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(21) Appl. No.: 12/547,772

(22) Filed: Aug. 26, 2009

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050125, filed on Feb. 26, 2008.(60) Provisional application No. 60/903,510, filed on Feb.
26, 2007, provisional application No. 60/903,509,
filed on Feb. 26, 2007.

(30) Foreign Application Priority Data

Jun. 5, 2007 (EP) PCT/EP2008/055537
Feb. 25, 2008 (GB) PCT/GB2008/050124

OGT002 (SEQ ID No: 1)

Peptide Source: 1D-GE, Breast cancer

MELRVLCWASLAALAEETLLNTKLETLADLKWVTFPQVGGQWELSGLDEEHSVRYTEVCDVQAPGQAHWLR
GWVPRGAVVYATLRFMTLECLSLPRAGRSCKETTFVYFYESDADTATATLPAWKENPY:KYDTVAEHLTKR
PGAEATGVNVTLRGLPLSKAGFYLAQDQGCAMALLSLHLYKKCAQLTVNLTRFETVPRELVPVAGSCVV
DAVPAFGSPSLYCREGQWAEQVPTGSCAPGFEAAGNTEKCRACAQGTFFPLSGEGSCQCPANSHSNTIGSA
VCQCRVGFYRARTDPRGAPCTTPPSAPRSVSRINGSSSLHLEWSAPLESGGREDLTALRCRECRPGGSCAPCGG
DLTFDGPFDLVEFWVVGRLRPDTYTFEVTALNGVSSLATGPVFPFVNTTDRVFPVAVSDIRVTSRSPSSL
SLAWAVPAPSGAVLDIEVKYHEKAGSGSVVRLKTSNRAELRLKRGASLYVQVRASEAAGYGP7QGEHHSQ
TOLDESGWREQLALAGTAVGVVLLVVIWVAVLCLRKQSGNREAYSDKHQYLIHGCTKYVIDPTEYEDPN
FAVREFAKEIDVSVYKIEVYGAGFGEVCRGRKAPGKESCAVKTLLKGGYTERORREPLSEASIMGCFHPN
IIRLEGVVTNSMPVILTEFMENGALDSFLRLNDGQFTVQLVQMLRGIASQMRVLAEMSVYHRDLAARNILVNS
NLVCKVSDPGLSRFLSENSDPTYSLLGGKIPIRWTAPEATAFRKFTSASDWSYGIWMEVMSFGERPYWMS
NQDVNAIQDYRLPFPDPTSLRLQMLDQWQKDRNARFPQVVSALDKMIRNPASLKIVARENGGASHPFLD
QROPHYSAFGSGVGLWRLAINGRYEESFAAGSGFSELVSQISAEDDLRLIGVTLAGHKKILASVQHMKSQAKPG
TFGGTGGAPQY

Mass Match Peptides (bold):

LNGSSLHLEWSAPLESGR [473]
QPHYSAGFSGVGLR [585]
SQAKPGTGGTGGAPQY [646]

Tandem Peptides (underline):

VDTVAEHLTR [749]

Peptide Source: 1D-GE, Colorectal cancer

MELRVLCWASLAALAEETLLNTKLETLADLKWVTFPQVGGQWELSGLDEEHSVRYTEVCDVQAPGQAHWLR
GWVPRGAVVYATLRFMTLECLSLPRAGRSCKETTFVYFYESDADTATATLPAWKENPY:KYDTVAEHLTKR
PGAEATGVNVTLRGLPLSKAGFYLAQDQGCAMALLSLHLYKKCAQLTVNLTRFETVPRELVPVAGSCVV
DAVPAFGSPSLYCREGQWAEQVPTGSCAPGFEAAGNTEKCRACAQGTFFPLSGEGSCQCPANSHSNTIGSA
VCQCRVGFYRARTDPRGAPCTTPPSAPRSVSRINGSSSLHLEWSAPLESGGREDLTALRCRECRPGGSCAPCGG
DLTFDGPFDLVEFWVVGRLRPDTYTFEVTALNGVSSLATGPVFPFVNTTDRVFPVAVSDIRVTSRSPSSL
SLAWAVPAPSGAVLDIEVKYHEKAGSGSVVRLKTSNRAELRLKRGASLYVQVRASEAAGYGP7QGEHHSQ
TOLDESGWREQLALAGTAVGVVLLVVIWVAVLCLRKQSGNREAYSDKHQYLIHGCTKYVIDPTEYEDPN
FAVREFAKEIDVSVYKIEVYGAGFGEVCRGRKAPGKESCAVKTLLKGGYTERORREPLSEASIMGCFHPN
IIRLEGVVTNSMPVILTEFMENGALDSFLRLNDGQFTVQLVQMLRGIASQMRVLAEMSVYHRDLAARNILVNS
NLVCKVSDPGLSRFLSENSDPTYSLLGGKIPIRWTAPEATAFRKFTSASDWSYGIWMEVMSFGERPYWMS
NQDVNAIQDYRLPFPDPTSLRLQMLDQWQKDRNARFPQVVSALDKMIRNPASLKIVARENGGASHPFLD
QROPHYSAFGSGVGLWRLAINGRYEESFAAGSGFSELVSQISAEDDLRLIGVTLAGHKKILASVQHMKSQAKPG
TFGGTGGAPQY

Mass Match Peptides (bold):

DLVEFWVVR [241]
EFLSEASIMGCFHPNTR [184]
EVPPAVSDIR [237]
GAPCTTPPSAPR [286]
ILASVQHMK [373]
LETDLK [456]
VDTVAEHLTR [749]
VYIDPTEYEDPNEAVR [818]
WTAPEATAFR [833]
YLAEMSVYHR [859]

Tandem Peptides (underline):

DLVEFWVVR [141]
FPQVVSALDK [263]

Peptide Source: 1D-GE, Hepatocellular carcinoma

MELRVLCWASLAALAEETLLNTKLETLADLKWVTFPQVGGQWELSGLDEEHSVRYTEVCDVQAPGQAHWLR
GWVPRGAVVYATLRFMTLECLSLPRAGRSCKETTFVYFYESDADTATATLPAWKENPY:KYDTVAEHLTKR
PGAEATGVNVTLRGLPLSKAGFYLAQDQGCAMALLSLHLYKKCAQLTVNLTRFETVPRELVPVAGSCVV
DAVPAFGSPSLYCREGQWAEQVPTGSCAPGFEAAGNTEKCRACAQGTFFPLSGEGSCQCPANSHSNTIGSA
VCQCRVGFYRARTDPRGAPCTTPPSAPRSVSRINGSSSLHLEWSAPLESGGREDLTALRCRECRPGGSCAPCGG
DLTFDGPFDLVEFWVVGRLRPDTYTFEVTALNGVSSLATGPVFPFVNTTDRVFPVAVSDIRVTSRSPSSL
SLAWAVPAPSGAVLDIEVKYHEKAGSGSVVRLKTSNRAELRLKRGASLYVQVRASEAAGYGP7QGEHHSQ
TOLDESGWREQLALAGTAVGVVLLVVIWVAVLCLRKQSGNREAYSDKHQYLIHGCTKYVIDPTEYEDPN
FAVREFAKEIDVSVYKIEVYGAGFGEVCRGRKAPGKESCAVKTLLKGGYTERORREPLSEASIMGCFHPN
IIRLEGVVTNSMPVILTEFMENGALDSFLRLNDGQFTVQLVQMLRGIASQMRVLAEMSVYHRDLAARNILVNS
NLVCKVSDPGLSRFLSENSDPTYSLLGGKIPIRWTAPEATAFRKFTSASDWSYGIWMEVMSFGERPYWMS
NQDVNAIQDYRLPFPDPTSLRLQMLDQWQKDRNARFPQVVSALDKMIRNPASLKIVARENGGASHPFLD
QROPHYSAFGSGVGLWRLAINGRYEESFAAGSGFSELVSQISAEDDLRLIGVTLAGHKKILASVQHMKSQAKPG
TFGGTGGAPQY

Mass Match Peptides (bold):

Tandem Peptides (underline):
VSDFGLSR [796]

Peptide Source: 1D-GE, Melanoma

MELRVLCWASLAALAEETLLNTKLETLADLKWVTFPQVGGQWELSGLDEEHSVRYTEVCDVQAPGQAHWLR
GWVPRGAVVYATLRFMTLECLSLPRAGRSCKETTFVYFYESDADTATATLPAWKENPY:KYDTVAEHLTKR
PGAEATGVNVTLRGLPLSKAGFYLAQDQGCAMALLSLHLYKKCAQLTVNLTRFETVPRELVPVAGSCVV
DAVPAFGSPSLYCREGQWAEQVPTGSCAPGFEAAGNTEKCRACAQGTFFPLSGEGSCQCPANSHSNTIGSA
VCQCRVGFYRARTDPRGAPCTTPPSAPRSVSRINGSSSLHLEWSAPLESGGREDLTALRCRECRPGGSCAPCGG
DLTFDGPFDLVEFWVVGRLRPDTYTFEVTALNGVSSLATGPVFPFVNTTDRVFPVAVSDIRVTSRSPSSL
SLAWAVPAPSGAVLDIEVKYHEKAGSGSVVRLKTSNRAELRLKRGASLYVQVRASEAAGYGP7QGEHHSQ
TOLDESGWREQLALAGTAVGVVLLVVIWVAVLCLRKQSGNREAYSDKHQYLIHGCTKYVIDPTEYEDPN
FAVREFAKEIDVSVYKIEVYGAGFGEVCRGRKAPGKESCAVKTLLKGGYTERORREPLSEASIMGCFHPN
IIRLEGVVTNSMPVILTEFMENGALDSFLRLNDGQFTVQLVQMLRGIASQMRVLAEMSVYHRDLAARNILVNS
NLVCKVSDPGLSRFLSENSDPTYSLLGGKIPIRWTAPEATAFRKFTSASDWSYGIWMEVMSFGERPYWMS
NQDVNAIQDYRLPFPDPTSLRLQMLDQWQKDRNARFPQVVSALDKMIRNPASLKIVARENGGASHPFLD
QROPHYSAFGSGVGLWRLAINGRYEESFAAGSGFSELVSQISAEDDLRLIGVTLAGHKKILASVQHMKSQAKPG
TFGGTGGAPQY

Mass Match Peptides (bold):

ENGASHPFLDOR [214]
FLENSDPTYSLLGGK [259]
FTMLECLSLR [276]
IEVYAGFGEVCR [360]
KESVATK [413]
LPFPDPTSLRLQMLDQWQK [479]

Tandem Peptides (underline):

VDTVAEHLTR [749]

Peptide Source: 1D-GE, Ovarian cancer

FIGURE 1

OGTA002 (SEQ ID No: 1)

Peptide Source: 1D-GE, Breast cancer

MELRVLLCWASLAAALEETLLNTKLETADLKWVTFPQVDGQWEELSGLDDEEQHSVRTYEVCDVQRAPGQAHWLRT
GWVPRRGAVHVYATLRFMTLECLSLPRAGRSCKETFTVFYYESDADTATALTPAWMENPYIKVDTVAAEHLTRKR
PGAETGKVNVTLRRLGPLSKAGFYLAQDQGACMALLSLHLFYKKCAQLTVNLTRFPETVPRELVPVAGSCVV
DAVPAPGPSPLYCREGQWAEQVPTGCSCAPGFEEAEGNTKCRACAQGTFKPLSGEGSCQPCPANSHSNTIGSA
VCQCRVGYFRARTDPRGAPCTTPPSAPRSVSRLNGSSLHLEWSAPLESGGREDLTALRCRECRPGGSCAPCGG
DLTFDPGPRDLVEPWVVRGLRPDFTYTFEVTALNGVSSLATGPVPFEPVNVTTDREVPPAVSDIRVTRSSPSSL
SLAWAVPRAPSGAVLDYEVKYHEKGAE GPSSVRFLKTSENRAELRGLKRGASYLVQVRARSEAGYGPFGQEHHSQ
TQDSEGWREQLALIAGTAVVGVLVVLVIVVAVLCLRKQSNGREAEYS DKHGQYLIGHGTKVYIDPFTYEDPN
EAVREFAKEIDVSYVKIEEVIGAGEFGEVCRGLKAPGKKESCVAIKTLKGGYTERQRREFLSEASIMQFEHPN
IIRLEGVVTNSMPVMILTEFMENGALDSFLRLNDGQFTVIQLVGMLRGIASGMRYLAEMSYVHRDLAARNILVNS
NLVCKVSDFGLSRFLEENSSDPTYTSSLGKIPIRWTAPEAIAFRKFTSASDAWSYGIVMWEVMSFGERPYWDMS
NQDVINAIEQDYRLPPPPDCPTSLHQLMLDCWQKDRNARPRFPQVVSALDKMIRNPASLKIVARENGGASHPLLD
QRQPHYSAFGSVGEWLRAIKMGRYEESFAAAGFGSFELVSQISAEDLLRIGVTLAGHQKKILASVQHMKSQAKPG
TPGGTGGPAPQY

Mass Match Peptides (bold):

LNGSSLHLEWSAPLES GGR [473]
QPHYSAFGSVGEWLR [585]
SQAKPGTPGGTGGPAPQY [646]

Tandem Peptides (underline):

VDTVAAEHLTR [749]

Peptide Source: 1D-GE, Colorectal cancer

MELRVLLCWASLAAALEETLLNTKLETADLKWVTFPQVDGQWEELSGLDDEEQHSVRTYEVCDVQRAPGQAHWLRT
GWVPRRGAVHVYATLRFMTLECLSLPRAGRSCKETFTVFYYESDADTATALTPAWMENPYIKVDTVAAEHLTRKR
PGAETGKVNVTLRRLGPLSKAGFYLAQDQGACMALLSLHLFYKKCAQLTVNLTRFPETVPRELVPVAGSCVV
DAVPAPGPSPLYCREGQWAEQVPTGCSCAPGFEEAEGNTKCRACAQGTFKPLSGEGSCQPCPANSHSNTIGSA
VCQCRVGYFRARTDPRGAPCTTPPSAPRSVVSRLNGSSLHLEWSAPLESGGREDLTALRCRECRPGGSCAPCGG
DLTFDPGPRDLVEPWVVRGLRPDFTYTFEVTALNGVSSLATGPVPFEPVNVTTDREVPPAVSDIRVTRSSPSSL
SLAWAVPRAPSGAVLDYEVKYHEKGAE GPSSVRFLKTSENRAELRGLKRGASYLVQVRARSEAGYGPFGQEHHSQ
TQDSEGWREQLALIAGTAVVGVLVVLVIVVAVLCLRKQSNGREAEYS DKHGQYLIGHGTKVYIDPFTYEDPN
EAVREFAKEIDVSYVKIEEVIGAGEFGEVCRGLKAPGKKESCVAIKTLKGGYTERQRREFLSEASIMQFEHPN
IIRLEGVVTNSMPVMILTEFMENGALDSFLRLNDGQFTVIQLVGMLRGIASGMRYLAEMSYVHRDLAARNILVNS
NLVCKVSDFGLSRFLEENSSDPTYTSSLGKIPIRWTAPEAIAFRKFTSASDAWSYGIVMWEVMSFGERPYWDMS
NQDVINAIEQDYRLPPPPDCPTSLHQLMLDCWQKDRNARPRFPQVVSALDKMIRNPASLKIVARENGGASHPLLD
QRQPHYSAFGSVGEWLRAIKMGRYEESFAAAGFGSFELVSQISAEDLLRIGVTLAGHQKKILASVQHMKSQAKPG
TPGGTGGPAPQY

Mass Match Peptides (bold):

DLVEPWVVR [141]
EFLSEASIMQFEHPNIIR [184]
EVPPAVSDIR [237]
CAPCTTPPSAPR [286]
ILASVQHMK [373]
LETADLK [456]
VDTVAAEHLTR [749]
VYIDPFTYEDPNEAVR [818]
WTAPEAIAFR [833]
YLAEMSYVHR [859]

Tandem Peptides (underline):

DLVEPWVVVR [141]
FPQVVSALDK [263]

Peptide Source: 1D-GE, Hepatocellular carcinoma

MELRVLLCWASLAAALEETLLNTKLETADLKWVTFPQVDGQWEELSGLDEEQHSVRTYEVC DVQRAPGQAHWLRT
GWVPRRGAVHVYATLRLFTMLECLSLPRAGRSCKETFTVFYYESDADTATALT PAWMENPYIKVDIVAAEHLTRKR
PGAEATGKVNVT LRLGPLSKAGFYLA FQDQGACMALLSLHLFYKKCAQLTVNLTRFPETVPREL VVPVAGSCVV
DAVPAPGPSPSLYCREDCQWAEQPV TGCSCAPGFEEAEGNTKCRACAQGT FKP LSGEGSCQPCPANSHSNTIGSA
VCQCRVGYFRARTDPRGAPCTTPPSAPRSVVSRLNGSSLHLEWSAPLES GGRDLYALRCRECRPGGSCAPCGG
DLTFDPGPRDLVEPWVVVRGLRPDFTYTFEVTALNGVSSLATGPVPFEPVNVTTDREVPPAVSDIRVTRSSPSSL
SLAWAVPRAPSGAVLDYEVKYHEKGAEGPSSVRFLKTSENRAELRGLKRGASYLVQVRARSEAGYGFPGQEHHSQ
TQLDESEGWRQALALIAGTAVVGVLVLVVI VVAVLCLRKQSNGREAEYS DKHGQYLIGHGTKVYIDPFTYEDPN
EAVREFAKEIDVSYVVKIEEVIGAGEFGEVCRGR LKAPGKKESCAVIAIKTLKGGYTERQRREFLSEASIMGQFEHPN
IIRLEGVVTNSMPVMILTEFMENGALDSFLRLNDGQFTVIQLVGMLRGIASGMRYLAEMS YVHRDLAARNILVNS
NLVCKVSDFGLSR FLEENSSDPTYTSSLGKIP IIRWTAPEAIAFRKFTSASDAWSYGI VMWEVMSFGERP YWDM
NQDVINAIEQDYRLPPPPDCPTSLHQLMLDCWQKDRNARPRFPQVVSALDKMIRNPASLKIVARENGGASHPLLD
QRQPHYSAFGSVGEWLRAIKMGRYEESFAAAGFGSFELVSQISAEDLLRIGVTLAGHQKKILASVQHMKSQAKPG
TPGGTGGPAPQY

Mass Match Peptides (bold):**Tandem Peptides (underline):**

VSDFGLSR [796]

Peptide Source: 1D-GE, Melanoma

MELRVLLCWASLAAALEETLLNTKLETADLKWVTFPQVDGQWEELSGLDEEQHSVRTYEVC DVQRAPGQAHWLRT
GWVPRRGAVHVYATLRL**FTMLECLSLPR**AGRSCKETFTVFYYESDADTATALT PAWMENPYIKVDIVAAEHLTRKR
PGAEATGKVNVT LRLGPLSKAGFYLA FQDQGACMALLSLHLFYKKCAQLTVNLTRFPETVPREL VVPVAGSCVV
DAVPAPGPSPSLYCREDCQWAEQPV TGCSCAPGFEEAEGNTKCRACAQGT FKP LSGEGSCQPCPANSHSNTIGSA
VCQCRVGYFRARTDPRGAPCTTPPSAPRSVVSRLNGSSLHLEWSAPLES GGRDLYALRCRECRPGGSCAPCGG
DLTFDPGPRDLVEPWVVVRGLRPDFTYTFEVTALNGVSSLATGPVPFEPVNVTTDREVPPAVSDIRVTRSSPSSL
SLAWAVPRAPSGAVLDYEVKYHEKGAEGPSSVRFLKTSENRAELRGLKRGASYLVQVRARSEAGYGFPGQEHHSQ
TQLDESEGWRQALALIAGTAVVGVLVLVVI VVAVLCLRKQSNGREAEYS DKHGQYLIGHGTKVYIDPFTYEDPN
EAVREFAKEIDVSYVVK**IEEVIGAGEFGEVCR**GR LKAPGKKESCAVIAIKTLKGGYTERQRREFLSEASIMGQFEHPN
IIRLEGVVTNSMPVMILTEFMENGALDSFLRLNDGQFTVIQLVGMLRGIASGMRYLAEMS YVHRDLAARNILVNS
NLVCKVSDFGLSR**FLEENSSDPTYTSSLGK**IP IIRWTAPEAIAFRKFTSASDAWSYGI VMWEVMSFGERP YWDM
NQDVINAIEQDYRL**PPPPDCPTSLHQLMLDCWQK**DRNARPRFPQVVSALDKMIRNPASLKIVARE**ENGGASHPLLD**
QRQPHYSAFGSVGEWLRAIKMGRYEESFAAAGFGSFELVSQISAEDLLRIGVTLAGHQKKILASVQHMKSQAKPG
TPGGTGGPAPQY

Mass Match Peptides (bold):

ENGGASHPLLDQR [214]
FLEENSSDPTYTSSLGK [258]
FTMLECLSLPR [276]
IEEVIGAGEFGEVCR [360]
KESCAVIAIK [413]
LPPPPDCPTSLHQLMLDCWQK [479]

Tandem Peptides (underline):

VDIVAAEHLTR [749]

Peptide Source: 1D-GE, Ovarian cancer

MELRVLLCWASLAAALEETLLNTKLETADLKWVTFPQVDGQWEELSGLDEEQHSVRTYEVC DVQ RAPGQAHWLRT
GWVPRRGAVHVYATLRFTMLECLSLPRAGRSCKETFTVFYYESDADTATALT PAWMENPYIKVDTVAAEHLTRKR
PGAEATGKVN VKTLRLGPLSKAGFYLA FQDQ GACMALLSLHLFYKKCAQLTVNLTRFPETVPREL VVPVAGSCVV
DAVPAPGPSFSLYCREDDGWAEQPV TGCSCAPGFEEAEGNTKCRACAQGT FKP LSGEGSCQPCPANSHSNTIGSA
VCQCRVGYFRARTDPRGAPCTTPPSAPRSVVSRLNGSSHLHLEWSAPLES GGGREDLT YALRCRECRPGGSCAPCGG
DLTFDPGPRDLVEPWVVVRGLRPDFTYTFEVTALNGVSSSLATGPVPFEPVNVTTDREVPPAVSDIRVTRSSPSSL
SLAWAVPRAPSGAVLDYEVKYHEKGAEGPSSVRFLKTSENRAELRGLKRGASYLVQVRARSEAGYGPFGQEHHSQ
TQLDESEGWREQLALIAGTAVVGVVLVVLVIVVAVLCLRKQSNGREAEYS DKHGQYLIHGHTKVYIDPFTYEDPN
EAVREFAKEIDVSYVKIEEVI GAGEFGEVCRGRLKAPGKKESCVAIKTLKGGYTERQREFLSEASIMGQFEHPN
IIRLEGVVTNSMPVMILTEFMENGALDSFLRLNDGQFTVIQLVGMRLGIASCMRYLAEMSYVHRDLAARNILVNS
NLVCKVSDFGLSRFLEENSSDPTYTSSLGGKIPIRWTAPEAIAFRKFTSASDAWSYGIVMWEVMSFGERPYWDMS
NQDVINAIEQDYRLPPPPDCPTSLHQLMLDCWQKDRNARPRFPQVVSALDKMIRNPASLKIVARENGGASHPLLD
QRQPHYSAPFGSVGEWLRAIKMGRYEESFAAAGFGSFELVVSQISAEDLLRIGVTLAGHQKKILASVQHMSQAKPG
TPGGTGGPAPQY

Mass Match Peptides (bold):**Tandem Peptides (underline):**

VSDFGLSR [796]

Peptide Source: 1D-GE, Pancreatic cancer

MELRVLLCWASLAAALEETLLNTKLETADLKWVTFPQVDGQWEELSGLDEEQHSVRT**TYEVC DVQ** RAPGQAHWLRT
GWVPRRGAVHVYATLRFTMLECLSLPRAGRSCKETFTVFYYESDADTATALT PAWMENPYIKVDTVAAEHLTRKR
PGAEATGKVN VKTLRLGPLSKAGFYLA FQDQ GACMALLSLHLFYKKCAQLTVNLTRFPETVPREL VVPVAGSCVV
DAVPAPGPSFSLYCREDDGWAEQPV TGCSCAPGFEEAEGNTKCRACAQGT FKP LSGEGSCQPCPANSHSNTIGSA
VCQCRVGYFRARTDPRGAPCTTPPSAPRSVVSRLNGSSHLHLEWSAPLES GGGREDLT YALRCRECRPGGSCAPCGG
DLTFDPGPRDLVEPWVVVRGLRPDFTYTFEVTALNGVSSSLATGPVPFEPVNVTTDREVPPAVSDIRVTRSSPSSL
SLAWAVPRAPSGAVLDYEVKYHEKGAEGPSSVRFLKTSENRAELRGLKRGASYLVQVRARSEAGYGPFGQEHHSQ
TQLDESEGWREQLALIAGTAVVGVVLVVLVIVVAVLCLRKQSNGREAEYS DK**HGQYLIHGHTK** VYIDPFTYEDPN
EAVREFAKEIDVSYVKIEEVI GAGEFGEVCRGRLKAPGKKESCVAIKTLKGGYTERQREFLSEASIMGQFEHPN
IIRLEGVVTNSMPVMILTEFMENGALDSFLRLNDGQFTVIQLVGMRLGIASCMRYLAEMSYVHRDLAARNILVNS
NLVCKVSDFGLSRFLEENSSDPTYTSSLGGKIPIRWTAPEAIAFRKFTSASDAWSYGIVMWEVMSFGERPYWDMS
NQDVINAIEQDYRLPPPPDCPTSLHQLMLDCWQKDRNARPRFPQVVSALDKMIRNPASLKIVARENGGASHPLLD
QRQPHYSAPFGSVGEWLRAIKMGRYEESFAAAGFGSFELVVSQISAEDLLRIGVTLAGHQKKILASVQHMSQAKPG
TPGGTGGPAPQY

Mass Match Peptides (bold):

HGQYLIHGHTK [335]

TYEVC DVQ [739]

Tandem Peptides (underline):

FPQVVSALDK [263]

Peptide Source: iTRAQ, Colorectal cancer

MELRVLLCWASLAAALEETLLNTKLETADLKWVTFPQVDGQWEELSGLDEEQHSVRTYEVC DVQ RAPGQAHWLRT
GWVPRRGAVHVYATLRFTMLECLSLPRAGRSCKETFTVFYYESDADTATALT PAWMENPYIKVDTVAAEHLTRKR
PGAEATGKVN VK**TLRLGPLSK** AGFYLA FQDQ GACMALLSLHLFYKKCAQLTVNLTRFPETVPREL VVPVAGSCVV
DAVPAPGPSFSLYCREDDGWAEQPV TGCSCAPGFEEAEGNTKCRACAQGT FKP LSGEGSCQPCPANSHSNTIGSA
VCQCRVGYFRARTDPRGAPCTTPPSAPRSVVSRLNGSSHLHLEWSAPLES GGGREDLT YALRCRECRPGGSCAPCGG
DLTFDPGPRDLVEPWVVVRGLRPDFTYTFEVTALNGVSSSLATGPVPFEPVNVTTDREVPPAVSDIRVTRSSPSSL
SLAWAVPRAPSGAVLDYEVKYHEKGAEGPSSVRFLKTSENRA**ELRLGLK** RGASYLVQVRARSEAGYGPFGQEHHSQ
TQLDESEGWREQLALIAGTAVVGVVLVVLVIVVAVLCLRKQSNGREAEYS DKHGQYLIHGHTKVYIDPFTYEDPN
EAVREFAKEIDVSYVKIEEVI GAGEFGEVCRGRLKAPGKKESCVAIKTLKGGYTERQREFLSEASIMGQFEHPN
IIRLEGVVTNSMPVMILTEFMENGALDSFLRLNDGQFTVIQLVGMRLGIASCMRYLAEMSYVHRDLAARNILVNS
NLVCKVSDFGLSRFLEENSSDPTYTSSLGGKIPIRWTAPEAIAFRKFTSASDAWSYGIVMWEVMSFGERPYWDMS
NQDVINAIEQDYRLPPPPDCPTSLHQLMLDCWQKDRNARPRFPQVVSALDKMIRNPASLKIVARENGGASHPLLD

QRQPHYSAFGSVGEWLRAIKMGRIEESFAAAGFGSFELVQSISAEDLLRIGVTLAGHQKKILASVQHMKSQAKPG
TPGGTGGPAPQY

Mass Match Peptides (bold):

AELRGLK [880]
ILASVQHMK [373]
TLRLGPLSK [983]

Tandem Peptides (underline):

AELRGLK [880]
ILASVQHMK [373]
TLRLGPLSK [983]

Peptide Source: iTRAQ, Hepatocellular cancer

MELRVLLCWASLAAALEETLLNTKLETADLKWVTFPQVDGQWEELSGLDEEQHSVRTYEVCVQRAPGQAHWLRT
GWVPRRGAVHVYATLRFTMLECLSLPRAGRSCKETFTVFYYESDADTATALTPAWMENPYIKVDTVAEHLTRKR
PGAETGKVNVTTLRLGPLSKAGFYLAQDQACMALLSLHLFYKKCAQLTVNLTRFPETVPRELVVPVAGSCVV
DAVPAZGPSFSLYCREDGQWAEQPVTCSCAPGFEEAEGNTKCRACAQGTFFKPLSGEGSCQPCPANSHSNTIGSA
VCQCRVGYFRARTDPRGAPCTTPPSAPRSVVSRLNGSSHLLEWSAPLES GGREDLTALRCRECRPGGSCAPCGG
DLTFDZGPRDLVEPWVVRGLRPDFTYTFEVTALNGVSSLATGPVPFEPVNVTTDREVPPAVSDIRVTRSSPSSL
SLAWAVPRAPSGAVLDYEVKYEKGAEGFPSSVRFLKTSENRAELRGLKRGASYLVQVRARSEAGYGPFGQEHHSQ
TQLDESEGWRQLALIACTAVGVVVLVVLVIVVAVLCLRKQSNGREAEYSKHKQYLIHGHTKVYIDFTTYEDPN
EAVREFAKEIDVSYVKIEEVIGAGEFGEVCRGLKAPGKKESCVAIKTLKGGYTERQRREFLSEASIMGQFEHPN
IIRLEGVVTNSMEVMILTEFMENGALDSFLRLNDGQFTVIQLVGMRLGIASGMRYLAEMS YVRDLAARNILVNS
NLVCKVSDFGLSRFLEENSSDPTYTSSLGKIPIRWTAPEAIAFRKFTSASDAWSYGIVMWEVMSFGERPYWMS
NQDVINAIEQDYRLPPPDCPTSLHQLMLDCWQKDRNARPRFPQVVSALDKMIRNPASLKIVARENGGASHPLLD
QRQPHYSAFGSVGEWLRAIKMGRIEESFAAAGFGSFELVQSISAEDLLRIGVTLAGHQKKILASVQHMKSQAKPG
TPGGTGGPAPQY

Mass Match Peptides (bold):

EIDVSYVK [899]

Tandem Peptides (underline):

EIDVSYVK [899]

Peptide Source: iTRAQ, Non-small cell lung cancer

MELRVLLCWASLAAALEETLLNTKLETADLKWVTFPQVDGQWEELSGLDEEQHSVRTYEVCVQRAPGQAHWLRT
GWVPRRGAVHVYATLRFTMLECLSLPRAGRSCKETFTVFYYESDADTATALTPAWMENPYIKVDTVAEHLTRKR
PGAETGKVNVTTLRLGPLSKAGFYLAQDQACMALLSLHLFYKKCAQLTVNLTRFPETVPRELVVPVAGSCVV
DAVPAZGPSFSLYCREDGQWAEQPVTCSCAPGFEEAEGNTKCRACAQGTFFKPLSGEGSCQPCPANSHSNTIGSA
VCQCRVGYFRARTDPRGAPCTTPPSAPRSVVSRLNGSSHLLEWSAPLES GGREDLTALRCRECRPGGSCAPCGG
DLTFDZGPRDLVEPWVVRGLRPDFTYTFEVTALNGVSSLATGPVPFEPVNVTTDREVPPAVSDIRVTRSSPSSL
SLAWAVPRAPSGAVLDYEVKYEKGAEGFPSSVRFLKTSENRAELRGLKRGASYLVQVRARSEAGYGPFGQEHHSQ
TQLDESEGWRQLALIACTAVGVVVLVVLVIVVAVLCLRKQSNGREAEYSKHKQYLIHGHTKVYIDFTTYEDPN
EAVREFAKEIDVSYVKIEEVIGAGEFGEVCRGLKAPGKKESCVAIKTLKGGYTERQRREFLSEASIMGQFEHPN
IIRLEGVVTNSMEVMILTEFMENGALDSFLRLNDGQFTVIQLVGMRLGIASGMRYLAEMS YVRDLAARNILVNS
NLVCKVSDFGLSRFLEENSSDPTYTSSLGKIPIRWTAPEAIAFRKFTSASDAWSYGIVMWEVMSFGERPYWMS
NQDVINAIEQDYRLPPPDCPTSLHQLMLDCWQKDRNARPRFPQVVSALDKMIRNPASLKIVARENGGASHPLLD
QRQPHYSAFGSVGEWLRAIKMGRIEESFAAAGFGSFELVQSISAEDLLRIGVTLAGHQKKILASVQHMKSQAKPG
TPGGTGGPAPQY

Mass Match Peptides (bold):

AELRGLK [880]
KCAQLTVNLTR [927]
QPHYSAFGSVGEWLRAIK [964]

Tandem Peptides (underline):

AELRGLK [880]
KCAQLTVNLTR [927]
QPHYSAFGSVGEWLRAIK [964]

Peptide Source: iTRAQ, Renal cell cancer

MELRVLLCWASLAAALEETLLNKTLETADLKWVTFPQVDGQWEELSGLDDEEQHSVRTYEVCVQRAPGQAHWLRT
GWVPRRGAVHVYATLRFMTLECLSLPRAGRSCKETFTVFYYESDADTATALTPAWMENPYIKVDTVAAEHLTRKR
PGAEATGKVNVTIIRLGLPSKAGFYLAQDQGACMALLSHLFYKKCAQLTVNLTRFETVPRELVPVAGSCVV
DAVPAPGPSPLSLYCREDGQWAEQPVTCSCAPGFEEAAGNTKCRACAQGTFFKPLSGEGSCQPCPANSHTIGSA
VCQCRVGYFRARTDPRGAPCTTPPSAPRSVVSRLNGSSHLLEWSAPLES GGREDLTALRCRECRPGGSCAPCGG
DLTFDPGPRDLVEPWVVRGLRPDFTYTFEVTALNGVSSLATGPVPFEPVNVTTDREVPPAVSDIRVTRSSPSSL
SLAWAVPRAPSGAVLDYEVKYHEKGAEGPSSVRFLKTSENRAELRGLKRGASYLVQVRARSEAGYGPFQGEHHSQ
TQLDESEGWREQLALITAGTAVVGVLVLVVIIVAVLCLRKQSNGREAEYS DKEGQYLIGHGTKVYIDPFTYEDPN
EAVREFAKEIDVS YVKIEEVIGAGEFGEVCRGLKAPGKKESCVAIKTLKGGYTERQRREFLSEASIMGQFEHPN
IIRLEGVVTNSMPVMILTEFMENGALDSFLRLNDGQFTVIQLVGMRLRGIASGMRYLAEMSYVHRDLAARNILVNS
NLVCKVSDFGLSRFLLEENSSDPTYTSSLGKIPIRWTAPEAIAFRKFTSASDAWSYGIVMWEVMSFGERPYWDMS
NQDVINAIEQDYRLPEPPDCPTSLHQLMLDCWQKDRNARPRFPQVVSALDKMIRNPASLKI VARENGGASHPLLD
QRQPHYSAFGSVGEWLRAIKMGREYESFAAAGFGSFELVSQISAEDLLRIGVTLAGHQKK **ILASVQHMK** SQAKPG
TPGGTGGFAPQY

Mass Match Peptides (bold):

ILASVQHMK [373]

Tandem Peptides (underline):

ILASVQHMK [373]

OGTA009 (SEQ ID No: 2)**Peptide Source: 1D-GE, Breast cancer**

MSMGLEITGTALAVLGWLGTIVCCALPMWRVSAFIGSNIITSQNIWEGLMWNCVVQSTGQMCKVYDSSLALPQD
LQAARALIVVAILLAFAFGLLVALVGAQCTNCVQDDTAKAKITIVAGVLFLLAALLTLVPVSW SANTIIIR **DFYNPV**
VPEAQKR EMGAGLYVGWAAAAALQLLGGALLCCSCPPREKKYTATKVVSAPR **STGPGASLGTGYDRK** DYV

Mass Match Peptides (bold):

DFYNPVVPEAQKR [120]
STGPGASLGTGYDR [657]
STGPGASLGTGYDRK [658]

Tandem Peptides (underline):

DFYNPVVPEAQK [119]
VYDSSLALPQDLQAAR [817]

Peptide Source: 1D-GE, Colorectal cancer

MSMGLEITGTALAVLGWLGTIVCCALPMWRVSAFIGSNIITSQNIWEGLMWNCVVQSTGQMCKVYDSSLALPQD
LQAARALIVVAILLAFAFGLLVALVGAQCTNCVQDDTAKAKITIVAGVLFLLAALLTLVPVSW SANTIIIR **DFYNPV**
VPEAQKR EMGAGLYVGWAAAAALQLLGGALLCCSCPPREKKYTATKVVSAPR **STGPGASLGTGYDRK** KDYV

Mass Match Peptides (bold):

DFYNPVVPEAQK [119]
DFYNPVVPEAQKR [120]

STGPGASLGTGYDR [657]

Tandem Peptides (underline):

STGPGASLGTGYDR [657]

Peptide Source: 1D-GE, Pancreatic cancer

MSMGLEITGTALAVLGWLGITIVCCALPMWRVSAFIGSNIITSQNIWEGLWMNCVVQSTGQMCKVYDSLLALPQDLQAARALIVVAILLAAFGLLVALVGAQCTNCVQDDTAKAKITIVAGVLFLLAALLTLVPVSW SANTIIIRDFYNPVVPEAQKREMGAGLYVGWAAAAALQLLGGALLCCSCPPREKKYTATKVVYSAPRSTGPGASLGTGYDRKDYV

Mass Match Peptides (bold):

STGPGASLGTGYDR [657]

VYDSLLALPQDLQAAR [817]

Tandem Peptides (underline):

STGPGASLGTGYDR [657]

VYDSLLALPQDLQAAR [817]

Peptide Source: 1D-GE, Prostate cancer

MSMGLEITGTALAVLGWLGITIVCCALPMWRVSAFIGSNIITSQNIWEGLWMNCVVQSTGQMCKVYDSLLALPQDLQAARALIVVAILLAAFGLLVALVGAQCTNCVQDDTAKAKITIVAGVLFLLAALLTLVPVSW SANTIIIRDFYNPVVPEAQKREMGAGLYVGWAAAAALQLLGGALLCCSCPPREKKYTATKVVYSAPRSTGPGASLGTGYDRKDYV

Mass Match Peptides (bold):

DFYNPVVPEAQK [119]

STGPGASLGTGYDR [657]

VVYSAPR [815]

VYDSLLALPQDLQAAR [817]

Tandem Peptides (underline):

DFYNPVVPEAQK [119]

Peptide Source: 1D-GE, Renal cell cancer

MSMGLEITGTALAVLGWLGITIVCCALPMWRVSAFIGSNIITSQNIWEGLWMNCVVQSTGQMCKVYDSLLALPQDLQAARALIVVAILLAAFGLLVALVGAQCTNCVQDDTAKAKITIVAGVLFLLAALLTLVPVSW SANTIIIRDFYNPVVPEAQKREMGAGLYVGWAAAAALQLLGGALLCCSCPPREKKYTATKVVYSAPRSTGPGASLGTGYDRKDYV

Mass Match Peptides (bold):

Tandem Peptides (underline):

STGPGASLGTGYDR [657]

Peptide Source: iTRAQ, Colorectal cancer

MSMGLEITGTALAVLGWLGITIVCCALPMWRVSAFIGSNIITSQNIWEGLWMNCVVQSTGQMCKVYDSLLALPQDLQAARALIVVAILLAAFGLLVALVGAQCTNCVQDDTAKAKITIVAGVLFLLAALLTLVPVSW SANTIIIRDFYNPVVPEAQKREMGAGLYVGWAAAAALQLLGGALLCCSCPPREKKYTATKVVYSAPRSTGPGASLGTGYDRKDYV

Mass Match Peptides (bold):

DFYNPVVPEAQK [119]

STGPGASLGTGYDR [657]

VYDSLLALPQDLQAAR [817]

Tandem Peptides (underline):

DFYNPVVPEAQK [119]
STGPGASLTGYDR [657]
VYDSLALPQDLQAAR [817]

Peptide Source: iTRAQ, Non-small cell lung cancer

MSMGLEITGTALAVLGWLGITIVCCALPMWRVSAFIGSNIITSQNIWEGLMNCVVQSTGQMCKVYDSLALPQDLQAARALIVVAILLAAGLLVALVGAQCTNCVQDDTAKAKITIVAGVLFLLAALLTLVPVSWASANTIIIRDFYNPVVPEAQKREMGAGLYVGWAAAALQLLGGALLCCSCPPREKKYTATKVVSAPRSTGPGASLTGYDRKDYV

Mass Match Peptides (bold):

VYDSLALPQDLQAAR [817]

Tandem Peptides (underline):

VYDSLALPQDLQAAR [817]

Peptide Source: iTRAQ, Ovarian cancer

MSMGLEITGTALAVLGWLGITIVCCALPMWRVSAFIGSNIITSQNIWEGLMNCVVQSTGQMCKVYDSLALPQDLQAARALIVVAILLAAGLLVALVGAQCTNCVQDDTAKAKITIVAGVLFLLAALLTLVPVSWASANTIIIRDFYNPVVPEAQKREMGAGLYVGWAAAALQLLGGALLCCSCPPREKKYTATKVVSAPRSTGPGASLTGYDRKDYV

Mass Match Peptides (bold):

DFYNPVVPEAQK [119]

Tandem Peptides (underline):

DFYNPVVPEAQK [119]

OGTA016 (SEQ ID No: 3)**Peptide Source: 1D-GE, Colorectal cancer**

MLLFVLTCLLAVFPAISTKSPIFGPEEVNSVEGNSVSITCYPPTSVNRHTRKYWCRQCARGGCITLISSEGYVS
SKYAGRANLTNFPENGTFVFNIAQLSQDDSGRYKCGLGINSRGLSFDVSLEVSQGPGLLNDTKVYTVDLGR
NCDFKTENAQKRKSLYKQIGLYPVLVIDSSGYVNPNTGRIRLDIQTGQLLFSVVINQLRLSDAGQYLCQAGDD
SNSNKKNADLQVLKPEPELVYEDLRGSVTFHCALGPEVANVAKFLCRQSSGENCDVVNTLGKRAPAFEGRILLN
PQDKDGSFSVVITGLRKEDAGRYLQGAHSDGLOEGSPIQAWOLFVNEESTIPRSPTVVKGAVGSSVAVLCPYNR
KESKSIKYWCLWEGAQNGRCPLLDSEGWVKAQYEGRLSLEEPGNGTFTVILNQLTSRDAGFYWCLTNGDTLWR
TTVEIKITIEGEPNLKVPGNVTAVLGETLKVPCHPCKFSSYEKYWCKWNNTGCQALPSQDEGFSKAFVNCDENSR
LVSLTLNLVTRADEGWYWCYVKQGHFYGETAAVYVAVEERKAAGSRDVSLEKADAAPDEKVLDSCFREIENKAIQ
DPRLFAGEEKAVADTRDQADGSRASVDSGSSEEQGGSSRALVSTLVPLGLVLAVGAVGVAVARARHRKNVDRVSR
SYRTDISMSDFENSREFGANDNMGASSITQETSLGGKEEFVATTESTETKEPKKAKRSSKEEAEMAYKDFLLQS
STVAEEAQDGPQEA

Mass Match Peptides (bold):

ADAAPDEK [57]
AFVNCDENSR [68]
ANLTNFPENGTFVFNIAQLSQDDSGR [79]
AQYEGR [85]
ASVDSGSSEEQGGSSR [86]
DFLLQSSTVAEEAQDGPQEA [116]
DGSFSVVITGLR [125]
DQADGSR [150]
EEFVATTESTETK [171]
FSSYEK [274]

GGCITLISSEGYVSSK [297]
GSVTFHCALGPEVANVAK [323]
IEGEPNLK [371]
ILLNPQDK [377]
KYWCR [443]
QGHFYGETAAVYVAVEER [574]
QGHFYGETAAVYVAVEERK [575]
QSSGENCDVVNTLGK [588]
QSSGENCDVVNTLGKR [589]
RAPAFEGR [597]
TDISMSDFENSR [684]
VLDGFR [776]
VPCHFCK [788]
VYTVDLGR [821]

Tandem Peptides (underline):

ASVDSGSSEEQGGSSR [86]
DGSFVSVITGLR [125]
EEFVATTESTTETK [171]
ILLNPQDK [377]
LSLLEEPGNGTFTVILNQLTSR [486]
TDISMSDFENSR [684]
VYTVDLGR [821]
YLCAHSDGQLQEGSPIQAWQLFVNEESTIPR [861]

Peptide Source: iTRAQ, Colorectal cancer

MLLFVLTCLLAVFPAISTKSPIFGPEEVNSVEGNSVSITCYPPPTSVNRHTRKYWCRQGARGGCITLISSEGYVS
SKYAGRANLTNFPENGTFVFNIAQLSQDDSGRYKCGLGINSRGLSFDVSLEVSQGPGLLNDTK**VYTVDLGR**TVTI
NCPFKTENAKRKSLYKQIGLYPVLVIDSSGYVNPNTGRIRLDIQGTGQLLFSVINQLRLSDAGQYLCQAGDD
SNSNKK**NADLQVLKPEPELVYEDLR**GSVTFHCALGPEVANVAKFLCR**QSSGENCDVVNTLGK**RAPAFEGR**ILLN**
PQDKDGSFVSVITGLRKEDAGRYLCAHSDGQLQEGSPIQAWQLFVNEESTIPRSPTVVKGVAGSSVAVLCPYNR
KESKSIKYCWLWEGAQNGRCPLLVDSEGWVKAQYEGRLSLLEEPGNGTFTVILNQLTSRDAGFYWCLTNGDTLWR
TTVEIK**IEGEPNLK**VPGNVTAVLGETLKVPCFCKFSSYEKYWCKWNNTCQALPSQDEGPK**AFVNCDENSR**
LVSLTLNLVTRADEGWYWCVKQGHFYGETAAVYVAVEERK**AAGSRDVSLAKADAAPDEK**VLDGFRFRIENKAIQ
DPRLEFAEEKAVADTRDQADGSR**ASVDSGSSEEQGGSSR**ALVSTLVPLGLVLAVGAVAVGVARARHRKNVDRVSIR
SYRTDISMSDFENSREFGANDNMGASSITQETSLGGKEEFVATTESTTETKEPKKAKRSSKEEAEMAYKDFLLQS
STVAEEAQDGPQEA

Mass Match Peptides (bold):

AAGSRDVSLAKADAAPDEK [877]
ADAAPDEK [57]
AFVNCDENSR [68]
ASVDSGSSEEQGGSSR [86]
IEGEPNLK [371]
ILLNPQDK [377]
LSDAGQYLCQAGDDSNSNKK [947]
NADLQVLKPEPELVYEDLR [955]
QSSGENCDVVNTLGK [588]
VYTVDLGR [821]

Tandem Peptides (underline):

AAGSRDVSLAKADAAPDEK [877]
ADAAPDEK [57]
AFVNCDENSR [68]
ASVDSGSSEEQGGSSR [86]
IEGEPNLK [371]
ILLNPQDK [377]
LSDAGQYLCQAGDDSNSNKK [947]
NADLQVLKPEPELVYEDLR [955]

QSSGENCDVVVNTLGK [588]
VYTVDLGR [821]

Peptide Source: iTRAQ, Non-small cell lung cancer

MLLFVLTCLLAVFPAISTKSPIFGPEEVNSVEGNSVSITCYPPTSVMNRHTRKYWCRQGARGGCITLISSEGYVS
SKYAGRANLTNFPENGTFVNNIAQLSQDDSGRYKCGLGINSRGLSFDVSLEVSQGPGLLNDTKVYTVDLGR**TVTI**
NCPFKTENAQKRKSLYKQIGLYPVLVIDSSGYVNPNTGRIRLDIQGTGQLLFSVVINQLRLSDAGQYLCQAGDD
SNSNKKNADLQVLKPEPELVYEDLRGSVTFHCALGPEVANVAKFLCRQSSGENCDVVVNTLGKRAPAFEGR**ILLN**
PQDKDGSFSVITGLRKEDAGRYLCCGAHSDGQLQEGSPIQAWQLFVNEESTIPRSPTVVKGVAGSSVAVLCFYNR
KESKSIKYWCLWEGAQNGRCPLLVDSEGWVKAQYEGRLSLLEPGNGTFTVILNQLTSRDAGFYWCLTNGDTLWR
TTVEIK**IEGEPNLK**VPGNVTAVLGETLKVPCFPCFSSYKYWCKWNNTGCQALPSQDEGPKAFVNCDENSR
LVSLTLNLVTRADEGWYWCQGVKQGHFYGETAAVYVAVEERKAAGSRDVS**ADAAPDEK**VLDSGFREIENKAIQ
DPRIFAEEKAVADTRDQADGSR**ASVDSGSSEEQGGSSR**ALVSTLVPLGLVLAVGAVAVGVARARHRKNVDVRSIR
SYRTDISMSDFENSREFGANDNMGASSITQETSLGGKEEFVATTESTTETKEPKAKRSSKEEAEMAYKDFLLQS
STVAABEAQDGPQEA

Mass Match Peptides (bold):

ADAAPDEK [57]
ASVDSGSSEEQGGSSR [86]
ESKSIK [907]
IEGEPNLK [371]
ILLNPQDK [377]
TVTINCPEK [987]

Tandem Peptides (underline):

ADAAPDEK [57]
ASVDSGSSEEQGGSSR [86]
ESKSIK [907]
IEGEPNLK [371]
ILLNPQDK [377]
TVTINCPEK [987]

OGTA028 (SEQ ID No: 4)**Peptide Source: 1D-GE, Ovarian cancer**

MSDVSTSVQSKFARLAK**KKENITYMKREQLTETDK**DIAPVLDLKCKDVSAIMNK**FVLMEIQDIMFEEMR**ETLKN
DLKAVLGKATIPVKNSENSSSR**TEFQOIINLALQK**TGMVGKIEGENSK**IGDDNENLTFK**LEVNELSGKLDNTN
EYNSNDGK**KLPQGESR**SYEVMGSMETLNCNIDDRGNRVHLETTRESRKDGEDEFVKEMREERKFQKLKNKEE
VLKASREEK**VLMDEGAVLT**LVADLSSATL**DISKQWSNVFNILR**ENDFE**FLCEVK**LAFKCDGEIK**TFSDQLQSLR**
KFASQKSSVKELLKDVL**PQKEEINQGGGRKYGIQEK**RDKTLIDSKHRAGEITSDGLSFLFLKEVK**VAKPEEMK**NLE
TQEEEFSELEELDEEASGMEDDEDTSGLEEEEEEPGLEEEEEEEASGLEEDEASGLEEEEEQTSEQDSTFQGH
LVDKHEVEITSDGMETTFIDSVEDSEEEEEEGKSSETGKVKTSLTEKKASRRQKEIPFSYLVGDSGKKKLK
HQVVHKTQEEETAVPTSQCTGTPCLTCLASPSK**SLEMSHDEHKKHSHTNLSISTGVTKLKKTEKKHRTLHTE**
ELTSKEADLTETEENLRSSVINSTREIKEEIGNLKSSHS**GVLEIENSVDLSSRMDILEERIDSLEDQIEEFSK**
DTMQMTKQIISKERORDIEERSRSCNIRLIGIPEKESYENRAEDI**KEIIDENFAELK**KGSSLEIVSACRVPSKI
DEKRLTPRHILVKFWNSSDKEKIIIRASRE**REITYQGTR**IR**TADES**LDTL**DARSKWSNVFK**VLEKGFNPRIY
PAK**MAFD**FRGKTK**VFLSIEEFRDYVLHMPTLRELLGNNIP**

Mass Match Peptides (bold):

DVSAIMNK [162]
DYVLHMPTLR [165]
EEIGNLK [175]
EEINQGGGR [177]
EIIDENFAELK [197]
EITYQGTR [200]
ELLGNNIP [203]

FLCEVK [256]
 HQVVHK [343]
 HSHTNLSISTGVTK [344]
 IDSLEDQIEEFSK [358]
 IGDDNENLTFK [366]
 KENITYMK [411]
 KENITYMKR [412]
 KKENITYMK [421]
 KLPQGSR [425]
 KTEEK [437]
 LPQGSR [480]
 MAFDFR [507]
 MDILEER [510]
 MSDVSTSVQSK [525]
 QWSNVFNILR [592]
 REITYQGTR [601]
 REQLTETDK [602]
 SLEMSHDEHKK [639]
 SSHSGVLEIENSVDDLSSR [649]
 TEFQIIINLALQK [687]
 TFSDLQSLR [690]
 TFSDLQSLRK [691]
 TLHTEELTSK [704]
 VAKPEEMK [743]
 VFLSIEEFR [761]
 VLMDEGAVLTLVADLSSATLDISK [782]
 VLMEIQDLMFEEMR [783]
 WSNVFK [832]
 YGIQEK [852]

Tandem Peptides (underline):

AGEITSDGLSFLFLK [70]
 EADLTEETEENLR [166]
 LTADLSLDTLDAR [494]
 NVHLEFTR [557]
 SSVINSIR [652]
 TEFQIIINLALQK [687]
 TFSDLQSLR [690]
 VLMEIQDLMFEEMR [783]

Peptide Source: iTRAQ, Colorectal cancer

MSDVSTSVQSKFARLAKKENITYMKREQLTETDKDIAPVLDLKCKDVSAIMNKFVKVLMEIQDLMFEEMRET LKN
 DLKAVLGGKATIPVKNSENSSSRTEFQIIINLALQKTGMVGKIEGENSKIGDDNENLTFKLEVNELSGKLDNTN
 EYNSNDGKKLPQGESRSYEVMGSMETLCNIDDRDGNRNHLEFTERESRKDGEDFVKEMREERKFQKLNKKEE
 VLKASREEKVLMDGAVLTLVADLSSATLDISKQWSNVFNILRENDPEPKFLCEVKLAFKCDGEIKTFSDLQSLR
 KFASQKSSVKELLKDVLPQKEEINQGGRKYGIQEKRDKTLDISKHRAGEITSDGLSFLFLKEVKVAKPEEMKNLE
 TQEEEFSELEELDEEASCMEDEDTSGLEEEEEEPSCLEEEEEEEASGLEEDEASGLEEEEEQTSEQDSTFQGH
 LVDKHEVEITSDGMEETFIDSVEDSESEEEEEEGKSSETGKVKTSLTEKKASRRQKEIPFSYLVGDSGKKKLVK
 HQVVHKTQEBEETAVPTSQGTGTPCLTLCLASPSKSLEMSHDEHKKHSHTNLSISTGVTKLKKTEKKHRTLHTE
 ELTSKEADLTEETEENLRSSVINSTRKEETIGNLKSSHSGVLEIENSVDDLSSRMDILEERIDSLEDQIEEFSK
 DTMQMTKQIISKERQRDIERSRSCNIRLIGIPEKESYENRAEDIIKEIIDENFAELKKGSSLEIVSACRVPSKI
DEKRLTTPRHILVKFWNSSDKEKIIIRASRRREITYQGTRIRLTADLSLDTLDARSKWSNVFKVLLEKGFNPRILY
 PAKMAFDGRGKTKVFLSIEEFRDYVLHMPTLRELLGNNIP

Mass Match Peptides (bold):

AEDIK [879]
 DIAPVLDLK [890]
 EEINQGGR [177]
 IDEKR [919]

SSVKELLK [973]

Tandem Peptides (underline):

AEDIIK [879]
DIAPVLDLK [890]
EEINQGGR [177]
IDEKR [919]
SSVKELLK [973]

Peptide Source: iTRAQ, Hepatocellular cancer

MSDVSTSVQSKFARLAKKKENITYMKREQLTETDK**DIAPVLDLK**CKDVSAIMNKFVKVLMETQDLMFEEMRETILKN
DLKAVILGGKATIEPVKNSENSSSRTEFQQIINLALQKTGMVGKIEGENSKIIGDDNENLTFKLEVNELSGKLDNTN
EYNSNDGKKLPQGESRSYEVMGSMETLCNIDDRDGNRNHLEFTEERESRKDGEDEFVKEMREERKFQKLKNKEE
VLKASREEKVLMDGAVLTLVADLSSATLDISKQWSNVFNILRENDPEPKFLCEVKLAFKCDGEIKTFSDQLSLR
KFASQSSVKELLKDVLPQKEEINQGGRKYGIQEKRDKTLDISKHRAGEITSDGLSFLFLKEVKVAKPEEMKNLE
TQEEEFSELEELDEEASGMEDDEDTSGLEEEEEEPGSGLEEEEEASGLEEDEASGLEEEEEQTSEQDSTFQGH
LVDKHEVEITSDGMETTFIDSVEDSESEEEEEEGKSSETGK**VKTSLTEKK**ASRRQKEIPFSYLVGDSGKKKLVK
HQVVHKTQEEETAVPTSQGTGTPCLTLCLASPSKSLEMSHDEHKKHSHTNLSISTGVTKLKKTEKKHRTLHTE
ELTSKEADLTEETENLRSSVINSIREIKEEIGNLKSSHSGVLEIENSVDLSSRMDILEERIDSLEDQIEEFSK
DTMQMTKQIISKERQRDIEERSRSCNIRLIGIPEKESYENRAEDIKEIIDENFAELKKGSSLEIVSACRVPSKI
DEKRLTPRHILVKFWNSSDKEKIIIRASRERREITYQGTRIRLTADLSLDTLDARSK**WSNVFK**VLEKGFNPRI
PAKMAFDPRGKTKVFLSIEEFRDYVLHMPFLRELLGNIP

Mass Match Peptides (bold):

DIAPVLDLK [890]
VKTSLTEKK [992]
WSNVFK [832]

Tandem Peptides (underline):

DIAPVLDLK [890]
VKTSLTEKK [992]
WSNVFK [832]

Peptide Source: iTRAQ, Non-small cell lung cancer

MSDVSTSVQSKFARLAKKKENITYMKREQLTETDK**DIAPVLDLK**CKDVSAIMNKFVKVLMETQDLMFEEMRETILKN
DLKAVILGGKATIEPVKNSENSSSRTEFQQIINLALQKTGMVGKIEGENSKIIGDDNENLTFKLEVNELSGKLDNTN
EYNSNDGKKLPQGESRSYEVMGSMETLCNIDDRDGNRNHLEFTEERESRKDGEDEFVKEMREERKFQ**LKNKEE**
VLKASREEKVLMDGAVLTLVADLSSATLDISKQWSNVFNILRENDPEPKFLCEVKLAFKCDGEIKTFSDQLSLR
KFASQSSVKELLK**DVLPQKEEINQGGR**KYGIQEKRDKTLDISKHRAGEITSDGLSFLFLKEVKVAKPEEMKNLE
TQEEEFSELEELDEEASGMEDDEDTSGLEEEEEEPGSGLEEEEEASGLEEDEASGLEEEEEQTSEQDSTFQGH
LVDKHEVEITSDGMETTFIDSVEDSESEEEEEEGKSSETGKVKTSLTEKKASRRQKEIPFSYLVGDSGKKKLVK
HQVVHKTQEEETAVPTSQGTGTPCLTLCLASPSKSLEMSHDEHKKHSHTNLSISTGVTKLKKTEKKHRTLHTE
ELTSKEADLTEETENLRSSVINSIREIKEEIGNLKSSHSGVLEIENSVDLSSRMDILEERIDSLEDQIEEFSK
DTMQMTKQIISKERQRDIEERSRSCNIRLIGIPEKESYENRAEDIKEIIDENFAELKKGSSLEIVSACRVPSKI
DEKRLTPRHILVKFWNSSDKEKIIIRASRERREITYQGTRIRLTADLSLDTLDARSK**WSNVFK****VLEK**GFNPRI
PAKMAFDPRGKTKVFLSIEEFRDYVLHMPFLRELLGNIP

Mass Match Peptides (bold):

DIAPVLDLK [890]
DVLPQK [897]
EEINQGGR [177]
LKNKEEVLK [933]
VLEK [995]

Tandem Peptides (underline):

DIAPVLDLK [890]

DVLPQK [897]
EEINQGG [177]
LKNKEEVK [933]
VLEK [995]

Peptide Source: iTRAQ, Ovarian cancer

MSDVSTSVQSKFARLAKKENITYMKREQLTETDKDIAPVLDLKCKDVSAIMNKFVLMETQDLMEEMRET LKN
DLKAVLGGKATIEVKNSSENSSRTEFQQIINLALQKTGMVGKIEGENSKI GDDNENLTFKLEVNELSGKLDNTN
EYNSNDGKKLPQGESRSYEVMGSMEEETLCNIDDRDGNRNVHLEFTERESRKDGEDFVKEMREERKFQKLKNKEE
VLKASREEKVLMDGAVLT LVLADLSSATL DISKQWSNVFNILREND FEPKFLCEVKLAFKCDGEIKTFSDLQSLR
KFASQKSSVKELLDVLPQKEEINQGGKRYGIQEKRDKT LIDSKHRAGEITSDGLSFLFLKEVKVAKPEEMKNLE
TQEEEFSELEELDEEASGMEDDEDTSGLEEEEEEP SGLEEEEEEASGLEEDEASGLEEEEEQTSEQDSTFQGH
LVDKHEVEITSDGMETTFIDSVEDSEEEEEEGKSSETGKVKTTSLTEKKASRRQKEIPFSYLVGDSGKKKLK
HQVVHKTQEEETAVPTSQGTGTPCLTLCLASPSKSLMSHDEHKKHSHNTLSISTGVTKLKKTEKKHRTLHTE
ELTSKEADLTEETENLRSSVINSIREIKEEIGNLKSSHSGVLEIENSVDLSSRMDILEERIDSLEDQIEEFK
DTMQMTKQIISKERQRDIERSRSCNIRLIGIPEKESYENRAEDIKEIIDENFAELKKGSSLEIVSACRVPSKI
DEKRLTPRHILVKFWNSSDKEKIRASRERREITYQGTRIRLTADLSLDTLDARSKWSNVFKVLEKGFNPRILY
PAKMAFDPRGKTKVFLSIEEFRDYVLHMP TLRLLGNIP

Mass Match Peptides (bold):

DIAPVLDLK [890]

Tandem Peptides (underline):

DIAPVLDLK [890]

Peptide Source: iTRAQ, Renal cell cancer

MSDVSTSVQSKFARLAKKENITYMKREQLTETDKDIAPVLDLKCKDVSAIMNKFVLMETQDLMEEMRET LKN
DLKAVLGGKATIEVKNSSENSSRTEFQQIINLALQKTGMVGKIEGENSKI GDDNENLTFKLEVNELSGKLDNTN
EYNSNDGKKLPQGESRSYEVMGSMEEETLCNIDDRDGNRNVHLEFTERESRKDGEDFVKEMREERKFQKLKNKEE
VLKASREEKVLMDGAVLT LVLADLSSATL DISKQWSNVFNILREND FEPKFLCEVKLAFKCDGEIKTFSDLQSLR
KFASQKSSVKELLDVLPQKEEINQGGKRYGIQEKRDKT LIDSKHRAGEITSDGLSFLFLKEVKVAKPEEMKNLE
TQEEEFSELEELDEEASGMEDDEDTSGLEEEEEEP SGLEEEEEEASGLEEDEASGLEEEEEQTSEQDSTFQGH
LVDKHEVEITSDGMETTFIDSVEDSEEEEEEGKSSETGKVKTTSLTEKKASRRQKEIPFSYLVGDSGKKKLK
HQVVHKTQEEETAVPTSQGTGTPCLTLCLASPSKSLMSHDEHKKHSHNTLSISTGVTKLKKTEKKHRTLHTE
ELTSKEADLTEETENLRSSVINSIREIKEEIGNLKSSHSGVLEIENSVDLSSRMDILEERIDSLEDQIEEFK
DTMQMTKQIISKERQRDIERSRSCNIRLIGIPEKESYENRAEDIKEIIDENFAELKKGSSLEIVSACRVPSKI
DEKRLTPRHILVKFWNSSDKEKIRASRERREITYQGTRIRLTADLSLDTLDARSKWSNVFKVLEKGFNPRILY
PAKMAFDPRGKTKVFLSIEEFRDYVLHMP TLRLLGNIP

Mass Match Peptides (bold):

DIAPVLDLK [890]

EEINQGG [177]

Tandem Peptides (underline):

DIAPVLDLK [890]

EEINQGG [177]

Peptide Source: iTRAQ, Small cell lung cancer

MSDVSTSVQSKFARLAKKENITYMKREQLTETDKDIAPVLDLKCKDVSAIMNKFVLMETQDLMEEMRET LKN
DLKAVLGGKATIEVKNSSENSSRTEFQQIINLALQKTGMVGKIEGENSKI GDDNENLTFKLEVNELSGKLDNTN
EYNSNDGKKLPQGESRSYEVMGSMEEETLCNIDDRDGNRNVHLEFTERESRKDGEDFVKEMREERKFQKLKNKEE
VLKASREEKVLMDGAVLT LVLADLSSATL DISKQWSNVFNILREND FEPKFLCEVKLAFKCDGEIKTFSDLQSLR
KFASQKSSVKELLDVLPQKEEINQGGKRYGIQEKRDKT LIDSKHRAGEITSDGLSFLFLKEVKVAKPEEMKNLE

TQEEEFSELEELDEEASGMEDDEDTSGLEEEEEEPGEEEEEEASGLEEDEASGLEEEEEQTSEQDSTFQGH
 LVDKHEVEITSDGMETTFIDSVDESESEEEEECKSSETGKVKTTSLTEKKASRRQKEIPFSYLVGDSGKKLVK
 HQVVHKTQEEEEETAVPTSQGTGTPCLTCLASPSKSLEMSHDEHKKHSHTNLSISTGVTKLKKTEKKHRTLHTE
 ELTSKEADLTEETEENLRSSVINSIREIKEEIGNLKSSSHSGVLEIENSVDLSSRMDILEERIDSLEDQIEEFSK
 DTMQMTKQIISKERQDIEERSRSNIRLIGIPEKESYENRAEDIKEIIDENFAELKKGSSLEIVSACRVPSKI
 DEKRLTPRHILVKFWNSSDKEKIRASRERREITYQGTRIRLTADLSLDTLDARSKWSNVFKVLEKGFNPRIY
 PAKMAFDFRGKTKVFLSIEEFRDYVLHMPRTLRELLGNINP

Mass Match Peptides (bold):

DIAPVLDLK [890]
 EEINQGR [177]

Tandem Peptides (underline):

DIAPVLDLK [890]
 EEINQGR [177]

OGTA037 (SEQ ID No: 5)

Peptide Source: 1D-GE, Gastric cancer

MAALIAENFRFLSLFFKSKDVMIFNGLVALGTVGSQELFSVVAFHCPSPARNYLYGLAAIGVPALVLFIIIGIIL
 NNHTWNLVAECQHRRTKNCSAAPTFLLLSSILGRAAVAPVTWSVISLLRGEAYVCALSEFVDPSSLTAREEHFPS
 AHATEILARFPCKENPDNLSDFREEVSRRLRYESQLFGWLLIGVVAILVFLTKCLKHYCSPLSYRQEAYWAQYRA
 NEDQLFQRTAEVHSRVLAANNVRRFFGFVALNKDDEELIANFPVEGTQPRPQWNAITGVVLYRENQGLPLYSLRH
 KWAQGLAGNGAAPDNVEMALLPS

Mass Match Peptides (bold):

Tandem Peptides (underline):

ENPDNLSDFR [215]

Peptide Source: iTRAQ, Colorectal cancer

MAALIAENFRFLSLFFKSKDVMIFNGLVALGTVGSQELFSVVAFHCPSPARNYLYGLAAIGVPALVLFIIIGIIL
 NNHTWNLVAECQHRRTKNCSAAPTFLLLSSILGRAAVAPVTWSVISLLRGEAYVCALSEFVDPSSLTAREEHFPS
 AHATEILARFPCKENPDNLSDFREEVSRRLRYESQLFGWLLIGVVAILVFLTKCLKHYCSPLSYRQEAYWAQYRA
 NEDQLFQRTAEVHSRV**VLAANNVR**RFFGFVALNKDDEELIANFPVEGTQPRPQWNAITGVVLYRENQGLPLYSLRH
 KWAQGLAGNGAAPDNVEMALLPS

Mass Match Peptides (bold):

VLAANNVR [993]

Tandem Peptides (underline):

VLAANNVR [993]

Peptide Source: iTRAQ, Non-small cell lung cancer

MAALIAENFRFLSLFFKSKDVMIFNGLVALGTVGSQELFSVVAFHCPSPARNYLYGLAAIGVPALVLFIIIGIIL
 NNHTWNLVAECQHRRTKNCSAAPTFLLLSSILGRAAVAPVTWSVISLLRGEAYVCALSEFVDPSSLTAREEHFPS
 AHATEILARFPCKENPDNLSDFREEVSRRLRYESQLFGWLLIGVVAILVFLTKCLKHYCSPLSYRQEAYWAQYRA
 NEDQLFQRTAEVHSRV**VLAANNVR**RFFGFVALNKDDEELIANFPVEGTQPRPQWNAITGVVLYRENQGLPLYSLRH
 KWAQGLAGNGAAPDNVEMALLPS

Mass Match Peptides (bold):

VLAANNVR [993]

Tandem Peptides (underline):

VLAANNVR [993]

Peptide Source: iTRAQ, Ovarian cancer

MAALIAENFRFLSLFFKSKDVMIFNGLVALGTVGSQELFSVVAFHCPSPARNYLYGLAAIGVPALVLFIIIGIIL
NNHTWNLVAECQHRRTKNCSAAPTFLLLSSILGRAAVAPVTWSVISLLRGEAYVCALSEFVDPSSLTAREEHFPS
AHATEILARFPCKENPDNLSDFREEVSRRLRYESQLFCWLLIGVVAILVFLTKCLKHYCSPLSYRQEAYWAQYRA
NEDQLFQRTAEVHSRVLAANNVRRFFGFVALNKDDEELIANFPVEGTQPRPQWNAITGVYLYRENQGLPLYSRHL
KWAQGLAGNGAAPDNVEMALLPS

Mass Match Peptides (bold):

VLAANNVR [993]

Tandem Peptides (underline):

VLAANNVR [993]

OGTA041 (SEQ ID No: 6)**Peptide Source: 1D-GE, Hepatocellular carcinoma**

MLTLQTWVVQALFIFLTTESTGELLDPGCIISPESPVVQLHSNFTAVCVLKEKCMDYFHVNNANYIVWKTINHFTIP
KEQYTIINRTASSVTFTDIASLNIQLTCNLTFFGQLEQNVYGITIIISGLPPEKPKNLSCIVNEGKKMRCEWDGGR
ETHLETNFTLSEWATHKFADCKAKRDTPTSTCTVDYSTVYFVNIEVWVEAENALGKVTS DHINFDPVYKVKPNPP
HNLSVINSEELSSILKLTWNTNPSIKSVIILKYNIQYRTKDASTWSQIPPEDTASTRSSFTVQDLKPFTEYVFRIR
CMKEDGKGYSDWSEEASGITYEDRPSKAPSFWKIDPSHTQGYRTVQLVWKTLPPEANGKILDYEVTLTRWKS
HLQNYTVNATKLTVNLTNDRYLATLTVRNLVGKSDAAVLTIPACDFQATHPVMDLKAFPKDNMLWVWETTPRESV
KKYILEWCVLSDKAPCITDWQQEDGTVHRTYLRGNLAESKCYLITVTPVYADGPGSPESIKAYLKQAPPSKGPTV
RTKKVCKNEAVLEWDQLPVDVQNGFIRNYTIFYRTIIGNETAVNVDSSHTEYTLSSSLTSDTLYMVRMAAYTDEGG
KDGPFTFTTPKFAQGEIEAIVVPVCLAFLLTLLGLVLCFNKRDLIKKHIWPNVPDPSKSHIAQWSPHTPPRHN
FNSKDQMYSDGNFTDVSVEIEANDKKFPFEDLKSLDLFKKEKINTEGHSSGIGGSSCMSSSRPSISSSDENESS
QNTSSTVQYSTVHSGYRHQVPSVQVFSRSESTQPLLDSEERPDLQLVDHVDGGDGILPRQQYFKQNCSSQHES
PDISHFERSKQVSSVNEEDFVRLKQQISDHISQSCGSGQMFMFQEVSAADAFGPGTEGQVERFETVGMEEATDEG
MPKSYLPQTVRQGGYMPQ

Mass Match Peptides (bold):

KFPFEDLK [431]

Tandem Peptides (underline):

DGPEFTFTTPK [124]

Peptide Source: 1D-GE, Lung cancer

MLTLQTWVVQALFIFLTTESTGELLDPGCIISPESPVVQLHSNFTAVCVLKEKCMDYFHVNNANYIVWKTINHFTIP
KEQYTIINRTASSVTFTDIASLNIQLTCNLTFFGQLEQNVYGITIIISGLPPEKPKNLSCIVNEGKKMRCEWDGGR
ETHLETNFTLSEWATHKFADCKAKRDTPTSTCTVDYSTVYFVNIEVWVEAENALGKVTS DHINFDPVYKVKPNPP
HNLSVINSEELSSILKLTWNTNPSIKSVIILKYNIQYRTKDASTWSQIPPEDTASTRSSFTVQDLKPFTEYVFRIR
CMKEDGKGYSDWSEEASGITYEDRPSKAPSFWKIDPSHTQGYRTVQLVWKTLPPEANGKILDYEVTLTRWKS
HLQNYTVNATKLTVNLTNDRYLATLTVRNLVGKSDAAVLTIPACDFQATHPVMDLKAFPKDNMLWVWETTPRESV
KKYILEWCVLSDKAPCITDWQQEDGTVHRTYLRGNLAESKCYLITVTPVYADGPGSPESIKAYLKQAPPSKGPTV
RTKKVCKNEAVLEWDQLPVDVQNGFIRNYTIFYRTIIGNETAVNVDSSHTEYTLSSSLTSDTLYMVRMAAYTDEGG
KDGPFTFTTPKFAQGEIEAIVVPVCLAFLLTLLGLVLCFNKRDLIKKHIWPNVPDPSKSHIAQWSPHTPPRHN
FNSKDQMYSDGNFTDVSVEIEANDKKFPFEDLKSLDLFKKEKINTEGHSSGIGGSSCMSSSRPSISSSDENESS
QNTSSTVQYSTVHSGYRHQVPSVQVFSRSESTQPLLDSEERPDLQLVDHVDGGDGILPRQQYFKQNCSSQHES
PDISHFERSKQVSSVNEEDFVRLKQQISDHISQSCGSGQMFMFQEVSAADAFGPGTEGQVERFETVGMEEATDEG
MPKSYLPQTVRQGGYMPQ

Mass Match Peptides (bold):

DNMLWVEWTPR [146]
QNCSEQHESPEISHFER [582]
QVSSVNEEDFVR [591]
SHLQNYTVNATK [635]

Tandem Peptides (underline):

QVSSVNEEDFVR [591]

Peptide Source: 1D-GE, Pancreatic cancer

MLTLQTWVVQALFIFLTTESTGELLDP CGYISPESPVVQLHSNFTAVCVLKEKCMDYFHV NANYIVWK**TNHFTIP**
KEQYTIINRTASSVTFTDIASLNIQLTCNILTFGQLEQNVYGITIIISGLPPEKPKNLSCIVNEGKKMRCEWDGGR
ETHLETNFTLTKSEWATHKFADCKAKRDTPTSTCTVDYSTVYFVNIEVWVEAENALGKVTS DHINFDPYKVKPNPP
HNLSVINSEELSSILKLTWNTNPSIKSVIILKYNIQYRTKDASTWSQIPPEDTASTRSSFTVQDLKPFTEYVFRIR
CMKEDGKGYWSDWSEEASGITYEDRPSKAPSFWKIDPSHTQGYRTVQLVWKTLP PFEANGKILDYEVTLTRWKS
HLQNYTVNATKLTVNLTNDRYLATLTVRNLVGKS DAAVLTIPACDFQATHFVMDLKAFPKDNMLWVEWTPPRESV
KKYILEWCVLSDKAPCITDWQQEDGTVHRTYLRGNLAESKCYLITVTPVYADGPGSPESIKAYLKQAPPSKGPTV
RTKKVGKNEAVLEWDQLPVDVQNGFIR**NYTIFYR**TIIGNETAVNVDSSHTEYTLSSLTSDTLYMVRMAAYTDEGC
KDGPEFTFTTPKFAQGEIEAIVVPVCLAFLLTTLLGVLF CFNKRDLIKK**HIWPNVPDPSK**SHIAQWSPHTPPRH
FNSKDQMYSDGNFTDVSVEIEANDKKPFPEDLKSLDLFKKEKINTEGHSSGIGGSSCMSSSRPSISSSDENESS
QNTSSTVQYSTVHSGYRHQVPSVQVFSRSESTQPLLDSEERPEDLQLVDHVDGGDGILPRQYFKQNCSEQHES
PDISHFERSKQVSSVNEEDFVRLKQQISDHISQSCGSGQMKMFQEVSAADAFPGTEGQVERFETVGM EATDEG
MPKSYLPQTVRQGGYMPQ

Mass Match Peptides (bold):

HIWPNVPDPSK [336]
NYTIFYR [564]
SHLQNYTVNATK [635]
TNHFTIPK [711]

Tandem Peptides (underline):

HIWPNVPDPSK [336]

Peptide Source: iTRAQ, Non-small cell lung cancer

MLTLQTWVVQALFIFLTTESTGELLDP CGYISPESPVVQLHSNFTAVCVLKEKCMDYFHV NANYIVWK**TNHFTIP**
KEQYTIINRTASSVTFTDIASLNIQLTCNILTFGQLEQNVYGITIIISGLPPEKPKNLSCIVNEGKKMRCEWDGGR
ETHLETNFTLTKSEWATHKFADCKAKRDTPTSTCTVDYSTVYFVNIEVWVEAENALGKVTS DHINFDPYKVKPNPP
HNLSVINSEELSSILK**LTWNTNPSIK**SVIILKYNIQYRTKDASTWSQIPPEDTASTRSSFTVQDLKPFTEYVFRIR
CMKEDGKGYWSDWSEEASGITYEDRPSKAPSFWKIDPSHTQGYRTVQLVWKTLP PFEANGKILDYEVTLTRWKS
HLQNYTVNATKLTVNLTNDRYLATLTVRNLVGKS DAAVLTIPACDFQATHFVMDLKAFPKDNMLWVEWTPPRESV
KKYILEWCVLSDKAPCITDWQQEDGTVHRTYLRGNLAESKCYLITVTPVYADGPGSPESIKAYLKQAPPSKGPTV
RTKKVGKNEAVLEWDQLPVDVQNGFIRNYTIFYRTIIIGNETAVNVDSSHTEYTLSSLTSDTLYMVRMAAYTDEGC
KDGPEFTFTTPKFAQGEIEAIVVPVCLAFLLTTLLGVLF CFNKRDLIKKHIWPNVPDPSKSHIAQWSPHTPPRH
FNSKDQMYSDGNFTDVSVEIEANDKKPFPEDLKSLDLFKKEKINTEGHSSGIGGSSCMSSSRPSISSSDENESS
QNTSSTVQYSTVHSGYRHQVPSVQVFSRSESTQPLLDSEERPEDLQLVDHVDGGDGILPRQYFKQNCSEQHES
PDISHFERSKQVSSVNEEDFVRLKQQISDHISQSCGSGQMKMFQEVSAADAFPGTEGQVERFETVGM EATDEG
MPKSYLPQTVRQGGYMPQ

Mass Match Peptides (bold):

LTWNTNPSIK [950]

Tandem Peptides (underline):

LTWNTNPSIK [950]

OGTA053 (SEQ ID No: 7)

Peptide Source: 1D-GE, Pancreatic cancer

MPGIVVFRRRWSVGSDDLVLPALFLFLHHTTFVILSVVLFGLVYNPHEACSLNLVDHGRGYLGILLSCMIAEMA
 IIWLSMRGGILYTEPRDSMQVLYVRLAILVIEFIYAIVGIVWLTQYYTSCNDLTAKNVTLMVVCNWVVILSVC
 ITVLCVFDPTGRTFVKLRATKRRQNRNLRTYNLRHRLLEEGQATSWSRRLKVFLCCTRTKDSQSDAYSEIAYLFAEF
 FRDLDIVPSDIIAGLVLLRQQRQAKRNAVLDEANNILAFLSGMPVTRNTKYLDLKNSEQEMLRYKEVCYYMLFAL
 AAYGWPMYLMRKPAACGLCQLARSCSCCLCPARPRFAPGVITIEDNCCGCNAIAIRRHFLDENMTAVDIVYTSCHD
 AVYETPFYVAVDHDKKKVVISIRGTLSPKDALDLDLTDGAERLPVEGHHGTWLGHKGMVLSAEYIKKKLEQEMVLS
 QAFGRDLGRGTHYGLIVVGHSLGAGTAAILSFLLRPQYPTLKCFAYSPPGGLLEDAMEYSKEFVTAVVLGKDL
 VPRIGLSQLEGFRRQLLDVLQRSTKPKWRIIVGATKCIKSELPEEVEVTTLASTRLWTHPSDLTIALSASTPLY
 PPGRIIHVVHNHPAEQCCCEQEPTYFAIWGDNKAFNEVIISPAMLEHHLFYVMEGLNKVLENYNGKGTALLS
 AAKVMVSPTEVDLTPELIFQQQLPTGPPMPTGLALELPTADHRNSSVRSKSQSEMSLEGFSEGRLLSPVAAAA
 RQDPVELLLLSTQERLAAELQARRAPLATMESLSDTESLSYFDSRRSSGFRSIRGSPSLHAVLERDEGHLFYIDP
 AIPENPSLSSRTELAAADSLKHSQDTQPLEAALGSGGVTPERPSSAAANDEEEVGGGGGGPASRGELALHNG
 RLGDSPSPQVLEFAEFIDSLFNLDKSSSFQDLYCMVVPESPTSDYAEQPKSPSQEILLRAQFEPNLVPPKPRIL
 FAGSADPSSGISLSPSPFLSSSGELMDLTPTGLSSQECLEADKIRTSTPTGHGASPAKQDELVISAR

Mass Match Peptides (bold):

FAPGVITIEDNCCGCNAIAIR [243]
 VLENYNG [780]

Tandem Peptides (underline):

LEEGQATSWSR [452]

Peptide Source: iTRAQ, Colorectal cancer

MPGIVVFRRRWSVGSDDLVLPALFLFLHHTTFVILSVVLFGLVYNPHEACSLNLVDHGRGYLGILLSCMIAEMA
 IIWLSMRGGILYTEPRDSMQVLYVRLAILVIEFIYAIVGIVWLTQYYTSCNDLTAKNVTLMVVCNWVVILSVC
 ITVLCVFDPTGRTFVKLRATKRRQNRNLRTYNLRHRLLEEGQATSWSRRLKVFLCCTRTKDSQSDAYSEIAYLFAEF
 FRDLDIVPSDIIAGLVLLRQQRQAKRNAVLDEANNILAFLSGMPVTRNTKYLDLKNSEQEMLRYKEVCYYMLFAL
 AAYGWPMYLMRKPAACGLCQLARSCSCCLCPARPRFAPGVITIEDNCCGCNAIAIRRHFLDENMTAVDIVYTSCHD
 AVYETPFYVAVDHDKKKVVVISIRGTLSPKDALDLDLTDGAERLPVEGHHGTWLGHKGMVLSAEYIKKKLEQEMVLS
 QAFGRDLGRGTHYGLIVVGHSLGAGTAAILSFLLRPQYPTLKCFAYSPPGGLLEDAMEYSKEFVTAVVLGKDL
 VPRIGLSQLEGFRRQLLDVLQRSTKPKWRIIVGATKCIKSELPEEVEVTTLASTRLWTHPSDLTIALSASTPLY
 PPGRIIHVVHNHPAEQCCCEQEPTYFAIWGDNKAFNEVIISPAMLEHHLFYVMEGLNKVLENYNGKGTALLS
 AAKVMVSPTEVDLTPELIFQQQLPTGPPMPTGLALELPTADHRNSSVRSKSQSEMSLEGFSEGRLLSPVAAAA
 RQDPVELLLLSTQERLAAELQARRAPLATMESLSDTESLSYFDSRRSSGFRSIRGSPSLHAVLERDEGHLFYIDP
 AIPENPSLSSRTELAAADSLKHSQDTQPLEAALGSGGVTPERPSSAAANDEEEVGGGGGGPASRGELALHNG
 RLGDSPSPQVLEFAEFIDSLFNLDKSSSFQDLYCMVVPESPTSDYAEQPKSPSQEILLRAQFEPNLVPPKPRIL
 FAGSADPSSGISLSPSPFLSSSGELMDLTPTGLSSQECLEADKIRTSTPTGHGASPAKQDELVISAR

Mass Match Peptides (bold):

IRTSTPTGHGASPAK [924]
 TELLAAADSLK [980]
 VVISIR [1002]

Tandem Peptides (underline):

IRTSTPTGHGASPAK [924]
 TELLAAADSLK [980]
 VVISIR [1002]

Peptide Source: iTRAQ, Hepatocellular cancer

MPGIVVFRRRWSVGSDDLVLPALFLFLHHTTFVILSVVLFGLVYNPHEACSLNLVDHGRGYLGILLSCMIAEMA
 IIWLSMRGGILYTEPRDSMQVLYVRLAILVIEFIYAIVGIVWLTQYYTSCNDLTAKNVTLMVVCNWVVILSVC
 ITVLCVFDPTGRTFVKLRATKRRQNRNLRTYNLRHRLLEEGQATSWSRRLKVFLCCTRTKDSQSDAYSEIAYLFAEF

FRDLDIVP^{SDII}IAGLVLLRQ^{RQRA}KRNAVLDEANNDILAF^{LSGMPV}TRNTKYLDL^{KNSQ}EMLRYKEVCYYMLFAL
 AAYGWPMYLMRKPACGLCQLARSCSCCLCPARPRFAPGV^{TI}EEDNCCGCNATAIRRHFLDENMTAVDIVYTSCHD
 AVYETPFYVAVDHDKKKVVISIRGTLSPKDALTDLTGAERLPVEGHHGTWLGHKGMVLSAEYIKKKLEQEMVLS
 QAFGRDLGRG^{IKHYGLIVVGHSLGAGTAAILSFLLRPQYPTL}KCFAYSPPGGLLSEDA^{MEYSKEFVTAVVLGKDL}
 VPRIGLSQLEGFRRQLLDVLQRSTKPKWRIIVGATKCI^{PKSELPEEVEVTTLASTRLWTHPSDLTIALSASTPLY}
 PPGRIIHVVHNHPAEQCCCEQE^{EPTYFAIWGDNKAFNEVII}SPAM^{LHEHL}PYVVM^{EGLNK}VLENYNKGKTALLS
 AAKVMVS^{PTEVDLTPELIFQQQPLPTGPPMPTGLALELPTADHRN}SSVRSKSQSEMSLEGFSEGRLLSPVAAAA
 RQDPVELLLLSTQERLAAELQARRAPLATMESLSDTESLYS^{FDSRRSSGFRSIRGSPSLH}AVLERDEGHLFYIDP
 AIPEEN^{PSLSSRTELLAADSLSKHSQDTQPLEAALGSGCVTP}ERPPSAAANDEEEVGGGGGGPASRGELALHNG
 RLGDSPSPQVLEFAEFIDSLFNLD^{SKSSSFQDLYCMVVPESPTS}DYAE^{GPKSPSQEILLRAQFEPNLV}PKPPRL
 FAGSAD^{SSGISLSPSFPLSSSGELMDLTPTGLSSQECLAADK}IRTSTPTGHGASPAKQDELVISAR

Mass Match Peptides (bold):

IRTSTPTGHGASPAK [924]

Tandem Peptides (underline):

IRTSTPTGHGASPAK [924]

Peptide Source: iTRAQ, Non-small cell lung cancer

MPGIVVFRRRWSVGSDDLVLP^{AI}FLFLLHTTW^{FVILSVVLFGLVYNPHEACSLNLVDHGRGYLGILLSCMIAEMA}
 IIWLSMRGGILYTEPRDSM^{QYVLYVRLAILVIEFIYAIVGIVWLTQYYTSCNDLTAKNVT}LGMVVCN^{WVVL}SVC
 ITVLCVFDPTGRTEFVKLRATKRRQRNLRTYNLRH^{RLEEGQATSWSRRLKVFLCCTRTKDSQSDAYSEIAYLFAEF}
 FRDLDIVP^{SDII}IAGLVLLRQ^{RQRA}KRNAVLDEANNDILAF^{LSGMPV}TRNTKYLDL^{KNSQ}EMLRYKEVCYYMLFAL
 AAYGWPMYLMRKPACGLCQLARSCSCCLCPARPRFAPGV^{TI}EEDNCCGCNATAIRRHFLDENMTAVDIVYTSCHD
 AVYETPFYVAVDHDKKKVVISIRGTLSPKDALTDLTGAERLPVEGHHGTWLGHKGMVLSAEYIKKKLEQEMVLS
 QAFGRDLGRG^{IKHYGLIVVGHSLGAGTAAILSFLLRPQYPTL}KCFAYSPPGGLLSEDA^{MEYSKEFVTAVVLGKDL}
 VPRIGLSQLEGFRRQLLDVLQRSTKPKWRIIVGATKCI^{PKSELPEEVEVTTLASTRLWTHPSDLTIALSASTPLY}
 PPGRIIHVVHNHPAEQCCCEQE^{EPTYFAIWGDNKAFNEVII}SPAM^{LHEHL}PYVVM^{EGLNK}VLENYNKGKTALLS
 AAKVMVS^{PTEVDLTPELIFQQQPLPTGPPMPTGLALELPTADHRN}SSVRSKSQSEMSLEGFSEGRLLSPVAAAA
 RQDPVELLLLSTQERLAAELQARRAPLATMESLSDTESLYS^{FDSRRSSGFRSIRGSPSLH}AVLERDEGHLFYIDP
 AIPEEN^{PSLSSRTELLAADSLSKHSQDTQPLEAALGSGCVTP}ERPPSAAANDEEEVGGGGGGPASRGELALHNG
 RLGDSPSPQVLEFAEFIDSLFNLD^{SKSSSFQDLYCMVVPESPTS}DYAE^{GPKSPSQEILLRAQFEPNLV}PKPPRL
 FAGSAD^{SSGISLSPSFPLSSSGELMDLTPTGLSSQECLAADK}IRTSTPTGHGASPAKQDELVISAR

Mass Match Peptides (bold):

GTLSPKDALTDLTGAER [916]

IRTSTPTGHGASPAK [924]

TELLAADSLSK [980]

Tandem Peptides (underline):

GTLSPKDALTDLTGAER [916]

IRTSTPTGHGASPAK [924]

TELLAADSLSK [980]

Peptide Source: iTRAQ, Renal cell cancer

MPGIVVFRRRWSVGSDDLVLP^{AI}FLFLLHTTW^{FVILSVVLFGLVYNPHEACSLNLVDHGRGYLGILLSCMIAEMA}
 IIWLSMRGGILYTEPRDSM^{QYVLYVRLAILVIEFIYAIVGIVWLTQYYTSCNDLTAKNVT}LGMVVCN^{WVVL}SVC
 ITVLCVFDPTGRTEFVKLRATKRRQRNLRTYNLRH^{RLEEGQATSWSRRLKVFLCCTRTKDSQSDAYSEIAYLFAEF}
 FRDLDIVP^{SDII}IAGLVLLRQ^{RQRA}KRNAVLDEANNDILAF^{LSGMPV}TRNTKYLDL^{KNSQ}EMLRYKEVCYYMLFAL
 AAYGWPMYLMRKPACGLCQLARSCSCCLCPARPRFAPGV^{TI}EEDNCCGCNATAIRRHFLDENMTAVDIVYTSCHD
 AVYETPFYVAVDHDKKKVVISIRGTLSPKDALTDLTGAERLPVEGHHGTWLGHKGMVLSAEYIKKKLEQEMVLS
 QAFGRDLGRG^{IKHYGLIVVGHSLGAGTAAILSFLLRPQYPTL}KCFAYSPPGGLLSEDA^{MEYSKEFVTAVVLGKDL}
 VPRIGLSQLEGFRRQLLDVLQRSTKPKWRIIVGATKCI^{PKSELPEEVEVTTLASTRLWTHPSDLTIALSASTPLY}
 PPGRIIHVVHNHPAEQCCCEQE^{EPTYFAIWGDNKAFNEVII}SPAM^{LHEHL}PYVVM^{EGLNK}VLENYNKGKTALLS
 AAKVMVS^{PTEVDLTPELIFQQQPLPTGPPMPTGLALELPTADHRN}SSVRSKSQSEMSLEGFSEGRLLSPVAAAA
 RQDPVELLLLSTQERLAAELQARRAPLATMESLSDTESLYS^{FDSRRSSGFRSIRGSPSLH}AVLERDEGHLFYIDP
 AIPEEN^{PSLSSRTELLAADSLSKHSQDTQPLEAALGSGCVTP}ERPPSAAANDEEEVGGGGGGPASRGELALHNG

RLGDSPPSPQVLEFAEFIDSLFNLDKSSSFQDLYCMVVPESPTSDYAEGPKSPSQQEILLRAQFEPNLVPKPPRL
FAGSADPSSGISLSPSPFLSSSGELMDLTPTGLSSQEC LAADK IRTSTPTGHGASPAK QDELVISAR

Mass Match Peptides (bold):

IRTSTPTGHGASPAK [924]
TELLAADSLSK [980]

Tandem Peptides (underline):

IRTSTPTGHGASPAK [924]
TELLAADSLSK [980]

Peptide Source: iTRAQ, Small cell lung cancer

MPGIVVFRRRWSVGSDDLVLPAIFLFLHHTTWVILSVVLFGLVYNPHEACSLNLVDHGRGYLGILLSCMIAEMA
IIWLSMRGGIlyTEPRDSMQYVLYVRLAILVIEFIYAIVGIVWLTQYYTSCNDLTAKNVTLMVVCNWVILSVC
ITVLCVFDPTGRTFVKLRATKRRQRNLRTYNLRHRLLEEGQATSWSRRLKVFLCCTRTKDSQSDAYSEIAYLFAEF
FRDLDIVPSDIIAGLVLLRQRQRAKRNAVLDEANNDILAFLSGMPVTRNTKYLDLKNSEQEMLRYKEVCYYMLFAL
AAYGWPMYLMRKPAACGLCQLARSCCCLCPARPRFAPGVTEEDNCCGCNAIAIRRHFLDENMTAVDIVYTSCHD
AVYETPFYVAVDHDKKKVVISIRGTLSPKDALTDLTGDARLPVEGHHGTWLGHKGMVLSAEYIKKKLEQEMVLS
QAFGRDLGRGTHYGLIVVGHSLGAGTAAILSFLLRPQYPTLKCFAYSPPGGLLSEDA MEYSKEFVTAVVLGKDL
VPRIGLSQLEGFRRLDVLQRSTKPKWRIIVGATKCI PKSELPEEVEVTTLASTRLWTHPSDLTIALSASTPLY
PPGRIITHVHNHPAEQCCCEQEPTTYFATWGDNKA FNEVIISPAMLHEHLPPYVMEGLNKVLENYNKGKTALLS
AAKVMVSPTFVDLTPELIFQQQPLPTGPPMPTGLALELPTADHRNSSVRSKSQSEMSLEGFSEGRLLSPVVAATA
RQDPVELLLLSTQERLAELQARRAPLATMESLSDTESLYSFDSSRRSSGFRSIRGSPSLHAVLERDEGHLFYIDP
AIPEENP SLSSR TELLAADSLSK HSQDTQFLEAALGSGGVTPERPSSAAANDEEEVGGGGGPASRGELALHNG
RLGDSPPSPQVLEFAEFIDSLFNLDKSSSFQDLYCMVVPESPTSDYAEGPKSPSQQEILLRAQFEPNLVPKPPRL
FAGSADPSSGISLSPSPFLSSSGELMDLTPTGLSSQEC LAADKIRTSTPTGHGASPAK QDELVISAR

Mass Match Peptides (bold):

TELLAADSLSK [980]

Tandem Peptides (underline):

TELLAADSLSK [980]

OGTA054 (SEQ ID No: 8)

Peptide Source: 1D-GE, Pancreatic cancer

MHK EEHEVAVLGAPPSTILPR STVINIHSETSVDPDHVVWSLFNTLFLNWCCLGFI AFAYSVKSRDRKMVG DVTGA
QAYASTAKCLNIWALILGILMTIGFILLVFGSVTVYHIMLQIIQEKRGY

Mass Match Peptides (bold):

Tandem Peptides (underline):

EEHEVAVLGAPPSTILPR [173]

Peptide Source: iTRAQ, Colorectal cancer

MHK EEHEVAVLGAPPSTILPR STVINIHSETSVDPDHVVWSLFNTLFLNWCCLGFI AFAYSVKSRDRK MVG DVTGA
QAYASTAK CLNIWALILGILMTIGFILLVFGSVTVYHIMLQIIQEKRGY

Mass Match Peptides (bold):

EEHEVAVLGAPPSTILPR [173]
MVG DVTGAQAYASTAK [954]

Tandem Peptides (underline):

EEHEVAVLGAPPSTILPR [173]
MVGDTVGAQAYASTAK [954]

Peptide Source: iTRAQ, Non-small cell lung cancer

MHKEEHEVAVLGAPPSTILPRSTVINIHSETSPVDHVVWSLFNTLFLNWCCLGFI AFAYSVKSRDRK MVGDTVGAQAYASTAK CLNIWALILGILMTIGFILLLVFGSVTVYHIMLQIIQE KRGY

Mass Match Peptides (bold):

MVGDTVGAQAYASTAK [954]

Tandem Peptides (underline):

MVGDTVGAQAYASTAK [954]

OGTA066 (SEQ ID No: 9)

Peptide Source: 1D-GE, Colorectal cancer

MMLHSALGLCLLLVTVSSNLAI A IKKEKRPPQTL SRGWGDDITWVQTYEEGLFYAQKSKKPLMVIHHLEDCQYSQ
ALKKVFAQNEEIQEMAQNK FIMLNL MHETTDKNLSPDGQYVPR IMFVDPSLTVR ADIAGRYSNRLYTYEPRDLPL
LIENMKKALRLIQSEL

Mass Match Peptides (bold):

IMFVDPSLTVR [380]

Tandem Peptides (underline):

IMFVDPSLTVR [380]

Peptide Source: 1D-GE, Pancreatic cancer

MMLHSALGLCLLLVTVSSNLAI A IKKEKRPPQTL SRGWGDDITWVQTYEEGLFYAQKSK KPLMVIHHLEDCQYSQ
ALKKVFAQNEEIQEMAQNK FIMLNL MHETTDKNLSPDGQYVPR IMFVDPSLTVR ADIAGRYSNRLYTYEPRDLPL
LIENMKKALRLIQSEL

Mass Match Peptides (bold):

IMFVDPSLTVR [380]

KPLMVIHHLEDCQYSQALK [432]

Tandem Peptides (underline):

IMFVDPSLTVR [380]

Peptide Source: iTRAQ, Colorectal cancer

MMLHSALGLCLLLVTVSSNLAI A IKKEKRPPQTL SRGWGDDITWVQTYEEGLFYAQKSKKPLMVIHHLEDCQYSQ
ALKKVFAQNEEIQEMAQNK FIMLNL MHETTDKNLSPDGQYVPR IMFVDPSLTVR ADIAGRYSNRLYTYEPR DLPL
LIENMK KALRLIQSEL

Mass Match Peptides (bold):

DLPLLIENMK [135]

IMFVDPSLTVR [380]

Tandem Peptides (underline):

DLPLLIENMK [135]

IMFVDPSLTVR [380]

Peptide Source: iTRAQ, Non-small cell lung cancer

MMLHSALGLCLLLTVSSNLAIKKEKRPPQTLNRGWGDDITWVQTYEEGLFYAQSKKKPLMVIHHLEDCQYSQ
 ALKKVFAQNEEIQEMAQNKFIMNLNHETTDKNLSPDGQYVPRIMFVDPSLTVRADIAGRYSNRLYTYEPRDLPL
LIENMKKALRLIQSEL

Mass Match Peptides (bold):

DLPLLIENMK [135]
 IMFVDPSLTVR [380]
 NLSPDGQYVPR [546]

Tandem Peptides (underline):

DLPLLIENMK [135]
 IMFVDPSLTVR [380]
 NLSPDGQYVPR [546]

Peptide Source: iTRAQ, Kidney cancer

MMLHSALGLCLLLTVSSNLAIKKEKRPPQTLNRGWGDDITWVQTYEEGLFYAQSKKKPLMVIHHLEDCQYSQ
 ALKKVFAQNEEIQEMAQNKFIMNLNHETTDKNLSPDGQYVPRIMFVDPSLTVRADIAGRYSNRLYTYEPRDLPL
LIENMKKALRLIQSEL

Mass Match Peptides (bold):

DLPLLIENMK [135]

Tandem Peptides (underline):

DLPLLIENMK [135]

OGTA072 (SEQ ID No: 10)

Peptide Source: 1D-GE, Colorectal cancer

MTTSGALFPSLVPGSRCASNKYLVEFRACKMSLKGTTPDKRKGLVYIQQTDDSLIHFCWKDRITSCNVEDDLII
 FDDCEFKRVPCPSGRVYVLKFKAGSKRLFFWMQEPKTDQDEEHCRKVNEYLNPPMPGALGASGSSGHELSAL
 GCEGGLQSLGNSMHSQMLQIGPAGLGGLGALTGPGLASLLGSSGPPGSSSSSSSRQSAAVTPSSTTSST
 RATPAPSAFAAASATSPSPAPSSGNGASTAASPTQPIQLSDLOSILATMNPVAGPAGGQVLDASVLTPEIMAPI
 LANADVQERLLPYLPAGESLPQTADAIQNTLTSPQFQALGMFSAALASGQLGPLMCQFGLPAEAVEAANKGDVE
 AFAKAMQNNAKPEQKEGDTKDKKDEEDMSLD

Mass Match Peptides (bold):

MTTSGALFPSLVPGSR [526]

Tandem Peptides (underline):

TDQDEEHCR [685]

OGTA074 (SEQ ID No: 11)

Peptide Source: 1D-GE, Colorectal cancer

MGDVKALLFVAAARARRLGGAAASESLAVSEAFCRVRSCQPKKACGPQRCLNVPVAVFSPSPSVRKRQVSLNWQP
 LTLQEARALLKRRRPRGPGGRGLLRPPQAPAGKAPVLCPLICHNGGVCVKPDRCLCPPDFAGKFCQLHSSGA
 RPPAPAVPGLTRSVYTMPLANERDDEHGVASVMVSVHVEHPQEAASVVVHQVERVSGPWEEADAEAVARAEAAAAAE
 AAA?YTVLAQSAFREDGYSDASGFGYCFRELRGGEASPLPGLRTQEVCCRGAGLAWGVHDCQLCSERLGNSESV
 SA?DGPCPTGFERVNGSCEDVDECATGGRCQHGEACANTRGGYTCVCPDGFLDSSRSSCISQHVISEAKGPCFRV
 LRDDGCSLPILRNITKQICCSRVGKAWGRGCQLCPPFGSEGFRICPAGPGYHYASDLRYNTRPLGQEPFRVS
 LSQ?RTLTPATSRPSAGFLPTRLERPRPEPRPDPRPGPELPLPSIPAWTGPEIPESGFSSGMCQRNPQVCGPGRCI

SRPSGYTCACDSGFRLSPQGTTRCIDVDECRRVPPPCAPGRCE NSPGSFRCVCGPGFRAGPRAAECLDVDECHRV P
 PCDLGRCENTPGSFLCVCAPAGYQAAPHGASCQDVDECTQSPGLCGRGACKNLPGSFRCVCPAGFRGSACEEDVD
 ECAQEPFPCCGPGRCNDTAGSFHCACFAGFRSRGFGAPCQDVDECARSPPPCTYGRCENTEGSFQCVCPMGFQNT
 AGSECEDVDECENHLACPGQECVNSPGSFQCRTPSGHHLHRGRCTDVDECSSGAPPCGPHGHCTNTEGSRFCSC
 APGYRA?SGRPGPCADVNECLEGDFCFPHGECLNTDGSFACTCAPGYRPGPRGASCLDVDECSEEDLCQSGICTN
 TDGSFECICPPGHRAGPDLASCLDVDECREGPALCGSQRCENSPGSYRCVRDCDPGYHAGPEGTCDVDEQCQY
 GPEICGAQRCENTPGSYRCTPACDPGYQPTPGGGCQDVDECRNRSFCGAHAVCQNLPGSFQCLCDQGYEGARDGR
 HCVDVNECETLQGVCGAALCENVEGSFLCVCNPSPPEEFDPMTGRCVPPRTSAGTFPGSQPAPASVLPARPPPP
 PLPRRPSTPR**QGPVGSGR**RECYFDTAAPDACDNILARNVTWQECCTVGEWGS GCRIQQCPGTETA EYQSLCPH
 GRGYLA?SGDLSLRDVDECQLFRDQVCKSGVCVNTAPGYSCYCSNGYYYHTQRLECIDNDECADEEPACEGGRC
 VNTVGSYHCTCEPPLVLDGSQRRCVSNESQSLDDNLGVWQEVGADLVCSHPRLD RQATYTECCCLYGEAWGMD C
 ALCPAQDSDDFEALCNVLRPPAYSPPRPGGFGLPYEYGPDLGPPYQGLPYGPPELYPPPALPYDPYPPPPGPFARR
 EAPYGA?RFDMPDFEDDGGPYGESEAPAPPGPCTRWPYRSRDRTRSFPEPEEPPEGGSYAGSLAEPYEELEAEEC
 GTLDGCTNGRCVR**VPEGFTCR**CFDGYRLDMTRMACVDINECDEAEAAASPLCVNARCLNTDGSFRCTCRPGFAPTH
 QPHHCA?ARPR A

Mass Match Peptides (bold):

QGPVGSGR [577]

VPEGFTCR [790]

Tandem Peptides (underline):

EDGYSDASGFYCFR [169]

Peptide Source: iTRAQ, Non-small cell lung cancer

MGDVKALLFVAAAARRLGGAASESLAVSEAFRCVRSCQPKKAGPQR**CLNPVPAVPSPSPSVRK**RQVSLNWQP
 LTLQEARALLKRRRPRGPGGRGLLRRRPPQRAPAGKAPVLCPLICHNGGVCKPDRCLCPPDFAGKFCQLHSSGA
 RPPAPAVPGLTRSVYTMPLANHRDDEHGVASMSVHVHHPQEASVVVHQVERVSGPWEEADAEAVARAEAAARAE
 AAAPYTVLAQSAPREDGYSDASGFYCFRELRGGECA SPLPGLRTQEVCCRGAGLAWGVHDCQLC SERLGNSE RV
 SAPDGPCTPTGFERVNGSCEDVDECATGGRCQHGE CANTRGGYTCVCPDGFLLDSSRSSCISQHVISEAKGPCFRV
 LRDDGCSLPLLRNITKQICCCSRVKGAWGRGQLCPPFGSEGFR EICPAGPGYHYASDLRYNTRPLGQEP RVS
 LSQPRTLPATSRPSAGFLPTHRLEPRPEPRDPRPGPELPLPSIPAWTGPEIPESGPPSSGMCQRNPQVCGPGRCI
 SRPSGYTCACDSGFRLSPQGTTRCIDVDECRRVPPPCAPGRCE NSPGSFRCVCGPGFRAGPRAAECLDVDECHRV P
 PCDLGRCENTPGSFLCVCAPAGYQAAPHGASCQDVDECTQSPGLCGRGACKNLPGSFRCVCPAGFRGSACEEDVD
 ECAQEPFPCCGPGRCNDTAGSFHCACFAGFRSRGFGAPCQDVDECARSPPPCTYGRCENTEGSFQCVCPMGFQNT
 AGSECEDVDECENHLACPGQECVNSPGSFQCRTPSGHHLHRGRCTDVDECSSGAPPCGPHGHCTNTEGSRFCSC
 APGYRA?SGRPGPCADVNECLEGDFCFPHGECLNTDGSFACTCAPGYRPGPRGASCLDVDECSEEDLCQSGICTN
 TDGSFECICPPGHRAGPDLASCLDVDECREGPALCGSQRCENSPGSYRCVRDCDPGYHAGPEGTCDVDEQCQY
 GPEICGAQRCENTPGSYRCTPACDPGYQPTPGGGCQDVDECRNRSFCGAHAVCQNLPGSFQCLCDQGYEGARDGR
 HCVDVNECETLQGVCGAALCENVEGSFLCVCNPSPPEEFDPMTGRCVPPRTSAGTFPGSQPAPASVLPARPPPP
 PLPRRPSTPRQGPVGSGRRECYFDTAAPDACDNILARNVTWQECCTVGEWGS GCRIQQCPGTETA EYQSLCPH
 GRGYLA?SGDLSLRDVDECQLFRDQVCKSGVCVNTAPGYSCYCSNGYYYHTQRLECIDNDECADEEPACEGGRC
 VNTVGSYHCTCEPPLVLDGSQRRCVSNESQSLDDNLGVWQEVGADLVCSHPRLD RQATYTECCCLYGEAWGMD C
 ALCPAQDSDDFEALCNVLRPPAYSPPRPGGFGLPYEYGPDLGPPYQGLPYGPPELYPPPALPYDPYPPPPGPFARR
 EAPYGA?RFDMPDFEDDGGPYGESEAPAPPGPCTRWPYRSRDRTRSFPEPEEPPEGGSYAGSLAEPYEELEAEEC
 GTLDGCTNGRCVR**VPEGFTCR**CFDGYRLDMTRMACVDINECDEAEAAASPLCVNARCLNTDGSFRCTCRPGFAPTH
 QPHHCA?ARPR A

Mass Match Peptides (bold):

CLNPVPAVPSPSPSVRK [888]

Tandem Peptides (underline):

CLNPVPAVPSPSPSVRK [888]

OGTA076 (SEQ ID No: 12)

Peptide Source: 1D-GE, Chronic lymphocytic leukaemia

MRTGWATPRR?AGLLMLLFWFFDLAEPSSGR**AANDPFTIVHGNTGK**CIKPVYGWIVADDCDEDEDKLLWK**WVSQHR**
FHLHSQKCLGLDITKSVNELRMFSCDSSAMLLWKK**CEHHSLYGAAR**YRLALKDGHGTAISNASDVWKKGGSEESLC
DQPYHEIYTRDGNISYGRPCFPFLIDGTWHHDCILDEHSGPWCATTLNIEYDRKWGICLKPENGCEDNWEKNEQ
FGSCYQFNTQTALSWKEAYVSCQNQGADLLSINSAAELTYLKEKEGTAKIFWIGLNQLYSARGWEWSDHKPLNFL
NWDPPDRPSAPTIGGSSCARMDAESGLWQSFSCFAQLPYVCRKPLNNTVELTDVWTYSSTRCDAGWLPNNGFCYLL
VNESNSWDKAHAKCAKFSSDLISIHSLADVEVVVTKLHNEDIKEEVWIGLKNINIPTLFQWSDGTETVLTLYWDEN
EPNVFYNKTPNCVSYLGELGQWKVQSCCEEKLYVCKRKEKLNDASSDKMCPPEGWKRHGETCYKIYEDEVFPFG
TNCNLITITSR**FEQBYLNDLMKK**YDKSLR**KYFWTGRL**RDVDSCEGYNWATVGGRRRAVTFSNWNFLEPASPGGCVAM
STGKSVGKWEVKDCRSFKALSICKKMSGPLGPEEASPKPDDPCPEGWQSFPAASLSCYK**VFHAER**IVRKR**NWEEAE**
RFCQALGAHLSSFSHVDEIKEFLHFLTDQFSGQHWLWIGLNKR**SPDLQGSWQWSDRTPVSTIIMPNEFQDDYDIR**
DCAAVK**VFHRPWR****GWHFYDDREFIYLRPFACDTK**LEWVCQIPKGRTPKTPDWYNPDRAIGHGPPLIEGSEYWF
VADLHLNYYEAVLYCASNHSFLATITISFVGLKAIKNKIANSIDGQKWWIR**ISEWPIDDHFTYSRYPWHRFPVTF**
GEECLYMSAKTWLIDLGKPTDCSTKLPFICEKYNVSSLEKYSPPSAK**VQCSEQWIPFQNK**CFLKIKPVSLTFSQ
ASDTCCHSYGGTLPVLSQIEQDFITSLPDMEATLWIGLRWTAYEKINKWTDNR**ELTYSNFHPLLVSGR****IPEN**
FFEEESRYHCALILNLQKSPFTGTWNFTSCSER**HFVSLCQK**YSEVKSQTILQNASETVYLNLYKIIPKTLTWH
SAKRECLKSNMQLVSITDPYQQAFLSVQALLHNSSLWIGLFSQDDELNFGWSDGKRLHFSRWAETNGQLEDCCVVL
DTDGFWKTVDCNDNQGAICYSGNETEKEVKPVDVSKCPSVLNTPWIPFQNCYNFIIITKNRHMATTQDEVHT
KCQKLNPKSHILSIRDEKENNFVLEQLLYFNYSWVWMLGITYRNNSLMWFDK**TPLSYTHWR**AGRPTIKNEKFLA
GLSTDGFWDIQTFFKVIIEAVYFHQHSILACKIEMVDYKEEHNTTLQFMPYEDGIYSVIQKKVTWYEALNMCSQS
GGHLASVHNQNGQLFLEDIVKRDGFPLWVGLSSHDSSESSFEWSGSGSTFDYIPWKGQTSFGNVCVLLDPKGTWKHE
KCNVSKDGAICYKPTKSKKLSRLTYSSRCPAAKENGSRWIKYKGHYK**SDQALHSFSEAK**KLCSKHDSATIVSI
KDEDENKFVSRLMRENNNITMRVWLGLSQHSVDQSWSWLDGSEVTFVKWENKSKSGVGR**CSMLIASNETWKKVEC**
EHGFGRVVCKVPLGPDYTAIAIIVATLSILVLMGGLIWFLEQRHRLHLAGFSSVRYAQGVNEDEIMLPSEHD

Mass Match Peptides (bold):

AANDPFTIVHGNTGK [52]
CEHHSLYGAAR [102]
CSMLIASNETWKK [108]
EFIYLRPFACDTK [183]
ELTYSNFHPLLVSGR [208]
FCQALGAHLSSFSHVDEIK [245]
FEQBYLNDLMK [247]
FEQBYLNDLMKK [248]
FPVTFGEECLYMSAK [265]
GWHFYDDR [328]
HFVSLCQK [333]
IPENFFEEESR [385]
ISEWPIDDHFTYSR [392]
KVECEHGFGR [439]
KYFWTGRL [442]
LFHLHSQK [460]
NWEEAER [563]
SDQALHSFSEAK [623]
SPDLQGSWQWSDR [644]
TPLSYTHWR [718]
TPVSTIIMPNEFQDDYDIR [722]
VFHAER [759]
VFHRPWR [760]
VQCSEQWIPFQNK [793]
WVSQHR [838]
YFWTGRL [851]
YPWHR [866]

Tandem Peptides (underline):

ELTYSNFHPLLVSGR [208]
IPENFFEEESR [385]
SDQALHSFSEAK [623]
SPDLQGSWQWSDR [644]
TPLSYTHWR [718]

Peptide Source: 1D-GE, Colorectal cancer

MRTGWATPRRPAGLLMLLFWFFDLAEPSCGRAANDPFTIVHGNTGKCIKPVYGWIVADDCDETDKWLKWSQHRL
 FHLHSQKCLGLDITKSVNELRMFSCDSSAMLWWKCEHHSLYGAARYRLALKDGHGTAISNASDVWKKGGSEESLC
 DQPYHEIYTRDGSYGRPCFEPFLIDGTWHHDCILDEHSGPWCAITLNEYEDRKWGICLKPENGCEDNWEKNEQ
 FGSCYQFNTQTALSWKEAYVSCQNQGADLLSINSAAELTYLKEKEGIAKIFWIGLNQLYSARGWEWS DHKPLNFL
 NWDPRPSAPTIGSSCARMDAESGLWQSFSCAQLPYVCRKPLNNTVELTDVWYSDTRCDAGWLPNNGFCYLL
 VNESNSWDKAHAKCKAFSSDLISIHSLADVEVVVTKLHNEDIKEEVWIGLKNINIPTLFQWSDGTEVTLTYWDEN
 EPNVPYNTKTPNCVSYLGELGQWKVQSCEEKLYVCKRKGEKLNDASSDKMCPDDEGWKRHGETCYKIYEDEVFPG
 TNCNLITITSRFEQEYLNLDLKKYDKSLRKYFWTGLRDVDSCEYNWATVGGRRRAVTFSNWNFLEPASPGGCAM
 STGKSVGKWEVKDCRSFKALSICKKMSGPLGPEEASPKPDDPCPEGWQSFPASLSYKVFHAERIVRKRNWEEAE
 RFCQALGAHLSSFSHVDEIKEFLHFLTDQFSGQHWLWIGLNKRSPDLQGSWQWSDRTPVSTIIMPNEFQQDYDIR
 DCAAVKVFHRPWRGWHFYDDREFIYLRPFACDTKLEWVCQIPKGRTPKTPDWYNPDRAIGHGPPLIIEGSEYWF
 VADLHLNYYYEAVLYCASNHSFLATITTSFVGLKAIKNKIANISGDGQKWWIRISEWPIDDHFTYSRYPWHRFPVTF
 GEECLYMSAKTWLIDLKPTDCSTKLPFICEKYNVSSLEKYS PDSA AKVQCSEQWIPFQNKCF LKIKPVSLTFSQ
 ASDTCHSYGGTLPVLSQIEQDFITSLLPDMEATLWIGLRWTAYEKINKWTDNRELTYSNFHPLLVSGRLRIPEN
FFEEESRYHCALILNLQKSPFTGTWNFTSCSERHFVSLCQKYSEVKSRQTLQNASETVKYLNLYKIIIPKTLTWH
 SAKRECLKSNMQLVSI TDPYQQAFLSVQALLHNSSLWIGLFSQDDELNFGWSDGKRLHFSRWAETNGQLEDCVVL
 DTDGFWKTVDNDNQPAGIACYSGNETEKEVKPVDSVKCPSVLPNTWPWIPFQNCYFIITKNRHMATTQDEVHT
 KCQKLNPKSHILSIRDEKENNFVLEQLLYFNIMASWVLMGITYRNNSLMWFDKTPLSYTHWRAGRPTIKNEKFLA
 GLSTDGFWDIQTFKVIIEAVYFHQHSILACKIEMVDYKEEHNTTLPQFMPYEDGIYSVIQKVTWYEALNMCSS
 GGHLASVHNQNGQLFLEDIVKRDGFPLWVGLSSHDGSESSFEWSDGSTFDYIPWKGTSPGNCVLLDPKGTWKHE
 KCNSVKDGAICYKPTKSKKLSRLTYSSRCPAAKENGSRWIQYKGHCYKSDQALHSFSEAKKLC SKHDHSATIVSI
 KDEDENKFVSRMLRENNNITMRVWLGSLQHSVDQSWWLDGSEVTFVKWENKSKSGVGRCSMLIASNETWKVEEC
 EHGFGRVVCVPLGPDYTAIAIIVATLSILVLMGGLIWFQRRHLHLAGFSSVRYAQGVNEDEIMLPSPFHD

Mass Match Peptides (bold):

IPENFFEEESR [385]
 TPVSTIIMPNEFQQDYDIR [722]

Tandem Peptides (underline):

IPENFFEEESR [385]

Peptide Source: 1D-GE, Pancreatic cancer

MRTGWATPRRPAGLLMLLFWFFDLAEPSCGRA**AANDPFTIVHGNTGK**CIKPVYGWIVADDCDETDKWLK**WVSQHRL**
 FHLHSQKCLGLDITKSVNELRMFSCDSSAMLWWKCEHHSLYGAARYRLALK**DGHGTAISNASDVWKKGGSEESLC**
 DQPYHEIYTRDGSYGRPCFEPFLIDGTWHHDCILDEHSGPWCAITLNEYEDRKWGICLKPENGCEDNWEKNEQ
 FGSCYQFNTQTALSWKEAYVSCQNQGADLLSINSAAELTYLKEKEGIAKIFWIGLNQLYSARGWEWS DHKPLNFL
 NWDPRPSAPTIGSSCARMDAESGLWQSFSCAQLPYVCRKPLNNTVELTDVWYSDTRCDAGWLPNNGFCYLL
 VNESNSWDKAHAKCK**AFSSDLISIHSLADVEVVVTK**LHNEDIKEEVWIGLKNINIPTLFQWSDGTEVTLTYWDEN
 EPNVPYNTKTPNCVSYLGELGQWKVQSCEEKLY**YVCKRK**GEKLNDASSDKMCPDDEGWKR**RHGETCYK**IYEDEVFPG
 TNCNLITITSRFEQEYLNLDLKKYDKSLR**KYFWTGLR**DVDSCEYNWATVGGRRRAVTFSNWNFLEPASPGGCAM
 STGKSVGKWEVKDCRSFKALSICKKMSGPLGPEEASPKPDDPCPEGWQSFPASLSYKVF**HAER**IVRKRNWEEAE
 RFCQALGAHLSSFSHVDEIKEFLHFLTDQFSGQHWLWIGLNKR**SPDLQGSWQWSDR**TPVSTIIMPNEFQQDYDIR
 DCAAVK**VFHRPWR**RGWHFYDDREFIYLRPFACDTKLEWVCQIPKGRTPKTPDWYNPDRAIGHGPPLIIEGSEYWF
 VADLHLNYYYEAVLYCASNHSFLATITTSFVGLKAIKNKIANISGDGQKWWIR**ISEWPIDDHFTYSRYPWHR**FPVTF
 GEECLYMSAKTWLIDLKPTDCSTKLPFICEKYNVSSLEKYS PDSA AKVQCSEQWIPFQNKCF LKIKPVSLTFSQ
 ASDTCHSYGGTLPVLSQIEQDFITSLLPDMEATLWIGLRWTAYEKINKWTDNRELTYSNFHPLLVSGRLRIPEN
FFEEESRYHCALILNLQKSPFTGTWNFTSCSERHFVSLCQKYSEVKSRQTLQNASETVKYLNLYKIIIPKTLTWH
 SAKRECLKSNMQLVSI TDPYQQAFLSVQALLHNSSLWIGLFSQDDELNFGWSDGKRLHFSRWAETNGQLEDCVVL
 DTDGFWKTVDNDNQPAGIACYSGNETEKEVKPVDSVKCPSVLPNTWPWIPFQNCYFIITKNR**HMATTQDEVHT**
KCQKLNPKSHILSIRDEKENNFVLEQLLYFNIMASWVLMGITYRNNSLMWFDKTPLSYTHWRAGRPTIKNEKFLA
 GLSTDGFWDIQTFK**VIEEAVYFHQHSILACKIEMVDYK**EEHNTTLPQFMPYEDGIYSVIQKVTWYEALNMCSS
 GGHLASVHNQNGQLFLEDIVKRDGFPLWVGLSSHDGSESSFEWSDGSTFDYIPWKGTSPGNCVLLDPKGTWKHE
 KCNSVKDGAICYKPTKSKKLSRL**LTYSR**CPAAKENGSRWIQYKGHCYKSDQALHSFSEAKKLC SKHDHSATIVSI
 KDEDENKFVSRMLRENNNITMRVWLGSLQHSVDQSWWLDGSEVTFVKWENKSKSGVGR**CSMLIASNETWK**VEEC
 EHGFGRVVCVPLGPDYTAIAIIVATLSILVLMGGLIWFQRRHLHLAGFSSVRYAQGVNEDEIMLPSPFHD

Mass Match Peptides (bold):

AANDPFTIVHGNTGK [52]
 AFSSDLISIHSLADVEVVVTK [67]
 CSMLIASNETWKK [108]
 DGHGTAISNASDVWKK [122]
 EFIYLRPFACDTK [183]
 ELTYSNFHPLLVSGR [208]
 HMATTQDEVHTK [338]
 IEMVDYK [362]
 IPENFFEEESR [385]
 ISEWPIDDHFTYSR [392]
 KYFWTGLR [442]
 LTYSSR [499]
 RHGETCYK [604]
 SPDLQGSWQWSDR [644]
 TPLSYTHWR [718]
 VFHAER [759]
 VFHRPWR [760]
 VIEEAVYFHQHSILACK [767]
 VQCSEQWIPFQNK [793]
 WVSQHR [838]
 YFWTGLR [851]
 YPWHR [866]
 YVCKRK [875]

Tandem Peptides (underline):

ELTYSNFHPLLVSGR [208]
 IPENFFEEESR [385]
 SPDLQGSWQWSDR [644]

Peptide Source: iTRAQ, Colorectal cancer

MRTGWATPRRPAAGLLMLLFWFFDLAEPSPGRAANDPFTIVHGNTGKCIKPVYGWIVADDCEDETKLWKWVSQHRRL
 FHLHSQKCLGLDITKSVNELRMFSCDSSAMLWWKCEHHSLYGAARYR**LALK**DGHGTAISNASDVWKKGGSEESLC
 DQPYHEIYTRDGSNSYGRPCFEPFLIDGTWHHDCLDEHSGFPWCATTLNIEYDRKWGICLKPENGCEDNWEKNEQ
 FGSCYQFNTQTALSWKEAYVSCQNQGADLLSINSAAELTYLKEK**EGIAK**IFWIGLNQLYSARGWEWSCHKPLNLF
 NWDPDPRPAPTIGSSCARMDAESGLWQSFSCEAQLPYVCRKPLNNTVELTDVWVTSYSDTRCDAGWLPNNGFCYLL
 VNESNSWDKAHAKCKAFSSDLTSIHSLADVEVVVTKLHNEDIKEEVWIGLKNINIPTLFQWSDGTEVTILTYWDEN
 EPNVPYNKTPNCVSYLGELGQWKVQSCEEKLYVCKRKGEKLNDASSDKMCPDDEGWKRHGETCYKIYEDEVFPFG
 TNCNLITISRFQEYLNLDLKKYDKSLRKYFWTGLRDVDSCGEYNWATVGGRRRAVTFSNWNFLEPASPGGCVAM
 STGKSVGKWEVKDCRSFKALSICKKMSGPLGPEEASPKPDDPCPEGWQSFPASLSICYKVFHAERIVRKRNWEEAE
 RFCQALGAHLSSFSHVDEIKEFLHFLTDQFSGQHWLWIGLNKRSPDLQGSWQWSDRTPVSTIIMPNEFQQDYDIR
 DCAAVKVVFHRPWRGWHFYDDREFIYLRPFACDTKLEWVCQIPKGRTPKTPDWYNPDRAIGHGPPLIEGSEYWF
 VADLHLNIEEAVLYCASNHSFLATITISFVGLKAIKNKIANISGDGQKWWIRISEWPIDDHFTYSRYPWHRFPVTF
 GEECLYMSAKTWLIDLKPTDCSTKLFPICEKYNVSSLEKYSFSAKVQCSEQWIPFQNKCFKIKPVSLTFPSQ
 ASDTCHSYGGTLPVSLSQIEQDFITSLLPDMEATLWIGLRWTAYEKINKWTDNRELTYSNFHPLLVSGRLRIPEN
 FFEESRYHCALILNLQKSPFTGTWNFTSCSERHFVSLCQKYSEVKSQTLQNASSETVYLNLYK**IIPK**TLTWH
 SAKRECLKSNMQLVSIITDPYQAFLSVQALLHNSSLWIGLFSQDDELNFGWSDGKRLHFSRWAETNGQLEDCEVVL
 DTDGEWKTVDNDNQPAGAIYYSGNETEKEVKPVDSVKCPSVLTNPWIPFQNCYFNITKNRHMATTQDEVHT
 KCQK**LNPK**SHILSIRDEKENNFVLEQLLYFNIMASWVMLGITYRNNSLMWFDKTPLSYTHWRAGRPTIKNEKFLA
 GLSTDGFWDIQTFFKIVIEEAVYFHQHSILACKIEMVDYKEEHNTTLPQFMPYEDGIYSVIQKKVTWYEALNMCSQS
 GGHLASVHNQNGQLFLEDIVKRDGFPLWVGLSSHGDSSESEFEWSDGSTFDYIPWKGQTSFGNCVLLDPKGTWKHE
 KCNSVKDGAICYKPTKSKKLSRLTYSSRCPAAKENGSRWIQYKGHCYKSDQALHSFSEAKKLCSKHDHSATIVSI
 KDEDENKFVSRLMRENNNITMRVWLGLSQHSVDQSWSLDGEVTFVKWENKSKSGVGRCSMLIASNETWKKVEEC
 EHGFRVVCVKPLGPDYTAIAIIVATLSILVLMGGLIWLFLQHRHLHLAGFSSVRYAQGVNEDEIMLPSPFHD

Mass Match Peptides (bold):

EGIAK [898]
 IIPK [921]
 LALK [929]
 LNPK [941]

Tandem Peptides (underline):

EGIAK [898]
IIPK [921]
LALK [929]
LNPK [941]

Peptide Source: iTRAQ, Kidney cancer

MRTGWATPRRPAGLLMLLFWFFDLAEPSCGRAANDPFTIVHGNTGKCIKPVYGWIVADDCDEDEDKLWKKVWSQHRL
FHLHSQKCLGLDITKSVNELRMFSCDSSAMLWWKCEHHSYGAARYRLALKDGHGTAISNASDVWKKGGSEESLC
DQPYHEIYTRDGNISYGRPCEFPFLIDGTWHHDCILDEHSGPWCATTNLNIEYDRKWGICLKPENGCEDNWEKNEQ
FGSCYQFNTQTALSWKEAYVSCQNGADLLSINSAEELTYLKEKEGIAKIFWIGLNQLYSARGWEWSDHKPLNFL
NWDPDPRPSAPTIGGSSCARMDAESGLWQSFSCAQPLPYVCRKPLNNTVELTDVWVTSYSDTRCDAGWLPNNGFCYLL
VNESNSWDKAHAKCKAFSSDLISIHSLADVEVVTKLHNEDIKEEVWIGLKNINIPITLFQWSDGTEVTLLTYWDEN
EPNVFPYKTPNCVSYLGLGQWKVQSCEEKLYVCKRKGEKLNDASSDKMCPPEDEGWRKHGETCYKIYEDEVFPFG
TNCNLITITSRFEQEYLNLDLMKKYDKSLRKYFWTGLRDVDSCEYNWATVGGRRRAVTFSNWNFLPASPGGCVM
STGKSVGKWEVKDCRSFKALSICKKMSGPLGPPEEASPKPDDPCPEGWQSFASLSYKVFHAERIVRKRNWEEAE
RFCQALGAHLSSFSHVDEIKEFLHFLTDQFSGQHWLWIGLNKRSPDLQGSWQWSDRTPVSTIIMPNEFQQDYDIR
DCAAVKVVFHRPWRGWHFYDDREFIYLRPFACDTKLEWVCQIPKGRTPKTPDWYNPDRAIGHGPPLIEGSEYWF
VADLHLNIEEAVLYCASNHSFLATITTSFVGLKAIKNKIANISGDGQKWWIRISEWPIDDHFTYSRYPWHRFPVTF
GEECLYMSAKTWLIDLKPTDCSTKLPFICEKYNVSSELEKYSPLSAKVQCSEQWIPFQNKCFLLKIPVSLTFSQ
ASDCHSYGGTLPVSLSQIEQDFITSLLPDMEATLWIGLRWTAYEKINKWTDNRELTYSNFHPLLVSGRLRIPEN
FEEESRYHCALILNLQKSPFTGTWNFTSCSERHFVSLCQKYSEVKSRQTLQNASSETVLYLNNLYKIIPKTLTWH
SAKRECLKSNMQLVSIITDPYQQAFLSVQALLHNSSLWIGLFSQDDELNFGWSDGKRLHFSRWAEATNGQLEDCCVVL
DTDGFWKTVDNDNQGAICYSGNETEKEVKPVDSVKCPSVLPNTPWIPFQNCYNFIITKNRHMATTQDEVHT
KCQKLNPKSHILSIRDEKENNFVLEQLLYFNMAWMLGITYRNNSLMWFDKTPLSYTHWRACRPTIKNEKFLA
GLSTDGFWDIQTFFKVEEAVYFHQHSILACKIEMVDYKEEHNTTLPQFMPYEDGIYSVIQKKVTWYEALNMCSQS
GGHLASVHNQNGQLFLEDIVKRDGFPLWVGLSSHDSSESSFEWSDGSTFDYIPWKQTSFGNCVLLDPKGTWKHE
KCNVSKDGAICYKPTKSKKLSRLTYSSRCPAAKENGSRWIQYKGHCYKSDQALHFSSEAKKLCCKHDHSATIVSI
KDEENKFVSRMLMRENNITMRVWGLSLQHSVDQSWWLDGSEVTFVKWENKSKSGVGRCSMLIASNETWKKVEC
EHGEGRVVCKVPLGPDYTAIAIIVATLSILVLMGGLIWFLFQRHRLHLACGFSSVRYAQGVNDEIMLPSEFHD

Mass Match Peptides (bold):

EGIAK [898]
LALK [929]
LNPK [941]
YLNNLYK [1006]

Tandem Peptides (underline):

EGIAK [898]
LALK [929]
LNPK [941]
YLNNLYK [1006]

Peptide Source: iTRAQ, Liver cancer

MRTGWATPRRPAGLLMLLFWFFDLAEPSCGRAANDPFTIVHGNTGKCIKPVYGWIVADDCDEDEDKLWKKVWSQHRL
FHLHSQKCLGLDITKSVNELRMFSCDSSAMLWWKCEHHSYGAARYRLALKDGHGTAISNASDVWKKGGSEESLC
DQPYHEIYTRDGNISYGRPCEFPFLIDGTWHHDCILDEHSGPWCATTNLNIEYDRKWGICLKPENGCEDNWEKNEQ
FGSCYQFNTQTALSWKEAYVSCQNGADLLSINSAEELTYLKEKEGIAKIFWIGLNQLYSARGWEWSDHKPLNFL
NWDPDPRPSAPTIGGSSCARMDAESGLWQSFSCAQPLPYVCRKPLNNTVELTDVWVTSYSDTRCDAGWLPNNGFCYLL
VNESNSWDKAHAKCKAFSSDLISIHSLADVEVVTKLHNEDIKEEVWIGLKNINIPITLFQWSDGTEVTLLTYWDEN
EPNVFPYKTPNCVSYLGLGQWKVQSCEEKLYVCKRKGEKLNDASSDKMCPPEDEGWRKHGETCYKIYEDEVFPFG
TNCNLITITSRFEQEYLNLDLMKKYDKSLRKYFWTGLRDVDSCEYNWATVGGRRRAVTFSNWNFLPASPGGCVM
STGKSVGKWEVKDCRSFKALSICKKMSGPLGPPEEASPKPDDPCPEGWQSFASLSYKVFHAERIVRKRNWEEAE
RFCQALGAHLSSFSHVDEIKEFLHFLTDQFSGQHWLWIGLNKRSPDLQGSWQWSDRTPVSTIIMPNEFQQDYDIR
DCAAVKVVFHRPWRGWHFYDDREFIYLRPFACDTKLEWVCQIPKGRTPKTPDWYNPDRAIGHGPPLIEGSEYWF
VADLHLNIEEAVLYCASNHSFLATITTSFVGLKAIKNKIANISGDGQKWWIRISEWPIDDHFTYSRYPWHRFPVTF
GEECLYMSAKTWLIDLKPTDCSTKLPFICEKYNVSSELEKYSPLSAKVQCSEQWIPFQNKCFLLKIPVSLTFSQ
ASDCHSYGGTLPVSLSQIEQDFITSLLPDMEATLWIGLRWTAYEKINKWTDNRELTYSNFHPLLVSGRLRIPEN

FFEEESRYHCALILNLQKSPFTGTWNFTSCSERHFVSLCQKYSEVKSQRQTLQNASETVK~~YLNNLYK~~IIPKTLTWH
SAKRECLKSNMQLVSI TD PYQQAFLSVQALLHNSSLWIGLFSQDDELNFGWSDGKRLHFSRWAETNGQLEDCVVL
DTDGFWKTVDNDNQGAICYSGNETEKEVKPVDSVKCPSVNLTPWIPFQNCYNFIITKNRHMATQDEVHT
KCQKLNPKSHILSIRDEKENNFVLEQLLYFNMYASWVMLGITYRNNSLMWFDKTPLSYTHWRAGRPTIKNEKFLA
GLSTDGFWDIQTFFKVEEAVYFHHQSILACKIEMVDYKEEHNTTLPQFMPYEDGIYSVIQKKVTWYEALNMCSQS
GGHLASVHNQNGQLFLEDIVKRDGFPLWVGLSSHDSSESSFEWSDGSTFDYIPWKGQTS PGNCVLLDPKGTWKHE
KCNSVKDGAICYKPTKSKKLSRLTYSSRCPAAKENGSRWIQYKGHCYKSDQALHSFSEAKKLC SKHDHSATIVSI
KDEDENKFVSRMLRENNNITMRVWLGLSQHSVDQSWSWLDGSEVTFVKWENKSKSGVGRCSMLIASNETWKKVEEC
EHGFGRVVKVPLGPDYTAIAIIVATLSILVLMGLIWFLEFQRHRLHLAGFSSVRYAQGVNEDEIMLPFSFH

Mass Match Peptides (bold):

YLNNLYK [1006]

Tandem Peptides (underline):

YLNNLYK [1006]

Peptide Source: iTRAQ, Non-small cell lung cancer

MRTGWATPRRPAGLLMLLFWFFDLAEPSCGRAANDPFTIVHGNTGKCIKPVYGWIVADDDEDEDKWKVWSQHRL
FHLHSQKCLGLDITKSVNELRMFSCDSSAMLLWKKCEHHSLYGAARYR~~LALK~~DGHGTAISNASDVWKKGGSEESLC
DQFYHEIYTRDGSYGRPCFEPFLIDGTWHDHDCILDEHSGPWCATTNLNIEYDRKWGICLK PENGCEDNWEKNEQ
FGSCYQFNTQTALSWKEAYVSCQNQGADLLSINSAAELTYLKEKEGIAKIFWIGLNQLYSARGWEWS DHKPLNFL
NWD PDRPSAPTIGGSSCARMDAESGLWQSFSCEAQLPYVCRKPLNNTVELTDVWYTS DTRCDAGWLPNNGFCYLL
VNESNSWDKAHAKCKAFSSDLISIHSLADVEVVVTKLHNEDIKEEVWIGLKNINIPITLFWQSDGTEVTLTYWDEN
EPNVYPNKTPNCVSYLGELGQWKVQSCEEKLYVCKRKGEKLN DASSDKMCPPEDEGWKRHCETCYKIYEDEVFPFG
TNCNLITISRFEEQEYLNDLMKKYDKSLRKYFWTGLRDVDS CGEYNWATVGGRRRAVTF SNWNFLEPASPGGCVM
STGKSVGKWEVKDCRSFKALSICKKMSGPLGPEEASPKDDPCPEGWQSFPASLSCYKVFHAERIVRKRNWEEAE
RFCQALGAHLSSFSHVDEIKEFLHFLTDQFSGQHVLWIGLNKRSPDLQGSWQWSDRTPVSTIIMPNEFQQDYDIR
DCAAVKV FHRPWRRGWHFYDDREFIYLRPFACDTKLEWVCQIPKGRTPKTPDWYNPD RAGIHGPPLIIEGSEYWF
VADLHLNIEEAVLYCASNHSFLATITSFVGLKAIKNKIANISGDGQKWWIRISEWPIDDHFTYSRYPWHRFPVTF
GEECLYMSAKTWLIDLKPTDCSTKL PFICEKYNVSSLEKYS PDSA AKVQCSEQWIPFQNKCFKIKPVSLTFSQ
ASDTC HSYGGTLP SVLSQIEQDFITSLLPDMEATLWIGLRWTAYEKINKWTDNRELTYSNFHPLLVSGRLRIPEN
FFEEESRYHCALILNLQKSPFTGTWNFTSCSERHFVSLCQKYSEVKSQRQTLQNASETVK~~YLNNLYKIIPK~~TLTWH
SAKRECLKSNMQLVSI TD PYQQAFLSVQALLHNSSLWIGLFSQDDELNFGWSDGKRLHFSRWAETNGQLEDCVVL
DTDGFWKTVDNDNQGAICYSGNETEKEVKPVDSVKCPSVNLTPWIPFQNCYNFIITKNRHMATQDEVHT
KCQKLNPKSHILSIRDEKENNFVLEQLLYFNMYASWVMLGITYRNNSLMWFDKTPLSYTHWRAGRPTIKNEKFLA
GLSTDGFWDIQTFFKVEEAVYFHHQSILACKIEMVDYKEEHNTTLPQFMPYEDGIYSVIQKKVTWYEALNMCSQS
GGHLASVHNQNGQLFLEDIVKRDGFPLWVGLSSHDSSESSFEWSDGSTFDYIPWKGQTS PGNCVLLDPKGTWKHE
KCNSVKDGAICYKPTKSKKLSRLTYSSRCPAAKENGSRWIQYKGHCYKSDQALHSFSEAKKLC SKHDHSATIVSI
KDEDENKFVSRMLRENNNITMRVWLGLSQHSVDQSWSWLDGSEVTFVKWENKSKSGVGRCSMLIASNETWKKVEEC
EHGFGRVVKVPLGPDYTAIAIIVATLSILVLMGLIWFLEFQRHRLHLAGFSSVRYAQGVNEDEIMLPFSFH

Mass Match Peptides (bold):

IIPK [921]

LALK [929]

YLNNLYK [1006]

Tandem Peptides (underline):

IIPK [921]

LALK [929]

YLNNLYK [1006]

Peptide Source: iTRAQ, Small cell lung cancer

MRTGWATPRRPAGLLMLLFWFFDLAEPSCGRAANDPFTIVHGNTGKCIKPVYGWIVADDDEDEDKWKVWSQHRL
FHLHSQKCLGLDITKSVNELRMFSCDSSAMLLWKKCEHHSLYGAARYRLALKDGHGTAISNASDVWKKGGSEESLC
DQFYHEIYTRDGSYGRPCFEPFLIDGTWHDHDCILDEHSGPWCATTNLNIEYDRKWGICLK PENGCEDNWEKNEQ
FGSCYQFNTQTALSWKEAYVSCQNQGADLLSINSAAELTYLKEK~~EGIAK~~IFWIGLNQLYSARGWEWS DHKPLNFL
NWD PDRPSAPTIGGSSCARMDAESGLWQSFSCEAQLPYVCRKPLNNTVELTDVWYTS DTRCDAGWLPNNGFCYLL
VNESNSWDKAHAKCKAFSSDLISIHSLADVEVVVTKLHNEDIKEEVWIGLKNINIPITLFWQSDGTEVTLTYWDEN
EPNVYPNKTPNCVSYLGELGQWKVQSCEEKLYVCKRKGEKLN DASSDKMCPPEDEGWKRHCETCYKIYEDEVFPFG

TNCNLTITSRFEQYLYNDLMKKYDKSLRKYFWTGLRDVDSCEYNWATVGGRRRAVTFSNWNFLEPASPGGCVAM
STGKSVGKWEVKDCRSFKALSICKKMSGPLGPPEEASPKPDDPCPEGWQSFPASLSCYKVFHAERIVRKRNWEEAE
RFCQALGAHLSSFSHVDEIKEFLHFLTDQFSGQHWLWIGLNKRSPDLQGSWQWSDRTPVSTIIMPNEFQQDYDIR
DCAAVKVFHRPWRGWHFYDDREFIYLRPFACDTKLEWVCQIPKGRTPKTPDWYNPDRAIGHGPPLIEGSEYWF
VADLHLNYYYEAVLYCASNHSFLATITSFVGLKAIKNKIANISGDGQKWWIRISEWPIDDHFTYSRYPWHRFPVTF
GEECLYMSAKTWLIDLGKPTDCSTKLFFICEKYNVSSLEKYSPPSAKVQCSEQWIPFQNKCFCLKIKPVSLTFSQ
ASDTCHSYGGTLPVSLSQIEQDFITSLLPDMEATLWIGLRWTAYEKINKWTDNRELTYSNFHPLLVSGLRLIPEN
FFEEESRYHICALILNLQKSPFTGTWNFTSCSERHFVSLCQKYSEVKSQTQLQNASETVKYLNLYKIIPKTLTWH
SAKRECLKSNMQLVSIIDPYQQAFLSVQALLHNSSLWIGLFSQDDELNFGWSDGKRLHFSRWAETNGQLEDCCVL
DTDGFWKTVDNDNQPGAICYSGNETEKEVKPVDVSKCPSVLPNTWIPFQNCYNFIITKNRHMATTQDEVHT
KCQKLNPKSHILSIRDEKENNFVLEQLLYFNYSASWVMLGITYRNNSLMWFDKTPLSYTHWRAGRPTIKNEKFLA
GLSTDGFWDIQTFFKIVIEEAVFYHQHSILACKIEMVDYKEEHNTTLPQFMPYEDGIYSVIQKKVTWYEALNMCSQS
GGHLASVHNQNGQLFLEDIVKRDGFPPLWVGLSSHDSSEFFEWSDGSTFDYIPWKGQTSFGNCVLLDPKGTWKHE
KCNSVKDGAICYKPTKSKKLSRLTYSSRCPAAKENGSRWIQYKGHCYKSDQALHSFSEAKKLCCKHDHSATIVSI
KDEDENKFVSRLMRENNNITMRVWLGLSQHSVDQSWSLDGSSEVTFVKWENKSKSGVGRCSMLIASNETWKKVEEC
EHGFGRVVCKVPLGPDYTAIAIIVATLSILVLMGGLIWFLFQRHRLHLAGFSSVRYAQGVNEDEIMLPSFHD

Mass Match Peptides (bold):

EGIAK [898]

Tandem Peptides (underline):

EGIAK [898]

Peptide Source: iTRAQ, Ovarian cancer

MRTGWATPRRPAGLLMLLFWFFDLAEPSSGRAANDPFTTIVHGNTGKCIKPVYGWIVADDCDETDKWLKWKVSQHRL
FHLHSQKCLGLDITKSVNELRMFSCDSSAMLWKKCEHHSYGAARY**LALK**DGHGTAISNASDVWKKGGSEESLC
DQPYHEIYTRDGNYSYGRPCFEPFLIDGTWHHDICILDEHSGPWCATTNLNYYEYDRKWGICLKPENGCEDNWEKNEQ
FGSCYQFNTQTALSWKEAYVSCQNQCADLLSINSAEALTYLKEKEGIAKIFWIGLNQLYSARGWEWSHKPLNFL
NWDPDRPSAPTIGGSSCARMDAESGLWQSFSCAQLPYVCRKPLNNTVELTDVWTYSSTRCDAGWLPNNGFCYLL
VNESNSWDKAHAKCAAFSSDLISIHSLADVEVVVTKLHNEDIKEEVWIGLKNINIPTLFQWSDGTEVTILTYWDEN
EPNVFYNTKTPNCVSYLGEGLQWKVQSCCEEKLYVCKRKEKLNDASSDKMCPPEDEGWKRHGETCYKIYEDEVFPG
TNCNLTITSRFEQYLYNDLMKKYDKSLRKYFWTGLRDVDSCEYNWATVGGRRRAVTFSNWNFLEPASPGGCVAM
STGKSVGKWEVKDCRSFKALSICKKMSGPLGPPEEASPKPDDPCPEGWQSFPASLSCYKVFHAERIVRKRNWEEAE
RFCQALGAHLSSFSHVDEIKEFLHFLTDQFSGQHWLWIGLNKRSPDLQGSWQWSDRTPVSTIIMPNEFQQDYDIR
DCAAVKVFHRPWRGWHFYDDREFIYLRPFACDTKLEWVCQIPKGRTPKTPDWYNPDRAIGHGPPLIEGSEYWF
VADLHLNYYYEAVLYCASNHSFLATITSFVGLKAIKNKIANISGDGQKWWIRISEWPIDDHFTYSRYPWHRFPVTF
GEECLYMSAKTWLIDLGKPTDCSTKLFFICEKYNVSSLEKYSPPSAKVQCSEQWIPFQNKCFCLKIKPVSLTFSQ
ASDTCHSYGGTLPVSLSQIEQDFITSLLPDMEATLWIGLRWTAYEKINKWTDNRELTYSNFHPLLVSGLRLIPEN
FFEEESRYHICALILNLQKSPFTGTWNFTSCSERHFVSLCQKYSEVKSQTQLQNASETVK**YLNLYK**IIPKTLTWH
SAKRECLKSNMQLVSIIDPYQQAFLSVQALLHNSSLWIGLFSQDDELNFGWSDGKRLHFSRWAETNGQLEDCCVL
DTDGFWKTVDNDNQPGAICYSGNETEKEVKPVDVSKCPSVLPNTWIPFQNCYNFIITKNRHMATTQDEVHT
KCQKLNPKSHILSIRDEKENNFVLEQLLYFNYSASWVMLGITYRNNSLMWFDKTPLSYTHWRAGRPTIKNEKFLA
GLSTDGFWDIQTFFKIVIEEAVFYHQHSILACKIEMVDYKEEHNTTLPQFMPYEDGIYSVIQKKVTWYEALNMCSQS
GGHLASVHNQNGQLFLEDIVKRDGFPPLWVGLSSHDSSEFFEWSDGSTFDYIPWKGQTSFGNCVLLDPKGTWKHE
KCNSVKDGAICYKPTKSKKLSRLTYSSRCPAAKENGSRWIQYKGHCYKSDQALHSFSEAKKLCCKHDHSATIVSI
KDEDENKFVSRLMRENNNITMRVWLGLSQHSVDQSWSLDGSSEVTFVKWENKSKSGVGRCSMLIASNETWKKVEEC
EHGFGRVVCKVPLGPDYTAIAIIVATLSILVLMGGLIWFLFQRHRLHLAGFSSVRYAQGVNEDEIMLPSFHD

Mass Match Peptides (bold):

LALK [929]

YLNLYK [1006]

Tandem Peptides (underline):

LALK [929]

YLNLYK [1006]

OGTA085 (SEQ ID No: 13)**Peptide Source: 1D-GE, Lung cancer**

MGQPPAEAEQPGALAREFLAAMEPEPAPAPAPEEWLDILGNGLLRKKTLPVGPFGSSRPVKQGVTVHLQTSLE
 NGTRVQEEPELVFTLGDCDVIQALDLSVPLMDVGETAMVTADSKYCYGPGGRSPYIPPHAALCLEVTLK**TAVDGP**
DLEMLTGQERVALANRRKRECGNAHYQRADEVLAANSYDLAIKAITSSAKVDMTFEEEAQLQLKVKCLNNLAASQ
 LKLDHYRAALRSCSLVLEHQPDNIKALFRKGK**VLAQQGEYSEAIPIILR**AALKLEPSNKT**TIHAELSK**LVKKHAAQR
STETALYRKMLGNPSRLPAKCPGKGAWSI PWKWLFGATAVALGGVALSVVIAARN

Mass Match Peptides (bold):

KMLGNPSR [427]
 STETALYR [655]
 TAVDGPDLEMLTGQER [677]
 VLAQQGEYSEAIPIILR [773]

Tandem Peptides (underline):

TIHAELSK [700]
VLAQQGEYSEAIPIILR [773]

Peptide Source: 1D-GE, Melanoma

MGQPPAEAEQPGALAREFLAAMEPEPAPAPAPEEWLDILGNGLLRKKTLPVGPFGSSRPVKQGVTVHLQTSLE
 NGTRVQEEPELVFTLGDCDVIQALDLSVPLMDVGETAMVTADSKYCYGPGGRSPYIPPHAALCLEVTLK**TAVDGP**
DLEMLTGQERVALANRRKRECGNAHYQRADEVLAANSYDLAIKAITSSAK**VDMTFEEEAQLQLK**VKCLNNLAASQ
 LKLDHYRAALRSCSLVLEHQPDNIKALFRKGK**VLAQQGEYSEAIPIILR**AALKLEPSNKT**TIHAELSK**LVKKHAAQR
STETALYRKMLGNPSRLPAKCPGKGAWSI PWKWLFGATAVALGGVALSVVIAARN

Mass Match Peptides (bold):

ADFLAANSYDLAIK [60]
 QGVTVHLQTSLENGTR [313]
 KMLGNPSR [427]
 LDHYR [447]
 MGQPPAEAEQPGALAR [516]
 SCSLVLEHQPDNIK [620]
 STETALYR [655]
 STETALYRK [656]
 TAVDGPDLEMLTGQER [677]
 VDMTFEEEAQLQLK [748]

Tandem Peptides (underline):

TAVDGPDLEMLTGQER [677]

Peptide Source: 1D-GE, Retinoblastoma

MGQPPAEAEQPGALAREFLAAMEPEPAPAPAPEEWLDILGNGLLRKKTLPVGPFGSSRPVKQGVTVHLQTSLE
 NGTRVQEEPELVFTLGDCDVIQALDLSVPLMDVGETAMVTADSKYCYGPGGRSPYIPPHAALCLEVTLK**TAVDGP**
DLEMLTGQERVALANRRKRECGNAHYQRADEVLAANSYDLAIKAITSSAKVDMTFEEEAQLQLKVKCLNNLAASQ
 LKLDHYRAALRSCSLVLEHQPDNIKALFRKGK**VLAQQGEYSEAIPIILR**AALKLEPSNKT**TIHAELSK**LVKKHAAQR
STETALYRKMLGNPSRLPAKCPGKGAWSI PWKWLFGATAVALGGVALSVVIAARN

Mass Match Peptides (bold):

KMLGNPSR [427]
 MGQPPAEAEQPGALAR [516]
 VLAQQGEYSEAIPIILR [773]

Tandem Peptides (underline):

VLAQQGEYSEAIPIILR [773]

Peptide Source: iTRAQ, Colorectal cancer

MGQPPAEEAEQPGALAREFLAAMEPEPAPAPAPEEWLDILGNLLRKKTLVPGPPGSSRPVKGQVVTVHLQTSLE
NGTRVQEEPELVFTLGDCDVIQALDLSVPLMDVGETAMVTADSKYCYGPQGRSPYIIPPHAALCLEVTLKTAVDGP
DLEMLTGQERVALANRKRCEGNAHYQRADFVLAANSYDLAIKAITSSAKVDMTFEEEAQLQLKVKCLNNLAASQ
LKLDHYRAALRSCSLVLEHQPDNIKALFRKGKVLAAQQGEYSEATPILRAALKLEPSNKTTHAELSKLVKKHAAQR
STETALYRKMLGNPSRLPAKCPGKGAWSI PWKWLFGATAVALGGVALSVVIAARN

Mass Match Peptides (bold):

KMLGNPSR [427]

Tandem Peptides (underline):

KMLGNPSR [427]

Peptide Source: iTRAQ, Non-small cell lung cancer

MGQPPAEEAEQPGALAREFLAAMEPEPAPAPAPEEWLDILGNLLRKKTLVPGPPGSSRPVKGQVVTVHLQTSLE
NGTRVQEEPELVFTLGDCDVIQALDLSVPLMDVGETAMVTADSKYCYGPQGRSPYIIPPHAALCLEVTLKTAVDGP
DLEMLTGQERVALANRKRCEGNAHYQRADFVLAANSYDLAIKAITSSAKVDMTFEEEAQLQLKVKCLNNLAASQ
LKLDHYRAALRSCSLVLEHQPDNIKALFRKGKVLAAQQGEYSEATPILRAALKLEPSNKTTHAELSKLVKKHAAQR
STETALYRKMLGNPSRLPAKCPGKGAWSI PWKWLFGATAVALGGVALSVVIAARN

Mass Match Peptides (bold):

KMLGNPSR [427]

Tandem Peptides (underline):

KMLGNPSR [427]

OGTA087 (SEQ ID No: 14)

Peptide Source: 1D-GE, B-cell non-Hodgkin's lymphoma

MATAAYEQLKLHITPEKFYVEACDDGADDVLTIDRVSTEVTLAVKKDVPPSAVTRPIFGILGTIHLVAGNYLIVI
TKKIKVGEFFSHVWVKATDFDVLSYKKTMLHLTDIQLQDNKTFLAMLNHVLNVDGFYFSTTYDLTHTLQRLSNTS
PEFQEMSLLERADQRFVWNGHLLRELSAQPEVHRFALPVLHGFTIMHSCSINGKYFDWILISRRSCFRAGVRYV
RGIDSEGHAAANFVETEIQIVHYNGSKASFVQTRGSI PVFWSQRPNLKYKPLPQISKVANHMDGFQRHFD SQV I IYG
KQVIINLINQKGSSEKPLEQTFATMVSSSLGSGMMRYIAFDHFKECKNMRWDRLSILLDQVAEMQDELSYFLVDSAG
QVVAHQEGVFRSNCMDCLDRTNVIQSLARRSLQAQLQRLGVLVHGQKLEEQDEFEKIYKNAWADNANACAKQYA
GTGALKTDFTRTGKRTHLGLIMDGWNSMIRYYKNNFSDGFRQDSIDLFLGNYSVDELESHSPLSVPRDWKFLALP
IIMVVAFSMCIICLLMAGDTWTETLAYVLFWGVASIGTFFIILYNGKDFVDAPRLVQKEKID

Mass Match Peptides (bold):

ATDFDVLSYK [89]
FVWNGHLLR [279]
KTMLHLTDIQLQDNK [438]
LHITPEK [466]
LSNTSPEFQEMSLLER [488]
NNFSDGFR [550]
QYAGTGALK [593]
VANHMDGFQR [744]

Tandem Peptides (underline):

LGVLHVGQK [464]
NNFSDGFR [550]
QVIINLINQK [590]
YIAFDHFK [854]
YKPLPQISK [856]

Peptide Source: 1D-GE, Breast cancer

MATAAYEQKLK**LHITPEK**FYVEACDDGADDVLTIDRVSTEVTLAVKKDVPPSAVTRPIFGILGTIHLVAGNYLIVI
TKKIKVGEFFSHVVK**ATDFDVL**SYKK**TMLHL**TDIQLQDNKTF~~L~~AMLNHVLNV~~D~~GFYFSTTYDLTHTLQRLSNTS
PEFQEMSLLE~~R~~ADQRFVWNGHLL**RELSA**QPEVHRFALPVLHGFI~~T~~MHSCSINGKYFDWILISRRSCFRAGVRYV
RGIDSEGHAA~~N~~FVETE~~Q~~IVHYNGSKASFVQTRGSI~~P~~VFW~~S~~QRPNLKYKPLPQISKVANHMDGFQRHFD~~S~~QV~~I~~IYG
KQVIINLINQKGSEKPLEQTFATMVSSLGSGMMRYIAFDFHKECKNMRWDRLSILLDQVAEMQDELSYFLVDSAG
QVVANQEGVFRSNCMDCLDR**TNVIQSL**LARRSLQAQLQRLGVLHV~~G~~QKLEE~~Q~~DEFEKIYKN~~A~~WADNANACAKQYA
GTGALKTD~~F~~TRTGK~~R~~THLGLIMDGWNSMIRYYKNNFSDGFRQDSID~~L~~FLGNYSVDELESHSPLSVPRDWKFLALP
IIMVVAFSMCII~~C~~LLMAGDTWTETLAYVLF~~W~~GVASIGTFFIILYNGKDFVDAPRLVQKEKID

Mass Match Peptides (bold):ATDFDVL**SYKK** [89]FVWNGHLL**R** [279]**Tandem Peptides (underline):**TNVIQSLLAR [714]**Peptide Source: 1D-GE, Colorectal cancer**

MATAAYEQKL**LHITPEK**FYVEACDDGADDVLTIDRVSTEVTLAVKKDVPPSAVTRPIFGILGTIHLVAGNYLIVI
TKKIKVGEFFSHVVK**KATDFDVL**SYKK**TMLHL**TDIQLQDNKTF~~L~~AMLNHVLNV~~D~~GFYFSTTYDLTHTLQRLSNTS
PEFQEMSLLE~~R~~ADQRFVWNGHLL**RELSA**QPEVHRFALPVLHGFI~~T~~MHSCSINGKYFDWILISRRSCFRAGVRYV
RGIDSEGHAA~~N~~FVETE~~Q~~IVHYNGSKASFVQTRGSI~~P~~VFW~~S~~QRPNLKYKPLPQISKVANHMDGFQRHFD~~S~~QV~~I~~IYG
KQVIINLINQKGSEKPLEQTFATMVSSLGSGMMRYIAFDFHKECKNMRWDRLSILLDQVAEMQDELSYFLVDSAG
QVVANQEGVFRSNCMDCLDR**TNVIQSL**LARRSLQAQLQRLGVLHV~~G~~QKLEE~~Q~~DEFEKIYKN~~A~~WADNANACAKQYA
GTGALKTD~~F~~TRTGK~~R~~THLGLIMDGWNSMIRYYKNNFSDGFRQDSID~~L~~FLGNYSVDELESHSPLSVPRDWKFLALP
IIMVVAFSMCII~~C~~LLMAGDTWTETLAYVLF~~W~~GVASIGTFFIILYNGKDFVDAPRLVQKEKID

Mass Match Peptides (bold):LHIT**PEK** [466]**Tandem Peptides (underline):**YIAFDFH**K** [854]**Peptide Source: 1D-GE, Gastric cancer**

MATAAYEQKLK**LHITPEK**FYVEACDDGADDVLTIDRVSTEVTLAVKKDVPPSAVTRPIFGILGTIHLVAGNYLIVI
TKKIKVGEFFSHVVK**KATDFDVL**SYKK**TMLHL**TDIQLQDNKTF~~L~~AMLNHVLNV~~D~~GFYFSTTYDLTHTLQRLSNTS
PEFQEMSLLE~~R~~ADQRFVWNGHLL**RELSA**QPEVHRFALPVLHGFI~~T~~MHSCSINGKYFDWILISRRSCFRAGVRYV
RGIDSEGHAA~~N~~FVETE~~Q~~IVHYNGSKASFVQTRGSI~~P~~VFW~~S~~QRPNLKYKPLPQISKVANHMDGFQRHFD~~S~~QV~~I~~IYG
KQVIINLINQKGSEKPLEQTFATMVSSLGSGMMRYIAFDFHKECKNMRWDRLSILLDQVAEMQDELSYFLVDSAG
QVVANQEGVFRSNCMDCLDR**TNVIQSL**LARRSLQAQLQRLGVLHV~~G~~QKLEE~~Q~~DEFEKIYKN~~A~~WADNANACAKQYA
GTGALKTD~~F~~TRTGK~~R~~THLGLIMDGWNSMIRYYKNNFSDGFRQDSID~~L~~FLGNYSVDELESHSPLSVPRDWKFLALP
IIMVVAFSMCII~~C~~LLMAGDTWTETLAYVLF~~W~~GVASIGTFFIILYNGKDFVDAPRLVQKEKID

Mass Match Peptides (bold):**Tandem Peptides (underline):**TNVIQSLLAR [714]**Peptide Source: 1D-GE, Lung cancer**

MATAAYEQKL**LHITPEK**FYVEACDDGADDVLTIDRV**STEVTLAVK**DVPPSAVTRPIFGILGTIHLVAGNYLIVI
TKKIKVGEFFSHVVK**ATDFDVL**SYKK**TMLHL**TDIQLQDNKTF~~L~~AMLNHVLNV~~D~~GFYFSTTYDLTHTLQRLSNTS
PEFQEMSLLERADQRFVWNGHLL**RELSA**QPEVHRFALPVLHGFI~~T~~MHSCSINGKYFDWILISRRSCFRAGVRYV
RGIDSEGHAA~~N~~FVETE~~Q~~IVHYNGSKASFVQTRGSI~~P~~VFW~~S~~QRPNLKYKPLPQISKVANHMDGFQRHFD~~S~~QV~~I~~IYG

KQVIINLINQKGSEKPLEQTFATMVSSLGSGMMRYIAFD~~FK~~ECKNMRWDRLSILLDQVAEMQDELSYFLVDSAG
QVVANQEGVFRSNCMDCLDRNTNVIQSLLARRSLQAQLQRLGVLHVGGKLEEQDEFEKIYKNWADNANACAKQYA
GTGALKTDFTRTGKRTHLGLIMDGWNSMIRYYKNNFSDGFRQDSIDLFLGNYSVDELESHSPLSVPRDWKFLALP
IIMVVAFSMCIICLLMAGDTWTETLAYVLFWGVASIGTFFIILYNGKDFVDAPRLVQKEKID

Mass Match Peptides (bold):

GSEKPLEQTFATMVSSLGSGMMR [314]
HFDSQVLIYVK [332]
LHITPEK [466]
LSNTSPEFQEMSLER [488]
NNFSDGFR [550]
QYAGTGALK [593]
RTHLGLIMDGWNSMIR [615]
THLGLIMDGWNSMIR [696]
VANHMDGFQR [744]
VSTEVTIAVK [797]
YFDWILISR [848]
YFDWILISRR [849]
YIAFD~~FK~~ [854]

Tandem Peptides (underline):

ATDFDVLSYK [88]
LEEQDEFEK [453]
NNFSDGFR [550]
TNVIQSLLAR [714]
YIAFD~~FK~~ [854]
YKPLPQISK [856]

Peptide Source: 1D-GE, Lymphoid leukaemia, unspecified

MATAAYEQLKLHITPEKIFYVEACDDGADDVLTIDRVSTEVTLAVKKDVPPSAVTRPIFGILGTIHLVAGNYLIVI
TKKIKVGEEFFSHVWVKATDFDVLSYKKTMLHLTDIQLQDNKTFLAMLNHVLNVDDGYFSTTYDLTHTLQRLSNTS
PEFQEMSLERADQRFVWNGHLLRELSAQPEVHRFALPVLEGFTIMHSCSINGKYFDWILISRRSCFRAGVRYV
RGIDSEGHAAANFVETEQIVHYNGSKASFVQTRGSIPVFSQRPNLKYKPLPQISKVANHMDGFQRHFDSQVLIYK
KQVIINLINQKGSEKPLEQTFATMVSSLGSGMMRYIAFD~~FK~~ECKNMRWDRLSILLDQVAEMQDELSYFLVDSAG
QVVANQEGVFRSNCMDCLDRNTNVIQSLLARRSLQAQLQRLGVLHVGGKLEEQDEFEKIYKNWADNANACAKQYA
GTGALKTDFTRTGKRTHLGLIMDGWNSMIRYYKNNFSDGFRQDSIDLFLGNYSVDELESHSPLSVPRDWKFLALP
IIMVVAFSMCIICLLMAGDTWTETLAYVLFWGVASIGTFFIILYNGKDFVDAPRLVQKEKID

Mass Match Peptides (bold):

LSNTSPEFQEMSLER [488]
NNFSDGFR [550]
THLGLIMDGWNSMIR [696]

Tandem Peptides (underline):

NNFSDGFR [550]
TNVIQSLLAR [714]
YKPLPQISK [856]

Peptide Source: 1D-GE, Ovarian cancer

MATAAYEQLKLHITPEKIFYVEACDDGADDVLTIDRVSTEVTLAVKKDVPPSAVTRPIFGILGTIHLVAGNYLIVI
TKKIKVGEEFFSHVWVKATDFDVLSYKKTMLHLTDIQLQDNKTFLAMLNHVLNVDDGYFSTTYDLTHTLQRLSNTS
PEFQEMSLERADQRFVWNGHLLRELSAQPEVHRFALPVLEGFTIMHSCSINGKYFDWILISRRSCFRAGVRYV
RGIDSEGHAAANFVETEQIVHYNGSKASFVQTRGSIPVFSQRPNLKYKPLPQISKVANHMDGFQRHFDSQVLIYK
KQVIINLINQKGSEKPLEQTFATMVSSLGSGMMRYIAFD~~FK~~ECKNMRWDRLSILLDQVAEMQDELSYFLVDSAG
QVVANQEGVFRSNCMDCLDRNTNVIQSLLARRSLQAQLQRLGVLHVGGKLEEQDEFEKIYKNWADNANACAKQYA
GTGALKTDFTRTGKRTHLGLIMDGWNSMIRYYKNNFSDGFRQDSIDLFLGNYSVDELESHSPLSVPRDWKFLALP
IIMVVAFSMCIICLLMAGDTWTETLAYVLFWGVASIGTFFIILYNGKDFVDAPRLVQKEKID

Mass Match Peptides (bold):

ATDFDVLSYKK [89]
FVWNGHLLR [279]
GSIPVFWSQRPNLK [316]
KTMHLHTDIQLQDNK [438]
RTHLGLIMDGWNSMIR [615]
TMLHLTDIQLQDNK [707]

Tandem Peptides (underline):

HFDSQVIYGYK [332]
LEEQDEFEK [453]

OGTA088 (SEQ ID No: 15)**Peptide Source: 1D-GE, Breast cancer**

MSDFDSNPFADPDLNNPFK**DPSVTQVTRNVPPGLDEYNPFSDSR**TPPPGGVKMPNVNTQPAIMKPTEEHPAYTQ
IAKE**HALAQAEELKRQEELER**KAAELDRRER**EMQNLSQHGR**KNNWPPLPSNFPVGPFCFYQDFSVDIPVEFQKTVK
LMYYLWMFHAVTLFLNIFGCLAWFCVDSARAVDFGLSILWFLFTPCSFVCWYRPLYGAFRSDSSFRFFVFFVY
ICQFAVHVLQAAGFHNWGNCGWISSLTGLNQNI PVGIMMIIIAALFTASAVISLVMFKKVHGLYRTTGASFEKAQ
QEFATGVMSNKT VQTAAANAATAASSAAQNAFKGNQI

Mass Match Peptides (bold):

DPSVTQVTR [149]
EMQNLSQHGR [211]
NVPPGLDEYNPFSDSR [560]
RQEELER [612]

Tandem Peptides (underline):

DPSVTQVTR [149]
EHALAQAEELK [190]
NVPPGLDEYNPFSDSR [560]

Peptide Source: 1D-GE, Gastric cancer

MSDFDSNPFADPDLNNPFK**DPSVTQVTRNVPPGLDEYNPFSDSR**TPPPGGVKMPNVNTQPAIMKPTEEHPAYTQ
IAKE**HALAQAEELKRQEELER**KAAELDRRER**EMQNLSQHGR**KNNWPPLPSNFPVGPFCFYQDFSVDIPVEFQKTVK
LMYYLWMFHAVTLFLNIFGCLAWFCVDSARAVDFGLSILWFLFTPCSFVCWYRPLYGAFRSDSSFRFFVFFVY
ICQFAVHVLQAAGFHNWGNCGWISSLTGLNQNI PVGIMMIIIAALFTASAVISLVMFKKVHGLYRTTGASFEKAQ
QEFATGVMSNKT VQTAAANAATAASSAAQNAFKGNQI

Mass Match Peptides (bold):

EMQNLSQHGR [211]

Tandem Peptides (underline):

EHALAQAEELK [190]

Peptide Source: 1D-GE, Glioblastoma

MSDFDSNPFADPDLNNPFK**DPSVTQVTRNVPPGLDEYNPFSDSR**TPPPGGVKMPNVNTQPAIMKPTEEHPAYTQ
IAKEHALAQAEELKRQEELERKAAELDRREREMQNLSQHGRKNNWPPLPSNFPVGPFCFYQDFSVDIPVEFQKTVK
LMYYLWMFHAVTLFLNIFGCLAWFCVDSARAVDFGLSILWFLFTPCSFVCWYRPLYGAFRSDSSFRFFVFFVY
ICQFAVHVLQAAGFHNWGNCGWISSLTGLNQNI PVGIMMIIIAALFTASAVISLVMFKK**VHGLYR**TTGASFEK**AO**
QEFATGVMSNKT VQTAAANAATAASSAAQNAFKGNQI

Mass Match Peptides (bold):

AQQEFATGVMSNK [84]
EHALAQAECLK [190]
EMQNLSQHGR [211]
KAAELDR [405]
MPNVNTQPAIMKPTEEHPAYTQIAK [522]
NVPPGLDEYNPFSDSR [560]
QEELER [566]
RQEELER [612]
TPPPGGVK [721]
TVQTAAANAASTAASSAAQNAFK [737]
VHGLYR [766]

Tandem Peptides (underline):

EHALAQAECLK [190]
NVPPGLDEYNPFSDSR [560]
TVQTAAANAASTAASSAAQNAFK [737]

Peptide Source: 1D-GE, Hepatocellular carcinoma

MSDFDSNPFADPDLNNPFKDPSVTQVTRNVPPGLDEYNPFSDSRTPPPGGVKMPNVNTQPAIMKPTEEHPAYTQ
TAKEHALAQAECLKRQEELERKAAELDRREREMQNLSQHGRKKNNWPLPSNFPVGPFCFYQDFSVDPVEFQKTVK
LMYYLWMFHAVTILFLNIFGCLAWFCVDSARAVDFGLSILWFLLFTPCSFVCWYRPLYGAFRSDSSFRFFVFFVY
ICQFAVHVLQAAGFHNWGNCGWISSLTGLNQNPVGGIMMIIAALFTASAVISLVMFKKVHGLYRITGASFEKAQ
QEFATGVMSNKTVQTAAANAASTAASSAAQNAFKGNQI

Mass Match Peptides (bold):

DPSVTQVTR [149]
EHALAQAECLK [190]
EMQNLSQHGR [211]
EMQNLSQHGRK [212]
KAAELDRR [406]
MPNVNTQPAIMKPTEEHPAYTQIAK [522]
NVPPGLDEYNPFSDSR [560]
QEELER [612]
RQEELERK [613]

Tandem Peptides (underline):

EHALAQAECLK [190]
NVPPGLDEYNPFSDSR [560]

Peptide Source: 1D-GE, Lung cancer

MSDFDSNPFADPDLNNPFKDPSVTQVTRNVPPGLDEYNPFSDSRTPPPGGVKMPNVNTQPAIMKPTEEHPAYTQ
TAKEHALAQAECLKRQEELERKAAELDRREREMQNLSQHGRKKNNWPLPSNFPVGPFCFYQDFSVDPVEFQKTVK
LMYYLWMFHAVTILFLNIFGCLAWFCVDSARAVDFGLSILWFLLFTPCSFVCWYRPLYGAFRSDSSFRFFVFFVY
ICQFAVHVLQAAGFHNWGNCGWISSLTGLNQNPVGGIMMIIAALFTASAVISLVMFKKVHGLYRITGASFEKAQ
QEFATGVMSNKTVQTAAANAASTAASSAAQNAFKGNQI

Mass Match Peptides (bold):

AQQEFATGVMSNK [84]
EMQNLSQHGR [211]
KVHGLYR [441]
MPNVNTQPAIMKPTEEHPAYTQIAK [522]
NVPPGLDEYNPFSDSR [560]
QEELER [566]
RQEELER [612]
TPPPGGVK [721]

TVQTAAANAASTAASSAAQNAFK [737]

Tandem Peptides (underline):

EHALAQAE LLK [190]

NVPPGLDEYNPFSDSR [560]

Peptide Source: 1D-GE, Lymphoid leukaemia, unspecified

MSDFDSNPFADPD LNNPFKDP SVTQVTR NVPPGLDEYNPFSDSR T P P P G G V K M P N V P N T Q P A I M K P T E E H P A Y T Q
I A K E EHALAQAE LLK R Q E E L E R K A A E L D R R E R EMQNLSQHGR K N N W P P L P S N F P V G P C F Y Q D F S V D I P V E F Q K T V K
L M Y Y L W M F H A V T L F L N I F G C L A W F C V D S A R A V D F G L S I L W F L L F T P C S F V C W Y R P L Y G A F R S D S S F R F F V F F F V Y
I C Q F A V H V L Q A A G F H N W G N C G W I S S L T G L N Q N I P V G I M M I I I A A L F T A S A V I S L V M F K K V H G L Y R T T G A S F E K A Q
Q E F A T G V M S N K T V Q T A A A N A A S T A A S S A A Q N A F K G N Q I

Mass Match Peptides (bold):

EMQNLSQHGR [211]

NVPPGLDEYNPFSDSR [560]

Tandem Peptides (underline):

EHALAQAE LLK [190]

Peptide Source: 1D-GE, Pancreatic cancer

MSDFDSNPFADPD LNNPFK DPSVTQVTRNVPPGLDEYNPFSDSR T P P P G G V K M P N V P N T Q P A I M K P T E E H P A Y T Q
I A K E EHALAQAE LLK R Q E E L E R K A A E L D R R E R EMQNLSQHGR K N N W P P L P S N F P V G P C F Y Q D F S V D I P V E F Q K T V K
L M Y Y L W M F H A V T L F L N I F G C L A W F C V D S A R A V D F G L S I L W F L L F T P C S F V C W Y R P L Y G A F R S D S S F R F F V F F F V Y
I C Q F A V H V L Q A A G F H N W G N C G W I S S L T G L N Q N I P V G I M M I I I A A L F T A S A V I S L V M F K KVHGLYR T T G A S F E K A Q
Q E F A T G V M S N K TVQTAAANAASTAASSAAQNAFK G N Q I

Mass Match Peptides (bold):

DPSVTQVTR [149]

EMQNLSQHGR [211]

KAAELDRR [406]

KVHGLYR [441]

NVPPGLDEYNPFSDSR [560]

RQEELER [612]

TVQTAAANAASTAASSAAQNAFK [737]

Tandem Peptides (underline):

DPSVTQVTR [149]

EHALAQAE LLK [190]

EMQNLSQHGR [211]

NVPPGLDEYNPFSDSR [560]

Peptide Source: 1D-GE, Renal cell cancer

MSDFDSNPFADPD LNNPFKDP SVTQVTR NVPPGLDEYNPFSDSR T P P P G G V K M P N V P N T Q P A I M K P T E E H P A Y T Q
I A K E EHALAQAE LLK R Q E E L E R K A A E L D R R E R EMQNLSQHGR K N N W P P L P S N F P V G P C F Y Q D F S V D I P V E F Q K T V K
L M Y Y L W M F H A V T L F L N I F G C L A W F C V D S A R A V D F G L S I L W F L L F T P C S F V C W Y R P L Y G A F R S D S S F R F F V F F F V Y
I C Q F A V H V L Q A A G F H N W G N C G W I S S L T G L N Q N I P V G I M M I I I A A L F T A S A V I S L V M F K KVHGLYR T T G A S F E K A Q
Q E F A T G V M S N K T V Q T A A A N A A S T A A S S A A Q N A F K G N Q I

Mass Match Peptides (bold):

EMQNLSQHGR [211]

KVHGLYR [441]

NVPPGLDEYNPFSDSR [560]

Tandem Peptides (underline):

EHALAQAELLK [190]
NVPPGLDEYNPFSDSR [560]

Peptide Source: 1D-GE, Retinoblastoma

MSDFDSNPFADPDLNNPFKDPSTQVTRNVPPGLDEYNPFSDSRTPPPGGVKMPNVPNTQPAIMKPTEEHPAYTQ
IAKEHALAQAELLK**RQEELER**KAAELDRREREMQNLSQHGRKNNWPPLPSNFPVGPFCFYQDFSVDIPVEFQKTVK
LMYLWFMFHAVTLFLNIFGCLAWFCVDSARAVDFGLSILWFLFTPCSFVCWYRPLYGAFRSDSSFRFFVFFVY
ICQFAVHVLQAAGFHNWGNCGWISSLTGLNQNI PVGIMMIIAALFTASAVISLVMFKK**VHGLYR**TTGASFEKAQ
QEFATGVMSNKT**TVQTAAANAATAASSAAQNAFK**GNQI

Mass Match Peptides (bold):

EHALAQAELLK [190]
EMQNLSQHGR [211]
NVPPGLDEYNPFSDSR [560]
RQEELER [612]
TVQTAAANAATAASSAAQNAFK [737]
VHGLYR [766]

Tandem Peptides (underline):

EHALAQAELLK [190]
NVPPGLDEYNPFSDSR [560]

Peptide Source: iTRAQ, Colorectal cancer

MSDFDSNPFADPDLNNPFKDPSTQVTRNVPPGLDEYNPFSDSRTPPPGGVKMPNVPNTQPAIMKPTEEHPAYTQ
IAKEHALAQAELLK**RQEELER**KAAELDRREREMQNLSQHGRKNNWPPLPSNFPVGPFCFYQDFSVDIPVEFQKTVK
LMYLWFMFHAVTLFLNIFGCLAWFCVDSARAVDFGLSILWFLFTPCSFVCWYRPLYGAFRSDSSFRFFVFFVY
ICQFAVHVLQAAGFHNWGNCGWISSLTGLNQNI PVGIMMIIAALFTASAVISLVMFKKVHGLYRTTGASFEKAQ
QEFATGVMSNKT**TVQTAAANAATAASSAAQNAFK**GNQI

Mass Match Peptides (bold):

RQEELERK [613]

Tandem Peptides (underline):

RQEELERK [613]

Peptide Source: iTRAQ, Non-small cell lung cancer

MSDFDSNPFADPDLNNPFKDPSTQVTRNVPPGLDEYNPFSDSRTPPPGGVKMPNVPNTQPAIMKPTEEHPAYTQ
IAKEHALAQAELLK**RQEELER**KAAELDRREREMQNLSQHGRKNNWPPLPSNFPVGPFCFYQDFSVDIPVEFQKTVK
LMYLWFMFHAVTLFLNIFGCLAWFCVDSARAVDFGLSILWFLFTPCSFVCWYRPLYGAFRSDSSFRFFVFFVY
ICQFAVHVLQAAGFHNWGNCGWISSLTGLNQNI PVGIMMIIAALFTASAVISLVMFKKVHGLYRTTGASFEKAQ
QEFATGVMSNKT**TVQTAAANAATAASSAAQNAFK**GNQI

Mass Match Peptides (bold):

RQEELERK [613]

Tandem Peptides (underline):

RQEELERK [613]

OGTA089 (SEQ ID No: 16)

Peptide Source: 1D-GE, Breast cancer

MEKRLGVKPNPASWILSGYYWQTSAKWLRSLYLFYTCFCFSVLWLSTDASESRCQQGKTQFGVGLRSGGENHLWL
 LEGTPSLQSCWAACQDSACHVFWWLEGMCIQADCSRPOQSCRAFRTHSSNSMLVFLKKFQTADDLGFLPEDDVPH
 LLGLGWNWASWRQSPRAALRPVSSSDQQLIRKLQKRGSFSDVVTPIVTQHSKVNDSELGGLTSSGSAEVHK
 AITISSPLTTDLTAELSGGPKNVSVQPEISEGLATTPSTQQVKSSEKTOIAPVQPVAPSYATPTPQASFQSTS
 APYPVikelVVSAGESVQITLTPKNEVQLNAYVLQEPPEKGETYTYDWQLITHPRDYSGEMEGKHSQILKLSKLTGP
 LYEFKVIVEGQNAHGEgyVNVTVKPEPRKNNRPPAIVSPQFQEISLPTTSTVIDGSQSTDDDKIVQYHWEELKGP
 LREEKISEDTAILKLSKLVPGNYTFSLTVVDSGATNSTTANLTVNKAVDYPPVANAGPNQVITLQNSTITLFGN
 QSTDHGHITSYEWLSLSPSSKKGKVVEMQGVRTPTQLSAMQEGDYTYQLTVTDTIGQQATAQVTVIVQPENNKPPQ
 ADAGPDKELTLPVDSTTLTGSKSSDDQKIISYLWEKTQGPDPGVQLENANSSVATVTGLQVGTYYVFTLTVKDERNL
 QSQSSVNVIVKKEEINKPPIAKITGNVITLPTSTAELDGSKSSDDKGIVSYLWTRDEGSPAAGEVLNHSDDHHPIL
 FLNLVEGTYTFHLKVTDAKGESDTRTTVEVKPDPRKNNLVEIILDINVSQTERLKGMFIRQIGVLLGLVLDSD
 IIVQKIQPYTEQSTKMVFFVQNEPPHQIFKGHEVAAMLKSELRKQKADFLIFRALEVNTVTCQLNCSDDHGHCDSE
 TKRCICDPFWMENFIKVLQRDGDSNCALTILIFLAWSVLYVIIATFVIVVALGILSWTVICCCKRQKQKPKRKS
 KYKILDATDQESLELKPTSRAIKQKGLLLSSSLMHSESELDSDDAIFTWPDREKGLLHGQNGSVPNGQTPLKA
 RSPREEIL

Mass Match Peptides (bold):

ADFLIFR [59]
 ELTLPVDSTTLTGSK [207]
 GETYTYDWQLITHPR [293]
 VVEMQGV [809]

Tandem Peptides (underline):

EEINKPPIAK [176]

Peptide Source: 1D-GE, Lung cancer

MEKRLGVKPNPASWILSGYYWQTSAKWLRSLYLFYTCFCFSVLWLSTDASESRCQQGKTQFGVGLRSGGENHLWL
 LEGTPSLQSCWAACQDSACHVFWWLEGMCIQADCSRPOQSCRAFRTHSSNSMLVFLKKFQTADDLGFLPEDDVPH
 LLGLGWNWASWRQSPRAALRPVSSSDQQLIRKLQKRGSFSDVVTPIVTQHSKVNDSELGGLTSSGSAEVHK
 AITISSPLTTDLTAELSGGPKNVSVQPEISEGLATTPSTQQVKSSEKTOIAPVQPVAPSYATPTPQASFQSTS
 APYPVikelVVSAGESVQITLTPKNEVQLNAYVLQEPPEKGETYTYDWQLITHPRDYSGEMEGKHSQILKLSKLTGP
 LYEFKVIVEGQNAHGEgyVNVTVKPEPRKNNRPPAIVSPQFQEISLPTTSTVIDGSQSTDDDKIVQYHWEELKGP
 LREEKISEDTAILKLSKLVPGNYTFSLTVVDSGATNSTTANLTVNKAVDYPPVANAGPNQVITLQNSTITLFGN
 QSTDHGHITSYEWLSLSPSSKKGKVVEMQGVRTPTQLSAMQEGDYTYQLTVTDTIGQQATAQVTVIVQPENNKPPQ
 ADAGPDKELTLPVDSTTLTGSKSSDDQKIISYLWEKTQGPDPGVQLENANSSVATVTGLQVGTYYVFTLTVKDERNL
 QSQSSVNVIVKKEEINKPPIAKITGNVITLPTSTAELDGSKSSDDKGIVSYLWTRDEGSPAAGEVLNHSDDHHPIL
 FLNLVEGTYTFHLKVTDAKGESDTRTTVEVKPDPRKNNLVEIILDINVSQTERLKGMFIRQIGVLLGLVLDSD
 IIVQKIQPYTEQSTKMVFFVQNEPPHQIFKGHEVAAMLKSELRKQKADFLIFRALEVNTVTCQLNCSDDHGHCDSE
 TKRCICDPFWMENFIKVLQRDGDSNCALTILIFLAWSVLYVIIATFVIVVALGILSWTVICCCKRQKQKPKRKS
 KYKILDATDQESLELKPTSRAIKQKGLLLSSSLMHSESELDSDDAIFTWPDREKGLLHGQNGSVPNGQTPLKA
 RSPREEIL

Mass Match Peptides (bold):

GETYTYDWQLITHPR [293]
 VNDSELGGLTSSGSAEVHK [786]

Tandem Peptides (underline):

IQPYTEQSTK [391]

Peptide Source: 1D-GE, Ovarian cancer

MEKRLGVKPNPASWILSGYYWQTSAKWLRSLYLFYTCFCFSVLWLSTDASESRCQQGKTQFGVGLRSGGENHLWL
 LEGTPSLQSCWAACQDSACHVFWWLEGMCIQADCSRPOQSCRAFRTHSSNSMLVFLKKFQTADDLGFLPEDDVPH
 LLGLGWNWASWRQSPRAALRPVSSSDQQLIRKLQKRGSFSDVVTPIVTQHSKVNDSELGGLTSSGSAEVHK
 AITISSPLTTDLTAELSGGPKNVSVQPEISEGLATTPSTQQVKSSEKTOIAPVQPVAPSYATPTPQASFQSTS
 APYPVikelVVSAGESVQITLTPKNEVQLNAYVLQEPPEKGETYTYDWQLITHPRDYSGEMEGKHSQILKLSKLTGP

LYEYFKVIVEGQNAHGEGYVNVTVKPEPRKNRPPIAIVSPQFQEISLPTTSTVIDGSQSTDDDKIVQYHWEELKGP
LREEKISEDTAILKLSKLVPGNYTFSLTVVDSGATNSTTANLTVNKAVDYPPVANAGPNQVITLPQNSITLFGN
QSTDDHGITSYEWLSLSPSSKGKVVEMQGVRTPTLQLSAMQEGDYTYQLTVTDTIGQQATAQVTVIVQPENNKPPQ
ADAGPDKELTLPVDSTTLDGSKSSDDQKIISYLWEKTQGPBGVQLENANSSVATVTGLQVGTYYVFTLTVKDERNL
QSQSSVNVIVKEEINKPPIAKITGNVITLPTSTAELDGSKSSDDKGIVSYLWTRDEGSPAAGEVLNHSDDHHPIL
FLSNLVEGTYTFHLKVTDAGESDTRTVEVKPDPRKNNLVEIILDINVSQTERLKGMFIRQIGVLLGVLDSD
IIVQK**IQPYTEQSTKMVFVQNEPPHQIFK**GHEVAAMLKSELRKQK**ADFLIFR**ALEVNTVTCQLNCSDHGHCDSD
TKRCICDPFWMENFIKVQLRDGDSNCALTILIFLAEWSVLYVIIATFVIVVALGILSWTVICCCRQKQKPKRKS
KYK**ILDATDQESLELKPTSR**AGIKQKGLLLSSSLMHSESELDSDDAIFTWPDREKGLLHGQNGSVPNGQTPPLKA
RSPREEIL

Mass Match Peptides (bold):

ADFLIFR [59]
GETYTYDWQLITHPR [293]
ILDATDQESLELKPTSR [374]
IQPYTEQSTK [391]
LTPGLYEFK [497]
MVFFVQNEPPHQIFK [528]
NVSQPEISEGLATTPSTQQVK [562]
THSSNSMLVFLK [699]

Tandem Peptides (underline):

EEINKPPIAK [176]
NLQSQSSVNVIVK [544]

Peptide Source: iTRAQ, Non-small cell lung cancer

MEKRLGVKPNPASWILSGYYWQTSAKWLRSLYLFYTCFCFSVLWLSTDASESRCQQGKTQFGVGLRSGGENHLWL
LEGTPSLQSCWAACQDSACHVFWWLEGMCIQADCSRPOSCRAFRTTHSSNSMLVFLKKFQTADDLGLFLPEDDVPH
LLGLGWNWASWRQSPPRALRPVSSSDQQLIRKLQKRGSPSDVVTPIVTQHSKVNDNELGGLTSSGSAEVHK
AITISSPLTTDLTAELSGGPKNVSVQPEISEGLATTPSTQQVKSSEKTQIAVPQPVAPSYSYATPTPQASQSTS
A?YPVIKELVVSAGESVQITLPKNEVQLNAYVLQEPKGETYTYDWQLITHPRDYSGEMEGKHSQILKLSKLTFG
LYEFKVVIVEGQNAHGEGYVNVTVKPEPRKNRPPIAIVSPQFQEISLPTTSTVIDGSQSTDDDKIVQYHWEELKGP
LREEKISEDTAILKLSKLVPGNYTFSLTVVDSGATNSTTANLTVNKAVDYPPVANAGPNQVITLPQNSITLFGN
QSTDDHGITSYEWLSLSPSSKGKVVEMQGVRTPTLQLSAMQEGDYTYQLTVTDTIGQQATAQVTVIVQPENNKPPQ
ADAGPDKELTLPVDSTTLDGSKSSDDQKIISYLWEKTQGPBGVQLENANSSVATVTGLQVGTYYVFTLTVKDERNL
QSQSSVNVIVKEEINKPPIAKITGNVITLPTSTAELDGSKSSDDKGIVSYLWTRDEGSPAAGEVLNHSDDHHPIL
FLSNLVEGTYTFHLKVTDAGESDTRTVEVKPDPRKNNLVEIILDINVSQTERLKGMFIRQIGVLLGVLDSD
IIVQK**IQPYTEQSTKMVFVQNEPPHQIFK**GHEVAAMLKSELRKQK**ADFLIFR**ALEVNTVTCQLNCSDHGHCDSD
TKRCICDPFWMENFIKVQLRDGDSNCALTILIFLAEWSVLYVIIATFVIVVALGILSWTVICCCRQKQKPKRKS
KYKILDATDQESLELKPTSRAGIKQKGLLLSSSLMHSESELDSDDAIFTWPDREKGL**LLHGQNGSVPNGQTPPLKA**
RSPREEIL

Mass Match Peptides (bold):

LLHGQNGSVPNGQTPLK [935]

Tandem Peptides (underline):

LLHGQNGSVPNGQTPLK [935]

Peptide Source: iTRAQ, Ovarian cancer

MEKRLGVKPNPASWILSGYYWQTSAKWLRSLYLFYTCFCFSVLWLSTDASESRCQQGKTQFGVGLRSGGENHLWL
LEGTPSLQSCWAACQDSACHVFWWLEGMCIQADCSRPOSCRAFRTTHSSNSMLVFLKKFQTADDLGLFLPEDDVPH
LLGLGWNWASWRQSPPRALRPVSSSDQQLIRKLQKRGSPSDVVTPIVTQHSKVNDNELGGLTSSGSAEVHK
AITISSPLTTDLTAELSGGPKNVSVQPEISEGLATTPSTQQVKSSEKTQIAVPQPVAPSYSYATPTPQASQSTS
A?YPVIKELVVSAGESVQITLPKNEVQLNAYVLQEPKGETYTYDWQLITHPRDYSGEMEGKHSQILKLSKLTFG
LYEFKVVIVEGQNAHGEGYVNVTVKPEPRKNRPPIAIVSPQFQEISLPTTSTVIDGSQSTDDDKIVQYHWEELKGP
LREEKISEDTAILKLSKLVPGNYTFSLTVVDSGATNSTTANLTVNKAVDYPPVANAGPNQVITLPQNSITLFGN
QSTDDHGITSYEWLSLSPSSKGKVVEMQGVRTPTLQLSAMQEGDYTYQLTVTDTIGQQATAQVTVIVQPENNKPPQ

ADAGPDKELTLPVDSTTLDGSKSSDDQKIISYLWEKTQGPBGVQLENANSSVATVTGLQVGTYYVFTLTVKDERNL
QSQSSVNVIVKKEINKPPIAKITGNVVITLPTSTAELDGSKSSDDKGIVSYLWTRDEGSPAAGEVLNHS DHPIL
FLSNLVEGTYTFHLKVTDAGGESDTRTTVEVKPDPRKNNLVEIILDINVSQTERLKGMFIRQIGVLLGVLDSD
IIVQKIQPYTEQSTKMVFFVQNEPPHQIFKGHEVAAMLKSELRKQKADFLIFRALEVNTVTCQLNCS DHGHCD SF
TKRCICDPFWMENFIKVQLRDGDSNCALTILIFLAESVLYVIIATFVIVVALGILSWTVICCCKRQKGPKRKS
KYKILDATDQESLELKPTSRAGIKQKGLLLSSSLMHSESELDSDDAIFTWPDREKGLLHGQNGSVNPGQTPLKA
RSPREIIL

Mass Match Peptides (bold):

NNLVEIILDINVSQTER [956]

Tandem Peptides (underline):

NNLVEIILDINVSQTER [956]

Peptide Source: iTRAQ, Renal cell cancer

MEKRLGVKPNPASWILSGYYWQTS AKWLRSLYLFYTCFCFSVLWLSTDAESRCQQGKTQFGVGLRSGGENHLWL
LEGTPSLQSCWAACQDSACHVFWWLEGMCIQADCSRQSCRAFRTTHSSNSMLVFLKKFQTADDLGFLPEDDVP
LLGLGWNWASWRQSPPRALRPVSSSDQQLIRKLKRGSPSDVVTPIVTQHSKVND SNELGGLTSSGSAEVHK
AITISSPLTTDLTAELSGGPKNVSVQPEISEGLATTPSTQQVKSSEKTQIAVPQPVAPSYATPTPOASFQSTS
APYPVikelVVSAGESVQITLPKNEVQLNAYVLQEPKGETYTYDWQLITHPRDYS GEMEGKHSQILKLSKLT PG
LYEFKVI VEGQNAHGEYVNVTVKPEPRKNRPPIAIVSPQFQEISLPTTSTVIDGSQSTDDDKIVQYHWEELKGP
LREEKISED TAILKLSKLVPGNYTFSLTVVDS DGATNSTTANLTVNKAVDYPPVANAGPNQVITLPONSITLFGN
QSTDDHGITSYEWLSLSPSSKGVVEMQGVRTPTLQLSAMQEGDYTYQLTVDITIGQQAQVTVIVQPENNKPPQ
ADAGPDKELTLPVDSTTLDGSKSSDDQKIISYLWEKTQGPBGVQLENANSSVATVTGLQVGTYYVFTLTVKDERNL
QSQSSVNVIVKKEINKPPIAKITGNVVITLPTSTAELDGSKSSDDKGIVSYLWTRDEGSPAAGEVLNHS DHPIL
FLSNLVEGTYTFHLKVTDAGGESDTRTTVEVKPDPRKNNLVEIILDINVSQTERLKGMFIRQIGVLLGVLDSD
IIVQKIQPYTEQSTKMVFFVQNEPPHQIFKGHEVAAMLKSELRKQKADFLIFRALEVNTVTCQLNCS DHGHCD SF
TKRCICDPFWMENFIKVQLRDGDSNCALTILIFLAESVLYVIIATFVIVVALGILSWTVICCCKRQKGPKRKS
KYKILDATDQESLELKPTSRAGIKQKGLLLSSSLMHSESELDSDDAIFTWPDREKGLLHGQNGSVNPGQTPLKA
RSPREIIL

Mass Match Peptides (bold):

GHEVAAMLK [913]

Tandem Peptides (underline):

GHEVAAMLK [913]

OGTA091 (SEQ ID No: 17)**Peptide Source: 1D-GE, Breast cancer**

MLRVFILYAENVHTPD TDISDAYCSAVFAGVKKRTKVIKNSVNPVWNEGFEWDLKGIPLDQGSSELHVVKDHETM
GRNRF LG EAKVPLREVLATP SLSASFNA PLLDTKKQPTGASLVLQVS YTPLPGAVPLFPPTPLEPSPTLPDL DV
VADTGG EEDTEDQGLTGDEAE PFLDQSGGPGAPTTPRKLPSRPPPHYPG IKRKRSAPTSRKL LSDKPQDFQIRVQ
VIEGRQLPGVNIKPVVKVTAAGQTKRTRIHKGNSPLFNETLFFNLFDSPGELFDEPIFITVVD SRSRLR TDALLGE
FRMDVGTIYREPRHAYLRKWL LLSDPDDFSAGARGYLKTS LCVLGP GDEAPLERKDPSEDKEDIESNLLRPTGVA
LRGAHFCLKVFR AEDLPQMDDAVMDNVKQIFGFESNKKNNLVDPFVEVVSFAGKMLCSKILEKTANPQWNQNTLPA
MFPSMCEKMRTRI IDWDR LTHNDIVATTYLSMSKISAPGGEIEEPAGAVKPSKASDLDDYLGLFLPTFGPCYINL
YGSFREFTGFPDYTELNTGKGEGVAYRGRLLLSLETKLVEHSEQVEDLPADDILRVEKYLR RKYSLFAAFYS
ATMLQDVDDAIQFEVSGNYGNKFDMTCLPLASTTQYSRAVFDGCHYYLPWGNVKPVVVLSSYWEDISHRIETQ
NQLLGIADRLEAGLEQVHLALKAQCSTEDVDSLVAQLTDELIAGCSQPLGDIHETPSATHLDQYLYQLRTHHLSQ
ITEAALALKLGHSELPAALEQAEDWLLRLRALAEPPQNSLPDIVIWM LQGDKR VAYQRPVPAHQVLF SRRGANYCG
KNCGLQTIIFLKYPMEKVP GARMVPQIRVKLWFLSVDEKEFNQFAEGKLSVFAETYENETK LALVGNWGT TGLT
YKPSDVTGKIKLPKDSFRPSAGWTWAGDWFCPEKTL LHDM DAGHLSFVEEVFENQTRLP GGQWIYMSDNYTDV
NGEKVLPKDDIECPLGWKWEDEEWS TDLNRAYDEQGWESYITIPPERKPKHWP AEKMYTHRRRRVRLRRRDL
SQMEALKRRHQAEAE GEGWEYASLFGWKFHLEYRKTDAFRRRRRRRRMEPLEKTGPAAVFALEGALGGVMDDKSE
DSMSVSTLSFGVNRPTISCIFDYG NRYHLRCYMYQARDLAAMDKDSFSDPYAIVSFLHQSQKT VVVKNLTLPNTWD

QTLIFYEIEIFGEPATVAEQPPSIVVELYDHDYGADEFMGRICQPSLERMPRLAWFPLTRGSQPSGELLASFE
LIQREKPAIHHPGFEVQETSRIILDESEDIDLPPYPPQREANIYMVPQNIKPALQRTAIEILAWGLRNMKSYQLA
NISSPSLVVECGGQTVQSCVIRNLRKNPNFDICTLFMEVMLPREELYCPPITVKVIDNRQFGRRPVVGQCTIRSL
ESFLCDPYSAESPSPOGGPDDVSLSPGEDVLIDIDDKLEPLIQEEEEFDWWSKFFASIGEREKCGSYLEKDFD
TLKVYDQLENVEAFEGLSDFCNTFKLYRGKTQEETEDPSVIGEFKGLFKIYPLPEDPAIPMPPRQFHQLAAQGP
QECLVRIYIVRAFGLPKDPNGKCDPYIKISIGKKSVDQDNYIPCTLEPVFGKMFELTCTLPLEKDLKITLYDY
DLLSKDEKIGETVVDLENRLLSKFGARCGLPQTYCVSGPNQWRDQLRPSQLLHLFCQQHRVKAPVYRTDRVMFQD
KEYSIEEIEAGRIPNPHLGPVEERLALHVLQQQGLVPEHVESRPLYSPLQPDIEQGLQMWVDFPKALGRPGPP
FNITPRRRARRFFLRCLIWNRDVLDDLSLTGEKMSDIYVKGWMI GFEEHKQKTDVHYRSLGGEGNFNWRFI'FPF
DYLPAEQVCTIAKKDAFWRLDKTESKIPARVVFQIWDNDKFSFDDFLGSLQLDLNRMKPKAKTAKKCSLDQLDDA
PHPEWFSVLFQKTVKGWPCVAEEGEKKILAGKLEMTLEIVAESSEHEERPAGQGRDEPNMNPKLEDPRRPDTSF
LWFTSPYKTMKFILWRRFRWAILFIILFILLFLAIFIYAFPNYAAMKLVKPPS

Mass Match Peptides (bold):

GEGVAYR [291]
NLVDPFVEVSFAGK [547]
TDVHYR [686]

Tandem Peptides (underline):

NLVDPFVEVSFAGK [547]

Peptide Source: 1D-GE, Cervical cancer

MLRVFILIYAENVHTPDTDISDAYCSAVFAGVKKRTKVIKNSVNPVWNEGFWDLGKIPLDQGSSELHVVKDHETM
GNNRFLGEAKVPLREVLATPSLSASFNAPLLDTKKQPTGASVLQVSYTLPAGAVLPFPPTPLEPSPTLPDLV
VADTGGEEDTEDQGLTGDEAEPLDQSGGPGAPTTPRKLPSPRPPHYPGIKRKRSAPTSRLKLLSDKPDQFQIRVQ
VIEGRQLPGVNIKPVVKVTAAGQTKRTRIHKGN SPLFNETLFFNLFDSPGELFDEPIFITVVDSSRLRTDALLGE
FRMDVGTIYREPRHAYLRKWL LSDPDDFSAGARGYLKTS LCVLGPGEAPLERKDPSEDKEDIESNLLRPTGVA
LRGAHFCLKVFRADLPQMDDAVMDNVKQIFGFESNKKNLVDPFVEVSFAGKMLCSKILEKTANPQWNQNTLPA
MFPSMCEKMRIRI IDWDRILTHNDIVATTYLSMSKISAPGGEIEEFPAAGVPSKASDLDDYLGFLPTFGPCYINL
YGS PREFTGFDPDZYTELNTGKGEGVAYRGRLLLSLETKLVEHSEQKVEDLPADDILRVEKYLRRRKYSLFAAFYS
ATMLQDVEDDAIQFEVSI GN YGNKFDMTCLPLASTTQYRAVFDGCHYYYLPWGNV KPVVVLSSYWEDISHRIETQ
NQLLGIADRLEAGLEQVHLALKAQCSTEDVDSLVAQLTDELIAGCSQPLGDIHETPSATHLDQYLYQLRTHHLSQ
ITEAALALKLGHSELPAALEQAEDWLLRLRALAEFPQNSLPDIVIWMQLQDKRVAYQRPVPAHQVLFSSRRGANYCG
KNCGLQTFILKYPMEKVPGARMPVQIRVKLWFGLSVDEKEFNQFAEGKLSVFAETYENETKLALVGNWGTGLT
YPKFSVDVTGKIKLPKDSFRPSAGWTWAGDWFVCPEKTLHDM DAGHLSFVEEVFENQTRLPGGQWIYMSDNYTDV
NGEKVLPKDDIECPLGWKWEDEEWSTDLNRAVDEQGWESITIPPERKPKHWVPAEKMYITHRRRRWVRLRRRDL
SQMEALKRHRQAEAE GEGWEYASLFGWKFHLEYRKTDAFRRRRRRRRMEPLEKTGPAAVFALEGALGGVMDKSE
DSMSVSTLSFGVNRPTISCFIDYGNRYHLRCYMYQARDLAAMDKDSFSDPYAIVSFLHQSQKTVVVKNTLNPTWD
QTLIFYEIEIFGEPATVAEQPPSIVVELYDHDYGADEFMGRICQPSLERMPRLAWFPLTRGSQPSGELLASFE
LIQREKPAIHHPGFEVQETSRIILDESEDIDLPPYPPQREANIYMVPQNIKPALQRTAIEILAWGLRNMKSYQLA
NISSPSLVVECGGQTVQSCVIRNLRKNPNFDICTLFMEVMLPREELYCPPITVKVIDNRQFGRRPVVGQCTIRSL
ESFLCDPYSAESPSPOGGPDDVSLSPGEDVLIDIDDKLEPLIQEEEEFDWWSKFFASIGEREKCGSYLEKDFD
TLKVYDQLENVEAFEGLSDFCNTFKLYRGKTQEETEDPSVIGEFKGLFKIYPLPEDPAIPMPPRQFHQLAAQGP
QECLVRIYIVRAFGLPKDPNGKCDPYIKISIGKKSVDQDNYIPCTLEPVFGKMFELTCTLPLEKDLKITLYDY
DLLSKDEKIGETVVDLENRLLSKFGARCGLPQTYCVSGPNQWRDQLRPSQLLHLFCQQHRVKAPVYRTDRVMFQD
KEYSIEEIEAGRIPNPHLGPVEERLALHVLQQQGLVPEHVESRPLYSPLQPDIEQGLQMWVDFPKALGRPGPP
FNITPRRRARRFFLRCLIWNRDVLDDLSLTGEKMSDIYVKGWMI GFEEHKQKTDVHYRSLGGEGNFNWRFI'FPF
DYLPAEQVCTIAKKDAFWRLDKTESKIPARVVFQIWDNDKFSFDDFLGSLQLDLNRMKPKAKTAKKCSLDQLDDA
PHPEWFSVLFQKTVKGWPCVAEEGEKKILAGKLEMTLEIVAESSEHEERPAGQGRDEPNMNPKLEDPRRPDTSF
LWFTSPYKTMKFILWRRFRWAILFIILFILLFLAIFIYAFPNYAAMKLVKPPS

Mass Match Peptides (bold):

GEGVAYR [291]
TDVHYR [686]

Tandem Peptides (underline):

Peptide Source: 1D-GE, Chronic lymphocytic leukaemia

MLRVFILYAENVHTPDTDISDAYCSAVFAGVKKRTKVIKNSVNPVWNEGFEDWLKGIPLDQGSELHVVKDHETM
GNRRLFLGEAKVPLREVLATPSLSASFNAPLLDTKKQPTGASLVLQVSYTPLPGAVPLFPPTPLEPSPTLPDLVDV
VADTGGEEDTEDQGLTGDEAEFFLDQSGGPGAPTTPRKLPSPRPPHYPGIKRKSAPT SRKLLSDKPQDFQIRVQ
VIEGRQLPGVNIKPVVKVTAAAGQTKRTRIHKGNSPLFNETLFFNLFDSPGELFDEPIFITVVDSSRLRTDALLGE
FRMDVGTIYREPRHAYLRKWLLSDPDDFSAGARGYLKTSCLVLPDGEAPLERKDPSEDKEDIESNLLRPTGVA
LRGAHFCLKVFRADLPQMDDAVMDNVKQIFGFESNKKNLVDPFVEVSFAGKMLCSKILEKTANPQWNQNTILPA
MFFSMCEKMRIRIIDWDRLTNDIVATTYLSMSKISAPGGEIEEEPAGAVKPSKASDLDDYLGLFPTFGPCYINL
YGSPREFTGFPDPYTELNTGKCEGVAYRGRLLLSLETCLVEHSEQVEDLPADDILRVEKYLRRRKYSLFAAFYS
ATMLQDVDDAIQFEVSI GNYGNKFDMTCLPLASTTQYSRAVFDGCHYYLPGWNVKPVVVLSSYWEDISHRIETQ
NQLLGIADRLEAGLEQVHLALKAQCSTEDVDSLVAQLTDELIAGCSQPLGDIHETPSATHLDQYLYQLRTHHLSQ
ITEAALALKLGHSELPAALEQAEDWLRLRALAEFPQNSLPDIVIWMQLQGDKRVA YQRPVPAHQVLFSSRRGANYCG
KNCGKQLQTI FLKYPMKVPGARMPVQIRVKLWFGLSVDEKEFNQFAEGKLSVFAETYENETKLALVGNWGTGLT
YPK**FSDVTGK**IKL PKDSFRPSAGWTWAGDWFVCPEKTLHDM DAGHLSFVEEVFENQTRLPGGQWIYMSDNYTDV
NGEKVL PKDDIECPLGWKWEDEEWSTDLNRAVDEQGWESITIPPERKPKHWVPAEKMYTHRRRRWVRLRRDL
SQMEALKRHRQAEEGEGWEYASLFGWKFHLEYRKTDAFRRRRWRRRMEPLEKTGPAAVFALEGALGGVMDKSE
DSMSVSTLSFGVNRPTISCFIDYGNRYHLRCYMYQARDLAAMDKDSFSDPYAIVSFLHQSQKT VVVKNTLNPTWD
QTLIFYEIEIFGEPATVAEQPPSIVVELYDHDYGADEFMGRICQPSLERMPLAWFPLTRGSQPSGELLASFE
LIQREKPAIHHPGFEVQETSRI LDESED TDLPYPPQREANIYMPQNIKPALQRTAIEILAWGLRNMKSYQLA
NISSPSLVVECGGTQVQSCVIRNLRKNPNFDICTLFMEVMLPREELYCPPITVKVIDNRQFGRRPVVGQCTIRSL
ESFLCDPYSAESPSPOGGPDDVSLSPGEDVLIDIDDKLEPLIQEEEFIDWWSKFFASIGEREKCGSYLEKDFD
TLKVYDTQLENVEAFEGLSDFCNTFKLYRGKTQEETEDPSVIGEFKGLFKIYPLPEDPAIPMPPRQFHQLAAQGP
QECLVRIYIVRAFGQLQPKDPNGKCDPYIKISIGKKSVSQDNYIPCTLEPVFGKMFELTCTLPLEKDLKITLYDY
DILSKDEKIGETVVDLENRLSKFGARCGLPQTYCVSGPNQWRDQLRPSQLHLFLCQHRVKAPVYRTDRVMFQD
KEYSIEETAGRI PNPHLGPVEERLALHVLQQGLVPEHVESRPLYSPLQPDIEQGLQMWVDLFPKALGRFGPP
FNITPRRARRFFLRCIWNTRDVILDDLSTGEKMSDIYVKGWMIGFEEHKQK**TDVHYR**SLGGEGNFNWRFIFF
DYLPAEQVCTIAKKDAFWRLDKTESKIPARVVFIQWDNKFSFDDFLGSLQLDLNRMPPKPAKTAKKCSLDQLDDA
FHPEWFVSLFEQKTVKGWPCVAEEGEEKILAGKLEMTLEIVAESHEERPAQGGRDEPNMNPKELEDRPRPDTSF
LWFTSPYKTMKFIWRFRFRAIILFIILFILLFLAIFTYAFPNYAAMKLVKPF'S

Mass Match Peptides (bold):

FSDVTGK [272]

TDVHYR [686]

Tandem Peptides (underline):**Peptide Source: 1D-GE, Gastric cancer**

MLRVFILYAENVHTPDTDISDAYCSAVFAGVKKRTKVIKNSVNPVWNEGFEDWLKGIPLDQGSELHVVKDHETM
GNRRLFLGEAKVPLREVLATPSLSASFNAPLLDTKKQPTGASLVLQVSYTPLPGAVPLFPPTPLEPSPTLPDLVDV
VADTGGEEDTEDQGLTGDEAEFFLDQSGGPGAPTTPRKLPSPRPPHYPGIKRKSAPT SRKLLSDKPQDFQIRVQ
VIEGRQLPGVNIKPVVKVTAAAGQTKRTRIHKGNSPLFNETLFFNLFDSPGELFDEPIFITVVDSSRLRTDALLGE
FRMDVGTIYREPRHAYLRKWLLSDPDDFSAGARGYLKTSCLVLPDGEAPLERKDPSEDKEDIESNLLRPTGVA
LRGAHFCLKVFRADLPQMDDAVMDNVKQIFGFESNKK**NLVDPFVEVSFAGK**MLCSKILEKTANPQWNQNTILPA
MFFSMCEKMRIRIIDWDRLTNDIVATTYLSMSKISAPGGEIEEEPAGAVKPSKASDLDDYLGLFPTFGPCYINL
YGSPREFTGFPDPYTELNTGK**CEGVAYR**GRLLLSLETCLVEHSEQVEDLPADDILRVEKYLRRRKYSLFAAFYS
ATMLQDVDDAIQFEVSI GNYGNKFDMTCLPLASTTQYSRAVFDGCHYYLPGWNVKPVVVLSSYWEDISHRIETQ
NQLLGIADRLEAGLEQVHLALKAQCSTEDVDSLVAQLTDELIAGCSQPLGDIHETPSATHLDQYLYQLRTHHLSQ
ITEAALALKLGHSELPAALEQAEDWLRLRALAEFPQNSLPDIVIWMQLQGDKRVA YQRPVPAHQVLFSSRRGANYCG
KNCGKQLQTI FLKYPMKVPGARMPVQIRVKLWFGLSVDEKEFNQFAEGKLSVFAETYENETKLALVGNWGTGLT
YPKFSDVTGKIKL PKDSFRPSAGWTWAGDWFVCPEKTLHDM DAGHLSFVEEVFENQTRLPGGQWIYMSDNYTDV
NGEKVL PKDDIECPLGWKWEDEEWSTDLNRAVDEQGWESITIPPERKPKHWVPAEKMYTHRRRRWVRLRRDL
SQMEALKRHRQAEEGEGWEYASLFGWKFHLEYRKTDAFRRRRWRRRMEPLEKTGPAAVFALEGALGGVMDKSE
DSMSVSTLSFGVNRPTISCFIDYGNRYHLRCYMYQARDLAAMDKDSFSDPYAIVSFLHQSQKT VVVKNTLNPTWD
QTLIFYEIEIFGEPATVAEQPPSIVVELYDHDYGADEFMGRICQPSLERMPLAWFPLTRGSQPSGELLASFE
LIQREKPAIHHPGFEVQETSRI LDESED TDLPYPPQREANIYMPQNIKPALQRTAIEILAWGLRNMKSYQLA
NISSPSLVVECGGTQVQSCVIRNLRKNPNFDICTLFMEVMLPREELYCPPITVKVIDNRQFGRRPVVGQCTIRSL
ESFLCDPYSAESPSPOGGPDDVSLSPGEDVLIDIDDKLEPLIQEEEFIDWWSKFFASIGEREKCGSYLEKDFD
TLKVYDTQLENVEAFEGLSDFCNTFKLYRGKTQEETEDPSVIGEFKGLFKIYPLPEDPAIPMPPRQFHQLAAQGP
QECLVRIYIVRAFGQLQPKDPNGKCDPYIKISIGKKSVSQDNYIPCTLEPVFGKMFELTCTLPLEKDLKITLYDY

DLISKDEKIGETVVDLENRLLSKFGARCGLPQTYCVSGPNQWRDQLRPSQLLHLCQQHRVKAPVYRTDRVMFQD
KEYSIEEIEAGRIIPNPHLGPVEERLALHVLQQQGLVPEHVESRPLYSPLOPDIEQGKLMWVDLFPKALGRPGPF
FNITPRRARFFLRCCIWNTRDVLDDLSLTGKMSDIYVKGWMI GFEEHKQKTDVHYRSLGGEGNFNWRFIFFP
DYLPAEQVCTIAKKDAFWRLDKTESKI PARVVFIWQNDKFSFDDFLGSLQLDLNRMFKPAKTAKKCSLDQLDDA
FHPEWVSVLFEQKTVKGWVPCVAEEGEEKILAGKLEMTLEIVAESHEERPAQGGRDEPNMNPKLEDPRRPDTSF
LWFTSPYKTMKFILWRRFRWAILFIILFILLFLAIFIYAFPNYAAMKLVKPF

Mass Match Peptides (bold):

GEGVAYR [291]
NLVDPFVEVSFAGK [547]
TDVHYR [686]

Tandem Peptides (underline):

NLVDPFVEVSFAGK [547]

Peptide Source: 1D-GE, Hepatocellular carcinoma

MLRVFILIYAENVHTPDIDISDAYCSAVFAGVKKRTKVIKNSVNPVWNEGFWDLGIPLDQGSSELHVVKDHETM
GRNRFELGEAKVPLREVLATPSLSASFNAPLDITKQPTGASLVQVSYTLPGLAVPLFPPTPLEPSPTLPDLDV
VADTGGEDTEDQGLTGDEAEPLDQSGGPGAPTTPRKLPSRPPHYPGIKRKSAPTSRKLLSDKPDQFQIRVQ
VIEGRQLPGVNIKPVVKVTAAGQTKRTRIHKGNSPLFNETLFFNLFDSPGELFDEPIFITVVDSSRLRTDALLGE
FRMDVGTTIYERPRHAYLRKWLLSDPDDFSAGARGYLKTSCLVGLPGDEAPLERKDPSEDKEDIESNLLRPTGVA
LRGAHFCLKVFRADLPQMDDAVMDNVKQIFGFESNKNLVDPFVEVSFAGKMCLSKILEKTANPQWNQNTITLPA
MFPSMCEKMRIRIIDWDRLTNDIVATTYLSMSKISAPGGEIEEPAGAVKPSKASDLDDYLGFLPTFGPCYINL
YGS PREFTGFPDPYTELNTGKGEGVAYRGRLLLSLETKLVEHSEQKVEDLPADDILRVEKYLRRRKYSLFAAFYS
ATMLQDVDDATQFEVSGNNGKFDMTCLPLASTTQYSRAVFDGCHYYYLPWGNVKNPVVLLSSYWEDISHRIETQ
NQLLGIADRLLEAGLEQVHLALKAQCSTEDVDSLVAQLTDELIAGCSQPLGDIHETPSATHLDQYLYQLRTHHLSQ
ITEAALALKLGHSELPAALQAEDWLLRLRALAEEPQNSLPDIVIWMQLQGDKRVAQRPVPAHQVLFSSRGANYCG
KNCGLQTIIFLYPMEKVPVGARMPVQIRVKLWFGLSVDEKEFNQFAEGKLSVFAETIYENETKLALVGNWGTGLT
YPKFSVDTGKIKLPKDSFRPSAGWTWAGDWFCPEKTLHDMAGHLSFVEEVFENQTRLPGGQWIYMSDNYTDV
NGEKVLPKDDIECPLGWKWEDEEWSTDLNRAVDEQWEYSITIPPERKPKHWPVPAEKMYTHRRRRWRVLRRLRDL
SQMEALKRHHQAEAEAGEGWEYASLFGWKFHLEYRKTDARRRRWRRRMEPLEKTGPAAVFALEGALGGVMDKSE
DSMSVSTLSFGVNRPTISCFDYGNYHLRCYMYQARDLAAMDKDSFSDPYAIVSFLHQSOKTVVVKNTLNPTWD
QTLIFYEIEIFGEPATVAEQPPSIVVELYDHDYGADEFMGRICQPSLERMPRLAWPLTRGSQPSGELLASFE
LIQREKPAIHHPGFEVQETSRIIDSESDTLPYPPPPQREANIYMVPQNIKPAQRTAIEILAWGLRNMKSYQLA
NISSPSLVVECGGQTVQSCVIRNLRKNPNFDICTLFMEVMLPREELYCPPITVKVIDNRQFGRPRVVGQCTIRSL
ESFLCDPYSAESPSQGGPDDVSLSPGEDVLIDIDDKEPLIPQEEEFIDWWSKFFASIGERLEKCGSYLEKDFD
TLKVYDTQLENVEAFEGLSDFCNTFKLYRGKTQEETEDPSVIGEFKGLFKTYPLPEDPAIPMPPRQFHQLAAQGP
QECLVR IYIVRAFLGQPKDPNGKCDPYIKISTIGKKSVDQDNYIPTCLEPVFGKMFELTCTLPLEKDLKITLYDY
DLISKDEKIGETVVDLENRLLSKFGARCGLPQTYCVSGPNQWRDQLRPSQLLHLCQQHRVKAPVYRTDRVMFQD
KEYSIEEIEAGRIIPNPHLGPVEERLALHVLQQQGLVPEHVESRPLYSPLOPDIEQGKLMWVDLFPKALGRPGPF
FNITPRRARFFLRCCIWNTRDVLDDLSLTGKMSDIYVKGWMI GFEEHKQKTDVHYRSLGGEGNFNWRFIFFP
DYLPAEQVCTIAKKDAFWRLDKTESKI PARVVFIWQNDKFSFDDFLGSLQLDLNRMFKPAKTAKKCSLDQLDDA
FHPEWVSVLFEQKTVKGWVPCVAEEGEEKILAGKLEMTLEIVAESHEERPAQGGRDEPNMNPKLEDPRRPDTSF
LWFTSPYKTMKFILWRRFRWAILFIILFILLFLAIFIYAFPNYAAMKLVKPF

Mass Match Peptides (bold):

AVDEQWEYSITIPPER [94]
DLSQMEALK [139]
DLSQMEALKR [140]
DSFSDPYAIVSFLHQSOK [155]
EKPAIHHPGFEVQETS [201]
EVLATPSLSASFNAPLDITK [234]
FFASIGER [250]
FHLEYR [254]
GEGVAYR [291]
GSQPSGELLASFELIQR [320]
IETQNQLLGIADR [363]
IGETVVDLENR [367]
IIDWDR [370]

ILDESEDTDLPPPPQR [375]
 IPNPHLGPEVER [386]
 IYPLPEDPAIPMPER [403]
 KNPNFICTLMEVMLPR [430]
 KTDAFRR [436]
 LLSDKPQDFQIR [469]
 LPPGQWIYMSDNYTDVNGEK [477]
 LSVFAETIYENETK [491]
 MDVGTIYR [511]
 MFELTCTLPLEK [515]
 MYYTHRRR [533]
 NLVDPFVEVSFAGK [547]
 NPNFICTLMEVMLPR [551]
 QFHQLAAQGFQECLVR [570]
 QIFGFESNK [579]
 RDLSQMEALK [599]
 RMEPLEK [607]
 RPDTSFLWFTSPYK [608]
 SLGGEGNFNWR [640]
 TANPQWNQNITLPAMFPSMCEK [670]
 TDAFRRR [680]
 TDALLGEFR [681]
 TDVHYR [686]
 TQEETEDPSVIGEFK [724]
 TSLCVLGPGEAPLER [728]
 TSLCVLGPGEAPLERK [729]
 VEDLPADDILR [753]
 VPAHQVLFSSR [787]
 VQVIEGR [794]
 VTAAGQTK [800]
 VVFQIWDNDK [810]
 WEDEEWSTDLNR [824]
 WLLLSDDPDDFSAGAR [827]

Tandem Peptides (underline):

FFASIGER [250]
 HWVPAEK [348]
 IGETVVDLENR [367]
 IYPLPEDPAIPMPER [403]
 LLSDKPQDFQIR [469]
 MDVGTIYR [511]
 NLVDPFVEVSFAGK [547]
 QIFGFESNK [579]
 SLGGEGNFNWR [640]
 TDALLGEFR [681]
 VEDLPADDILR [753]

Peptide Source: 1D-GE, Lung cancer

MLRVFILIYAENVHTPDTDISDAYCSAVFAGVKRRTKVIKNSVNPVWNEGFWDLGKIPLDQGSSELHVVKDHETM
 GRNRFLGEAKVPLREVLA TP SLSASFNA PLLDTKKQPTGASLVLQVSYTPLPGAVPLFPPTPLEPSPTLPDL DV
 VADTGGEEDTEDQGLTGDEAEFLDQSGGPGAPTTPRKLPSRPPPHYPGIKRKRSAPTSRKLLSDKPQDFQIRVQ
 VIEGRQLPGVNIKPVVKVTAAGQTKRTRIHKGNSPLFNETLFFNLFDSPGELEDEPIFITVVDSSRLRTDALLGE
 FRMDVGTIYREPRHAYLRKWL LLSDDPDDFSAGARGYLKTS LCVLGPGEAPLERKDPSSEDKEDIESNLLRPTGVA
 LRGAHFCLKVFRAEDLPQMDDAVMDNVKQIFGFESNK **KNLVDPFVEVSFAGK** MLCSKILEKTANPQWNQNITLPA
 MFPSMCEKMRIRIIDWRLTHNDIVATTYLSMSKISAPGGEIEEEPAGAVKPSKASDLD DYLGLPFTFGPCYINL
 YGSPREFTGFDPYTELNTGK **CEGVAYR** GRLLLSLETCLVEHSEQVEDLPADDILRVEKYLRRRKYSLFAAFYS
 ATMLQDVDDATQFEVSI GNYGNKFDMTCLPLASTTQYSRAVFDGCHYYL PWGNVKPVVVLSSYWEDISHRIETQ
 NQLLGIADRL EAGLEQVHLALKAQCSTEDVDSLVAQLTDELIAGCSQPLGDIHETPSATHLDQYLYQLRTHHSQ
 ITEAALALKLGHSELPAALEQAEDWLLRLRALAEEPQNSLPDIVIWM LQGDKRVAYQRPVPAHQVLFSSRCANYCG
 KNCKGLQTI FLKYPMEKVP GARMVPQIRVKLWFLSVDEKEFNQFAEGKLSVFAETIYENETKLALVGNWGT TGLT

YPKFSDVTGKIKLPKDSFRPSAGWTWAGDWFVCPEKTLHDM DAGHLSFVEEVFENQTRLPGGQWIYMSDNYTDV
 NGEKVLPKDDIECPLGWKWEDEEWSTDLNRAVDEQGW EYSITIPPERKPKHWVPAEKMYTHRRRRWVRLRRDL
 SQMEALKRHRQAEAE GEGWEYASLFGWKFHLEYRKTD AFRRRRWRRRMEPLEKTPGAAVFALEGALGGVMDDKSE
 DSM SVSTLSFGVNRPTISCFDYGNRYHLRCYMYQARDLAAMDKDSFSDPYAIVSFLHQSQKTVVVKNTLNPTWD
 QTLIFYEIEIFGEPATVAEQPPSIVVELYDHD TYGADEFMGR C ICQPSLERM PRLAWFPLTRGSQPSGELLASFE
 LIQREKPAIHHPGFVQETSRILDESED TLPYPPPPQREANIYMPQNIKPA LQRTAIEILAWGLRNMKSYQLA
 NISSPSLVVECGGQTVQSCVIRNLRKNPNFDICTLFMEVMLPREEL YCPPITVKVIDNRQFGRRPVVGQCTIRSL
 ESFLCDPYSAESPS PQGGPDDVSLSPGEDVLIDIDKEPLIPIQEEEFIDWWSKFFASIGEREKCGSYLEKDFD
 TLKVYDTQLENVEAFEGLSDFCNTFKLYRGKTQEETEDPSVIGEFKGLFKIYPLPEDPAIPMPPRQFHQLAAQGP
 QECLVRIYIVRAFLQPKDPNGKCDPYIKISIGKKSVDQDNYIPCTLEPVFGKMFELTCTLPLEKDLKITLYDY
 DLLSKDEKIGETVVDLENRLLSKFGARCGLPQTYCVSGPNQWRDQLRPSQLLHLFCQQHRVKAPVYRTDRVMFQD
 KEYSIEEIEAGRIPNPHLGPVEERIALHVLQQQGLVPEHVESRPLYSPLQPDIEQGKLMWVDLFPKALGRPGPP
 FNITPRRARRFFLRCIIWNTRDVILDDLSTGEEKMSDIYVKGWMIGFEEHKQKTDVHYRSLGGEGNFNWRFIFPF
 DYLP AEQVCTIAKKDAFWRLDKTESKIPARVVFQIWDNDKFSFDDFLGSLQLDLNRMKPAKTAKKCSLDQLDDA
 FHEWFSVLFEQKTVKGWPCVAEEGEKKILAGKLEMTLEIVA ESEHEERPAGQGRDEPNMNPKLEDPRRPDTSF
 LWFTSPYKTMKFIWRRFRWAILFIILFILLFLAIFIYAFPNYAAMKLVKPS

Mass Match Peptides (bold):

GEGVAYR [291]
 ILDESED TLPYPPPPQR [375]
 IPNPHLGPVEER [386]
 KNLVDPFVEVSFAGK [429]
 MEPLEK [513]
 RMEPLEK [607]
 TDVHYR [686]

Tandem Peptides (underline):

EYSIEEIEAGR [241]
 SLGGEGNFNWR [640]

Peptide Source: 1D-GE, Melanoma

MLRVFILIYAENVHPTD TDISDAYCSAVFAGVKKRTKVIKNSVNPVWNEGFEWDLKGIPLDQGSSELHVVKDHETM
 GRNRFLEAKVPLREVLATPSLSASFNAFLD TTKKQPTGASIVLQVS YTPLPGAVPLFPPTPLEPSPTLPDL DV
 VADTGG EEDTEDQGLTGDEAE PFLDQSGGPGAPTTPRKLPSRPPPHYPGIKRKRSAPTSRKLLSDK PQDFQIRVQ
 VIEGRQLPGVNIKPVVKVTAAGQTKRTRIHKNSPLFNETLFFNLFDSPGELFDEPIFITVVD SRSRLRTDALLGE
 FRMDVGTIYREPRHAYLRKWL LLSDPDDFSAGARGYLKTSCLV LGPGDEAPLERKDPSDEKEDIESNLLRP TGVA
 LRGAHFCLKVFR AEDLPQMDDAVMDNVKQIFGFESNKKNLVDPFVEVSFAGKMLCSKILEKTANPQWNQNTLPA
 MFPSMCEKMRIRIIDWDR LTHNDIVATTYLSMSKISAPGGEIEEPPAGAVKPSKASDLDYLGFLPTFGPCYINL
 YGSPREFTFGFPDPTYELNTGKGEGVAYRGRILLLSLETKLVEHSEQKV EDLPADDLVEKYLRRRKYSLFAAFYS
 ATMLQDVDDAIQFEVSI GNKFDMTCLPLASTTQYSRAVFDGCHYYLPWGNV KPVVVLSSYWEDISHRIETQ
 NQLLGIADRLEAGLEQVHLAKAQCSTEDVDSLVAQLTDELIAGCSQPLGDIHETPSATHLDQYLYQLRTHHLSQ
 ITEAALALKLGHSELPAALEQAEDWLLRLRALAEPPQNSLPDIVIWM LQGDKRVA YQRPVPAHQVLF SRRCANYCG
 KNCGLQTI FLKYPM EKVPGARMPVQIRVKLWFGLSVDEKEFNQFAEGKLSVFAET YENETKLALVGNWGT TGLT
 YPKFSDVTGKIKLPKDSFRPSAGWTWAGDWFVCPEKTLHDM DAGHLSFVEEVFENQTRLPGGQWIYMSDNYTDV
 NGEKVLPKDDIECPLGWKWEDEEWSTDLNRAVDEQGW EYSITIPPERKPKHWVPAEKMYTHRRRRWVRLRRDL
 SQMEALKRHRQAEAE GEGWEYASLFGWKFHLEYRKTD AFRRRRWRRRMEPLEKTPGAAVFALEGALGGVMDDKSE
 DSM SVSTLSFGVNRPTISCFDYGNRYHLRCYMYQARDLAAMDKDSFSDPYAIVSFLHQSQKTVVVKNTLNPTWD
 QTLIFYEIEIFGEPATVAEQPPSIVVELYDHD TYGADEFMGR C ICQPSLERM PRLAWFPLTRGSQPSGELLASFE
 LIQREKPAIHHPGFVQETSRILDESED TLPYPPPPQREANIYMPQNIKPA LQRTAIEILAWGLRNMKSYQLA
 NISSPSLVVECGGQTVQSCVIRNLRKNPNFDICTLFMEVMLPREEL YCPPITVKVIDNRQFGRRPVVGQCTIRSL
 ESFLCDPYSAESPS PQGGPDDVSLSPGEDVLIDIDKEPLIPIQEEEFIDWWSKFFASIGEREKCGSYLEKDFD
 TLKVYDTQLENVEAFEGLSDFCNTFKLYRGKTQEETEDPSVIGEFKGLFKIYPLPEDPAIPMPPRQFHQLAAQGP
 QECLVRIYIVRAFLQPKDPNGKCDPYIKISIGKKSVDQDNYIPCTLEPVFGKMFELTCTLPLEKDLKITLYDY
 DLLSKDEKIGETVVDLENRLLSKFGARCGLPQTYCVSGPNQWRDQLRPSQLLHLFCQQHRVKAPVYRTDRVMFQD
 KEYSIEEIEAGRIPNPHLGPVEERIALHVLQQQGLVPEHVESRPLYSPLQPDIEQGKLMWVDLFPKALGRPGPP
 FNITPRRARRFFLRCIIWNTRDVILDDLSTGEEKMSDIYVKGWMIGFEEHKQKTDVHYRSLGGEGNFNWRFIFPF
 DYLP AEQVCTIAKKDAFWRLDKTESKIPARVVFQIWDNDKFSFDDFLGSLQLDLNRMKPAKTAKKCSLDQLDDA
 FHEWFSVLFEQKTVKGWPCVAEEGEKKILAGKLEMTLEIVA ESEHEERPAGQGRDEPNMNPKLEDPRRPDTSF
 LWFTSPYKTMKFIWRRFRWAILFIILFILLFLAIFIYAFPNYAAMKLVKPS

Mass Match Peptides (bold):

FSDVTGK [272]

NLVDPFVEVSFAGK [547]

Tandem Peptides (underline):**Peptide Source: 1D-GE, Osteosarcoma**

MLRVFILYAENVHTPDTDISDAYCSAVFAGVKKRTKVIKNSVNPVWNEGFWDLKGIPLDQGSSELHVVKDHETM
GRNRFLGEAKVPLREVLATPSLSASFNAPLLDTKKQPTGASVLVQVSYTPLPGAVPLFPPPTPLEPSPTLPDLVDV
VADTGGEDTEDQGLTGDEAEFPLDQSGGPGAPTTPRKLPSRPPPHYPGIKRRKSAPTSRKLLSDKPKQDFQIRVQ
VIEGRQLPGVNIKPVKVTAAGQTKRTRIHKGNPLFNETLFFNLFDSPGELFDEPIFITVVDSSRLRTDALLGE
FRMDVGTIYREPRHAYLRKWLILLSDPDDFSAGARGYLKTSCLVLPDDEAPLERKDPSEDKEDIESNLLRP TGVA
LRGAHFCLKVFRADLPQMDDAVMDNVKQIFGFESNKK**NLVDPFVEVSFAGK**MLCSKILEKTANPQWNQNTLPA
MFPSMCEKMRIRIIDWDRILTHNDIVATTYLSMSKISAPGGEIEEEPAGAVKPSKASDLDDYLGLPTFGPCYINL
YGS PREFTGFPDPYTELNTGKGEGVAYRGRLLLSLETKLVEHSEQKVEDLPADDILRVEKYLRRRKYSLFAAFYS
ATMLQDVDDAIQFEVSI GNYGNKFDMTCLPLASTTQYSRAVFDGCHYYLPWGNVKPVVVLSSYWEDISHRIETQ
NQLLGIADRLEAGLEQVHLALKAQCSTEDVDSLVAQLTDELIAGCSQPLGDIHETFSATHLDQYLYQLRTHHLSQ
ITEAALALKLGHSELPAALEQAEDWLLRLRALAEEPQNSLPDIVIWMQLQGDKRVAHQVLFSSRRGANYCG
KNCGLQTIIFLKYPMEKVPGARMPVQIRVKLWFGLSVDEKEFNQFAEGKLSVFAETYENETKLALVGNWGTGTLT
YPKFSDVTGKIKLPKDSFRPSAGWTWAGDWFCPEKTL LHDM DAGHLSFVEEVFENQTRLPGGQWIYMSDNYTDV
NGEKVLPKDDIECPLGWKWEDEEWSTDLNRAVDEQGEYSITIPPERKPKHWVPAEKMYTHRRRRWVLRRLRDL
SQMEALKRHRQAAEGEGWEYASLFGWKFHLEYRKTDAFRRRRRRRRMEPLEKTGFAAVFALEGALGGVMDKSE
DSMSVSTLSFGVNRPTISCI FDYGNRYHLRCYMYQARDLAAMDKDSFSDPYAIVSFLHQSQKT VVVKNTLNPTWD
QTLIFYEIEIFGEPATVAEQPPSIVVELYDHDYGADEFMGRICQPSLERMPRLAWFPLTRGSQPSGELLASFE
LIQREKPAIHHPGFEVQETSRILDESED TDLPPPPQREANIYMPQNIKPALQRTAIEILAWGLRNMKSYQLA
NISSPSLVVECGQTQVQSCVIRNLRKNPNFDICTLFMEVMLPREELYCPIITVKVIDNRQFGRRPVVGQCTIRSL
ESFLCDPYSAESPSPQGGPDDVSLSPGEDVLI DDDKEPLIPIQEEEFIDWWSKFFASIGEREKCGSYLEKDFD
TLKVYDTQLENVEAFEGLSDFCNTFKLYRGKTQEETEDPSVIGEFKGLFKIYPLPEDPAIMPMPRQFHQLAAQGP
QECLVRIYIVRAFGLPKDPNGKCDPYIKISIGKKSVDQDNYIPTCLEPVFGKMFELTCTLPLEKDLKITLYDY
DLSKDEKIGETVVDLENRLLSKFGARCGLPQTYCVSGPNQWRDQLRPSQLLHLFCQQHRVKAPVYRTDRVMFQD
KEYSIEEIEAGRIPNPHLGPVEERLALHVLQQGLVPEHVESRPLYSPLQPDIEQGKLQMWVDLFPKALGRPGPP
FNITPRRARRFFLRCCIWNTRDVILDDLSTGEXMSDIYVKGWMI GFEEHKQ**TDVHYR**SLGGEGNFNWRFIFFP
DYLPAEQVCTIAKKDAFWRLDKTESKIPARVVFQIWDNDKFSFDDFLGSLQLDLNRMPKPAKTAKKCSLDQLDDA
FHPEWFSVSLFEQKTVKGNWPCVAEEGEKKILAGKLEMTLEIVAESHEERPAGQGRDEPNMNPKLEDP RPDPSTF
LWFTSPYKTMKFIWRRFRWAIILFIILFILLLLFLAIFIYAFPNYAAMKLVKPF

Mass Match Peptides (bold):

NLVDPFVEVSFAGK [547]

TDVHYR [686]

Tandem Peptides (underline):**Peptide Source: 1D-GE, Ovarian cancer**

MLRVFILYAENVHTPDTDISDAYCSAVFAGVKKRTKVIKNSVNPVWNEGFWDLKGIPLDQGSSELHVVKDHETM
GRNRFLGEAKVPLREVLATPSLSASFNAPLLDTKKQPTGASVLVQVSYTPLPGAVPLFPPPTPLEPSPTLPDLVDV
VADTGGEDTEDQGLTGDEAEFPLDQSGGPGAPTTPRKLPSRPPPHYPGIKRRKSAPTSRKLLSDKPKQDFQIRVQ
VIEGRQLPGVNIKPVKVTAAGQTKRTRIHKGNPLFNETLFFNLFDSPGELFDEPIFITVVDSSRLRTDALLGE
FRMDVGTIYREPRHAYLRKWLILLSDPDDFSAGARGYLKTSCLVLPDDEAPLERKDPSEDKEDIESNLLRP TGVA
LRGAHFCLKVFRADLPQMDDAVMDNVKQIFGFESNKK**NLVDPFVEVSFAGK**MLCSKILEKTANPQWNQNTLPA
MFPSMCEKMRIRIIDWDRILTHNDIVATTYLSMSKISAPGGEIEEEPAGAVKPSKASDLDDYLGLPTFGPCYINL
YGS PREFTGFPDPYTELNTGK**GEGVAYR**GRLLLSLETKLVEHSEQKVEDLPADDILRVEKYLRRRKYSLFAAFYS
ATMLQDVDDAIQFEVSI GNYGNKFDMTCLPLASTTQYSRAVFDGCHYYLPWGNVKPVVVLSSYWEDISHRIETQ
NQLLGIADRLEAGLEQVHLALKAQCSTEDVDSLVAQLTDELIAGCSQPLGDIHETFSATHLDQYLYQLRTHHLSQ
ITEAALALKLGHSELPAALEQAEDWLLRLRALAEEPQNSLPDIVIWMQLQGDKRVAHQVLFSSRRGANYCG
KNCGLQTIIFLKYPMEKVPGARMPVQIRVKLWFGLSVDEKEFNQFAEGKLSVFAETYENETKLALVGNWGTGTLT
YPKFSDVTGKIKLPKDSFRPSAGWTWAGDWFCPEKTL LHDM DAGHLSFVEEVFENQTRLPGGQWIYMSDNYTDV

NGEKVLPKDDIECPLGWKWEDEEWSTDLNRAVDEQGWEYSITIPPERKPKHWPVPAEKMYTHRRRRWVRLRRDL
 SQMEALKRHRQAEAE GEGWEYASLFGWKFHLEYRKTD AFRRRRWRRRMEPLEKTGPAAVFALEGALGGVMDKSE
 DSM SVSTLSFGVNRPTISCIFDYGNRYHLRCYMYQARDLAAMDKDSFSDPYAIVSFLHQSQKT VVVKNTLNPTWD
 QTLIFYEIEIFGEPATVAEQPPSIVVELYDHD TYGADEFMGRCICQPSLERMPRLAWFPLTRGSQPSGELLASFE
 LIQREKPAIHHPGFEVQETSRI LDESED TDL PYPQQREANIYMPQNIK PALQRTAIEILAWGLRNMKSYQLA
 NISSPSLVVECGGQTVQSCVIRNLRKNPNFDICTLFMEVMLPREELYCPPITVKVIDNRQFGRPRPVVGQCTIRSL
 ESFLCDPYSAESPSQGGPDDVSLSPGEDVLIDIDKEPLIPIQEEEFIDWWSKFFASIGEREKCGSYLEKDFD
 TLKVYDTQLENVEAFEGLSDFCNTFKLYRGKTQEETEDPSVIGEFKGLFKIYPLPEDPAIPMPPRQFHQLAAQGP
 QECLVRIYIVRAFG LQPKDPNGKCDPYIKISIGKKSVDQDNYIPCTLEPVFGKMFELTCTLPLEKDLKITLYDY
 DLLSKDEKIGETVVDLENRLLSKFGARCGLPQTYCVSGPNQWRDQLRPSQLLHLFCQQHRVKAPVYRTDRVMFQD
 KEYSIEEIEAGRIPNPHLGPVEERLALHVLQOQGLVPEHVESRPLYSP LQPDIEQGKLQMWVDLFPKALGRPGPP
 FNITPRRARREFLRCIIWNTRDVLDDLSLTGKMSDIYVKGWMI GFEEHKQKTDVHYRSLGGEGNFENWRFIFPF
 DYLPAEQVCTIAKKDAFWRLDKTESKIPARVVFQIWDNDKFSFDDFLGSLQLDLNRMKPKAKTAKKCSLDQLDDA
 FHPEW FVSLFEQKTVKGWWPCVAEEGEEKILAGKLEMTLEIVA ESEHEERPAGQGRDEPNMNP KLEDPRRPDTSF
 LWFTSPYKTMKFILWRRFRWAIILFIILFILLFLAIFIAFPNYAAMKLVKPFSS

Mass Match Peptides (bold):

GEGVAYR [291]
 KNLVDPFVEVSFAGK [429]
 NLVDPFVEVSFAGK [547]

Tandem Peptides (underline):

Peptide Source: 1D-GE, Pancreatic cancer

MLRVFILIYAENVHTPD TDISDAYCSAVFAGVKRRTKVIKNSVNPVWNEGFWD LKGIPLDQGSSELHVVKDHETM
 GRNRFLGEAKVPLREVLATPSLSASFNA PLLDTKKQPTGASLVLQVSYTPLPGAVPLFPPTPLEPSPTLPDL DV
 VADTGG EEDTEDQGLTGDEAEFLDQSGGPGAPTTPRKLPSRPPHYPGIKRKSAPT SRKLLSDKPDQDFQIRVQ
 VIEGRQLPGVNIKPVVKVTAAGQTKRTRIHKGNSPLFNETLFFNFLFDSPGELFDEPIFITVVD SRSRLRTDALLGE
 FRMDVGTIYREPRHAYLRKWL LLSDPDDFSAGARGYLKTS LCVLPGDEAPLERKDPSEDKEDIESNLLRPTGVA
 LRGAHFLKLVFRAEDLPQMDDAVMDNVKQIFGFESNK**KNLVDPFVEVSFAGK**MLCSKILEKTANPQWNQNTLP
 MFPSMCEKMRIRIIDWRDLTHNDIVATTYLSMSKISAPGGEIEEEPAGAVKPSKASDLDDYLGFLPTFGPCYINL
 YGSFREFTGFPDPYTELNTGK**GEGVAYR**GRLLLSLETKLVEHSEQKVEDLPADDILRVEKYLRRRKYSLFAAFYS
 ATMLQD VDDAIQFEVSGNYGNKFDMTCLPLASTTQYSRAVFDGCHYYYLPWGNVKPVVVLSSYWEDISHRIETQ
 NQLLGTADRLEAGLEQVHLALKAQCSTEDVDSLVAQLTDELIAGCSQPLGDIHETPSATHLDQYLYQLRTHHLSQ
 ITEAALALKLGHSELPAALQAE DWLLRLRALAEFPQNSLPDIVIWM LQGDKRVA YQRPVPAHQVLF SRRGANYCG
 KNCGKQLQITFLKYPMEKVPGARMPVQIRVKLWFGLSVDEKEFNQFAEGKLSVFAETYENETKLALVGNWGTGLT
 YPK**FSDVTGK**IKLPKDSFRPSAGWTWAGDWFCPEKTL LHDM DAGHLSFVEEVFENQTRLPGGQWIYMSDNYTDV
 NGEKVLPKDDIECPLGWKWEDEEWSTDLNRAVDEQGWEYSITIPPERKPKHWPVPAEKMYTHRRRRWVRLRRDL
 SQMEALKRHRQAEAE GEGWEYASLFGWKFHLEYRKTD AFRRRRWRRRMEPLEKTGPAAVFALEGALGGVMDKSE
 DSM SVSTLSFGVNRPTISCIFDYGNRYHLRCYMYQARDLAAMDKDSFSDPYAIVSFLHQSQKT VVVKNTLNPTWD
 QTLIFYEIEIFGEPATVAEQPPSIVVELYDHD TYGADEFMGRCICQPSLERMPRLAWFPLTRGSQPSGELLASFE
 LIQREKPAIHHPGFEVQETSRI LDESED TDL PYPQQREANIYMPQNIK PALQRTAIEILAWGLRNMKSYQLA
 NISSPSLVVECGGQTVQSCVIRNLRKNPNFDICTLFMEVMLPREELYCPPITVKVIDNRQFGRPRPVVGQCTIRSL
 ESFLCDPYSAESPSQGGPDDVSLSPGEDVLIDIDKEPLIPIQEEEFIDWWSKFFASIGEREKCGSYLEKDFD
 TLKVYDTQLENVEAFEGLSDFCNTFKLYRGKTQEETEDPSVIGEFKGLFKIYPLPEDPAIPMPPRQFHQLAAQGP
 QECLVRIYIVRAFG LQPKDPNGKCDPYIKISIGKKSVDQDNYIPCTLEPVFGKMFELTCTLPLEKDLKITLYDY
 DLLSKDEKIGETVVDLENRLLSKFGARCGLPQTYCVSGPNQWRDQLRPSQLLHLFCQQHRVKAPVYRTDRVMFQD
 KEYSIEEIEAGRIPNPHLGPVEERLALHVLQOQGLVPEHVESRPLYSP LQPDIEQGKLQMWVDLFPKALGRPGPP
 FNITPRRARREFLRCIIWNTRDVLDDLSLTGKMSDIYVKGWMI GFEEHKQKTDVHYRSLGGEGNFENWRFIFPF
 DYLPAEQVCTIAKKDAFWRLDKTESKIPARVVFQIWDNDKFSFDDFLGSLQLDLNRMKPKAKTAKKCSLDQLDDA
 FHPEW FVSLFEQKTVKGWWPCVAEEGEEKILAGKLEMTLEIVA ESEHEERPAGQGRDEPNMNP KLEDPRRPDTSF
 LWFTSPYKTMKFILWRRFRWAIILFIILFILLFLAIFIAFPNYAAMKLVKPFSS

Mass Match Peptides (bold):

FSDVTGK [272]
 GEGVAYR [291]
 KNLVDPFVEVSFAGK [429]
 NLVDPFVEVSFAGK [547]
 TDVHYR [686]

Tandem Peptides (underline):

NLVDPFVEVSFAGK [547]

Peptide Source: 1D-GE, Prostate cancer

MLRVFILYAENVHTPDTDISDAYCSAVFAGVKKRTKVIKNSVNPVWNEGFWDLGKIPLDQGSSELHVVKDHETM
GRNRFLEAKVPLREVLPATPSLSASFNAPLLDTKKQPTGASLVLQVSYTLPAGAVLFPPTPLEPSPTLPDLVDV
VADTGGEEDTEDQGLTGDEAEPLDQSGGPGAPTTPRKLPSPRPHPHYPGIKRKRSAPTSRLKLLSDKPDQDFQIRVQ
VIEGRQLPGVNIKPVVKVTAAGQTKRTRIHKGNSPLFNETLFFNLFDSPGELFDEPIFITVVDSSRLRTDALLGE
FRMDVGTIYREPRHAYLRKWLLSDPDDFSAGARGYLKTSCLVLGPGDEAPLERKDPSEDKEDIESNLLRPTGVA
LRGAHFCLKVFRAEDLPQMDDAVMDNVKQIFGFESNKKNLVDPFVEVSFAGKMLCSKILEKTANPQWNQNTILPA
MPSMCEKMRIRI LDWDRLTNDIVATTYLSMSKISAPGGEIEEEPAGAVKPSKASDLDDYLGFLPTFGPCYINL
YGSPREFTGFDPDYTELNTGK**GEGVAYR**GRLLLSLETKLVEHSEQKVEDLPADDILRVEKYLRRRKYSLFAAFYS
ATMLQDVDDAIQFEVSIGNYGNKFDMTCLPLASTTQYSRAVFDGCHYYLFWGNVKKPVVVLSSYWEDISHRIETQ
NQLGLIADRLAEGLEQVHLALKAQCSTEDVDSLVLAQLTDELIAGCSQPLGDIHETPSATHLDQYLYQLRTHHLSQ
ITEAALALKLGHSELPAALEQAEDWLLRLRALAEFPQNSLPDIVIWMQLQGDKRVAQYQVPAHQVLFSSRGANYCG
KNCGLQTIIFLKYPMEKVPGARMPVQIRVKLWFGLSVDEKEFNQFAEGKLSVFAETYENETKLALVGNWGTGLT
YPKFSDVTGKIKLPKDSFRPSAGWTWAGDFVFCPEKTLHDM DAGHLSFVEEVFENQTRLPGGQWIYMSDNYTDV
NGEKVLPKDDIECLPGWKWEDEEWSTDLNRAVDEQGWESITIPPERKPKHWVPAEKMYTHRRRRWVLRRLRDL
SQMEALKRHRQAEEGEGWEYASLFGWKFHLEYRKTDAFRRRRWRRRMEPLEKTGPAAVFALEGALGGVMDKSE
DSMSVSTLSFGVNRPTISCIIFYGNRYHLRCYMYQARDLAAMDKDSFSDPYAIVSFLHQSQKT VVVKNLTNP TWD
QTLIFYEIEIFGEPATVAEQPPSIVVELYDHDYCADEFMGRICQPSLERMPRLAWFPLTRGSQPSGELLASFE
LIQREKPAIHHPGFVQETSRILDESEDTDLPPPPQREANIYMPQNIKALQRTAIEILAWGLRNMKSYQLA
NISSPSLVVECGGQTVQSCVIRNLRKNPNFDICTLFMEVMLPREELYCPPITVKVIDNRQFGRRPVVGQCTIRSL
ESFLCDPYSAESPSQGGPDDVSLSPGEDVLIDIDKEPLIQEEEFIDWWSKFFASIGEREKCSYLEKDFD
TLKVYDTQLENVEAFEGLSDFCNTFKLYRGKTQEETEDPSVIGEFKGLFKIYPLPEDPAIPMPRQFHQLAAQGP
QECLVRIYIVRAFGLPKDPNGKCDPYIKISIGKKSVDQDNYIPTCLEPVFGKMFELTCTLPLEKDKLTLYDY
DLSKDEKIGETVVDLENRLLSKFGARCGLPQTYCVSGPNQWRDQLRPSQLLHLFCQQRHVKAQVYRTDRVMFQD
KEYSIEEIEACRIPNPHLGPVEERLALHVLQQGLVPEHVESRPLYSPLQPDIEQGLQMWVDLPFKALGRPGPP
FNITPRRRARFFLRCIIWNTRDVIDDLSLTGKMSDIYVKGWMI GFEEHKQK**TDVHYR**SLGGEGNFNWRIFPP
DYLPAEQVCTIAKKDAFWRLDKTESKIPARVVFQIWDNDKFSFDDFLGSLQLDLNRMKPAKTAKKCSLDQLDDA
FHEPWFVSLFEQKTVKGWPCVAEEGEEKILAGKLEMTLEIVAEESEHEERPAQQRDEPNMNPKLEDPRRPDTSF
LWFTSPYKTMKFIWRRFRWAILFIFILLFILLFLAIFIAFNPYAAMKLVKPPS

Mass Match Peptides (bold):

GEGVAYR [291]

TDVHYR [686]

Tandem Peptides (underline):**Peptide Source: 1D-GE, Renal cell cancer**

MLRVFILYAENVHTPDTDISDAYCSAVFAGVKKRTKVIKNSVNPVWNEGFWDLGKIPLDQGSSELHVVKDHETM
GRNRFLEAKVPLREVLPATPSLSASFNAPLLDTKKQPTGASLVLQVSYTLPAGAVLFPPTPLEPSPTLPDLVDV
VADTGGEEDTEDQGLTGDEAEPLDQSGGPGAPTTPRKLPSPRPHPHYPGIKRKRSAPTSRLKLLSDKPDQDFQIRVQ
VIEGRQLPGVNIKPVVKVTAAGQTKRTRIHKGNSPLFNETLFFNLFDSPGELFDEPIFITVVDSSRLRTDALLGE
FRMDVGTIYREPRHAYLRKWLLSDPDDFSAGARGYLKTSCLVLGPGDEAPLERKDPSEDKEDIESNLLRPTGVA
LRGAHFCLKVFRAEDLPQMDDAVMDNVKQIFGFESNKKNLVDPFVEVSFAGKMLCSKILEKTANPQWNQNTILPA
MPSMCEKMRIRI **ITDWDRL**THNDIVATTYLSMSKISAPGGEIEEEPAGAVKPSKASDLDDYLGFLPTFGPCYINL
YGSPREFTGFDPDYTELNTGK**GEGVAYR**GRLLLSLETKLVEHSEQK**VEDLPADDILR**VEKYLRRRKYSLFAAFYS
ATMLQDVDDAIQFEVSIGNYGNKFDMTCLPLASTTQYSRAVFDGCHYYLFWGNVKKPVVVLSSYWEDISHRIETQ
NQLGLIADRLAEGLEQVHLALKAQCSTEDVDSLVLAQLTDELIAGCSQPLGDIHETPSATHLDQYLYQLRTHHLSQ
ITEAALALKLGHSELPAALEQAEDWLLRLRALAEFPQNSLPDIVIWMQLQGDKRVAQYQVPAHQVLFSSRGANYCG
KNCGLQTIIFLKYPMEKVPGARMPVQIRVKLWFGLSVDEKEFNQFAEGKLSVFAETYENETKLALVGNWGTGLT
YPK**FSDVTGK**IKLPKDSFRPSAGWTWAGDFVFCPEKTLHDM DAGHLSFVEEVFENQTRLPGGQWIYMSDNYTDV
NGEKVLPKDDIECLPGWK**WEDEEWSTDLNRAVDEQGWESITIPPER**KPKHWVPAEK**MYTHRR**RRWVLRRLRDL
SOMEALKRHRQAEEGEGWEYASLFGWK**FHLEYR**KTDAFRRRRWRRR**RMEPLEK**TGPAAVFALEGALGGVMDKSE
DSMSVSTLSFGVNRPTISCIIFYGNRYHLRCYMYQARD**DLAAMDK**DSFSDPYAIVSFLHQSQKT VVVKNLTNP TWD

QTLIFYEIEIFGEPATVAEQPPSIVVELYDHDYGADEFMGRICQPSLERMPRLAWFPLTRGSQPSGELLASFE
 LIQR**EKPAIHHPGFVEQETSRILDESEDTLPYPPPPQR**EANIYMPQNIKPALQRTAIEILAWGLRNMK**SYQLA**
NISSPSLVVECGGQTVQSCVIRNLRKNPNFDICTLFMEVMLPREELYCPPIITVKVIDNRQFGRRPVVGQCTIRSL
 ESFLCDPYSAESPSQGGPDDVSLSPGEDVLIDIDDKEPLIPTQEEEFIDWWSKFFASIGEREKCGSYLEKDFD
 TLKVYDTQLENVEAFEGLSDFCNTFKLYRGK**TQEETEDPSVIGEFK**GLFK**IYPLPEDPAIPMPPR**QFHQLAAQGP
 QECLVRIYIVRAFGQLQPKDPNGKCDPYIKISIGKKSVDQDNYIPTCLEPVFGKMFELTCTLPLEKDLKITLYDY
 DLLSKDEK**IGETVVDLENR**LLSKFGARCGLPQTYCVSGPNQWRDQLRPSQLLHLFCQQHRVKAPVYRTDRVMFQD
KEYSIEEIEAGRINPHIGPVEERLALHVLQQQGLVPEHVESRPLYSPQPDIEQGLQMWVDLFPKALGRPGPE
FNITERRARRFFLCIIWNTRDVILDDLSLTGEKMSDIYVKGWMI GFEEHK**TDVHYRSLGEGNFNWR**FIFFPF
 DYLPAEQVCTIAKKDAFWRLDKTESKIPARVVFIWDNDK**FSFDDFLGSLQLDLNR**MPKPAKTAKKCSLDQLDDA
 FHPEWVSVLFEQKTVKGWVPCVAEEGEKKILAGKLEMTLEIVAESSEHEERPAQGRDEPNMNPKELEDPFRPDTSF
 LWFTSPYKTMKFILWRRFRWAILFIILFILLFLAIFIYAFPNYAAMKLVKPPS

Mass Match Peptides (bold):

AVDEQGWESITIPPER [94]
 CIIWNTR [104]
 DLAAMDK [132]
 DLSQMEALK [139]
 EFNQFAEGK [185]
 EKPAIHHPGFVEQETSR [201]
 EYSIEEIEAGR [241]
 FHLEYR [254]
 FSDVTGK [272]
 FSFDDFLGSLQLDLNR [273]
 GEGVAYR [291]
 IETQNQLLGIADR [363]
 IGETVVDLENR [367]
 IIDWDR [370]
 ILDESEDTLPYPPPPQR [375]
 IYPLPEDPAIPMPPR [403]
 KLPSRPPPHYPGIK [426]
 LLSDKPQDFQIR [469]
 MDVGTIYR [511]
 MYYTHR [531]
 MYYTHRR [532]
 NLVDPFVEVSFAGK [547]
 RMEPLEK [607]
 SLGEGGNFNWR [640]
 SYQLANISSPSLVVECGGQTVQSCVIR [667]
 TDALLGEFR [681]
 TDVHYR [686]
 TQEETEDPSVIGEFK [724]
 VEDLPADDILR [753]
 VQVIEGR [794]
 WEDEEWSTDLNR [824]
 WLLSDPDDFSAGAR [827]

Tandem Peptides (underline):

ALGRPGPPFNITPR [76]
 DLSQMEALK [139]
 GWMIGFEEHK [329]

Peptide Source: iTRAQ, Colorectal cancer

MLRVFILIYAENVHTPDTDISDAYCSAVFAGVKKRTKVIKNSVNPVWNEGFWDLKGIPLDQGSSELHVVKDHETM
 GRNRFGLGEAKVPLREVLA TPSSLASFNAPLLDTKKQPTGASVLQVSYTLPFGAVPLFPPTPLEPSPTLPDLIDV
 VADTGGEEDTEDQGLTGDEAEFFLDQSGGPGAPTTPRKLPSPRPPPHYPGIK**KRSAPTSR**KLLSDKPQDFQIRVQ
 VIEGRQLPGVNIKPVVKVTAAGQTKRTRIHKGNSPLFNETLFFNLFDSPGELFDEPIFITVVDSSRLRTDALLGE
 FRMDVGTIYREPRHAYLRKWL LLSDPDDFSAGARGYLKTSCLVLFSGDEAPLERKDPSEDKEDIESNLLRFTGVA
 LRGAHFCLKVFR AEDLPQMDDAVMDNVKQIFGFESNKKNLVDPPFVEVSFAGKMLCSKILEKTANPQWNQNTILPA

MFPSMCEKMRIRIIDWDRDLTHNDIVATTYLSMSKISAPGGEIEEEPAGAVKPSKASDLDDYLGLFPTFGPCYINL
YGS?REFTGFDPYTELNTGKGEVAYRGRLLLSLETKLVEHSEQKVEDLPADDILRVEKYLRRRKYSLFAAFYS
ATMLQDVDDAIQFEVSIQNYGNKFDMTCLPLASTTQYSRAVFDGCHYYLPLWGNVKNPVVVLSSYWEDISHRIETQ
NQLLGIADRLEAGLEQVHLALKAQCSTEDVDSLVAQLTDELIAGCSQPLGDIHETPSATHLDQYLYQLRTHHLSQ
ITEAALALKLGHSELPAALEQAEDWLLRLRALAEFPQNSLPDIVIWMQLQGDKRVAQYQVPAHQVLFSSRRGANYCG
KNCCKLQITIFLKYPMEKVPGARMPVQIRVKLWFGLSVDEKEFNQFAEGKLSVFAETYENETKLALVGNWGTGLT
YPKFSDVTGKIKLPKDSFRPSAGWTWAGDWFCPEKTLHDMADAGHLSFVEEVFENQTRLPGGQWIYMSDNYTDV
NGEKVLPKDDIECPLGKWEDEEWSTDLNRAVDEQGWYSITIPPERKPKHWVPAEKMYTHRRRRWVRLRRRDL
SQMEALKRHRQAEAEEGEGWEYASLFGWKHFHLEYRKTDFAFRRRRWRRRMEPLEKTGPAAVFALEGALGGVMDKSE
DSMSVSTLSFGVNRPTISCIFDYGNRYHLRCYMYQARDLAAMDKDSFSDPYAIVSFLHQSQKTVVVKNLTNPTWD
QTLIFYEIEIFGEPATVAEQPPSIVVELYDHDYGADEFMGRCICQPSLERMPRLAWFPLTRGSQPSGELLASFE
LIQREKPAIHHPGFEVQETSRIILDESEDTDLPPPPQREANIYMPQNIKALQRTAIEILAWGLRNMKSYQLA
NISSPSLVVECGGQTVQSCVIRNLRKNPNFDICTLFMEVMLPREELYCPPITVKVIDNRQFGRRPVVGQCTIRSL
ESFLCDPYSAESPSQGGPDDVSLSPGEDVLIDDDKEPLIPIQEEEFIDWWSKFFASIGEREKCGSYLEKDFD
TLKVYDTQLENVEAFEGLSDFCNTFKLYRGKTQEETEDPSVIGEFKGLFKIYPLPEDPAIPMPPRQFHQLAAQGP
QECLVRIYIVRAFLQPKDPNGKCDPYIKISIGKKSVDQDNYIPTLEPVFGKMFELTCTLPLEKDLKITLYDY
DLLSKDEKIGETVVDLENRLSKFGARCGLPQTYCVSGPNQWRDQLRPSQLHLFCQHRVKAPVYRTDRVMFQD
KEYSIEEIEACRIPNPHLCPVEERLALHVLQQGLVPEHVESRPLYSPLQPDIEQCKLQMWVDLFPKALGRPGPP
FNITPRRARFFLRCCIWNTRDVLDDLSLTGEKMSDIYVKGWMIGFEEHKQKTDVHYRSLGGEGNFNWRFIFFP
DYLPAEQVCTIAKKDAFWRLDKTESKIPARVVVFQIWDNDKFSFDDFLGSLQLDLNRMKPAKTAKKCSLDQLDDA
FHPWFVSLFEQKTVKGWPCVAEEGKKILAGKLEMTLEIVAESEHEERPAQGRDEPNMNPKEDEPRRPTDTSF
LWFTSPYKTMKFIWRRFRWAILFIILFILLFLAIFIYAFPNYAAMKLVKPFPS

Mass Match Peptides (bold):

IYIVR [926]
KRSAPTISR [928]

Tandem Peptides (underline):

IYIVR [926]
KRSAPTISR [928]

Peptide Source: iTRAQ, Hepatocellular cancer

MLRVFILIYAENVHTPDTDISDAYCSAVFAGVKKRTKVIKNSVNPVWNEGFWDKLGIPLDQGSSELHVVKDHETM
GRNRFLEAKVPLREVLATPSLSASFNAPLLDTKKQPTGASLVLVQVSYTPLPGAVPLFPPTPLEPSPTLPDLV
VADTGGEEDTEDQGLTGDEAEFFLDQSGGPGAPTTPRKLPSRPPPHYPGIIKRRSAPTISRKLLSDKPDQFQIRVQ
VIEGRQLPGVNIKPVVKVTAAGQTKRTRIHKGSNPLFNETLFFNLFDSPGELFDEPIFITVVDSSRLRDTALLGE
FRMDVGTIYREPRHAYLRKWLILLSDDPDSAGARGYLKTSCLVGLGPGDEAPLERKDPSEDKEDIESNLLRPTGVA
LRGAHFCLKVFRADLPQMDDAVMDNVKQIFGFESNKKNLVDPFVEVSFAGKMLCSKILEKTANPQWNQNTILPA
MFPSMCEKMRIRIIDWDRDLTHNDIVATTYLSMSKISAPGGEIEEEPAGAVKPSKASDLDDYLGLFPTFGPCYINL
YGS?REFTGFDPYTELNTGKGEVAYRGRLLLSLETKLVEHSEQKVEDLPADDILRVEKYLRRRKYSLFAAFYS
ATMLQDVDDAIQFEVSIQNYGNKFDMTCLPLASTTQYSRAVFDGCHYYLPLWGNVKNPVVVLSSYWEDISHRIETQ
NQLLGIADRLEAGLEQVHLALKAQCSTEDVDSLVAQLTDELIAGCSQPLGDIHETPSATHLDQYLYQLRTHHLSQ
ITEAALALKLGHSELPAALEQAEDWLLRLRALAEFPQNSLPDIVIWMQLQGDKRVAQYQVPAHQVLFSSRRGANYCG
KNCCKLQITIFLKYPMEKVPGARMPVQIRVKLWFGLSVDEKEFNQFAEGKLSVFAETYENETKLALVGNWGTGLT
YPKFSDVTGKIKLPKDSFRPSAGWTWAGDWFCPEKTLHDMADAGHLSFVEEVFENQTRLPGGQWIYMSDNYTDV
NGEKVLPKDDIECPLGKWEDEEWSTDLNRAVDEQGWYSITIPPERKPKHWVPAEKMYTHRRRRWVRLRRRDL
SQMEALKRHRQAEAEEGEGWEYASLFGWKHFHLEYRKTDFAFRRRRWRRRMEPLEKTGPAAVFALEGALGGVMDKSE
DSMSVSTLSFGVNRPTISCIFDYGNRYHLRCYMYQARDLAAMDKDSFSDPYAIVSFLHQSQKTVVVKNLTNPTWD
QTLIFYEIEIFGEPATVAEQPPSIVVELYDHDYGADEFMGRCICQPSLERMPRLAWFPLTRGSQPSGELLASFE
LIQREKPAIHHPGFEVQETSRIILDESEDTDLPPPPQREANIYMPQNIKALQRTAIEILAWGLRNMKSYQLA
NISSPSLVVECGGQTVQSCVIRNLRKNPNFDICTLFMEVMLPREELYCPPITVKVIDNRQFGRRPVVGQCTIRSL
ESFLCDPYSAESPSQGGPDDVSLSPGEDVLIDDDKEPLIPIQEEEFIDWWSKFFASIGEREKCGSYLEKDFD
TLKVYDTQLENVEAFEGLSDFCNTFKLYRGKTQEETEDPSVIGEFKGLFKIYPLPEDPAIPMPPRQFHQLAAQGP
QECLVRIYIVRAFLQPKDPNGKCDPYIKISIGKKSVDQDNYIPTLEPVFGKMFELTCTLPLEKDLKITLYDY
DLLSKDEKIGETVVDLENRLSKFGARCGLPQTYCVSGPNQWRDQLRPSQLHLFCQHRVKAPVYRTDRVMFQD
KEYSIEEIEACRIPNPHLCPVEERLALHVLQQGLVPEHVESRPLYSPLQPDIEQCKLQMWVDLFPKALGRPGPP
FNITPRRARFFLRCCIWNTRDVLDDLSLTGEKMSDIYVKGWMIGFEEHKQKTDVHYRSLGGEGNFNWRFIFFP
DYLPAEQVCTIAKKDAFWRLDKTESKIPARVVFQIWDNDKFSFDDFLGSLQLDLNRMKPAKTAKKCSLDQLDDA

FHPEWFSVLFEQKTVKGWWPCVAEEGEKKILAGKLEMTLEIVAESSEHEERPAGQGRDEPNMNPKEDEPRRPDTSF
LWFTSYPYKTMKFIWRRFRWAILFIILFILLFLAIFIYAFPNYAAMKLVKPF

Mass Match Peptides (bold):

VVFQIWDNDK [810]

Tandem Peptides (underline):

VVFQIWDNDK [810]

Peptide Source: iTRAQ, Non-small cell lung cancer

MLRVFILYAENVHTPDTDISDAYCSAVFAGVKKRTKVIKNSVNPVWNEGFEDLKGIFLDQGSSELHVVKDIETM
GRNRFLEAKVPLREVLPATPSLSASFNAPLLDTKKQPTGASVLVQVSYTLPFGAVPLFPPTPLEPSTLPDLVDV
VADTGGEDTEDQGLTGDEAEFPLDQSGGPGAPTTPRKLPSRPPPHYPGKIKRKSAPT SRKLLSDKPDQFQIRVQ
VIEGRQIPGVNIKPVVKVTAAGQTKRTRIHKGNSPLFNETLFFNLFDS PGELFDEPIFITVVDSSRLTDALLGE
FRMDVGTIYREPRHAYLRKWLILSDPDDFSAGARGYLKTS LCVLGPGEAPLERKDPSEDKEDIESNLLRPTGVA
LRGAHFCLKVFRADLPQMDDAVMDNVKQIFGFESNKKNLVDPFVEVSFAGKMLCSKILEKTANPQWNQNTLPA
MFPSMCEKMRIRIIDWDRLTNDIVATTYLSMSKISAPGGEIEEPAGAVKPSKASDLDYLGFLPTFGPCYINL
YGS PREFTGFPDPYTELNTGKGEVAYRGRLLLSLETKLVEHSEQKVEDLPADDILRVEKYLRRRKYSLFAAFYS
ATMLQDVDDAIQFEVSI GNNGKFDMTCLPLASTTQYSRAVFDGCHYYYLPWGNVVKPVVLSY WEDISHRIETQ
NQLLGIADRLEAGLEQVHLALKAQCSTEDVDSLVAQLTDELIAGCSQPLGDIHETPSATHLDQYLYQLRTHHLSQ
ITEAALALKLGHSELPAALEQAEDWLLRLRALAEEPQNSLPDIVIWM LQGDKRVA YQRPVPAHQVLF SRRGANYCG
KNCGLQTIIFLKYPM EKVPGARMPVQIRVKLWFGLSVDEKEFNQFAEGKLSVFAETYENETKLALVGNWGT TGLT
YPKFS DVTGKIKL PKDSFRPSAGWTWAGDWFVCPEKTL LHDMDAGHLSFVEEVFENQTRLPGGQWIYMSDNYTDV
NGEKVLPKDDIECPLGWKWEDEEWSTDLNRAVDEQGW EYSITIPPERKPKHWVPAEKMYTHRRRRWVRLRRDL
SOMEALKRHRQAEAE GEGWEYASLFGWKFHLEYRKTDAFRRRRRRRRMEPLEKTGPAAVFALE GALGVMDDKSE
DSMSVSTLSFGVNRPTISCFIDYGNRYHLRCYMYQARDLAAMDKDSFSDPYAIVSFLHQSQKT VVVKNTLNPTWD
QTLIFYEIEIFGEPATVAEQPPSIVVELYDHD TYGADEFMGRICQPSLERMPRLAWFPLTRGSQPSGELLASFE
LIQREKPAIHHPGFEVQETSRI LDESED TDLPYPPQREANIYMPQNIKPALQRTAIEILAWGLRNMKSYQLA
NISSPSLVVECGQTQVQSCVIRNLRKNPNFDICTLFMEVMLPREELYC PPI TVKVIDNRQFGRRPVVGQCTIRSL
ESFLCDPYSAESPSPQGGPDVSLSPGEDVLI DIDDKEPLIPIQEEFIDWWSKFFASIGEREKCGSYLEKDFD
TLKVYDTQLENVEAFEGLSDFCNTFKLYRCKTQEETEDPSVIGEFKGLFKIYPLPEDPAIPMPPRQFHQLAAQGP
QECLVR IYIVRAFGLQPKDPNGKCDPYIKISIGKKSVDQDNYIPCTLEPVFGKMFELTCTLPLEKDLKITLYDY
DLSKDEKIGETVVDLENRLLSKFGARCLPQTYCVSGPNQWRDQLRPSQLLHLFCQQRHV KAPVYRTDRVMFQD
KEYSIEEIEAGRIPNPHLGPVEERLALHVLQOQGLVPEHVESRPLYSP LQPDIEQGKLQMWVDLFPKALGRPGPP
FNITPRRARRFFLRCTIWNTRDVLDDLSLTGEKMSDIYVKGWMIGFEEHKQKTDVHYRSLGGEGNFNWRFI FPF
DYLPAEQVCTIAKKDAFWRLDKTESKIPARVVFIQIWDNDKFSFDDFLGSLQLDLNRM PKPAKTAKKCSLDQLDDA
FHPEWFSVLFEQKTVKGWWPCVAEEGEKKILAGKLEMTLEIVAESSEHEERPAGQGRDEPNMNPKEDEPRRPDTSF
LWFTSYPYKTMKFIWRRFRWAILFIILFILLFLAIFIYAFPNYAAMKLVKPF

Mass Match Peptides (bold):

FSDVTGK [272]

IPNPHLGPVEER [386]

IYIVR [926]

RRDLSQMEALK [966]

TAIEILAWGLR [976]

VTAAGQTK [800]

Tandem Peptides (underline):

FSDVTGK [272]

IPNPHLGPVEER [386]

IYIVR [926]

RRDLSQMEALK [966]

TAIEILAWGLR [976]

VTAAGQTK [800]

Peptide Source: iTRAQ, Ovarian cancer

MLRVFILYAENVHTPDTDISDAYCSAVFAGVKRRTKVIKNSVNPVWNEGFEDLKGIFLDQGSSELHVVKDHETM
GRNRFLEGAQVPLREVLA TP SL SASFNAPLLDTKKQPTGASLVLVQVSYTFLPGAVPLFPPTPLEPSPTLPDLVDV
VADTGGSEEDTEDQGLTGDEAEFPFLDQSGGPGAPTTPRKLPSRPPPHYPGIKRKRSAPTSRKLLSDKPDQDFQIRVQ
VIEGRQLPGVNIKPVVKVTAAGQTKRTRIHKGNSPLFNETLFFNLFDSPGELFDEPIFITVVDSSRLRTDALLGE
FRMDVGTIYREPRHAYLRKWL L L S D P D F S A G A R G Y L K T S L C V L G P G D E A P L E R K D P S E D K E D I E S N L L R P T G V A
LRGAHFCLKVFAEDLPQMDDAVMDNVKQIFGFESNKNLVDPFVEVSFAGKMLCSKILEKTANPQWNQNTLPA
MFPSMCEKMRIRIIDWDR L T H N D I V A T T Y L S M S K I S A P G G E I E E P A G A V K P S K A S D L D D Y L G F L P T F G P C Y I N L
YGS PREFTGFDPYTELNTGKGEGVAYRGRLLLSLET KLVEHSEQKVEDLPADDILRVEKYLR R R K Y S L F A A F Y S
ATMLQDVDDAIQFEVSI G N Y G N K F D M T C L P L A S T T Q Y S R A V F D G C H Y Y L P W G N V K P V V L S S Y W E D I S H R I E T Q
NQLLG I A D R L E A G L E Q V H L A L K A Q C S T E D V D S L V A Q L T D E L I A G C S Q P L G D I H E T P S A T H L D Q Y L Y Q L R T H H L S Q
I T E A A L A L K L G H S E L P A A L E Q A E D W L L R L R A L A E E P Q N S L P D I V I W M L Q G D K R V A Y Q R V P A H Q V L F S R R G A N Y C G
K N C G K L Q T I F L K Y P M E K V P G A R M P V Q I R V K L W F G L S V D E K E F N Q F A E G K L S V F A E T Y E N E T K L A L V G N W G T T G L T
Y P K F S D V T G K I K L P K D S F R P S A G W T A G D W F V C P E K T L L H D M D A G H L S F V E E V F E N Q T R L P G G Q W I Y M S D N Y T D V
N G E K V L P K D D I E C P L G W K W E D E E W S T D L N R A V D E Q G W E Y S I T I P P E R K P K H W P A E K M Y Y T H R R R R W V L R R R D L
S Q M E A L K R H R Q A E A E G E G W E Y A S L F G W K F H L E Y R K T D A F R R R R W R R R M E P L E K T G P A A V F A L E G A L G G V M D D K S E
D S M S V T L S F G V N R P T I S C I F D Y G N R Y H L R C Y M Y Q A R D L A A M D K D S F S D F Y A I V S F L H Q S Q K T V V V K N T L N P T W D
Q T L I F Y E I E I F G E P A T V A E Q P P S I V E L Y D H D T Y G A D E F M G R C I C Q P S L E R M P R L A W F L P L T R G S Q P S G E L L A S F E
N I S S P S L V V E C G G Q T V Q S C V I R N L R K N P N F D I C T L F M E V M L P R E E L Y C P P I T V K V I D N R Q F G R R P V V G Q C T I R S L
E S F L C D P Y S A E S P S P Q G G P D D V S L L S P G E D V L I D I D D K E P L I P I Q E E E F I D W S K F F A S I G E R E K C G S Y L E K D F D
T L K V Y D T Q L E N V E A F E G L S D F C N T F K L Y R G K T Q E E T D P S V I G E F K G L F K I Y P L P E D P A I P M P P R Q F H Q L A A Q G P
Q E C L V R I Y I V R A F G L Q P K D P N G K C D P Y I K I S I G K K S V S D Q D N Y I P C T L E P V F G K M F E L T C T L P L E K D L K I T L Y D Y
D L L S K D E K I G E T V V D L E N R L L S K F G A R C G L P Q T Y C V S G P N Q W R D Q L R P S Q L L H L F C Q Q H R V K A P V Y R T D R V M F Q D
K E Y S I E E I E A G R I P N P H L G P V E E R L A L H V L Q Q Q G L V P E H V E S R P L Y S P L Q P D I E Q G K L Q M W V D L F P K A L G R P G P P
F N I T P R R A R R F F L R C I I W N T R D V I L D D L S L T G E K M S D I Y V K G W M I G F E E H K Q K T D V H Y R S L G G E G N F N W R F I F P T
D Y L P A E Q V C T I A K K D A F W R L D K T E S K I P A R V V F Q I W N D N K F S F D D L G S L Q L D L N R M E K P A K T A K K C S L D Q L D D A
F H P E W F V S L F E Q K T V K G W W P C V A E E G E K K I L A G K L E M T L E I V A E S E H E E R P A G Q G R D E P N M N F K L E D P R R P D T S F
L W F T S P Y K T M K F I L W R R F R W A I I L F T I L F I L L F L A I T Y A F P N Y A A M K L V K P F S

Mass Match Peptides (bold):

VPAHQVLFSSRR [997]

VTAAGQTKRTR [999]

Tandem Peptides (underline):

VPAHQVLFSSRR [997]

VTAAGQTKRTR [999]

Peptide Source: iTRAQ, Renal cell cancer

MLRVFILYAENVHTPDTDISDAYCSAVFAGVKRRTKVIKNSVNPVWNEGFEDLKGIFLDQGSSELHVVKDHETM
GRNRFLEGAQVPLREVLA TP SL SASFNAPLLDTKKQPTGASLVLVQVSYTFLPGAVPLFPPTPLEPSPTLPDLVDV
VADTGGSEEDTEDQGLTGDEAEFPFLDQSGGPGAPTTPRKLPSRPPPHYPGIKRKRSAPTSRKLLSDKPDQDFQIRVQ
VIEGRQLPGVNIKPVVKVTAAGQTKRTRIHKGNSPLFNETLFFNLFDSPGELFDEPIFITVVDSSRLRTDALLGE
FRMDVGTIYREPRHAYLRKWL L L S D P D F S A G A R G Y L K T S L C V L G P G D E A P L E R K D P S E D K E D I E S N L L R P T G V A
LRGAHFCLKVFAEDLPQMDDAVMDNVKQIFGFESNKNLVDPFVEVSFAGKMLCSKILEKTANPQWNQNTLPA
MFPSMCEKMRIRIIDWDR L T H N D I V A T T Y L S M S K I S A P G G E I E E P A G A V K P S K A S D L D D Y L G F L P T F G P C Y I N L
YGS PREFTGFDPYTELNTGKGEGVAYRGRLLLSLET KLVEHSEQKVEDLPADDILRVEKYLR R R K Y S L F A A F Y S
ATMLQDVDDAIQFEVSI G N Y G N K F D M T C L P L A S T T Q Y S R A V F D G C H Y Y L P W G N V K P V V L S S Y W E D I S H R I E T Q
NQLLG I A D R L E A G L E Q V H L A L K A Q C S T E D V D S L V A Q L T D E L I A G C S Q P L G D I H E T P S A T H L D Q Y L Y Q L R T H H L S Q
I T E A A L A L K L G H S E L P A A L E Q A E D W L L R L R A L A E E P Q N S L P D I V I W M L Q G D K R V A Y Q R V P A H Q V L F S R R G A N Y C G
K N C G K L Q T I F L K Y P M E K V P G A R M P V Q I R V K L W F G L S V D E K E F N Q F A E G K L S V F A E T Y E N E T K L A L V G N W G T T G L T
Y P K F S D V T G K I K L P K D S F R P S A G W T A G D W F V C P E K T L L H D M D A G H L S F V E E V F E N Q T R L P G G Q W I Y M S D N Y T D V
N G E K V L P K D D I E C P L G W K W E D E E W S T D L N R A V D E Q G W E Y S I T I P P E R K P K H W P A E K M Y Y T H R R R R W V L R R R D L
SOMEALKRHRQAEEAEGEGWEYASLFGWK F H L E Y R K T D A F R R R R W R R R RMEPLEKTGPAAVFALEGALGGVMDKSE
DSMSVSTLSFGVNRPTISCIFDYGNRYHLRCYMYQARDLAAMDKDSFSDFYAIVSFLHQSQKT VVVKN T L N P T W D
Q T L I F Y E I E I F G E P A T V A E Q P P S I V E L Y D H D T Y G A D E F M G R C I C Q P S L E R M P R L A W F L P L T R G S Q P S G E L L A S F E
L I Q R E K P A I H H I P G F E V Q E T S R I L D E S E D T D L P Y P P P Q R E A N I Y M V P Q N I K P A L Q R T A I E I L A W G L R N M K S Y Q L A
N I S S P S L V V E C G G Q T V Q S C V I R N L R K N P N F D I C T L F M E V M L P R E E L Y C P P I T V K V I D N R Q F G R R P V V G Q C T I R S L
E S F L C D P Y S A E S P S P Q G G P D D V S L L S P G E D V L I D I D D K E P L I P I Q E E E F I D W S K F F A S I G E R E K C G S Y L E K D F D
T L K V Y D T Q L E N V E A F E G L S D F C N T F K L Y R G K T Q E E T D P S V I G E F K G L F K I Y P L P E D P A I P M P P R Q F H Q L A A Q G P

QECLVRIYIVRAFLQPKDPNGKCDPYIKISIGKKSVDQDNYIPCTLEPVFGKMFELTCTLPLEKDLKITLYDY
DLSKDEKIGETVVDLENRLLSKFGARCGLPQTYCVSGPNQWRDQLRPSQLLHLFCQQHRVKAPVYRTDRVMFQD
KEYSIEIEACRIPNPHLGPVEERLALHVLQQQGLVPEHVESRPLYSPLQPDIEQGKLMWVDLFPKALGRPGPP
FNITPRRARFFLRICIWNTRDVLDDSLTGEKMSDIYVKGWMIGFEEHKQKTDVHYRSLGGEGNFWRFIFPF
DYLPAEQVCTIAKKDAFWRLDKTESKIPARVVFQIWDNDKFSFDDFLGSLQLDLNRMKPAKTAKKCSLDQLDDA
FHPEWVSVLFEQKTVKGWWPCVAEEGEKKILAGKLEMTLEIVAEESEHEERPAGQGRDEPNMNPKLEDPRRPDTSF
LWFTSPYKTMKFIWRRFRWAILFIILFILLFLAIFIYAFPNYAAMKLVKPF

Mass Match Peptides (bold):

FSDVTGKIK [912]
IGETVVDLENR [367]
LLSDK [938]
RMEPLEK [607]
RRDLSQMEALK [966]

Tandem Peptides (underline):

FSDVTGKIK [912]
IGETVVDLENR [367]
LLSDK [938]
RMEPLEK [607]
RRDLSQMEALK [966]

Peptide Source: iTRAQ, Small cell lung cancer

MLRVFILIYAENVHTPDTDISDAYCSAVFAGVKKRRTKVIKNSVNPVWNEGFEWDLKGIPLDQGSSELHVVKDHETM
GRNRFGLGEAKVPLREVLATPSLSASFNAPLLDTKKQPTGASLVLVQVSYTLPGLAVPLFPPPTPLEPSPTLPDLVDV
VADTGGEEDTEDQGLTGDEAEFLDQSGGPGAPTTPRKLPSRPPPHYPGIKRKRSAPTSRL**LLSDK**PQDFQIRVQ
VIEGRQLPGVNIKPVKVTAAGQTKRTRIHKGNSPLFNETLFFNLFDSPGELFDEPIFITVVDSSRLRTDALLGE
FRMDVGTIYREPRHAYLRKWL**LLSD**PDDFSAGARGYLKTSCLVLPGEDEAPLERKDPSEDKEDIESNLLRPTGVA
LRGAHFCLKVFRADLPQMDDAVMDNVKQIFGFESNKKNLVDPFVEVSFAGKMLCSKILEKTANPQWNQNTILPA
MFPSMCEKMRIRIIDWRLTHNDIVATTYLSMSKISAPGGEIEEPAGAVKPSKASDLDYLGFLPTFGPCYINL
YGSPREFTGFPDPYTELNTGKGEVAYRGRLLLSLETCLVEHSEQKVEDLPADDILRVEKYLRKKYSLFAAFYS
ATMLQDVDDAIQFEVSGNYGNKFDMTCLPLASTTQYSRAVFDGCHYYLPGWNVKPVVVLSSYWDISHRIETQ
NQLGIADRLEAGLEQVHLAKAQCTSTEDVDSLVAQLTDELIAGCSQPLGDIHETPSATHLDQYLYQLRTHHLSQ
ITEAALAKLKGSELPAALEQAEDWLLRLRALAEEPQNSLPDIVIWMQLQGDKRVAQVRPAHQVLFSSRRGANVCG
KNCCKLQITIFLKYPMEKVPGARMPVQIRVKLWFGLSVDEKEFNQFAEGKLSVFAETYENETKLALVGNWGTGLT
YKFSFSDVTGKIKLPKDSFRPSAGWTWAGDWFVCPKTLHMDAGHLSFVEEVFENQTRLPGGQWIYMSDNYTDV
NGEVLPLKDDIECPGKWEDEEWSTDLNRAVDEQWEYSITIPPERKPKHWVPAEKMYTHRRRRWVRLRRDL
SQMEALKRRHQAEAEGEWEYASLFGWKFHLEYRKTDAFRRRRWRRRMEPLEKTGPAAVFALEGALGGVMDDKSE
DSMSVSTLSFGVNRPTISCI FDYGNRYHLRCYMYQARDLAAMDKDSFSDPYAIVSFLHQSQKTVVVKNTLNPTWD
QTLIFYEIEIFGEPATVAEQPPSIVVELYDHDYGADEFMGRICQPSLERMPLAWFPLTRGSQPSGELLASFE
LIQREKPAIHHPGFEVQETSRLIDESEDTLPPPPQREANIYMPQNIKPAIQRTAIEILAWGLRNMKSYQLA
NISSPSLVVECGQTQVQSCVIRNLRKNPNFDICTLFMEVMLPREELYCPPITVKVIDNRQFGRRPVVGQCTIRSL
ESFLCDPYSAESPSPOGGPDDVSLSPGEDVLIDIDKEPLIPIQEEEFIDWWSKTFASIGEREKCGSYLEKDFD
TLKVYDTQLENVEAFEGLSDFCNTFKLYRGKTQEETEDPSVIGEFKGLFKIYPLPEDPAIPMPPRQFHQLAAQGP
QECLVRIYIVRAFLQPKDPNGKCDPYIKISIGKKSVDQDNYIPCTLEPVFGKMFELTCTLPLEKDLKITLYDY
DLSKDEKIGETVVDLENRLLSKFGARCGLPQTYCVSGPNQWRDQLRPSQLLHLFCQQHRVKAPVYRTDRVMFQD
KEYSIEIEACRIPNPHLGPVEERLALHVLQQQGLVPEHVESRPLYSPLQPDIEQGKLMWVDLFPKALGRPGPP
FNITPRRARFFLRICIWNTRDVLDDSLTGEKMSDIYVKGWMIGFEEHKQKTDVHYRSLGGEGNFWRFIFPF
DYLPAEQVCTIAKKDAFWRLDKTESKIPARVVFQIWDNDKFSFDDFLGSLQLDLNRMKPAKTAKKCSLDQLDDA
FHPEWVSVLFEQKTVKGWWPCVAEEGEKKILAGKLEMTLEIVAEESEHEERPAGQGRDEPNMNPKLEDPRRPDTSF
LWFTSPYKTMKFIWRRFRWAILFIILFILLFLAIFIYAFPNYAAMKLVKPF

Mass Match Peptides (bold):

LLSDK [938]

Tandem Peptides (underline):

LLSDK [938]

OGTA098 (SEQ ID No: 18)

Peptide Source: 1D-GE, Breast cancer

MARTRDRVRLLLLLLIFCNVGSGLHLQVLSTRNENKLLPKHPLVLRQKRAWITAPVALREGEDLSKKNPIAKIHSD
LAEERGLKITYKYTGKITEPPFGIFVFNKDTGELNVTSLDR**EETPFFLLTGYALDAR**GNNVEKPLELRIKVL
INDNEPVFTQDVFGSVEELSAATLVMKINATDAEPNTLSKISYRIVSLEPAYPPVFYLNK**DTGEIYTTSVT**
LDREEHSSYTLTVEARDGNCEVTDKPVKQAVQIRILDVNDNIPVVENKVLEGMVEENQVNVETRIKVFDADEI
GSDNWLANFTFASGNEGgyFHIETDAQTNEGIVTLIKEVDYEMKNLDFSVIVANKAAFHKSIKSKYKPTPIPIK
VKVKNVKEGIHFkSSVISIYVESMDRSSKGQIIGNFQAFDEDTGLPAHARYVKLEDRDNWISVDSVTSEIKLAK
LPDFESRYVQNGTYTVK**IVAISEDYPR**KTITGTVLINVEDINDNCPTLIEPVQTICHDAEYVNVTAEDLDGHPNS
GPFSSVIDKPPGMAEKWKIAR**QUESTSVLLQQSEKK**LG RSEIQFLISDNQGFSCPEKQVLTTLTVCEVLHGSGCRE
AQHDSYVGLGPAAIALMILAFLLLLLVPLLLLMCHCGKAKAFTPIPGTIEMLHPWNNEGAPPEDK**VVPSFLPVD**
QGGSLVGRNGVGGMAKEATMKGSSSASIVKGQHEMSEMDGRWEEHRSLLSGRATQFTGATGAIMTTETTKTARAT
GASRD**DMAGAQAALNEEFLLR**NYFTDKAASYTEEDENHTAKDCLLVYSQEETESLNASIGCCSFIEGELDDR**FL**
DDLGLKFKTLAEVCLGQKIDINKEIEQRQKPATETSMNTASHSLCEQTMVNSENTYSSGSSFPVPKSLQEAANAEK
VTQEIIVTERSVSSRQAQKVATPLPDPMASRNVIAETETSYVTGSTMPPTTVILGPSQPQSLIVTER**VYAPASTLVD**
QPYANEGTVVTERVIQPHGGGNNPLEGTQHLQDVPYVMVRERESFLAPSSGVQPTLAMPNIAVGQNVTVTERVL
APASTLQSSYQIPTENSMTARNTTVSGAGVPGPLPDFGLEESGHSNSTITTSSTRVTKHSTVQHSYS

Mass Match Peptides (bold):

ATQFTGATGAIMTTETTK [93]
DGNCEVTDKPVK [123]
DMAGAQAALNEEFLLR [142]
DNWISVDSVTSEIK [148]
DTGEIYTTSVTLDR [159]
EETPFFLLTGYALDAR [182]
FLDDLGLK [257]
IVAISEDYPR [400]
NGVGGMAK [536]
QUESTSVLLQQSEK [568]
QUESTSVLLQQSEKK [569]
VTQEIIVTER [806]
VVPSFLPVDQGGSLVGR [812]
VYAPASTLVDQPYANEGTVVTER [816]
VQNGTYTVK [876]

Tandem Peptides (underline):

VVPSFLPVDQGGSLVGR [812]

Peptide Source: 1D-GE, Cervical cancer

MARTRDRVRLLLLLLIFCNVGSGLHLQVLSTRNENKLLPKHPLVLRQKRAWITAPVALREGEDLSKKNPIAKIHSD
LAEERGLKITYKYTGKITEPPFGIFVFNKDTGELNVTSLDR**EETPFFLLTGYALDAR**GNNVEKPLELRIKVL
INDNEPVFTQDVFGSVEELSAATLVMKINATDAEPNTLSKISYRIVSLEPAYPPVFYLNK**DTGEIYTTSVT**
LDREEHSSYTLTVEARDGNCEVTDKPVKQAVQIRILDVNDNIPVVENKVLEGMVEENQVNVETRIKVFDADEI
GSDNWLANFTFASGNEGgyFHIETDAQTNEGIVTLIKEVDYEMKNLDFSVIVANKAAFHKSIKSKYKPTPIPIK
VKVKNVKEGIHFkSSVISIYVESMDRSSKGQIIGNFQAFDEDTGLPAHARYVKLEDRDNWISVDSVTSEIKLAK
LPDFESRYVQNGTYTVK**IVAISEDYPR**KTITGTVLINVEDINDNCPTLIEPVQTICHDAEYVNVTAEDLDGHPNS
GPFSSVIDKPPGMAEKWKIAR**QUESTSVLLQQSEKK**LG RSEIQFLISDNQGFSCPEKQVLTTLTVCEVLHGSGCRE
AQHDSYVGLGPAAIALMILAFLLLLLVPLLLLMCHCGKAKAFTPIPGTIEMLHPWNNEGAPPEDK**VVPSFLPVD**
QGGSLVGRNGVGGMAKEATMKGSSSASIVKGQHEMSEMDGRWEEHRSLLSGRATQFTGATGAIMTTETTKTARAT
GASRD**DMAGAQAALNEEFLLR**NYFTDKAASYTEEDENHTAKDCLLVYSQEETESLNASIGCCSFIEGELDDRFL
DDLGLKFKTLAEVCLGQKIDINKEIEQRQKPATETSMNTASHSLCEQTMVNSENTYSSGSSFPVPKSLQEAANAEK
VTQEIIVTERSVSSRQAQKVATPLPDPMASRNVIAETETSYVTGSTMPPTTVILGPSQPQSLIVTERVYAPASTLVD
QPYANEGTVVTERVIQPHGGGNNPLEGTQHLQDVPYVMVRERESFLAPSSGVQPTLAMPNIAVGQNVTVTERVL
APASTLQSSYQIPTENSMTARNTTVSGAGVPGPLPDFGLEESGHSNSTITTSSTRVTKHSTVQHSYS

Mass Match Peptides (bold):

DTGEIYTTSVTLDR [159]

EEHSSYTLTVEAR [174]

IVAISEDYPR [400]

Tandem Peptides (underline):

IVAISEDYPR [400]

Peptide Source: 1D-GE, Hepatocellular carcinoma

MARTRDRVRLLLLLICFNVGSGHLQVLSTRNENKLLPKHPLVLRQKRAWITAPVALREGEDLSKKNPIAKIHSD
 LAERGLKITTYKGTGKITEPPFGIFVFNKDTGELNVTSLDREETPFFLLTGYALDARGNNVEKPLELR IKVLD
 INDNEPVFTQDVFVGSVEELSAHTLVMKINATDADEPNTLNSKISYRIVSLEPAYPPVFYLNKDTGEIYTTSVT
 LDR EEHSSYTLTVEARDGNGEVDKPVKQAQVQIRILDVNDNIPVVENKVLEGMVEENQVNVEVTRIKVFDADI
 GSDNWLANFTFASGNEGGYFHIETDAQTNEGIVTLIKEVDYEEEMKNLDFSVIVANKAAFHKSIRSKYKPTPIPIK
 VKVKNVKEGIHFKSSVISIYVSESMRDSKQGIIGNFQAFDEDTGLPAHARYVKLEDRDNWISVDSVTSEIKLAK
 LPDFESRYVQNGTYTVKIVAISEDYPRKTIITGTVLINVEDINDNCPTLIEPVQTICHDAEYVNVTAEDLDGHPNS
 GPFESVIDKPPGMAEKWKIARQESTSVLLQQSEK KLGRSEIQFLISDNQGFSCPEKQVLTTLVCEVLHGSGCRE
 AQHDSYVGLGPAALMILAFLLLLVPLLLLMCHCGKAKAFTPIPGTIEMLHPWNNEGAPPEDKVVP SFLPVD
 QGGSILVGRNGVGGMAKEATMKGSSSASIVKGQHEMSEMDGRWEEHRSLLSGRATQFTGATGAIMTTETTKTARAT
 GASRDMAGAAVAALNEEFRLNYFTDKAASYTEEDENHTAKDCLLVYSQEETESLNASIGCCSFIEGELDDRFL
 DDGLGLKFKTLAEVCLGQKIDINKEIEQRQKPATETSMNTASHSLCEQTMVNSENTYSSGSSFPVPKSLQEANA
 EKVQEIIVTERSVSSRQAQKVATPLPDPMASRNVIAETETSYVTGSTMPPTTVILGPSQPQSLIVTERVYAPASTLVD
 QPYANEGTVVTVTERVIQPHGGGSPLEGTQHLQDVPYVMVRERESFLAPSSGVQPTLAMPNIAVGQNVTVTERVL
 APASTLQSSYQIPTENSMTARNTTVSGAGVGPPLPDFGLEESGHSNSTITTSSTRVTKHSTVQHSYS

Mass Match Peptides (bold):

ATQFTGATGAIMTTETTK [93]

DNWISVDSVTSEIK [148]

DTGEIYTTSVTLDR [159]

FLDDLGLK [257]

GNNVEKPLELR [304]

GQIIGNFQAFDEDTGLPAHAR [311]

INATDADEPNTLNSK [381]

IVAISEDYPR [400]

QESTSVLLQQSEK [568]

VATPLPDPMASR [746]

VLEGMVEENQVNVEVTR [778]

VTQEIIVTER [806]

VVPSFLPVDQGGSILVGR [812]

WEEHR [825]

Tandem Peptides (underline):

ATQFTGATGAIMTTETTK [93]

Peptide Source: 1D-GE, Lung cancer

MARTRDRVRLLLLLICFNVGSGHLQVLSTRNENKLLPKHPLVLRQKRAWITAPVALREGEDLSKKNPIAKIHSD
 LAERGLKITTYKGTGKITEPPFGIFVFNKDTGELNVTSLDREETPFFLLTGYALDARGNNVEKPLELR IKVLD
 INDNEPVFTQDVFVGSVEELSAHTLVMKINATDADEPNTLNSKISYRIVSLEPAYPPVFYLNKDTGEIYTTSVT
 LDREHSSYTLTVEARDGNGEVDKPVKQAQVQIRILDVNDNIPVVENKVLEGMVEENQVNVEVTRIKVFDADI
 GSDNWLANFTFASGNEGGYFHIETDAQTNEGIVTLIKEVDYEEEMKNLDFSVIVANKAAFHKSIRSKYKPTPIPIK
 VKVKNVKEGIHFKSSVISIYVSESMRDSKQGIIGNFQAFDEDTGLPAHARYVKLEDRDNWISVDSVTSEIKLAK
 LPDFESRYVQNGTYTVKIVAISEDYPRKTIITGTVLINVEDINDNCPTLIEPVQTICHDAEYVNVTAEDLDGHPNS
 GPFESVIDKPPGMAEKWKIARQESTSVLLQQSEK KLGRSEIQFLISDNQGFSCPEKQVLTTLVCEVLHGSGCRE
 AQHDSYVGLGPAALMILAFLLLLVPLLLLMCHCGKAKAFTPIPGTIEMLHPWNNEGAPPEDKVVP SFLPVD
 QGGSILVGRNGVGGMAKEATMKGSSSASIVKGQHEMSEMDGRWEEHRSLLSGRATQFTGATGAIMTTETTKTARAT
 GASRDMAGAAVAALNEEFRLNYFTDKAASYTEEDENHTAKDCLLVYSQEETESLNASIGCCSFIEGELDDRFL
 DDGLGLKFKTLAEVCLGQKIDINKEIEQRQKPATETSMNTASHSLCEQTMVNSENTYSSGSSFPVPKSLQEANA
 EKVQEIIVTERSVSSRQAQKVATPLPDPMASRNVIAETETSYVTGSTMPPTTVILGPSQPQSLIVTERVYAPASTLVD

QPYANEGTVVTERVIQPHGGGSPLEGTQHLQDVPYVMVRERESFLAPSSGVQPTLAMPNIAVGQNVTVTERVL
APASTLQSSYQIPTENSMTARNNTTVSGAGVPGPLPDFGLEESGHSNSTITTSSTRVTKHSTVQHSYS

Mass Match Peptides (bold):

ATQFTGATGAIMTTETTK [93]
DNWISVDSVTSEIK [148]
DTGEIYTTSVTLDR [159]
EEHSSYTLTVEAR [174]
GNNVEKPLELR [304]
GQIIGNFQAFDEDTGLPAHAR [311]
INATDADEPNTLNSK [381]
IVAISEDYPR [400]
LPDFESR [476]
QUESTSVLLQQSEK [568]
VLAPASTLQSSYQIPTENSMTAR [772]
VLEGMVEENQVNVEVTR [778]
VTQEIIVTER [806]
VVPSFLPVDQGGSLVGR [812]
VYAPASTLVDQPYANEGTVVTER [816]

Tandem Peptides (underline):

FLDDLGLK [257]
VATPLPDPMASR [746]
YKPTPIPIK [858]

Peptide Source: 1D-GE, Osteosarcoma

MARTRDRVRLLLLLICFNVGSGHLQVLSTRNENKLLPKHPLVRQKRAWITAPVALREGEDLSKKNPIAKIHSD
LAERGLKITYKYTGKITEPPFGIFVFNKDTGELNVTSLDREETPFFLLTGYALDARGNNVEKPLELRKIVLD
INDNEPVFTQDVFVGSVEELSAHTLVMKINATDADEPNTLNSKISYRIVSLEPAYPPVFYLNKDTGEIYTTSVT
LDREEHSSYTLTVEARDGNGEVTDKPVKQAQVQIRILDVNDNIPVVENK**VLEGMVEENQVNVEVTR**IKVFDADAI
GSDNWLANFTFASGNEGgyFHIETDAQTNEGIVTLIKEVDYEMKNLDFSVIVANKAAFHKSIRSKYKPTPIPIK
VKVKNVKEGIHFkSSVISIYVESMDRssKGQIIIGNFQAFDEDTGLPAHARYVKLEDR**DNWISVDSVTSEIK**LAK
LPDFESRYVQNGTYTVK**IVAISEDYPR**KTITGTVLINVEDINDNCPTLIEPVQTICHDAEYVNVTAEDLDGHPNS
GPFSFVIDKPPGMAEKWKIARQUESTSVLLQQSEKKLGRSEIQFLISDNQGFSCPEKQVLTTLTVCEVLHGSGCRE
AQHDSYVGLGPAATIALMILAFLLLLVPLLLLMCHCGKAKAFTPIPGTIEMLHPWNNEGAPPEDKVVPFLPVD
QGGSLVGRNGVGGMAKEATMKGSSSASIVKGQHEMSEMMDGRWEEHRSLLSGRATQFTGATGAIMTTETTKTARAT
GASRMAGAQAANAVALNEEFLRNYFTDKAASYTEEDENHTAKDCLLVYSQEETESLNASIGCCSFIEGELDDRFL
DDLGLKFKTLAEVCLGQKIDINKEIEQRQKPATETSMNTASHSLCEQTMVNSENTYSSGSSFPVPKSLQEANA
VTQEIIVTERSVSSRQAQKVATPLPDPMASRNVIAETSYVTGSTMPPTTVILGPSQPQSLIVTERVYAPASTLVD
QPYANEGTVVTERVIQPHGGGSPLEGTQHLQDVPYVMVRERESFLAPSSGVQPTLAMPNIAVGQNVTVTERVL
APASTLQSSYQIPTENSMTARNNTTVSGAGVPGPLPDFGLEESGHSNSTITTSSTRVTKHSTVQHSYS

Mass Match Peptides (bold):

DNWISVDSVTSEIK [148]
IVAISEDYPR [400]
VLEGMVEENQVNVEVTR [778]

Tandem Peptides (underline):

GITEPPFGIFVFNK [301]
IVAISEDYPR [400]

Peptide Source: 1D-GE, Pancreatic cancer

MARTRDRVRLLLLLICFNVGSGHLQVLSTRNENKLLPKHPLVRQKRAWITAPVALR**EGEDLSKKNPIAKIHSD**
LAERGLKITYKYTGKITEPPFGIFVFNK**DTGELNVTSLDREETPFFLLTGYALDARGNNVEKPLELR**KIVLD
INDNEPVFTQDVFVGSVEELSAHTLVMK**INATDADEPNTLNSK**ISYRIVSLEPAYPPVFYLNKDT**DTGEIYTTSVT**
LDREEHSSYTLTVEARDGNGEVTDKPVKQAQVQIRILDVNDNIPVVENK**VLEGMVEENQVNVEVTR**IKVFDADAI
GSDNWLANFTFASGNEGgyFHIETDAQTNEGIVTLIKEVDYEMKNLDFSVIVANKAAFHKSIRSKYKPTPIPIK

VKVKNVKEGIHFHFKSSVISIYVSESMRDRSSKGQIIGNFQAFDEDTGLPAHARYVKLEDRDNWISVDSVTSEIKLAK
 LPDFESRYVQNGTYTVKIVAISEDYPRKTTITGTVLINVEDINDNCPTLIEPVQTIChDAEYVNVTAEDLDGHPNS
 GPFSFSVIDKPPGMAEKWKIARQESTSVLLQQSEK KLGRSEIQFLISDNQGFSCPEKQVLTTLTVCEVLHGSGCRE
 AQHDSYVGLGPAAIALMILAFLLLLLVPLLLLMCHCGKAKAFTPIPGTIEMLHPWNNEGAPPEDKVVPSFLPVD
 QGGSLVGRNGVGGMAKEATMKGSSSASIVKGQHEMSEMDGRWEEHRSLLSGRATQFTGATGAIMTTETTKTARAT
 GASRDMAGAQAAVALNEEFRLRNYFTDKAASYTEEDENHTAKDCLLVYSQEETESLNASIGCCSFIEGELDDRFL
 DDLGLKFKTLAEVCLGQKIDINKEIEQROK PATETSMNTASHSLCEQTMVNSENTYSSGSSFPVPKSLQEANA EK
 VTQEIVTERSVSSRQAQKVATPLPDPMASRNVIAETETSYVTGSTMPPTTVILGPSQPSLIVTERVYAPASTLVD
 QPYANEGTVVVTERVIQPHGGGSPNLEGTQHLQDVPYVMVRERESFLAPSSGVQPTLAMPNIAVGQNVTVTERVL
 APASTLQSSYQIPTENSMTARNNTTVSGAGVPGLPDPFGLSESGHSNSTITTSSTRVTKHSTVQHSYS

Mass Match Peptides (bold):

ATQFTGATGAIMTTETTK [93]
 DNGEVTDKPVK [123]
 DMAGAQAAVALNEEFRL [142]
 DNWISVDSVTSEIK [148]
 DTGEIYTTSVTLDR [159]
 DTGELNVTSLDR [160]
 EEHSSYTLTVEAR [174]
 EETPFLLTGALDAR [182]
 EGEDLSKK [187]
 GNNVEKPLELR [304]
 GQIIGNFQAFDEDTGLPAHAR [311]
 GSSSASIVK [322]
 IHSDLAEER [369]
 INATDAEPNTLNSK [381]
 IVAISEDYPR [400]
 QESTSVLLQQSEK [568]
 SEIQFLISDNQGFSCPEK [628]
 SSVISIYVSESMR [653]
 VATPLPDPMASR [746]
 VLAPASTLQSSYQIPTENSMTAR [772]
 VLEGMVEENQVNVEVTR [778]
 VTQEIVTER [806]
 VVPSFLPVDQGGSLVGR [812]
 VYAPASTLVDQPYANEGTVVVTER [816]
 WEEHR [825]

Tandem Peptides (underline):

ATQFTGATGAIMTTETTK [93]
 DMAGAQAAVALNEEFRL [142]
 DTGEIYTTSVTLDR [159]
 EEHSSYTLTVEAR [174]
 ESFLAPSSGVQPTLAMPNIAVGQNVTVTER [223]
 GNNVEKPLELR [304]
 QESTSVLLQQSEK [568]
 VATPLPDPMASR [746]
 VLEGMVEENQVNVEVTR [778]
 VVPSFLPVDQGGSLVGR [812]

Peptide Source: 1D-GE, Prostate cancer

MARTRDRVRLLLLLLICFNVGSGHLQVLSTRNENKLLPKHPLVRQKRAWITAPVALREGEDLSKKNPIAKIHSD
 LAERGLKITYKYTGKITEPPFGIFVFVKNDTGELNVTSLDRREETPFLLTGALDARGNNVEKPLELRKIVLD
 INDNEPVFTQDVFGVSEELSAATLVMKINATDAEPNTLNSKISYRIVSLEPAYPPVFYLNKDTGEIYTTSVT
 LDR EEHSSYTLTVEARDNGEVTDKPVKQAQVQIRILDVNDNIPVENKVLEGMVEENQVNVEVTRIKVFDADI
 GSDNWLANFTFASGNEGCFHIEDAQTNEGIVTTLIKEVDYEEEMKNLDFSIVANKAAAFHKSIRSKEYKPTPIPIK
 VKVKNVKEGIHFHFKSSVISIYVSESMRDRSSKGQIIGNFQAFDEDTGLPAHARYVKLEDRDNWISVDSVTSEIKLAK
 LPDFESRYVQNGTYTVKIVAISEDYPRKTTITGTVLINVEDINDNCPTLIEPVQTIChDAEYVNVTAEDLDGHPNS
 GPFSFSVIDKPPGMAEKWKIARQESTSVLLQQSEK KLGRSEIQFLISDNQGFSCPEKQVLTTLTVCEVLHGSGCRE

AQHDSYVGLGPAAIALMILAFLLLLLVLPLLLLMCHCGKGAKAFTPIPGTIEMLHPWNNEGAPPEDKVVPSTFLPVD
 QGGSLVGRNGVGGMAKEATMKGSSSASIVKGQHEMSEMDGRWEEHRSLLSGRATQFTGATGAIMTTETTTKTARAT
 GASRDMAGAQAVALNEEFRLNYFTDKAASYTEEDENHTAKDCLLVYSQEETESLNASIGCCSFIEGELDDREFL
DDLGLKFKFTLAEVCLGQKIDINKEIEQRQKPATETSMNTASHSLCEQTMVNSENTYSSGSSFFVPKSLQEANA
 VTQEIIVTERSVSRRQAQKVATPLPDPMASRNVIATETSYVTGSTMPPTTVILGPSQPQSLIVTERVYAPASTLVD
 QPYANEGTVVVTERRVIQPHGGGSPLEGTQHLQDVPYVMVRERESFLAPSSGVQPTLAMPNIAVGQNVTVTERVL
 APASTLQSSYQIPTENSMTARNTTVSGAGVPGPLPDFGLEESGHSNSTITTSSTRVTKHSTVQHSYS

Mass Match Peptides (bold):

DTGEIYTTSVTLDR [159]
 VATPLPDPMASR [746]

Tandem Peptides (underline):

FLDDLGLK [257]

Peptide Source: 1D-GE, Renal cell cancer

MARTRDRVRLLLLLLFCFNVGSGHLHLQVLSTRNENKLLPKHPLHVRQKRAWITAPVALREGEDLSKKNPIAKIHSD
 LAEERGLKITYKYTGKGITEPPFGIFVFNKDTGELNVTSLDREETPFLLTGALDARGNNVEKPLELRKIKVLD
 INDNEPVFTQDVFVGSVEELSAHTLMKINATDADEPNTLSKISYRIVSLEPAYPPVFYLNKDTGEIYTTSVT
 LDREEHSSYTTLVEARDGNGEVTDKPVKQAQVQIRILDVNDNIPVVENKVLGEMVEENQVNVETRIKVFDADEI
 GSDNWLANFTFASGNEGgyFHIETDAQTNNEGIVTLIKEVDYEMKNLDFSVIVANKAAAFHKSIRSKYKPTPIPIK
 VKVKNVKEGIHFKSSVISIYVSESMRDSKQIIGNFQAFDEDTGLPAHARYVKLEDRDNWISVDSVTSEIKLAK
LPDFESRYVQNGTYTVKIVAISEDYPRKITITGTVLINVEDINDNCPTLIEPVQTIChDAEYVNVTAEDLDGHPNS
 GPFSSVIDKPPGMAEKWKIARQESTSVLLQQSEKKLGRSEIQFLISDNQGFSCPEKQVLTTLTCEVLHGSGCRE
 AQHDSYVGLGPAAIALMILAFLLLLLVLPLLLLMCHCGKGAKAFTPIPGTIEMLHPWNNEGAPPEDKVVPSTFLPVD
 QGGSLVGRNGVGGMAKEATMKGSSSASIVKGQHEMSEMDGRWEEHRSLLSGRATQFTGATGAIMTTETTTKTARAT
 GASRDMAGAQAVALNEEFRLNYFTDKAASYTEEDENHTAKDCLLVYSQEETESLNASIGCCSFIEGELDDREFL
 DDLGLKFKFTLAEVCLGQKIDINKEIEQRQKPATETSMNTASHSLCEQTMVNSENTYSSGSSFFVPKSLQEANA
 VTQEIIVTERSVSRRQAQKVATPLPDPMASRNVIATETSYVTGSTMPPTTVILGPSQPQSLIVTERVYAPASTLVD
 QPYANEGTVVVTERRVIQPHGGGSPLEGTQHLQDVPYVMVRERESFLAPSSGVQPTLAMPNIAVGQNVTVTERVL
 APASTLQSSYQIPTENSMTARNTTVSGAGVPGPLPDFGLEESGHSNSTITTSSTRVTKHSTVQHSYS

Mass Match Peptides (bold):

Tandem Peptides (underline):

GNNVEKPLELR [304]
 IVAISEDYPR [400]
 LPDFESR [476]
 VTQEIIVTER [806]

Peptide Source: iTRAQ, Colorectal cancer

MARTRDRVRLLLLLLFCFNVGSGHLHLQVLSTRNENKLLPKHPLHVRQKRAWITAPVALREGEDLSKKNPIAKIHSD
 LAEERGLKITYKYTGKGITEPPFGIFVFNKDTGELNVTSLDREETPFLLTGALDARGNNVEKPLELRKIKVLD
 INDNEPVFTQDVFVGSVEELSAHTLMKINATDADEPNTLSKISYRIVSLEPAYPPVFYLNKDTGEIYTTSVT
 LDREEHSSYTTLVEARDGNGEVTDKPVKQAQVQIRILDVNDNIPVVENKVLGEMVEENQVNVETRIKVFDADEI
 GSDNWLANFTFASGNEGgyFHIETDAQTNNEGIVTLIKEVDYEMKNLDFSVIVANKAAAFHKSIRSKYKPTPIPIK
 VKVKNVKEGIHFKSSVISIYVSESMRDSKQIIGNFQAFDEDTGLPAHARYVKLEDRDNWISVDSVTSEIKLAK
 LPDFESRYVQNGTYTVKIVAISEDYPRKTAEDLDGHPNS
 GPFSSVIDKPPGMAEKWKIARQESTSVLLQQSEKKLGRSEIQFLISDNQGFSCPEKQVLTTLTCEVLHGSGCRE
 AQHDSYVGLGPAAIALMILAFLLLLLVLPLLLLMCHCGKGAKAFTPIPGTIEMLHPWNNEGAPPEDKVVPSTFLPVD
 QGGSLVGRNGVGGMAKEATMKGSSSASIVKGQHEMSEMDGRWEEHRSLLSGRATQFTGATGAIMTTETTTKTARAT
 GASRDMAGAQAVALNEEFRLNYFTDKAASYTEEDENHTAKDCLLVYSQEETESLNASIGCCSFIEGELDDREFL
 DDLGLKFKFTLAEVCLGQKIDINKEIEQRQKPATETSMNTASHSLCEQTMVNSENTYSSGSSFFVPKSLQEANA
 VTQEIIVTERSVSRRQAQKVATPLPDPMASRNVIATETSYVTGSTMPPTTVILGPSQPQSLIVTERVYAPASTLVD
 QPYANEGTVVVTERRVIQPHGGGSPLEGTQHLQDVPYVMVRERESFLAPSSGVQPTLAMPNIAVGQNVTVTERVL
 APASTLQSSYQIPTENSMTARNTTVSGAGVPGPLPDFGLEESGHSNSTITTSSTRVTKHSTVQHSYS

Mass Match Peptides (bold):

INATDADEPNTLNSK [381]
SLQEANA EK [970]
TLAEVCLGQK [982]

Tandem Peptides (underline):

INATDADEPNTLNSK [381]
SLQEANA EK [970]
TLAEVCLGQK [982]

Peptide Source: iTRAQ, Non-small cell lung cancer

MARTDRVRLLLLLICFNVGSLHLQVLSTRNENKLLPKHPLVRQKRAWITAPVALREGEDLSKK**NPIAK**IHSD
LAERGLKITYKYTGKGITEPPFGIFVFNKDTGELNVTSILDREETPFLLTGYALDARGNNVEKPLELRKIVLD
INDNEPVFTQDVFGVGSVEELSAHTLVMKINATDADEPNTLNSKISYRIVSLEPAYPPVFYLNKDTGEIYTTSVT
LDREEHSSYTLTVEARDGNGEVTDKPVKQAQVQIRILDVNDNIPVVENKVLEGMVEENQVNVEVTRIKVFDADI
GSDNWLANFTFASGNEGgyFHIETDAQTNEGIVTLIKEVDYEEMKNLDFSVIVANKAAFHKSIRSKEYKPTPIPIK
VKVKNVKEGIHFKSSVISIYVSESMRSSKGQIIIGNFQAFDEDTGLPAHARYVKLEDRDNWISVDSVTSEIKLAK
LPDFESRYVQNGTYTVKIVAISEDYPRKTTITGTVLINVEDINDNCPTLIEPVQTICHDAEYVNVTAEDLDGHPNS
GPFESFVIDKPPGMAEKWKIARQUESTSVLLQQSEKKLGRSEIQFLISDNQGFSCPEKQVLTTLTVCEVLHGSGCRE
AQHDSYVCLGPAAIAMILAFLLLLLVPLLLLMCHCCGKAKAFTPIPGTIEMLHPWNNEGAPPEDKVVPSEFLPVD
QGGSLVGRNGVGGMAKEATMKGSSSASIVKGQHEMSEMDGRWEEHRSLLSGRATQFTGATGAIMTTETTKTARAT
GASRDMAGAAVAALNEEFLRNYFTDKAASYTEEDENHTAKDCLLVYSQEETESLNASIGCCSFIEGELDDRFL
DDLGLKFKTLAEVCLGQKIDINKEIEQRQKPATETSMNTASHSLCEQTMVNSENTYSSGSSFPVPKSLQEANA EK
VTQEIIVTERSVSSRQAQKVATPLPDPMASRNVIAETTSYVTGSTMPPTTVILGPSQPQSLIVTERVYAPASTLVD
QPYANEGTVVVTERVIQPHGGGNSPLEGTQHLQDVPYVMVRERESFLAPSSGVQPTLAMPNIAVGQNVTVTERVL
APASTLQSSYQIPTENSMTARNTTVSGACVPGPLPDFGLEESGHSNSTITTSSTRVTKHSTVQHSHS

Mass Match Peptides (bold):

INATDADEPNTLNSK [381]
NPIAK [957]

Tandem Peptides (underline):

INATDADEPNTLNSK [381]
NPIAK [957]

Peptide Source: iTRAQ, Ovarian cancer

MARTDRVRLLLLLICFNVGSLHLQVLSTRNENKLLPKHPLVRQKRAWITAPVALREGEDLSKK**NPIAK**IHSD
LAERGLKITYKYTGKGITEPPFGIFVFNKDTGELNVTSILDREETPFLLTGYALDARGNNVEKPLELRKIVLD
INDNEPVFTQDVFGVGSVEELSAHTLVMKINATDADEPNTLNSKISYRIVSLEPAYPPVFYLNKDTGEIYTTSVT
LDREEHSSYTLTVEARDGNGEVTDKPVKQAQVQIRILDVNDNIPVVENKVLEGMVEENQVNVEVTRIKVFDADI
GSDNWLANFTFASGNEGgyFHIETDAQTNEGIVTLIKEVDYEEMKNLDFSVIVANKAAFHKSIRSKEYKPTPIPIK
VKVKNVKEGIHFKSSVISIYVSESMRSSKGQIIIGNFQAFDEDTGLPAHARYVKLEDRDNWISVDSVTSEIKLAK
LPDFESRYVQNGTYTVKIVAISEDYPRKTTITGTVLINVEDINDNCPTLIEPVQTICHDAEYVNVTAEDLDGHPNS
GPFESFVIDKPPGMAEKWKIARQUESTSVLLQQSEKKLGRSEIQFLISDNQGFSCPEKQVLTTLTVCEVLHGSGCRE
AQHDSYVCLGPAAIAMILAFLLLLLVPLLLLMCHCCGKAKAFTPIPGTIEMLHPWNNEGAPPEDKVVPSEFLPVD
QGGSLVGRNGVGGMAKEATMKGSSSASIVKGQHEMSEMDGRWEEHRSLLSGRATQFTGATGAIMTTETTKTARAT
GASRDMAGAAVAALNEEFLRNYFTDKAASYTEEDENHTAKDCLLVYSQEETESLNASIGCCSFIEGELDDRFL
DDLGLKFKTLAEVCLGQKIDINKEIEQRQKPATETSMNTASHSLCEQTMVNSENTYSSGSSFPVPKSLQEANA EK
VTQEIIVTERSVSSRQAQKVATPLPDPMASRNVIAETTSYVTGSTMPPTTVILGPSQPQSLIVTERVYAPASTLVD
QPYANEGTVVVTERVIQPHGGGNSPLEGTQHLQDVPYVMVRERESFLAPSSGVQPTLAMPNIAVGQNVTVTERVL
APASTLQSSYQIPTENSMTARNTTVSGACVPGPLPDFGLEESGHSNSTITTSSTRVTKHSTVQHSHS

Mass Match Peptides (bold):

NPIAK [957]

Tandem Peptides (underline):

NPIAK [957]

Peptide Source: iTRAQ, Renal cell cancer

MARTDRVRLLLLLICFNVGSGCLHLQVLSTRNENKLLPKHPLVLRQKRAWITAPVALREGEDLSKKNPIAKIHSD
 LAEERGLKITYKYTGKGITTEPPFGIFVFNKDTGELNVTSLDREETPFFLLTGYALDARGNNVEKPLELRIKVLD
 INDNEPVFTQDVFVGSVEELSAHAITLVMKINATDAEPNTLNSKISYRIVSLEPAYPPVFYLNKDTGEIYTTSTVT
 LDREEHSSYTLTVEARDGNGEVTDKPVKQAQVQIRILDVNDNIPVVENKVLGEMVEENQVNVETRIKVFDADEI
 GSDNWLANFTFASGNEGgyFHIETDAQTNEGIVTLIKEVDYEEEMKNLDFSIVANKAAAFHKSIRSKEYKPTPIPIK
 VKVKNVKEGIFHKSSVISIYVSESMRSSKQIIGNFQAFDEDTGLPAHARYVKLEDRDNWISVDSVTSEIKLAK
 LPDFESRYVQNGTYTVKIVAISEDYPRKTIITCTVLINVEDINDNCPTLIEFPVQTICHDAEYVNVTAEDLDGHPNS
 GPFESFVIDKPPGMAEKWKIARQESTSVLLQQSEKKLGRSEIQFLISDNQGFSCPEKQVLTITVCEVLHGSGCRE
 AQHDSYVGLGPAIAIMILAFLLLLLVPLLLLMCHCGKAKAFTPIPGTIEMLHPWNNEGAPPEDKVVPSFLPVD
 QGGSVLGRNGVGGMAKEATMKGSSSASIVKGQHEMSEMDGRWEEHRSLLSGRATQFTGATGAIMTTETTKTARAT
 GASRDMAGAQAVALNEEFRLNYFTDKAASYTEEDENHTAKDCLLVYSQEETESLNASIGCCSFIEGELDDRFL
 DDLGLKFKTLAEVCLGQKIDINKEIEQRQKPATETSMNTASHSLCEQTMVNSENTYSSGSSFPVPK**SLQEANA****AEK**
 VTQEIIVTERSVSSRQAQKVATPLPDPMASRNVATETSYVTGSTMPPTTVILGPSQPQSLIVTERVYAPASTLVD
 QPYANEGTVVVTERTVIQPHGGGSPLEGTQHLQDVYPYVMVRERESFLAPSSGVQPTLAMPNIAVGQNVTVTERVL
 APASTLQSSYQIPTENSMTARNTTVSGAGVPGPLPDFGLEESGHSNSTITTSSTRVTKHSTVQHSYS

Mass Match Peptides (bold):

SLQEANA**EK** [970]

Tandem Peptides (underline):

SLQEANA**EK** [970]

Peptide Source: iTRAQ, Small cell lung cancer

MARTDRVRLLLLLICFNVGSGCLHLQVLSTRNENKLLPKHPLVLRQKRAWITAPVALREGEDLSKKN**NPIAK**IHSD
 LAEERGLKITYKYTGKGITTEPPFGIFVFNKDTGELNVTSLDREETPFFLLTGYALDARGNNVEKPLELRIKVLD
 INDNEPVFTQDVFVGSVEELSAHAITLVMKINATDAEPNTLNSKISYRIVSLEPAYPPVFYLNKDTGEIYTTSTVT
 LDREEHSSYTLTVEARDGNGEVTDKPVKQAQVQIRILDVNDNIPVVENKVLGEMVEENQVNVETRIKVFDADEI
 GSDNWLANFTFASGNEGgyFHIETDAQTNEGIVTLIKEVDYEEEMKNLDFSIVANKAAAFHKSIRSKEYKPTPIPIK
 VKVKNVKEGIFHKSSVISIYVSESMRSSKQIIGNFQAFDEDTGLPAHARYVKLEDRDNWISVDSVTSEIKLAK
 LPDFESRYVQNGTYTVKIVAISEDYPRKTIITCTVLINVEDINDNCPTLIEFPVQTICHDAEYVNVTAEDLDGHPNS
 GPFESFVIDKPPGMAEKWKIARQESTSVLLQQSEKKLGRSEIQFLISDNQGFSCPEKQVLTITVCEVLHGSGCRE
 AQHDSYVGLGPAIAIMILAFLLLLLVPLLLLMCHCGKAKAFTPIPGTIEMLHPWNNEGAPPEDKVVPSFLPVD
 QGGSVLGRNGVGGMAKEATMKGSSSASIVKGQHEMSEMDGRWEEHRSLLSGRATQFTGATGAIMTTETTK**TARAT**
GASRDMAGAQAVALNEEFRLNYFTDKAASYTEEDENHTAKDCLLVYSQEETESLNASIGCCSFIEGELDDRFL
 DDLGLKFKTLAEVCLGQKIDINKEIEQRQKPATETSMNTASHSLCEQTMVNSENTYSSGSSFPVPKSLQEANA**EK**
 VTQEIIVTERSVSSRQAQKVATPLPDPMASRNVATETSYVTGSTMPPTTVILGPSQPQSLIVTERVYAPASTLVD
 QPYANEGTVVVTERTVIQPHGGGSPLEGTQHLQDVYPYVMVRERESFLAPSSGVQPTLAMPNIAVGQNVTVTERVL
 APASTLQSSYQIPTENSMTARNTTVSGAGVPGPLPDFGLEESGHSNSTITTSSTRVTKHSTVQHSYS

Mass Match Peptides (bold):

NPIAK [957]

TARAT**GASR** [977]

Tandem Peptides (underline):

NPIAK [957]

TARAT**GASR** [977]

OGTA101 (SEQ ID No: 19)

Peptide Source: 1D-GE, Breast cancer

MVHVARLLLLLTFFLRDAETPPRFTRTPVDQTVSGGVASFICQATGDERPKIVWNKKGKKVSNQRFEVIEFD
 DGSGSVLRIQPLRTPRDEAIYECVASNNVGEISVSTRLTVLREDQIPRGFPTIDMGPOLKVVVERTR**TATMLCAAS**
GNPDPEITWFKDFLPVDTSNNNGRIKQLRSEISIGGTPIRGALQIEQSEESDQGYECVATNSAGTRYAPANLYV
 RELREVRRVPPRFIPPTNHEIMPCCSVNITCVAVGSPMPYVWMLGAEDLTPEDDMPICRNVLELNDVQRQANY
 TCVAMSTLGVIEAIAQITVKALPKPPGIPVVTTESTATSITLTWDSGNPEVSYIIQHKPKNSEELYKEIDGVAT
 TRYSVAGLSPYSYDIEFRVAVNNIGR**GPPSEPVLTQTSEQAPSSAPR**VDQARMLSSSTILVQWKEPEEPNGQIQG
 YRVYYTMDPTQHVNNWMMKHNVDASQITTTIGNLVPQKTYSVKVLAFTSIGDGPLSSDIQVITQTGVPQGPLNFK**AE**
PESETILLSWTTPRSDTIANYELVYKDGEGHEEQRTIEPGTSYRLQGLKPNLSLYYFRLAARSPQGLGASTAEI
 SARTMQSKPSAPPQDISCTSPSSSTILVSWQPPPVEKQNGIITEYSIKYTAVDGEDDKPHEILGIPSDTTKYLL
 QLEKWTEYRITVTAHTDVGPGPESLSVLIR**TNEDVPSGPPRK**VEVEAVNSTSVKVSWSRSPVFNK**QHGQIR**GYQVH
 YVRMENGEPKQPMKLDVMLADAQWEDDTTEHDMIIISGLQPETSYSLTVTAYTTKDGARSKEPKLVSTTGAVPG
 K3RLVINHTQMNTALIQWHPPVDTFGLQGYRLKFGKRDMEPLTTLEFSEKEDHFTATDIHKGASYVFRLSARNK
VGFGGEEMVKEISIDPEEVPFGPQNLHSEGTTSVSVQLSWQPPVLAERNGIITKYTLRYDINIPLLPMEQLIVPA
 DTTMTLTGLKPDTTYDVKVAHTSKGPGPYSPSVQFRTLTPVDQVFAKNFHVKAVMK**TSVLLSWEIPENYNSAMPF**
KILYDDGKMVEEVDGRATQKLVNLKPEK**SYSFVLNTR**GNSAGGLQHRVTAKTAPDVLRTKPAFIGKTNLDGMIT
 VQLPEVPANENIKGYIIIVPLKKSARG**FIKPWESPDEMEDELLEK**EISRKRRSIRYGREVELKPYIAAHFDVLP
 TEFTLGDGDKHYGGFTNKQLQSGQBYVFFVLAVMEHAESKMYATSPYSDPVVSMDLDPQIPITDEEEGLIWWVGPVL
 AVVFIICIVIAILLYKRKRAESDRKSSIPNNK**EIPSHHPTDPVELR**RLNLFQTPGMASHPPPIPILELADHIERLK
 ANDNLKFSQYESIDPGQFTWEHSNLEVNKPKNRYANVIAYDHSRVLLSAIEGIPGSDYVNANYIDGYRKQAY
 IATQGSPLPETFGDFWRMIWEQSRATVMMTKLEERSRVKCDQYWPSSRGTEHGLVQVTLTLDVELATYCVTRFAL
 YKNGSSEKREVRQFTAWPDHGVPEHPTPFLAFLRRVKTCPDAGPMVVHCSAGVGR**TGCFIVIDAMLER**IKH
 EKTVDIYGHVTLMAQRNVMVQTEDQYIFHDALLEAVTCGNTVEPARNLYAYIQK**LTQIETGENVTGMELEFK**
 LASSKAHTSRFISANLPCNKFKNL**LVNIMPYESTR**VCLQPIR**GVEGSDYINASFIDGYR**QOKAYIATQGPLAETT
 EDFWR**MLWEHNSTIVVMLTK**LREMGREKCHQYWPASARS**YQYFVVDPMAEYNMPQYILR**EKVIDDARDGQSRTV
RQFQFTDWPEQGVPKSGEGFIDFIGQVHKTKEQFGQDGPISVHCSAGVGRIGVFTILSIVLERMRYEGVVDIFQT
 VKMLRTRQRPAMVQTEDQYQFSYR**AALEYLGSFDHYAT**

Mass Match Peptides (bold):

AALEYLGSFDHYAT [51]
 AEPESETILLSWTTPR [63]
 EIPSHHPTDPVELR [198]
 FIKPWESPDEMEDELLEK [255]
 GFPTIDMGPOLK [295]
 GPPSEPVLTQTSEQAPSSAPR [309]
 GVEGSDYINASFIDGYR [325]
 LTQIETGENVTGMELEFK [498]
 LVNIMPYESTR [503]
 MLWEHNSTIVVMLTK [520]
 MVEEVDGR [527]
 QFQFTDWPEQGVPK [572]
 QHGQIR [578]
 SYSFVLNTR [668]
 TATMLCAASGNPDPEITWFK [675]
 TGCFIVIDAMLER [692]
 TNEDVPSGPPRK [709]
 TSVLLSWEIPENYNSAMPF [731]
 VGFGGEEMVK [763]
 YQYFVVDPMAEYNMPQYILR [869]

Tandem Peptides (underline):

AALEYLGSFDHYAT [51]
 GVEGSDYINASFIDGYR [325]

Peptide Source: 1D-GE, Cervical cancer

MVHVARLLLLLTFFLRDAETPPRFTRTPVDQTVSGGVASFICQATGDERPKIVWNKKGKKVSNQRFEVIEFD
 DGSGSVLRIQPLRTPRDEAIYECVASNNVGEISVSTRLTVLREDQIPRGFPTIDMGPOLKVVVERTRATATMLCAAS
 GNPDPEITWFKDFLPVDTSNNNGRIKQLRSEISIGGTPIRGALQIEQSEESDQGYECVATNSAGTRYAPANLYV
 RELREVRRVPPRFIPPTNHEIMPCCSVNITCVAVGSPMPYVWMLGAEDLTPEDDMPICRNVLELNDVQRQANY

TCVAMSTLGVIEAIAQITVKALPKPPGTPVVTESTATSITLTWDSGNPEPVSYIIQHKPKNSEELYKEIDGVAT
 TRYSVAGLSPYSDYEFVAVNNIGRGPSEPVLTTQTSEQAPSSAPRDVQARMLSSSTILVQWKEPEEPNGQIQG
 YRVYITMDPTQHVNNWMKHNVDQSITITIGNLVPKTYSVKVLAFTSIGDGPLSSDIQVITQTGVPGQPLNFKAE
 PESETSILLSWTPPRSDTIANVELVYKDGEGHEEQRITIEPGTSYRLQGLKPNLSYYFRLAARSPOGLGASTAEI
 SARTMQSKPSAPPQDISCTSPSSSTILVSWQPPPEVEKQNGIITEYSIKYTAVDGEDDKPHEILGIPSDTTKYLLE
 QLEKWTEYRITVTAHTDVGCPGESLSVLIRTNEDVPSGPPRKVEVEAVNSTSVKVSWSRSPVFNKQHGQIRIRGYQVH
 YVRMENGEPKGPMLKDVMLADAQWFEFDDTTEHDMIISGLQPETSYSLSLTVTAYTTKGDGARSKPKLVSTTGAVPG
 KPRLVINHTQMNTALIQWHPPVDTFGLQGYRLKFGKDMELTTLEFSEKEDHFTATDIHKGASYVFRLSARNK
 VGFGEMVKEISIEPEVPTGFPQNLHSECTTSTSVQLSWQPPVLAERNGIITKYTLTYRDINIPLLPMEQLIVPA
 DTTMTLTGLKPDTTYDVKVRATSKGPGPYSPSVQFRTLPVDQVFAKNFHVKAVMKTSVLLSWEIPENYNSAMPF
 KILYDDGKMVEVDGRATQKLIJNLKPEKSYSFVLTRNGNSAGGLQHRVTAKTAPDVLRTKPAFIGKTNLDGMIT
 VQLPEVPANENIKGYIIIVPLKKSARGKFIKPWESFDEMELDELLKEISRKRIRYGREVELKPYIAAHFDVLP
 TEFTLGDDKHGCGFTNKQLQSGQYVFFVLAVMEHAESKMYATSPYSDPVVSMDLDPQIPITDEEEGLIWWVGPVL
 AVVFIIICIVIAILLYKRKRAESDSRKSSIPNNKEIPSHHPTDPVELRRLNFQTPGMASHPPPIPIELADHIERLK
 ANDNLKFSQYESI DPQQFTWEHSNLEVNKPKNRYANVIAYDHSRVLLSAIEGIPGSDYVNANYIDGYRKQNAV
 IATQGSPLPETFGDFWRMIWEQRSATVVMMTKLEERSRVKCDQYWPSRGTEETHGLVQVTLTDLTVELATYCVRTFAL
 YKNGSSEKREVRQFQTAWPDHGVPEHPTPFLAFLRRVKTCNPPDAGPMVVHCSAGVGRGTGCFIVIDAMLERIKH
 EKTVDIYGHVTLMRAQRNMYVQTEDQYIFIHDALEAVTCGNTEVPARNLYAYIQKLTQIETGENVTGMELEFKR
 LASSKAHTRSFISANLPCNKFKNRLVNIMPYESTRVCLQPIRGVEGSDYINASFIDGYRQOKAYIATQGPLAETT
 EDFWRMLWEHNSTIVMLTKLREMGREKCHQYWPASARYQYFVVDPMAYNMPQYILREFKVDARDGQSRTV
 RQFQFTDWPEQGVPKSGEGFIDFIGQVHKTEQFGQDGPISVHCSAGVGRGTGVFITLSIVLERMRYEGVVDIFQT
 VKMLRTQRPAMVQTEDQYQFSYRAALEYLGSDHYAT

Mass Match Peptides (bold):

QHGQIR [578]

WTEYR [836]

Tandem Peptides (underline):

Peptide Source: 1D-GE, Colorectal cancer

MVHVARLLLLLLLLTFFLRDAETPPRFTRTPVDQTVSGGVASFICQATGDPKPKIVWNKKGKKVSNQRFEVIEFD
 DGSGSVLRIOPLRTPRDEAIYECVASNNVGEISVSTRLTVLREDQIPRGFPITDMGPQLKVVERTRTATMLCAAS
 GNPDEIITWFKDFLPVDTSNNGRIKQLRSESIGTPIRGALQIEQSEESDQKYECAVNTSAGTRYSSAPANLYV
 RELREVRVPPRFISIPPTNHEIMPGGSVNITCVAVGSPMPYVKWMLGAEDLTPEDDMPICRNVLELNDVRSANY
 TCVAMSTLGVIEAIAQITVKALPKPPGTPVVTESTATSITLTWDSGNPEPVSYIIQHKPKNSEELYKEIDGVAT
 TRYSVAGLSPYSDYEFVAVNNIGRGPSEPVLTTQTSEQAPSSAPRDVQARMLSSSTILVQWKEPEEPNGQIQG
 YRVYITMDPTQHVNNWMKHNVDQSITITIGNLVPKTYSVKVLAFTSIGDGPLSSDIQVITQTGVPGQPLNFKAE
 PESETSILLSWTPPRSDTIANVELVYKDGEGHEEQRITIEPGTSYRLQGLKPNLSYYFRLAARSPOGLGASTAEI
 SARTMQSKPSAPPQDISCTSPSSSTILVSWQPPPEVEKQNGIITEYSIKYTAVDGEDDKPHEILGIPSDTTKYLLE
 QLEKWTEYRITVTAHTDVGCPGESLSVLIRTNEDVPSGPPRKVEVEAVNSTSVKVSWSRSPVFNKQHGQIRIRGYQVH
 YVRMENGEPKGPMLKDVMLADAQWFEFDDTTEHDMIISGLQPETSYSLSLTVTAYTTKGDGARSKPKLVSTTGAVPG
 KPRLVINHTQMNTALIQWHPPVDTFGLQGYRLKFGKDMELTTLEFSEKEDHFTATDIHKGASYVFRLSARNK
 VGFGEMVKEISIEPEVPTGFPQNLHSECTTSTSVQLSWQPPVLAERNGIITKYTLTYRDINIPLLPMEQLIVPA
 DTTMTLTGLKPDTTYDVKVRATSKGPGPYSPSVQFRTLPVDQVFAKNFHVKAVMKTSVLLSWEIPENYNSAMPF
 KILYDDGKMVEVDGRATQKLIJNLKPEKSYSFVLTRNGNSAGGLQHRVTAKTAPDVLRTKPAFIGKTNLDGMIT
 VQLPEVPANENIKGYIIIVPLKKSARGKFIKPWESFDEMELDELLKEISRKRIRYGREVELKPYIAAHFDVLP
 TEFTLGDDKHGCGFTNKQLQSGQYVFFVLAVMEHAESKMYATSPYSDPVVSMDLDPQIPITDEEEGLIWWVGPVL
 AVVFIIICIVIAILLYKRKRAESDSRKSSIPNNKEIPSHHPTDPVELRRLNFQTPGMASHPPPIPIELADHIERLK
 ANDNLKFSQYESI DPQQFTWEHSNLEVNKPKNRYANVIAYDHSRVLLSAIEGIPGSDYVNANYIDGYRKQNAV
 IATQGSPLPETFGDFWRMIWEQRSATVVMMTKLEERSRVKCDQYWPSRGTEETHGLVQVTLTDLTVELATYCVRTFAL
 YKNGSSEKREVRQFQTAWPDHGVPEHPTPFLAFLRRVKTCNPPDAGPMVVHCSAGVGRGTGCFIVIDAMLERIKH
 EKTVDIYGHVTLMRAQRNMYVQTEDQYIFIHDALEAVTCGNTEVPARNLYAYIQKLTQIETGENVTGMELEFKR
 LASSKAHTRSFISANLPCNKFKNRLVNIMPYESTRVCLQPIRGVEGSDYINASFIDGYRQOKAYIATQGPLAETT
 EDFWRMLWEHNSTIVMLTKLREMGREKCHQYWPASARYQYFVVDPMAYNMPQYILREFKVDARDGQSRTV
 RQFQFTDWPEQGVPKSGEGFIDFIGQVHKTEQFGQDGPISVHCSAGVGRGTGVFITLSIVLERMRYEGVVDIFQT
 VKMLRTQRPAMVQTEDQYQFSYRAALEYLGSDHYAT

Mass Match Peptides (bold):

Tandem Peptides (underline):

YSAPANLYVR [870]

Peptide Source: 1D-GE, Hepatocellular carcinoma

MVHVARLLLLLLTFFLRDAETPPRFTRTPVDQTCVSGGVASFCQATGDP RP KIVWNKKGKKVSNQRFEVIEFD
DGSGSVLRIQPLRTPRDEAIYECVASNNVGEISVSTRLTVLREDQIPR**GFPTIDMGPOLK**VVERTR**TATMLCAAS**
GNPDPEITWFKDFLPVDTSNNGRIKQLRSESIGGTPIRGALQIEQSEESDQGYECVATNSAGTRY**YSAPANLYV**
RELREVRRVPPRFSIPPTNHEIMPGGSVNITCVAVGSPMPYVKWMLGAEDLTPEDDMPIGRNVLELNDVRSANY
TCVAMSTLGVIEAIAQITVKALPKPPGTPVVTESTATSIITLTWDSGNPEPVSYIIQHKPKNSEELYKEIDGVAT
TRYSVAGLSPYSDEFRVAVNNIGRGPPSEPVLTQTSEQAPSSAPRDVQARMLSSTTIIVQWKEPEEPNGQIQG
YRVYYTMDPTQHVNNWMKHNVADSQITITGNLVPQKTYSVKVLAFSTISGDGPLSSDIQVITQTGVPGPPLNFKAE
PESETSIILLSWTPPRSDTIANYELVYKDGEGHEEQRTIEPGTSYRLQGLKPNLSLYYFRLAARSPOGLGASTAEI
SARTMQSKPSAPPQDISCTSPSSSILVSWQPPPVVEKQNGIITEYSIKYTAVDGEDDKPHEILGIPSDTTKYLL
QLEKWTEYRITVTAHTDVGP GPESLSVLIRTNEDVPSGPPRKVEVEAVNSTSVKVSWSRSPVFNKQHGQIRGYQVH
YVRMENGEPKGQPMKDVMLADAQWFEDDTTEHDMIISGLQPETSYSLTAYTTKGDGARSKPKLVSTTGAVPG
KPLRVINHTQMNTALIQWHPPVDTFGPLQGYRLKFGRK**DMEPLTTLEFSEK**EDHFTATDTHKGASYVFRLSARNK
VGFGEEMVKEISIPPEEVP TGFPQNLHSEGTSTTSVQLSWQPPVLAERNGIITKYTLLYRDNIPILPMEQLIVPA
DTTMTLTGLKPDITYDVKVRHAHTSK**GPGPYSPSVQFR**TTLPVDQVFAKNFHVAVMKTSVLLSWEIPENYNSAMPF
KILYDDGKMVEEVDGRATQKLIVNLKPEKSYSFVLNTRGNSAGGLQHRVTAKTAPDVLRTKPAFIGTKNLNMGMIT
VQLPEVPANENIKGYIIIVPLKKS RGKFIKPWESPDEMEDELLEKISRKRRSIRYGREVELKPYIAAHFDVLP
TEFTLGDDKHGGFTNKQLQSGQYVFFVLAVMEHAESKMYATSPYSDPVVSMDDLDPQIPITDEEGLIWWVGPVL
AVVFIICIVIAILLYKRKRAESDSRKSSIPNNKEIPSHHPTDPVELRLNLFQTPGMASHPIPILELADHIERLK
ANDNLKFSQEYESIDPGQQFTWEHSNLEVNKPKNRY**YANVIAYDHSR**VLLSAIEGIPGSDYVNANYIDGYRKQNAV
IATQGSLEPTFGDFWRMTIWEQRSATVVMMTKLEERSRVKCDQYWP SRGTETHGLVQVTLTLDVETATYCVRTFAL
YKNGSSEKREVRQFQFTAWPDHGVPEHPTPFLAFLRRVKT CNPPDAGPMVVHCSAGVGR TGCFVIDAMLERIKH
EKTVDIYGHVTLMRAQRNYMVQTEDQYIFIHDALLEAVTCGNTEVPARNLYAYIQKLTQIETGENVTGMELEFKR
LASSKAHTSRFISANLPCNKFKNRLVNMIPYESTRVCLQPIRGVEGSDYINASFIDGYRQQKAYIATQCPLAETT
EDFWRMLWEHNSITLVMLTKLREMGREKCHQYWP AERSARYQYFVVDPMAEYNMPQYILREFKVT DARDGQSRTV
RQFQFTDWPEQGVPK**SGEGFIDFIGQVHK**TKEQFGQDGPISVHCSAGVGR TGVFITLSIVLERMRYEGVVDIFQT
VKMLRTQR PAMVQTEDQYQFSYRAALEYLG SFDHYAT

Mass Match Peptides (bold):

DMEPLTTLEFSEK [143]
GFPTIDMGPOLK [295]
GPGPYSPSVQFR [306]
SGEGFIDFIGQVHK [632]
TATMLCAASGNPDPEITWFK [675]
YSAPANLYVR [870]

Tandem Peptides (underline):

YANVIAYDHSR [840]

Peptide Source: 1D-GE, Lung cancer

MVHVARLLLLLLTFFLRDAETPPRFTRTPVDQTCVSGGVASFCQATGDP RP KIVWNKKGKKVSNQRFEVIEFD
DGSGSVLRIQPLRTPRDEAIYECVASNNVGEISVSTRLTVLREDQIPR**GFPTIDMGPOLK**VVERTR**TATMLCAAS**
GNPDPEITWFKDFLPVDTSNNGRIKQLRSESIGGTPIRGALQIEQSEESDQGYECVATNSAGTRY**YSAPANLYV**
RELREVRRVPPRFSIPPTNHEIMPGGSVNITCVAVGSPMPYVKWMLGAEDLTPEDDMPIGRNVLELNDVRSANY
TCVAMSTLGVIEAIAQITVKALPKPPGTPVVTESTATSIITLTWDSGNPEPVSYIIQHKPKNSEELYKEIDGVAT
TRYSVAGLSPYSDEFRVAVNNIGRGPPSEPVLTQTSEQAPSSAPRDVQARMLSSTTIIVQWKEPEEPNGQIQG
YRVYYTMDPTQHVNNWMKHNVADSQITITGNLVPQKTYSVKVLAFSTISGDGPLSSDIQVITQTGVPGPPLNFKAE
PESETSIILLSWTPPRSDTIANYELVYKDGEGHEEQRTIEPGTSYRLQGLKPNLSLYYFRLAARSPOGLGASTAEI
SARTMQSKPSAPPQDISCTSPSSSILVSWQPPPVVEKQNGIITEYSIKYTAVDGEDDKPHEILGIPSDTTKYLL
QLEKWTEYRITVTAHTDVGP GPESLSVLIRTNEDVPSGPPRK**VEVEAVNSTSVK**VSWSRSPVFNKQHGQIRGYQVH
YVRMENGEPKGQPMKDVMLADAQWFEDDTTEHDMIISGLQPETSYSLTAYTTKGDGARSKPKLVSTTGAVPG
KPLRVINHTQMNTALIQWHPPVDTFGPLQGYRLKFGRK**DMEPLTTLEFSEK**EDHFTATDTHKGASYVFRLSARNK
VGFGEEMVKEISIPPEEVP TGFPQNLHSEGTSTTSVQLSWQPPVLAERNGIITKYTLLYRDNIPILPMEQLIVPA

DTTMTLTGLKPDTTYDVKVRHAETSKGPGPYSPSVQFRTLPLVDQVFAKNFHVKAVMKTSVLLSWEIPENYNNSAMPF
KILYDDGKMVEEVDGRATQKLIVNLKPEKSYSFVLTNRGNSAGGLQHRVTAKTAPDVLRTKPAFIGKTNLDGMIT
VQLPEVPANENIKGYIIIVPLKKSRRGKFIKPWESPDEMEIDELLKEISRKRRSIRYGREVELKPYIAAHFDVLP
TEFTLGDGDKHYGGFTNKQLQSGQEYVFFVLAVMEHAESKMYATSPYSDPVVSMDDLDPQIPITDEEEGLIWVVG PVL
AVVFIIICIVIAILLYKRKRAESDSRKSSIPNNKEIPSHHPTDPVELRRLNFQTPGMASHPPPIPIELADHIERLK
ANDNLKFSQEYESIDPGQQTWEHSNLEVNKPKNRYANVIAYDHSRVLLSAIEGIPGSDYVNANYIDGYRKQNAV
IATQGSLPETFGDFWRMIWEQRSATVMMTKLEERSRVKCDQYWPSRGTEHGLVQVTLTDLTVELATYCVRTFAL
YKNGSSEKREVRQFQFTAWPDHGVPEHPTPFLAFLRRVKTCPDAGPMVVHCSAGVGRGTGCFIVIDAMLERIKH
EKTVDIYGHVTLMRARQNYMVQTEDQYIFIHDALLEAVTCGNTEVPARNLYAYIQKLTQIETGENVTGMELEFKR
LASSKAHTSRFISANLPCNKFKNRLVNIMPYESTRVCLQPIRGVEGSDYINASFIDGYRQQKAYIATQGPIAETT
EDFWRLWEHNSTIVVMLTKLREMGREKCHQYWPASERSARYQYFVVDPMAEYNMPQYILREFKVTDARDGQSRTV
RQFQFTDWPEQGVPKSGEGFIDFIGQVHKTKEQFGQDGPISVHCSAGVGRGTGVFITLSIVLERMR YEGVVDIFQT
VKMLRTQRPAMVQTEDQYQFSYRAALEYLGSEFDHYAT

Mass Match Peptides (bold):

FIKPWESPDEMEIDELLK [255]
GFPTIDMG PQLK [295]
GVEGSDYINASFIDGYR [325]
LTQIETGENVTGMELEFK [498]
QFQFTDWPEQGVPK [572]
SDTIANYELVYK [625]
TATMLCAASGNPDPEITWFK [675]
TVDIYGHVTLMR [736]
VEVEAVNSTSVK [755]
YEGVVDIFQTVK [843]
YSAPANLYVR [870]

Tandem Peptides (underline):

QFQFTDWPEQGVPK [572]
YANVIAYDHSR [840]

Peptide Source: 1D-GE, Osteosarcoma

MVHVARLLLLLLTFFLRDAETPPRFTRTPVDQTVSGGVASFICQATGDPRPKIVWNKKGKKVSNQRFEVIEFD
DGSGSVLRIRQLRTPRDEAIYECVASNNVGEISVSTRLTVLREDQIPRGFPPTIDMG PQLKVVERTRTATMLCAAS
GNPDPEITWFKDFLPVDTSNNGRIKQLRSESIGGTPTRGATQTEQSEESDQGYECVATNSAGTRY SAPANLYV
RELREVRVRPPRESIPPTNHEIMPGGSVNITCVAVGSPMPYVKWMLGAEDLTPEDDMPIGRNVLELNDVRQSANY
TCVAMSTLGVIAIAQITVKALPKPGTPPVVTESTATSITLWDSGNPEPVSYIIQHKPKNSEELYKEIDGVAT
TRYSVAGLSPSYDYEFRVAVNNIGRPPSEPVLTQTSEQAPSSAPRDVQARMLSSTTILVQWKEPEEPNGQIQG
YRVYYTMDPTQHVNNWMKHNVADSQITIGNLVPOKTYSVKVLAFSTIGDGPLSSDIQVITQTGVPGQPLNFKAE
PESETSIILLSWTPERSDTIANYELVYKDGEHGEQRITIEPGTSYRLQGLKPNSLYYFRLAARSPOGLGASTAEI
SARTMQSKPSAPPQDISCTSPSSSTILVSWQPPPVEKQNGIITEYSIKYTAVDGEDDKPHEILGIPSDTTKYLL
QLEKWEYRITVTAHTDVGPGESLSVLIRTNEDVPSGPPRKVEVEAVNSTSVKVSWSRSEVPNK QHGQIRGYQVH
YVRMENGEPKGPMLKDVMLADAQWEDDTTEHDMIISGLQPETSYSLTVTAYTTKGDGARSKPKLVSTTGAVPG
KPRVLINHTQMNTALIQWHPPVDTFGLQGYRLKFRKDMPLTTLEFSEKEDHFTATDIHKGASYVFRLSARNK
VGFGEMVKEISIPPEVPTGFPQNLHSEGTSTSVQLSWQPPVLAERNGIITKYTLTYRDNIPLLPMEQLIVPA
DTTMTLTGLKPDTTYDVKVRHAETSKGPGPYSPSVQFRTLPLVDQVFAKNFHVKAVMKTSVLLSWEIPENYNNSAMPF
KILYDDGKMVEEVDGRATQKLIVNLKPEKSYSFVLTNRGNSAGGLQHRVTAKTAPDVLRTKPAFIGKTNLDGMIT
VQLPEVPANENIKGYIIIVPLKKSRRGKFIKPWESPDEMEIDELLKEISRKRRSIRYGREVELKPYIAAHFDVLP
TEFTLGDGDKHYGGFTNKQLQSGQEYVFFVLAVMEHAESKMYATSPYSDPVVSMDDLDPQIPITDEEEGLIWVVG PVL
AVVFIIICIVIAILLYKRKRAESDSRKSSIPNNKEIPSHHPTDPVELRRLNFQTPGMASHPPPIPIELADHIERLK
ANDNLKFSQEYESIDPGQQTWEHSNLEVNKPKNRYANVIAYDHSRVLLSAIEGIPGSDYVNANYIDGYRKQNAV
IATQGSLPETFGDFWRMIWEQRSATVMMTKLEERSRVKCDQYWPSRGTEHGLVQVTLTDLTVELATYCVRTFAL
YKNGSSEKREVRQFQFTAWPDHGVPEHPTPFLAFLRRVKTCPDAGPMVVHCSAGVGRGTGCFIVIDAMLERIKH
EKTVDIYGHVTLMRARQNYMVQTEDQYIFIHDALLEAVTCGNTEVPARNLYAYIQKLTQIETGENVTGMELEFKR
LASSKAHTSRFISANLPCNKFKNRLVNIMPYESTRVCLQPIRGVEGSDYINASFIDGYRQQKAYIATQGPIAETT
EDFWRLWEHNSTIVVMLTKLREMGREKCHQYWPASERSARY QYFVVDPMAEYNMPQYILREFKVTDARDGQSRTV
RQFQFTDWPEQGVPKSGEGFIDFIGQVHKTKEQFGQDGPISVHCSAGVGRGTGVFITLSIVLERMR YEGVVDIFQT
VKMLRTQRPAMVQTEDQYQFSYRAALEYLGSEFDHYAT

Mass Match Peptides (bold):

QHGQIR [578]
YQYFVVDPMAEYNMPQYILR [869]

Tandem Peptides (underline):

Peptide Source: 1D-GE, Pancreatic cancer

MVHVARLLLLLLTFFLRDAETPPRFTRTPVDQTVSGGVASFICQATGDPKPKIVWNKKGKKVSNQRFVIEFD
DGSGSVLRIQPLRTPRDEAIYECVASNNVGEISVSTRLTVLREDQIPR**GFPTIDMGPQLK**VVERTRTATMLCAAS
GNPDPEITWFK**DFLPVDTSNNGR**IKQLRSESIGGTPIRGALQIEQSEESDQGYECVATNSAGTRY**YSAPANLYV**
RELREVRVVP**PRFS**IPPTNHEIMPGGSVNITCVAVGSPMPYVKWMLGAEDLTPEDDMPIGRNVLELNDVRQSANY
TCVAMSTLGVIEAIAQITVKALPKPGTPVVTTESTATSITLTWDSGNPEPVSYIIQHKPKNSEELYKEIDGVAT
TRY**YSVAGLSPYSDYEF**RVAVNNIGRGPSEPVLTTQTSQAPSSAPRDVQARMLSSSTILVQWKEPEEPNGQIQG
YRVYITMDPTQHVNNMKHNVDASQITITIGNLVPQKTSVKVLAFTSIGDGPLSSDIQVITQTGVPGQPLNFKA
PESETSILLSWTPPR**SDTIANYELVYK**DGEHGEEQRITIEPGTSYRLQGLKPNLSLYYFRLAARSPQGLGASTAEI
SARTMQSKPSAPPQDISCTSPSSSTILVSWQPPPEVKQNGIITEYSIKYTAVDGEDDKPHEILGIPSDTTKYLL
QLEKWTEYRITVTAHTDVGPGPESLSVLIRTNEDVPSPGPRKVEVEAVNSTSVKVSWSRSPVPNKQHGQIRGYQVH
YVRMENGEPKGPMLKDVMLADAQWFFDDTTEHDMIISGLQPETSYSLTVTAYTTKGDGARSKPKLVSTTGAVPG
KRLVINHTQMNTALIQWHPPVDTFGPLQGYRLKFGKRDMEPLTTLEFSEKEDHFTATDIHKGASYVFRLSARNK
VGFGEMVKEISIPPEVPTGFPQNLHSEGTSTSVQLSWQPPVLAERNGLITKYTLTYRDINIPILPMEQLIVPA
DTTMTLTGLKPDTTYDVKVRHAHTSKGPGPYSPSVQFRTLPVDQVFAKNFHVKAVMKTSVLLSWEIPENYNSAMPF
KILYDDGKMVEEDVGRATQKLIVNLKPEKSYSFVLTNR**GNSAGGLQHR**VTAKTAPDVLRTKPAFIGKTNLDMIT
VQLPEVPANENIKGYIIIVPLKKSRLKFIKPWESPDEMEDELLEISRKRRSIRYGREVELKPYIAAHFDVLP
TEFTLGDDKHGGFTNKQLQSGQEYVFFVLAVMEHAESKMYATSPSYSDPVVSMDLDPQIPITDEEGLIWWVGPVL
AVVFICIVIAILLYKRR**KRAESDSRK**SSIPNNK**EIPSHHPTDPVELRR**LNFTQPGMASHPIPILELADHIERLK
ANDNLKFSQYESIDPGQFTWEHSNLEVNKPKNR**YANVIAYDHSR**VLLSAIEGIPGSDYVNANYIDGYRKQNAV
IATQCSLPETFGDFWRMIWEQRSATVMMTKLEERSRVKCDQYWPSRGTEHGLVQVTLTLDVETATYCVRTFAL
YKNGSSEKREVQFQFTAWPDHGVPEHPTPFLAFLRVKTCNPPDAGPMVVHCSAGVGR**TGCFIVIDAMLER**IKH
EK**TVDIYGHVTLMR**AQRNYMVQTEDQYIFIHDALLEAVTCGNTEVPARNLYAYIQ**LTQIETGENVTGMELEFK**R
LASSKAHTSRFISANLPCNKFKNR**LVNIMPYESTR**VCLQPIRG**VEGSDYINASFIDGYR**QKAYIATQGPLAETT
EDFWRMLWEHNSTIVVMLTKLREMGREKCHQYWPASARS**YQYFVVDPMAEYNMPQYILR**REFKVTDARDGQSRV
RQFQFTDWPEQGVPK**SGEGFIDFIGQVHK**TK**EQFGQDGPISVHCSAGVGR**TGVFITLSIVLERMRYEGVVDIFQT
VKMLRTQRPAMVQTEDQYQFSYRAALEYLGSDHYAT

Mass Match Peptides (bold):

DFLPVDTSNNGR [118]
EIPSHHPTDPVELRR [199]
EQFGQDGPISVHCSAGVGR [219]
GFPTIDMGPQLK [295]
GNSAGGLQHR [305]
GVEGSDYINASFIDGYR [325]
KRAESDSR [434]
LTQIETGENVTGMELEFK [498]
LVNIMPYESTR [503]
RAESDSRK [595]
SDTIANYELVYK [625]
SGEGFIDFIGQVHK [632]
TGCFIVIDAMLER [692]
TVDIYGHVTLMR [736]
YANVIAYDHSR [840]
YQYFVVDPMAEYNMPQYILR [869]
YSAPANLYVR [870]
YSVAGLSPYSDYEF [873]

Tandem Peptides (underline):

YANVIAYDHSR [840]
YSAPANLYVR [870]

Peptide Source: iTRAQ, Colorectal cancer

MVHVARLLLLLLTFFLRDAETPPRFTRTPVDQTVSGGVASFCQATGDPKPKIVWNKKGKVSNQRFVIEFD
 DGSGSVLRIQPLRTPRDEAIYECVASNNVGEISVSTRLTVLREDQIPRGFPTIDMGPKLVVERTRTATMLCAAS
 GNPDPFITWFKDFLPVDTSNNNGR**IKQLR**SESIGGTPIRGALQIEQSEESDQGYECVATNSAGTRYSAPANLYV
 RELREVRVPFRFSIPPTNHEIMPGGSVNITCVAVGSPMPYVKWMLGAEDLTPEDDMPIGRNVLELNDVRQSANY
 TCVAMSTLGVIEAIAQITVKALPKPPGTPVVTTESTATSIITLWDSGNPEPVSYIIQHKPKNSEELYKEIDGVAT
 TRYSVAGLSPYSYDFRVVAVNNIGRGPPSEPVLTQTSEQAPSSAPRDVQARMLSSSTILVQWKEPEEPNGQIQG
 YRVYYTMDPTQHVNNWMKHNVDQSITITIGNLVPQKTSYVKVLAFTSIGDGPLSSDIQVITQTGVPGQPLNFKAE
 PESETSILLSWTPPRSDTIANYELVYKDGEGEEQRITIEPGTSYRLQGLKPNLSLYYFRLAARSPQGLGASTAEI
 SARTMQSKSPAPPQDISCTSPSSSTISLVSWQPPPEKQNGIITEYSIKYTAVDGEDDKPHEILGIPSDTTKYLL
 QLEKWTEYRITVTAHTDVGPGPESLSVLIRTNEDVPSGPPRKVEEAVNSTSVKVSWSRSPVFNKQHGQIRGYQVH
 YVRMENGEPKQPMKLDVMLADAQWEDDTTEHDMIISGLQPETSYSLTVTAYTTKGDGARSKPKLVSTTGAVPG
 KPRLVINHTQMNTALIQWHPPVDTFGFLQGYRLKFGKRDMEPLTTLEFSEKEDHFTATDIHKGASYVFR**LSARNK**
 VGFGEEMVKEISIPPEEVPFGFPQNLHSEGTSTSVQLSWQPPVLAERNGIITKYTLLYRDINIPLLPMEQLIVPA
 DTTMTLTGLKPDTTYDVVKRAHTSKGPGPYSPSVQFRTLPVDQVFAKNFHVKAAMKTSVLLSWEIPENYNSAMPF
 KILYDDGKMVEEVDGRATQKLIVNLKPEKSYFVLTNRCNSAGGLQHRVTAKTAPDVLRTKPAFIGKTNLDGMIT
 VQLPEVPANENIKGYYIIIVPLKKSCKFIKPWESPDMEDELDELKEISRKRIRYGREVELKPYIAAHFDVLP
 TEFTLGGDKHYGGFTNKQLQSGQYVFFVLAVMEHAESKMYATSPYSDPVVSMDLDPQIPITDEEEGLIWWVGPVL
 AVVFIICIVIAILLYKRAESDSRKSSIPNNKEIPSHHPTDPVELRRLNFQTPGMASHPPPIPILEADHIERLK
 ANDNLKFSQYIESIDPGQQTWEHSNLEVNKPKNRYANVIAYDHSRVLLSAIEGIPGSDYVNANYIDGYRKQNAV
 IATQGSGLPETFGDFWRMIWEQRSATVVMMTKLEERSRVKCDQYWPARGTETHGLVQVTLDDTVELATYCVRTFAL
 YKNGSSEKREVRQFQFTAWPDHGVPEHPTPFLAFLRRVKTCPNPPDAGPMVHCSAGVGRGCFIVIDAMLERIKH
 EKTVDIYGHVTLMAQRNVMVQTEDQYIFIHDALEAVTCGNTEVPARNLYAYIQKLTQIETGENVTGMELEFKR
LASSKAHTSRFI SANLPCNKFKNRLVNIMPYESTRVCLQPIRGVEGSDYINASFIDGYRQOKAYIATQGPLAETT
 EDFWRMLWEHNSTIVVMLTKLREMGREKCHQYWPASARYQYFVVDPMAYNMPQYILREFKVTDARDGQSRTV
 RQFQFTDWPEQGVKSGEGFIDFIGVHKTKQFGQDGPISVHCSAGVGRGCFITLSIVLERMRYEGVVDIFQT
 VKMLRTQRPAMVQTEDQYQFSYRAALEYLGSPDHYAT

Mass Match Peptides (bold):

IKQLR [922]
 LASSKAHTSR [930]
 LSARNK [946]

Tandem Peptides (underline):

IKQLR [922]
 LASSKAHTSR [930]
 LSARNK [946]

Peptide Source: iTRAQ, Hepatocellular cancer

MVHVARLLLLLLTFFLRDAETPPRFTRTPVDQTVSGGVASFCQATGDPKPKIVWNKKGKVSNQRFVIEFD
 DGSGSVLRIQPLRTPRDEAIYECVASNNVGEISVSTRLTVLREDQIPRGFPTIDMGPKLVVERTRTATMLCAAS
 GNPDPFITWFKDFLPVDTSNNNGR**IKQLR**SESIGGTPIRGALQIEQSEESDQGYECVATNSAGTRYSAPANLYV
 RELREVRVPFRFSIPPTNHEIMPGGSVNITCVAVGSPMPYVKWMLGAEDLTPEDDMPIGRNVLELNDVRQSANY
 TCVAMSTLGVIEAIAQITVKALPKPPGTPVVTTESTATSIITLWDSGNPEPVSYIIQHKPKNSEELYKEIDGVAT
 TRYSVAGLSPYSYDFRVVAVNNIGRGPPSEPVLTQTSEQAPSSAPRDVQARMLSSSTILVQWKEPEEPNGQIQG
 YRVYYTMDPTQHVNNWMKHNVDQSITITIGNLVPQKTSYVKVLAFTSIGDGPLSSDIQVITQTGVPGQPLNFKAE
 PESETSILLSWTPPRSDTIANYELVYKDGEGEEQRITIEPGTSYRLQGLKPNLSLYYFRLAARSPQGLGASTAEI
 SARTMQSKSPAPPQDISCTSPSSSTISLVSWQPPPEKQNGIITEYSIKYTAVDGEDDKPHEILGIPSDTTKYLL
 QLEKWTEYRITVTAHTDVGPGPESLSVLIRTNEDVPSGPPRKVEEAVNSTSVKVSWSRSPVFNKQHGQIRGYQVH
 YVRMENGEPKQPMKLDVMLADAQWEDDTTEHDMIISGLQPETSYSLTVTAYTTKGDGARSKPKLVSTTGAVPG
 KPRLVINHTQMNTALIQWHPPVDTFGFLQGYRLKFGKRDMEPLTTLEFSEKEDHFTATDIHKGASYVFR**LSARNK**
 VGFGEEMVKEISIPPEEVPFGFPQNLHSEGTSTSVQLSWQPPVLAERNGIITKYTLLYRDINIPLLPMEQLIVPA
 DTTMTLTGLKPDTTYDVVKRAHTSKGPGPYSPSVQFRTLPVDQVFAKNFHVKAAMKTSVLLSWEIPENYNSAMPF
 KILYDDGKMVEEVDGRATQKLIVNLKPEKSYFVLTNRCNSAGGLQHRVTAKTAPDVLRTKPAFIGKTNLDGMIT
 VQLPEVPANENIKGYYIIIVPLKKSCKFIKPWESPDMEDELDELKEISRKRIRYGREVELKPYIAAHFDVLP
 TEFTLGGDKHYGGFTNKQLQSGQYVFFVLAVMEHAESKMYATSPYSDPVVSMDLDPQIPITDEEEGLIWWVGPVL
 AVVFIICIVIAILLYKRAESDSRKSSIPNNKEIPSHHPTDPVELRRLNFQTPGMASHPPPIPILEADHIERLK
 ANDNLKFSQYIESIDPGQQTWEHSNLEVNKPKNRYANVIAYDHSRVLLSAIEGIPGSDYVNANYIDGYRKQNAV

IATQGSLEPETFGDFWRMIWEQRSATVMMTKLEERSRVKCDQYWPSRGTEHGLVQVTLTDLTVELATYCVRTFAL
YKNGSSEKREVRQFQFTAWPDHGVPEHPTPFLAFLRRVKTCPNPDAGPMVVHCSAGVGRGTGCTFIVIDAMLERIKH
EKTVDIYGHVTLMRQQRNMYMVQTEDQYIFLHDALLEAVTCGNTEVPARNLYAYIQKLTQIETGENVTGMELEFKR
LASSKAHTSRFISANLPCNKFKNRLVNIIMPYESTRVCLQPIRGVEGSDYINASFIDGYRQQKAYIATQGPLAETT
EDFWRMLWEHNSTIVVMTKLREMGREKCHQYWPASERSARYQYFVVDPMAYNMPQYILREFKVTDARDGQSRTV
RQFQFTDWPEQGVPKSGEGFIDFIGQVHKTEQFGQDGPISVHCSAGVGRGTGVFTLISIVLERMRYEGVVDIFQT
VKMLRTQRPAMVQTEDQYQFSYRAALEYLGSEFDHYAT

Mass Match Peptides (bold):

IKQLR [922]

Tandem Peptides (underline):

IKQLR [922]

Peptide Source: iTRAQ, Non-small cell lung cancer

MVHVARLLLLLLTFFLRDAETPPRFTRTPVDQTVGSSGVASFICQATGDPKPKIVWNKKGKKVSNQRFVIEFD
DGSGSVLRIQPLRTPRDEAIYECVASNNVGEISVSTRLTVLREDQIPRGFTIDMGFQLKVVERTRTATMLCAAS
GNPDPEITWFKDFLPVDTSNNGRIKQLRSESIGGTPIRGALQIEQSESDQKGYECVATNSAGTRYSAANLYV
RELREVRRVPPRFISIPPTNHEIMPSSSVNITCVAVGSPMPYVWMLGAEDLTPEDDMPIGRNVLELNDVRQSANY
TCVAMSTLGVIEAIAQITVKALPKPPGTPVVTTESTATSITLTWDSGNPEFVSYYIIQHKPKNSEELYKEIDGVAT
TRYSVAGLSPYSDYEFVAVNNIGRGPPEPVLQTSEQAPSSAPRDVQARMLSTTILVQWKEPEEPNGQIQG
YRVYTTMDPTQHVNNWMKHNVADSQITITIGNLVLPQKTSVKVLAFTSIGDGPLSSDIQVITQTGVPGQPLNFKAE
PESETSILLSWTPPRSDTIANYELVYKDGEGHEEQRTIEPGTSYRLQGLKPNSLYYFRLAARSPQGLGASTAEI
SARTMQSKPSAPPQDISCTSPSSSTILVSWQPPPVVEKQNGIITEYSIKYTAVDGEDDKPHEILGIPSDTTKYLL
QLEKWTEYRITVTAHTDVGGPESLSVLIRTNEDVPSGPPRKVEVEAVNSTSVKVSWRSPVPNKQHGQIRGYQVH
YVRMENGEPKQPMKDVMLADAQWFEFDDTTEHDMIISGLQPETSYSLTVTAYTKGDGARSKPKLVSTTGAVPG
KPLRVINHTQMNTALIQWHPVDTFGPLQGYRLKFGKRDMEPLTTLEFSEKEDHFTATDIHKGASYVFRLSARNK
VGFGEMVKEISIPPEVPTGFPQNLHSEGTSTSVQLSWQPPVLAERNGIITKYTLLYRDINIPLLPMEQLIVPA
DTTMTLTGLKPDTTYDVKVRHTSKGPGPYSPSVQFRTLVPDQVFAKNFHVKAVMKTSLVLSWEIPENYNSAMPF
KILYDDGKMVEVDGRATQKLIVNLKPEKSYSFVLTNRGNSAGGLQHRVTAKTAPDVLRTKPAFIGKTNLDGMIT
VQLPEVPANENIKGYIIIVPLKKSARGKFIKPWESPDEMEDELLEKISRKRRSIRYGREVELKPYIAAHFDVLP
TEFTLGDGKHGGFTNKQLQSGQEYVFFVLAVMEHAESKMYATSPYSDPVPVSMOLDPQPIITDEEGLIWWVGPVL
AVVFIICIVIAILLYKRRKRAESDSRKSSIPNKEIPSHHPTDPVELRRLNFQTPGMASHPPPIILELADHIERLK
ANDNLKFSQYYESIDPGQFTWEHSNLEVNPKPNRYANVIAYDHSRVLLSAIEGIPGSDYVNANYIDGYRKQNAY
IATQGSLEPETFGDFWRMIWEQRSATVMMTKLEERSRVKCDQYWPSRGTEHGLVQVTLTDLTVELATYCVRTFAL
YKNGSSEKREVRQFQFTAWPDHGVPEHPTPFLAFLRRVKTCPNPDAGPMVVHCSAGVGRGTGCTFIVIDAMLERIKH
EKTVDIYGHVTLMRQQRNMYMVQTEDQYIFLHDALLEAVTCGNTEVPARNLYAYIQKLTQIETGENVTGMELEFKR
LASSKAHTSRFISANLPCNKFKNRLVNIIMPYESTRVCLQPIRGVEGSDYINASFIDGYRQQKAYIATQGPLAETT
EDFWRMLWEHNSTIVVMTKLREMGREKCHQYWPASERSARYQYFVVDPMAYNMPQYILREFKVTDARDGQSRTV
RQFQFTDWPEQGVPKSGEGFIDFIGQVHKTEQFGQDGPISVHCSAGVGRGTGVFTLISIVLERMRYEGVVDIFQT
VKMLRTQRPAMVQTEDQYQFSYRAALEYLGSEFDHYAT

Mass Match Peptides (bold):

ELREVR [901]

GNSAGGLQHRVTAK [914]

LASSKAHTSR [930]

LSARNK [946]

LTVLR [949]

MRYEGVVDIFQTVK [952]

TVDIYGHVTLMR [736]

VEVEAVNSTSVK [755]

Tandem Peptides (underline):

ELREVR [901]

GNSAGGLQHRVTAK [914]

LASSKAHTSR [930]

LSARNK [946]

LTVLR [949]

MRYEGVVDIFQTVK [952]

TVDIYGHVTLMR [736]
VEVEAVNSTSVK [755]

Peptide Source: iTRAQ, Ovarian cancer

MVHVARLLLLLLTFFLRDAETPPRFTRTPVDQTGVSGGVASFCQATGDPKPKIVWNKKGKKVSNQRFEVIEFD
DGSGSVLRIQPLRTPRDEAIYECVASNNVGEISVSTRLTVLREDQIPRGFPTIDMGPQLKVVERTRTATMLCAAS
GNPDPEITWFKDFLPVDTSNNGRIKQLRSESIGGTPIRGALQIEQSEESDQKGYECVATNSAGTRYSAPANLYV
RELREVRVPPRFSIPPTNHEIMPGGSVNITCVAVGSPMPYVKWMLGAEDLTPEDDMPIGRNVLELNDVRQSANY
TCVAMSTLGVIEAIAQITVKALPKPPGTPVVTSTATSITLTWDSGNPEPVSYIIQHKPKNSEELYKEIDGVAT
TRYSVAGLSPYSYEFVRVAVNNIGRGPPSEPVLTQTSEQAPSSAPRDVQARMLSTTILVQWKEPEEPNGQIQG
YRVYYTMDPTQHVNNWMKHNVDQSITTIGNLVPQKTSYVKVLAFTSIGDGPLSSDIQVITQTGVPGQPLNFKAE
PESETSIILSWTPPRSDTIANYELVYKDGEGEEQRITIEPGTSYRLQGLKPNLSYYFRLAARSPQGLGASTAEI
SARTMQSKPSAPPQDISCTSPSSSILVSWQPPPVEKQNGIITEYSIKYTAVDGEDDKPHEILGIPSDTTKYLLE
QLEKWTEYRITVTAHTDVGPGPESLSVLIRTNEDVPSGPPRKVEVEAVNSTSVKVSWSRSPVFNKQHGQIRGYQVH
YVRMENGEPKQGMPLKDVMLADAQWFEFDDTTEHDMIISGLQPETSYSLTVTAYTTKGDGARSKPKLVSTTGAVPG
KPRLVINHTQMNTALIQWHPVDTFGPLQGYRLKFGKRDMEPLTTLEFSEKEDHFTATDIHKGASYVFRLSARNK
VGFGEEMVKEISIPPEVPTGFPQNLHSEGTSTSVQLSWQPPVLAERNGIITKYTLLYRDINIPLLPMEQLIVPA
DTMTLTGLKPDITTYDVKVRHAHTSKGPGPYSPSVQFRTLTPVDQVFAKNFHVKAVMKTSVLLSWEIPENYNSAMPF
KILYDDGKMVEEVDGRATQKLIVNLKPEKSYSEFVLNTRGNSAGGLQHRVTAKTAPDVLRTKPAFIGTNDLGMIT
VQLPEVPANENIKGYYIIIVPLKKSARGKFIKPWESPDMELEDELLKEISRKRRSIRYGREVELKPYIAAHFDVLP
TEFTLGDDKHGGFTNKQLQSGQYVFFVLAVMEHAESKMYATSPYSDPVVSMOLDPQPIITDEEEGLIWWVGVPV
AVVFIICIVIAILLYKRKRAESDSRKSSIPNNKEIPSHHPTDPVELLRLNFQTPGMASHPPPILELADHIERLK
ANDNLKFSQYYESIDPGQFTWEHSNLEVNPKPNRYANVIAYDHSRVLLSAIEGIPGSDYVNANYIDGYRKQNAV
IATQGSPLPETFGDFWRMIWEQRSATVVMMTKLEERSVKCDQYWPSSRGTEHGLVQVTLTLDVELATYCVRTFAL
YKNGSSEKREVRQFQTAWPDHGVPEHPTPFLAFLRRVKTCPNPDAGPMVVHCSAGVGRGTGCFIVIDAMLERIKH
EKTVDIYGHVTLMRQARNYMQTEDQYIFIHDALEAVTCGNTEVPARNLYAYIQKLTQIETGENVTGMELEFKR
LASSKAHTSRFISANLPCNKFKNRLVNIMPYESTRVCLOPIRGVEGSDYINASFIDGYRQKAYIATQGPLAETT
EDFWRMLWEHNSTIVVMLTKLREMGREKCHQYWPAAERSARYQYFVVDMAEYNMPQYILREFKVTDARDGQSRV
RQFQFTDWPEQGVKSGEGFIDFIGQVHKTKEQFGQDGPISVHCSAGVGRGTGVFTLSIVLERMRYEGVVDIFQT
VKMLRTQRPAMVQTEDQYQFSYRAALEYLGSFDHYAT

Mass Match Peptides (bold):
YEGVVDIFQTVK [843]

Tandem Peptides (underline):
YEGVVDIFQTVK [843]

Peptide Source: iTRAQ, Renal cell cancer

MVHVARLLLLLLTFFLRDAETPPRFTRTPVDQTGVSGGVASFCQATGDPKPKIVWNKKGKKVSNQRFEVIEFD
DGSGSVLRIQPLRTPRDEAIYECVASNNVGEISVSTRLTVLREDQIPRGFPTIDMGPQLKVVERTRTATMLCAAS
GNPDPEITWFKDFLPVDTSNNGRIKQLRSESIGGTPIRGALQIEQSEESDQKGYECVATNSAGTRYSAPANLYV
RELREVRVPPRFSIPPTNHEIMPGGSVNITCVAVGSPMPYVKWMLGAEDLTPEDDMPIGRNVLELNDVRQSANY
TCVAMSTLGVIEAIAQITVKALPKPPGTPVVTSTATSITLTWDSGNPEPVSYIIQHKPKNSEELYKEIDGVAT
TRYSVAGLSPYSYEFVRVAVNNIGRGPPSEPVLTQTSEQAPSSAPRDVQARMLSTTILVQWKEPEEPNGQIQG
YRVYYTMDPTQHVNNWMKHNVDQSITTIGNLVPQKTSYVKVLAFTSIGDGPLSSDIQVITQTGVPGQPLNFKAE
PESETSIILSWTPPRSDTIANYELVYKDGEGEEQRITIEPGTSYRLQGLKPNLSYYFRLAARSPQGLGASTAEI
SARTMQSKPSAPPQDISCTSPSSSILVSWQPPPVEKQNGIITEYSIKYTAVDGEDDKPHEILGIPSDTTKYLLE
QLEKWTEYRITVTAHTDVGPGPESLSVLIRTNEDVPSGPPRKVEVEAVNSTSVKVSWSRSPVFNKQHGQIRGYQVH
YVRMENGEPKQGMPLKDVMLADAQWFEFDDTTEHDMIISGLQPETSYSLTVTAYTTKGDGARSKPKLVSTTGAVPG
KPRLVINHTQMNTALIQWHPVDTFGPLQGYRLKFGKRDMEPLTTLEFSEKEDHFTATDIHKGASYVFRLSARNK
VGFGEEMVKEISIPPEVPTGFPQNLHSEGTSTSVQLSWQPPVLAERNGIITKYTLLYRDINIPLLPMEQLIVPA
DTMTLTGLKPDITTYDVKVRHAHTSKGPGPYSPSVQFRTLTPVDQVFAKNFHVKAVMKTSVLLSWEIPENYNSAMPF
KILYDDGKMVEEVDGRATQKLIVNLKPEKSYSEFVLNTRGNSAGGLQHRVTAKTAPDVLRTKPAFIGTNDLGMIT
VQLPEVPANENIKGYYIIIVPLKKSARGKFIKPWESPDMELEDELLKEISRKRRSIRYGREVELKPYIAAHFDVLP
TEFTLGDDKHGGFTNKQLQSGQYVFFVLAVMEHAESKMYATSPYSDPVVSMOLDPQPIITDEEEGLIWWVGVPV
AVVFIICIVIAILLYKRKRAESDSRKSSIPNNKEIPSHHPTDPVELLRLNFQTPGMASHPPPILELADHIERLK

ANDNLKFSQEYESIDPGQQFTWEHSNLEVNKPKNRYANVIAYDHSRVLLSAIEGIPGSDYVNANYIDGYRKQNAV
IATQGSLEPETFGDFWRMIWEQRSATVMMTKLEERSRVKCDQYWPSRGTEHGLVQVTLTDLTVELATYCVRTFAL
YKNGSSEKREVRQFQFTAWPDHGVPEHPTPFLAFLRRVKT CNFPDAGPMVVHCSAGVGRTGCFIVIDAMLERIKH
EKTVDIYGHVTLMRAQRNMYVQTEDQYIFIHDALEAVTCGNTIEVPARNLYAYIQKLTQIETGENVTGMELEFKR
LASSKAHTRSFI SANLPCKNFKNRLVNIIMPYESTRVCLQPIRGVEGSDYINASFIDGYRQQKAYIATQGPLAETT
EDFWRMLWEHNSTIVVMLTKLREMGREKCHQYWPASARYQYFVVDPMAYNMPQYIILREFKVT DARDGQSRTV
RQFQFTDWPEQGVKPSGEGFIDFIGQVHKTKEQFGQDGPISVHCSAGVGRTGVFITLSIVLERMRYEGVVDIFQT
VKMLRTQRPFAMVQTEDQYQFSYRAALEYLG SFDHYAT

Mass Match Peptides (bold):

ILYDDGKMVEEVDGR [923]

Tandem Peptides (underline):

ILYDDGKMVEEVDGR [923]

OGTA104 (SEQ ID No: 20)**Peptide Source: 1D-GE, Breast cancer**

MGSGARFPSGTLRVRWLLLLGLVGPVLGAARPGFQQTSHLSSYEIITPWRLTRERREAPRPYSKQVS YVIAEGK
EHIIHLERNKDLLPEDFVVYTYNKECTLITDHPNIQNHCHYRGYVEGVHNSSIALSDCFGLRGLLHLENASYGIE
PLQNSSHEFHIIYRMDDVYKEPLKCGVSNKDIEKETAKDEEEEP SMTQLLRRRAVL P QTRYVELFIVVDKERY
DMMGRNQTA VREEMILLANYLDSMYIMLNIRIVLVGLEIWTNGNLINIVGGAGDVLGNFVQWREKFLITRRRHDS
AQLVLKKGFGGTAGMAFVGTVC SRSHAGGINVFGQITVETFA SIVAH ELGHNLMNHDDGRDCSCGAKSCIMNSG
ASGSRNFSSCSAEDFEKLT LNKGGNCLLNIPK PDEAYSAPSCGNKLVDAGEECD CGTPKECELDPCCEGSTCKLK
SFAECAYGDCCKDCRFLPGGTL CRGKTSECDVPEYCN GSSQFCQPDVFIQNGYPCQNNKAYCYNGMCQYYDAQCQ
VIFGSKAKAAPKDCFIEVNSKGD RFGNCGFSGNEYKKCATGNALCGKLQCE NVQEIPVFGIVPAIIQTPSRGTKC
WGVDFQLGSDVPDPGMVNEG TKCGAGKICRN FQCVDASVLNYDCDVQKKCHGHGVCNSNKNCHCENGWAPPNCET
KGYGGSVD SGPTYNEMNTALRDGLLVFFFLIVPLIVCAIFIFIKRDQLWRSYFRKKRSQTYESDGKNQANPSRQP
GSVPRHVSFVTPPR **EVPIYANR**FAVPTYAAK **QPQQFPSRPPPPQPK**VSSQGNLIPARPAPAPPLYSSLT

Mass Match Peptides (bold):

EVPIYANR [236]

QPQQFPSRPPPPQPK [586]

Tandem Peptides (underline):

FAVPTYAAK [244]

Peptide Source: 1D-GE, Hepatocellular carcinoma

MGSGARFPSGTLRVRWLLLLGLVGPVLGAARPGFQQTSHLSSYEIITPWRLTRERREAPRPYSKQVS YVIAEGK
EHIIHLERNK**DLLPEDFVVYTYNK**EGTLITDHPNIQNHCHYRGYVEGVHNSSIALSDCFGLRGLLHLENASYGIE
PLQNSSHEFHIIYRMDDVYKEPLKCGVSNKDIEKETAK**DEEEPPSMTQLLR**RRRAVL P QTRYVELFIVVDKERY
DMMGRNQTA VREEMILLANYLDSMYIMLNIRIVLVGLEIWTNGNLINIVGGAGDVLGNFVQWREKFLITRRRHDS
AQLVLK**KGFGGTAGMAFVGTVC SR**SHAGGINVFGQITVETFA SIVAH ELGHNLMNHDDGRDCSCGAKSCIMNSG
ASGSRNFSSCSAEDFEKLT LNKGGNCLLNIPK PDEAYSAPSCGNKLVDAGEECD CGTPKECELDPCCEGSTCKLK
SFAECAYGDCCKDCRFLPGGTL CRGKTSECDVPEYCN GSSQFCQPDVFIQNGYPCQNNKAYCYNGMCQYYDAQCQ
VIFGSKAKAAPKDCFIEVNSKGD RFGNCGFSGNEYKKCATGNALCGKLQCE NVQEIPVFGIVPAIIQTPSRGTKC
WGVDFQLGSDVPDPGMVNEG TKCGAGKICRN FQCVDASVLNYDCDVQKKCHGHGVCNSNKNCHCENGWAPPNCET
KGYGGSVD SGPTYNEMNTALRDGLLVFFFLIVPLIVCAIFIFIK**RDQLWR**SYFRKKRSQTYESDGKNQANPSR**QP**
GSVPRHVSFVTPPR **EVPIYANR**FAVPTYAAK **QPQQFPSRPPPPQPK**VSSQGNLIPARPAPAPPLYSSLT

Mass Match Peptides (bold):

DEEEPPSMTQLLR [113]

DLLPEDFVVYTYNK [134]

EVPIYANR [236]

KGFGGTAGMAFVGTVC SR [419]

QPGSVPR [584]

QPQQFPSRPPPPQPK [586]

RDQLWR [600]

Tandem Peptides (underline):

EVPIYANR [236]

Peptide Source: 1D-GE, Ovarian cancer

MGSGAR**FPSGTLR**VRWLLLLGLVGPVLGAARPGFQQTSHLSSYEIITPWRLTRERREAPRPYSKQVSYVIQAEKG
 EHIHLEARNKDLLPEDFVVYTYNKEGTLTIDHPNIQNHCHYRGYVEGVHNSIALSDCFGLRGLLHLENASYGIE
 PLQNSSHFEHIIYRMDDVYKEPLKCGVSNKDIEKETAKDEEEPPSMTQLRRRRRAVLPPQTRYVELFIVVDKERY
 DMMGRNQTAVEREEMILLANYLDSMYIMLNIRIVLVGLEIWTNGNLINIVGGAGDVLGNFVQWREKFLITRRRHDS
 AQLVLK**KGFGGTAGMAFVGTVCSR**SHAGGINVFGQITVETFAIVAHELGHNLMNHDDGRDCSCGAKSCIMNSG
 ASGSRNFSSCSAEDFEKLTNLKGGNCLLNIPKPDEAYSAPSCGNKLVDAGEECDGTPKECELDPCCEGSTCKLK
 SFAECAYGDCCKDCR**FLPGGTLCR**GKTSECDVPEYCNSSQFCQPDVFIQNGYPCQNNKAYCYNGMCQYYDAQCQ
 VIFGSKAKAAPKDCFIENVSKGDRFGNCGFSGNEYKKCATGNALCGKLQCEENVQEIIPVFGIVPAIIQTPSRGTKC
 WGVDFQLGSDVPDPGMVNEGTCGAGKICRNFQCVDAVLNDCDVQKKCHGHGVCNSNKNCHCENGWAPPNCET
 KGYGGSVDSGPTYNEMNTALRDGLLVFFFLIVPLIVCAIFIFIKR**DQLWRSYFRK**KRSQTYESDGKNQANPSRQP
 GSVPR**HVSPVTPPREVPIYANR**FAVPTYAA**QPQQFPSRPPPPQPK**VSSQGNLIPARPAPAPPLYSSLT

Mass Match Peptides (bold):

DQLWR [152]

EVPIYANR [236]

FLPGGTLCR [260]

FPSGTLR [264]

HVSPVTPPR [346]

KGFGGTAGMAFVGTVCSR [419]

QPQQFPSRPPPPQPK [586]

SYFRK [666]

Tandem Peptides (underline):

EVPIYANR [236]

FAVPTYAAK [244]

Peptide Source: 1D-GE, Pancreatic cancer

MGSGAR**FPSGTLR**VRWLLLLGLVGPVLGAARPGFQQTSHLSSYEIITPWRLTRERREAPRPYSKQVSYVIQAEKG
 EHIHLEARNKDLLPEDFVVYTYNKEGTLTIDHPNIQNHCHYRGYVEGVHNSIALSDCFGLRGLLHLENASYGIE
 PLQNSSHFEHIIYRMDDVYKEPLKCGVSNKDIEKETAKDEEEPPSMTQLRRRRRAVLPPQTRYVELFIVVDKERY
 DMMGRNQTAVEREEMILLANYLDSMYIMLNIRIVLVGLEIWTNGNLINIVGGAGDVLGNFVQWREKFLITRRRHDS
 AQLVLK**KGFGGTAGMAFVGTVCSR**SHAGGINVFGQITVETFAIVAHELGHNLMNHDDGRDCSCGAKSCIMNSG
 ASGSRNFSSCSAEDFEKLTNLKGGNCLLNIPKPDEAYSAPSCGNKLVDAGEECDGTPKECELDPCCEGSTCKLK
 SFAECAYGDCCKDCRFLPGGTLCRGKTSECDVPEYCNSSQFCQPDVFIQNGYPCQNNKAYCYNGMCQYYDAQCQ
 VIFGSKAKAAPKDCFIENVSKGDRFGNCGFSGNEYKKCATGNALCGKLQCEENVQEIIPVFGIVPAIIQTPSRGTKC
 WGVDFQLGSDVPDPGMVNEGTCGAGKICRNFQCVDAVLNDCDVQKKCHGHGVCNSNKNCHCENGWAPPNCET
 KGYGGSVDSGPTYNEMNTALRDGLLVFFFLIVPLIVCAIFIFIKR**DQLWRSYFRK**KRSQTYESDGKNQANPSRQP
 GSVPR**HVSPVTPPREVPIYANR**FAVPTYAA**QPQQFPSRPPPPQPK**VSSQGNLIPARPAPAPPLYSSLT

Mass Match Peptides (bold):

EEMILLANYLDSMYIMLNIR [179]

EVPIYANR [236]

KGFGGTAGMAFVGTVCSR [419]

QPQQFPSRPPPPQPK [586]

Tandem Peptides (underline):

HVSPVTPPR [346]

Peptide Source: iTRAQ, Colorectal cancer

MGSGAR**FPSGTLR**VRWLLLLGLVGPVLGAARPGFQQTSHLSSYEIITPWRLTRERREAPRPYSKQVSVYVIAEGK
 EHIIHLERNKDLLPEDFVVYTYNKEGTITDHPNIQNHCHYRGYVEGVHNSIALSDCFGLRGLLHLENASYGIE
 PLQNSSHFEHIIYRMDVYKEPLKCGVSNKDIEKETAKDEEEPPSMTQLRRRRRAVLPPQTRYVELFIVVDKERY
 DMMGR**NQTAVR**EMILLANYLDSMYIMLNIRIVLVGLEIWTNGNLINIVGGAGDVLGNFVQWREKFLITRRRHDS
 AQLVLKKGGGGTAGMAFVGTVCSSRHAGGINVFGQITVETFAIVAHELGHNLGMNHDDGRDCSCGAKSCIMNSG
 ASGSRNFSSCSAEDFEKLTNLKGGNCLLNIPKPDEAYSAPSCGNKLVDAGEECDGTPKECELDPCCEGSTCKLK
 SFAECAYGDCCKDCRFLPGGTLCRGKTSECDVPEYCNSSQFCQPDVFIQNGYPCQNNKAYCYNGMCQYYDAQCQ
 VIFGSKAKAAPKDCFIEVNSKGRDFGNCGFSGNEYKKCATGNALCGK**LQCEENVQEIIPVFGIVPAIIQTTPSR**GTTC
 WGVDFQLGSDVDPDGMVNEGTCGAGKICRNFQCVDA SVLN YDCDVQKKCHGHGVCNSNKNCHCENGWAPPNCET
 KGYGGSVDSGPTYNEMNTALRDGLLVFFFLIVPLIVCAIFIFIKRQDLWRSYFRKKRSQTYESDGKNQANPSRQP
 GSVPRHVSPTPTPREVPIYANRFVPTTYAAKQPQQFPSRPPPPQPKVSSQGNLIPARPAPAPPLYSSLT

Mass Match Peptides (bold):

FPSGTLR [264]
 LQCEENVQEIIPVFGIVPAIIQTTPSR [943]
 NQTAVR [959]

Tandem Peptides (underline):

FPSGTLR [264]
 LQCEENVQEIIPVFGIVPAIIQTTPSR [943]
 NQTAVR [959]

Peptide Source: iTRAQ, Hepatocellular cancer

MGSGARF**FPSGTLR**VRWLLLLGLVGPVLGAARPGFQQTSHLSSYEIITPWRLTRERREAPRPYSKQVSVYVIAEGK
 EHIIHLERNKDLLPEDFVVYTYNKEGTITDHPNIQNHCHYRGYVEGVHNSIALSDCFGLRGLLHLENASYGIE
 PLQNSSHFEHIIYRMDVYKEPLKCGVSNKDIEKETAKDEEEPPSMTQLRRRRRAVLPPQTRYVELFIVVDKERY
 DMMGRNQTAVREEMILLANYLDSMYIMLNIRIVLVGLEIWTNGNLINIVGGAGDVLGNFVQWREKFLITRRRHDS
 AQLVLKKGGGGTAGMAFVGTVCSSRHAGGINVFGQITVETFAIVAHELGHNLGMNHDDGRDCSCGAKSCIMNSG
 ASGSRNFSSCSAEDFEKLTNLKGGNCLLNIPKPDEAYSAPSCGNKLVDAGEECDGTPKECELDPCCEGSTCKLK
 SFAECAYGDCCKDCRFLPGGTLCRGKTSECDVPEYCNSSQFCQPDVFIQNGYPCQNNKAYCYNGMCQYYDAQCQ
 VIFGSKAKAAPKDCFIEVNSKGRDFGNCGFSGNEYKKCATGNALCGKLQCEENVQEIIPVFGIVPAIIQTTPSRGTTC
 WGVDFQLGSDVDPDGMVNEGTCGAGKICRNFQCVDA SVLN YDCDVQKKCHGHGVCNSNKNCHCENGWAPPNCET
 KGYGGSVDSGPTYNEMNTALRDGLLVFFFLIVPLIVCAIFIFIKRQDLWRSYFRKKRS**SQTYESDGK**NQANPSRQP
 GSVPRHVSPTPTPREVPIYANRFVPTTYAAKQPQQFPSRPPPPQPKVSSQGNLIPARPAPAPPLYSSLT

Mass Match Peptides (bold):

SQTYESDGK [972]

Tandem Peptides (underline):

SQTYESDGK [972]

Peptide Source: iTRAQ, Non-small cell lung cancer

MGSGARF**FPSGTLR**VRWLLLLGLVGPVLGAARPGFQQTSHLSSYEIITPWRLTRERREAPRPYSKQVSVYVIAEGK
 EHIIHLERNKDLLPEDFVVYTYNKEGTITDHPNIQNHCHYRGYVEGVHNSIALSDCFGLRGLLHLENASYGIE
 PLQNSSHFEHIIYRMDVYKEPLK**CGVSNKDIEK**ETAKDEEEPPSMTQLRRRRRAVLPPQTRYVELFIVVDKERY
 DMMGRNQTAVREEMILLANYLDSMYIMLNIRIVLVGLEIWTNGNLINIVGGAGDVLGNFVQWREK**FLITRRRHDS**
 AQLVLKKGGGGTAGMAFVGTVCSSRHAGGINVFGQITVETFAIVAHELGHNLGMNHDDGRDCSCGAKSCIMNSG
 ASGSRNFSSCSAEDFEKLTNLKGGNCLLNIPKPDEAYSAPSCGNKLVDAGEECDGTPKECELDPCCEGSTCKLK
 SFAECAYGDCCKDCRFLPGGTLCRGKTSECDVPEYCNSSQFCQPDVFIQNGYPCQNNKAYCYNGMCQYYDAQCQ
 VIFGSKAKAAPKDCFIEVNSKGRDFGNCGFSGNEYKKCATGNALCGKLQCEENVQEIIPVFGIVPAIIQTTPSRGTTC
 WGVDFQLGSDVDPDGMVNEGTCGAGKICRNFQCVDA SVLN YDCDVQKKCHGHGVCNSNKNCHCENGWAPPNCET
 KGYGGSVDSGPTYNEMNTALRDGLLVFFFLIVPLIVCAIFIFIKRQDLWRSYFRKKRSQTYESDGKNQANPSRQP
 GSVPRHVSPTPTPREVPIYANRFVPTTYAAKQPQQFPSRPPPPQPKVSSQGNLIPARPAPAPPLYSSLT

Mass Match Peptides (bold):

CGVSNKDIEK [887]

FLITRRR [910]

Tandem Peptides (underline):

CGVSNKDIEK [887]

FLITRRR [910]

Peptide Source: iTRAQ, Ovarian cancer

MGSGARFPSTGLRVRWLLLLGLVGPVLGAARPGFQQTSHLSSYEIITPWRLTRERREAPRPYSKQVSYVIQAEKG
EHIIHLERNKDLLPEDFVVYTYNKEGTLITDHPNIQNHCHYRGYVEGVHNSIALSDCFGLRGLLHLENASYGIE
PLQNSSHFEHIIYRMDVYKEPLKCGVSNKDIEKETAKDEEEPPSMTQLLRRRRRAVLTPQTRYVELFIVVDKERY
DMMGRNQTAVREEMILLANYLDSMYIMLNIRIVLVGLEIWTNGNLINIVGGAGDVLGNFVQWREK**FLITRRR**HDS
AQLVLKKGFGGTAGMAFVGTVCSSRHAGGINVFGQITVETFASTVAHELGHNLGMNHDDGRDCSCGAKSCIMNSG
ASGSRNFSSCSAEDFEKLTNLKGGNCLLNIPKPDEAYSAPSCGNKLVDAGEECDGTPKECELDPCCEGSTCKLK
SFAECAYGDCKDCRFLPGGTLRCRGKTSECDVPEYCNSSQFCQPDVFIQNGYPCQNNKAYCYNGMCQYYDAQCQ
VIFGSKAKAAPKDCFIEVNSKGRDFGNCGFSGNEYKKCATGNALCGKLQCEENVQEIPVFGIVPAIIQTPSRGTKC
WGVDFQLGSDVDPDGMVNEGTCGAGKICRNFCVDASVLNYDCDVQKKCHGHGVCNSNKNCHCENGWAPPNCET
KGYGGSVDGSPTYNEMNTALRDGLLVFFFLIVPLIVCAIFIFIKRDQLWRSYFRKKRSQTYESDGKNQANPSRQP
GSVPRHVSPTTPPREVPIYANRFAVPTYAAKQPQQFPSRPPPPQPKVSSQGNLIPARPAPAPPLYSSLT

Mass Match Peptides (bold):

FLITRRR [910]

Tandem Peptides (underline):

FLITRRR [910]

Peptide Source: iTRAQ, Renal cell cancer

MGSGARFPSTGLRVRWLLLLGLVGPVLGAARPGFQQTSHLSSYEIITPWRLTRERREAPRPYSKQVSYVIQAEKG
EHIIHLERNKDLLPEDFVVYTYNKEGTLITDHPNIQNHCHYRGYVEGVHNSIALSDCFGLRGLLHLENASYGIE
PLQNSSHFEHIIYRMDVYKEPLKCGVSNKDIEKETAKDEEEPPSMTQLLRRRRRAVLTPQTRYVELFIVVDKERY
DMMGRNQTAVREEMILLANYLDSMYIMLNIRIVLVGLEIWTNGNLINIVGGAGDVLGNFVQWREK**FLITRRR**HDS
AQLVLKKGFGGTAGMAFVGTVCSSRHAGGINVFGQITVETFASTVAHELGHNLGMNHDDGRDCSCGAKSCIMNSG
ASGSRNFSSCSAEDFEKLTNLKGGNCLLNIPKPDEAYSAPSCGNKLVDAGEECDGTPKECELDPCCEGSTCKLK
SFAECAYGDCKDCRFLPGGTLRCRGKTSECDVPEYCNSSQFCQPDVFIQNGYPCQNNKAYCYNGMCQYYDAQCQ
VIFGSKAKAAPKDCFIEVNSKGRDFGNCGFSGNEYKKCATGNALCGKLQCEENVQEIPVFGIVPAIIQTPSRGTKC
WGVDFQLGSDVDPDGMVNEGTCGAGKICRNFCVDASVLNYDCDVQKKCHGHGVCNSNKNCHCENGWAPPNCET
KGYGGSVDGSPTYNEMNTALRDGLLVFFFLIVPLIVCAIFIFIKRDQLWRSYFRKKRSQTYESDGKNQANPSRQP
GSVPRHVSPTTPPREVPIYANRFAVPTYAAKQPQQFPSRPPPPQPKVSSQGNLIPARPAPAPPLYSSLT

Mass Match Peptides (bold):

FLITRRR [910]

Tandem Peptides (underline):

FLITRRR [910]

OGTA106 (SEQ ID No: 21)**Peptide Source: 1D-GE, Cervical cancer**

MQPPSLLLLLLLLLLLLCVSVVRPRGLLCGSFPEPCANGGTCLSLSLGQGTCCAPGFLGETCQFPDPCQNAQLCQ
NGGSCQALLPAPLGLPSSPSPLTPSFLCTCLPGFTGERCQAKLEDPCPPSFCSKRGRCHIQASGRPQCSCMPGWT
GEQCQIRDFCSANPCVNGGVCLATYPQIQCHCPPGFEGHACERDVNECFQDPGPCPKGTSCHNTLGSFQCLCPVG
QEGPRCELRAGPCPPRGCSNGGTCQLMPEKDSTFHLCLCPPGFIGPDCEVNPDCVSHQCQNGGTCQDGLDITYTC
LCPETWTGWDCESEDVDECETQGPFHCRNGGTCQNSAGSFHCVSVSGWGGTSCEENLDDCIAATCAPGSTCIDRVG

SFSCLCPPGRTGLLCHLEDMCLSQPCHGDAQCSTNPLTGSTLCLCQPGYSGPTCHQDLDECLMAQQGSPSPCEHGG
 SCLNTPGSFNCLCPPGYTGSRCADHNECLSQPCHPGSTCLDLLATFHCLCPPGLEQQLCEVETNECASAPCLNH
 ADCHDLLNGFQCICLPGFSGTRCEEDIDECRSSPCANGGQCQDQPGAFHCKCLPGFEGPRCQTEVDECLSDPCPV
 GASCLDLPGAFFCLCPSGFTGQLCEVPLCAPNLCPKQICKDQKDKANCLCPDGSPGCAPPEDNCTCHHGHCCQRS
 SCVCDVGWGTGPECEAELGGCISAPCAHGGTCYPQPSGYNCTCPTGYTGPTCSEEMTACHSGPCLNGGSCNPSPGG
 YYCTCPPSHTGPQCQTSTDYCVSAPCFNGGTCVNRPGTFSCLCAMGFQGPCEGKLRPSCADSPCRNRATCQDSP
 QGPRCLCPTGYTGGSQCOTLMDLCAQKPCPRNSHCLQTGPSFHCLCLQGTGPLCNLPLSSCQKAALSQGIDVSSL
 CHNGGLCVDSGPSYFCHCPGFGSLCQDHVNPCESRPCQNGATCMAQPSGYLCQCAPGYDGNCSKELDACQSQ
 PCHNHCTCTPKPGGFHCACPPGFVGLRCEGDVDECLDQPCHTCTAACHSLANAFYCQCLPGHTGQWCEVEIDPC
 HSQPCFHGGTCEATAGSPLGFICHCPKGFEGPTCSHRAPSCGFHHCHHGGLCLPSKPGFPFPRACLSGYGGPDC
 LTPPAKPGCGPPSPCLYNGSCSETTGLGGPGFRCSCPHSSPGPRCQKPGAKGCEGRSGDGACDAGCSGPGGNWDG
 GDGSLGVDPDPWKCPSHSRCWLLFRDGGQCHPQCDSEECLEFDGYDCETPPACTPAYDQYCHDHFNHGHCKEKGNTA
 ECGWDGGDCRPEGDGPEWGPSLALLVLSPPALDQQLFALARVLSLTLRVGLWVRKDRDGRDMVYPYPGARAEK
 LGGTRDPTYQERAAPQTQPLGKETDLSAGFVVVMGVDLRSCGPDHPASRCPWDPGLLLRFLAAMAAGVALEPLL
 PGPLLAVHPHAGTAPPANQLPWPVLCSPVAGVILALGALLVLQIRRRRREHGALWLPFGFTRRERTQSAPHRR
 RPPLGEDSIGLKALKPKAEVDEDGVVMCSGPEEGEEVQAEETGPPSTCQLWSLSGGCGALPQAAMLTTPQESEM
 EAPDLDRGPDGVTPLMSAVCCGEVQSGTFQGAWLGCPEPWEPLLDGGACPAHTVGTGETPLHLAARFSRPTAA
 RRLLEAGANPNQPDRAGRTPPLHAAVAADAREVCQLLLRSRQTAVDARTEDGTTPLMLAARLAVEDLVEELIAAQA
 DVGARDKWKGTALHWAANAARARSLLQAGADKDAQDNREQTPLFLAAREGAVEVAQQLLGLGAARELRDQAG
 LAPADVAHQNRNWDLLTLLEGAGPPEARHKATPGREAGFPFPRARTVSVVPPHGGGALPRCRTL SAGAGPRGGGA
 CLQARTWSVDLAARGGGAYSHCRSLSGVGAGGGPTPRGRRF SAGMRGPRNPAIMRGYGVAAAGRGGRVSTDWDP
 CDWVALGACGSASNIPIPPCLTPSPERGSPQLDCGPPALQEMPINQGGEGKK

Mass Match Peptides (bold):

Tandem Peptides (underline):

LSLGVGAGGGPTPR [642]

Peptide Source: 1D-GE, Melanoma

MQPPSLLLLLLLLLLLLLCVSVVRPRLGCGSFPEPCANGGTCLSLSLGQGTCCAPGFLGETCQFPDPCQNAQLCQ
 NGGSCQALLPAPLGLPSSPSPLTPSFLCTCLPGFTGERCQAKLEDPCPPSFCSKRGR**CHI QASGRPQCSCMPGWT**
GEQCQLRDFCSANPCVNGGVCLATYPQIQCHCPPGFEGHACERDVNECFQDGPGPCPKGTSCHNTLGSFQCLCPVG
 QEGPRCELRAGPCPPRGCSNGGTCQLMPEKDDSTFHLCLCPPGFIGPDCEVNPDCNVSHQCQNGGTCQDGLDIYTC
 LCPETWTGWDCSEDVDECETQGPPHCRNGGTCQNSAGSFHCVCVSGWGGTSCEENLDDCIAATCAPGSTCIDRVG
 SFSCLCPPGRTGLLCHLEDMCLSQPCHGDAQCSTNPLTGSTLCLCQPGYSGPTCHQDLDECLMAQQGSPSPCEHGG
 SCLNTPGSFNCLCPPGYTGSRCADHNECLSQPCHPGSTCLDLLATFHCLCPPGLEQQLCEVETNECASAPCLNH
 ADCHDLLNGFQCICLPGFSGTRCEEDIDECRSSPCANGGQCQDQPGAFHCKCLPGFEGPRCQTEVDECLSDPCPV
 GASCLDLPGAFFCLCPSGFTGQLCEVPLCAPNLCPKQICKDQKDKANCLCPDGSPGCAPPEDNCTCHHGHCCQRS
 SCVCDVGWGTGPECEAELGGCISAPCAHGGTCYPQPSGYNCTCPTGYTGPTCSEEMTACHSGPCLNGGSCNPSPGG
 YYCTCPPSHTGPQCQTSTDYCVSAPCFNGGTCVNRPGTFSCLCAMGFQGPCEGKLRPSCADSPCRNRATCQDSP
 QGPRCLCPTGYTGGSQCOTLMDLCAQKPCPRNSHCLQTGPSFHCLCLQGTGPLCNLPLSSCQKAALSQGIDVSSL
 CHNGGLCVDSGPSYFCHCPGFGSLCQDHVNPCESRPCQNGATCMAQPSGYLCQCAPGYDGNCSKELDACQSQ
 PCHNHCTCTPKPGGFHCACPPGFVGLRCEGDVDECLDQPCHTCTAACHSLANAFYCQCLPGHTGQWCEVEIDPC
 HSQPCFHGGTCEATAGSPLGFICHCPKGFEGPTCSHRAPSCGFHHCHHGGLCLPSKPGFPFPRACLSGYGGPDC
 LTPPAKPGCGPPSPCLYNGSCSETTGLGGPGFRCSCPHSSPGPRCQKPGAKGCEGRSGDGACDAGCSGPGGNWDG
 GDGSLGVDPDPWKCPSHSRCWLLFRDGGQCHPQCDSEECLEFDGYDCETPPACTPAYDQYCHDHFNHGHCKEKGNTA
 ECGWDGGDCRPEGDGPEWGPSLALLVLSPPALDQQLFALARVLSLTLRVGLWVRKDRDGRDMVYPYPGARAEK
 LGGTRDPTYQERAAPQTQPLGK**ETDLSAGFVVVMGVDLR**SCGPDHPASRCPWDPGLLLRFLAAMAAGVALEPLL
 PGPLLAVHPHAGTAPPANQLPWPVLCSPVAGVILALGALLVLQIRRRRREHGALWLPFGFTRRERTQSAPHRR
 RPPLGEDSIGLKALKPKAEVDEDGVVMCSGPEEGEEVQAEETGPPSTCQLWSLSGGCGALPQAAMLTTPQESEM
 EAPDLDRGPDGVTPLMSAVCCGEVQSGTFQGAWLGCPEPWEPLLDGGACPAHTVGTGETPLHLAARFSRPTAA
 RRLLEAGANPNQPDRAGR**TPPLHAAVAADAR**EVQQLLLRSRQTAVDARTEDGTTPLMLAARLAVEDLVEELIAAQA
 DVGARDKWKGTALHWAANAARARSLLQAGADKDAQDNRE**EQTPLFLAAR**EGAVEVAQQLLGLGAARELRDQAG
 LAPADVAHQNRNWDLLTLLEGAGPPEARHKATPGREAGFPFPRARTVSVVPPHGGGALPRCRTL**TSAGAGPR**GGGA
 CLQARTWSVDLAARGGGAYSHCRSLSGVGAGGGPTPRGRRF SAGMR**GPRPNPAIMR**GRYGVAAAGRGGRVSTDWDP
 CDWVALGACGSASNIPIPPCLTPSPERGSPQLDCGPPALQEMPINQGGEGKK

Mass Match Peptides (bold):

CHI QASGRPQCSCMPGWTGEQCQLR [103]

EQTPLFLAAR [221]
 EIDSLSAGFVVVMGVDLR [229]
 GPRPNPAIMR [310]
 GSPQLDCGPPALQEMPINQGEGKK [318]
 TLSACAGPR [705]
 TPLHAAVAADAR [717]

Tandem Peptides (underline):

EQTPLFLAAR [221]

Peptide Source: 1D-GE, Pancreatic cancer

MQPPSLLLLLLLLLLLLCVSVVRPRGLLCGSFPEPCANGGTCLSLSLGQGTQCQCAPGFLGETCQFPDPCQNAQLCQ
 NGGSCQALLPAPLGLPSSPSPLTPSFLCTCLPGFTGERCQAKLEDPCPPSFCSKRGRCHI QASGRPQCSCMPGWT
 GEQCQLRDFCSANPCVNGGVCLATYPQIQCHCPPGFEGHACERDVNECFQDPGPCPKGTSCHNTLGSTFQCLCPVG
 QEGPRCELRAAGCPPPRGCSNNGGTCQLMPEKDSFHLCLCPPPGFIGPDCEVNPNCVSHQCQNGGTCQDGLDIYTC
 LCPETWTGWDCSEEDVDECETQCPPHCRNNGGTCQNSAGSFHCVCVSGWGGTSCEENLDDCIAATCAPGSTCIDRVG
 SFSCCLCPPGRTGLLCHLEDMCLSQPCHGDAQCSTNPLTGSTLCLCQPGYSGPTCHQDLDECLMAQQGSPCEHGG
 SCLNTPGSFNCLCPPGYTGSRCADHNECLSQPCHPGSTCLDLLATFHLCLCPPGLEQLCEVETNECASAPCLNH
 ADCHDLLNGFQCICLPGFSGTRCEEDI DECRSSPCANGGQCQDQPGAFFHCKCLPGFEGPRCQTEVDECLSDPCPV
 GASCLDLPGAFFCLCPSPGFTGQLCEVPLCAPNLCQPKQICKDQKDKANCLCPDGSPGCAPPEDNCTCHHGHGQRS
 SCVCDVGTWGPCEFAELGGCISAPCAHGGTCYPQPSGYNCTCPTGYTGPTCSEEMTACHSGPCLNGGSCNPSPGG
 YYCTCPPSHTGPPCQTSTDYCVSAPCFNNGTCVNRPGTFSCLCAMGFQGPCEGKLRPSCADSPCRNRATCQDSF
 QGPRCLCPTGYTGGSCQTLMDLCAQKPCPRNSHCLQTGPSFHCLCLQGWTPGLCNLPLSSCQKAALSQGIDVSSL
 CHNGGLCVDGSGPSYFCHCPPPGFQGSCLQDHVNPCESEPCQNGATCMAQPSGYLCQCAPGYDQNCSEKELDACQSQ
 PCHNHGCTCPKPGGFHCACPPGFVGLRCEGDVDECLDQPCPHTGTAAACHSLANAFYQCLPGHTGQWCEVEIDPC
 HSQPCFHGGTCEATAGSPLGFICHCPKGFEGPTCSHRAPSCGFHHCHHGLCLPSPKPGFPPRCACLSGYGGPDC
 LTFPAPKGCQPPSPCLYNGSCSETTGLGGPGRFCSCPHSSPGPRCQKPGAKGCEGRSGDGACDAGCSGPGGNWDG
 GDCSLGVDPDWKGCPSHRCWLLFRDQCHPQCDSECLFDGYDCETPPACTPAYDQYCHDHFNHGHCEKGCNTA
 ECGWDCGDCRPEDCDPEWGPSLALLVLSPPALDQQLFALARVLSLTLRVCLWVRKDRDGRDMVYPYPGARAEK
 LGGTRDPTYQERAAQTQPLGKETDLSAGFVVVMGVDLRSCGPDHPASRCPWDPGLLLRFLAAMAAGVALEPLL
 PGFLAVHPHAGTAPPANQLPWPVLCSPVAGVILLALGALLVLQILRRRRRREHGALWLPFGFTRRPRTQSAPHRR
 RPELGEDSIGLKKPKAEVDEDGVVMCSGPEEGEEVGQAEETGPPSTCQLWSLSGGCGALPQAAMLTTPQSESEM
 EAPDLDRGPDGVTPLMSAVCCGEVQSGTFQGAWLGCPEPWEPLLDGGACPAHTVGTGETPLHLAARFSRPTAA
 RRLLEAGANPNQPDRAGRTPHAAVAADAREVCQLLLRSRQTAVDARTEDGTTPLMLAARLAVEDIVEELTAAQA
 DVGARDKWGKTALHWAANVNARAARSLQAGADKDAQDNREQTPFLFLAAREGAVEVAQLLLGLGAARELRDQAG
 LAPADVAHQNRNWDLLTLLEGAGPPEARHKATPGREAGFPFRARTVSVSVPPHGGGALPRCRTLSACAGPRGGGA
 CLQARTWSVDLAARGGGAYSHCRSLSGVAGGGGPTPRGRRFSAGMRGPRPNPAIMRGRYGVAAGRGGRVSTDDWF
 CDWVALGACGSASNIPIPPCLTPSPERGPSQLDCGPPALQEMPINQGEGKK

Mass Match Peptides (bold):

EQTPLFLAAR [221]

Tandem Peptides (underline):

EQTPLFLAAR [221]

Peptide Source: iTRAQ, Hepatocellular cancer

MQPPSLLLLLLLLLLLLCVSVVRPRGLLCGSFPEPCANGGTCLSLSLGQGTQCQCAPGFLGETCQFPDPCQNAQLCQ
 NGGSCQALLPAPLGLPSSPSPLTPSFLCTCLPGFTGERCQAKLEDPCPPSFCSKRGRCHI QASGRPQCSCMPGWT
 GEQCQLRDFCSANPCVNGGVCLATYPQIQCHCPPGFEGHACERDVNECFQDPGPCPKGTSCHNTLGSTFQCLCPVG
 QEGPRCELRAAGCPPPRGCSNNGGTCQLMPEKDSFHLCLCPPPGFIGPDCEVNPNCVSHQCQNGGTCQDGLDIYTC
 LCPETWTGWDCSEEDVDECETQCPPHCRNNGGTCQNSAGSFHCVCVSGWGGTSCEENLDDCIAATCAPGSTCIDRVG
 SFSCCLCPPGRTGLLCHLEDMCLSQPCHGDAQCSTNPLTGSTLCLCQPGYSGPTCHQDLDECLMAQQGSPCEHGG
 SCLNTPGSFNCLCPPGYTGSRCADHNECLSQPCHPGSTCLDLLATFHLCLCPPGLEQLCEVETNECASAPCLNH
 ADCHDLLNGFQCICLPGFSGTRCEEDI DECRSSPCANGGQCQDQPGAFFHCKCLPGFEGPRCQTEVDECLSDPCPV
 GASCLDLPGAFFCLCPSPGFTGQLCEVPLCAPNLCQPKQICKDQKDKANCLCPDGSPGCAPPEDNCTCHHGHGQRS
 SCVCDVGTWGPCEFAELGGCISAPCAHGGTCYPQPSGYNCTCPTGYTGPTCSEEMTACHSGPCLNGGSCNPSPGG
 YYCTCPPSHTGPPCQTSTDYCVSAPCFNNGTCVNRPGTFSCLCAMGFQGPCEGKLRPSCADSPCRNRATCQDSF

QGPRCLCPTGYTGGSCQTLMDLCAQKPCPRNSHCLQTGPSFHCCLCQGTGPLCNLPLSSCQKAALSQGIDVSSL
CHNGGLCVDSGPSYFCHCPPGFQGSILCQDHVNPCESRPCQNGATCMAQPSGYLCQCAPGYDQNCSEKLDACQSQ
PCHNHGTCTPKPGGFHCACPPGFVGLRCEGDVDECLDQPCHTGTAAACHSLANAFYCQCLPGHTGQWCEVEIDPC
HSQPCFHGGTCEATAGSPLGFICHCPKGFEGPTCSHRAPSCGFHHCHHGGGLCLPSKPGFFPRCACLSGYGGPDC
LTPPAPKGGCFPSPLYNGSCSETTGLGGPGFRCSCPHSSPGPRCQKPKGAKGCEGRSGDGACDAGCSGPGGNWDG
GDCSLGVDPDWKGCPSHSRCWLLFRDGGQCHPQCDSEECLEFDGYDCETPPACTPAYDQYCHDHFHNGHCEKGCNTA
ECGWDDGDCRDEGDGDEWGPSLALLVVLSPPALDQQLFALARVLSLTLRVGLWVRKDRDGRDMVYPYPGARAEK
LGGTRDPTYQERAAQTQPLGKETDSLSAGFVVVMGVLSRCGPDHPASRCPWDPGLLLRFLAAMAAVGALEPLL
PGPLLAVHPHAGTAPPANQLPWPVLCSPVAGVILLALGALLVLQLIRRRRREHGALWLPPGFTRRPRTQSAPHRR
RPPLGEDSIGLKALKPKAEVDEDDGVVMCSGP EEGEEVCQAEETGPPSTCQLWSLSGGCGALFQAAMLTTPQESSEM
EAPDLDTRGPDGVTPLMSAVCCGEVQSGTFQGAWLGCPEPWEPLLDGGACPAHTVGTGETPLHLAARFSRPTAA
RRLEAGANPNQPDRAGRTPHLAAVAADAREVCQLLLRSRQTAVDARTEDGTTPLMLAARLAVEDLVEELIAAQA
DVGARDKWKGTALHWAAAVNNARAARSLAQAGADKDAQDNREQTPLFLAAREGAVEVAQLLGLGAARELRDQAG
LAPADVAHQNRHWDLLTLEAGAPPEARHKAATPGREAGFPFPRARTVSVSVPPHGGGALPRCRTLASAGAPRGGA
CLQARTWSVDLAARGGGAYSHCRSLSGVGAGGGPTPRGRRFSAGMRGPRENPATMRGRYGVAAGRGRVSTDDWP
CDWVALGACGSASNIPPPCLTPSPERGSPQLDCGPPALQEMPINQGGEGKK

Mass Match Peptides (bold):

EVCQLLLR [908]

Tandem Peptides (underline):

EVCQLLLR [908]

OGTA112 (SEQ ID No: 22)**Peptide Source: 1D-GE, Breast cancer**

MNSLSEANTKFMFDLFQQFRSKKENNIFYSPISITSALGMVLLGAKDNTAQQISKVLHFDQVTENTTEKAATYHV
DRSGNVHHQFQKLLTEFNKSTDAYELKIANLFGKEKTYQFLQEYLDIAIKKIFYQTSVESTDFANAPEESRKKINSW
VESQTNEKIKNLFPDGTIGNDTTLVLVNAIYFKGQWENKFKKENTKEEFWPNKNTYKSVQMMRQYNSFNFALLE
DVQAKVLEIPYKGDLSMIVLLPNEIDGLQKLEEKLTAEKLMEWTSLQNMRETCDLHLPRFKMEESYDLKDTLR
TMGMVNIENGDADLSGMTWSHGLSVSKVLHKAFFVEVTEEGVEAAAATAVVVVVELSSPSTNEEFCCNHPFLFFIRQ
NKTNSILFYGRFSSP

Mass Match Peptides (bold):

ETCVDLHLPR [228]

FMFDLFQQFR [261]

FYQTSVESTDFANAPEESR [280]

FYQTSVESTDFANAPEESRKK [281]

KFYQTSVESTDFANAPEESRK [416]

KINSWVESQTNEK [420]

LMEWTSLQNM [470]

QYNSFNFALLEDVQAK [594]

TNSILFYGR [713]

TYQFLQEYLDIAIK [741]

VLHFDQVTENTTEK [781]

Tandem Peptides (underline):

FMFDLFQQFR [261]

LMEWTSLQNM [470]

Peptide Source: 1D-GE, Cervical cancer

MNSLSEANTKFMFDLFQQFRSKKENNIFYSPISITSALGMVLLGAKDNTAQQISKVLHFDQVTENTTEKAATYHV
DRSGNVHHQFQKLLTEFNKSTDAYELKIANLFGKEKTYQFLQEYLDIAIKKIFYQTSVESTDFANAPEESRKKINSW
VESQTNEKIKNLFPDGTIGNDTTLVLVNAIYFKGQWENKFKKENTKEEFWPNKNTYKSVQMMRQYNSFNFALLE
DVQAKVLEIPYKGDLSMIVLLPNEIDGLQKLEEKLTAEKLMEWTSLQNMRETCDLHLPRFKMEESYDLKDTLR

TMGMVNIFNGDADLSGMTWSHGLSVSKVLHKA FVEVTEEGVEAAAAATAVVVVELSSPSTNEEFCCNHPFLFFIRQ
NKTNSILFYGRFSSP

Mass Match Peptides (bold):

FMFDLFQQFRK [262]
LMEWTSLQNM [470]
SVQMMR [665]
TMGMVNIFNGDADLSGMTWSHGLSVSK [706]

Tandem Peptides (underline):

LMEWTSLQNM [470]
VLEIPYK [779]

Peptide Source: 1D-GE, Chronic lymphocytic leukaemia

MNSLSEANTK**FMFDLFQQFR**SKENNIFYSPI SITSALGMVLLGAKDNTAQQISKVLHFDQVTENTTEKAATYHV
DRSGNVHHQFQKLLTEFNKSTDAYELKIANKLFGKTYQFLQEYLD AIKKFYQTSVESTDFANAPEESRKKINSW
VESQTNEKIKNLFPDGTIGNDTTLVLVNAIYFKGQWENKFKKENTKEEFWPNKNTYKSVQMMRQYNSFNFALLE
DVQAKVLEIPYKGKDL SMIVLLPNEIDGLQKLEEKLTAEKLMWTSLQNM**ETCVDLHLPR**FKMEESYDLKDTLR
TMGMVNIFNGDADLSGMTWSHGLSVSKVLHKA FVEVTEEGVEAAAAATAVVVVELSSPSTNEEFCCNHPFLFFIRQ
NKTNSILFYGRFSSP

Mass Match Peptides (bold):

ETCVDLHLPR [228]

Tandem Peptides (underline):

FMFDLFQQFR [261]

Peptide Source: 1D-GE, Hepatocellular carcinoma

MNSLSEANTK**FMFDLFQQFR**SKENNIFYSPI SITSALGMVLLGAKDNTAQQISK**VLHFDQVTENTTEKAATYHV**
DRSGNVHHQFQKLLTEFNKSTDAYELKIANKLFGKTYQFLQEYLD AIKKFYQTSVESTDFANAPEESRKKINSW
VESQTNEKIKNLFPDGTIGNDTTLVLVNAIYFKGQWENKFKKENTKEEFWPNKNTYKSVQMMR**QYNSFNFALLE**
DVQAKVLEIPYKGKDL SMIVLLPNEIDGLQKLEEKLTAEKLMWTSLQNM**ETCVDLHLPR**FKMEESYDLKDTLR
TMGMVNIFNGDADLSGMTWSHGLSVSKVLHKA FVEVTEEGVEAAAAATAVVVVELSSPSTNEEFCCNHPFLFFIRQ
NKT**NSILFYGR**FSSP

Mass Match Peptides (bold):

AATYHVDR [54]
ETCVDLHLPR [228]
FMFDLFQQFR [261]
QYNSFNFALLEDVQAK [594]
TNSILFYGR [713]
VLHFDQVTENTTEK [781]

Tandem Peptides (underline):

INSWVESQTNEK [384]
LMEWTSLQNM [470]

Peptide Source: 1D-GE, Pancreatic cancer

MNSLSEANTK**FMFDLFQQFR**SKENNIFYSPI SITSALGMVLLGAKDNTAQQISK**VLHFDQVTENTTEK**AATYHV
DRSGNVHHQFQKLLTEFNKSTDAYELKIANKLFGKTYQFLQEYLD AIKKFYQTSVESTDFANAPEESRKKINSW
VESQTNEKIKNLFPDGTIGNDTTLVLVNAIYFKGQWENKFKKENTKEEFWPNKNTYK**SVQMMR**QYNSFNFALLE
DVQAKVLEIPYKGKDL SMIVLLPNEIDGLQKLEEKLTAEKLMWTSLQNM**ETCVDLHLPR**FKMEESYDLKDTLR
TMGMVNIFNGDADLSGMTWSHGLSVSKVLHKA FVEVTEEGVEAAAAATAVVVVELSSPSTNEEFCCNHPFLFFIRQ
NKT**NSILFYGR**FSSP

Mass Match Peptides (bold):

ETCVDLHLPR [228]
 FMFDLFQQFR [261]
 FMFDLFQQFRK [262]
 LMEWTSLQNM [470]
 SVQMMR [665]
 TNSILFYGR [713]
 VLHFDQVTENTTEK [781]

Tandem Peptides (underline):

FMFDLFQQFR [261]
 INSWVESQTNEK [384]
 LMEWTSLQNM [470]
 QYNSFNFALLEDVQAK [594]

Peptide Source: 1D-GE, Renal cell cancer

MNSLSEANTKFMFDLFQQFRKSKENNIFYSPISITSALGMVLLGAKDNTAQQISKVLHFDQVTENTTEKAAATYHV
 DRSGNVHHQFQKLLTEFNKSTDAYELKIANKLFGKTYQFLQEYLDAIKKFYQTSVESTDFANAPEESRKKINSW
 VESQTNEKIKNLFPGDTIGNDTTLVLVNAIYFKGQWENKFKKENTKEEFWPNKNTYKSVQMMRQYNSFNFALLE
 DVQAKVLEIPYKGDLSMIVLLPNEIDGLQKLEELTAELMEWTSLQNMRETCDLHLPRFKMEESYDLKDTLR
 TMGMVNIENGADLSGMTWSHGLSVSKVLHKAFFVEVTEEGVEAAAAATAVVVVVELSSPSTNEEFCCNHPFLFFIRQ
 NKTNSILFYGRFSSP

Mass Match Peptides (bold):

LMEWTSLQNM [470]
 SVQMMR [665]
 TNSILFYGR [713]
 VLHFDQVTENTTEK [781]

Tandem Peptides (underline):

INSWVESQTNEK [384]
 LMEWTSLQNM [470]

Peptide Source: iTRAQ, Renal cell cancer

MNSLSEANTKFMFDLFQQFRKSKENNIFYSPISITSALGMVLLGAKDNTAQQISKVLHFDQVTENTTEKAAATYHV
 DRSGNVHHQFQKLLTEFNKSTDAYELKIANKLFGKTYQFLQEYLDAIKKFYQTSVESTDFANAPEESRKKINSW
 VESQTNEKIKNLFPGDTIGNDTTLVLVNAIYFKGQWENKFKKENTKEEFWPNKNTYKSVQMMRQYNSFNFALLE
 DVQAKVLEIPYKGDLSMIVLLPNEIDGLQKLEELTAELMEWTSLQNMRETCDLHLPRFKMEESYDLKDTLR
 TMGMVNIENGADLSGMTWSHGLSVSKVLHKAFFVEVTEEGVEAAAAATAVVVVVELSSPSTNEEFCCNHPFLFFIRQ
 NKTNSILFYGRFSSP

Mass Match Peptides (bold):

LFGEK [932]

Tandem Peptides (underline):

LFGEK [932]

OGTA113 (SEQ ID No: 23)

Peptide Source: 1D-GE, Pancreatic cancer

MAANYSTSTREHVVKVKTSSQPGFLERLSETSGGMFVGLMAFLLSFYLIFTNEGRALKTATSLAEGSLVSPD
 SIHSVAPENEGRLVHIIGALRTSKLLSDPNYGVHLPVAVKLRRHVEMYQWVETEESREYTEDGQVKKETRYSYNTE
 WRSEIINSKNFREIGHKNPSAMAVESFMATAPFVQIGRFFLSGLIDKVDNFKSLSLSKLEDPHVDIIRRGDFF

YHSENPKEYPEVGDLRVSFSYAGLSGDDPDLGPAHVVTVIARQRGDQLVPFSTKSGDTLLLLHHGDFSAAEEVFHRE
 LRSNSMKTWGLRAACWMAMFMGLNLMTRILYTLVDWFPVFRDLVNI GLKAFACVATSLTLLTVAAGWLFYRPLW
 ALLIAGLALVPILVARTRVPAKKLE

Mass Match Peptides (bold):

HVEMYQWVETESR [345]
 LEDPHVDIIR [449]
 LVHIIGALR [500]
 RGDDFFYHSENP [603]
 SEIINSK [627]
 TSSQPGFLER [730]
 YPEVGDLR [865]
 YSYNTEWR [874]

Tandem Peptides (underline):

LEDPHVDIIR [449]
 LVHIIGALR [500]
 YPEVGDLR [865]

Peptide Source: iTRAQ, Colorectal cancer

MAANYSSSTSTREHVVKVTSSQPGFLERLSETSGGMFVGLMAFLLSFYLIFTNEGRALKTATSLAEGLSLVVSPD
 SIHSAVAPENEGRLVHIIGALRTSK**LLSDPNYGVHLP**AVKLRRHVEMYQWVETESREYTEDGQVKKETRYSYNTE
 WRSEIINSKNFDR EIGHKNPSAMAVESFMATAPFVQIGRFFLSSGLIDKVDNFKSLSLSK**LEDPHVDIIR**RGDDFF
 YHSENP**KEYPEVGDLR**VSFSYAGLSGDDPDLGPAHVVTVIARQRGDQLVPFSTKSGDTLLLLHHGDFSAAEEVFHRE
 LRSNSMKTWGLRAACWMAMFMGLNLMTRILYTLVDWFPVFRDLVNI GLKAFACVATSLTLLTVAAGWLFYRPLW
 ALLIAGLALVPILVARTRVPAKKLE

Mass Match Peptides (bold):

LEDPHVDIIR [931]
 LLSDPNYGVHLP [939]
 YPEVGDLR [865]

Tandem Peptides (underline):

LEDPHVDIIR [931]
 LLSDPNYGVHLP [939]
 YPEVGDLR [865]

Peptide Source: iTRAQ, Non-small cell lung cancer

MAANYSSSTSTREHVVKVTSSQPGFLERLSETSGGMFVGLMAFLLSFYLIFTNEGRALKTATSLAEGLSLVVSPD
 SIHSAVAPENEGRLVHIIGALRTSKLLSDPNYGVHLPVAVKLRRHVEMYQWVETESREYTEDGQVKKETRY**YSYNTE**
WRSEIINSKNFDR EIGHKNPSAMAVESFMATAPFVQIGRFFLSSGLIDKVDNFKSLSLSKLEDPHVDIIRRGDDFF
 YHSENP**KEYPEVGDLR**VSFSYAGLSGDDPDLGPAHVVTVIARQRGDQLVPFSTKSGDTLLLLHHGDFSAAEEVFHRE
 LRSNSMKTWGLRAACWMAMFMGLNLMTRILYTLVDWFPVFRDLVNI GLKAFACVATSLTLLTVAAGWLFYRPLW
 ALLIAGLALVPILVARTRVPAKKLE

Mass Match Peptides (bold):

YPEVGDLR [865]
 YSYNTEWR [874]

Tandem Peptides (underline):

YPEVGDLR [865]
 YSYNTEWR [874]

Peptide Source: iTRAQ, Ovarian cancer

MAANYSSSTRREHVVKVKTSSQPGFLERLSETSGGMFVGLMAFLLSFYLIIFTNEGRALKTATSLAEGSLVVS
 SIHSVAPENEGRLVHIIGALRTSKLLSDPNYGVHLPVAVKLRRHVEMYQWVETTESREYTEDGQVKKETRYSYNTE
 WRSEIINSKNFDRIGHKNPSAMAVESFMATAPFVQIGRFFLSSGLIDKVDNFKSLSLSKLEDPHVDIIRRGDFF
 YHSENPXYEVGDLRVFSYAGLSGDDPDLGPAHVVTVIARQRGDQLVFFSTKSGDTLLLLLHHGDFSAAEEVFHRE
 LRSNSMKTWGLRAAGWMAMFMGLNLMTRILYTLVDWFPVFRDLVNI GLKAFACVATSLTLLTVAAGWLFYRPLW
 ALLIAGLALVPILVARTRVPARKLE

Mass Match Peptides (bold):

LEDPHVDIIR [449]

Tandem Peptides (underline):

LEDPHVDIIR [449]

Peptide Source: iTRAQ, Renal cell cancer

MAANYSSSTRREHVVKVKTSSQPGFLERLSETSGGMFVGLMAFLLSFYLIIFTNEGRALKTATSLAEGSLVVS
 SIHSVAPENEGRLVHIIGALRTSKLLSDPNYGVHLPVAVKLRRHVEMYQWVETTESREYTEDGQVKKETRYSYNTE
 WRSEIINSKNFDRIGHKNPSAMAVESFMATAPFVQIGRFFLSSGLIDKVDNFKSLSLSKLEDPHVDIIRRGDFF
 YHSENPXYEVGDLRVFSYAGLSGDDPDLGPAHVVTVIARQRGDQLVFFSTKSGDTLLLLLHHGDFSAAEEVFHRE
 LRSNSMKTWGLRAAGWMAMFMGLNLMTRILYTLVDWFPVFRDLVNI GLKAFACVATSLTLLTVAAGWLFYRPLW
 ALLIAGLALVPILVARTRVPARKLE

Mass Match Peptides (bold):

LEDPHVDIIR [449]

Tandem Peptides (underline):

LEDPHVDIIR [449]

OGTA119 (SEQ ID No: 24)

Peptide Source: 1D-GE, B-cell non-Hodgkin's lymphoma

MTPPSRAEAGVRRSRVPSEGRWRGAEPGGISASTQPASAGRAARHCGAMSGARGE GPEAGAGGAGGRAAPENPGG
 VLSVELPGLLAQLARSFALLLPVYALGYLGLSFSWVLLALALLAWCRRSRGLKALRLCRA LALLEDEERVVRLGV
 RACDLPANVHFPDTERAEWLNTVKHMPFICQFIEKLFRETIEPAVRGANTHLSTFSFTKVDVGQQLRINGVK
 VYTENVDKRQIILDLQISFVGNCEIDLEIKRYFCRAGVKSQIHGTMRVILEPLIGDMPLVGALSIFFLRKPLLE
 INWTGLTNLLDVPGNLGLSDTIILDIISNYLVLPNRITVPLVSEVQIAQLRFPVPKGVLRHIFIEAQDLQ GKDTY
 LKGLVKGKSDPYGIIRVGNQIFQSRVIKENLSPKWNEVYEALVYEHPCQELEIELFDEDPDKDDFLGSLMIDLE
 VEKERLLDEWFTLDEVPGKGLHLRLLEWLTMPNASNLDKVLTDIKADKDQANDGLSSALLILYLD SARNLP SGKK
 ISSNPNPVQMSVGHKAQESKIRYKTNEPVWEENFTFFIHNPKRQDLEVEVRDEQHQC SLGNLKVPLSQLLTSED
 MTVSQRFQLSNSGPNSTIKMKIALRVLHLEKRERPPDHQHS AQVKRPSVSKEGRKTSIKSHMSGSPGPGGSNTAP
 STPVIGGSDKPGMEEKAQPPEAGPQGLHDLGRSSSSSLASPGHISVKEPTPSIASDISLP IATQELRQRLRQLEN
 GTTLGQSPLGQIQLTIRHSSQRNKLIVVHACRNLIASFEDGSDPYVRMYLLPDKRRSGRRKTHVSKKTLNPVFD
 QSFDFSLSLPEVQRRITLDVAVKNSGGFLSKDKGLLCKVLVALASEELAKGWTQWYDLTEDGTRPQAMT

Mass Match Peptides (bold):

AQPPEAGPQGLHDLGR [83]

DEQHQC SLGNLK [115]

ERPPDHQHS AQVK [222]

GANTHLSTFSFTK [285]

VGNQIFQSR [765]

Tandem Peptides (underline):

VGNQIFQSR [765]

Peptide Source: 1D-GE, Breast cancer

MTPPSRAEAGVRRSRVPSEGRWRGAEPGGISASTQPASAGRAARHCGAMSGARGEPEAGAGGAGGRAAPENPGG
VLSVELPGLLAQLARSFALLLPVYALGYLGLSFSWVLLALALLAWCRRSRGLKALRLCRALALLEDEERVVRLGV
RACDLPAWVHFPDTERAEWLNKTVKHMWPFICQFIEKLFRETIEPAVRGANTHLSTFSFTKVDVGQQPLRINGVK
VYTENVDKRQIILDQLISFVGNCEIDLEIKRYFCRAGVKSQIHGTMRVILEPLIGDMPLVGALSIFFLRKPLLE
INWTGLTNLLDVPGLNGLSDTIILDIIISNYLVLPNRITVPLVSEVQIAQLRFPVPKGVLRHIFIEAQDLQGGKDTY
LKGLVKGKSDPYGIIRVGNQIFQSRVRIKENLSPKWNEVEYALVYEHFGQELEIELFDEDDPKDDFLGSLMIDLIE
VEKERLLDEWFTLDEVKPKGLHLRLLEWLTLMPNASNLDKVLTDIKADKDQANDGLSSALLILYLDARSNLPSGKK
ISSNPNPVVQMSVGHKAQESKIRYKTNEPVWEENFTFFIHNPKRQDLEVEVRDEQHQCSLGNLKVPLSQLLTSED
MTVSQR**FQLSNSGPNSTIK**MKIALRVLHLEKRERFPDHQSAQVKRPSVSKGRKTSIKSHMSGSPGPGGSNTAP
STPVIGGSDKPGMEEK**AQPPEAGPQGLHDLGR**SSSSLLASPGHISVKEPTPSIASDISLPIATQELRQLRQLEN
GTTLCQSPPLGQIQLTIRHSSQRNKLIVVHACR**NLIAFSEDGSDPYVR**MYLLPKRRSGRRKTHVSKKTLNPVFD
QSFDFSVSLPEVQRRTLDVAVKNSGGFLSKDKGLLGKVLVALASEELAKGWTQWYDLTEDGTRPQAMT

Mass Match Peptides (bold):

AEWLNK [64]
AQPPEAGPQGLHDLGR [83]
FQLSNSGPNSTIK [268]
ISSNPNPVVQMSVGHK [393]
NLIAFSEDGSDPYVR [542]
VGNQIFQSR [765]

Tandem Peptides (underline):

ALALLEDEER [75]

Peptide Source: 1D-GE, Colorectal cancer

MTPPSRAEAGVRRSRVPSEGRWRGAEPGGISASTQPASAGRAARHCGAMSGARGEPEAGAGGAGGRAAPENPGG
VLSVELPGLLAQLARSFALLLPVYALGYLGLSFSWVLLALALLAWCRRSRGLKALRLCRALALLEDEERVVRLGV
RACDLPAWVHFPDTERAEWLNKTVKHMWPFICQFIEKLFRETIEPAVRGANTHLSTFSFTKVDVGQQPLRINGVK
VYTENVDKRQIILDQLISFVGNCEIDLEIKRYFCRAGVKSQIHGTMRVILEPLIGDMPLVGALSIFFLRKPLLE
INWTGLTNLLDVPGLNGLSDTIILDIIISNYLVLPNRITVPLVSEVQIAQLRFPVPKGVLRHIFIEAQDLQGGKDTY
LKGLVKGKSDPYGIIRVGNQIFQSRVRIKENLSPKWNEVEYALVYEHFGQELEIELFDEDDPKDDFLGSLMIDLIE
VEKERLLDEWFTLDEVKPKGLHLRLLEWLTLMPNASNLDKVLTDIKADKDQANDGLSSALLILYLDARSNLPSGKK
ISSNPNPVVQMSVGHKAQESKIRYKT**TNEPVWEENFTFFIHNPKRQDLEVEVR**DEQHQC
SLGNLKVPLSQLLTSED
MTVSQR**FQLSNSGPNSTIK**MKIALRVLHLEKR**ERPPDHQSAQVK**RPSVSKGRKTSIKSHMSGSPGPGGSNTAP
STPVIGGSDKPGMEEK**AQPPEAGPQGLHDLGR**SSSSLLASPGHISVKEPTPSIASDISLPIATQELRQLRQLEN
GTTLCQSPPLGQIQLTIRHSSQRNKLIVVHACR**NLIAFSEDGSDPYVR**MYLLPKRRSGRRKTHVSKKTLNPVFD
QSFDFSVSLPEVQRRTLDVAVKNSGGFLSKDKGLLGKVLVALASEELAKGWTQWYDLTEDGTRPQAMT

Mass Match Peptides (bold):

AQPPEAGPQGLHDLGR [83]
ERPPDHQSAQVK [222]
FQLSNSGPNSTIK [268]
LEWLTLMPNASNLDK [457]
NLIAFSEDGSDPYVR [542]
RQDLEVEVR [611]
TNEPVWEENFTFFIHNPK [710]

Tandem Peptides (underline):

ALALLEDEER [75]

Peptide Source: 1D-GE, Gastric cancer

MTPPSRAEAGVRRSRVPSEGRWRGAEPGGISASTQPASAGRAARHCGAMSGARGEPEAGAGGAGGRAAPENPGG
VLSVELPGLLAQLARSFALLLPVYALGYLGLSFSWVLLALALLAWCRRSRGLKALRLCRALALLEDEERVVRLGV
RACDLPAWVHFPDTERAEWLNKTVKHMWPFICQFIEKLFRETIEPAVRGANTHLSTFSFTKVDVGQQPLRINGVK
VYTENVDKRQIILDQLISFVGNCEIDLEIKRYFCRAGVKSQIHGTMRVILEPLIGDMPLVGALSIFFLRKPLLE
INWTGLTNLLDVPGLNGLSDTIILDIIISNYLVLPNRITVPLVSEVQIAQLRFPVPKGVLRHIFIEAQDLQGGKDTY
LKGLVKGKSDPYGIIRVGNQIFQSRVRIKENLSPKWNEVEYALVYEHFGQELEIELFDEDDPKDDFLGSLMIDLIE

VEKERLLDEWFTLDEVKPKGLHLRLLEWLTLMPNASNLDKVLTDIKADKDQANDGLSSALLILYLDARSARNLPSGKK
ISSNPNPVVQMSVGHKAQESKIRYKTNEPVWEEENFTFFIHNPKRQDLEVEVRDEQHQCISLGNLKVPLSQLLTSED
MTVSQRFQLSNSGPNSTIKMKIALRVLHLEKRRERPPDHQHSQVVRPSVSKEGRKTSIKSHMSGSPGPGGSNTAP
STPVIIGSDKPGMEEKAPPEAGPQGLHDLGRSSSSLLASPGHISVKEPTPSIASDISLPATQELRQRLRQLEN
GTTLGQSPLGQIQLTIRHSSQRNKLIVVHACRNLIASFSEDGSDPYVRMYLLPDKRRSGRRKTHVSKKTLNPFVD
QSFDFSVSLPEVQRRTLDVAVKNSGGFLSKDKGLLGKVLVALASEELAKGWTQWYDLTEDGTRPQAMT

Mass Match Peptides (bold):

Tandem Peptides (underline):

VDVGQQPLR [750]

Peptide Source: 1D-GE, Hepatocellular carcinoma

MTPPSRAEAGVRRSRVPSEGRWRGAEPGGISASTQPASAGRAARHCGAMSGARGEPEAGAGGAGGRAAPENPGG
VLSVELPGLLAQLARSFALLLPVYALGYLGLSFSWVLLALALLAWCRRSRGLKALRLCRALALLEDEERVVRLGV
RACDLPAAWHFPTDERAEWLNKTVKHMWPFICQFIEKLFRETIEPAVRGANTHLSTFSFTKVDVGQQPLRINGVK
VYTENVDKRQIILDQLISFVGNCEIDLEIKRYFCRAGVKSIIQIHGTMRVILEPLIGDMPLVGALSIFFLRKPLLE
INWTGLTNLLDVPGLNGLSDTIILDIISNYLVLPNRITVPLVSEVQIAQLRFPVPGVLRHFIIEAQDLQKDTY
LKGLVKGKSDPYGIIRVGNQIFQSRVIKENLSPKWNEVEALVYEHPCQELEIELFDEDPDKDDFLGSLMIDLIE
VEKERLLDEWFTLDEVKPKGLHLRLLEWLTLMPNASNLDKVLTDIKADKDQANDGLSSALLILYLDARSARNLPSGKK
ISSNPNPVVQMSVGHKAQESKIRYKTNEPVWEEENFTFFIHNPKRQDLEVEVRDEQHQCISLGNLKVPLSQLLTSED
MTVSQRFQLSNSGPNSTIKMKIALRVLHLEKRRERPPDHQHSQVVRPSVSKEGRKTSIKSHMSGSPGPGGSNTAP
STPVIIGSDKPGMEEKAPPEAGPQGLHDLGRSSSSLLASPGHISVKEPTPSIASDISLPATQELRQRLRQLEN
GTTLGQSPLGQIQLTIRHSSQRNKLIVVHACRNLIASFSEDGSDPYVRMYLLPDKRRSGRRKTHVSKKTLNPFVD
QSFDFSVSLPEVQRRTLDVAVKNSGGFLSKDKGLLGKVLVALASEELAKGWTQWYDLTEDGTRPQAMT

Mass Match Peptides (bold):

AEWLNK [64]
AQPPEAGPQGLHDLGR [83]
DEQHQCISLGNLK [115]
ERPPDHQHSQVVK [222]
FQLSNSGPNSTIK [268]
HMWPFICQFIEK [339]
NLIASFSEDGSDPYVR [542]
RQDLEVEVR [611]
SDPYGIIR [622]
TNEPVWEEENFTFFIHNPK [710]
VDVGQQPLR [750]
VGNQIFQSR [765]
VPLSQLLTSEDMTVSQR [792]

Tandem Peptides (underline):

ALALLEDEER [75]
AQPPEAGPQGLHDLGR [83]
FQLSNSGPNSTIK [268]
HFIIEAQDLQK [368]
NLIASFSEDGSDPYVR [542]
VGNQIFQSR [765]

Peptide Source: 1D-GE, Lung cancer

MTPPSRAEAGVRRSRVPSEGRWRGAEPGGISASTQPASAGRAARHCGAMSGARGEPEAGAGGAGGRAAPENPGG
VLSVELPGLLAQLARSFALLLPVYALGYLGLSFSWVLLALALLAWCRRSRGLKALRLCRALALLEDEERVVRLGV
RACDLPAAWHFPTDERAEWLNKTVKHMWPFICQFIEKLFRETIEPAVRGANTHLSTFSFTKVDVGQQPLRINGVK
VYTENVDKRQIILDQLISFVGNCEIDLEIKRYFCRAGVKSIIQIHGTMRVILEPLIGDMPLVGALSIFFLRKPLLE
INWTGLTNLLDVPGLNGLSDTIILDIISNYLVLPNRITVPLVSEVQIAQLRFPVPGVLRHFIIEAQDLQKDTY
LKGLVKGKSDPYGIIRVGNQIFQSRVIKENLSPKWNEVEALVYEHPCQELEIELFDEDPDKDDFLGSLMIDLIE
VEKERLLDEWFTLDEVKPKGLHLRLLEWLTLMPNASNLDKVLTDIKADKDQANDGLSSALLILYLDARSARNLPSGKK

ISSNPNPVVQMSVGEKAQESKIRYKTNEPVWEENFTFFIHNPKRQDLEVEVRDEQHQC SLGNLKVPLSQLLTSED
MTVSQRFQLSNSGPNSTIKMKIALRVLHLEKREPPDHQHSQVVRPSVSKEGRKTSIKSHMSGSPGPGGSNTAP
STPVIGGSDKPGMEEEKAQPEAGPQGLHDLGRSSSSSLASPGHISVKEPTPSIASDISLPATQELRQRLQLEN
GTTLGQSPLGQIQLTIRHSSQRNKLI VVVHACRNLI AFSE DGS DPYVRMYLLPDKRRSGRRKTHVSKKTLNPVFD
QSFDFSVSLPEVQRRITLDVAVKNSGGFLSKDKGLLGKVLVALASEELAKGWTQWYDLTEDGTRPQAMT

Mass Match Peptides (bold):

AQPPEAGPQGLHDLGR [83]
ERPPDHQHSQVVR [222]
HMWPFICQFIEK [339]

Tandem Peptides (underline):

ITVPLVSEVQIAQLR [398]

Peptide Source: 1D-GE, Lymphoid leukaemia, unspecified

MT?PSRAEAGVRRSRVPSEGRWRGAEPFGISASTQPASAGRAARHCGAMSGAR**GEGPEAGAGGAGGR**AAPENPGG
VLSVELPGLLAQLARSFALLLPVYALGYLGLSF~~SWVLLALALLAWCRRSRGLKALRLCRALALLEDEERVVRLGV~~
RACDLPAWVHFPDTERAEWLNKTVK**HMWPFICQFIEK**LFR**ETIEPAVR**GANTHLSTFSFTK**VDVGGQQLR**INGVK
VYTENVDKRQIILDLQISFVGNCEIDLEIKRYFCRAGVKS IQIHGTMRVILEPLIGDMPLVGALSIFFLRKPLLE
INWTGLTNLLDVPGLNGLSDTIILDIISNYLVLNRTITVPLVSEVQIAQLRFPVPKGVLR**IHFIEAQDLQK**DTY
LKGLVKGKSDPYGIIRVGNQIFQSRVIKENLSPKWNVEYEAALVYEHGQELEIELFDEDPKDDFLGSLMIDLIE
VEKERLLDEWFTLDEVPKGLHLRLLEWLTLMPNASNLDKVLTDIKADKDQANDGLSSALLILYLD SARNLPSCGK
ISSNPNPVVQMSVGHKAQESKIRYKTNEPVWEENFTFFIHNPKRQDLEVEVRDEQHQC SLGNLKVPLSQLLTSED
MTVSQRF**QLSNSGPNSTIK**MKIALRVLHLEKREPPDHQHSQVVRPSVSKEGRKTSIKSHMSGSPGPGGSNTAP
STPVIGGSDKPGMEEEKAQPEAGPQGLHDLGRSSSSSLASPGHISVKEPTPSIASDISLPATQELRQRLQLEN
GTTLGQSPLGQIQLTIRHSSQRNKLI VVVHACRN**LI AFSE DGS DPYVR**MYLLPDKRRSGRRKTHVSKKTLNPVFD
QSFDFSVSLPEVQRRITLDVAVKNSGGFLSKDKGLLGKVLVALASEELAKGWTQWYDLTEDGTRPQAMT

Mass Match Peptides (bold):

AQPPEAGPQGLHDLGR [83]
ERPPDHQHSQVVR [222]
ETIEPAVR [230]
FQLSNSGPNSTIK [268]
GEGPEAGAGGAGGR [290]
HMWPFICQFIEK [339]
ISSNPNPVVQMSVGHK [393]
NLIAFSE DGS DPYVR [542]
RQDLEVEVR [611]
VDVGGQQLR [750]

Tandem Peptides (underline):

FQLSNSGPNSTIK [268]
IHFIEAQDLQK [368]
VLVALASEELAK [784]

Peptide Source: 1D-GE, Neuroblastoma

MT?PSRAEAGVRRSRVPSEGRWRGAEPFGISASTQPASAGRAARHCGAMSGAR**GEGPEAGAGGAGGR**AAPENPGG
VLSVELPGLLAQLARSFALLLPVYALGYLGLSF~~SWVLLALALLAWCRRSRGLKALRLCRALALLEDEERVVRLGV~~
RACDLPAWVHFPDTER**AEWLNK**TVK**HMWPFICQFIEK**LFR**ETIEPAVR**GANTHLSTFSFTKVDVGGQQLRINGVK
VYTENVDKRQIILDLQISFVGNCEIDLEIKRYFCRAGVKS IQIHGTMRVILEPLIGDMPLVGALSIFFLRKPLLE
INWTGLTNLLDVPGLNGLSDTIILDIISNYLVLNRTITVPLVSEVQIAQLRFPVPKGVLR**IHFIEAQDLQK**DTY
LKGLVKGKSDPYGIIRVGNQIFQSRVIKENLSPKWNVEYEAALVYEHGQELEIELFDEDPKDDFLGSLMIDLIE
VEKERLLDEWFTLDEVPKGLHLRLLEWLTLMPNASNLDKVLTDIKADKDQANDGLSSALLILYLD SARNLPSCGK
ISSNPNPVVQMSVGEKAQESKIRYKTNEPVWEENFTFFIHNPKRQDLEVEVRDEQHQC SLGNLKVPLSQLLTSED
MTVSQRFQLSNSGPNSTIKMKIALRVLHLEKREPPDHQHSQVVRPSVSKEGRKTSIKSHMSGSPGPGGSNTAP
STPVIGGSDKPGMEEEKAQPEAGPQGLHDLGRSSSSSLASPGHISVKEPTPSIASDISLPATQELRQRLQLEN

GTTLGQSPGLGQIQLTIRHSSQRNKLIVVHACRNLI AFSE DGS DPYVRMYLLPDKRRSGRRKTHVSKKTLNPVFD
QSFDFSVSLPEVQRRTLDVAVKNSGGFLSKDKGLLGKVLVALASEELAKGWTQWYDLTEDGTRPQAMT

Mass Match Peptides (bold):

AEWLNK [64]

Tandem Peptides (underline):

Peptide Source: 1D-GE, Osteosarcoma

MTPPSRAEAGVRRSRVPSEGRWRGAEP PGISASTQPASAGRAARHCGAMSGAR **GEGPEAGAGGAGGR** AAPENPGG
VLSVELPGLLAQLARSFALLLPVYALGYLGLSFSWVLLALALLAWCRRSRGLKALRLCRALALLEDEERVRLGV
RACDLPAWVHFPDTER **AEWLNK** TVKHMWPFICQFIEKLFRETIEPAVRCANTHLSTFSFTKVDVGQOPLRINGVK
VYTENVDKRQIILDLQISFVGNCEIDLEIKRYFCRAGVKSIIHGTMRVILEPLIGDMPLVGALSIFFLRKPLLE
INWGTGLTNLLDVPGLNGLSDTIILDIISNYLVLPNRITVPLVSEVQIAQLRFPVPKGVLR IHFIEAQDLQKDTY
LKGLVKGKSDPYGIIRVGNQIFQSRVIKENLSPKWNEVYEALVYEHPPGQELEIELFDEDPDKDDFLGSLMIDLIE
VEKERLLDEWFTLDEVKPKGLHLRLEWLTMPNASNLDKVLTDIKADKDQANDGLSSALLILYLD SARNLP SGKK
ISSNPNPVVQMSVGHKAQESKIRYKTNEPVWEENFTFFIHNPKRQDLEVEVRDEQHQC SLGNLKVPLSQLLTSED
MTVSQRFQLSNSGPNSTIKMKIALRVLHLEKRERPPDHQHS AQVKRPSVSKEGRKTSIKSHMSGSPGPGGSNTAP
STPVIGSDKPGMEEKAPPEAGPQGLHDLGRSSSSSLLASPGHISVKEPTPSIASDISLP IATQELRQRLRQLEN
GTTLGQSPGLGQIQLTIRHSSQRNKLIVVHACRNLI AFSE DGS DPYVRMYLLPDKRRSGRRKTHVSKKTLNPVFD
QSFDFSVSLPEVQRRTLDVAVKNSGGFLSKDKGLLGKVLVALASEELAKGWTQWYDLTEDGTRPQAMT

Mass Match Peptides (bold):

AEWLNK [64]

Tandem Peptides (underline):

Peptide Source: 1D-GE, Pancreatic cancer

MTPPSRAEAGVRRSRVPSEGRWRGAEP PGISASTQPASAGRAARHCGAMSGAR **GEGPEAGAGGAGGR** AAPENPGG
VLSVELPGLLAQLARSFALLLPVYALGYLGLSFSWVLLALALLAWCRRSRGLKALRLCRALALLEDEERVRLGV
RACDLPAWVHFPDTERAEWLNKTVK **HMWPFICQFIEK** LFRETIEPAVRCANTHLSTFSFTKVDVGQOPLRINGVK
VYTENVDK RQIILDLQISFVGNCEIDLEIKRYFCRAGVKSIIHGTMRVILEPLIGDMPLVGALSIFFLRKPLLE
INWGTGLTNLLDVPGLNGLSDTIILDIISNYLVLPNRITVPLVSEVQIAQLRFPVPKGVLR **IHFIEAQDLQK** DTY
LKGLVKCK **SDPYGIIRVGNQIFQSR** VIKENLSPKWNEVYEALVYEHPPGQELEIELFDEDPDKDDFLGSLMIDLIE
VEKERLLDEWFTLDEVKPKGLHLRLEWLTMPNASNLDKVLTDIKADKDQANDGLSSALLILYLD SARNLP SGKK
ISSNPNPVVQMSVGHKAQESKIRYKTNEPVWEENFTFFIHNPKRQDLEVEVR **DEQHQC SLGNLKVPLSQLLTSED**
MTVSQRFQLSNSGPNSTIKMKIALRVLHLEKRERPPDHQHS AQVK RPSVSKEGRKTSIKSHMSGSPGPGGSNTAP
STPVIGSDKPGMEEKAPPEAGPQGLHDLGRSSSSSLLASPGHISVKEPTPSIASDISLP IATQELRQRLRQLEN
GTTLGQSPGLGQIQLTIRHSSQRNKLIVVHACRNLI **AFSE DGS DPYVR** MYLLPDKRRSGRRKTHVSKKTLNPVFD
QSFDFSVSLPEVQRRTLDVAVKNSGGFLSKDKGLLGKVLVALASEELAKGWTQWYDLTEDGTRPQAMT

Mass Match Peptides (bold):

AQPPEAGPQGLHDLGR [83]
DEQHQC SLGNLK [115]
ERPPDHQHS AQVK [222]
GEGPEAGAGGAGGR [290]
HMWPFICQFIEK [339]
IHFIEAQDLQK [368]
ISSNPNPVVQMSVGHK [393]
NLI AFSE DGS DPYVR [542]
SDPYGIIR [622]
VGNQIFQSR [765]
VPLSQLLTSEDMTVSQR [792]
VYTENVDK [819]

Tandem Peptides (underline):

ALALLEDEER [75]
NLIAFSEDGSDPYVR [542]

Peptide Source: 1D-GE, Prostate cancer

MTPPSRAEAGVRRSRVPSEGRWRGAEPGGISASTQPASAGRAARHCGAMSGARGEGPEAGAGGAGGAAAPENPGG
VLSVELPGLLAQLARSFALLLPVYALGYLGLSFSWVLLALALLAWCRRSRGLKALRLCRALALLEDEERVVRLGV
RACDLPAWVHFPDTERAEWLNTVKHMPFFICQFIEKLFRETIEPAVRGANHTLSTFSFTKVDVGQQPLRINGVK
VYTENVDKRQIILDLQISFVGNCEIDLEIKRYFCRAGVKSQIHGTMRVILEPLIGDMPLVGALSIFFLRKPLLE
INWTGLTNLLDVPGLNGLSDTIILDIISNYLVLPNRITVPLVSEVQIAQLRFPVPGVLRHIFIEAQDLQCKDQTY
LKGLVKGKSDPYGIIRVGNQIFQSRVIKENLSPKWNEVEYALVYEHHPGQELEIELFDEDPDKDDFLGSLMIDLIE
VEKERLLDEWFTLDEVPGKGLHLRLEWLTLPNPNASNLDKVLTDIKADKQANDGLSSALLILYLDARSNLPSGKK
ISSNPNPVQMSVGHKAQESKIRYKTNEPVWEENFTFFIHNPKRDLEVEVRDEQHQCSLGNLKVPLSQLLTSED
MTVSQRFQLSNSGPNSTIKMKIALRVHLHLEKREPPDHQHSQAQVKRPSVSKEGRKTSIKSHMSGSPGPGGSNTAP
STPVIGGSDKPGMEEKAPPEAGPQGLHDLGRSSSSLLASPGHISVKEPTPSIASDISLPATQELRQRLRQLEN
GTTLGQSPLGQIQLTIRHSSQRNKLIVVHACRNLIASFSEDGSDPYVRMYLLPDKRRSGRRKTHVSKKTLNPFVD
QSFDFSVSLPEVQRRTLDAVKNSGGFLSKDKGLLGKVLVALASEELAKGWTQWYDLTETDTRPQAMT

Mass Match Peptides (bold):

AEWLNK [64]

Tandem Peptides (underline):

Peptide Source: 1D-GE, Renal cell cancer

MTPPSRAEAGVRRSRVPSEGRWRGAEPGGISASTQPASAGRAARHCGAMSGARGEGPEAGAGGAGGAAAPENPGG
VLSVELPGLLAQLARSFALLLPVYALGYLGLSFSWVLLALALLAWCRRSRGLKALRLCRALALLEDEERVVRLGV
RACDLPAWVHFPDTERAEWLNTVKHMPFFICQFIEKLFRETIEPAVRGANHTLSTFSFTKVDVGQQPLRINGVK
VYTENVDKRQIILDLQISFVGNCEIDLEIKRYFCRAGVKSQIHGTMRVILEPLIGDMPLVGALSIFFLRKPLLE
INWTGLTNLLDVPGLNGLSDTIILDIISNYLVLPNRITVPLVSEVQIAQLRFPVPGVLRHIFIEAQDLQCKDQTY
LKGLVKGKSDPYGIIRVGNQIFQSRVIKENLSPKWNEVEYALVYEHHPGQELEIELFDEDPDKDDFLGSLMIDLIE
VEKERLLDEWFTLDEVPGKGLHLRLEWLTLPNPNASNLDKVLTDIKADKQANDGLSSALLILYLDARSNLPSGKK
ISSNPNPVQMSVGHKAQESKIRYKTNEPVWEENFTFFIHNPKRDLEVEVRDEQHQCSLGNLKVPLSQLLTSED
MTVSQRFQLSNSGPNSTIKMKIALRVHLHLEKREPPDHQHSQAQVKRPSVSKEGRKTSIKSHMSGSPGPGGSNTAP
STPVIGGSDKPGMEEKAPPEAGPQGLHDLGRSSSSLLASPGHISVKEPTPSIASDISLPATQELRQRLRQLEN
GTTLGQSPLGQIQLTIRHSSQRNKLIVVHACRNLIASFSEDGSDPYVRMYLLPDKRRSGRRKTHVSKKTLNPFVD
QSFDFSVSLPEVQRRTLDAVKNSGGFLSKDKGLLGKVLVALASEELAKGWTQWYDLTETDTRPQAMT

Mass Match Peptides (bold):

AEWLNK [64]
AQPPEAGPQGLHDLGR [83]
ERPPDHQHSQAQVK [222]
HMPFFICQFIEK [339]
SIQIHGTMR [638]
TNEPVWEENFTFFIHNPK [710]
VDVGQQPLR [750]
VYTENVDKR [820]

Tandem Peptides (underline):

AQPPEAGPQGLHDLGR [83]

Peptide Source: iTRAQ, Colorectal cancer

MTPPSRAEAGVRRSRVPSEGRWRGAEPGGISASTQPASAGRAARHCGAMSGARGEGPEAGAGGAGGAAAPENPGG
VLSVELPGLLAQLARSFALLLPVYALGYLGLSFSWVLLALALLAWCRRSRGLKALRLCRALALLEDEERVVRLGV
RACDLPAWVHFPDTERAEWLNTVKHMPFFICQFIEKLFRETIEPAVRGANHTLSTFSFTKVDVGQQPLRINGVK
VYTENVDKRQIILDLQISFVGNCEIDLEIKRYFCRAGVKSQIHGTMRVILEPLIGDMPLVGALSIFFLRKPLLE

INWTGLTNLLDVPGLNGLSDTIILDIISNYLVLPNRITVPLVSEVQIAQLRFPVPKGVLRHIFIEAQDLQKQDITY
LKGLVKGKSDPYGIIRVGNQIFQSRVIKENLSPKWNEVYEALVYEHHPGQELEIELFDEDDPKDDFLGSLMIDLIE
VEKERLLDEWFTLDEVPKCKLHLRLEWLTLPNPNASNLDKVLTADKQDQANDGLSSALLILYLDARSNLPSPGKK
ISSNPNPVVQMSVGHKAQESKIRYKTNEPVWEENFTFFIHNPKRQDLEVEVRDEQHQCSLGNLKVPLSQLLTSED
MTVSQRFQLSNSGPNSTIKMKIALRVLHLEKRERPPDQHSAQVKRPSVSKEGRKTSIKSHMSGSPGPGGSNTAP
STPVIGGSDKPGMEEKAQPPEAGPQGLHDLGRSSSSLLASPGHISVKEPTPSIASDISLPATQELRQRLRQLEN
GTTLQGSPLGQIQTLIRHSSQRNKLIVVHACRNLIASFEDGSDPYVRMYLLPDKRRSGRRKTHVSKKTLNPNVFD
QSFDFSVSLPEVQRRTLDVAVKNSGGFLSKDKGLLGKVLVALASEELAKGWTQWYDLTEDGTRPQAMT

Mass Match Peptides (bold):

ALALLEDEER [75]
GEGPEAGAGGAGGR [290]
MTPPSRAEAGVRR [953]
VLTADIK [996]

Tandem Peptides (underline):

ALALLEDEER [75]
GEGPEAGAGGAGGR [290]
MTPPSRAEAGVRR [953]
VLTADIK [996]

Peptide Source: iTRAQ, Non-small cell lung cancer

MTPPSRAEAGVRRSRVPSEGRWRGAEPGGISASTQPASAGRAARHCGAMSGAR**GEGPEAGAGGAGGR**AAPENPGG
VLSVELPGLLAQLARSFALLLPVYALGYLGSLFSWVLLALALLAWCRRSRGLKALRLCRALALLEDEERVRLGV
RACDLPAWVHF²PTER**AEWLNK**TVKHMW²FCQFIEKLFRETIEPAVRGANTHLSTFSFTKVDVGQOPLRINGVK
VYTENVDKRQIILDLQISFVGNCIEDLEIKRYFCRAGVKSIIHGTMRVILEPLIGDMPLVGALSIFFLRKPLLE
INWTGLTNLLDVPGLNGLSDTIILDIISNYLVLPNRITVPLVSEVQIAQLRFPVPKGVLRHIFIEAQDLQKQDITY
LKGLVKGKSDPYGIIRVGNQIFQSRVIKENLSPKWNEVYEALVYEHHPGQELEIELFDEDDPKDDFLGSLMIDLIE
VEKERLLDEWFTLDEVPKCKLHLRLEWLTLPNPNASNLDKVLTADKQDQANDGLSSALLILYLDARSNLPSPGKK
ISSNPNPVVQMSVGHKAQESKIRYKTNEPVWEENFTFFIHNPKRQDLEVEVRDEQHQCSLGNLKVPLSQLLTSED
MTVSQRFQLSNSGPNSTIKMKIALRVLHLEKRERPPDQHSAQVKRPSVSKEGRKTSIKSHMSGSPGPGGSNTAP
STPVIGGSDKPGMEEKAQPPEAGPQGLHDLGRSSSSLLASPGHISVKEPTPSIASDISLPATQELRQRLRQLEN
GTTLQGSPLGQIQTLIRHSSQRNKLIVVHACRNLIASFEDGSDPYVRMYLLPDKRRSGRRKTHVSKKTLNPNVFD
QSFDFSVSLPEVQRRTLDVAVKNSGGFLSKDKGLLGKVLVALASEELAKGWTQWYDLTEDGTRPQAMT

Mass Match Peptides (bold):

AEWLNK [64]
DTYLK [896]
GEGPEAGAGGAGGR [290]

Tandem Peptides (underline):

AEWLNK [64]
DTYLK [896]
GEGPEAGAGGAGGR [290]

Peptide Source: iTRAQ, Ovarian cancer

MTPPSRAEAGVRRSRVPSEGRWRGAEPGGISASTQPASAGRAARHCGAMSGAR**GEGPEAGAGGAGGR**AAPENPGG
VLSVELPGLLAQLARSFALLLPVYALGYLGSLFSWVLLALALLAWCRRSRGLKALRLCR**ALALLEDEER**VRLGV
RACDLPAWVHF²PTERAEWLNKTVKHMW²FCQFIEKLFRETIEPAVRGANTHLSTFSFTKVDVGQOPLRINGVK
VYTENVDKRQIILDLQISFVGNCIEDLEIKRYFCRAGVKSIIHGTMRVILEPLIGDMPLVGALSIFFLRKPLLE
INWTGLTNLLDVPGLNGLSDTIILDIISNYLVLPNRITVPLVSEVQIAQLRFPVPKGVLRHIFIEAQDLQKQDITY
LKGLVKGKSDPYGIIRVGNQIFQSRVIKENLSPKWNEVYEALVYEHHPGQELEIELFDEDDPKDDFLGSLMIDLIE
VEKERLLDEWFTLDEVPKCKLHLRLEWLTLPNPNASNLDKVLTADKQDQANDGLSSALLILYLDARSNLPSPGKK
ISSNPNPVVQMSVGHKAQESKIRYKTNEPVWEENFTFFIHNPKRQDLEVEVRDEQHQCSLGNLKVPLSQLLTSED
MTVSQRFQLSNSGPNSTIKMKIALRVLHLEKRERPPDQHSAQVKRPSVSKEGRKTSIKSHMSGSPGPGGSNTAP
STPVIGGSDKPGMEEKAQPPEAGPQGLHDLGRSSSSLLASPGHISVKEPTPSIASDISLPATQELRQRLRQLEN

GTTLLGQSPLGQIQLTIRHSSQRNKLIVVHACRNLIASFSEDGSDPYVRMYLLPDKRRSGRRKTHVSKKTLNPFVD
QSFDFSVSLPEVQRRITLDVAVKNSGGFLSKDKGLLGKVLVALASEELAKGWTQWYDLTEDGTRPQAMT

Mass Match Peptides (bold):

ALALLEDEER [75]

Tandem Peptides (underline):

ALALLEDEER [75]

OGTA124 (SEQ ID No: 25)

Peptide Source: 1D-GE, Hepatocellular carcinoma

MPHFTVVPVDGPRRGDYDNLEGLSWVDYGERAELDDSDGHGNHRESSPFLSPLEASERGIDYYDRNLALFEEELDI
RPKVSSLLGKLVSYTNLTQGAKEHEEAESGEGTRRRAAEAPSMGTLMGVYLPCLQNI FGVI LFLRLTWMVGTAGV
LQALLIVLICCCCTLLTAISMAIATNGVVPAGGSYFMISRLGPEFGGAVGLCFYLGTTFAAAMYILGAIEILL
TYIAPPAIFYPGADTSNATLNNMRVYGTIFLTFMTLVVFGVKYVNKFASLFLACV IISILSIYAGGIK**SIF**
DPPVFPVCMLGNRTLSRDQFDICAKTAVVDNETVATQLWSFFCHSPNLITDSCDPYFMLNNVTEIPGIPGAAAGV
LQENLWSAYLEKGDIVEK**HGLPSADAPSLK**ESLPLYVVADIATSFTVLVGIFFPSTGIMAGSNRSGDLRDAQKS
IPVGTILAIITTSLVYFSSVVLFGACIEGVLRDKYGDGVSRLNVVGTALWPSPPWVIVIGSFFSTCGAGLQSLTG
APRLLOAIADNIIPFLRVFGHGKVNGETWALLLTALIAELGILIASLDMVAPILSMFFLMCYL FVNACAVQT
LLR**TPNWRPR**FKYYHWALSFLGMSLCLALMFVSSWYYALVAMLIAGMIYKY**YIEYQGAKEWGDGIR**GLSLSAARY
ALLR**LEEPPHTK**NWRPOLLVLLK**LDEDLHV**KYPRLLTFASQLKAGKGLTIVGSVIQGSFLESYGEAQAAEOTIK
NMMEIEKVKGFCQVVVASKVR**EGLAHLIQSCGLGGMHNSVVLGWPGWR**QSEDPRAWK**TFIDTVR**CTTAHLAL
LVPK**NIAFYPSNHER**YLEGHIDVWVIVHDGMLMLLPFLLRQHVKVRKCRMRIFTVAQMDDNSIQMK**DLAVFLY**
HLRLEAEVEVEMHNSDISAYTYERTLMMEQRSQMLRQMLTKTEREREALVKDRHSALRLESLSYDEEDESAV
GADKIQMTWTRDK**YMTETWDPSHAPDNFR**ELVHIKPDQSNVRMHTAVKLNIEVIVTRSHDAR**LVLLNMPGPPRNS**
EGDENYMEFLEVLTEGLERVLLVRGGRE**EVITIYS**

Mass Match Peptides (bold):

AELDDSDGHGNHR [62]
DLAVFLYHLR [133]
EGLAHLIQSCGLGGM [188]
EHEEAESGEGTRRR [192]
ESSPFLSPLEASER [227]
EVITIYS [233]
EWGDGIR [240]
HGLPSADAPSLK [334]
HNSVVLGWPGWR [340]
LDEDLHV [446]
LEEPPHTK [451]
MPHFTVVPVDGPR [521]
NIAFYPSNHER [539]
NLALFEEELDIRPK [541]
NSEGDENYMEFLEVLTEGLER [553]
SIFDPPVFPVCMLGNR [636]
TFIDTVR [689]
TPNWRPR [720]
YIEYQGAEK [855]
YMTETWDPSHAPDNFR [863]

Tandem Peptides (underline):

HGLPSADAPSLK [334]
LVLLNMPGPPR [501]
LVSYTNLTQGAKE [504]

Peptide Source: 1D-GE, Lung cancer

MPHFTVVPVDGPRRGDYDNLEGLSWVDYGERAELEDDSDGHGNHRESSPFLSPLEASRGIDYYDRNLALFEEELDI
 RPKVSSLLGKLVSYTNLTQGAKEHEEAESGEGTRRRRAAEAPSMGTLMGVYLPCLQNI FGVILFLRLTWMVGTAGV
 LQALLIVLICCCCTLLTAISMSAIATNGVVPAGGSYFMISRSLGPEFGGAVGLCFYLGTTFAAAMYILGAIEILL
 TYIAPPAATFYPSGAHDTSNATLNNMRVYGTIFLTMTLVVFGVKYVNFASFLLACVLIISILSIYAGGIKSIF
 DPPVFPVCMGLGNRTLSRDQFDICAKTAVVDNETVATQLWSFFCHSPNLTTDSCDPYFMLNNVTEIPGIPGAAAGV
 LQENLWSAYLEKGDIVEKHGLPSADAPSLKESLPLYVVADIATSFTVLVGIFFPSVTGIMAGSNRSGDLRDAQKS
 IPVGTILAIITTSLVYFSSVVLFGACIEGVVLRDKYGDGVSRLNVVGT LAWPSPWVIVIGSFFSTCGAGLQSLTG
 APRLLQAIADKNII PFLRVF'GHGKVNGEPTWALLLTALIAELGILIASLDMVAPILSMFFLMCYLFVNLACAVQT
 LLRTPNWRPRFKYHWALESFLGMSLCLALMFVSSWYALVAMLIAGMIYKYIEYQGAKEWGDGIRGLSLSAARY
 ALLRLEEGPPHTKNWRPQLLVLLKLDLHVKYPRLLTFASQLKAGKGLTIVGSVIQGSFLESYGEAQAAEQTIK
 NMMEIEKVKGFCQVVASKVREGLAHLIQSCGLGMRHNSVVLGWPGWQSEDPRAWKTFIDTVRCTTAAHLAL
 LVPKNIAFYPSNHERYLEGHIDVWVIHVDGGMMLLPFLLRQHKVWRKCRMRIFTVAQMDDNSIQMKKDLAVFLY
 HLRLEAEVEVVMHNSDISAYTYERTLMMEQSQMLRQMLTKTEREREQQLVKDRHSALRLESLSYDEEDES AV
 GADKIQMTWTRDKYMTETWDP SHAPDNFRELVHIKPDQSNVRRMHTAVKLENEIVTRSHDARLVLLNMPGPPRNS
 EGDENYMEFLEVLTEGLERVLLVRGGGREVITIYS

Mass Match Peptides (bold):

DQFDICAK [151]
 EHEEAESGEGTR [191]
 EHEEAESGEGTRRR [192]
 ESSPFLSPLEASR [227]
 EVITIYS [233]
 LVLLNMPGPPER [501]
 LVSYTNLTQGAKE [504]

Tandem Peptides (underline):

LVSYTNLTQGAKE [504]

Peptide Source: 1D-GE, Ovarian cancer

MPHFTVVPVDGPRRGDYDNLEGLSWVDYGERAELEDDSDGHGNHRESSPFLSPLEASRGIDYYDRNLALFEEELDI
 RPKVSSLLGKLVSYTNLTQGAKEHEEAESGEGTRRRRAAEAPSMGTLMGVYLPCLQNI FGVILFLRLTWMVGTAGV
 LQALLIVLICCCCTLLTAISMSAIATNGVVPAGGSYFMISRSLGPEFGGAVGLCFYLGTTFAAAMYILGAIEILL
 TYIAPPAATFYPSGAHDTSNATLNNMRVYGTIFLTMTLVVFGVKYVNFASFLLACVLIISILSIYAGGIKSIF
 DPPVFPVCMGLGNRTLSRDQFDICAKTAVVDNETVATQLWSFFCHSPNLTTDSCDPYFMLNNVTEIPGIPGAAAGV
 LQENLWSAYLEKGDIVEKHGLPSADAPSLKESLPLYVVADIATSFTVLVGIFFPSVTGIMAGSNRSGDLRDAQKS
 IPVGTILAIITTSLVYFSSVVLFGACIEGVVLRDKYGDGVSRLNVVGT LAWPSPWVIVIGSFFSTCGAGLQSLTG
 APRLLQAIADKNII PFLRVF'GHGKVNGEPTWALLLTALIAELGILIASLDMVAPILSMFFLMCYLFVNLACAVQT
 LLRTPNWRPRFKYHWALESFLGMSLCLALMFVSSWYALVAMLIAGMIYKYIEYQGAKEWGDGIRGLSLSAARY
 ALLRLEEGPPHTKNWRPQLLVLLKLDLHVKYPRLLTFASQLKAGKGLTIVGSVIQGSFLESYGEAQAAEQTIK
 NMMEIEKVKGFCQVVASKVREGLAHLIQSCGLGMRHNSVVLGWPGWQSEDPRAWKTFIDTVRCTTAAHLAL
 LVPKNIAFYPSNHERYLEGHIDVWVIHVDGGMMLLPFLLRQHKVWRKCRMRIFTVAQMDDNSIQMKKDLAVFLY
 HLRLEAEVEVVMHNSDISAYTYERTLMMEQSQMLRQMLTKTEREREQQLVKDRHSALRLESLSYDEEDES AV
 GADKIQMTWTRDKYMTETWDP SHAPDNFRELVHIKPDQSNVRRMHTAVKLENEIVTRSHDARLVLLNMPGPPRNS
 EGDENYMEFLEVLTEGLERVLLVRGGGREVITIYS

Mass Match Peptides (bold):

ESSPFLSPLEASR [227]
 EVITIYS [233]
 IQMTWTR [389]
 LNEIVTR [472]
 MHTAVK [517]
 NIAFYPSNHER [539]
 NSEGDENYMEFLEVLTEGLER [553]
 TFIDTVR [689]
 TPNWRPR [720]

Tandem Peptides (underline):

ESSPFLSPLEASR [227]
 GIDYYDR [300]

Peptide Source: 1D-GE, Pancreatic cancer

MPHFTVVPVDGPRRGDYDNLEGLSWVDYGERAELDDSDGHGNHRESSPFLSPLEASRGIDYYDRNLALFEEELDI
 RPKVSSLLGKLVSYTNLTQGAKHEEEAESGEGTRRRAAEAPSMGTLMGVYLPCLQNI FGVI LFLRLTWMVGTAGV
 LQALLIVLICCCCTLLTAISMSAIATNGVVPAGGSYFMISRLGPEFGGAVGLCFYLGTTFAAAMYILGAIEILL
 TYIAPPAAIFYPSGAHDTSNATLNNMRVYGTIFLTFMTLVVFGVKYVNKFASLFLACVII SILSIYAGGIK**SIF**
DPPVFPVCMLGNRTLSRDQFDICAKTAVVDNETVATQLWSFFCHSPNLITDSCDPYFMLNNVTEIPGIPGAAAGV
 LQENLWSAYLEKGDIVEKHGLPSADAPSLKESLPLYVADIATSFTVLVGIFFPSTGIMAGSNRSGDLRDAQKS
 IPVGTILAIITTSLVYFSSVVLFGACIEGVVLRDKYGDGVSRLVVGTLAWPSPWVIVIGSFFSTCGAGLQSLTG
 APRLLQAIADKNIIPFLRVFGHGKVNGETWALLLTALIAELGILIASLDMVAPILSMFFLMCYLTVNLACAVQT
 LLRTPNWRPRFKYYHWALSFLGMSLCLALMFVSSWYALVAMLIAGMIYKYIEYQGAKEWGDGIRGLSLSAARY
 ALLRLEEGPPHTKNWRPQLLVLLKLEDEHLVKYPRLLTFASQLKAGKGLTIVGSIQGSFLESYGEAQAAEQTIK
 NMMEIEKVKGFCQVVVASKVREGLAHLIQSCGLGGMREHNSVVLGWPGYGWRQSEDPRAWKTFIDTVRCTTAAHLAL
 LVPK**NIAFYPSNHER**YLEGHIDVWVIVHDGCMMLLPFLLRQHKVWRKCRMRIFTVAQMDDNSIQMKKDLAVFLY
 HLRLEAEVEVVMHNSDISAYTYERTLMMEQORSQMLRQMRITKTEREREQLVKDRHSALRLESLSYDEEDESAV
 GADKIQMTWTRDKYMTETWDPSHAPDNFRELVHIKPDQSNVRMHTAVKLNVEIVTRSHDARLVLLNMPGPPRNS
 EGDENYMEFLEVLTTEGLERVLLVRGGGREGVITIYS

Mass Match Peptides (bold):

ELVHIKPDQSNVR [209]
 ESSPFLSPLEASR [227]
 HNSVVLGWPGYGWR [340]
 LEEGPPHTK [451]
 LVSYTNLTQGAK [504]
 NIAFYPSNHER [539]
 SIFDPPVFPVCMLGNR [636]

Tandem Peptides (underline):

LVSYTNLTQGAK [504]

Peptide Source: 1D-GE, Renal cell cancer

MPHFTVVPVDGPRRGDYDNLEGLSWVDYGERAELDDSDGHGNHRESSPFLSPLEASRGIDYYDRNLALFEEELDI
 RPKVSSLLGKLVSYTNLTQGAKHEEEAESGEGTRRRAAEAPSMGTLMGVYLPCLQNI FGVI LFLRLTWMVGTAGV
 LQALLIVLICCCCTLLTAISMSAIATNGVVPAGGSYFMISRLGPEFGGAVGLCFYLGTTFAAAMYILGAIEILL
 TYIAPPAAIFYPSGAHDTSNATLNNMRVYGTIFLTFMTLVVFGVKYVNKFASLFLACVII SILSIYAGGIK**SIF**
DPPVFPVCMLGNRTLSRDQFDICAKTAVVDNETVATQLWSFFCHSPNLITDSCDPYFMLNNVTEIPGIPGAAAGV
 LQENLWSAYLEKGDIVEKHGLPSADAPSLKESLPLYVADIATSFTVLVGIFFPSTGIMAGSNRSGDLRDAQKS
 IPVGTILAIITTSLVYFSSVVLFGACIEGVVLRDKYGDGVSRLVVGTLAWPSPWVIVIGSFFSTCGAGLQSLTG
 APRLLQAIADKNIIPFLRVFGHGKVNGETWALLLTALIAELGILIASLDMVAPILSMFFLMCYLTVNLACAVQT
 LLRTPNWRPRFKYYHWALSFLGMSLCLALMFVSSWYALVAMLIAGMIYKYIEYQGAKEWGDGIRGLSLSAARY
 ALLRLEEGPPHTKNWRPQLLVLLKLEDEHLVKYPRLLTFASQLKAGKGLTIVGSIQGSFLESYGEAQAAEQTIK
 NMMEIEKVKGFCQVVVASKVREGLAHLIQSCGLGGMREHNSVVLGWPGYGWRQSEDPRAWKTFIDTVRCTTAAHLAL
 LVPK**NIAFYPSNHER**YLEGHIDVWVIVHDGCMMLLPFLLRQHKVWRKCRMRIFTVAQMDDNSIQMKKDLAVFLY
 HLRLEAEVEVVMHNSDISAYTYERTLMMEQORSQMLRQMRITKTEREREQLVKDRHSALRLESLSYDEEDESAV
 GADKIQMTWTRDKYMTETWDPSHAPDNFRELVHIKPDQSNVRMETAVKLNVEIVTRSHDARLVLLNMPGPPRNS
 EGDENYMEFLEVLTTEGLERVLLVRGGGREGVITIYS

Mass Match Peptides (bold):

ESSPFLSPLEASR [227]
 HNSVVLGWPGYGWR [340]
 IFTVAQMDDNSIQMK [364]
 IFTVAQMDDNSIQMKK [365]
 LVSYTNLTQGAK [504]
 MPHFTVVPVDGPR [521]
 NIAFYPSNHER [539]
 SIFDPPVFPVCMLGNR [636]

Tandem Peptides (underline):

LVSYTNLTQGAK [504]

Peptide Source: iTRAQ, Colorectal cancer

MPHFTVPVDGPRRGDYDNLEGLSWVDYGERAELEDDSDGHNHRESSPFLSPLEASRGIDYYDRNLALFEEELDI
RPKVSSLLGKLVSYTNLTQGAKEHEEAESGEGTRRRAAEAPSMCTLMGVYLPCLQNI FGVILFLRLTWMVGTAGV
LQALLIVLICCCCTLLTAISMSAIATNGVVPAGGSYFMISRLGPEFGGAVGLCFYLGTTFAAAMYILGAIEILL
TYIAPPAAIFYPSCAHDTSNATLNNMRVYGTIFLTFMTLVVFVGKYNKFFASLFLACVVISILSIYAGGIKSIF
DPPVFVPCMLGNRTLSDQDFDCAKTAVVDNETVATQLWSFFCHSPNLTTDSCDPYFMLNNVTEIPGIPGAAAGV
LQENLWSAYLEKGDIVEKHGLPSADAPSLKESLPLYVVADIATSFTVLVGIFFPSTGIMAGSNRSGDLRDAQS
IPVGTILAIITTSLVYFSSVVLFGACIEGVVLRDKYGDGVSRLNVVGT LAWPSPWVIVIGSFFSTCGAGLQSLTG
APRLLQAIKAKDNIPFLRVFGHGKVNGETWALLLTALIAELGILIASLDMVAPILSMFFLMCYLFVNILACAVQT
LLRTPNWRPRFRYYHWALSFLGMSLCLALMFVSSWYALVAMLIAGMIYKYIEYQGAKEKWDGTRGLSLSAARY
ALLRLEEGPPTHKNWRPQLLVLLKLDLHVKYPRLLTFASQLKAGKGLTIVGSGVSIQGSFLESYGEAQAAEQTIK
NMMEIEKVKGFQVQVVASKVREGLAHLIQSCGLGMRHNSVVLGWPGWRQSEDPRAWKTFIDTVRCTTAAHLAL
LVPKNIAFYPSNHERYLEGHIDVWVIVHDGGMMLLPFLLRQHKKVWRKCRMRIFTVAQMDNDSIQMKKDLAVFLY
HLRLEAEVEVVMHNSDISAYTYERTLMMEQRSQMLRQMRITKTEREREQVLKDRHSALRLESLSYDDEESAV
GADKIQMTWTRDKYMTETWDP SHAPDNFREL VHIKPDQSNVRMHTAVKLNEVIVTRSHDARLVLLNMPGPPRNS
EGDENYMEFLEVLTEGLERVLLVRGGGREVITIYS

Mass Match Peptides (bold):

LLQAIKAK [937]

Tandem Peptides (underline):

LLQAIKAK [937]

Peptide Source: iTRAQ, Hepatocellular cancer

MPHFTVPVDGPRRGDYDNLEGLSWVDYGERAELEDDSDGHNHRESSPFLSPLEASRGIDYYDRNLALFEEELDI
RPKVSSLLGKLVSYTNLTQGAKEHEEAESGEGTRRRAAEAPSMCTLMGVYLPCLQNI FGVILFLRLTWMVGTAGV
LQALLIVLICCCCTLLTAISMSAIATNGVVPAGGSYFMISRLGPEFGGAVGLCFYLGTTFAAAMYILGAIEILL
TYIAPPAAIFYPSCAHDTSNATLNNMRVYGTIFLTFMTLVVFVGKYNKFFASLFLACVVISILSIYAGGIKSIF
DPPVFVPCMLGNRTLSDQDFDCAKTAVVDNETVATQLWSFFCHSPNLTTDSCDPYFMLNNVTEIPGIPGAAAGV
LQENLWSAYLEKGDIVEKHGLPSADAPSLKESLPLYVVADIATSFTVLVGIFFPSTGIMAGSNRSGDLRDAQS
IPVGTILAIITTSLVYFSSVVLFGACIEGVVLRDKYGDGVSRLNVVGT LAWPSPWVIVIGSFFSTCGAGLQSLTG
APRLLQAIKAKDNIPFLRVFGHGKVNGETWALLLTALIAELGILIASLDMVAPILSMFFLMCYLFVNILACAVQT
LLRTPNWRPRFRYYHWALSFLGMSLCLALMFVSSWYALVAMLIAGMIYKYIEYQGAKEKWDGTRGLSLSAARY
ALLRLEEGPPTHKNWRPQLLVLLKLDLHVKYPRLLTFASQLKAGKGLTIVGSGVSIQGSFLESYGEAQAAEQTIK
NMMEIEKVKGFQVQVVASKVREGLAHLIQSCGLGMRHNSVVLGWPGWRQSEDPRAWKTFIDTVRCTTAAHLAL
LVPKNIAFYPSNHERYLEGHIDVWVIVHDGGMMLLPFLLRQHKKVWRKCRMRIFTVAQMDNDSIQMKKDLAVFLY
HLRLEAEVEVVMHNSDISAYTYERTLMMEQRSQMLRQMRITKTEREREQVLKDRHSALRLESLSYDDEESAV
GADKIQMTWTRDKYMTETWDP SHAPDNFREL VHIKPDQSNVRMHTAVKLNEVIVTRSHDARLVLLNMPGPPRNS
EGDENYMEFLEVLTEGLERVLLVRGGGREVITIYS

Mass Match Peptides (bold):

EWGDGIR [240]

Tandem Peptides (underline):

EWGDGIR [240]

Peptide Source: iTRAQ, Non-small cell lung cancer

MPHFTVPVDGPRRGDYDNLEGLSWVDYGERAELEDDSDGHNHRESSPFLSPLEASRGIDYYDRNLALFEEELDI
RPKVSSLLGKLVSYTNLTQGAKEHEEAESGEGTRRRAAEAPSMCTLMGVYLPCLQNI FGVILFLRLTWMVGTAGV
LQALLIVLICCCCTLLTAISMSAIATNGVVPAGGSYFMISRLGPEFGGAVGLCFYLGTTFAAAMYILGAIEILL
TYIAPPAAIFYPSCAHDTSNATLNNMRVYGTIFLTFMTLVVFVGKYNKFFASLFLACVVISILSIYAGGIKSIF

DPPVFPVCM LGNRTL SRDQFDICAKTAVVDNETVATQLWSFFCHSPNLTTDSCDPYFMLNNVTEIPGIPGAAAGV
LQENLWSAYLEKGDIVEKHGLPSADAPSLKESLPLYVVADIATSF TVLVGIFFP SVTGIMAGSNRSGDLRDAQKS
IPVGTILAIITTS LVYFSSVVLFGACIEGVVLRDKYGDGVSRLVVGTLAWPSPWVIVIGSFFSTCGAGLQSLTG
APRL LQAI AKDNII PFLRVFGHGKVNGEPTWALLLTALIAELGILIASLDMVAPILSMFFLMCYLFVNLC AVQT
LLRTPNWRPRFKYYHWALSFLGMSLCLALMFVSSWYYALVAMLIAGMIYKYIEYQGAKEWGDGIRGLSLSAARY
ALLRLEEGP PHTKNWRPQLLVLLK LDEDLHVK YPRLLTFASQLKAGKGLTIVG SVIQGSFLESYGEAQAAEQTIK
NMMEIEKVKGFCQVVVASKVREGLAHLIQSCGLGMRHNSVVLGWPYGWRQSEDPRAWKTFIDTVRCTTAHAHAL
LVPKNIAFYPSNHERYLEGHIDVWWIVHDGGM LMLLPFLLRQHKVWRKCRMRIFTVAQMDDNSIQMKKDLAVFLY
HLRLEAEVEVVMHNSDISAYTYERTLMMEQRSQMLRQMLRTKTEREREQAQLVKDRHSALRLESLSYDEEDES AV
GADKI QMTWTRDKYMTETWDP SHAPDNFREL VHIKPDQSNVRRMHTAVKLN EVIVTRSHDARLVLLNMPGPPRNS
EGDENYMEFLEVLTEGLERVLVLRGGGREVITITYS

Mass Match Peptides (bold):

LDEDLHVK [446]

Tandem Peptides (underline):

LDEDLHVK [446]

Peptide Source: iTRAQ, Ovarian cancer

MPHFTVVPVDGPRRGDYDNLEGLSWVDYGERAE LDDSDGHGHNHRESSPFLS PLEASRGIDYYDRNLALFEEELDI
RPKVSSLLGKLVSYTNLTQGAKEHEEAESGEGTRRRAEAPSMTGLMGVYLPCLQNI FGVILFLRLTWMVGTAGV
LQALLIVLICCCTLLTAISMSAIATNGVVPAGGSYFMISRS LGPEFGGAVGLCFYLGTTFAAAMYILGAIEILL
TYIAPPAAI FYP SGADHTSNATLNNMRVYGTIFLTFMTLVV FVGKYNKFASLFLACV IISILSIYAGGIKSIF
DPPVFPVCM LGNRTL SRDQFDICAKTAVVDNETVATQLWSFFCHSPNLTTDSCDPYFMLNNVTEIPGIPGAAAGV
LQENLWSAYLEKGDIVEKHGLPSADAPSLKESLPLYVVADIATSF TVLVGIFFP SVTGIMAGSNRSGDLRDAQKS
IPVGTILAIITTS LVYFSSVVLFGACIEGVVLRDKYGDGVSRLVVGTLAWPSPWVIVIGSFFSTCGAGLQSLTG
APRL LQAI AKDNII PFLRVFGHGKVNGEPTWALLLTALIAELGILIASLDMVAPILSMFFLMCYLFVNLC AVQT
LLRTPNWRPRFKYYHWALSFLGMSLCLALMFVSSWYYALVAMLIAGMIYKYIEYQGAKEWGDGIRGLSLSAARY
ALLRLEEGP PHTKNWRPQLLVLLK LDEDLHVK YPRLLTFASQLKAGKGLTIVG SVIQGSFLESYGEAQAAEQTIK
NMMEIEKVKGFCQVVVASKVREGLAHLIQSCGLGMRHNSVVLGWPYGWRQSEDPRAWKTFIDTVRCTTAHAHAL
LVPKNIAFYPSNHERYLEGHIDVWWIVHDGGM LMLLPFLLRQHKVWRKCRMRIFTVAQMDDNSIQMKKDLAVFLY
HLRLEAEVEVVMHNSDISAYTYERTLMMEQRSQMLRQMLRTKTER EREQAQLVK DRHSALRLESLSYDEEDES AV
GADKI QMTWTRDKYMTETWDP SHAPDNFREL VHIKPDQSNVRRMHTAVKLN EVIVTRSHDARLVLLNMPGPPRNS
EGDENYMEFLEVLTEGLERVLVLRGGGREVITITYS

Mass Match Peptides (bold):

EREQAQLVK [905]

Tandem Peptides (underline):

EREQAQLVK [905]

Peptide Source: iTRAQ, Renal cell cancer

MPHFTVVPVDGPRRGDYDNLEGLSWVDYGERAE LDDSDGHGHNHRESSPFLS PLEASRGIDYYDRNLALFEEELDI
RPKVSSLLGKLVSYTNLTQGAKEHEEAESGEGTRRRAEAPSMTGLMGVYLPCLQNI FGVILFLRLTWMVGTAGV
LQALLIVLICCCTLLTAISMSAIATNGVVPAGGSYFMISRS LGPEFGGAVGLCFYLGTTFAAAMYILGAIEILL
TYIAPPAAI FYP SGADHTSNATLNNMRVYGTIFLTFMTLVV FVGKYNKFASLFLACV IISILSIYAGGIKSIF
DPPVFPVCM LGNRTL SRDQFDICAKTAVVDNETVATQLWSFFCHSPNLTTDSCDPYFMLNNVTEIPGIPGAAAGV
LQENLWSAYLEKGDIVEKHGLPSADAPSLKESLPLYVVADIATSF TVLVGIFFP SVTGIMAGSNRSGDLRDAQKS
IPVGTILAIITTS LVYFSSVVLFGACIEGVVLRDKYGDGVSRLVVGTLAWPSPWVIVIGSFFSTCGAGLQSLTG
APRL LQAI AKDNII PFLRVFGHGKVNGEPTWALLLTALIAELGILIASLDMVAPILSMFFLMCYLFVNLC AVQT
LLRTPNWRPRFKYYHWALSFLGMSLCLALMFVSSWYYALVAMLIAGMIYKYIEYQGAKEWGDGIRGLSLSAARY
ALLRLEEGP PHTKNWRPQLLVLLK LDEDLHVK YPRLLTFASQLKAGKGLTIVG SVIQGSFLESYGEAQAAEQTIK
NMMEIEKVKGFCQVVVASKVREGLAHLIQSCGLGMRHNSVVLGWPYGWRQSEDPRAWKTFIDTVRCTTAHAHAL
LVPKNIAFYPSNHERYLEGHIDVWWIVHDGGM LMLLPFLLRQHKVWRKCRMRIFTVAQMDDNSIQMKKDLAVFLY
HLRLEAEVEVVMHNSDISAYTYERTLMMEQRSQMLRQMLRTKTEREREQAQLVKDRHSALRLESLSYDEEDES AV
GADKI QMTWTRDKYMTETWDP SHAPDNFREL VHIKPDQSNVRRMHTAVKLN EVIVTRSHDARLVLLNMPGPPRNS
EGDENYMEFLEVLTEGLERVLVLRGGGREVITITYS

Mass Match Peptides (bold):

IFTVAQMDDNSIQMKK [365]
LDEDLHVK [446]

Tandem Peptides (underline):

IFTVAQMDDNSIQMKK [365]
LDEDLHVK [446]

OGTA126 (SEQ ID No: 26)**Peptide Source: 1D-GE, Breast cancer**

MAGLNCGVSIALLGVLLGAARLPR**GAEAFETALPR**ESNITVLIKLGTPTLIAKPCYIVISKRHITMLSIKSGER
IVFTFSCQSPENHFVIEIQKNIDCMGSPCFGEVQLQPSTSLPTLNRTFIWDVKAHKSIGLELQFSIPRLRQIG
PGESCPDGVTHSISGRIDATVVRIGTFCSNGTVSRIKM**QEGVKMALHLFWFHR**NVSGFSIANRSSIKRLCIES
VFEGEGSATLMSANYPEGFPPEDELMTWQFVVPAAHLRASVSFLNFNLSNCERKEERVEYYIPGSTTNPEVFKLEDK
QPGNMAGNFNLSLQGCQDAQSPGILRLQFQVLVQHFPQNESNKI**YVVDLSNER**AMSLTIEPRPVKQSRKTFVPGCF
VCLESRTCSSNLTLTSGSKHKISFLCDDLTRLWMNVKTIISCTDHRYCQRKSYSLQVPSDILHLFVELHDFSWKL
LVPKDRLSLVLPAAQLQQHTHEKPCNTSFSYLVASAIPSQDLYFGSFCPGGSIKQIQVKQNISVTLRTEFAPSFR
QEASRQGLTVSFIPYFKEEGVFTVTPDTKSKVYLRTPNWDR**GLPSLTSVSWNISVPR**DQVACLTFFKERSGVVCQ
TGRA**AFMIIQEQR**TRAEIIFSLDEDVLPKPSFHHHSFWVNIISNCSPSTSGKQLDLLFSVTLTPRTVDLTVILIAAVG
GGVLLLSALGLIICCVKKKKKTKNGPAVGIIYNGNINTEMPRQPKKFQKGRKDNDSHVYAVIEDTMVYGHLQDS
SGSFLQPEVDTYRPFQGTMGVCPSPPTICSRAPTAKLATEEPPPSPPPESESEPYTFSHPNNGDVSSKDTDIPL
LSTQEPMEPAE

Mass Match Peptides (bold):

AFMIIQEQR [66]
GAEAFETALPR [282]
GLPSLTSVSWNISVPR [302]
MALHLFWFHR [508]

Tandem Peptides (underline):

IYVVDLSNER [404]

Peptide Source: 1D-GE, Colorectal cancer

MAGLNCGVSIALLGVLLGAARLPRGAEAFETALPRESNITVLIKLGTPTLIAKPCYIVISKRHITMLSIKSGER
IVFTFSCQSPENHFVIEIQKNIDCMGSPCFGEVQLQPSTSLPTLNRTFIWDVKAHKSIGLELQFSIPRLRQIG
PGESCPDGVTHSISGRIDATVVRIGTFCSNGTVSRIKM**QEGVKMALHLFWFHR**NVSGFSIANRSSIKRLCIES
VFEGEGSATLMSANYPEGFPPEDELMTWQFVVPAAHLR**ASVSFLNFNLSNCER**KEERVEYYIPGSTTNPEVFKLEDK
QPGNMAGNFNLSLQGCQDAQSPGILRLQFQVLVQHFPQNESNKIYVVDLSNERAMSLTIEPRPVKQSRKTFVPGCF
VCLESRTCSSNLTLTSGSKHKISFLCDDLTRLWMNVKTIISCTDHRYCQRKSYSLQVPSDILHLFVELHDFSWKL
LVPKDRLSLVLPAAQLQQHTHEKPCNTSFSYLVASAIPSQDLYFGSFCPGGSIKQIQVKQNISVTLRTEFAPSFR
QEASRQGLTVSFIPYFKEEGVFTVTPDTKSKVYLRTPNWDRGLPSLTSVSWNISVPRDQVACLTFFKERSGVVCQ
TGRAFMIIQEQRTRAEIIFSLDEDVLPKPSFHHHSFWVNIISNCSPSTSGKQLDLLFSVTLTPRTVDLTVILIAAVG
GGVLLLSALGLIICCVKKKKKTKNGPAVGIIYNGNINTEMPRQPKKFQKGRKDNDSHVYAVIEDTMVYGHLQDS
SGSFLQPEVDTYRPFQGTMGVCPSPPTICSRAPTAKLATEEPPPSPPPESESEPYTFSHPNNGDVSSKDTDIPL
LSTQEPMEPAE

Mass Match Peptides (bold):

ASVSFLNFNLSNCER [87]
MALHLFWFHR [508]

Tandem Peptides (underline):

VEYYIPGSTTNPEVFK [757]

Peptide Source: 1D-GE, Hepatocellular carcinoma

MAGLNCGVSIALLGVLLGAARLPRGAFAFEIALPRESNITVLIKLGTPPTLLAKPCYIVISKRHITMLSIKSGER
IVFTFSCQSPENHFVIEIQKNIDCMMSGPCPFGEVQLQPSTSLPTLNRTFIWDVKAHKSIGLELQFSIPRLR**QIG**
PGESCPDGVTHSISGRIDATVVRI GTFCSNGTVSRIKMQEGVK**MALHLPWFHPRNVSGFSIANR**SSIKRLCIIES
VFEGEGSATLMSANYPEGFPEDELMTWQFVVPAAHLR**ASVSFLNFNLSNCER**KEERVEYYYIPGSTTNPEVFKLEDK
QPGNMAGNFNLSLQGCDDAQSPGILRLQFQVLVQHPPONESNK**IYVVDLSNER**AMSLTIEPRPVKQSRKFVPGCF
VCLESR**TCSSNLTLTSGSK**HKISFLCDDLTRL**LWMNVEK**TISCTDHRYCQRKSYSLQVPSDILHLPVELHDFSWKL
LVPKDRLSLVLVPAQKLQOHTHEKPCNTSFSYLVASAIQSDLYFGSFCPGGSIKQIQVKQNI SVTLRTFAPSFR
QEASRQGLTVSFIPYFK**EEGVFTVTPDTK**SKVYLRTPNWDRGLPSLTSVSWNISVPRDQVACLTFKKERSGVVCQ
TGR**AFMIIQEQR**TRAEEIFSLDEDVLPKPSFHHHSFWVNISNCSPTSGKQLDLLFSVTLTPTVDTLVILIAAVG
GGVLLLSALGLIICCVKKKKKTNKGPAVG IYNGNINTEMPRQPKKFQKGRKDNDSHVYAVIEDTMVYGHLQDS
SGSFLQPEVD TYRPFQGTMGVCPSPPTICSRAPTAK**LATEEPPPR**SPPPESESEPYTF SHPNNGDVSSKDTDIPL
LSTQEPMEPAE

Mass Match Peptides (bold):

AFMIIQEQR [66]
ASVSFLNFNLSNCER [87]
EEGVFTVTPDTK [172]
IYVVDLSNER [404]
LATEEPPPR [444]
LWMNVEK [505]
MALHLPWFHPR [508]
NVSGFSIANR [561]
QIGPGESCPDGVTHSISGR [580]
TCSSNLTLTSGSK [679]

Tandem Peptides (underline):

LATEEPPPR [444]

Peptide Source: 1D-GE, Melanoma

MAGLNCGVSIALLGVLLGAARLPRGAFAFEIALPRESNITVLIKLGTPPTLLAKPCYIVISKRHITMLSIKSGER
IVFTFSCQSPENHFVIEIQKNIDCMMSGPCPFGEVQLQPSTSLPTLNRTFIWDVKAHKSIGLELQFSIPRLR**QIG**
PGESCPDGVTHSISGRIDATVVRI GTFCSNGTVSRIKMQEGVK**MALHLPWFHPR**NVSGFSIANRSSIKRLCIIES
VFEGEGSATLMSANYPEGFPEDELMTWQFVVPAAHLR**ASVSFLNFNLSNCER**KEERVEYYYIPGSTTNPEVFKLEDK
QPGNMAGNFNLSLQGCDDAQSPGILRLQFQVLVQHPPONESNK**IYVVDLSNER**AMSLTIEPRPVKQSR**KFVPGCF**
VCLESRTCSSNLTLTSGSKHKISFLCDDLTRL**LWMNVEK**TISCTDHRYCQRKSYSLQVPSDILHLPVELHDFSWKL
LVPKDRLSLVLVPAQKLQOHTHEKPCNTSFSYLVASAIQSDLYFGSFCPGGSIKQIQVKQNI SVTLRTFAPSFR
QEASRQGLTVSFIPYFK**EEGVFTVTPDTK**SKVYLRTPNWDRGLPSLTSVSWNISVPRDQVACLTFKKERSGVVCQ
TGR**AFMIIQEQR**TRAEEIFSLDEDVLPKPSFHHHSFWVNISNCSPTSGKQLDLLFSVTLTPTVDTLVILIAAVG
GGVLLLSALGLIICCVKKKKKTNKGPAVG IYNGNINTEMPRQPKKFQKGRKDNDSHVYAVIEDTMVYGHLQDS
SGSFLQPEVD TYRPFQGTMGVCPSPPTICSRAPTAK**LATEEPPPR**SPPPESESEPYTF SHPNNGDVSSKDTDIPL
LSTQEPMEPAE

Mass Match Peptides (bold):

AFMIIQEQR [66]
ASVSFLNFNLSNCER [87]
DQVACLTFEK [153]
IYVVDLSNER [404]
KFVPGCFVCLESR [415]
LATEEPPPR [444]
MALHLPWFHPR [508]

Tandem Peptides (underline):

IYVVDLSNER [404]
LATEEPPPR [444]

Peptide Source: 1D-GE, Pancreatic cancer

MAGLNCGVSIALLGVLLGAARLPRGAFAFEIALPRESNITVLIKLGTPILLAKPCYIVISKRHITMLSIKSGER
IVFTFSCQSPENHFVIEIQKNIDCMGSPCFGEVQLQPSTSLPLNRTFIWDVKAHKSIGLELQFSIFRLRQIG
PGESCPDGVTHSISGRIDATVVRIGTFCSNGTVSRIKMQEGVKMALHLPWFHPRNVSGFSIANRSSIKRLCIES
VFEGEGSATILMSANYPEGFPEDELMTWQFVVPALHRSVSFLNFNLSNCERKEERVEYYIPGSTTNPEVFKLEDK
QPGNMAGNFNLSLQGCDDAQSPGILRLQFQVLVQHQPONESNKIYVVDLSNERAMSLTIEPRPVKQSRKFVPGCF
VCLESRTCSSNLTSLTSGSKHKISFLCDDLTRLWMNVEKTICTDHRYCQRKSYSLQVPSDILHLPVELHDFSWKL
LVPKDRLSLVLVPAQKLQOHTHEKPCNTSFSYLVASAIQSDLYFGSFCPGGSIKQIQVKQNISVTLRTFAPSFR
QEASRQGLTVSFIPYFKEEGVFTVTPDTKSKVYLRTPNWDRGLPSLTSVSWNISVPRDQVACLTFKKERSGVVCQ
TGRAFMIIQEQRTRAEIIFSLDEDVLPKPSFHHSFWVNISNCSPTSGKQLDLLFSVTLTPRTVDLTVILIAAVG
GGVLLLSALGLIICCVKKKKKTKNGPAVGIYNGNINTEMPRQPKKFQKGRKDNDSHVYAVIEDTMVYGHLLQDS
SGSFLQPEVDTYRPFQGTMGVCPSPPTICSRAPTAKLATEEPPRSPPESESEPYTFSHPNNGDVSSKDTDIPL
LSTQEPMEPAE

Mass Match Peptides (bold):

QGLTVSFIPYFK [576]
QIGPGESCPDGVTHSISGR [580]
QPGNMAGNFNLSLQGCDDAQSPGILR [583]
VEYYIPGSTTNPEVFK [757]

Tandem Peptides (underline):

QGLTVSFIPYFK [576]

Peptide Source: 1D-GE, Prostate cancer

MAGLNCGVSIALLGVLLGAARLPRGAFAFEIALPRESNITVLIKLGTPILLAKPCYIVISKRHITMLSIKSGER
IVFTFSCQSPENHFVIEIQKNIDCMGSPCFGEVQLQPSTSLPLNRTFIWDVKAHKSIGLELQFSIFRLRQIG
PGESCPDGVTHSISGRIDATVVRIGTFCSNGTVSRIKMQEGVKMALHLPWFHPRNVSGFSIANRSSIKRLCIES
VFEGEGSATILMSANYPEGFPEDELMTWQFVVPALHRSVSFLNFNLSNCERKEERVEYYIPGSTTNPEVFKLEDK
QPGNMAGNFNLSLQGCDDAQSPGILRLQFQVLVQHQPONESNKIYVVDLSNERAMSLTIEPRPVKQSRKFVPGCF
VCLESRTCSSNLTSLTSGSKHKISFLCDDLTRLWMNVEKTICTDHRYCQRKSYSLQVPSDILHLPVELHDFSWKL
LVPKDRLSLVLVPAQKLQOHTHEKPCNTSFSYLVASAIQSDLYFGSFCPGGSIKQIQVKQNISVTLRTFAPSFR
QEASRQGLTVSFIPYFKEEGVFTVTPDTKSKVYLRTPNWDRGLPSLTSVSWNISVPRDQVACLTFKKERSGVVCQ
TGRAFMIIQEQRTRAEIIFSLDEDVLPKPSFHHSFWVNISNCSPTSGKQLDLLFSVTLTPRTVDLTVILIAAVG
GGVLLLSALGLIICCVKKKKKTKNGPAVGIYNGNINTEMPRQPKKFQKGRKDNDSHVYAVIEDTMVYGHLLQDS
SGSFLQPEVDTYRPFQGTMGVCPSPPTICSRAPTAKLATEEPPRSPPESESEPYTFSHPNNGDVSSKDTDIPL
LSTQEPMEPAE

Mass Match Peptides (bold):

AFMIIQEQR [66]
EEGVFTVTPDTK [172]
IDATVVR [353]
IYVVDLSNER [404]
LATEEPPR [444]
LWMNVEK [505]
TENWDR [719]
VEYYIPGSTTNPEVFK [757]

Tandem Peptides (underline):

AFMIIQEQR [66]
IYVVDLSNER [404]

Peptide Source: 1D-GE, Renal cell cancer

MAGLNCGVSIALLGVLLGAARLPRGAFAFEIALPRESNITVLIKLGTPILLAKPCYIVISKRHITMLSIKSGER
IVFTFSCQSPENHFVIEIQKNIDCMGSPCFGEVQLQPSTSLPLNRTFIWDVKAHKSIGLELQFSIFRLRQIG
PGESCPDGVTHSISGRIDATVVRIGTFCSNGTVSRIKMQEGVKMALHLPWFHPRNVSGFSIANRSSIKRLCIES

VFEGEGSATLMSANYPEGFPPEDELMTWQFVVPAPHLRASVSFLNFNLSNCERKEERVEYYIPGSTTNPEVFKLEDK
QPGNMAGNFNLSLQGCDDAQSPGILRLQFQVLVQHPQNESNKIYVVDLSNERAMSLTIEPRPVKQSR**KFVPGCF**
VCLSRTCSSNLTLTSGSKHKISFLCDDLTRLWMNVEKTISCTDHYRCQRKSYSLQVPSDILHLPVELHDFSWKL
LVLPKDR**LSLVPAQK**LQQTHEKPCNTSFSYLVASAI PSQDLYFGSFCPGGSIKQIQVKQNISVTTLRTFAPSFR
QEASRQGLTVSFIPYFKEEGVFTVTPDTKSKVYL RTPNWDRGLPSLTSVSWNISVPRDQVACLTFKKER**SGVVCQ**
TGRAFMIIQEQRTRAEIIFSLDEDVLPKPSFHHHSFVWNISNCSPSTSGKQLDLLFSVTLTPTVDTLVILIAAVG
GGVLLLSALGLIICCVKKKKKTKNGPAVGIYNGNINTEMPROPKKFKGRKDNDSHVYAVIEDTMVYGHLLQDS
SGSFLQPEVDITYRPFQGTMGVCPSPPTICSRAPTAKLATEEPPPSPPPESESEPYTFSHPNNGDVSSKDTDIPL
LSTQEPMEPAE

Mass Match Peptides (bold):

KFVPGCFVCLSR [415]

SGVVCQTGR [633]

Tandem Peptides (underline):

LSLVLPVPAQK [487]

Peptide Source: iTRAQ, Non-small cell lung cancer

MAGLNCGVSIALLGVLLGAARLPRGAEEFIALPRESNITVLIKLGTPTLAKPCYIVISKRHITMLSIKSGER
IVFTFSCQSPENHFVIEIQKNIDCMSPGCPFGEVQLQPSTSLPLTLNRTFIWDVKAHKSIGLELQFSIPRLRQIG
PGESCPDGWTHSISGRIDATVVR**IGTFCSNGTVSRIK**MQEGVKMALHLPWFHPRNVSGFSIANRSSIKRLCIIES
VFEGEGSATLMSANYPEGFPPEDELMTWQFVVPAPHLRASVSFLNFNLSNCERKEERVEYYIPGSTTNPEVFKLEDK
QPGNMAGNFNLSLQGCDDAQSPGILRLQFQVLVQHPQNESNKIYVVDLSNERAMSLTIEPRPVKQSRKFVPGCF
VCLSR**TCSSNLTLTSGSKHKISFLCDDLTRL****LWMNVEK**TISCTDHYRCQRKSYSLQVPSDILHLPVELHDFSWKL
LVPKDRLSLVLPVPAQKLQQTHEKPCNTSFSYLVASAI PSQDLYFGSFCPGGSIKQIQVKQNISVTTLRTFAPSFR
QEASRQGLTVSFIPYFKEEGVFTVTPDTKSKVYL RTPNWDRGLPSLTSVSWNISVPRDQVACLTFKKERSGVVCQ
TGRAFMIIQEQRTRAEIIFSLDEDVLPKPSFHHHSFVWNISNCSPSTSGKQLDLLFSVTLTPTVDTLVILIAAVG
GGVLLLSALGLIICCVKKKKKTKNGPAVGIYNGNINTEMPROPKKFKGRKDNDSHVYAVIEDTMVYGHLLQDS
SGSFLQPEVDITYRPFQGTMGVCPSPPTICSRAPTAKLATEEPPPSPPPESESEPYTFSHPNNGDVSSKDTDIPL
LSTQEPMEPAE

Mass Match Peptides (bold):

IGTFCSNGTVSRIK [1007]

LLVPKDR [940]

LWMNVEK [505]

Tandem Peptides (underline):

IGTFCSNGTVSRIK [1007]

LLVPKDR [940]

LWMNVEK [505]

OGTA156 (SEQ ID No: 27)**Peptide Source: 1D-GE, Acute T-cell leukaemia**

MFPTESAWLGKRGANPGPEAAVRETVMLLCLGVPTGRPYNVDTESALLYQGPHNTLFGYSVVLHSHGANRWLLV
GAPTANWLANASVINPGAIYRCRIGKNPGQTCEQLQLGSPNGEPCGKTCLEER**DNQWLGVTL**SRQPGENGSIIVTC
GHRWKNIFYIKNENK**LPTGGCGYVPPDLR**TELSKRIAPCYQDYVKKFGENFASCQAGISSFYTKDLIVMGAPGSS
YWTGSLFVYINITTNKYKAFLDKQNVKFGSYLGYSVGAGHFR**SOHTTEVVGGAPQHEQIGKAYIFSIDEK**ELNLL
HEMKGKKLGSYFGASCAVDLNADGFSDLLVGAPMQSTIREEGRVFVYINSMSGAVMNAMEINLVGSDKYAARFG
ESIVNLGDDNDGFEDVAIGAPQEDDLQGAIIYNGR**ADGISSTFSQR**IEGLQISKSLSMFGQSSISGQIDADNNG
YVDVAVGAFRSDSAVLLRTRPVVIVDASLSHPESVNRKFDCEVNGWPSVCIDLTLCSYKGEVPGYIVLFYNM
SLDVNRKAESPFRFYSSNGTSDVITGSIQVSSREANCR**THQAFMR**KDVRDILTPIQIEAAYHLGPHVISKRSTE
EFPLQPILOQKKEKDIMKK**TINFAR**CAHENCADLQVSAKIGFLKPHENKTYLAVGSMKTLMLNVSLFNAGDD
AYETTLHVKLPGVLYFIKILELEEKQINCEVTDNSGGVQLDCSIGYIYVDHLSRIDISFLLDVSSLSRAEEDLSI
TVHATCENEEMDNLKHRSR**VTVATPLK**YEVKLTVHGTVNPTSFVYGSNDENE PETCMVEKMNLTFHVINTGNSMA
PNVSVEIMVPNSFSPQTDKLFNILDVQTTTGECHFENYQRVCALEQQKSAMQTLKGIVRFLSKTDKRLLYCIKAD

PHCLNFLCNFGKMEASVHIQLEGRPSILEMDETSALKFEIRATGFPEPNPRVIELNKDENVAHVLEGLHH
QRPKRYFTIIVISSLILLGLIVLLISYVMWKAGFFKQYKSILQEENRRDSWSYINSKSNDD

Mass Match Peptides (bold):

ADGISSTFSQR [61]
ATGFPEPNPR [90]
AYIFSIDEK [99]
DNQWLGVTLR [147]
LPTGGCYGVPPDLR [482]
SILQEENR [637]
SQHTTEVVGAPQHEQIGK [648]
THQAFMR [697]
TINFAR [701]
VIVAIPLK [807]

Tandem Peptides (underline):

ADGISSTFSQR [61]
ATGFPEPNPR [90]
AYIFSIDEK [99]
LPTGGCYGVPPDLR [482]
SILQEENR [637]

Peptide Source: 1D-GE, B-cell non-Hodgkin's lymphoma

MFPTESAWLGKRGANPGPEAAVRETVMLLLCIGVPTGRPYNVDTESALLYQGPHNTLFGYSVVLHSHGANRWLLV
GAPTANWLANASVINPGAIRYCRIGKNPGQTCEQLQLGSPNGEPCGKTCLERDNQWLGVTLRQPGENGSIIVTC
GHRWKNIIFYIKNENKLPTGGCYGVPPDLRTELRSKRITAPCYQDYVKKFGENFASCQAGISSFYTKDLIVMGAPGSS
YWTGSLFVYNITTNKYKAFLDKQNVKFGSYLGYSVGAGHFRSQHTTEVVGAPQHEQIGKAYIFSIDEKELNIL
HEMKGKGLGSYFGASVCAVDLNADGFSDDLVGAPMQSTIREGRVVFVYINSGSGAVMNAMEINLVGSDKYAAREFG
ESIVNLGDDIDNDGFEDVAIGAPQEDDLQGAIIYNGRAADGISSTFSQRIEGLQISKSLSMFQGISQIDADNNG
YVDVAVGAFRSDSAVLLRTRPVVIVDASLSHPESVNRIKFDCVENGWPSVCIDLTLCSYKGEVPCYIVLFYNM
SLDVNRKAESPFRFYFSSNGTSDVITGSIQVSSREANCRTHQAFMRKDVRDILTPIQIEAAYHLGPHVISKRSITE
EEFPLQPILOQKKEKDIMKKTINFARFCAHENCADLQVSAKIGFLKPHENKTYLAVGSMKTMLNVSILFNAGDD
AYETTLHVKLPLVGLYFIKILELEEKQINCEVTDNSGVVQLDCSIGYIYVDHLSRIDISFLLDVSSLSRAEEDLSI
TVHATCENEEEMDNLKHRSRTVAIPLKYEVLTVHGFVNPTSFVYGSNDENEPETCMVEKMNLTFHVINTGNSMA
PNVSVEIMVPSNFSPTDKLFNILDVQTTTGECHFENYQRVCALEQQKSAMQTLKGIVRFLSKTDKRLLYCIKAD
PHCLNFLCNFGKMEASVHIQLEGRPSILEMDETSALKFEIRATGFPEPNPRVIELNKDENVAHVLEGLHH
QRPKRYFTIIVISSLILLGLIVLLISYVMWKAGFFKQYKSILQEENRRDSWSYINSKSNDD

Mass Match Peptides (bold):

ADGISSTFSQR [61]
ATGFPEPNPR [90]
AYIFSIDEK [99]
DNQWLGVTLR [147]
IAPCYQDYVK [351]
KAESPFR [407]
NIFYIK [540]
SDSAVLLR [624]
SILQEENR [637]
SQHTTEVVGAPQHEQIGK [648]
TCLEER [678]
THQAFMRK [698]
TINFAR [701]
TYLAVGSMK [740]

Tandem Peptides (underline):

EASVHIQLEGRPSILEMDETSALK [167]
LPVGLYFIK [484]
STEEFPLQPILOQK [654]

Peptide Source: 1D-GE, Chronic lymphocytic leukaemia

MFPTESAWLGKRGANPGPEAAVRETVMALLCLGVPTGRPYNVDTESALLYQGPHNTLFGYSVVLHSHGANRWLLV
CAPTANWLANASVINPGAIYRCRIGKNPGQTCEQLQLGSPNGEPCGKTCLEERDNQWLGVTLRSRQPGENGSIIVTC
GHRWKNIFYIKNENKLP TGCCYGVPPDLRTEL SKRIAPCYQDYVKKFGENFASCQAGISSFYTKDLIVMGAPGSS
YWTGSLFVYNIITNKYKAFLDKQNVKFGSYLGYSVGAGHFRSQHTTEVVGGAPQHEQIGKAYIFSIDEKELNII
HEMKGKKLGSYFGASVCAVDLNADGFSDDL VGAPMQSTIREEGRVVFYINSGSGAVMNAMETNLVGS DKYAAARFG
ESIVNLGDI DNDGFEDVAIGAPQEDDLQGAIIYNGRADGISSTFSQRIEGLQISKSLSMFGQSSISGQIDADNNG
YVDVAVGAFRSDSAVLLRTRPVVIVDASLSHPESVNR TKFDCVENGWPSVCIDLTLCF SYKGKEVPGYIVLFYNM
SLDVNRKAESP RRYFSSNGTSDVITGSIQVSSREANCRT HQAFMRKDVRDILTPIQIEAAYHLGPHVISKRS TE
EFPFLQPI LQKKKEKDIMKKTINFARFCAHENC SADLQVSAKIGFLKPHENKTYLAVGSMKTLMLNVSLFNAGDD
AYETTLHVKL PVLGYFIKILELEEKQINCEVTDNSGVVQLDCSIGYIYVDHLSRIDISFLLDVSSLSRAEEDLSI
TVHATCENE EEMDNLKH SRVTVAIPLKYEVKLT VHGFVNPTSFVYGSNDENE PETCMVEKMNLTFHVINTGNSMA
PNVSVEIMVNSFS PQTDKLFNILDVQTTTGECHFENYQ RVCAL EQQKSAMQTLKGIVRFLSKTDKRLLYCIKAD
PHCLNFLCNFGKME SGKEASVHIQLEGRPS ILEMDETSALKFEIRATGFPEPNRVI ELNKDENVAHVLLGLEGLHH
QRPKRYFTI VIIS SLLLGLIVLLLISYVMWKAGFFKRQYKSILQEENRRDSWSYINSKSNDD

Mass Match Peptides (bold):

DNQWLGVTLRSR [147]
ELNIIHEMK [205]
EVPGYIVLFYNM SLDVNR [235]
ILELEEK [376]
SQHTTEVVGGAPQHEQIGK [648]

Tandem Peptides (underline):

ELNIIHEMK [205]
STEEFPLQPI LQKK [654]

Peptide Source: 1D-GE, Hepatocellular carcinoma

MFPTESAWLGKRGANPGPEAAVRETVMALLCLGVPTGRPYNVDTESALLYQGPHNTLFGYSVVLHSHGANRWLLV
CAPTANWLANASVINPGAIYRCRIGKNPGQTCEQLQLGSPNGEPCGKTCLEERDNQWLGVTLRSRQPGENGSIIVTC
GHRWKNIFYIKNENKLP TGCCYGVPPDLRTEL SKRIAPCYQDYVKKFGENFASCQAGISSFYTKDLIVMGAPGSS
YWTGSLFVYNIITNKYKAFLDKQNVKFGSYLGYSVGAGHFRSQHTTEVVGGAPQHEQIGKAYIFSIDEKELNII
HEMKGKKLGSYFGASVCAVDLNADGFSDDL VGAPMQSTIREEGRVVFYINSGSGAVMNAMETNLVGS DKYAAARFG
ESIVNLGDI DNDGFEDVAIGAPQEDDLQGAIIYNGRADGISSTFSQRIEGLQISKSLSMFGQSSISGQIDADNNG
YVDVAVGAFRSDSAVLLRTRPVVIVDASLSHPESVNR TKFDCVENGWPSVCIDLTLCF SYKGKEVPGYIVLFYNM
SLDVNRKAESP RRYFSSNGTSDVITGSIQVSSREANCRT HQAFMRKDVRDILTPIQIEAAYHLGPHVISKRS TE
EFPFLQPI LQKKKEKDIMKKTINFARFCAHENC SADLQVSAKIGFLKPHENKTYLAVGSMKTLMLNVSLFNAGDD
AYETTLHVKL PVLGYFIKILELEEKQINCEVTDNSGVVQLDCSIGYIYVDHLSRIDISFLLDVSSLSRAEEDLSI
TVHATCENE EEMDNLKH SRVTVAIPLKYEVKLT VHGFVNPTSFVYGSNDENE PETCMVEKMNLTFHVINTGNSMA
PNVSVEIMVNSFS PQTDKLFNILDVQTTTGECHFENYQ RVCAL EQQKSAMQTLKGIVRFLSKTDKRLLYCIKAD
PHCLNFLCNFGKME SGKEASVHIQLEGRPS ILEMDETSALKFEIRATGFPEPNRVI ELNKDENVAHVLLGLEGLHH
QRPKRYFTI VIIS SLLLGLIVLLLISYVMWKAGFFKRQYKSILQEENRRDSWSYINSKSNDD

Mass Match Peptides (bold):

VIELNK [768]

Tandem Peptides (underline):

IEGLQISK [361]

Peptide Source: iTRAQ, Colorectal cancer

MFPTESAWLGKRGANPGPEAAVRETVMALLCLGVPTGRPYNVDTESALLYQGPHNTLFGYSVVLHSHGANRWLLV
CAPTANWLANASVINPGAIYRCRIGKNPGQTCEQLQLGSPNGEPCGKTCLEERDNQWLGVTLRSRQPGENGSIIVTC
GHRWKNIFYIKNENKLP TGCCYGVPPDLRTEL SKRIAPCYQDYVKKFGENFASCQAGISSFYTKDLIVMGAPGSS
YWTGSLFVYNIITNKYKAFLDKQNVKFGSYLGYSVGAGHFRSQHTTEVVGGAPQHEQIGKAYIFSIDEKELNII

HEMKGKKLGSYFGASVCAVDLNADGFSDDLVGAPMQSTIREEGRVVFVYINSGSGAVMNAMEINLVGSDKYAARFG
 ESIVNLGDIIDNDGFEDVAIGAPQEDDLQGAIIYINCRADGISSTFSQRIEGLQISKSLSMFGQSSISGQIDADNNG
 YVDVAVGAFRSDSAVLLRTRPVVIVDASLSHPESVNRKTKFDCVENGWPSVCIDLTLCSFYKGEVPGYIVLFYNM
 SLDVNRKAESPFRFYSSNGTSDVITGSIQVSSREANCRTHQAFMRKDVRDILTPIQIEAAYHLGPHVISKRSTE
 EFPPLQPILOQKKEK**DIMKKTINFAR**FCAHENC SADLQVSAKIGFLKPHENKTYLAVGSMKTLMLNVSLFNAGDD
 AYETTLHVKLPVGLYFIKILELEEKQINCEVTDNSGVVQLDCSIGYIYVDHLSRIDISFLLDVSSLSRAEEDLSI
 TVHATCENEEEMDNLKHSRVTVAIPLKYEVKLTVHG FVNPTSFVYGSNDENE PETCMVEKMNLTFHVINTGNSMA
 PNVSV EIMVPNSFSPQTDKLFNILDVQTTTGECHFENYQRVCALEQQKSAMQTLKGIVRFLSKTDKRLLYCIKAD
 PHCLNFCNFGKMEGKEASVHIQLEGRPSILEMDETSALKFEIRATGFPEPNPRVIELNKDENVAHVILLEGLHH
 QRPKRYFTIVIISSSLLGLIVLLLSYVMWKAGFFKRQYKSILQEENRRDSWSYINSKSNDD

Mass Match Peptides (bold):

DIMKKTINFAR [891]

Tandem Peptides (underline):

DIMKKTINFAR [891]

Peptide Source: iTRAQ, Non-small cell lung cancer

MFPTESAWLGKRGANPGPEAAVRETVMLLLC LGVPTGRPYNVDTESALLYQGPHNTLFGYSVVLHSHGANRWLLV
 GAPTANWLANASVINPGAIIYRCRIGKNPGQTCEQLQLGSPNGEPCGKTCLEERDNQWLGVTL SRQPGENGSI VTC
 GHRWKNIFYIKNENKLPTGGCYGVPPDLRTELSKRIAPCYQDYVKKFGENFASCQAGISSFYTKDLIVMGAPGSS
 YWTGSLFVYNITTNKYKAFLDKQNVKFGSYLGYSVGAGHFRSQHTTEVVGGAPQHEQIGKAYIFSIDEKELNIL
 HEMKGKKLGSYFGASVCAVDLNADGFSDDLVGAPMQSTIREEGRVVFVYINSGSGAVMNAMEINLVGSDKYAARFG
 ESIVNLGDIIDNDGFEDVAIGAPQEDDLQGAIIYINCRADGISSTFSQRIEGLQISKSLSMFGQSSISGQIDADNNG
 YVDVAVGAFRSDSAVLLRTRPVVIVDASLSHPESVNRKTKFDCVENGWPSVCIDLTLCSFYKGEVPGYIVLFYNM
 SLDVNRKAESPFRFYSSNGTSDVITGSIQVSSREANCRTHQAFMRKDVRDILTPIQIEAAYHLGPHVISKRSTE
 EFPPLQPILOQKKEK**DIMKKTINFAR**FCAHENC SADLQVSAKIGFLKPHENK**TYLAVGSMK**TLMLNVSLFNAGDD
 AYETTLHVKLPVGLYFIKILELEEKQINCEVTDNSGVVQLDCSIGYIYVDHLSRIDISFLLDVSSLSRAEEDLSI
 TVHATCENEEEMDNLK**HSRVTVAIPLK**YEVKLTVHG FVNPTSFVYGSNDENE PETCMVEKMNLTFHVINTGNSMA
 PNVSV EIMVPNSFSPQTDKLFNILDVQTTTGECHFENYQRVCALEQQKSAMQTLKGIVRFLSKTDKRLLYCIKAD
 PHCLNFCNFGKMEGKEASVHIQLEGRPSILEMDETSALKFEIRATGFPEPNPRVIELNKDENVAHVILLEGLHH
 QRPKRYFTIVIISSSLLGLIVLLLSYVMWKAGFFKRQYKSILQEENRRDSWSYINSKSNDD

Mass Match Peptides (bold):

HSRVTVAIPLK [918]

TYLAVGSMK [740]

Tandem Peptides (underline):

HSRVTVAIPLK [918]

TYLAVGSMK [740]

Peptide Source: iTRAQ, Ovarian cancer

MFPTESAWLGKRGANPGPEAAVRETVMLLLC LGVPTGRPYNVDTESALLYQGPHNTLFGYSVVLHSHGANRWLLV
 GAPTANWLANASVINPGAIIYRCRIGKNPGQTCEQLQLGSPNGEPCGKTCLEERDNQWLGVTL SRQPGENGSI VTC
 GHRWKNIFYIKNENKLPTGGCYGVPPDLRTELSKRIAPCYQDYVKKFGENFASCQAGISSFYTKDLIVMGAPGSS
 YWTGSLFVYNITTNKYKAFLDKQNVKFGSYLGYSVGAGHFRSQHTTEVVGGAPQHEQIGKAYIFSIDEKELNIL
 HEMKGKKLGSYFGASVCAVDLNADGFSDDLVGAPMQSTIREEGRVVFVYINSGSGAVMNAMEINLVGSDKYAARFG
 ESIVNLGDIIDNDGFEDVAIGAPQEDDLQGAIIYINCRADGISSTFSQRIEGLQISKSLSMFGQSSISGQIDADNNG
 YVDVAVGAFRSDSAVLLRTRPVVIVDASLSHPESVNRKTKFDCVENGWPSVCIDLTLCSFYKGEVPGYIVLFYNM
 SLDVNRKAESPFRFYSSNGTSDVITGSIQVSSREANCRTHQAFMRKDVRDILTPIQIEAAYHLGPHVISKRSTE
 EFPPLQPILOQKKEK**DIMKKTINFAR**FCAHENC SADLQVSAKIGFLKPHENKTYLAVGSMKTLMLNVSLFNAGDD
 AYETTLHVKLPVGLYFIKILELEEKQINCEVTDNSGVVQLDCSIGYIYVDHLSRIDISFLLDVSSLSRAEEDLSI
 TVHATCENEEEMDNLKHSRVTVAIPLKYEVKLTVHG FVNPTSFVYGSNDENE PETCMVEKMNLTFHVINTGNSMA
 PNVSV EIMVPNSFSPQTDKLFNILDVQTTTGECHFENYQRVCALEQQKSAMQTLKGIVRFLSKTDKRLLYCIKAD
 PHCLNFCNFGKMEGKEASVHIQLEGRPSILEMDETSALKFEIRATGFPEPNPRVIELNKDENVAHVILLEGLHH
 QRPKRYFTIVIISSSLLGLIVLLLSYVMWKAGFFKRQYKSILQEENRRDSWSYINSKSNDD

Mass Match Peptides (bold):

DIMKKTINFAR [891]

Tandem Peptides (underline):

DIMKKTINFAR [891]

Peptide Source: iTRAQ, Renal cell cancer

MFPTESAWLGKRGANPGPEAAVRETVMLLLCLGVPTGRPYNVDTESALLYQGPHNTLFGYSVVLHSHGANRWLLV
GAPTANWLANASVINPGAIYRCRIGKNPGQTCEQLQLGSPNGEPCGKTCLEERDNQWLGVTLRQPGENGSIIVTC
GHRWKNIFYIKNENKLTGGCYGVPPDLRTELSKRIAPCYQDYVKKFGENFASCQAGISSFYTKDLIVMGAPGSS
YWTGSLFVYNITTNKYKAFLDKQNQVKFGSYLGYSVGAGHFRSQHTTEVVGGAPQHEQIGKAYIFSIDEKELNIL
HEMKGKKLGSYFGASVCAVDLADGFSDDLGVGAPMQSTIREEGRVVFYINSGSGAVMNAMETNLVGSDKYAARFG
ESTVNLGDDIDNDGFEDVAIGAPQEDDLQGAIIYNGRADGISSTFSQRIEGLQISKSLSMFGQSISGQIDADNNG
YVDVAVGAFRSDSAVLLRTRPVVIVDASLSHPESVNRTKFDCEVNGWPSVCIDLTLCFYSYKGEVPGYIVLFYNM
SLDVNRKAESPFRFYSSNGTSDVITGSIQVSSREANCRTHQAFMRKDVRDILTPIQIEAAYHLGPHVISKRSTE
EFPPLQPILOQKKEK**DIMKKTINFAR**FCAHENC SADLQVSAKIGFLKPHENKTYLAVGSMKTLMLNVSLFNAGDD
AYETTLHVKLPGVGLYFIKILELEEKQINCEVTDNSSGVQLDCSIGIYVDHLSRIDISFLLDVSSLSRAEEDLSI
TVHATCENEEMDNLKH**HSRVTVAIPLK**YEVKLTVHGFVNPTSEFVYGSNDENEPECTMVEKMNLTFHVINTGNSMA
PNVSVEIMVNSFSPQTDKLFNILDVQTTTGECHFENYQRVCALEQQKSAMQTLKGIVRFLSKTDKRLLYCIKAD
PHCLNFLCNFGKMEESGKEASVHTQLEGREPSILEMDETSALKFEIRATGFPEPNPRVIELNKDENVAEVLLEGLHH
QRPKRYFTTIVIISSSLLLGLIVLLLISYVMWKAGFFKRQYKSLQEEENRRDSWSYINSKSNDD

Mass Match Peptides (bold):

DIMKKTINFAR [891]

HSRVTVAIPLK [918]

Tandem Peptides (underline):

DIMKKTINFAR [891]

HSRVTVAIPLK [918]

OGTA159 (SEQ ID No: 28)

Peptide Source: 1D-GE, Breast cancer

MVAPVWYLVA AALLVGFTILFLTRSRGRAASAGQEPLHNEELAGAG**VAQPGPLEPEEPR**AGGRPRRRRDLGSRLQ
AQRRAQRVAWAEADENEEAVILAQEEEGVEKPAETHLSGKIGAKKLRKLEEKQARKAQREAEAEEREERKRLES
QREAEWKKEEERLRLEEEQKEEEERKAREEQAQREHEEYLLKKEAFVVEEEGVGETMTTEEQSQSFLTEFINYIKQ
SKVVLLEDLASQVGLRTQDTINRIQDLLAEGTITGVIDDRGKFIYITPEELAAVANFIRQGRVSI AELAQASNS
LIAWGR**ESPAQAPA**

Mass Match Peptides (bold):

ESPAQAPA [226]

VAQPGPLEPEEPR [745]

Tandem Peptides (underline):

VAQPGPLEPEEPR [745]

Peptide Source: 1D-GE, Chronic lymphocytic leukaemia

MVAPVWYLVA AALLVGFTILFLTRSRGRAASAGQEPLHNEELAGAG**VAQPGPLEPEEPR**AGGRPRRRRDLGSRLQ
AQRRAQRVAWAEADENEEAVILAQEEEGVEKPAETHLSGKIGAKKLRKLEEKQARKAQREAEAEEREERKRLES
QREAEWKKEEERLR**LEEEQK**EEERKAREEQAQREHEEYLLKKEAFVVEEEGVGETMTTEEQSQSFLTEFINYIKQ
SKVVLLEDLASQVGLRTQDTINRIQDLLAEGTITGVIDDRGKFIYITPEELAAVANFIRQGRVSI AELAQASNS
LIAWG**RESPAQAPA**

Mass Match Peptides (bold):

LEEEQK [450]

Tandem Peptides (underline):

Peptide Source: 1D-GE, Colorectal cancer

MVAPVWYLVA AALLVGFILFLTRSRGR**AASAGQEP**PLHNEELAGAGR**VAQPGPLEPEEPR**AGGRPRRRRDLGSRLQ
 AQRRAQRVAWAEADENEEEA VILAQEEEGVEKPAETHLSGKIGAKKLRKLEEKQARKAQREAEAEEREERKRLES
 QREAEWKKEERLRLEEEQKEEEERKARE**EEQAQR**EHEEYLKLKEAFVVEEEGVGETMTTEEQSQSFLTEFINYIKQ
 SKVVLLLEDLASQVGLRTQDTINRIQDLLAEGTITGVIDDRGKFIYITPEELAAVANFIRQGRVSI AELAQASNS
 LIAWGRESPAQAPA

Mass Match Peptides (bold):

AASAGQEPPLHNEELAGAGR [53]

EEQAQR [180]

VAQPGPLEPEEPR [745]

Tandem Peptides (underline):

VAQPGPLEPEEPR [745]

Peptide Source: 1D-GE, Hepatocellular carcinoma

MVAPVWYLVA AALLVGFILFLTRSRGRAASAGQEPPLHNEELAGAGR**VAQPGPLEPEEPR**AGGRPRRRRDLGSRLQ
 AQRRAQRVAWAEADENEEEA VILAQEEEGVEKPAETHLSGKIGAKKLRKLEEKQARKAQREAEAEEREERKRLES
 QREAEWKKEERLRLEEEQKEEEERKAREEQAQREHEEYLKLKEAFVVEEEGVGETMTTEEQSQSFLTEFINYIKQ
 SKVVLLLEDLASQVGLRTQDTINRIQDLLAEGTITGVIDDRGKFIYITPEELAAVANFIRQGRVSI AELAQASNS
 LIAWGRESPAQAPA

Mass Match Peptides (bold):

VAQPGPLEPEEPR [745]

Tandem Peptides (underline):

VAQPGPLEPEEPR [745]

Peptide Source: 1D-GE, Melanoma

MVAPVWYLVA AALLVGFILFLTRSRGRAASAGQEPPLHNEELAGAGRVAQPGPLEPEEPRAGGRPRRR**RDLGSR**LQ
 AQRRAQRVAWAEADENEEEA VILAQEEEGVEKPAETHLSGKIGAKKLRKLEEKQARKAQREAEAEEREERKRLES
 QREAEWKKEERLRLEEEQKEEEERKAREEQAQREHEEYLKLKEAFVVEEEGVGETMTTEEQSQSFLTEFINYIKQ
 SK**VVLLLEDLASQVGLR**TQDTINR**IQDLLAEGTITGVIDDR**GKFIYITPEELAAVANFIRQGRVSI AELAQASNS
 LIAWGRESPAQAPA

Mass Match Peptides (bold):

IQDLLAEGTITGVIDDR [387]

RDLGSR [598]

VVLLLEDLASQVGLR [811]

Tandem Peptides (underline):

VVLLLEDLASQVGLR [811]

Peptide Source: 1D-GE, Pancreatic cancer

MVAPVWYLVA AALLVGFILFLTRSRGR**AASAGQEP**PLHNEELAGAGR**VAQPGPLEPEEPR**AGGRPRRRRDLGSRLQ
 AQRRAQRVAWAEADENEEEA VILAQEEEGVEKPAETHLSGKIGAKKLRKLEEKQARKAQREAEAEEREERKRLES

QREAEWKKEERLRLEEEQKEEEERKAREEQAR**EHEEYLK**LKEAFVVEEGVGETMTEEQSQSFLTEFINYIKQ
SKVVLLEDLASQVGLRTQDTINRIQDLLAEGTITGVIDDRGKFIYITPEELAAVANFIRQGRVSI AELAQASNS
LIAWGRESPAQAPA

Mass Match Peptides (bold):

AASAGQEPLHNEELAGAGR [53]
EHEEYLK [193]
VAQPGPLEPEEPR [745]

Tandem Peptides (underline):

VAQPGPLEPEEPR [745]

Peptide Source: iTRAQ, Non-small cell lung cancer

MVAPVWYLVA AALLVGFILFLTRSRGRAASAGQEPLHNEELAGAGRVAQPGPLEPEEPRAGGRPRRR**RDLGSRLO**
AQRRAQRVAWAEADENEEFAVILAQEEEGVEKPAETHLSGKIGAKKLRLKEEKQARKAQREAEFAEREERKRLES
QREAEWKKEERLRLEEEQKEEEERKAREEQAREHEEYLKLEAFVVEEGVGETMTEEQSQSFLTEFINYIKQ
SKVVLLEDLASQVGLRTQDTINRIQDLLAEGTITGVIDDRGKFIYITPEELAAVANFIRQGRVSI AELAQASNS
LIAWGRESPAQAPA

Mass Match Peptides (bold):

RDLGSRLOAQR [965]

Tandem Peptides (underline):

RDLGSRLOAQR [965]

Peptide Source: iTRAQ, Renal cell cancer

MVAPVWYLVA AALLVGFILFLTRSRGRAASAGQEPLHNEELAGAGRVAQPGPLEPEEPRAGGRPRRR**RDLGSRLO**
AQRRAQRVAWAEADENEEFAVILAQEEEGVEKPAETHLSGKIGAKKLRLKEEKQARKAQREAEFAEREERKRLES
QREAEWKKEERLRLEEEQKEEEERKAREEQAREHEEYLKLEAFVVEEGVGETMTEEQSQSFLTEFINYIKQ
SKVVLLEDLASQVGLRTQDTINRIQDLLAEGTITGVIDDRGKFIYITPEELAAVANFIRQGRVSI AELAQASNS
LIAWGRESPAQAPA

Mass Match Peptides (bold):

RDLGSRLOAQR [965]

Tandem Peptides (underline):

RDLGSRLOAQR [965]

OGTA168 (SEQ ID No: 29)

Peptide Source: 1D-GE, Glioblastoma

MKDDFAEEEEVQSFYKRFQIQEGTQCTKCKNNWALKFSIILLYILCALLTITVAILGYKVVEKMDNVTGGMETS
RQTYDDKLTAVESDLK**KLGDQTGKKAISTNSELSTFR**SDILDLRQQLREITEKTSKNKDTLEK**LOASGDALVDRQ**
SQLKETLENNISFLITTVNKTLQAYNGYVTNLQQDTSVLQGNLQNMYSHNVVIMNLNNLNLTVQVQQR**NLITNLQR**
SVDDTQSQTQRIKNDFOQLQOVFLQAKKDQTDWLKEKVQSLQTLAANNSALAKANNDTLEDMNSQLNSFTGQMENT
TTISQANEQNLKDLQDLHKDAENRTAIFNQLEERFQLFETDIVNIISNISYTAHHLRTLSTNLNEVRTTCTDTL
TKHTDDLTSLNNTLANIRLDSVSLRMQQDLMRSL**LDTEVANLSVIMEEMK**LVDSKHGOLIKNFTILQGPFGPRGP
RGDR**GSGQPPPGPTGNK**GQKGEKGEPPGPAGERGPIGPAGPPGERGGKSGSKSGQPKGSR**GSPGKPGQGSSGD**
PGPPPGPGKEGLPGQGPFGQCLQGTVGEPCVPGPRGLPGLPGVPGMPGPKGPPGPPGPGSGAVVPLALQNEPTP
APEDNGCPSHHWKNFTDKCYYSVEKEIFEDAKLFCEDKSSHLVFINTREEQQWIKKQMVGR**ESHWIGLTDSEREN**
EWKWLDTGSPDYKNWKAGQPDNWHGHGPGEDCAGLIYAGQWDFQCEDVNNFICEKDRETVLSSAL

Mass Match Peptides (bold):

AISTNSELSTFR [74]
ESHWIGLTDSE [225]
GSPGKPGPQGSSGDPGPPGPPGK [317]
GSQGPPGPTGNK [319]
KLGDQGTGK [423]
LDTEVANLSVIMEEMK [448]
LGDQGTGKK [461]
NDFQNLQQVFLQAK [534]
NLITNLQR [543]

Tandem Peptides (underline):

AISTNSELSTFR [74]
LQASGDALVDR [485]
SVDDTSQAIQR [661]

Peptide Source: 1D-GE, Melanoma

MKDDFAEEEEVQSFYKRFQIEGTQCTCKNNWALKFSIILLYILCALLTITVAILGYKVVEKMDNVTGGMETS
RQTYDDKLTAVESDLKKLGDQGTGKKAISTNSELSTFRSDIILDLRQQLREITEKTSKNKDTLEKLQASGDALVDRQ
SQLKETLENNSEFLITTVNKTQLAYNGYVTNLQQDTSVLQGNLQNMYSNNVIMNLLNNLNTQVQQRNLTNLQR
SVDDTSQAIQR IKNDFQNLQQVFLQAKKDDTLKEKVSQSLQTLAANNALAKANNDDTLEDMSQLNSFTGQMENI
TTISQANEQNLKDLQDLHKDAENRTAIFKNQLEERFQLFETDIVNIIISNISTAHHLRLTSLNNEVVRTTCTDTL
TKHTDDLTSLNNTLANIRLDSVSLRMQQDLMSRLDTEVANLSVIMEEMKLVDSKHGQLIKNFTTILQGPPEGPRGP
RGDRGSQGPPGPTGNKGQKGEKGEPPGPPGAGERGPIGPAGPPGERGGKSGSKSGQGPKGSRGSPGKPGPQGSSGD
PGPPGPPGKEGLPGPQPPGPFQGLQGTVGEPGVPGRGLPLGVPVGMPPGKPPGPPGPSGAVVPLALQNEPTP
APEDNGCPPHWKNFTDKCYFVSVEKEIFEDAKLFCEDKSSHLVFINTREEQQWIKQMVGRESHWIGLTDSEREN
EWKWLDTSPDYKNWKAGQPDNWDGHHGPGEDCAGLIYAGQWDFQCEDVNNFICEKDRETVLSSAL

Mass Match Peptides (bold):

GEPPGPPGAGER [292]
SVDDTSQAIQR [661]

Tandem Peptides (underline):

LTAVESDLK [495]

OGTA169 (SEQ ID No: 30)**Peptide Source: 1D-GE, Breast cancer**

MTRTRAALLLFTALATSLGFNLDTEELTAFRVDSAGFGDSVVQYANSWVVVGAPQKITAANQTGGLYQCGYSTGA
CEPIGLQVPPEAVNMSLGLSLASTTSPSQLLACGPTVHHECGRNMVLTGLCFLLGPTQLTQRLPVSQRQECPRQEQ
DIVFLIDGSGSISRRNFATMMNFVRAVISQFQRPSTQFSLMQFSNKFQTHFTFEFFRRTSNPLSLLASVHQLQGF
TYTATAIQNVVHRLFHASYGARRDATKILIVITDGKKEGDSLDYKDVIPMADAAGIIRYAIGVGLAFQNRNSWKE
LNDIASKPSQEHIFKVEDFDALKDQNLKEKIFAIEGTETSSSSFELEMAQEGFSAVFTPDGPVLGAVGSFTW
SGGAFLYPPNMSPTFINMSQENVDMDRDSYLGYSTELALWKGVSQSLVLGAPRYQHTGKAVIFTQVSRQWRMKA EVT
GTQIGSYFGASLCSVDVDTDGSTDLVLIGAPHYYEQTRGGQVSVCPLPRGWRWWCDVLYGEQGHWPGRFGAAL
TVLGDVNGDKLTDVVIGAPGEEENRGAVYLFHGVLGPSISPSHSQRIAGSQLSSRLQYFGQALSGGQDLTQDGLV
DLAVGARGQVLLLRTRPVLWVGVSMMQFIPAEIPRSAFEQVSEQTLVQSNICLYIDKRSKNLLGSRDLQSSV
TLDLALDPGRLSPRATFQETKNRSLSRVRVLGLKAHCENFNLLLPSCVEDSVTPITLRLNFTLVCKPLLAFRNLR
PMLAADAQRYFTASLPFEKNCGADHICQDNLGISFSFPGLKSLLVGSNLELNAEVMVWNGEDSYGTTITTFSHA
GLSYRYVAEGQKQGLRSLHLTCDAPVGSQGTWSTSCRINHIFRGGQITFLATFDVSPKAVLGDRLLLTANV
SSENNTPRTSKTTFQLELPVKYAVYTVVSSHEQFTKYLNFSESEKESHVAMHRYQVNNLGQRDLPSINFWVPV
ELNQEAVMMDVEVSHPPQNPSLRCSSEKIAPPASDFLAHIQKNPVLDCSIAGCLRFRCDVPSFSVQEELDFTLKGN
LSFGWVRQILQKKVSVVSAEITFDTSVYSQLPGQEAFMRAQTTTVLEKYKVHNPTPLIVGSSIGGLLLALLALITA
VLYKVGFFKRYKEMMEEANGQIAPENGQTTPSPSEK

Mass Match Peptides (bold):

FGAALTVLGDVNGDK [252]

Tandem Peptides (underline):

Peptide Source: 1D-GE, Chronic lymphocytic leukaemia

MTRTRAALLFTALATSLGFNLDTEELTAFRVDSAGFGDSVVQYANSWVVVGAPOKITAANQTGGLYQCGYSTGA
CEPIGLQVPPPEAVNMSLGLSLASTTSPSQLLACGPTVHHECGRNMYLTGLCFLLGPTQLTQRLPVSRQECPRQEQ
DIVFLIDSGSGSISSRNFMNFVRAVISQFORPSTQFSLMQFSNKFQTHFTFEEFRTSNPLSLLASVHQLQGF
TYTATAIQNVVHRLFHASYGARRDATKILIVITDGKKEGDSL~~YK~~DVIPMADAAGIIRYAIGVGLAFQNRNSWKE
LNDIASKPSQEHIKVEDFDALKDIQNQLKEKIFAIEGTETSSSSFELEMAQEGFSAVFTPDGPVLGAVGSFTW
SGGAFLYPPNMSPTFINMSQENVDMRDSYLG~~Y~~STELALWKGVS~~LV~~L~~G~~APRYQHTGKAVIF~~TQ~~VS~~R~~QWRMKA EVT
GTQIGSYFGASLCSVDVDTDCSTDVLIGAPHYYEQTRGGQVSVCPLPRGWRWWCDVLYGEQCHPWGRFGAAL
TVLGDVNGDKLTDVVIGAPGEEENRGAVYLFHGVLGPSISPSHSQRIAGSQLSSRLQYFGQALSGGQDLTQDGLV
DLAVGARGVLLLRTRPVLWVGVSQFIPAEIPSAFECREQVVEQTLVQSNICLYIDKRSKNLLGSRDLQSSV
TLDLALDPGRLSPRATFOETKNRSLSRVRVLGLKAHCENFNLLPSCVEDSVTPITLRLNFTLVGKPLLAFRNLR
PMLAADAQR~~Y~~FTASLPFEKNCGADHICQDNLGISFSFPGKSLLVGSNLELNAEVMVWNDGEDSYGTTITFSHPA
GLSYRYVAEGQKQGLRSLHLTCD~~S~~APVGSQGTWSTSCRINHLIFRGGCAQITFLATFDVSEKAVLGDRLLLTANV
SSENTPRTSKTTFQLELPVKYAVYTVVSSHEQFTKYLNFSESEEEKESHVAMHRYQVNNLGQRDLPSINFWVPV
ELNQEA~~V~~WMDVEVSHQPNSLRCSSEKIAPPASDFLAHIQKNPVLD~~C~~SIAGCLRFRC~~D~~VPSFVSQEELDFTLKGN
LSFGWVRQILQKKVSVSVAEITDTSVYSQLPQEA~~F~~MRQTTTVLEKYKVENPTPLIVGSSIGL~~L~~LALITA
VLYKVGFFKRQYKEMMEEANGQIAPENGQTQTPSPPEK

Mass Match Peptides (bold):

AVIFTQVSR [96]
CDVPSFSVQEELDFTLK [100]
DIQNQLK [130]
DLQSSVTLDLALDPGR [138]
DSYLG~~Y~~STELALWK [158]
DVIPMADAAGIIR [161]
ELNDIASKPSQEHIK [204]
EMMEEANGQIAPENGQTQTPSPPEK [210]
ESHVAMHR [224]
FGAALT~~V~~LGDVNGDK [252]
FQTHFTFEEFR [269]
FQTHFTFEEFR [270]
GAVYLFHGVLGPSISPSHSQR [287]
GGQVSVCPLPR [299]
GNLSFGWVR [303]
GVQSLVLGAPR [327]
IAGSQLSSR [350]
IAPPASDFLAHIQK [352]
INHLIFR [383]
KEGDSL~~YK~~ [409]
LFHASYGAR [458]
LFHASYGARR [459]
LTDVVIGAPGEEENR [496]
NFATMMNFVR [535]
NLRPMLAADAQR [545]
NMYLTGLCFLLGPTQLTQR [548]
NPVLD~~C~~SIAGCLR [552]
QE~~Q~~DIVFLIDSGSGSISSR [567]
SLHLTCD~~S~~APVGSQGTWSTSCR [641]
VEDFDALK [752]
YAIGVGLAFQNR [839]
YAVYTVVSSHEQFTK [841]
YQHTGK [867]
YQVNNLGQR [868]

Tandem Peptides (underline):

AVIFTQVSR [96]
AVISQFORPSTQFSLMQFSNK [97]

DVIPMADAAGIIR [161]
 FQTHFTFEEFR [269]
 GGAQITFLATFDVSPK [296]
 GVQSLVLGAPR [327]
 INHLIFR [383]
 LTDVVICAPGEEENR [496]
 NFATMMNFVR [535]
 NMYLTGLCFLLGPTQLTQR [548]
 YAVYTVVSSHEQFTK [841]
 YQVNNLGQR [868]

Peptide Source: iTRAQ, Colorectal cancer

MTRTRAALLLFTALATSLGFNLDTEELTAFRVDSAGFGDSVVQYANSWVVVGAPQKITAANQTGGLYQCGYSTGA
 CEPIGLQVPPEAVNMISLGLSLASTTSPSQLLACGPTVHHECGRNMYLTGLCFLLGPTQLTQRLPVSQRQECPRQEQ
 DIVFLIDGSGSISRRNFATMMNFVRAVISQFQRPSTQFSLMQFSNKFQTHFTFEEFRRTSNPLSLLASVHQLQGF
 TYTATAIQNVVHRLFHASYGARRDATKILIVITDGKKEGDSLDYKDVIPMADAAGIIRYAIGVGLAFQNRNSWKE
 LNDIASKPSQEHIFKVEDFDALKDIQNQLKEKIFAIEGTETTTSSSSFELEMAQEGFSAVFTPDGPNLGAAGSFTW
 SGGAFLYPPNMSPTFINMSQENVDMRDSYLGSTELALWKGVSQSLVLGAPRYQHTGKAVIFTQVSRQWRMKA EVT
 GTQIGSYFGASLCSVDVDTDGSTDVLVIGAPHYYEQTR**GGQVSVCPPLPR**GWRRWWCDVAVLYGEQGHFWGRFGAAL
 TVLGDVNGDKLTDVVICAPGEEENRGAVYLFHGVLGPSISPSHSQRIAGSQLSSRLQYFGQALSGGQDLTQDGLV
 DLAVGARGQVLLLRTRPVLWVGVMQFIPAEIPRSAFEQREQVSEQTLVQSNICLYIDKRSKNLLGSRDLQSSV
 TLDLALDPCRLSPRATFQETK**NRSLSRVR**VVLGLKAHCENFNLLPSCVEDSVTPITLRLNFTLVGKPLLAFFNLR
 PMLAADAQRYFTASLPEKNCADHICQDNLGIFSFPGLKSLLVGSNLELNAEVMVWNDGEDSYCTTITFSHPA
 GLSYRYVAEGQKQGLRSLHLTCD SAPVGSQGTWSTSCRINHLIFRGAQITFLATFDVSPKAVLGDRLLLTANV
 SSENTPR**TSKTTFQLELPVK**YAVYTVVSSHEQFTKYLNFSESEEKESHVAMHRYQVNNLGQRDLFPVSINFWVPV
 ELNQEA VWMDEVSHQNP SLRCSSEKIAPPASDFLAHIQKNPVLDCSIAGCLRFRCDVPSFSVQEELDFTLKGN
 LSFQWVRQILQKKVSVSVSAEITFDTSVYSQPLPGQEA FMRAQT TTVLEKYKVHNPTPLIVGSSIGGLLLLALITA
 VLYKVGFFKRQYKEMMEEANGQIAPENGQTTPSPPEK

Mass Match Peptides (bold):

GGQVSVCPPLPR [299]
 NRSLSRVR [961]
 TSKTTFQLELPVK [985]

Tandem Peptides (underline):

GGQVSVCPPLPR [299]
 NRSLSRVR [961]
 TSKTTFQLELPVK [985]

Peptide Source: iTRAQ, Non-small cell lung cancer

MTRTRAALLLFTALATSLGFNLDTEELTAFRVDSAGFGDSVVQYANSWVVVGAPQKITAANQTGGLYQCGYSTGA
 CEPIGLQVPPEAVNMISLGLSLASTTSPSQLLACGPTVHHECGRNMYLTGLCFLLGPTQLTQRLPVSQRQECPRQEQ
 DIVFLIDGSGSISRRNFATMMNFVRAVISQFQRPSTQFSLMQFSNKFQTHFTFEEFRRTSNPLSLLASVHQLQGF
 TYTATAIQNVVHRLFHASYGARRDATKILIVITDGKKEGDSLDYKDVIPMADAAGIIRYAIGVGLAFQNRNSWKE
 LNDIASKPSQEHIFKVEDFDALKDIQNQLKEKIFAIEGTETTTSSSSFELEMAQEGFSAVFTPDGPNLGAAGSFTW
 SGGAFLYPPNMSPTFINMSQENVDMRDSYLGSTELALWKGVSQSLVLGAPRYQHTGKAVIFTQVSRQWRMKA EVT
 GTQIGSYFGASLCSVDVDTDGSTDVLVIGAPHYYEQTR**GGQVSVCPPLPR**GWRRWWCDVAVLYGEQGHFWGRFGAAL
 TVLGDVNGDKLTDVVICAPGEEENRGAVYLFHGVLGPSISPSHSQRIAGSQLSSRLQYFGQALSGGQDLTQDGLV
 DLAVGARGQVLLLRTRPVLWVGVMQFIPAEIPRSAFEQREQVSEQTLVQSNICLYIDKRSKNLLGSRDLQSSV
 TLDLALDPCRLSPRATFQETK**NRSLSRVR**VVLGLKAHCENFNLLPSCVEDSVTPITLRLNFTLVGKPLLAFFNLR
 PMLAADAQRYFTASLPEKNCADHICQDNLGIFSFPGLKSLLVGSNLELNAEVMVWNDGEDSYCTTITFSHPA
 GLSYRYVAEGQKQGLRSLHLTCD SAPVGSQGTWSTSCRINHLIFRGAQITFLATFDVSPKAVLGDRLLLTANV
 SSENTPR**TSKTTFQLELPVK**YAVYTVVSSHEQFTKYLNFSESEEKESHVAMHRYQVNNLGQRDLFPVSINFWVPV
 ELNQEA VWMDEVSHQNP SLRCSSEKIAPPASDFLAHIQKNPVLDCSIAGCLRFRCDVPSFSVQEELDFTLKGN
 LSFQWVRQILQKKVSVSVSAEITFDTSVYSQPLPGQEA FMRAQT TTVLEKYKVHNPTPLIVGSSIGGLLLLALITA
 VLYKVGFFKRQYKEMMEEANGQIAPENGQTTPSPPEK

Mass Match Peptides (bold):

GGQVSVCPLEP [299]
 LTDVVIGAPGEEENR [496]
 TSKTTFQLELPVK [985]
 YFTASLPFEK [1004]

Tandem Peptides (underline):

GGQVSVCPLEP [299]
 LTDVVIGAPGEEENR [496]
 TSKTTFQLELPVK [985]
 YFTASLPFEK [1004]

Peptide Source: iTRAQ, Renal cell cancer

MTRTRAALLLFTALATSLGFNLDTEELTAFRVDSAGFGDSVVQYANSWVVGAPQKITAANQTGGLYQCGYSTGA
 CEFIGLQVPPPEAVNMISLGLSLASTTSPSQLIACGPTVHHECGRNMVLTGLCFLLGPTQLTQRLPVSQRCPQREQ
 DIVFLIDGSGSISRNFAATMMNFVRAVISQFQRPSTQFSLMQFSNKFQTHFTFEFRRTSNPLSLLASVHQLQGF
 TYTATAIQNVVHRLPHASYGARRDATKILIVITDGKKEGDSLDDYKDVIPMADAAGIIRYAIGVGLAFQNRNSWKE
 LNDIASKPSQEHIFKVEDFDALKDIQNQLKEKIFAIEGTETTTSSSSFELEMAQEGFSAVFTPDGPVLGAVGSFTW
 SGGAFLYPPNMSPTFINMSQENVDMRDSYLGSTELALWKGVSILVGLAPRYQHTGKAVIFTQVSRQWRMKA EVT
 GTQIGSYFGASLCSDVDVTDGSTDVLVIGAPHYYEQTRGGQVSVCPLEPRGWRWWCDVAVLYGEQGHWPGRFGAAL
 TVLGDVNGDKLTDVVIGAPGEEENRGAVYLFHGVGLGPSISPSHSQRIAGSQLSSRLQYFGQALSGGQDLTQDGLV
 DLAVGARGQVLLLRTRPVLVWGVSMQFIPAEIPRSFAFECREQVVSEQTLVQSNICLYIDKRSKNLLGSRDLQSSV
 TLDLALDPGRSPRATFQETKNRSLSRVRLGLKAHCENFNLLPSCVEDSVTPITLRLNFTLVGKPLLAFRNLRL
 PMLAADAQRYFTASLPFEKNCADHICQDNLGISFSFPGKSLLVGSNLELNAEVMVWNGEDSYGTTITFSHPA
 GLSYRYVAEGQKQGLRSLHLTCD SAPVGSQGTWSTSCRINHLIFRGAQITFLATFDVSPK**AVLGDR**LLLTANV
 SSENNTPTSKTTFQLELPVKYAVYTVVSSHEQFTKYLNFSESEEKESHVAMHRYQVNNLGQRDLVPSINFWVPV
 ELNQEA VWMVDVESHQPNPSLRCSSEKIAAPPASDFLAHIQKNPVLDCSIAGCLRFRCDVPSFSVQEELEDFTLKG
 NLSFGWVRQILQKVS VVSAEITFDTSVYSQLPQGEAFMRAQT TTVLEKYKVHNPTPLIVGSSIGLLLLLALITA
 VLYKVGFFKRQYKEMMEEANGQIAPENGQTPTSPSPSEK

Mass Match Peptides (bold):

AVLGDR [885]

Tandem Peptides (underline):

AVLGDR [885]

OGTA174 (SEQ ID No: 31)

Peptide Source: 1D-GE, Acute T-cell leukaemia

MPMGSLOPLATLYLLGMLVASCLGR**LSWYDPDFQAR**LTRSNSK**COGQLEVYLK**DGWHMVCSQSWGRSSKQWEDPS
 QASKVCORLNCGVPLSLGPFLVYTPQSSII CYGQLGSFNC SHSRNDMCHSLGLTCLPQK**TPPTTREPPTTT**
PEPTAPPRLQLVAQSGGQHCAGVVEFYSGSLGGTISYEAQDKTQDLENFLCENNLQCGSFLK**HLPETEAGRAQDPG**
 EPREHQPLPIQWKIQNSSCTSL EHCERKIKPKQKSGR**VLALLCSGFQPK**VQSRVLVGGSSICEGTVEVR**QGAQWAAL**
CDSSSARSSSLR**WEEVCR**EQQCGSVNSYR**VLDAGDPTSR**GLFCPHQK**LSQCHELWERN**SYCKKVFVTCQDPNPAGL
 AAGTVASIIILALVLLVLLVVCPLAYKKLVKKFRQKKQWIGPTGMNQNM SFHRNHTATVR**SHAENPTASHVD**
NEYSQPPRNSRLSAYPALEGVLHRSSMQPDNSSDSYDLHGAQRL

Mass Match Peptides (bold):

CQGQLEVYLK [107]
 HLPETEAGR [337]
 LSQCHELWER [490]
 LSWYDPDFQAR [493]
 NSYCKK [554]
 QGAQWAALCDSSSAR [573]
 SHAENPTASHVDNEYSQPPR [634]

TPPTTRPPPTTTPEPTAPPR [734]
VLALLCSGFQPK [771]
VLDAGDPTSR [775]
WEEVCR [826]

Tandem Peptides (underline):

LSWYDPDFQAR [493]
VLDAGDPTSR [775]

Peptide Source: 1D-GE, Chronic lymphocytic leukaemia

MPMGSLQPLATLYLLGMLVASCLGR**LSWYDPDFQAR**LTRNSNKCQGQLEVYLKDGWHMVCSQSWGRSSKQWEDPS
QASKVCQRLNCGVPLSLGPFVLTYPQSSIICYGQLGSFNSCHSRNDMCHSLGLTCLEPQKTTPPTTRPPPTTT
PEPTAPPRQLVAQSGGQHCAGVVEFYSGSLGGTISYEAQDK**TQDLENFLCNNLQCGSFLKHLPETEAGRAQDPG**
EPREHOPLPIQWKIQNSSCTSLEHCFRKIKPKQSGRVLALLCSGFQPKVQSRLVGGSSICEGTVEVRQGAQWAAL
CDSSSARSSLRWEEVCREQQCGSVNSYR**VLDAGDPTSR**GLFCPHQK**LSQCHELWER**NSYCKKVFVTCQDPNPAGL
AAGTVASIIILALLVLLVLLVVCPLAYKKLVKKFRQKKQKQWIGPTGMNQNMFSFRNHTATVR**SHAENPTASHVD**
NEYSQPPRNSRLSAYPALEGVLHRSSMQPDNSSDSYDLHGAQRL

Mass Match Peptides (bold):

AQDPGEPR [81]
EHQPLPIQWK [194]
HLPETEAGR [337]
IQNSSCTSLEHCFRK [390]
LSQCHELWER [490]
LSWYDPDFQAR [493]
SHAENPTASHVDNEYSQPPR [634]
TQDLENFLCNNLQCGSFLK [723]
VLDAGDPTSR [775]

Tandem Peptides (underline):

LSWYDPDFQAR [493]
VLDAGDPTSR [775]

Peptide Source: iTRAQ, Non-small cell lung cancer

MPMGSLQPLATLYLLGMLVASCLGRLSWYDPDFQARLTRNSNKCQGQLEVYLKDGWHMVCSQSWGRSSKQWEDPS
QASKVCQRLNCGVPLSLGPFVLTYPQSSIICYGQLGSFNSCHSRNDMCHSLGLTCLEPQKTTPPTTRPPPTTT
PEPTAPPRQLVAQSGGQHCAGVVEFYSGSLGGTISYEAQDKTQDLENFLCNNLQCGSFLKHLPETEAGRAQDPG
EPREHOPLPIQWKIQNSSCTSLEHCFRKIKPKQSGRVLALLCSGFQPKVQSRLVGGSSICEGTVEVRQGAQWAAL
CDSSSARSSLRWEEVCREQQCGSVNSYRVLDAGDPTSRGLFCPHQK**LSQCHELWER**NSYCKKVFVTCQDPNPAGL
AAGTVASIIILALLVLLVLLVVCPLAYKKLVKKFRQKKQKQWIGPTGMNQNMFSFRNHTATVRSHAENPTASHVD
NEYSQPPRNSRLSAYPALEGVLHRSSMQPDNSSDSYDLHGAQRL

Mass Match Peptides (bold):

LSQCHELWER [490]

Tandem Peptides (underline):

LSQCHELWER [490]

OGTA176 (SEQ ID No: 32)

Peptide Source: 1D-GE, B-cell non-Hodgkin's lymphoma

MAEAITYADLRVFKAPLKKSISRLGQDPGADDDGEITYENVQVPAVLGVPSSLASSVLGDKAAVKSEQPTASWR
AVTSPA VGRILPCRTTCLRYLLGLLLTCLLLGVTAICLGVR**YLOVSQQLQOTNR**VLEVTNSSLRQQLRLK**ITQL**
GQSAEDLQGSRRRLAQSQEALQVEQRAHQAAEQQLQACQADRQKTK**ETLQSEEQORR**ALEQKLSNMENRLKPFFFT

CGSADTCCPSGWIMHQKSCFYISLTSKNWQESQKQCETLSSKLATFSEIYPQSHSYFFLNSLLPNGGSGNSYWTG
LSSNKDWKLTDDTQRTRYAQSSKCNKVHKTWSWWTLESESCRSSLPYICEMTAFRFPD

Mass Match Peptides (bold):

ELAQSQEALQVEQR [202]
ETLQSEEQQR [231]
ITQLGQSAEDLQGSR [396]
ITQLGQSAEDLQGSRR [397]
YLQVSQQLQQTNR [862]

Tandem Peptides (bold):

ETLQSEEQQR [231]

Peptide Source: 1D-GE, Chronic lymphocytic leukaemia

MAEAITYADLRVFKAPLKSSISRLGQDPGADDDGEITYENVQVPAVLGVPSSLASSVLGDKAAVK**SEQPTASWR**
AVTSPAVGRILPCRTTCLRYLLGLLLTCLLLGVTAICLGVR**YLQVSQQLQQTNR**VLEVTNSSLRQQLRLK**ITQL**
GQSAEDLQGSRRELAQSQEALQVEQRAHQAAEGQLQACQADRQKTK**ETLQSEEQRR**ALEQKLSNMENRLKPFFT
CGSADTCCPSGWIMHQKSCFYISLTSKNWQESQKQCETLSSKLATFSEIYPQSHSYFFLNSLLPNGGSGNSYWTG
LSSNKDWKLTDDTQRTRYAQSSKCNKVHKTWSWWTLESESCR**SSLPYICEMTAFR**FPD

Mass Match Peptides (bold):

ELAQSQEALQVEQR [202]
ETLQSEEQQR [231]
ETLQSEEQRR [232]
ITQLGQSAEDLQGSR [396]
SEQPTASWR [630]
SSLPYICEMTAFR [650]
YLQVSQQLQQTNR [862]

Tandem Peptides (underline):

ELAQSQEALQVEQR [202]
ETLQSEEQQR [231]
ITQLGQSAEDLQGSR [396]
YLQVSQQLQQTNR [862]

Peptide Source: iTRAQ, Colorectal cancer

MAEAITYADLRVFKAPLKSSISRLGQDPGADDDGEITYENVQVPAVLGVPSSLASSVLGDKAAVKSEQPTASWR
AVTSPAVGRILPCRTTCLRYLLGLLLTCLLLGVTAICLGVR**YLQVSQQLQQTNR**VLEVTNSSLRQQLRLKITQL
GQSAEDLQGSRR**ELAQSQEALQVEQRAHQAAEGQLQACQADRQKTKETLQSEEQRR**ALEQKLSNMENRLKPFFT
CGSADTCCPSGWIMHQKSCFYISLTSKNWQESQKQCETLSSKLATFSEIYPQSHSYFFLNSLLPNGGSGNSYWTG
LSSNKDWKLTDDTQRTRYAQSSKCNKVHKTWSWWTLESESCRSSLPYICEMTAFRFPD

Mass Match Peptides (bold):

AVTSPAVGR [886]

Tandem Peptides (underline):

AVTSPAVGR [886]

Peptide Source: iTRAQ, Non-small cell lung cancer

MAEAITYADLRVFKAPLKSSISRLGQDPGADDDGEITYENVQVPAVLGVPSSLASSVLGDKAAVKSEQPTASWR
AVTSPAVGRILPCRTTCLRYLLGLLLTCLLLGVTAICLGVR**YLQVSQQLQQTNR**VLEVTNSSLRQQLRLKITQL
GQSAEDLQGSRR**ELAQSQEALQVEQRAHQAAEGQLQACQADRQKTKETLQSEEQRR**ALEQKLSNMENRLKPFFT
CGSADTCCPSGWIMHQKSCFYISLTSKNWQESQKQCETLSSKLATFSEIYPQSHSYFFLNSLLPNGGSGNSYWTG
LSSNKDWKLTDDTQRTRYAQSSKCNKVHKTWSWWTLESESCRSSLPYICEMTAFRFPD

Mass Match Peptides (bold):

AVTSPAVGR [886]

Tandem Peptides (underline):

AVTSPAVGR [886]

Peptide Source: iTRAQ, Renal cell cancer

MAEAITYADLRVFKAPLKKSISRLGQDPGADDDGEITYENVQVPAVLGVPSSLASSVLGDKA AVKSEQPTASWR
AVTSPAVGRILPCRTTCLRYLLGLLLTCLLLGVTAICLGVRYLQVSQQQLQQTNRVLEVTNSSLRQQLRLKITQL
 GQSAEDLQGSRRRLAQSQEALQVEQRAHQAAEGQLQACQADRQKTKETLQSEEQRRALEQKLSNMENRLKPFFT
 CGSADTCCPSGWIIMHQKSCFYISLTSKNWQESQKQCETLSSKLATFSEIYPQSHSYFFLNSLLPNGGSGNSYWTG
 LSSNKDWKLTDDTQRTRTYAQSSKCNKVHKTWSWWTLESESCRSSLPYICEMTAFRFPD

Mass Match Peptides (bold):

AVTSPAVGR [886]

Tandem Peptides (underline):

AVTSPAVGR [886]

Peptide Source: iTRAQ, Small cell lung cancer

MAEAITYADLRVFKAPLKKSISRLGQDPGADDDGEITYENVQVPAVLGVPSSLASSVLGDKA AVKSEQPTASWR
AVTSPAVGRILPCRTTCLRYLLGLLLTCLLLGVTAICLGVRYLQVSQQQLQQTNRVLEVTNSSLRQQLRLKITQL
 GQSAEDLQGSRRRLAQSQEALQVEQRAHQAAEGQLQACQADRQKTKETLQSEEQRRALEQKLSNMENRLKPFFT
 CGSADTCCPSGWIIMHQKSCFYISLTSKNWQESQKQCETLSSKLATFSEIYPQSHSYFFLNSLLPNGGSGNSYWTG
 LSSNKDWKLTDDTQRTRTYAQSSKCNKVHKTWSWWTLESESCRSSLPYICEMTAFRFPD

Mass Match Peptides (bold):

AVTSPAVGR [886]

Tandem Peptides (underline):

AVTSPAVGR [886]

OGTA177 (SEQ ID No: 33)

Peptide Source: 1D-GE, Chronic lymphocytic leukaemia

MEDTKESNVKTFCSKNILAILGFSSIIAVIALLAVGLTQNKALPENVK**YGIVLDAGSSHTSLYIYK**WPAEKENDT
 GVVHQVEECRVKGPISKFVQKVNEIGIYLTDCMERAREVIPR**SQHQETPVYLGATAGMR**LLRMESEELADRVLD
 VVER**SLSNYFFDFQGAR**IITGQEEGAYGWITINYL LGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVP
 QNQTIESPDNALQFRLYGKDYNVYTHSFLCYGKDQALWQKLAK**DIQVASNEILR**PCFHPGYKKVVNVSDLYKTP
 CTKRFEMTLFPQQFEIQGIGNYQQCHQSILELNTSYCPYSQCAFNGIFLPLQGDFFGAFAFYFVVMK**FLNLTSE**
KVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYILSLLQGYHFTADSWEHIFFIGKIQGS DAGW
 TLGYMLNLTNMI PAEQPLSTPLSHSTYVFLMVLFSLVLFVVAIIIGLLIFHKPSYFWKDMV

Mass Match Peptides (bold):

DIQVASNEILR [131]
 FLNLTSEK [259]
 SLSNYFFDFQGAR [643]
 SQHQETPVYLGATAGMR [647]
 VTEMMK [801]
 VTEMMKK [802]
 YGIVLDAGSSHTSLYIYK [853]

Tandem Peptides (underline):

MESEELADR [514]
SLSNYPDFQGAR [643]
SQHQETPVYLGATAGMR [647]

Peptide Source: iTRAQ, Colorectal cancer

MEDTKESNVKTFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDT
GVVHQVEECRVK**GPGISK** FVQKVNEIGIYLTDCMERAR**AREVIPRSQHQPVPVYLGATAGMRLLR**MESEELADR**VLD**
VVERSLSNYPDFQGAR**IITGQEEGAYGWITINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVP**
QNQTIESPDNALQFRLYGKDYNVYTHSFLCYGKDQALWQKLAK**DIQVASNEILR**DPCFHPGYKK**VVNVSDLYK**TP
CTKRFEMTL**FQQFEIQGIGNYQQCHQSILEFNTSYCPYSQCAFNGIFLPPLQGDGAFSAFYFVMKFLNLTSE**
KVSQEKVTEMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYILSLLQGYHFTADSWEHIHFIGKIQGSDAGW
TLGYMLNLTNMIPAEQPLSTPLSHSTYVFLMVLFSLVLFVVAIIIGLLIFHKPSYFWKDMV

Mass Match Peptides (bold):

AREVIPR [883]
DIQVASNEILR [131]
GPGISK [915]
SQHQETPVYLGATAGMRLLR [971]
VLDVVER [994]
VVNVSDLYK [1003]

Tandem Peptides (underline):

AREVIPR [883]
DIQVASNEILR [131]
GPGISK [915]
SQHQETPVYLGATAGMRLLR [971]
VLDVVER [994]
VVNVSDLYK [1003]

Peptide Source: iTRAQ, Non-small cell lung cancer

MEDTKESNVKTFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDT
GVVHQVEECRVK**GPGISK**FVQKVNEIGIYLTDCMERAR**EVIPRSQHQPVPVYLGATAGMRLLR**MESEELADR**VLD**
VVER**SLSNYPDFQGAR****IITGQEEGAYGWITINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVP**
QNQTIESPDNALQFRLYGKDYNVYTHSFLCYGKDQALWQKLAK**DIQVASNEILR****DPCFHPGYK**KVVNVSDLYKTP
CTKRFEMTL**FQQFEIQGIGNYQQCHQSILEFNTSYCPYSQCAFNGIFLPPLQGDGAFSAFYFVMK****FLNLTSE**
KVSQEKVTEMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYILSLLQGYHFTADSWEHIHFIGKIQGSDAGW
TLGYMLNLTNMIPAEQPLSTPLSHSTYVFLMVLFSLVLFVVAIIIGLLIFHKPSYFWKDMV

Mass Match Peptides (bold):

DIQVASNEILR [131]
DPCFHPGYK [892]
EVIPR [909]
FLNLTSEKVSQEK [911]
SLSNYPDFQGAR [643]
SQHQETPVYLGATAGMR [647]

Tandem Peptides (underline):

DIQVASNEILR [131]
DPCFHPGYK [892]
EVIPR [909]
FLNLTSEKVSQEK [911]
SLSNYPDFQGAR [643]
SQHQETPVYLGATAGMR [647]

Peptide Source: iTRAQ, Ovarian cancer

MEDTKESNVKTFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDT
GVVHQVEECRVK**GPGISK**FEVQKVNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLD
VVERSLSNYPDFDQGARIIITGQEEGAYGWITINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVP
QNQTIESPDNALQFRLYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCHFPGYKKVVNVSDLYKTP
CTKRFEMLTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPQLQDGFAGSAFYFVMKFLNLTSE
KVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHFIGIKIQGSDAGW
TLGYMLNLTNMIPAEQPLSTPLSHSTYVFLMVLFSLVLFVTAIIGLLIFHKPSYFWKDMV

Mass Match Peptides (bold):

GPGISK [915]

Tandem Peptides (underline):

GPGISK [915]

Peptide Source: iTRAQ, Renal cell cancer

MEDTKESNVKTFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDT
GVVHQVEECRVK**GPGISK**FEVQKVNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLD
VVERSLSNYPDFDQGARIIITGQEEGAYGWITINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVP
QNQTIESPDNALQFRLYGKDYNVYTHSFLCYGKDQALWQKLAK**DIQVASNEILR**DPCHFPGYKKVVNVSDLYKTP
CTKRFEMLTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPQLQDGFAGSAFYFVMKFLNLTSE
KVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHFIGIKIQGSDAGW
TLGYMLNLTNMIPAEQPLSTPLSHSTYVFLMVLFSLVLFVTAIIGLLIFHKPSYFWKDMV

Mass Match Peptides (bold):

DIQVASNEILR [131]
GPGISK [915]
SLSNYPDFDQGAR [643]
VLDVVER [994]

Tandem Peptides (underline):

DIQVASNEILR [131]
GPGISK [915]
SLSNYPDFDQGAR [643]
VLDVVER [994]

Peptide Source: iTRAQ, Small cell lung cancer

MEDTKESNVKTFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDT
GVVHQVEECRVK**GPGISK**FEVQKVNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLD
VVERSLSNYPDFDQGARIIITGQEEGAYGWITINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVP
QNQTIESPDNALQFRLYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCHFPGYKKVVNVSDLYKTP
CTKRFEMLTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPQLQDGFAGSAFYFVMKFLNLTSE
KVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHFIGIKIQGSDAGW
TLGYMLNLTNMIPAEQPLSTPLSHSTYVFLMVLFSLVLFVTAIIGLLIFHKPSYFWKDMV

Mass Match Peptides (bold):

AREVIPR [883]

Tandem Peptides (underline):

AREVIPR [883]

OGTA197 (SEQ ID No: 34)

Peptide Source: 1D-GE, Colorectal cancer

MELQAARACFALLWGCALAAAAAQQGKEVLLDFAAAGGELGWLTHPYGKGWDLMQNIMNDMPIYMSVCNVMSG
DQDNWLRTNWVYRGEAERNNFELNFTVRDCNSFPGGASSCKETFNLYYAESDLGYGTNFQKRLFTKIDTIAPDEI
TVSSDFEARHVKLNV EERSVGP LTRKGFYLA FQDIGACVALLSVRVYYKKCP ELLQGLAHFPETIAGSDAPSLAT
VAGTCVDHAVVPPGGEEPRMHCAVDGEWLVP I GQCLCQAGYEKVEDACQACSPGFFKFEASESPCLECPEHTLPS
PEGATSCCEEGGFRAPQDPASMPCTRPPSAPHYLTA VGMGAKVELRWTPPQDSGGREDIVYSVTCEQCWPESGE
CGPCEASVRYSEPPHGLTRTSVTVSDLEPHMNYTFTVEARNGVSGLVTSR SFR TASVSINQTEPPKVRLEGRSTT
SLSVSWSI PPPQSRVWKYEV TYRKKGDSNSYNVRRTEGFSVTLDD LAPD TTYLVQVQALTQEGQGAGSKVHEFQ
T LSP EGSNLA VIGGVAVGVVLLLVLAGVGFFIHRRRKNQ RARQSPEDVYFSKSEQLKPLKTYVDPHTYEDPNQA
VLKFTTEIHPSCVTRQKVIGAGEFGEVYK GMLKTSSGKKEVPVAIKTLKAGYTEKQ RVD FLGEAGIMQF SHHNI
IRLEGVISKYKPMMIITEYMENGALDKFLREKDG EFSVLQLVGMLRGIAAGMKYLANMNYVHRDLAARNILVNSN
LVCKVSD FGLSRVLEDDPEATYTTSGGKIPIRWTAPEAISYRKFTSASDVWSFGIVMWEVMTYGERPYWELSNHE
VMKAINDGFR LPTPMDCP SAIYQLMMQCWQERARRPKFADIVSILDKLIRAPDSLKT LADFDPRVSIRLPSTSG
SEGVPFR TVSEWLESIKMQQYTEHFMAAGYTAIEKVVQMTNDDIKRIGVRLPGHQKRIAYSLGLKQDQVNTVGIP
I

Mass Match Peptides (bold):

MQQYTEHFMAAGYTAIEK [523]
TSVTVSDLEPHMNYTFTVEAR [733]
TYVDPHTYEDPNQAVLK [742]
WTPPQDSGGR [837]
YKPMMIITEYMENGALDK [857]

Tandem Peptides (underline):

NGVSGLVTSR [538]
QSPEDVYFSK [587]
VIGAGEFGEVYK [769]

Peptide Source: 1D-GE, Hepatocellular carcinoma

MELQAARACFALLWGCALAAAAAQQGKEVLLDFAAAGGELGWLTHPYGKGWDLMQNIMNDMPIYMSVCNVMSG
DQDNWLRTNWVYRGEAERNNFELNFTVRDCNSFPGGASSCKETFNLYYAESDLGYGTNFQKRLFTKIDTIAPDEI
TVSSDFEARHVKLNV EERSVGP LTRKGFYLA FQDIGACVALLSVRVYYKKCP ELLQGLAHFPETIAGSDAPSLAT
VAGTCVDHAVVPPGGEEPRMHCAVDGEWLVP I GQCLCQAGYEKVEDACQACSPGFFKFEASESPCLECPEHTLPS
PEGATSCCEEGGFRAPQDPASMPCTRPPSAPHYLTA VGMGAKVELRWTPPQDSGGREDIVYSVTCEQCWPESGE
CGPCEASVRYSEPPHGLTRTSVTVSDLEPHMNYTFTVEARNGVSGLVTSR SFR TASVSINQTEPPKVRLEGRSTT
SLSVSWSI PPPQSRVWKYEV TYRKKGDSNSYNVRRTEGFSVTLDD LAPD TTYLVQVQALTQEGQGAGSKVHEFQ
T LSP EGSNLA VIGGVAVGVVLLLVLAGVGFFIHRRRKNQ RARQSPEDVYFSKSEQLKPLKTYVDPHTYEDPNQA
VLKFTTEIHPSCVTRQKVIGAGEFGEVYK GMLKTSSGKKEVPVAIKTLKAGYTEKQ RVD FLGEAGIMQF SHHNI
IRLEGVISKYKPMMIITEYMENGALDKFLREKDG EFSVLQLVGMLRGIAAGMKYLANMNYVHRDLAARNILVNSN
LVCKVSD FGLSRVLEDDPEATYTTSGGKIPIRWTAPEAISYRKFTSASDVWSFGIVMWEVMTYGERPYWELSNHE
VMKAINDGFR LPTPMDCP SAIYQLMMQCWQERARRPKFADIVSILDKLIRAPDSLKT LADFDPRVSIRLPSTSG
SEGVPFR TVSEWLESIKMQQYTEHFMAAGYTAIEKVVQMTNDDIKRIGVRLPGHQKRIAYSLGLKQDQVNTVGIP
I

Mass Match Peptides (bold):

AINDGFR [73]
EVVLLDFAAAGGELGWLTHPYGK [239]
FTEIHPSCVTR [278]
IDTIAPDEITVSSDFEAR [359]
KGDSNSYNVR [417]
LPGHQKR [478]
LPSTSGSEGVPR [481]
MELQAAR [512]
MQQYTEHFMAAGYTAIEK [523]
QSPEDVYFSK [587]
RKNQR [605]
TLADFDPR [702]
TYVDPHTYEDPNQAVLK [742]

VDFLGEAGIMGQFSHHNIIR [747]
VIGAGEFGEVYK [769]
VVQMTNDDIK [813]
VVQMTNDDIKR [814]
VYYKK [822]
WTAPEAISYR [834]
WTAPEAISYRK [835]
YKPMIITEYMENGALDK [857]
YLANMNYVHR [860]
YSEPPHGLTR [871]

Tandem Peptides (underline):

LPSTSGSEGVFPR [481]
QSPEDVYFSK [587]
VIGAGEFGEVYK [769]
VSDFGLSR [796]
YSEPPHGLTR [871]

Peptide Source: 1D-GE, Lung cancer

MELQAARACFALLWGCALAAAAAQQKEVVLLDFAAAGGELGWLTHPYGKGWDLQNMNDMPIYMYSVCNVMSG
DQDNWLRTNWVYRGEAERNNFELNFTVRDCNSFPGGASSCKETFNLYYAESLDYGTNFQKRLFTK**IDTIAPDEI**
TVSSDFEARHVKLNVEERSVGPLTRKGFYLAQDIGACVALLSV**VYYKK**CPELLQGLAHFPETIAGSDAPSLAT
VAGTCVDHAVVPPGGEPRMHCAVDGEWLVPIGQCLCQAGYEKVEDACQACSPGFFKFEASESPCLEPHEHTLPS
PEGATSCCEEGFFRAPQDPASMPCTRPPSAPHYLTAVGMGAKVELR**WTPPDSSGGR**EDIVYSVTCEQCWPESGE
CGPCEASVRYSEPPHGLTR**TSVTVSDLEPHMNYTFTVEAR**NGVSGLVTSR**SFTASVSINQTEPPK**VRLEGRSTT
SLSVSWSIPPPQSRVWK**YEVTYRKKGDSNSYNVRR**TEGFSVTLLDDLAPDTTYLVQVQALTQEGQGAGSKVHEFQ
TLPSEGSGLNAVIGGVAVGVLLLVLAGVGFFIHR**RKNQR**AR**QSPEDVYFSK**SEQLKPLKTYVDPHTYEDPNOA
VLK**FTTEIHPSCVTR**Q**VIGAGEFGEVYK**GMLKTSSGK**KEVPVAIK**TLKAGYTEKQ**RVDFLGEAGIMGQFSHHNI**
IRLEGVISK**YKPMIITEYMENGALDK**FLREK**DGEFSVLQLVGMLR**GIAAGMK**YLANMNYVHR**DLAARNILVNSN
LVCKVSDFGLS**VLEDDPEATYTTSGGK**IP**IRWTAPEAISYRK**FTSASDVWSFGIVMWVMTYGERPYWELSNHE
VMK**AINDGFR**LPTPMDCPSAIYQLMMQCNQGERAR**RPFADIVSILDK**LIRAPDSLK**TLADFDPR**VSIR**LPSTSG**
SEGVFPRTVSEWLESIKMQQYTEHFMAAGYTAIEKVVQMTNDDIKRIGVRLPGHQKRIAYSLGLKQDVNTVGIP
I

Mass Match Peptides (bold):

AINDGFR [73]
DGEFSVLQLVGMLR [121]
EVPVAIK [238]
FADIVSILDK [242]
FTTEIHPSCVTR [278]
GDSNSYNVRR [288]
IDTIAPDEITVSSDFEAR [359]
KEVPVAIK [414]
KKGDSNSYNVR [422]
LPSTSGSEGVFPR [481]
MQQYTEHFMAAGYTAIEK [523]
NGVSGLVTSR [538]
RKNQR [605]
TASVSINQTEPPK [673]
TLADFDPR [702]
TSVTVSDLEPHMNYTFTVEAR [733]
TVSEWLESIK [738]
VDFLGEAGIMGQFSHHNIIR [747]
VIGAGEFGEVYK [769]
VLEDDPEATYTTSGGK [777]
VVQMTNDDIKR [814]
VYYKK [822]
WTAPEAISYRK [835]
WTPPDSSGGR [837]

YEVTYR [845]
YKPMIITEYMENGALDK [857]
YLANMNYVHR [860]

Tandem Peptides (underline):

DQVNTVGIPI [154]
LPSTSGSEGVPPR [481]
QSPEDVYFSK [587]
VIGAGEFGEVYK [769]
VLEDDPEATYTTSGGK [777]
VVQMTNDDIK [813]
WTPPDSSGGR [837]
YLANMNYVHR [860]
YSEPPHGLTR [871]

Peptide Source: 1D-GE, Melanoma

MELQAARACFALLWGICALAAAAAQQKEVVLLDFAAAGGELGWLTHPYGKGWDLQNMIMNDMPIYMSVCNVMMSG
DQDNWLRNTNWVYRGEAERNNFELNFTVRDCNSFPGGASSCKETFNLYYAESDLGYGTNFQKRLFTKIDTIAPDEI
TVSSDFEARHVKLNVEERSVGPLTRKGFYLAQDYGACVALLSVRVYKKCPPELLQGLAHFPETIAGSDAPSLAT
VAGTCVDHAVVPPGGEEPRLMCAVDGEWLVPYGQCLCQAGYEKVEDACQACSPGFFKFEASESPCLECPEHTLPS
PEGATSCECEEGFFRAPQDPASMPCTRPPSAPHYLTAVGMGAKVELRWTPPDSSGGREDIVYSVTCEQCWPESGE
CGPCEASVRYSEPPHGLTRTSVTVSDLEPHMNYTFTVEARNGVSGLYTSRSFRTASVSINQTEPPKVRLEGRSTT
SLSVSWSI PPPQQRVWKYEVTYRKKGDSNSYNVRTEGFSVTLDLAPDITYLVQVQALTQEGQGAGSKVHEFQ
TSLPEGSGNLAVIGGVAVGVVLLLVLAGVGFFIHRRRKNQARQSPEDVYFSKSEQLKPLKTYVDPHTYEDPNQA
VLKFTTEIHPSCVTRQKVIGAGEFGEVYKGMKTSSGKKEVPVAIKILKAGYTEKQQRVDFLGEAGIMGQFHHNI
IRLEGVISKYKPMIITEYMENGALDKFLREKDGEFSVLQLVGMLRGIAAGMKYLANMNYVHRDLAARNILVNSN
LVCKVSDFLSRVLEDDPEATYTTSGGKIPRWTAPEAISYRKFTSASDVWSFGIVMWEVMTYGERPYWELSNHE
VMKAINDGFRLLPTMDCPSAIYQLMMQCWQERARRPKFADIVSILDKLIRAPDSLKTADFDPRVSIRLPSTSG
SEGVPPFRIVSEWLESIKMQQYTEHFMAAGYTAIEKVQMTNDDIKRIGVRLPGHQKRIAYSLLGLKQVNTVGIP
I

Mass Match Peptides (bold):

APQDPASMPCTRPPSAPHYLTAVGMGAK [80]
DGEFSVLQLVGMLR [121]
EVPVAIK [238]
MELQAAR [512]
STTSLSVSWSI PPPQQR [660]
SVGPLTR [662]
TASVSINQTEPPK [673]
TSVTVSDLEPHMNYTFTVEAR [733]
YKPMIITEYMENGALDK [857]
YLANMNYVHR [860]

Tandem Peptides (underline):

FADIVSILDK [242]
VIGAGEFGEVYK [769]

Peptide Source: 1D-GE, Osteosarcoma

MELQAARACFALLWGICALAAAAAQQKEVVLLDFAAAGGELGWLTHPYGKGWDLQNMIMNDMPIYMSVCNVMMSG
DQDNWLRNTNWVYRGEAERNNFELNFTVRDCNSFPGGASSCKETFNLYYAESDLGYGTNFQKRLFTKIDTIAPDEI
TVSSDFEARHVKLNVEERSVGPLTRKGFYLAQDYGACVALLSVRVYKKCPPELLQGLAHFPETIAGSDAPSLAT
VAGTCVDHAVVPPGGEEPRLMCAVDGEWLVPYGQCLCQAGYEKVEDACQACSPGFFKFEASESPCLECPEHTLPS
PEGATSCECEEGFFRAPQDPASMPCTRPPSAPHYLTAVGMGAKVELRWTPPDSSGGREDIVYSVTCEQCWPESGE
CGPCEASVRYSEPPHGLTRTSVTVSDLEPHMNYTFTVEARNGVSGLYTSRSFRTASVSINQTEPPKVRLEGRSTT
SLSVSWSI PPPQQRVWKYEVTYRKKGDSNSYNVRTEGFSVTLDLAPDITYLVQVQALTQEGQGAGSKVHEFQ
TSLPEGSGNLAVIGGVAVGVVLLLVLAGVGFFIHRRRKNQARQSPEDVYFSKSEQLKPLKTYVDPHTYEDPNQA

VLKFTTEIHPSCVTRQKVIGAGEFGEVYKGM LKTS SSGKKEVPVAIKTLKAGYTEKQRVDFLGEAGIMQGFSSHNI
IRLEGVISKYKPMMIITEYMENGALDKFLREKDGEFSVLQLVGMLRGIAAGMKYLANMNYVHRDLAARNILVNSN
LVCKVSDFGLSRVLEDDPEATYTTSGGKIPIRWTAPPAISYRKFTSASDVWSFGIVMWEVMTYGERPYWELSNHE
VMKAINDGFR LPTMDCPSAIYQLMMQCWQQRARRPKFADIVSILDKLIRAPDSLKT LADFDPRVSIRLPSTSG
SEGVPFR TVSEWLESIKMQQYTEHFMAAGYTAIEKVVQMTNDDIKRIGVRLPGHQKRIAYSLLGLKDQVNTVGIP
I

Mass Match Peptides (bold):

ACFALLWGCAAAAAAQGK [55]
AINDGFR [73]
APQDPASMPCTRPPSAPHYLTAVGMGAK [80]
DGEFSVLQLVGMLR [121]
FTTEIHPSCVTR [278]
IDTIAPDEITVSSDFEAR [359]
KGDSNSYNVR [417]
LPTMDCPSAIYQLMMQCWQQR [483]
MQQYTEHFMAAGYTAIEK [523]
RKNQR [605]
STTSLSVWSI PPPQQR [660]
SVGPLTR [662]
TASVSINQTEPPK [673]
TLADFDPR [702]
TNWVYR [715]
TSVTVSDLEPHMNYTFTVEAR [733]
TYVDPHTYEDPNQAVLK [742]
VDFLGEAGIMQGFSSHNIIR [747]
VVQMTNDDIK [813]
VVQMTNDDIKR [814]
WTPPDQSGGR [837]
YEVTYRK [846]
YKPMMIITEYMENGALDK [857]
YLANMNYVHR [860]
YSEPPHGLTR [871]

Tandem Peptides (underline):

LPSTSGSEGVPFR [481]
NGVSGLVTSR [538]
TLADFDPR [702]
VIGAGEFGEVYK [769]
VLEDDPEATYTTSGGK [777]

Peptide Source: 1D-GE, Ovarian cancer

MELQAARACFALLWGCAAAAAAQGKEVVLLDFAAAGGELGWLTHPYGKGWDLMQNIMNDMPIYMSVCNVMSG
DQDNWLR TNWVYRGEAERNNFELNFTVRDCNSFPGGASSCKETFNLYAESDLDYGTNFQKRLFTK IDTIAPDEI
TVSSDFEARHVKLNVEER SVGPLTRKGFYLAFQDIGACVALLSVRVYKKCPPELLQGLAHFPETIAGSDAPSLAT
VAGTCVDHAVVPPCGEPRMHCADVGEWLVPICQCLCQAGYEKVEDACQACSPGFFKFEASESPCLECPEHTLPS
PEGATSCCEEGFFRAPQDPASMPCTRPPSAPHYLTAVGMGAKVELRWTPPDQSGGRDIVSVTCEQCWPESGE
CGPCEASVRYSEPPHGLTRTSVTVSDLEPHMNYTFTVEARNGVSGLVTSRSFR TASVSINQTEPPKVRLEGRSTT
SLSVWSI PPPQQRVWKYEVTYRKKGDSNSYNVRRTGFSVTLLDAPDTTYLVQVQALTQEGQGAGSKVHEFQ
TLPSEGSGLNAVIGGVAVGVVLLVLAVGVGFFIHRRRKNQRRARQSPEDVYTSKSEQLKPLKTYVDPHTYEDPNQA
VLKFTTEIHPSCVTRQKVIGAGEFGEVYKGM LKTS SSGKKEVPVAIKTLKAGYTEKQRVDFLGEAGIMQGFSSHNI
IRLEGVISKYKPMMIITEYMENGALDKFLREKDGEFSVLQLVGMLRGIAAGMKYLANMNYVHRDLAARNILVNSN
LVCKVSDFGLSRVLEDDPEATYTTSGGKIPIRWTAPPAISYRKFTSASDVWSFGIVMWEVMTYGERPYWELSNHE
VMKAINDGFR LPTMDCPSAIYQLMMQCWQQRARRPKFADIVSILDKLIRAPDSLKT LADFDPRVSIRLPSTSG
SEGVPFR TVSEWLESIKMQQYTEHFMAAGYTAIEKVVQMTNDDIKRIGVRLPGHQKRIAYSLLGLKDQVNTVGIP
I

Mass Match Peptides (bold):

ACFALLWGCALAAAAAQQGK [55]
 AINDGFR [73]
 DGEFSLQLVGMRL [121]
 FTTEIHPSCVTR [278]
 IDTIAPDEITVSSDFEAR [359]
 KGDSNSYNVRR [418]
 RKNQR [605]
 STTSLSVSWSIPPPQQR [660]
 SVGPLTR [662]
 TASVSINQTEPPK [673]
 TLADFDPR [702]
 TNWVYR [715]
 TSVTVSDLEPHMNYTFTVEAR [733]
 TYVDPHTYEDPNQAVLK [742]
 VDFLGEAGIMGQFSHHNIIR [747]
 VIGAGEFGEVYK [769]
 VVQMTNDDIKR [814]
 WTPPQDSGGR [837]
 YEVTYR [845]
 YKPMIITEYMENGALDK [857]
 YLANMNYVHR [860]
 YSEPPHGLTR [871]

Tandem Peptides (underline):

FADIVSILDK [242]
 LPSTSGSEGVPR [481]
 QSPEDVYFSK [587]
 TASVSINQTEPPK [673]
 VIGAGEFGEVYK [769]
 VSDFGLSR [796]
 WTPPQDSGGR [837]

Peptide Source: 1D-GE, Pancreatic cancer

MELQAARACFALLWGCALAAAAAQQGKEVLLDFAAAGGELGWLTHPYGKGWDLMNIMNDMPIYMSVCNVMSG
DQDNWLRTNWVYRGEAERNNFELNFTVRDCNSFPFGASSCKETFNLYYAESDLDYGTNFQKRLFTKIDTIAPDEI
TVSSDFEARHVKLNVEERSVGPLTRKGFYLAQDQIGACVALLSVRVYYYKKCPELLQGLAHFPETIAGSDAPSLAT
VAGTCVDHAVVPPGGEEPRMCAVDGEWLVPIGQCLCQAGYEKVEDACQACSPGFFKFEASESPCLECPEHTLPS
PEGATSCCEEGFFRAPQDPASMPCTRPPSAPHYLTAVGMAKVELRWTPPQDSGGREDIVSVTCEQCWPESGE
CGPCRASVRYSEPPHGLTRTSVTVSDLEPHMNYTFTVEARNGVSGLVTSRFRTASVSINQTEPPKVRLEGRSTT
SLSVSWSIPPPQQRVWKYEVTYRKKGDSNSYNVRRTEGFSVTLDDLPDITLVQVQALTQEGQAGSKVHEFQ
TLSPGSGNLAVIGGAVGVLLLVLAGVGFFIHRRRKNQRRQSPEDVYFSKSEQLKPLKTYVDPHTYEDPNQA
VLKFTTEIHPSCVTROKVIGAGEFGEVYKGMLKTSSGKKEVPVAIKTLKAGYTEKQRVDFLGEAGIMGQFSHHNI
IRLEGVISKYKPMIITEYMENGALDKFLREKDGESVLQVGMRLGIAAGMKYLANMNYVHRDLAARNILVNSN
LVCKVSDFGLSRVLEDDPEATYTTSGGKIPIRWTAPEAISYRKFTSASDVWSFGIVMWEVMTYGERPYWELSNHE
VMKAINDGFRLPTPMDCPSAIYQLMMQCWQERARRPKFADIVSILDKLIRAPDSLTLADFDPRVSIRLPSTSG
SEGVPRFTVSEWLESIKMQQYTEHFMAAGYTAIEKVVQMTNDDIKRIGVRLPGHQKRIAYSLGLKQVNTVGIP
 I

Mass Match Peptides (bold):

ACFALLWGCALAAAAAQQGK [55]
 AINDGFR [73]
 IDTIAPDEITVSSDFEAR [359]
 KGDSNSYNVR [417]
 KGDSNSYNVRR [418]
 LEGVISK [454]
 LNVEER [474]
 LPSTSGSEGVPR [481]
 MELQAAR [512]
 MQQYTEHFMAAGYTAIEK [523]

QSPEDVYFSK [587]
 SEQLKPLK [629]
 STTSLSVSWSIPPPQQR [660]
 SVGPLTR [662]
 SVGPLTRK [663]
 TLADFDPR [702]
 TNWVYR [715]
 TVSEWLESIK [738]
 TYVDPHTYEDPNQAVLK [742]
 VIGAGEFGEVYK [769]
 VLEDDPEATYTTSGGK [777]
 VVQMTNDDIK [813]
 VVQMTNDDIKR [814]
 VYYKK [822]
 WTAPEAISYR [834]
 WTPPQDSGGR [837]
 YEVTYR [845]
 YEVTYRK [846]
 YEVTYRKK [847]
 YKPMMIITEYMENGALDK [857]
 YLANMNYVHR [860]
 YSEPPHGLTR [871]

Tandem Peptides (underline):

FADIVSILDK [242]
 LPSTSGSEGVPFR [481]
 QSPEDVYFSK [587]
 TASVSINQTEPPK [673]
 TLADFDPR [702]
 VIGAGEFGEVYK [769]
 WTAPEAISYR [834]
 WTPPQDSGGR [837]
 YLANMNYVHR [860]
 YSEPPHGLTR [871]

Peptide Source: 1D-GE, Prostate cancer

MELQAARACFALLWGCALAAAAAQQGKEVVLLDFAAAGGELGWLTHPYGKGWDLMQNIMNDMPIYMSVCNVMSG
 DQDNWLRNTNWVYRGEAERNNFELNFTVRDCNSFPGGASSCKETFNLYYAESDLDYGTNFQKRLFTKIDTIAPDEI
 TVSSDFEARHVKNVEERSVGPLTRKGFYLAQDIGACVALLSVRVYKKCPPELLQGLAHPETIAGSDAPSLAT
 VAGTCVDHAVVP?GGEEP?RMHCAVDGEWLVP?IGQCLCQAGYEKVEDACQACSPGFFKFEASESPCLECEHTLPS
 PEGATSCCEEGFRAPQDPASMPCTRPSPAPHYLTAVGMGAKVELR**WTPPQDSGGR**EDIVYSVTCEQCWPESGE
 CGPCEASVR**YSEPPHGLTR**TSVTVSDLEPHMNYTFTVEAR**NGVSGLVTSR**SFRTASVSINQTEPPKVRLEGRSTT
 SLSVSWSIPPPQCSRVMKY**YEVTYR**KKKGDNSNSYNVRRTEGFSVTLDDLAPDTTYLVQVQALTQEGQGAGSKVHEFQ
 TLSPEGSGNLAVIGGVAVGVVLLLVLAGVGFFIHRRRKNQRARQSPEDVYFSKSEQLKPLKTYVDPHTYEDPNQA
 VLKFTTEIHPSCVTRQKVIGAGEFGEVYKGMKLTSSGKKEVPVAIKTLKAGYTEKQRVDFLGEAGIMGQFSHNH
 IRLEGVISKYKPMMIITEYMENGALDKFLREKDGFEFSVLQLVGMLRGIAAGMKYLANMNYVHRDLAARNIIVNSN
 LVCKVSDFGLSRVLEDDPEATYTTSGGKIPIRWTAPEAISYRKFTSASDVWSFGIVMWEVMTYGERPYWELSNHE
 VMKAINDFRLPTPMDCPSAIYQLMMQCWQOERARRPKFADIVSILDKLIRAPDSLKTLADFDPRVSIR**LPSTSG**
SEGVPFRTVSEWLESIKMQQYTEHFMAAGYTAIEK**VVQMTNDDIK**RIGVRLPGHQKRIAYSLLGLKDQVNTVGIP
 I

Mass Match Peptides (bold):

LPSTSGSEGVPFR [481]
 MELQAAR [512]
 NGVSGLVTSR [538]
 VVQMTNDDIK [813]
 WTPPQDSGGR [837]
 YEVTYR [845]
 YSEPPHGLTR [871]

Tandem Peptides (underline):

LPSTSGSEGVPPFR [481]

Peptide Source: 1D-GE, Renal cell cancer

MELQAARAC**ACFALLWG**CALAAAAA**Q**GKEVVLLDFAAAGGELGWLTHPYGKGWDLMQNIMNDMPIYMYSVCNVMSG
DQDNWLR**TNWVYR**GGEAERNNFELNFTVRDCNSFPGGASSCKETFNLYYAESDLDYGTNFKRLFTKIDTIAPDEI
TVSSDFEARHVKLNVEER**SVGPLTR**KGFYLAFQDIGACVALLSVRVYKKCPPELLQGLAHFPETIAGSDAPSLAT
VAGTCVDHAVVPPGGEFPRMHCAVDGEWLVPIGQCLCQAGYEKVEDACQACSPGFFKFEASESPCLECPEHTLPS
PEGATSCCECEGFFRAPQDPASMPCTRPPSAPHYLTAVGMCAKVELRW**TPPDQSGGR**EDIVYSVTECQCWPESGE
CGPCEASVR**YSEPPHGLTR**TSVTVSDLEPHMNYTFTVEARNGVSGLVTSRSTASVSINQTEPPKVRLEGRSTT
SLSVSWSIPPPQCSRVMKY**YEVTYRKKGDSNSYNVRR**TEGFSVTLDDLAPDTTYLVQVQALTQEGQGAGSKVHEFQ
TSLPEGSGNLAVIGGVAVGVVLLVLAGVGFFIHRRRKNQRRARQSPEDVYFSKSEQLKPLK**TYVDPHTYEDPNQA**
VLKFTTEIHFPSCVTRQ**VIGAGEFGEVYK**GMLKTSSGKKEVPVAIKTLKAGYTEKQRVDFLGEAGIMGQFSHHNI
IRLEGVISYKPMIITEYMENGALDKFLREKDGESVLQVLGMLRGIAAGMK**YLANMNYVHR**DLAARNILVNSN
LVCKVSDFGLSRVLEDDPEATYTTSGGKIPIR**WTAPEAISYR**KFTSASDVWSFGIVMWEVMTYGERPYWELSNHE
VMK**AINDGFR**LPTPMDCPSAIYQLMMQCWQQRARRPKFADIVSILDKLIRAPDSLKTLDADFDPVRSIR**LPSTSG**
SEGVPPFRTVSEWLESIKMQQYTEHFMAAGYTAIEK**VVQMTNDDIKR**IGVRLPGHQKRIAYSLGLCKDQVNTVGIP
I

Mass Match Peptides (bold):

ACFALLWGCAAAAAA**Q**GK [55]
AINDGFR [73]
KGDSNSYNVRR [418]
LPSTSGSEGVPPFR [481]
SVGPLTR [662]
TNWVYR [715]
TYVDPHTYEDPNQAVLK [742]
VIGAGEFGEVYK [769]
VVQMTNDDIK [813]
VVQMTNDDIKR [814]
WTAPEAISYR [834]
WTPPDQSGGR [837]
YEVTYR [845]
YEVTYRK [846]
YLANMNYVHR [860]
YSEPPHGLTR [871]

Tandem Peptides (underline):

LPSTSGSEGVPPFR [481]
VIGAGEFGEVYK [769]
WTAPEAISYR [834]
YSEPPHGLTR [871]

Peptide Source: iTRAQ, Colorectal cancer

MELQAARACFALLWGCAAAAAA**Q**GKEVVLLDFAAAGGELGWLTHPYGKGWDLMQNIMNDMPIYMYSVCNVMSG
DQDNWLR**TNWVYR**GGEAERNNFELNFTVRDCNSFPGGASSCKETFNLYYAESDLDYGTNFKRLFTKIDTIAPDEI
TVSSDFEARHVKLNVEER**SVGPLTR**KGFYLAFQDIGACVALLSVRVYKKCPPELLQGLAHFPETIAGSDAPSLAT
VAGTCVDHAVVPPGGEFPRMHCAVDGEWLVPIGQCLCQAGYEKVEDACQACSPGFFKFEASESPCLECPEHTLPS
PEGATSCCECEGFFRAPQDPASMPCTRPPSAPHYLTAVGMCAKVELRW**TPPDQSGGR**EDIVYSVTECQCWPESGE
CGPCEASVR**YSEPPHGLTR**TSVTVSDLEPHMNYTFTVEAR**NGVSGLVTSR**SFTASVSINQTEPPKVRLEGRSTT
SLSVSWSIPPPQCSRVMKYEVTYRKKGDSNSYNVRRTEGFSVTLDDLAPDTTYLVQVQALTQEGQGAGSKVHEFQ
TSLPEGSGNLAVIGGVAVGVVLLVLAGVGFFIHRRRKNQRRARQSPEDVYFSKSEQLKPLKTYVDPHTYEDPNQA
VLKFTTEIH**FPSCVTRQ**VIGAGEFGEVYK**GMLKTSSGKKEVPVAIKTLKAGYTEKQRVDFLGEAGIMGQFSHHNI**
IRLEGVISYKPMIITEYMENGALDKFLREKDGESVLQVLGMLRGIAAGMKYLANMNYVHRDLAARNILVNSN
LVCKVSDFGLSRVLEDDPEATYTTSGGKIPIR**WTAPEAISYR**KFTSASDVWSFGIVMWEVMTYGERPYWELSNHE
VMK**AINDGFR**LPTPMDCPSAIYQLMMQCWQQRARRPKFADIVSILDKLIRAPDSLKTLDADFDPVRSIR**LPSTSG**

SEGVPFRITVSEWLESIKMQQYTEHFMAAGYTAIEKVVQMTNDDIKRIGVRLPGHQKRIAYSLGLKQVNTVGIP
I

Mass Match Peptides (bold):

LNVEERSVGPLTR [942]
NGVSGGLVTSR [538]
TASVSINQTEPPK [673]

Tandem Peptides (underline):

LNVEERSVGPLTR [942]
NGVSGGLVTSR [538]
TASVSINQTEPPK [673]

Peptide Source: iTRAQ, Hepatocellular cancer

MELQAARACFALLWGCALAAAAAQQKEVVLLDFAAAGGELGWLTHPYGKGWDLMQNIMNDMPIYMSVCNVMSG
DQDNWLRITNWVYRGEAERNNFELNFTVRDCNSFPGGASSCKETFNLYAESDLGYGTNFQKRLFTKIDTIAPDEI
TVSSDFEARHVKLNVEERSVGPLTRKGFYLAQDIGACVALLSVRVYKKCPPELLQGLAHFPETIAGSDAPSLAT
VAGTCVDHAVVPPGGEEPRMHCAVDGEWLVPVIGQCLCQAGYEKVEDACQACSPGFFKFEASESPCLECPEHTLPS
PEGATSCCEEGFFRAPQDPASMPCTRPPSAPHYLTAVGMGAKVELRWTPPDSSGGREDIVYSVTCEQCWPESGE
CGPCEASVRYSEPPHGLTRTSVTVDLEPHMNYTFTVEARNGVSGGLVTSRSFRTASVSINQTEPPKVRLEGRSTT
SLSVSWSIPTPPQSRVWKYEVTYRKKGDSNSYNVRRTEGFSVTLLDAPDITYLVQVQALTQEGQGAGSKVHEFQ
TLSPEGSGNLAVIGGVAVGVVLLLVLAGVGFFIHRRRKNQARQSPEDVYFSKSEQLKPLKTYVDPHTYEDPNQA
VLKFTTEIHPSCVTRQKVIAGEFGEVYKGLMTSSGKKEVPVAIKTLKAGYTEKQRVDFLGEAGIMQGFSHHNI
IRLEGVLSKYKPMMLITEYMENGALDKFLREKDGESVLQVLGMLRGLAAGMKYLANMNYVHRDLAARNILVNSN
LVCKVSDFGLSRVLEDDPEATYTTSGGKIPIRWTAPEAISIYRKFTSASDVWSFGIVMWEVMTYGERPYWELSNHE
VMKAINDGFRLLPTMDCPSAIYQLMMQCWQERARRPKFADIVSILDKLIRAPDSLKTLDLDFDPRVSIRLPSTSG
SEGVPFRITVSEWLESIKMQQYTEHFMAAGYTAIEKVVQMTNDDIKRIGVRLPGHQKRIAYSLGLKQVNTVGIP
I

Mass Match Peptides (bold):

TASVSINQTEPPK [673]

Tandem Peptides (underline):

TASVSINQTEPPK [673]

Peptide Source: iTRAQ, Non-small cell lung cancer

MELQAARACFALLWGCALAAAAAQQKEVVLLDFAAAGGELGWLTHPYGKGWDLMQNIMNDMPIYMSVCNVMSG
DQDNWLRITNWVYRGEAERNNFELNFTVRDCNSFPGGASSCKETFNLYAESDLGYGTNFQKRLFTKIDTIAPDEI
TVSSDFEARHVKLNVEERSVGPLTRKGFYLAQDIGACVALLSVRVYKKCPPELLQGLAHFPETIAGSDAPSLAT
VAGTCVDHAVVPPGGEEPRMHCAVDGEWLVPVIGQCLCQAGYEKVEDACQACSPGFFKFEASESPCLECPEHTLPS
PEGATSCCEEGFFRAPQDPASMPCTRPPSAPHYLTAVGMGAKVELRWTPPDSSGGREDIVYSVTCEQCWPESGE
CGPCEASVRYSEPPHGLTRTSVTVDLEPHMNYTFTVEARNGVSGGLVTSRSFRTASVSINQTEPPKVRLEGRSTT
SLSVSWSIPTPPQSRVWKYEVTYRKKGDSNSYNVRRTEGFSVTLLDAPDITYLVQVQALTQEGQGAGSKVHEFQ
TLSPEGSGNLAVIGGVAVGVVLLLVLAGVGFFIHRRRKNQARQSPEDVYFSKSEQLKPLKTYVDPHTYEDPNQA
VLKFTTEIHPSCVTRQKVIAGEFGEVYKGLMTSSGKKEVPVAIKTLKAGYTEKQRVDFLGEAGIMQGFSHHNI
IRLEGVLSKYKPMMLITEYMENGALDKFLREKDGESVLQVLGMLRGIAAGMKYLANMNYVHRDLAARNILVNSN
LVCKVSDFGLSRVLEDDPEATYTTSGGKIPIRWTAPEAISIYRKFTSASDVWSFGIVMWEVMTYGERPYWELSNHE
VMKAINDGFRLLPTMDCPSAIYQLMMQCWQERARRPKFADIVSILDKLIRAPDSLKTLDLDFDPRVSIRLPSTSG
SEGVPFRITVSEWLESIKMQQYTEHFMAAGYTAIEKVVQMTNDDIKRIGVRLPGHQKRIAYSLGLKQVNTVGIP
I

Mass Match Peptides (bold):

DGEFSVLQVLGMLR [121]
LNVEERSVGPLTR [942]
NGVSGGLVTSR [538]

TASVSINQTEPPK [673]

Tandem Peptides (underline):

DGEFSVLQLVGMLR [121]

LNVEERSVGPLTR [942]

NGVSGGLVTSR [538]

TASVSINQTEPPK [673]

Peptide Source: iTRAQ, Renal cell cancer

MELQAARACFALLWGCALAAAAAQQKEVVLLDFAAAGGELGWLTHPYGKGWDLMQNIMNDMPIYMSVCNVMSG
DQDNWLRTNWVYRGEAERNNFELNFTVRDCNSFPGGASSCKETFNLYYAESDLGYGTNFKRLFTKIDTIAPDEI
TVSSDFEARHVKNLVEERSVGPPLTRKGFYLAQDQIGACVALLSVRVYKKCPPELLQGLAHFPETIAGSDAPSLAT
VAGTCVDHAVVPPGGEPRMHCAVDGEWLVPVIGQCLCQAGYEKVEDACQACSPGFFKFEASESPCLECPEHTLPS
PEGATSCCEEGFFRAPQDPASMPCTRPPSAPHYLTAVGMGAKVELRWTPPDQSGGREDIVYSVTCEQCWPESGE
CGPCEASVRYSEPPHGLTRTSVTVSDLEPHMNYTFTVEARNGVSGGLVTSRSFRTASVSINQTEPPKVRLEGRSTT
SLSVSWSIPPPQQSRVWKYEVITYRKKGDSNSYNVRRTEGFSVTLDDLPDPTTYLVQVQALTQEGQGAGSKVHEFQ
TLSPEGSGNLAVIGGVAVGVVLLVLAVGVGFIIHRRKNQRRARQSPEDVYFSKSEQLKPLKTYVDPHTYEDPNQA
VLKFTTEIHPSCVTRQKVI GAGEFGEVYKGLMKTSSGKKEVPVAIKTLKAGYTEKQRVDFLGEAGIMGQFSSHNI
IRLEGVISKYKPMIITEYMENGALDKFLREKDGFEFSVLQLVGMLRGIAAGMKYLANMNYVHRDLAARNILVNSN
LVCKVSDFGLSRVLEDDPEATYTTSGGKIPIRWTAPEAISIYRKFTSASDVWSFGIVMWEVMTYGERPYWELSNHE
VMKAINDFRLPTPMDCPSAIYQLMMQCWQERARRPKFADIVSILDKLIRAPDSLKTDLADFDPVRSIRLPSTSG
SEGVPFRTVSEWLESIKMQQYTEHFMAAGYTAIEKVQMTNDDIKRIGVRLLPGHQKRIAYSLLGLKDQVNTVGIP
I

Mass Match Peptides (bold):

LPGHQKR [478]

NGVSGGLVTSR [538]

TASVSINQTEPPK [673]

Tandem Peptides (underline):

LPGHQKR [478]

NGVSGGLVTSR [538]

TASVSINQTEPPK [673]

Peptide Source: iTRAQ, Small cell lung cancer

MELQAARACFALLWGCALAAAAAQQKEVVLLDFAAAGGELGWLTHPYGKGWDLMQNIMNDMPIYMSVCNVMSG
DQDNWLRTNWVYRGEAERNNFELNFTVRDCNSFPGGASSCKETFNLYYAESDLGYGTNFKRLFTKIDTIAPDEI
TVSSDFEARHVKNLVEERSSVGPLTRKGFYLAQDQIGACVALLSVRVYKKCPPELLQGLAHFPETIAGSDAPSLAT
VAGTCVDHAVVPPGGEPRMHCAVDGEWLVPVIGQCLCQAGYEKVEDACQACSPGFFKFEASESPCLECPEHTLPS
PEGATSCCEEGFFRAPQDPASMPCTRPPSAPHYLTAVGMGAKVELRWTPPDQSGGREDIVYSVTCEQCWPESGE
CGPCEASVRYSEPPHGLTRTSVTVSDLEPHMNYTFTVEARNGVSGGLVTSRSFRTASVSINQTEPPKVRLEGRSTT
SLSVSWSIPPPQQSRVWKYEVITYRKKGDSNSYNVRRTEGFSVTLDDLPDPTTYLVQVQALTQEGQGAGSKVHEFQ
TLSPEGSGNLAVIGGVAVGVVLLVLAVGVGFIIHRRKNQRRARQSPEDVYFSKSEQLKPLKTYVDPHTYEDPNQA
VLKFTTEIHPSCVTRQKVI GAGEFGEVYKGLMKTSSGKKEVPVAIKTLKAGYTEKQRVDFLGEAGIMGQFSSHNI
IRLEGVISKYKPMIITEYMENGALDKFLREKDGFEFSVLQLVGMLRGIAAGMKYLANMNYVHRDLAARNILVNSN
LVCKVSDFGLSRVLEDDPEATYTTSGGKIPIRWTAPEAISIYRKFTSASDVWSFGIVMWEVMTYGERPYWELSNHE
VMKAINDFRLPTPMDCPSAIYQLMMQCWQERARRPKFADIVSILDKLIRAPDSLKTDLADFDPVRSIRLPSTSG
SEGVPFRTVSEWLESIKMQQYTEHFMAAGYTAIEKVQMTNDDIKRIGVRLLPGHQKRIAYSLLGLKDQVNTVGIP
I

Mass Match Peptides (bold):

NGVSGGLVTSR [538]

SVGPLTRK [663]

TASVSINQTEPPK [673]

Tandem Peptides (underline):

NGVSGLVTSR [538]
 SVGPLTRK [663]
 TASVSINQTEPPK [673]

OGTA202 (SEQ ID No: 35)

Peptide Source: 1D-GE, Colorectal cancer

MGLPRGPLASLLLLQVCWLQCAASEPCRAVFREAEVTL EAGGAEQEPGQALGKVFMGCPGQEPALFSTDND DFTV
 RNGETVQERRSLKERNPLKIFPSKRILRRHKRDWV VAPISVPENGKGFPFQRLNQLKSNKDRD TKIFYSITGPGA
 DSPPEGVFAVEKETGWLLLNKPLDREEIAKYELFGH AVSENGASVEDPMNISIIIVTDQNDHKPKFTQD TFRGSVL
 EGVLPGTSMQVTATDEDDAIYTYNGVVAYSISHSQ EPKDPHDLMTIHRSTGTISVISSGLDREKVPEY TLT IQA
 TDMDGDGSTTTAVAVVEILDANDNAPMFD PQKYEAHVPENAVGHEVQRLTVTDLDAPNSPAWRATY LIMGGDDGD
 HFTITTHPESNQILTTTRKGLDFAKNQHTLYVEVT NEAPFVLKLP TSTATIVVHVEDVNEAPVFVPPSKVVEVQ
 EGIPTGEPVCVYTAEDPDKENQKISYRILRDPAGW LAMPDPSGQVTAVGTL DREDEQFVRNNIYEV MVLAMDNGS
 PPTTGTGTTTTLIDVNDHGPVPEPRQITICNQSPVRHVLNITDKDLSPH TSPFQAQLTDDSDIYWTA EVNEEGD
 TVVLSLKKFLKQD TYDVHLSLSDHGNKEQLTVIRATVCDCHGHVETCPGPWKGGF ILPVLGAVLALLFLLL VLLL
 LVRKKRKIKEPLLLPEDDTRDNV FYYGEEGGGEEDQDYDITQLHRGLEARPEVVL RNDVAPTIIPTPMYRPRPAN
 PDEIGNFIIENLKAANTDPTAPPYDTLLVFDYEGSGSDAASLSLTSSASDQDQDYDYLNEWGSRFKKLADMYGG
 GEDD

Mass Match Peptides (bold):

Tandem Peptides (underline):

FTQD TFR [277]

Peptide Source: iTRAQ, Colorectal cancer

MGLPRGPLASLLLLQVCWLQCAASEPCRAVFREAEVTL EAGGAEQEPGQALGKVFMGCPGQEPALFSTDND DFTV
 RNGETVQERRSLKERNPLKIFPSKRILRRHKRDWV VAPISVPENGKGFPFQRLNQLKSNKDRD TKIFYSITGPGA
 DSPPEGVFAVEKETGWLLLNKPLDREEIAKYELFGH AVSENGASVEDPMNISIIIVTDQNDHKPKFTQD TFRGSVL
 EGVLPGTSMQVTATDEDDAIYTYNGVVAYSISHSQ EPKDPHDLMTIHRSTGTISVISSGLDREKVPEY TLT IQA
 TDMDGDGSTTTAVAVVEILDANDNAPMFD PQKYEAHVPENAVGHEVQRLTVTDLDAPNSPAWRATY LIMGGDDGD
 HFTITTHPESNQILTTTRKGLDFAKNQHTLYVEVT NEAPFVLKLP TSTATIVVHVEDVNEAPVFVPPSKVVEVQ
 EGIPTGEPVCVYTAEDPDKENQKISYRILRDPAGW LAMPDPSGQVTAVGTL DREDEQFVRNNIYEV MVLAMDNGS
 PPTTGTGTTTTLIDVNDHGPVPEPRQITICNQSPVRHVLNITDKDLSPH TSPFQAQLTDDSDIYWTA EVNEEGD
 TVVLSLKKFLKQD TYDVHLSLSDHGNKEQLTVIRATVCDCHGHVETCPGPWKGGF ILPVLGAVLALLFLLL VLLL
 LVRKKRKIKEPLLLPEDDTRDNV FYYGEEGGGEEDQDYDITQLHRGLEARPEVVL RNDVAPTIIPTPMYRPRPAN
 PDEIGNFIIENLKAANTDPTAPPYDTLLVFDYEGSGSDAASLSLTSSASDQDQDYDYLNEWGSRFKKLADMYGG
 GEDD

Mass Match Peptides (bold):

EQLTVIR [904]
 ISYRILR [925]
 STGTISVISSGLDREK [975]

Tandem Peptides (underline):

EQLTVIR [904]
 ISYRILR [925]
 STGTISVISSGLDREK [975]

Peptide Source: iTRAQ, Non-small cell lung cancer

MGLPRGPLASLLLLQVCWLQCAASEPCRAVFREAEVTL EAGGAEQEPGQALGKVFMGCPGQEPALFSTDND DFTV
 RNGETVQERRSLKERNPLKIFPSKRILRRHKRDWV VAPISVPENGKGFPFQRLNQLKSNKDRD TKIFYSITGPGA
 DSPPEGVFAVEKETGWLLLNKPLDREEIAKYELFGH AVSENGASVEDPMNISIIIVTDQNDHKPKFTQD TFRGSVL

EGVLPGTSVMQVTATDEDDAIYTYNGVVAYSISHSQEPKDPHDLMTIHRSTGTISVISSGLDREKVPEYTLTIQA
 TDMGDGSGSTTAVAVVEILDANDNAPMFDPOKYEAHVPENAVGHEVQRLTVTDLDAPNSPAWRATYILMGDDGD
 HFTITTHPESNQGILTRKGLDFEAKNQHTLYVEVTNEAPFVLKLPSTATIVVHVEDVNEAPVFVPPSKVVEVQ
 EGIPTEGPVCVYTAEDPDKENQKISYRILRDPAGWLAMDPSGQVAVGTLGREDEQFVRNNIYEVMLAMDNGS
 PPTTGTGTLTLLIDVNDHGPVPEPRQITICNQSPVRHVLNITDKDLSPHTSPPQAQLTDDSDIYWTAEVNEEGD
 TVVLSLKKFLKQDQTYDVHLSLSDHGNKEQLTVIRATVCDCHGHVETCPGPKWGGFILPVLGAVLALLFLLVLL
 LVRKKRKIKEPLLLPEDDTRDNVIFYGEEGGGEEDQDYDTQLHRGLEARPEVVLNRNDVAPTIIPTPMYRPRPAN
 PDEIGNFIENLKAANTDPTAPPYDTLLVFDYEGSGSDAASLSSLTSSASDQDQDYDYLNEWGSRFKKLADMYGG
 GEDD

Mass Match Peptides (bold):

EQLTVIR [904]

Tandem Peptides (underline):

EQLTVIR [904]

OGTA203 (SEQ ID No: 36)

Peptide Source: 1D-GE, Ovarian cancer

MRTYRYFLLLFVWGQPYPTLSTPLSKRTSGFPAKKRALELSGNSKNELNRSKRSMWNQFFLLEEYTGSDYQYVG
 KLHSDQDRGDGSLKYILSGDGAGDLFIINENTGDIQATKRLDREEKPVYILRAQAINRRRTGRPVPESEFIKIH
 DINDNEPIFTKEVYTATVPMSDVGTFFVQVTATDADDPTYGNSAKVVYSILQGQPYFSVESETGIKKTALLNMD
 RENREQYQVVIQAKDMGCGMGLSGTTTNNITLTDVNDNPPRFQSTYQFKTPESSPPGTPIGRIRIKASDADVGEN
 AEIEYSITDGEGLDMFDVITDQETQEGIIITVKLLDFEKKKVYTLKVEASNYPYVEPRFLYLGPFKDSATVRIIVE
 DVDEPPVFSKLAYILQIREDAQINTTIGSVTAQDPDAARNPVKYSVDRHTMDRIFNIDSGNGSIFTSKLLDRET
 LLWHNITVIATEINNPKQSSRVPLYIKVLDVNDNAPEFAEFYETVCEKAKADQLIQTILHAVDKDDPYSGHQFSF
 SLAPEAASGSNFTIQDNKDNTAGILTRKNGYNRHEMSTYLLPVVISDNDYPVQSSSTGTVTVRVCACDHGNGMQSC
 HAEALIHPTGLSTGALVAILLCIVILLVTVVLFAALRRQRKKEPLIISKEDIRDNIVSYNDEGGGEEDTQAFDIG
 TLRNPEAIEDNKLRRDIVPEALFLPRRTPTARDNTDVRDIFNQRLEKENDTPTAPPYDSLATYAYEGTGSVADSL
 SSLESVTTDADQDYDYLSDWGPFRFKKLADMYGGVDSKDS

Mass Match Peptides (bold):

DNIVSYNDEGGGEEDTQAFDIGTLR [144]

EDAQINTTIGSVTAQDPDAAR [168]

RTPTAR [618]

TALLNMDR [669]

TPESSPPGTPIGR [716]

TSGFPAKK [727]

VEASNYPYVEPR [751]

Tandem Peptides (underline):

VEASNYPYVEPR [751]

Peptide Source: 1D-GE, Renal cell cancer

MRTYRYFLLLFVWGQPYPTLSTPLSKRTSGFPAKKRALELSGNSKNELNRSKRSMWNQFFLLEEYTGSDYQYVG
 KLHSDQDRGDGSLKYILSGDGAGDLFIINENTGDIQATKRLDREEKPVYILRAQAINRRRTGRPVPESEFIKIH
 DINDNEPIFTKEVYTATVPMSDVGTFFVQVTATDADDPTYGNSAKVVYSILQGQPYFSVESETGIKKTALLNMD
 RENREQYQVVIQAKDMGCGMGLSGTTTNNITLTDVNDNPPRFQSTYQFKTPESSPPGTPIGRIRIKASDADVGEN
 AEIEYSITDGEGLDMFDVITDQETQEGIIITVKLLDFEKKKVYTLKVEASNYPYVEPRFLYLGPFKDSATVRIIVE
 DVDEPPVFSKLAYILQIREDAQINTTIGSVTAQDPDAARNPVKYSVDRHTMDRIFNIDSGNGSIFTSKLLDRET
 LLWHNITVIATEINNPKQSSRVPLYIKVLDVNDNAPEFAEFYETVCEKAKADQLIQTILHAVDKDDPYSGHQFSF
 SLAPEAASGSNFTIQDNKDNTAGILTRKNGYNRHEMSTYLLPVVISDNDYPVQSSSTGTVTVRVCACDHGNGMQSC
 HAEALIHPTGLSTGALVAILLCIVILLVTVVLFAALRRQRKKEPLIISKEDIRDNIVSYNDEGGGEEDTQAFDIG
 TLRNPEAIEDNKLRRDIVPEALFLPRRTPTARDNTDVRDIFNQRLEKENDTPTAPPYDSLATYAYEGTGSVADSL
 SSLESVTTDADQDYDYLSDWGPFRFKKLADMYGGVDSKDS

Mass Match Peptides (bold):

KNGYNR [428]
TSGFPAKK [727]

Tandem Peptides (underline):

IVVEDVDEPPVFSK [402]

Peptide Source: iTRAQ, Non-small cell lung cancer

MRTYRYFLLLFWVGQPYPTLSTPLSKRTSGFPAKKRALELSGNSKNELNRSKRSMWNQFFLLEEYTGSDYQYVG
KLHSDQDRGDGSLKYILSGDGAGDLFIINENTGDIQATKRLDREEKPVYILRAQAINRRTGRPVEPESEFIKIH
DINDNEPIFTKEVYTATVPMSDVGTFFVQVTATDADDDPTYGNSAKVVYSILQGQPYFSVESETGIKKTALLNMD
RENREQYQVVIQAKDMGGQMGGLSGTTTNNITLTDVNDNPPRFPOSTYQFKTPESSPPGTPIGRIKASDADVGEN
AEIEYSITDGEGLDMFDVITDQETQEGIIITVKKLLDFEKKKVYTLK**VEASNPYVEPRFLYLGPFK**KDSATVRIVVE
DVDEPPVFSKLAYILQIREDAQINTTIGSVTAQDDAARNPVKYSVDRHTDMDRIFNIDSGNGSIFTSKLLDRET
LLWHNITVIATEINNPKQSSRVPLYIKVLDVNDNAPEFAEFYETFVCEKAKADQLIQTTLHAVDKDDPYSGHQFSF
SLAPEAASGSNFTIQDNKDNTAGILTRKNGYNRHEMSTYLLPVVISDNDYPVQSSTGTVTVRVACDHHGNMQSC
HAEALIHPTGLSTGALVAILLCIVILLVTVVLFAALRRQRKKEPLIISKEDIRDNIIVSYNDEGGGEEDTQAFDIG
TLRNPEAIEDNKLRRDIVPEALFLPRRTPTARDNTDVRDFINQRLKENDTDPTAPPYDSLATYAYEGTGSVADSL
SSLESVTTDADQDYDYLSDWGPFRKKLADMYGGVDSKDKS

Mass Match Peptides (bold):

VEASNPYVEPRFLYLGPFK [989]

Tandem Peptides (underline):

VEASNPYVEPRFLYLGPFK [989]

Peptide Source: iTRAQ, Renal cell cancer

MRTYRYFLLLFWVGQPYPTLSTPLSKRTSGFPAKKRALELSGNSKNELNRSKRSMWNQFFLLEEYTGSDYQYVG
KLHSDQDRGDGSLKYILSGDGAGDLFIINENTGDIQATKRLDREEKPVYILRAQAINRRT**TGRPVEPESEFIK**IH
DINDNEPIFTKEVYTATVPMSDVGTFFVQVTATDADDDPTYGNSAKVVYSILQGQPYFSVESETGIKKTALLNMD
RENREQYQVVIQAKDMGGQMGGLSGTTTNNITLTDVNDNPPRFPOSTYQFKTPESSPPGTPIGRIKASDADVGEN
AEIEYSITDGEGLDMFDVITDQETQEGIIITVKK**LLDFEK**KKKVYTLKVEASNPYVEPRFLYLGPFKDSATVRIVVE
DVDEPPVFSKLAYILQIREDAQINTTIGSVTAQDDAARNPVKYSVDRHTDMDRIFNIDSGNGSIFTSKLLDRET
LLWHNITVIATEINNPKQSSRVPLYIKVLDVNDNAPEFAEFYETFVCEKAKADQLIQTTLHAVDKDDPYSGHQFSF
SLAPEAASGSNFTIQDNKDNTAGILTRKNGYNRHEMSTYLLPVVISDNDYPVQSSTGTVTVRVACDHHGNMQSC
HAEALIHPTGLSTGALVAILLCIVILLVTVVLFAALRRQRKKEPLIISKEDIRDNIIVSYNDEGGGEEDTQAFDIG
TLRNPEAIEDNKLRRDIVPEALFLPRRTPTARDNTDVRDFINQRLKENDTDPTAPPYDSLATYAYEGTGSVADSL
SSLESVTTDADQDYDYLSDWGPFRKKLADMYGGVDSKDKS

Mass Match Peptides (bold):

LLDFEK [934]
TGRPVEPESEFIK [981]

Tandem Peptides (underline):

LLDFEK [934]
TGRPVEPESEFIK [981]

OGTA206 (SEQ ID No: 37)

Peptide Source: 1D-GE, Breast cancer

MASMGLOVMGIALAVLGLAVMLCCALPMWRVTAFIGSNIVTSQTIWEGLWMNCVVQSTGQMCKVYD**SLALPQ**
DLQAARALVIIISIIAALGVLLSVVGGKCTNCLEDESAAKTMIVAGVVFLLAGLMVIVPVSWTAHNI**IQDFYNP**
LVASGQKREMGASLYVGWAASGLLLLGGLLCCNCPPRTDKPYSAKYSAAARSAAASNYV

Mass Match Peptides (bold):

Tandem Peptides (bold):

VYDSLALPQDLQAAR [817]

Peptide Source: 1D-GE, Pancreatic cancer

MASMGQLQVMGIALAVLGWLAVMLCCALPMWRVTAFIGSNIVTSQTIWEGLMNCVVQSTGQMCK**VYDSLALPQDLQAAR**ALVIISIIVAALGVLLSVVGKCTNCLEDESAAKATMIVAGVVFLLAGLMVIVPVSWTAHNIIQDFYNP
LVASGQKREMGASLYVGWAASGLLLGGGLCCNCPPRTDKPYSAKYSAARSAAASNYV

Mass Match Peptides (bold):

VYDSLALPQDLQAAR [817]

Tandem Peptides (underline):

VYDSLALPQDLQAAR [817]

Peptide Source: 1D-GE, Prostate cancer

MASMGQLQVMGIALAVLGWLAVMLCCALPMWRVTAFIGSNIVTSQTIWEGLMNCVVQSTGQMCK**VYDSLALPQDLQAAR**ALVIISIIVAALGVLLSVVGKCTNCLEDESAAKATMIVAGVVFLLAGLMVIVPVSWTAHNIIQDFYNP
LVASGQKREMGASLYVGWAASGLLLGGGLCCNCPPRTDKPYSAKYSAARSAAASNYV

Mass Match Peptides (bold):

VYDSLALPQDLQAAR [817]

Tandem Peptides (underline):

Peptide Source: iTRAQ, Colorectal cancer

MASMGQLQVMGIALAVLGWLAVMLCCALPMWRVTAFIGSNIVTSQTIWEGLMNCVVQSTGQMCK**VYDSLALPQDLQAAR**ALVIISIIVAALGVLLSVVGKCTNCLEDESAAKATMIVAGVVFLLAGLMVIVPVSWTAHNIIQDFYNP
LVASGQKREMGASLYVGWAASGLLLGGGLCCNCPPRTDKPYSAKYSAAR**SAAASNYV**

Mass Match Peptides (bold):

SAAASNYV [968]
VYDSLALPQDLQAAR [817]

Tandem Peptides (underline):

SAAASNYV [968]
VYDSLALPQDLQAAR [817]

Peptide Source: iTRAQ, Non-small cell lung cancer

MASMGQLQVMGIALAVLGWLAVMLCCALPMWRVTAFIGSNIVTSQTIWEGLMNCVVQSTGQMCK**VYDSLALPQDLQAAR**ALVIISIIVAALGVLLSVVGKCTNCLEDESAAKATMIVAGVVFLLAGLMVIVPVSWTAHNIIQDFYNP
LVASGQKREMGASLYVGWAASGLLLGGGLCCNCPPRTDKPYSAKYSAARSAAASNYV

Mass Match Peptides (bold):

VYDSLALPQDLQAAR [817]

Tandem Peptides (underline):

VYDSLALPQDLQAAR [817]

OGTA213 (SEQ ID No: 38)

Peptide Source: 1D-GE, Lung cancer

MRPRTKARSPGRALRNPWRGFLPLTLALFVGAGHAQRDPVGRYEPAGGDANRLRRPGGSYPAAAAAKVYSLFREQ
 DAPVAGLQPVRAQPGWGSPPRRPTEAEARRPSRAQQSRRVQPPAQTRRSTPLGQQQPAPRTRAAPALPRIGTPQR
 SGAAPPPTPPRGLTGRNVCGGQCCPGWTTANSTNHCIKPVCEPPCQNRGSCSRPQLCVCRSRGFRGARCEEVIPDE
 EFDPQNSRLAPRRWAERSPNLRRSSAAGEGTLARAQPPAPQSPAPQSPAGTSLGLSQTHPSQQHVGLSRTVRL
 HPTATASSQLSSNALPPGPGLEQRDGTQQAVPLEHPSSPWGLNLTEKIKKIKIVFTPTICKQTCARGHCANSCE
 GDTTTLYSQGGHGHDPKSGFRIYFCQIPCLNGRCIGRDECWCPANSTGKFCHLPQPDPREPPGRGSRPRALLE
 APLKQSTFTLPLSNQLASVNPVSLVKVHIHHPPEASVQIHQVAQVRGGVEEALVENSVETRPPFWLPASPGHSLWD
 SNNIPARSGEPPRPLPPAAPRRPGLLGRCYLNTVNGQCANPLLELTQEDCCGSVGAFWGVTLCAPCPPRPASPV
 IENGQLECPQGYKRLNLTHCQDINECLTLGLCKDAECVNTRGSYLCTCRPGLMLDPSRSRCVSDKATISMLQGLCY
 RSLPGTCTLPLAQIRITKQICCCSRVGKAWGSECEKCLPGTEAFREICPAGHGYTYASSDIRLSMRKAEIEEELA
 RPPREQQRRSSGALPGPAERQPLRVVDTWLEAGTIPDKGDSQAGQVTTSVTHAPAWVTGNATTPPMPEQGI
 QEEQVTPSTDVLTSTPGIDRCAAGATNVCGPGTCVNLDPGYRCVCSPGYQLHPSQAYCTDDNECLRDFCKGKG
 RCINRVGSYSFCYPGYTLATSGATQECQDINECEQPGVCSGGQCTNTEGSYHCECDQGYIMVRKGHCQDINECR
 HPGTCTPDGRCVNSPGSYTCLACEEGYRGQSGSCVDVNECLTPGVCAHGKCTNLEGSFRCSCEQGYEVTSD
 DVDECASTRASCPTGLCLNTEGSFACSAACENGYWVNEGTACEDLDECAFPGVCPGVCNTNAGSFSCDKCDGGY
 PSPLGDSCEDVDECEDPQSSCLGGECKNTVGSYQCLCPQGFQLANGTVCEDEVNECMGEEHCAPHGECLNSHGSFF
 CLCAPGFVSAEGGTSCQDVDECATTDPCVGGHCVNTEGSFNCCLCETGTFQSPESGECVDIDECEDYDGPVCGTWK
 CENSPGSYRCVLGCQPGFHMAPNGDCIDIDECANDTMCGSHGFCNDTDCSFRCLCDQGFETSPSGWDCVDVNECE
 LMLAVCGAALCENVEGSFLCLCASDLEEYDAQEGHCRPRGAGQSMSEAPTGDHAPAPTRMDCYSQGKHAPCSS
 VLGRNTTQAECCTQGATWGDACDLCPSEDSAEFSEICPSGKGYIPVEGAWTFGQTMYTDADECVIIFGPGLCFNG
 RCLNTVPGYVCLCNPGFHYDASHKKCEDHDECQDLACENGEVNTESGFHCFCSPPLTLDLSSQRCMNSTSSTED
 LPDHDHMDICWKVNTDVCSEPLRGHRTTYTECCQDQKAWSQQCALCPPRSSEVYAQLCNVARI
 EAREAGVHFRPGYEGYGGPDDLHYSIYGPDPGAPFNYLGPEDTVPFAFPNTAGHSADRTPILESPLQPS
 ELQPHYVASHPEPAGFEGQLAECEGILNCGENRCVRVREGYTCDCEFGFQLDAAHMACVDVNECDLNGPAVLCV
 HGYCENTEGSYRCHCSPGYVAEAGPPHCTAKE

Mass Match Peptides (bold):

Tandem Peptides (underline):

IVFTPTICK [401]

Peptide Source: iTRAQ, Colorectal cancer

MRPRTKARSPGRALRNPWRGFLPLTLALFVGAGHAQRDPVGRYEPAGGDANRLRRPGGSYPAAAAAKVYSLFREQ
 DAPVAGLQPVRAQPGWGSPPRRPTEAEARRPSRAQQSRRVQPPAQTRRSTPLGQQQPAPRTRAAPALPRIGTPQR
 SGAAPPPTPPRGLTGRNVCGGQCCPGWTTANSTNHCIKPVCEPPCQNRGSCSRPQLCVCRSRGFRGARCEEVIPDE
 EFDPQNSRLAPRRWAERSPNLRRSSAAGEGTLARAQPPAPQSPAPQSPAGTSLGLSQTHPSQQHVGLSRTVRL
 HPTATASSQLSSNALPPGPGLEQRDGTQQAVPLEHPSSPWGLNLTEKIKKIKIVFTPTICKQTCARGHCANSCE
 GDTTTLYSQGGHGHDPKSGFRIYFCQIPCLNGRCIGRDECWCPANSTGKFCHLPQPDPREPPGRGSRPRALLE
 APLKQSTFTLPLSNQLASVNPVSLVKVHIHHPPEASVQIHQVAQVRGGVEEALVENSVETRPPFWLPASPGHSLWD
 SNNIPARSGEPPRPLPPAAPRRPGLLGRCYLNTVNGQCANPLLELTQEDCCGSVGAFWGVTLCAPCPPRPASPV
 IENGQLECPQGYKRLNLTHCQDINECLTLGLCKDAECVNTRGSYLCTCRPGLMLDPSRSRCVSDKATISMLQGLCY
 RSLPGTCTLPLAQIRITKQICCCSRVGKAWGSECEKCLPGTEAFREICPAGHGYTYASSDIRLSMRKAEIEEELA
 RPPREQQRRSSGALPGPAERQPLRVVDTWLEAGTIPDKGDSQAGQVTTSVTHAPAWVTGNATTPPMPEQGI
 QEEQVTPSTDVLTSTPGIDRCAAGATNVCGPGTCVNLDPGYRCVCSPGYQLHPSQAYCTDDNECLRDFCKGKG
 RCINRVGSYSFCYPGYTLATSGATQECQDINECEQPGVCSGGQCTNTEGSYHCECDQGYIMVRKGHCQDINECR
 HPGTCTPDGRCVNSPGSYTCLACEEGYRGQSGSCVDVNECLTPGVCAHGKCTNLEGSFRCSCEQGYEVTSD
 DVDECASTRASCPTGLCLNTEGSFACSAACENGYWVNEGTACEDLDECAFPGVCPGVCNTNAGSFSCDKCDGGY
 PSPLGDSCEDVDECEDPQSSCLGGECKNTVGSYQCLCPQGFQLANGTVCEDEVNECMGEEHCAPHGECLNSHGSFF
 CLCAPGFVSAEGGTSCQDVDECATTDPCVGGHCVNTEGSFNCCLCETGTFQSPESGECVDIDECEDYDGPVCGTWK
 CENSPGSYRCVLGCQPGFHMAPNGDCIDIDECANDTMCGSHGFCNDTDCSFRCLCDQGFETSPSGWDCVDVNECE
 LMLAVCGAALCENVEGSFLCLCASDLEEYDAQEGHCRPRGAGQSMSEAPTGDHAPAPTRMDCYSQGKHAPCSS
 VLGRNTTQAECCTQGATWGDACDLCPSEDSAEFSEICPSGKGYIPVEGAWTFGQTMYTDADECVIIFGPGLCFNG
 RCLNTVPGYVCLCNPGFHYDASHKKCEDHDECQDLACENGEVNTESGFHCFCSPPLTLDLSSQRCMNSTSSTED
 LPDHDHMDICWKVNTDVCSEPLRGHRTTYTECCQDQKAWSQQCALCPPRSSEVYAQLCNVARI
 EAREAGVH

FRPGYEGPGPDDLHYSIYCPDGAFFNYLGPEDTVPEPAFPNTAGHSADRTPILESPLQPSSELQPHYVASHPEP
PAGFEGQLAECEGILNGCENGRCVRVREGYTCDCFEFGQLDAAHMACVDVNECDDLNGPAVLGVHGYCENTEGSY
RCHCSPGYVAEAGPPHCTAKE

Mass Match Peptides (bold):

RSSAAGEGTLAR [967]

Tandem Peptides (underline):

RSSAAGEGTLAR [967]

Peptide Source: iTRAQ, Non-small cell lung cancer

MRPRTKARSPGRALRNPWRGFLPLTLALFVGAGHAQRDPVGRYEPAGGDANRLRRPGGSYPAAAAAKVYSLFREQ
DAPVAGLQPVERAQPGWGSPPRRPTEAEARRPSRAQQSRRVQPPAQTRRSTPLGQQQPAPRTRAAPALPRLGTPQR
SGAAPPTPPRGRLTGRNVCGGQCCPGWTTANSTNHCIKPVCEPPCQNRGSCSRPQLCVCRSGFRGARCEEVIPDE
EFDPQNSRLAPRRWAERSPNLRRSSAAGEGTLARQAQPAPQSPAPQSPAGTSLGLSQTHTPSQQHVLRSRTVRL
HPTATASSQLSSNALPPGPGLEQRDGTQQAQVPLEHPSSPWGLNLTEKIKKIKIVFTPTICKQTCARGHCANSCER
GDTTTLYSQGGHGHDPKSGFRIYFCQIPCLNGGRCIGRDECWCPANSTGKFCFLPIPPQDREPPGRGSRPRALLE
APLKQSTFTTLPLSNQLASVNPVSLVKVHIHHPPEASVQIHQVAQVRGGVEEALVENSVEPTRPPWLPASPGHSLWD
SNNIPARSGEPPLPLPPAAPRPRGLLGRCYLNTVNGQCANPLLELTQEDCCGSVGAFWGVTLCAPCPPRPASPV
IENGQLECPQGYKRLNLTHCQDINECLTLGLCKDAECVNTRGSYLCTCRPGLMLDPSRRCVSDKAISMLQGLCY
RSLGPGTCTTLPLAQRIITKQICCSRVGKAWGSECEKCPLEGTAEFREICPAGHGTYTASSDIRLSMRKAEELLA
RPPREQGQRSSGALPGFAERQPLRVVTDTWLEAGTIPDKGDSQAGQVTTSVTHAPAWVTGNATTPMPPEQGIABE
QEEQVTFSTDLVLTSTPGIDRCAAGATNVCGPGTCVNLDPGYRCVCSPGYQLHPSQAYCTDDNECLRDPCCKGK
RCINRVGSYSCFCYPGYTLATSGATQECQDINECEQPGVCSGGQCTNTEGSYHCECDQGYIMVRKGHCQDINECR
HPGTCPDGRCVNSPGSYTCLACEEYRGQSGSCVDVNECLTPGVCAHGKCTNLEGSFRCSCQGYEVTSDKEGCO
DVDECASTRASCTPTGLCLNTEGSFACSACENGYWVNEGTACEDLDECAFPVGVCPSGVCTNTAGSFCKDCDGGYR
PSPGLDSCEDVDECEDPQSSCLGGECKNTVGSYQCLCPQGFQLANGTVCEDEVNECMGEEHCAPHGECLNSHGSFF
CLCAGFVSAEAGTSCQDVDECATTDPCVGGHCVNTEGSFNCLCETGFGQPSPESGECVDIDECEGYDGPVCGTWK
CENSPGSYRCVLGCQPGFHMAPNGDCIDIDECAANDTMCGSHGFCNDTSGSFRCLCDQGFELSPSGWDCVDVNECE
IMLAVCGAALCENVEGSLCLCASDLEEDYDAQEGHCRPRGAGGQSMSEAPTGDHAPAPTRMDCYSGQKGHAPCSS
VLGRNTTQAECCCTQGATWGDACDLCPSEDSAEFSEICPSGKGYIPVEGAWTFGQTMYTDADECIVFGPGLCPNG
RCLNTVPGYVCLCNPGFHYDASHKKCEDHDECQDLACENGECVNTEGSFHCFCSPPLTDLDSQQRCMNSTSTED
LPDHDTHMDICWKKVTNDVCSEPLRGHRTTYTECCQDQKAWSQCALCPPRSSEVYQALCNVARI EAEREAGVH
FRPGYEGPGPDDLHYSIYCPDGAFFNYLGPEDTVPEPAFPNTAGHSADRTPILESPLQPSSELQPHYVASHPEP
PAGFEGQLAECEGILNGCENGRCVRVREGYTCDCFEFGQLDAAHMACVDVNECDDLNGPAVLGVHGYCENTEGSY
RCHCSPGYVAEAGPPHCTAKE

Mass Match Peptides (bold):

RSSAAGEGTLAR [967]

Tandem Peptides (underline):

RSSAAGEGTLAR [967]

OGTA214 (SEQ ID No: 39)

Peptide Source: 1D-GE, Ovarian cancer

MKAIHILTLALLSVNTATNQNSADAVTTTETATSGPTVAAADTTETNFPETASTTANTPSFPTATSPAPPIIS
THSSSTIPTPAPPIISTHSSSTIPTAADSESTTNVNSLATSDIITASSPNDGLITMVPSETQSNEMSPPTED
NQSSGPPTGTALLETSTLNSTGPNPCQDDPCADNSLCKVLHNTSFCLCLEGYYSNSTCKKGKVPKGKISVTVS
ETFDPEEKHSMAYQDLHSEITSLFKDVFSTSVYQQTIVILTSTLSRSEMRADDKFNVTIVTILAETTSNEK
TVTEKINKAIRSSSSNFLNYDLTLRCDDYGCNQATADDCLNGLACDCKSDLQRPNPQSPFCVASSLKCPDACNAQH
KQCLIKKSGGAPEACACVPGYQEDANGNCQKCAFYSGLDCKDKFQLILTIVGTIAGIVILSMIILIVTARSNNK
TKHIEENLIDEDFQNLKLRSTGFTNLGAEGSVFPKVRITASRDSQMQNPYSRHSSMPRPDY

Mass Match Peptides (bold):

QCLIKK [565]

SSSSNFLNYDLTLR [651]

Tandem Peptides (underline):

ISVTVSETFDPEEK [394]

SSSSNFLNYDLTLR [651]

Peptide Source: iTRAQ, Colorectal cancer

MKAIHLLTLLALLSVNTATNQGNSADAVTTTETATSGPTVAAADTTETNFPETASTTANTPSFPTATSPAPPIIS
THSSSTIPTPAPPIISTHSSSTIPIPTAADSESTTNVNSLATSDIITASSPNDGLITMVPSETQSNNEMSPTTED
NQSSGPTGTALLETSTLNSTGPSNPCQDDPCADNSLCVKLHNTSFCLCLEGYYSNSTCKKGVVFPKGISVTVS
ETFDPEEKHSMAYQDLHSEITSFKDVFQTSVYGQTVILTSTLSRSEMRADDKFNVTIVTILAETSDNEK
TVTEKINKAIRSSSSNFLNYDLTLRCDYYGCNQTTADDCLNGLACDCKSDLQRPNPQSPFCVASSLKCPDACNAQH
KQCLIKKSGGAPEACVPGYQEDANGNCQKCAFYSGLDCKDKFQLILTIIVGTIAGIVILSMIILIVTARSNNK
TKHIEENLIDEDFQNLKLRSTGFTNLGAEGSVFVKVRITASRDSQMQNPYSRRHSSMPRPDY

Mass Match Peptides (bold):

DSQMQNPYSR [895]

HIEENLIDEDFQNLK [917]

SDLQRPNPQSPFCVASSLK [969]

STGFTNLGAEGSVFVK [974]

VFPGK [990]

Tandem Peptides (underline):

DSQMQNPYSR [895]

HIEENLIDEDFQNLK [917]

SDLQRPNPQSPFCVASSLK [969]

STGFTNLGAEGSVFVK [974]

VFPGK [990]

OGTA216 (SEQ ID No: 40)**Peptide Source: 1D-GE, Breast cancer**

MEPRPTA?SSGAPGLAGVGETPSAAALAAARVELPGTAVPSVPEDAAPASRDGGGVREDEGPAAAGDCLGRPLGPT
PSQSRFQVDLVSENAGRAAAAAAAAAAAAAAAAAAGAGAGAKQTPADGEASGESEPAKGSEEAAGRFRVNFVDPAASS
SAEDSLSDAAGVGVGDGPNVSFQNGGDTVLSEGSLLHSGGGGGSGHHQHYYYDTHNTIYYLRTFGHNTMDAVPRID
HYRHTAAQLGEKLLRPSLAELHDELEKEPFEDCFANGEESTPTRDAVVITYAESKGVVKFGWIKGVLVRCMLNIW
GVMLFIRLSWIVGQAGIGLSVLVIMMATVVTITIGLSTSAIATNGFVRGGGAYYLISRLGPEFGGAIGLIFAF
NAVAVAMYVVGFAETVVELLKEHSILMIDEINDIRIIGAITVVILLGISVAGMEWEAKAQIVLLVILLILAIGDFV
IGTFIPLESKKPKGFFGYKSEIFNENFGPDFREREETFSVFATFFPAATGILAGANISGDLADPQSAIPKGTLLA
ILITTLVYVGLAVSVGSCVVRDATGNVNDTIVIELTNCITSAACKLNFDSSCESSPCSYGLMNNFQVMSMVSGFT
PLISAGIFSATLSSALASLVSAKIFQALCKDNIYPAFQMFAGYKGNNEPLRGYILTFLIALGFIILAEINLVIA
PIISNFFLASALINFSVFHASLAKSPGWRPAFKYYNMWISLLGAILCCIVMFVINWWAALLTYVIVLGLYIYVT
YKPDVNWGSSQTALTYLNAHQHSIRLSGVEDHVKNFRPQCLVMTGAPNSRPALLHLVHDFTKNVGLMICGHVHM
GPRRQAMKEMSIDQAKYQRWLIKNNKMAFYAPVHADDLREGAQYLMQAAGLGRMKPNTLVLGFKKDWLQADMRDV
DMYINLFHDAFDIQYGVVIRLKEGLDISHLQCGEELLSSQEKSPGTDVVVSVEYSKKSDLDTSKPLSEKPITH
KVEEEDGKTATQPLLKESKGPVPLNVADCKLLEASTQFQKKQGNKNTIDVWWLFDDGGLTLLIPYLLTTKKKWK
DCKIRVFIGGKINRIDHDDRARAMATLLSKFRIDFSDIMVLGDINTKPKKENIIFAEELIEPYRLHEDDKEQDIADK
MKEDEPWRTDNELEYKTKTYRQIRLNELLKEHSSSTANIIVMSLPVARKGAVSSALYMAWLEALSKDLPPILLV
RGNHQSVLTFYS

Mass Match Peptides (bold):

AFYAPVHADDLR [69]

DVVSVEYSK [163]

EGAQYLMQAAGLGR [186]

FQVDLVSENAGR [271]

IDHDDR [356]

KDWLQADMR [408]
 NVGLMICGHEVHMGP [555]
 NVGLMICGHEVHMGP [556]

Tandem Peptides (underline):

DEGPAAAGDGLGRPLGPTPSQSR [114]
 GPIVPLNVADQK [307]
 SEIFNENFGPD [626]

Peptide Source: 1D-GE, Colorectal cancer

MEPRPTAPSSGAPGLAGVGETPSAAALAAAR**VELPGTAVPSVPEDAAPASR**DGGGVVRDEGPAAAGDGLGRPLGPT
 PSQSR**FQVDLVSENAGRA**AAAAAAAAAGAGAGAKQTFADGEASGESEPAKGSEEAAGRFRVNFVDPASS
 SAEDSLSDAAGVVDGPNVVSFQNGGDTVLSGSSLHSGGGGSGHHQHYYDTHNTYYLR**TFGHNTMDAVPRID**
HYRHTAAQLGEKLLRPSLAELHDELEK**EPFEDGFANGEESTPTRDAVVITYTAESK**GVVKFGWIKGVLVRC**MLNIW**
GVMLFIRLSWIVGQAGIGLSVLVIMMATVVTTITGLSTSAIATNGFVR**GGGAYYLISR**SLGPEFGGAIGLIFAF
 NAVAVAMYVVGFAETVVELLKEHSILMIDEINDIRIIGAITVVILLGTSVAGMEWEAKAQIVLLVILLAIIGDFV
 IGTIFPLESKKPK**GFFGYKSEIFNENFGPD**EEETFFSVFAIFFPAATGILAGANISGDLADPQSAIPKGTLLA
 ILITLVYVGIASVSGCVVRDATGNVNDTIVTELTNCTSAACKLNDFSSCESSPCSYGLMNNFQVMSMVSGFT
 PLISAGIFSATLSSALASLVSAPKIFQALCK**DNIYPAFQMF**AKGYGK**NNEPLR**GYILTFLIALGFILIAELNVIA
 PIISNFFLASALINFSVFHASLAK**SPGWRPAFK**YYNMWISLLGAILCCIVMFVINWWAALLTYVIVLGLYIYVT
 YKKPDVNWGSSTQALTYLNALQHSIRLSGVEDHVKNFRPQCLVMTGAPNSRPALLHLVHDFTK**NVGLMICGHEVHM**
GPRRQAMK**EMSIDQAK**YQWLKIKMK**AFYAPVHADDLREGAQYLMQAAGLGR**MPNTLVLGFK**KDWLQADMR**DV
 DMYINLFHDAFDIQYGVVIRLKEGLDISHLQGEELLSSQEKSPGTDVVVSVEYS**KSDLDTSKPLSEKPITH**
KVEEDGKTATQPLLKESK**GPIVPLNVADQK**LLEASTQFQKKQKNTIDVWWLFDDGGLTLLIPYLLTTKKKKW
 DCKIRVFIGGKINR**IDHRRAMATLLSK**FRIDFSDIMVLGDINTKPKKENIIAFEEIIEPYRLHEDDKQDIADK
 MKEDEPWRTDNELELYKTQYRQIR**LNELLKEHSSTANIIVMSLPVAR**KGAVSSALYMAWLEALSK**DLPPILLV**
RGNHQSVLTFYS

Mass Match Peptides (bold):

AFYAPVHADDLR [69]
 AMATLLSK [78]
 CMLNIWGVMLFIR [106]
 DAVVITYTAESK [110]
 DLPPILLV [136]
 DNIYPAFQMF [145]
 DWLQADMR [164]
 EGAQYLMQAAGLGR [186]
 EHSSTANIIVMSLPVAR [195]
 EMSIDQAK [213]
 EPFEDGFANGEESTPTR [216]
 FQVDLVSENAGR [271]
 GFFGYK [294]
 GGGAYYLISR [298]
 IDFSDIMVLGDINTKPK [354]
 IDFSDIMVLGDINTKPKK [355]
 IDHRR [356]
 IDHYR [357]
 KDWLQADMR [408]
 KENIIAFEEIIEPYR [410]
 KSDLDTSKPLSEKPITHK [435]
 LHEDDK [465]
 LNELLK [471]
 NNEPLR [549]
 NVGLMICGHEVHMGP [555]
 NVGLMICGHEVHMGP [556]
 RAMATLLSK [596]
 SEIFNENFGPD [626]
 SPGWRPAFK [645]
 TFGHNTMDAVPR [688]
 VELPGTAVPSVPEDAAPASR [754]

Tandem Peptides (underline):

AAAAAAAAAAAAAAAAAGAGAGAK [49]
DAVVTYTAESK [110]
DEGFAAAGDGLGRPLGPTPSQSR [114]
DLPPILLVR [136]
DVVVSVEYSK [163]
DWLQADMR [164]
EGAQYLMQAAGLGR [186]
EHSSTANIIVMSLPVAR [195]
FQVDLVSENAGR [271]
GPIVPLNVADQK [307]
ITDNELEYK [395]
SEIFNENFGPDFR [626]
TFGHNTMDAVPR [688]

Peptide Source: 1D-GE, Pancreatic cancer

MEPRPTAPSSGAPGLAGVGETPSAAALAAAR**VELPGTAVPSVPEDAAPASR**DGGGVREDEGPAAAGDGLGRPLGPT
PSQSRFQVDLVSENAGRAAAAAAAAAAGAGAGAKQTPADGEASGESEPAKGSEEAAGRFRVNFVDPAASS
SAEDSLSDAAGVGVDGPNVSFQNGGDTVLSEGSLLHSGGGGSGHHQHYYDTHNTYYLRTFGHNTMDAVPRID
HYRHTAAQLGEKLLRPSLAELHDELEK**EPFEDGFANGEESTPTR**DAVVTYTAESKGVVKFGWIKGVLVRCMLNIW
GVMLFIRLSWIVGQAGIGLSVLVIMMATVVTITGLSTSAIATNGFVR**GGGAYYLISR**SLGPFGGAIGLIFAF
NAVAVAMYVVGFAETVVELLKEHSILMIDEINDIRIIGAITVVILLGISVAGMEWEAKAQIVLLVILLLLAIGDFV
IGTFIPLESKKPKCFFGYK**SEIFNENFGPDFR**REEETFFSVFAIFFPAATGILAGANISGDLADPQSAIPKGTLLA
ILITTLVYVGIAVSVGSCVVRDATGNVNDTIVTELTNCTSAACKLNDFSSCESSPCSYGLMNNFQVMSMVSGFT
PLISAGIFSATLSSALASLVSAKIFQALCKDNIYPAPQMFAGYGYK**NNEPLR**GYILTFLIALGFILIAELNVIA
PIISNFFLASALINFSVFHASLAKSPGWRPAFKYYNMWISLLGAILCCIVMFVINWWAALLTYVIVLGLYIYVT
YKKPDVNWGSSTQALTYLNALQHSIRLSGVEDHVKNFRPQCLVMTGAPNSRPALLHLVHDFTK**NVGLMICGHVHM**
GPRRQAMKEMSIDQAKYQRWLIKNNMK**AFYAPVHADDLR**EGAQYLMQAAGLGRMKPNTLVLGFKKDWLQADMRDV
DMYINLFHDAFDIQYGVVIRLKEGLDISHLQOEELLSSQEKSPGTD**DVVVSVEYSK**KSDLDTSKPLSEKPIH
KVEEEDGKTATQPLLKESKGPIVPLNVADQKLLEASTQFOKKQGNKNTIDVWVLFDDGGTLTLLIPYLLTTKKKWK
DCKIRVFIGGKINRIDHRRAMATLLSKFRIDFSDIMVLGDINTKPKKENIIAFEEIIEPYRLHEDDKEQDIADK
MKEDEPWRTDNELEYKTKTYRQIRLNELLKEHSSTANIIVMSLPVARKGAVSSALYMAWLEALS KDLPPIILLV
RGNHQSVLTFYS

Mass Match Peptides (bold):

AFYAPVHADDLR [69]
DVVVSVEYSK [163]
EPFEDGFANGEESTPTR [216]
GGGAYYLISR [298]
NNEPLR [549]
NVGLMICGHVHMGR [555]
VELPGTAVPSVPEDAAPASR [754]

Tandem Peptides (underline):

GPIVPLNVADQK [307]
SEIFNENFGPDFR [626]

Peptide Source: iTRAQ, Colorectal cancer

MEPRPTAPSSGAPGLAGVGETPSAAALAAAR**VELPGTAVPSVPEDAAPASR**DGGGVREDEGPAAAGDGLGRPLGPT
PSQSRFQVDLVSENAGR**AAAAAAAAAGAGAGAKQTPADGEASGESEPAK**GSEEAAGRFRVNFVDPAASS
SAEDSLSDAAGVGVDGPNVSFQNGGDTVLSEGSLLHSGGGGSGHHQHYYDTHNTYYLRTFGHNTMDAVPRID
HYRHTAAQLGEKLLRPSLAELHDELEK**EPFEDGFANGEESTPTR**DAVVTYTAESKGVVKFGWIKGVLVRCMLNIW
GVMLFIRLSWIVGQAGIGLSVLVIMMATVVTITGLSTSAIATNGFVR**GGGAYYLISR**SLGPFGGAIGLIFAF
NAVAVAMYVVGFAETVVELLKEHSILMIDEINDIRIIGAITVVILLGISVAGMEWEAKAQIVLLVILLLLAIGDFV
IGTFIPLESKKPKCFFGYK**SEIFNENFGPDFR**REEETFFSVFAIFFPAATGILAGANISGDLADPQSAIPKGTLLA
ILITTLVYVGIAVSVGSCVVRDATGNVNDTIVTELTNCTSAACKLNDFSSCESSPCSYGLMNNFQVMSMVSGFT

PLISAGIFSATLSSALASLSVAPKIFQALCKDNIPAFQMFAGYKGNNEPLRGYILTFILIALGFILIAELNVIA
 PIISNFFLASALINFSVFHASLAKSPGWRPAFKYYNMWISLLGAILCCIVMFVINWAAALLTYVIVLGLYIYVT
 YKKPDVNWGSSTQALTYLNLQHSIRLSGVEDHVKNFRPQCLVMTGAPNSRPALLHLVHDFTKNVGLMICGHVHM
 GPRRQAMKEMSIDQAKYQRWLKKNMKAFYAPVHADDLREGAQYLMQAAGLGRMKPNTLVLGFKKDWLQADMRDV
 DMYINLFHDAFDIQYGVVIRLKEGLDISHLQGGQEELLSSQEKSPGTDVVVSVEYSKKSDDLTSKPLSEKPIH
 KVEEEDGKTATQPLLKESKGPVPLNVADQKLEASTQFQKKQGNKNTIDVWWLFDGGLTLLIPYLLTTKKKWK
 DCKIRVFIGGKINRIDHRRAMATLLSKFRIDFSDIMVLGDINTKPKKENIIAFEEIIEPYRLHEDDKEQDIADK
 MKEDEPWRITDNELELYKTKTYRQIRLNELLKHSSTANIIVMSLPVARKGAVSSALYMAWLEALS~~DLPPILLV~~
~~RGNHQSVLTFYS~~

Mass Match Peptides (bold):

AAAAAAAAAAAAAAAAAGAGAGAK [49]
 AFYAPVHADDLR [69]
 AMATLLSK [78]
 DLPPILLVR [136]
 EGAQYLMQAAGLGR [186]
 GGGAYYLISR [298]
 GPIVPLNVADQK [307]
 ITDNELELYK [395]
 QTPADGEASGESEPAK [1008]

Tandem Peptides (underline):

AAAAAAAAAAAAAAAAAGAGAGAK [49]
 AFYAPVHADDLR [69]
 AMATLLSK [78]
 DLPPILLVR [136]
 EGAQYLMQAAGLGR [186]
 GGGAYYLISR [298]
 GPIVPLNVADQK [307]
 ITDNELELYK [395]
 QTPADGEASGESEPAK [1008]

Peptide Source: iTRAQ, Hepatocellular cancer

MEPRPTAPSSCAPGLAGVCETPSAAALAAARVELPCTAVPSVPEDAAPASRDGGGVRDEGPAAAGDGLGRPLGPT
 PSQSRFQVDLVSENAAGRAAAAAAAAAAAAAAAAAAGAGAGAKQTPADGEASGESEPAKGSSEAKGRFRVNFVDPAASS
 SAEDSLSDAAGVGDGPNVSVFQNGGDTVLSEGSSLSHSGGGGSGHHQHYYDTHNTYLRFTGHNTMDAVERID
 HYRHTAAQLGEKLLRPSLAELHDELEKEPFEDGFANGEESTPTRDAVVITYAESKGVVKFGWIKGVLRCLMLNIW
 GVMLFIRLSWIVGQAGIGLSVLVIMMATVVTITITGLSTSAIATNGFVRGGGAYYLISRSLGPEFGGAIGLIFAF
 NAVAVAMYVVGFAETVVELLKEHSILMIDEINDIRIICAITVVILLGISVAGMEWEAKAQIVLLVILLIAIGDFV
 IGTPIPLESKKPKGFFGYKSEIFNENFGPDFREETFFSVFAIFPPAATGILAGANISGLADPQSAIPKGTLLA
 ILITTLVYVGIASVSGCVVRDATCNVNDTIVTELTNCTSAACKLNFDSSCESSPCSYGLMNNFQVMSMVSCFT
 PLISAGIFSATLSSALASLSVAPKIFQALCKDNIPAFQMFAGYKGNNEPLRGYILTFILIALGFILIAELNVIA
 PIISNFFLASALINFSVFHASLAKSPGWRPAFKYYNMWISLLGAILCCIVMFVINWAAALLTYVIVLGLYIYVT
 YKKPDVNWGSSTQALTYLNLQHSIRLSGVEDHVKNFRPQCLVMTGAPNSRPALLHLVHDFTKNVGLMICGHVHM
 GPRRQAMKEMSIDQAKYQRWLKKNMKAFYAPVHADDLREGAQYLMQAAGLGRMKPNTLVLGFKKDWLQADMRDV
 DMYINLFHDAFDIQYGVVIRLKEGLDISHLQGGQEELLSSQEKSPGTDVVVSVEYSKKSDDLTSKPLSEKPIH
 KVEEEDGKTATQPLLKESKGPVPLNVADQKLEASTQFQKKQGNKNTIDVWWLFDGGLTLLIPYLLTTKKKWK
 DCKIRVFIGGKINRIDHRRAMATLLSKFRIDFSDIMVLGDINTKPKKENIIAFEEIIEPYRLHEDDKEQDIADK
 MKEDEPWRITDNELELYKTKTYRQIRLNELLKHSSTANIIVMSLPVARKGAVSSALYMAWLEALS~~DLPPILLV~~
~~RGNHQSVLTFYS~~

Mass Match Peptides (bold):

IFQALCK [920]
 SPGWRPAFK [645]

Tandem Peptides (underline):

IFQALCK [920]
 SPGWRPAFK [645]

Peptide Source: iTRAQ, Non-small cell lung cancer

MEPRPTAPSSGAPGLAGVGETPSAAALAAARVELPGTAVPSVPEDAAPASRDGGGVRDEGPAAAGDGLGRPLGPT
 PSQSRFQVDLVSENAGRAAAAAAAAAAGAGAGAKQTPADGEASGESEPAKGSEEAAGRFRVNFVDPAASS
 SAEDSLSDAAGVGVDGPNVSFQNGGDTVLSGSSLSHSGGGGSGHHQHYYDTHNTYYLRTFGHNTMDAVPRID
 HYRHTAAQLGEKLLRPSLAELHDELEKEPFEDGFANGEESTPTRDAVVITYAESKGVVKFGWIKGVLVRCMLNIW
 GVMLFIRLSWIVGQAGIGLSVLVIMMATVVTITGLSTSAIATNGFVRGGGAYYLISRSLGPEFGGAIGLIFAF
 NAVAVAMYVVGFAETVVELLKEHSILMIDEINDIRIIGAITVVILLGTSVAGMEWEAKAQIVLLVILLILAIGDFV
 IGTFIPLSKKPKGFFGYKSEIFNENFGPDFREEETFFSVFAIFFPAATGILAGANISGDLADPQSAIPKGTLLA
 ILITTLVYVGIAVSVGSCVVRDATGNVNDTIVTELTNCTSAACKLNDFSSCESSPCSYGLMNNFQVMSMVSGFT
 PLISAGIFSATLSSALASLVSAPIFQALCKDNIYPAFQMFAGYKGNNEPLRGYILTFLIALGFIILAEINLVIA
 PIISNFFLASALINFSVFHASLAKSPGWRPAFKYYNMWISLLGAILCCIVMFVINWWAALLTYVIVLGLYIYVT
 YKKFDVNWGSSTQALTYLNALQHSIRLSGVEDHVKNFRPQCLVMTGAPNSRPALLHLVHDFTKNVGLMICGHVHM
 GPRRQAMK**EMSIDQAK**YQRWLIKNNKMAFYAPVHADDLREGAQYLMQAAGLGRMKPNTLVLGFKKDWLQADMRDV
 DMYINLFHDAFDIQYGVVIRLKEGLDISHLQGEELLSSQEKSPGTDVVSVEYSKKSOLDTSKPLSEKPI
 KVEEEDGKT**TATQPLLK**KESKGPVPLNVADQKLEASTQFQKKQKNTIDVWWLFDGGLTLLIPYLLTTKKKKW
DCKIRVFIGGKINRIDHDDR**AMATLLSK**FRIDFSDIMVLGDINTKPKKENIIAFEETIEPYRL**HEDDK****EQDIADK**
 MKEDEPWRTDNELEYKTKTYRQIRLNELLKEHSSTANIIVMSLPVARKGAVSSALYMAWLEALSK**DLPPILLV**
RGNHQSVLTFYS

Mass Match Peptides (bold):

AMATLLSK [78]
 DCKIRVFIGGK [889]
 DLPPILLVR [136]
 EMSIDQAK [213]
 EQDIADK [903]
 LHEDDK [465]
 TATQPLLK [978]

Tandem Peptides (underline):

AMATLLSK [78]
 DCKIRVFIGGK [889]
 DLPPILLVR [136]
 EMSIDQAK [213]
 EQDIADK [903]
 LHEDDK [465]
 TATQPLLK [978]

Peptide Source: iTRAQ, Ovarian cancer

MEPRPTAPSSGAPGLAGVGETPSAAALAAARVELPGTAVPSVPEDAAPASRDGGGVRDEGPAAAGDGLGRPLGPT
 PSQSRFQVDLVSENAGRAAAAAAAAAAGAGAGAKQTPADGEASGESEPAKGSEEAAGRFRVNFVDPAASS
 SAEDSLSDAAGVGVDGPNVSFQNGGDTVLSGSSLSHSGGGGSGHHQHYYDTHNTYYLRTFGHNTMDAVPRID
 HYRHTAAQLGEKLLRPSLAELHDELEKEPFEDGFANGEESTPTRDAVVITYAESKGVVKFGWIKGVLVRCMLNIW
 GVMLFIRLSWIVGQAGIGLSVLVIMMATVVTITGLSTSAIATNGFVRGGGAYYLISRSLGPEFGGAIGLIFAF
 NAVAVAMYVVGFAETVVELLKEHSILMIDEINDIRIIGAITVVILLGTSVAGMEWEAKAQIVLLVILLILAIGDFV
 IGTFIPLSKKPKGFFGYKSEIFNENFGPDFREEETFFSVFAIFFPAATGILAGANISGDLADPQSAIPKGTLLA
 ILITTLVYVGIAVSVGSCVVRDATGNVNDTIVTELTNCTSAACKLNDFSSCESSPCSYGLMNNFQVMSMVSGFT
 PLISAGIFSATLSSALASLVSAPIFQALCKDNIYPAFQMFAGYKGNNEPLRGYILTFLIALGFIILAEINLVIA
 PIISNFFLASALINFSVFHASLAKSPGWRPAFKYYNMWISLLGAILCCIVMFVINWWAALLTYVIVLGLYIYVT
 YKKFDVNWGSSTQALTYLNALQHSIRLSGVEDHVKNFRPQCLVMTGAPNSRPALLHLVHDFTKNVGLMICGHVHM
 GPRRQAMK**EMSIDQAK**YQRWLIKNNKMAFYAPVHADDLREGAQYLMQAAGLGRMKPNTLVLGFKKDWLQADMRDV
 DMYINLFHDAFDIQYGVVIRLKEGLDISHLQGEELLSSQEKSPGTDVVSVEYSKKSOLDTSKPLSEKPI
 KVEEEDGKT**TATQPLLK**KESKGPVPLNVADQKLEASTQFQKKQKNTIDVWWLFDGGLTLLIPYLLTTKKKKW
DCKIRVFIGGKINRIDHDDR**AMATLLSK**FRIDFSDIMVLGDINTKPKKENIIAFEETIEPYRL**HEDDK****EQDIADK**
 MKEDEPWRTDNELEYKTKTYRQIRLNELLKEHSSTANIIVMSLPVARKGAVSSALYMAWLEALSK**DLPPILLV**
RGNHQSVLTFYS

Mass Match Peptides (bold):

AMATLLSK [78]

Tandem Peptides (underline):

AMATLLSK [78]

Peptide Source: iTRAQ, Renal cell cancer

MEPRPTAPSSGAPGLAGVGETPSAAALAAARVELPGTAVPSVPEDAAPASRDGGGVRDEGPAAAGDGLGRPLGPT
 PSQSREQVDLVSENAGRAAAAAAAAAAGAGAGAKQTPADGEASGESEPAKGSEEAKGRFRVNFVDPAAASS
 SAEDSLSDAAGVGVDGPNVSFQNGGDTVLESGSSLSHSGGGGSGHHQHYYDDHTNTYYLRTFGHNTMDAVPRID
 HYRHATAQLGKLLRPSLAELHDELEKEPFEDGFANGEESTPTRDAVVITYTAESKGVVKGWIKGVLVRCMLNIW
 GVMLFIRLSWIVGQAGIGLSVLVIMMATVVTITIGLSTSAIATNGFVRGGGAYYLISRLGPEFGGAIGLIFAF
 NAVAVAMYVVGFAETVVELLKEHSILMIDEINDIRIIGAITVVILLGISVAGMEWEAKAQIVLLVILLLLAIGDFV
 IGTIFPLESKKPKGFFGYKSEIFNENFGPDFREEETFFSVFAIFFPAATGILAGANISGDLADPQSAIPKGTLLA
 ILITTLVYVGIASVSGCVVRDATGNVNDTIVTELNTCTSAACKLNDFESSCESSPCSYGLMNNFQVMSMVSGFT
 PLISAGIFSATLSSALASLVSAPIFQALCKDNIYPAFQMFAGYKGNNEPLRGYILTFLIALGFIILAEINLVIA
 PIISNFFLASALINFSVFHASLAKSPGWRPAFKYYNMWISLLGAILCCIVMFVINWWAALLTYVIVLGLYIYVT
 YKKPDVNWGSSQTALTYLALQHSIRLSGVEDHVKNFRPQCLVMTGAPNSRPALLHLVHDFTKNVGLMICGHVHM
 GPRRQAMKEMSIDQAKYQRWLIKMKAFYAPVHADDLREGAQYLMQAAGLGRMKPNTLVLGFKKDWLQADMRDV
 DMYINLFHDAFDIQYGVVIRLKEGLDISHLQGGQELLSSQEKSPGTDVVSVEYSKSDLDTSKPLSEKPIH
 KVEEEDGKTATQFLKESKGPVPLNVADQKLEASTQFQKKQGNKNTIDVWWLFDGGLTLLIPYLLTTKKKKW
 DCKIRVFIGGKINRIDHRRAMATLLSKFRIDFSDIMVLGDINTKPKKENIAFEEIIEPYRLHEDDKEQDIADK
 MKEDEPWRTDNELELYKTKTYRQIRLNELLKEHSSTANIIVMSLPVARKGAVSSALYMAWLEALSCKDLPPILLV
 RGNHQSULTFYS

Mass Match Peptides (bold):

RAMATLLSK [596]

SPGWRPAFK [645]

Tandem Peptides (underline):

RAMATLLSK [596]

SPGWRPAFK [645]

Peptide Source: iTRAQ, Small cell lung cancer

MEPRPTAPSSGAPGLAGVGETPSAAALAAARVELPGTAVPSVPEDAAPASRDGGGVRDEGPAAAGDGLGRPLGPT
 PSQSREQVDLVSENAGRAAAAAAAAAAGAGAGAKQTPADGEASGESEPAKGSEEAKGRFRVNFVDPAAASS
 SAEDSLSDAAGVGVDGPNVSFQNGGDTVLESGSSLSHSGGGGSGHHQHYYDDHTNTYYLRTFGHNTMDAVPRID
 HYRHATAQLGKLLRPSLAELHDELEKEPFEDGFANGEESTPTRDAVVITYTAESKGVVKGWIKGVLVRCMLNIW
 GVMLFIRLSWIVGQAGIGLSVLVIMMATVVTITIGLSTSAIATNGFVRGGGAYYLISRLGPEFGGAIGLIFAF
 NAVAVAMYVVGFAETVVELLKEHSILMIDEINDIRIIGAITVVILLGISVAGMEWEAKAQIVLLVILLLLAIGDFV
 IGTIFPLESKKPKGFFGYKSEIFNENFGPDFREEETFFSVFAIFFPAATGILAGANISGDLADPQSAIPKGTLLA
 ILITTLVYVGIASVSGCVVRDATGNVNDTIVTELNTCTSAACKLNDFESSCESSPCSYGLMNNFQVMSMVSGFT
 PLISAGIFSATLSSALASLVSAPIFQALCKDNIYPAFQMFAGYKGNNEPLRGYILTFLIALGFIILAEINLVIA
 PIISNFFLASALINFSVFHASLAKSPGWRPAFKYYNMWISLLGAILCCIVMFVINWWAALLTYVIVLGLYIYVT
 YKKPDVNWGSSQTALTYLALQHSIRLSGVEDHVKNFRPQCLVMTGAPNSRPALLHLVHDFTKNVGLMICGHVHM
 GPRRQAMKEMSIDQAKYQRWLIKMKAFYAPVHADDLREGAQYLMQAAGLGRMKPNTLVLGFKKDWLQADMRDV
 DMYINLFHDAFDIQYGVVIRLKEGLDISHLQGGQELLSSQEKSPGTDVVSVEYSKSDLDTSKPLSEKPIH
 KVEEEDGKTATQFLKESKGPVPLNVADQKLEASTQFQKKQGNKNTIDVWWLFDGGLTLLIPYLLTTKKKKW
 DCKIRVFIGGKINRIDHRRAMATLLSKFRIDFSDIMVLGDINTKPKKENIAFEEIIEPYRLHEDDKEQDIADK
 MKEDEPWRTDNELELYKTKTYRQIRLNELLKEHSSTANIIVMSLPVARKGAVSSALYMAWLEALSCKDLPPILLV
 RGNHQSULTFYS

Mass Match Peptides (bold):

LSGVEDHVK [948]

Tandem Peptides (underline):

LSGVEDHVK [948]

OGTA222 (SEQ ID No: 41)

Peptide Source: 1D-GE, B-cell non-Hodgkin's lymphoma

MWSGWWLWPLVAVCTADFFRDEAERIMRDSVIDGHNDLPWQLLDMFNNRLQDERANLTTLAGHTNIPKLRAGF
VGGQFWSVYTPCDTQNKDAVRR**TLEQMDVVHR**MCRMYPETFLYVTSSAGIRQAFREGKVASLIGVEGGHSIDSSL
GVLR**ALYQLGMR**YLTTLTHSCNTPWADNWLVDTGDEPQSQGLSPFGQRVVKELNRLGVLLIDLAHVSVATMK**ATLQ**
LSRAPVIFSHSSAYSVCASRRNVPDDVLRLVKQTDLSVMVNFYNNYISCTNKANLSQVADHLDDHIKEVAGAR**AVG**
FGGDFDGVPRVPEGLEDVSK**YPDLIAELLR**RRNWTEAEVK**GALADNLLR**VFEAVEQASNLTAPEEEPIPLDQLGG
SCRTHYGYSSGASSLHRHWGLLLASLAPLVLCLSLL

Mass Match Peptides (bold):

ALYQLGMR [77]
ATLQLSR [91]
AVGFGGDFDGVPR [95]
GALADNLLR [283]
MYPETFLYVTSSAGIR [530]
NVPDDVLR [559]
RTLEQMDVVHR [617]
TLEQMDVVHR [703]
YPDLIAELLR [864]

Tandem Peptides (underline):

AVGFGGDFDGVPR [95]
VPEGLEDVSK [791]

Peptide Source: 1D-GE, Colorectal cancer

MWSGWWLWPLVAVCTADFFRDEAERIMRDSVIDGHNDLPWQLLDMFNNRLQDERANLTTLAGHTNIPKLRAGF
VGGQFWSVYTPCDTQNKDAVRR**TLEQMDVVHR**MCRMYPETFLYVTSSAGIRQAFREGKVASLIGVEGGHSIDSSL
GVLR**ALYQLGMR**YLTTLTHSCNTPWADNWLVDTGDEPQSQGLSPFGQRVVKELNRLGVLLIDLAHVSVATMK**ATLQ**
LSRAPVIFSHSSAYSVCASRRNVPDDVLRLVKQTDLSVMVNFYNNYISCTNKANLSQVADHLDDHIKEVAGAR**AVG**
FGGDFDGVPRVPEGLEDVSK**YPDLIAELLR**RRNWTEAEVK**GALADNLLR**VFEAVEQASNLTAPEEEPIPLDQLGG
SCRTHYGYSSGASSLHRHWGLLLASLAPLVLCLSLL

Mass Match Peptides (bold):

ALYQLGMR [77]
AVGFGGDFDGVPR [95]
GALADNLLR [283]
TLEQMDVVHR [703]

Tandem Peptides (underline):

AVGFGGDFDGVPR [95]
GALADNLLR [283]
TLEQMDVVHR [703]

Peptide Source: iTRAQ, Colorectal cancer

MWSGWWLWPLVAVCTADFFRDEAERIMR**DSPVIDGHNDLPWQLLDMFNNR**LQDERANLTTLAGHTNIPKLR**AGF**
VGGQFWSVYTPCDTQNKDAVRR**TLEQMDVVHR**MCRMYPETFLYVTSSAGIRQAFREGK**VASLIGVEGGHSIDSSL**
GVLRALYQLGMRYLTTLTHSCNTPWADNWLVDTGDEPQSQGLSPFGQRVVKELNRLGVLLIDLAHVSVATMK**ATLQ**
LSRAPVIFSHSSAYSVCASRRNVPDDVLRLVKQTDLSVMVNFYNNYISCTNKANLSQVADHLDDHIKEVAGAR**AVG**
FGGDFDGVPRVPEGLEDVSK**YPDLIAELLR**RRNWTEAEVK**GALADNLLR**VFEAVEQASNLTAPEEEPIPLDQLGG
SCRTHYGYSSGASSLHRHWGLLLASLAPLVLCLSLL

Mass Match Peptides (bold):

AGFVGGQFWSVYTPCDTQNK [881]
 ALYQLGMR [77]
 ATLQLSR [91]
 AVGFGGDFDGVPR [95]
 DSPVIDGHNDLPWQLDMFNNR [894]
 GALADNLLR [283]
 NVPDDVLR [559]
 TLEQMDVVHR [703]
 VASLIGVEGGHSIDSSLGVLR [988]
 VPEGLEDVSK [791]
 YPDLIAELLR [864]

Tandem Peptides (underline):

AGFVGGQFWSVYTPCDTQNK [881]
 ALYQLGMR [77]
 ATLQLSR [91]
 AVGFGGDFDGVPR [95]
 DSPVIDGHNDLPWQLDMFNNR [894]
 GALADNLLR [283]
 NVPDDVLR [559]
 TLEQMDVVHR [703]
 VASLIGVEGGHSIDSSLGVLR [988]
 VPEGLEDVSK [791]
 YPDLIAELLR [864]

Peptide Source: iTRAQ, Non-small cell lung cancer

MWSGWWLWPLVAVCTADFFRDEAERIMRDSVIDGHNDLPWQLDMFNNRLQDERANLTTLAGTHTNIPKLRAGF
 VGGQFWSVYTPCDTQNKDAVRRITLEQMDVVHRMCRMPETFLYVTSSAGIRQAFREGKVASLIGVEGGHSIDSSL
 GVLRLALYQLGMRYLTLTHSCNTPWADNWLVDIGDSEPSQGLSPFGQRVVKELNRLGVLDLAHVSVATMKATLQ
 LSRAPVIFSHSSAYSVCASRNNVPDDVLRVLVKQTDLSVMVNFYNNYISCTNKANLSQVADHLDHIKEVAGARAVG
 FCGDFDGVPR**VPEGLEDVSK**YPDLIAELLRRNWTEAEVKGALADNLLRVFEAVEQASNLQAPEEEPIPLDQLGG
 SCRTHYGYSSGASSLHRHWGLLLASLAPLVLCLSLL

Mass Match Peptides (bold):

ANLSQVADHLDHIK [882]
 VPEGLEDVSK [791]

Tandem Peptides (underline):

ANLSQVADHLDHIK [882]
 VPEGLEDVSK [791]

Peptide Source: iTRAQ, Renal cell cancer

MWSGWWLWPLVAVCTADFFRDEAERIMRDSVIDGHNDLPWQLDMFNNRLQDERANLTTLAGTHTNIPKLRAGF
 VGGQFWSVYTPCDTQNKDAVRRITLEQMDVVHRMCRMPETFLYVTSSAGIRQAFREGKVASLIGVEGGHSIDSSL
 GVLRL**ALYQLGMR**YLTLTHSCNTPWADNWLVDIGDSEPSQGLSPFGQRVVKELNRLGVLDLAHVSVATMKATLQ
 LSRAPVIFSHSSAYSVCASRNNVPDDVLRVLVKQTDLSVMVNFYNNYISCTNKANLSQVADHLDHIKEVAGAR**AVG**
FCGDFDGVPRVPEGLEDVSKYPDLIAELLRRNWTEAEVKG**GALADNLLR**VFEAVEQASNLQAPEEEPIPLDQLGG
 SCRTHYGYSSGASSLHRHWGLLLASLAPLVLCLSLL

Mass Match Peptides (bold):

ALYQLGMR [77]
 AVGFGGDFDGVPR [95]
 GALADNLLR [283]
 NVPDDVLR [559]

VPEGLEDVSK [791]
YPDLIAELLR [864]

Tandem Peptides (underline):

ALYQLGMR [77]
AVGFGGDFDGVPR [95]
GALADNLLR [283]
NVPDDVLR [559]
VPEGLEDVSK [791]
YPDLIAELLR [864]

OGTA236 (SEQ ID No: 42)**Peptide Source: 1D-GE, Pancreatic cancer**

MSSESKEQHNVSPRDSAEGNDSYPSGIHLELQRESSTDFKQFETNDQCRPYHRILIERQEKS DTFNFKEFVIKKLQ
KNCQCSPAKAKNMILGFLPVLPKYDLKKNILGDVMSGLIVGILLVPQSIAYSLLAGQEPVYGLYTSFFASII
YFLLGTSRHIISVGIFGVLCMIGETVDRELQKAGYDNAHSAPSLGMVSNGSTLLNHTSDRICDKSCYAIMVGSTV
TFIAGVYQVAMGFFQVGFVS VYLS DALLSGFVTGASFTILTSQAKYLLG LNLPR TNGVGS LITTWI HVFERNIHT
NLCDLITSLCLLVLLPTKELNEHFKSKLKAPIELVVVVAATLASHFGKLHENYNSSIAGHIPTGFMPPKVPE
WNLIPSAVDAIAISIIIGFAITVSLSEMPAKKHGYTVKANQEMYAIGFCNIIPSFFHCFTTSAALAKTLVKESTG
CHTQLSGVVTALVLLLVLVIAPLFYSLQKSVLGVIITIVNLRGALRKFRDLPKMWSISRMDTVIWFVTMLSSALL
STEIGLLVGVCFSIFCVILRTQKPKSSLLGLVEESEVFESVSAYKNLQTKPGIKIFRFVAPLYYINKECFKSALY
KQTVNPILIKVAWKKAARKRIKEKVVTLGGIQDEMSVQLSHDPLELHTIVIDCSAIQFLDTAGIHTLKEVRRDYE
AIGIQVLLAQCNPTVRDSL TNGEYCKKEEENLLFYSVYEAMAFAEVSKNQKGVCPNGLSLSSD

Mass Match Peptides (bold):**Tandem Peptides (underline):**

SVLGVIITIVNLR [664]

Peptide Source: iTRAQ, Colorectal cancer

MSSESKEQHNVSPRDSAEGNDSYPSGIHLELQRESSTDFKQFETNDQCRPYHRILIERQEKS DTFNFKEFVIKKLQ
KNCQCSPAKAKNMILGFLPVLPKYDLKKNILGDVMSGLIVGILLVPQSIAYSLLAGQEPVYGLYTSFFASII
YFLLGTSRHIISVGIFGVLCMIGETVDRELQKAGYDNAHSAPSLGMVSNGSTLLNHTSDRICDKSCYAIMVGSTV
TFIAGVYQVAMGFFQVGFVS VYLS DALLSGFVTGASFTILTSQAKYLLG LNLPR TNGVGS LITTWI HVFERNIHT
NLCDLITSLCLLVLLPTK**ELNEHFKSK**LKAPIELVVVVAATLASHFGKLHENYNSSIAGHIPTGFMPPKVPE
WNLIPSAVDAIAISIIIGFAITVSLSEMPAKKHGYTVKANQEMYAIGFCNIIPSFFHCFTTSAALAKTLVKESTG
CHTQLSGVVTALVLLLVLVIAPLFYSLQKSVLGVIITIVNLRGALRKFRDLPKMWSISRMDTVIWFVTMLSSALL
STEIGLLVGVCFSIFCVILRTQKPKSSLLGLVEESEVFESVSAYKNLQTKPGIKIFRFVAPLYYINKECFKSALY
KQTVNPILIKVAWKKAARKRIKEKVVTLGGIQDEMSVQLSHDPLELHTIVIDCSAIQFLDTAGIHTLKEVRRDYE
AIGIQVLLAQCNPTVRDSL TNGEYCKKEEENLLFYSVYEAMAFAEVSKNQKGVCPNGLSLSSD

Mass Match Peptides (bold):

ELNEHFKSK [900]

Tandem Peptides (underline):

ELNEHFKSK [900]

OGTA237 (SEQ ID No: 43)**Peptide Source: 1D-GE, B-cell non-Hodgkin's lymphoma**

MRLLLALLGVLLSVPGPPVLSLEASEEVELEPCLAPSLEQQEQELTVALGQFVRLCCGRAERGGHWYKEGSRLAP
AGRVRGWRGRLEIASFLPEDAGRYLCLARGSMIVLQNLTLITGDSL TSSNDEDPKSHRDP SNRHSYPQQAPYWT
HPQRMKKLHAVPAGNTVKFRCPAAGNPTPTIRWLKDGQAFHGENRIGGIRLRHQHWSLVMSVVPVSDRGTYTCL

VENAVGSIRYNYLLDVLEERSPHRPILQAGLPANTTAVVGSDELCKVYSDAQPHIQWLKHIVINGSFSGADGFP
YVQVLKTADINSSEVEVLYLRNVSAEDAGEYTCLAGNSIGLSYQSAWLTVLPEEDPTWTAAAPARYTDIILYAS
GSLALAVLLLLAGLYRGQALHGRHPRPPATVQKLSRFPLARQFSLESSESGSSKSSSSSLVRGVRLSSSGPALLAGLV
SLDLPLDPLWEFFPRDRLVLGKPLGEGCFGQVVRAEAFGMDPARPDQASTVAVKMLKDNASDKDLADLVSEMEVMK
LIGRHKNIINLLGVCTQEGPLYVIVECAAKGNLREFLRARRPPGPDLSPDGPRSSSEGPLSFPLVSCAYQVARGM
QYLESRKCIHRDLAARNVLVTEDNVMKIADFGLARGVHHIDYYKKTSGRLPVKWMAPALFDRVYTHQSDVWSF
GILLWEIFTLGGSPYPGIPVEELFSLREGHRMDRPPHCPPELYGLMRECWAAPSQRPTFKQLVEALDKVLLAV
SEYIDLRLTTFGPYSPSGGDASSTCSSSDSVFSDPLPLGSSSFPPFGSGVQT

Mass Match Peptides (bold):

IADFGLAR [349]

Tandem Peptides (underline):

IADFGLAR [349]

Peptide Source: 1D-GE, Lymphoid leukaemia

MRLLLALLGVLLSVPGPPVLSLEASEEVELEPCAPSLEQQEQELTVALGQPVRLLCCGRAERGHHWYKEGSRAP
AGRVGRWRGRLEIASFLPEDAGRYLCLARGSMIVLQNLTLITGDSLTSNDDDEPKSHRDPNSRHSYPQQAPYWT
HPQRMEKKLHVPAGNTVKFRCPAAGNPTPTIRWLKDGQAFHGENRIGGIRLRHQHWSLVMSVVPDRGTYTCL
VENAVGSIRYNYLLDVLEERSPHRPILQAGLPANTTAVVGSDELCKVYSDAQPHIQWLKHIVINGSFSGADGFP
YVQVLKTADINSSEVEVLYLRNVSAEDAGEYTCLAGNSIGLSYQSAWLTVLPEEDPTWTAAAPARYTDIILYAS
GSLALAVLLLLAGLYRGQALHGRHPRPPATVQKLSRFPLARQFSLESSESGSSKSSSSSLVRGVRLSSSGPALLAGLV
SLDLPLDPLWEFFPRDRLVLGKPLGEGCFGQVVRAEAFGMDPARPDQASTVAVKMLKDNASDKDLADLVSEMEVMK
LIGRHKNIINLLGVCTQEGPLYVIVECAAKGNLREFLRARRPPGPDLSPDGPRSSSEGPLSFPLVSCAYQVARGM
QYLESRKCIHRDLAARNVLVTEDNVMKIADFGLARGVHHIDYYKKTSGRLPVKWMAPALFDRVYTHQSDVWSF
GILLWEIFTLGGSPYPGIPVEELFSLREGHRMDRPPHCPPELYGLMRECWAAPSQRPTFKQLVEALDKVLLAV
SEYIDLRLTTFGPYSPSGGDASSTCSSSDSVFSDPLPLGSSSFPPFGSGVQT

Mass Match Peptides (bold):

Tandem Peptides (underline):

IADFGLAR [349]

Peptide Source: 1D-GE, Prostate cancer

MRLLLALLGVLLSVPGPPVLSLEASEEVELEPCAPSLEQQEQELTVALGQPVRLLCCGRAERGHHWYKEGSRAP
AGRVGRWRGRLEIASFLPEDAGRYLCLARGSMIVLQNLTLITGDSLTSNDDDEPKSHRDPNSRHSYPQQAPYWT
HPQRMEKKLHVPAGNTVKFRCPAAGNPTPTIRWLKDGQAFHGENRIGGIRLRHQHWSLVMSVVPDRGTYTCL
VENAVGSIRYNYLLDVLEERSPHRPILQAGLPANTTAVVGSDELCKVYSDAQPHIQWLKHIVINGSFSGADGFP
YVQVLKTADINSSEVEVLYLRNVSAEDAGEYTCLAGNSIGLSYQSAWLTVLPEEDPTWTAAAPARYTDIILYAS
GSLALAVLLLLAGLYRGQALHGRHPRPPATVQKLSRFPLARQFSLESSESGSSKSSSSSLVRGVRLSSSGPALLAGLV
SLDLPLDPLWEFFPRDRLVLGKPLGEGCFGQVVRAEAFGMDPARPDQASTVAVKMLKDNASDKDLADLVSEMEVMK
LIGRHKNIINLLGVCTQEGPLYVIVECAAKGNLREFLRARRPPGPDLSPDGPRSSSEGPLSFPLVSCAYQVARGM
QYLESRKCIHRDLAARNVLVTEDNVMKIADFGLARGVHHIDYYKKTSGRLPVKWMAPALFDRVYTHQSDVWSF
GILLWEIFTLGGSPYPGIPVEELFSLREGHRMDRPPHCPPELYGLMRECWAAPSQRPTFKQLVEALDKVLLAV
SEYIDLRLTTFGPYSPSGGDASSTCSSSDSVFSDPLPLGSSSFPPFGSGVQT

Mass Match Peptides (bold):

IADFGLAR [349]

Tandem Peptides (underline):

Peptide Source: iTRAQ, Colorectal cancer

MRLLALLGVLLSVPGPPVLSLEASEEVELEPCLAPSLEQQEQELTVALGQPVRLCCGRAERGGHWHYKEGSRLAP
 AGRVRGWRGRLEIASFLPEDAGRYLCLARGSMIVLQNLTLITGDSLTSSNDDDEDPKSHRDPSNRHSYPQQAPYWT
 HPQRMKKLHAVPAGNTVKFRCPAAGNPTPTIRWLKDGQAFHGENRIGGIRLRHQHWSLVMESVVPSPDRGTYTCL
 VENAVGSIRYNYLLDVLSRPHRPILQAGLPANTTAVVGSDELCKVYSDAQPHIQWLKHIVINGSFSGADGFP
 YVQVLKTADINSSEVEVLYLRNVSAEDAGEYTCLAGNSIGLSYQSAWLTVLPEEDPTWTAAAPARYTDIILYAS
 GSLALAVLLLLAGLYRGQALHGRHPRPPATVQKLSRFPLARQFSLESSESGSKSSSSSVRGVRLSSSGPALLAGLV
 SLDLPLDPLWEFPRDRLVLGKPLGEGCFQGVVRAEAFGMDPARPDQASTVAVKMLKDNASDKDLADLVSEMEVMK
 LIGRHKNIINLLGVCTQEGPLYVIVECAAKGNLREFLRARRPPGPDLSPDGPRSSEGPLSFVPLVSCAYQVARGM
 QYLESRCKIHRDLAARNVLVTEDNMKIADFLARGVHHIDYKKTSNGRLPVKWMPEALFDRVYTHQSDVWSF
 GILLWEIFTLGGSPYPGIPVEELFSLREGHRMDRPPHCPPELYGLMRECWAAPSQRPTFKQLVEALDKVLLAV
 SEEYDLRLTLFGPYSPSGDASSTCSSSDSVFSDHPLPLGSSSFPFGSGVQT

Mass Match Peptides (bold):

QLVEALDK [963]

Tandem Peptides (underline):

QLVEALDK [963]

Peptide Source: iTRAQ, Non-small cell lung cancer

MRLLALLGVLLSVPGPPVLSLEASEEVELEPCLAPSLEQQEQELTVALGQPVRLCCGRAERGGHWHYKEGSRLAP
 AGRVRGWRGRLEIASFLPEDAGRYLCLARGSMIVLQNLTLITGDSLTSSNDDDEDPKSHRDPSNRHSYPQQAPYWT
 HPQRMKKLHAVPAGNTVKFRCPAAGNPTPTIRWLKDGQAFHGENRIGGIRLRHQHWSLVMESVVPSPDRGTYTCL
 VENAVGSIRYNYLLDVLSRPHRPILQAGLPANTTAVVGSDELCKVYSDAQPHIQWLKHIVINGSFSGADGFP
 YVQVLKTADINSSEVEVLYLRNVSAEDAGEYTCLAGNSIGLSYQSAWLTVLPEEDPTWTAAAPARYTDIILYAS
 GSLALAVLLLLAGLYRGQALHGRHPRPPATVQKLSRFPLARQFSLESSESGSKSSSSSVRGVRLSSSGPALLAGLV
 SLDLPLDPLWEFPRDRLVLGKPLGEGCFQGVVRAEAFGMDPARPDQASTVAVKMLKDNASDKDLADLVSEMEVMK
 LIGRHKNIINLLGVCTQEGPLYVIVECAAKGNLREFLRARRPPGPDLSPDGPRSSEGPLSFVPLVSCAYQVARGM
 QYLESRCKIHRDLAARNVLVTEDNMKIADFLARGVHHIDYKKTSNGRLPVKWMPEALFDRVYTHQSDVWSF
 GILLWEIFTLGGSPYPGIPVEELFSLREGHRMDRPPHCPPELYGLMRECWAAPSQRPTFKQLVEALDKVLLAV
 SEEYDLRLTLFGPYSPSGDASSTCSSSDSVFSDHPLPLGSSSFPFGSGVQT

Mass Match Peptides (bold):

TSNGRLPVK [986]

Tandem Peptides (underline):

TSNGRLPVK [986]

Peptide Source: iTRAQ, Renal cell cancer

MRLLALLGVLLSVPGPPVLSLEASEEVELEPCLAPSLEQQEQELTVALGQPVRLCCGRAERGGHWHYKEGSRLAP
 AGRVRGWRGRLEIASFLPEDAGRYLCLARGSMIVLQNLTLITGDSLTSSNDDDEDPKSHRDPSNRHSYPQQAPYWT
 HPQRMKKLHAVPAGNTVKFRCPAAGNPTPTIRWLKDGQAFHGENRIGGIRLRHQHWSLVMESVVPSPDRGTYTCL
 VENAVGSIRYNYLLDVLSRPHRPILQAGLPANTTAVVGSDELCKVYSDAQPHIQWLKHIVINGSFSGADGFP
 YVQVLKTADINSSEVEVLYLRNVSAEDAGEYTCLAGNSIGLSYQSAWLTVLPEEDPTWTAAAPARYTDIILYAS
 GSLALAVLLLLAGLYRGQALHGRHPRPPATVQKLSRFPLARQFSLESSESGSKSSSSSVRGVRLSSSGPALLAGLV
 SLDLPLDPLWEFPRDRLVLGKPLGEGCFQGVVRAEAFGMDPARPDQASTVAVKMLKDNASDKDLADLVSEMEVMK
 LIGRHKNIINLLGVCTQEGPLYVIVECAAKGNLREFLRARRPPGPDLSPDGPRSSEGPLSFVPLVSCAYQVARGM
 QYLESRCKIHRDLAARNVLVTEDNMKIADFLARGVHHIDYKKTSNGRLPVKWMPEALFDRVYTHQSDVWSF
 GILLWEIFTLGGSPYPGIPVEELFSLREGHRMDRPPHCPPELYGLMRECWAAPSQRPTFKQLVEALDKVLLAV
 SEEYDLRLTLFGPYSPSGDASSTCSSSDSVFSDHPLPLGSSSFPFGSGVQT

Mass Match Peptides (bold):

AEAFGMDPARPDQASTVAVK [878]

Tandem Peptides (underline):

AEAFGMDPARPDQASTVAVK [878]

Peptide Source: iTRAQ, Small cell lung cancer

MRLLLALLGVLLSVPGPPVLSLEAEEVELEPCLAPSLQQEQELTVALGQPVRLCCGRAERGGHWYKEGSRLAP
 AGRVRGWRGRLEIASFLPEDAGRYLCLARGSMIVLQNLTLITGDSLTSNDDDEDPKSHRDPNSNRHSYPQQAPYWT
 HPQRMKKLHAVPAGNTVKFRCPAAGNPTPTIRWLKDGQAFHGENRIGGIRLRHQHWSLVMSVVPSTRGTYTCL
 VENAVGSIRYNYLLDVLERSPHRPILQAGLPANTTAVVGSDELCKVYSDAQPHIQWLKHIVINGSFGADGFP
 YVQVLKTADINSSEVEVLYLRNVSAEDAGEYTCLAGNSIGLSYQSAWLTVLPEDPTWTAAAPARYTDIILYAS
 GSLALAVLLLAGLYRGQALHGRHPRPATVQKLSRFPLARQFSLES GSSGKSSSSSLVRGVRLSSSGPALLAGLV
 SLDPLDPLWEFPRDRLVLGKPLGEGCFGQVRAEAFGMDPARPDQASTVAVKMLKDNASDKDLADLVSEMEVMK
 LIGRHKNIINLLGVCTQEGPLYVIVECAAKGNLREFLRARRPPGPDLSPDGPRSEGLSFPVLVSCAYQVARGM
 QYLESRCKIHRDLAARNVLVTEDNVMKIADFGLARGVHHIDYKKTSGRLPVKWMAPALFDRVYTHQSDVWSF
 GILLWEIFTLGSGPYPGIPVEELFSLREGHRMDRPHCPPELYGLMRECWHAAFSQRPFTFKQLVEALDKVLLAV
 SEEYLDLRLTFGPYSPSGDASSTCSSSDSVFSDHPLPLGSSSFPFGSGVQT

Mass Match Peptides (bold):

LVLGK [951]

Tandem Peptides (underline):

LVLGK [951]

OGTA247 (SEQ ID No: 44)

Peptide Source: 1D-GE, Hepatocellular carcinoma

MVVALRYVWPLLLCSPCLLIQIPEEYEGHEVMEPPVITEQSPRRLVVFPTDDISLK**CEASGKPEVQFR**WTRDGVH
 FKPKRELGVTVYQSPHSGSETITGNNSNFAQR**FOGIYR**CFASNK**LGTAMSHEIR**LMAGAPKWPKETVKPVEVEE
 GESVVLPCNPSPSAEPLRIYWMNSKILHIKQDERVTMGQNGNLYFANVLTSNDHSDYICAHFPGTRTIIQ**EPI**
DLRVK**ATNSMIDR**KPRLLFPTNSSSHLVALQGQPLVLECIAGEFPPTIK**WLRPSGMPADRVTYQNHNK**ILQLL
 KVGEEDDGEYRCLAENSLGSARHAYYVTVAAAPYWLHKPQSHLYGPGETARLDCQVQGRPOPEVTWRINGIPVEE
 LAKDQKYRIQR**GALILSNVQPSDTMVTQCEARN**RHGLLANAYIYVVLPAKILTADNQTYMAVQGSTAYLLCKA
 FGAPVPSVQWLDEDGTTVLQDER**FFPYANGTLGIR**DLQANDTGRYFCLAANDQNNVTIMANLKVK**DATQITQGPR**
STIEKKGS**RVTF**TCQASFDPSLQPSITWRGDGRDLQELGDSK**YFIEDGR**LVIHSLDYSQGNYSVASTELDVV
 ESR**AQLLVGSPGPVPR**LVLSDLHLLTQSQVR**VSWSPAEDHNAPIEKYDIEFED**KEMAPEKWYSLGKVPGNQST
 TLK**LSPYVHYTFR**VTAINKYGPGEPSVSETVVTPEAAPEKNPVDVKEGNETTNMVTWKPLR**WMDWNAPQVOY**
RVQWRPQGRGPWQEIVSDPFLVVSNTSTFVPYIEKVQAVNSQKGPEPQVTIGYSGEDYPQAIPELEGIEILN
 SSAVLVKWRPVDLAQVKGHLR**GYNVTYWR**EGSQKHSKRHIHKDHVVVPANTTSVILSGLRPYSSYHLEVQAFNG
 RSGSPASEFTFTSTPEGVPGHPEALHLECQSNLSLLRWQPPLSHNGVLTGYVLSYHPLDEGGKQLSFNLDP
 RTHNLTDLSPHLRYRFQLQATTK**EGPGEAIVR**EGGTMAISGIDFGNISATAGENYSVSVWPKEGQCNR**FHIL**
FKALGEEKGGASLSPQYVSYNQSSYTQWDLQPDTDYIEHLFKERMF**HQMAVK**INGTGRVRLPPAGFATEGWFIG
 FVSAILLLLLVLLILCFIKRSKGGKYSVKDK**EDTQVDSEARPMK**DETTFGEYRSLESNDNEEKAFGSSQPSLNGDIK
 PLGSDDSLADYGGSDVQFNEDGSFIGQYSGKKEKAAGNDSSGATSPINPAVALE

Mass Match Peptides (bold):

AQLLVGSPGPVPR [82]
 ATNSMIDR [92]
 CEASGKPEVQFR [101]
 DATQITQGPR [109]
 EDTQVDSEARPMK [170]
 EGPGEAIVR [189]
 EPIDLR [217]
 FFPYANGTLGIR [251]
 FHILFK [253]
 FOGIYR [266]
 GALILSNVQPSDTMVTQCEAR [284]
 GYNVTYWR [330]
 HQMAVK [342]
 LGTAMSHEIR [463]
 LSPYVHYTFR [489]

STIEKK [659]
VQWRPQGTR [795]
VSWSPAEDHNAPIEK [798]
VTFTCQASFDPQLQPSITWR [804]
VTYQNHNK [808]
WLRPSGMPADR [828]
WMDWNAPQVQYR [829]
YFIEDGR [850]

Tandem Peptides (underline):

AQLLVGSPGPVPR [82]
DATQITQGPR [109]
DLQELGDSK [137]
EGPGEAIVR [189]
INGIPVEELAK [382]
LDCQVQGRPQPEVTWR [445]
LGTAMSHEIR [463]
VGEEDDGEYR [762]
YDIEFEDK [842]
YFIEDGR [850]

Peptide Source: 1D-GE, Melanoma

MVVALRYVWPLLLCSPCLLIQIPEEYEGHHVMEPPVITEQSPRRLLVFPTDDISLK**CEASGKPEVQFR**WTRDGVH
FKPKEELGVTVYQSPHSGSFTITGNNSNFAQR**FQGIYR**CFASNK**LGTAMSHEIR**LMAGAPKWPKETVKPVEVEE
GESVVLPCNPPPSAEPLRIYWMNSKILHIKQDERVTMGQNGNLYFANVLTSDNHSDYICHAHFPGTRTIIQ**KEPI**
DLRVKATNSMIDRKPRLLFPTNSSSHLVALQGQPLVLECIAEGFPTPTIK**WLRPSGMPADR**VTYQNHNKTLQLL
KVGEEDDGEYR**CLAENSLGSAR**HAYYVTVEAAPYWLHKPQSHLYGPGETARLDCQVQGRPQPEVTWR**INGIPVEE**
LAKDQKYRIQR**GALILSNVQPSDTMTQCEAR**NRHGLLLANAYIYVQLPAKILTADNOTYMAVQGSTAYLLCKA
FGAPVPSVQWLDEDEGTTVLQDERFFPYANGTLGIRDLQANDTGRYFCLAANDQNNVTIMANLKVK**DATQITQGPR**
STIEKKGSRVTFFTCQASFDPQLQPSITWRGDGRDLQELGDSK**YFIEDGR**LVIHSLDYSQDQNYSCVASTELDVV
ESR**AQLLVGSPGPVPR****LVLSDLHLLTQSQVRVSWSPAEDHNAPIEK**YDIEFEDKEMAPEKWYSLGKVPGNQTST
TLK**LSPVVHYTFR**VTAINKYGPGEPSVSETVVTPEAAPEKNPVDVK**GEGNETTNMVITWKPLRWMDWNAPQVQY**
RVQWRPQGTRGPWQEIQIVSDPFLVVSNTSTFVPEYIKVQAVNSQKGPEPQVTIGYSGEDYPQAIPELEGIEILN
SSAVLVK**WRPVDLAQVK**GHLRGYNVTYWREGSQRKHSKRHIHKDHVVVPANTTSVTLGSLRPYSSYHLEVQAFNG
RGSGPASEFTFSTPEGVPGHPEALHLEQSNSTSLLRWQPLSHNGVLTGYVLSYHPLDEGGK**QLSFNLR**DP
RTHNLTDLSPHLRYPQLQATT**EGPGEAIVR**EGGTMAISGIDFGNISATAGENYSVSVWPKEGQCNFR**FHIL**
FKALGEEKGGASLSPQYVSYNQSSYTQWDLQPDTDYIEHLFKERMFRHQMAVKTNGTGRVRLPPAGFATEGWFIG
FVSAIILLVLLILCFIKRSKGGKYSVKDKEDTQVDSEARPMKDETFGEYRSLESNDNEKAFGSSQPSLNGDIK
PLGSDDSLADYGGSDVDQFNEDGSFIGQYSGKKEKEAAGGNDSSGATSPINPAVALE

Mass Match Peptides (bold):

AFGAPVPSVQWLDEDEGTTVLQDER [65]
AQLLVGSPGPVPR [82]
CEASGKPEVQFR [101]
CLAENSLGSAR [105]
DATQITQGPR [109]
DGVHFKPK [126]
EGPGEAIVR [189]
EPIDLR [217]
FFPYANGTLGIR [251]
FHILFK [253]
FQGIYR [266]
GALILSNVQPSDTMTQCEAR [284]
GEGNETTNMVITWKPLR [289]
QLSFNLR [312]
INGIPVEELAK [382]
LGTAMSHEIR [463]
LSPVHYTFR [489]
LVLSDLHLLTQSQVR [502]

VGEEDDGEYR [762]
VQWRPQGTR [795]
VSWSPAEDHNAPIEK [798]
WLRPSGMPMPADR [828]
WMDWNAPQVQYR [829]
WRPVDLAQVK [831]
YFIEDGR [850]

Tandem Peptides (underline):

AQLLVVGSPGPVPR [82]
DATQITQGPR [109]
DHVVVPANTTSVILSGLRPYSSYHLEVQAFNGR [128]
EELGVTIVYQSPHSGSFITIGNNSNFAQR [178]
EGPGEAIVR [189]
VQWRPQGTR [795]
WMDWNAPQVQYR [829]
WRPVDLAQVK [831]

Peptide Source: iTRAQ, Non-small cell lung cancer

MVVALRYVWPLLLCSPCLLIQIPEEYEGHHVMEFPVITEQSPRRLVVFPTDDISLKCEASGKPEVQFRWTRDGVH
FKPKEELGVTVYQSPHSGSFITIGNNSNFAQRFGGIYRCFASNKLGTAMSHIEIRLMAEGAPKWPKETVVKPVEVEE
GESVVLPCNPPPSAEPLRIYWMNSKILHIKQDERVTMGQNGNLYFANVLTSDNESDYICAHFPGTRTIIQKEPI
DLRVKATNSMIDRKPRLLFPTNSSSHLVALQGCPLVLECIAGFPPTTIKWLRLPSGMPMPADRVTYQNHNTLQLL
KVGEEDDGEYRCLAENSLGSARHAYVTVVEAAPYWLHKPQSHLYGPGETARLDCQVQGRPQPEVTWRINGIPVEE
LAKDQKYRIQRGALILSNVQPSDTMTVQCEARNRHGLLLANAYIYVQLPAKILTADNQT YMAVQGSTAYLLCKA
FGAPVPSVQWLDEGTTVLQDERFFPYANGTLGIRDLOANDTGRYFCLAANDQNNVTIMANLKVKDQITQGP
STIEKKGSRVTFTCQASFDPSLQPSITWRGDGRDLQELGSDSKYFIEDGRLVIHSLDYSDQGNYS CVASTELDVV
ESRAQLLVVGSPGPVPRVLVSLDLHLITQSQVRVSWSPAEDHNAPIEKYDIEFEDKEMAPEKWYSLGKVPNGQTST
TLKLSPYVHYTFRTAINKYGPGEPSPVSETVVTPEAAPEKNPVDVKGEGETTNMVTITWKPLRWMDWNAPQVQY
RVQWRPQGRGPNQEQIVSDPFLVVSNTSTFVPEYIEKVQAVNSQKGPEPQVTIGYSGEDYPQAIPELEGIEILN
SSAVLVKWRPVDLAQVKGHLRGYNVTYWRGSGQRKHSKRHIKHDHVVVPANTTSVILSGLRPYSSYHLEVQAFNG
RGSGPASEFTFTSTPEGVPGHPEALHLECCQSNSTSLLLRWQPPPLSHNCVLTGYVLSYHPLDEGGKQLSFNLDP
RTHNLTDLSPLRLRYFQLQATTKEGPGEAIVREGGTMALSGISDFGNISATAGENYSVSVWVPKEGQCNRPHIL
FKALGEEKGGASLSPQYVSYNQSSYTQWDLQPDYDYEIHLFEKERMFRHQMAVKTNGTGRVRLPPAGFATECWFIC
FVSAIILLLLVLILCFIKRSKGGKYSVKDKEDTQVDSEARPMKDETFGEYRSLESNDNEEKAFGSSQPSLNGDIK
PLGSDDSLADYGGSDVDQFNEDGSFIGQYSGKKEKEAAGGNDSSGATSPINPAVALE

Mass Match Peptides (bold):

ERMFR [906]
TNGTGRVR [984]
WRPVDLAQVK [831]

Tandem Peptides (underline):

ERMFR [906]
TNGTGRVR [984]
WRPVDLAQVK [831]

Peptide Source: iTRAQ, Small cell lung cancer

MVVALRYVWPLLLCSPCLLIQIPEEYEGHHVMEFPVITEQSPRRLVVFPTDDISLKCEASGKPEVQFRWTRDGVH
FKPKEELGVTVYQSPHSGSFITIGNNSNFAQRFGGIYRCFASNKLGTAMSHIEIRLMAEGAPKWPKETVVKPVEVEE
GESVVLPCNPPPSAEPLRIYWMNSKILHIKQDERVTMGQNGNLYFANVLTSDNESDYICAHFPGTRTIIQKEPI
DLRVKATNSMIDRKPRLLFPTNSSSHLVALQGCPLVLECIAGFPPTTIKWLRLPSGMPMPADRVTYQNHNTLQLL
KVGEEDDGEYRCLAENSLGSARHAYVTVVEAAPYWLHKPQSHLYGPGETARLDCQVQGRPQPEVTWRINGIPVEE
LAKDQKYRIQRGALILSNVQPSDTMTVQCEARNRHGLLLANAYIYVQLPAKILTADNQT YMAVQGSTAYLLCKA
FGAPVPSVQWLDEGTTVLQDERFFPYANGTLGIRDLOANDTGRYFCLAANDQNNVTIMANLKVKDQITQGP
STIEKKGSRVTFTCQASFDPSLQPSITWRGDGRDLQELGSDSKYFIEDGRLVIHSLDYSDQGNYS CVASTELDVV
ESRAQLLVVGSPGPVPRVLVSLDLHLITQSQVRVSWSPAEDHNAPIEKYDIEFEDKEMAPEKWYSLGKVPNGQTST

TLKLSPYVHYTFRVTAINKYGPGEPSPVSETVVTPEAAPEKNPVDVKGEGNETTNMVTWKPLRWMDWNAPQVQY
RVQWRPQGTGRGPWQEQIVSDPFLVVSNTSTFVPYEIKVQAVNSQGKCGPEPQVTIGYSGEDYPQAIPELEGIEILN
SSAVLVKWRPVDLAQVKGHLRGYNVTYWREGSQRKHSKRHIHKDHVVVPANTTSVILSGLRPYSSYHLEVQAFNG
RGSGPASEFTTFTPEGVPGHPEALHLECSNTSLLLRWQPPLSHNGVLTGYVLSYHPLDEGGKQQLSFNLRDPELR
RTHNLTDLSPHLRFRYFQLQATTKEGPGGEAIVREGGTMALSGISDFGNISATAGENYSVVSVPKEGQCNRFRHIL
FKALGEEKGGASLSPQYVSYNQSSYTQWDLQPDTDYEIHLFKERMFRHQMAYKTNGTGRVRLPPAGFATEGWFEG
FVSAIILLVLLVLLLCFIKRSKGGKYSVKDKEDTQVDSEARPMKDETFCGYRSLSDNEEKAFGSSQPSLNGDIK
PLGSDDSLADYGGSVDVQFNEDGSFIGQYSGKKEKEAAGGNDSSGATSPINPAVALE

Mass Match Peptides (bold):

AQLLVVGSPPGVPR [82]
DATQITQGER [109]
DLQELGDSDK [137]
DPELR [893]
EGPGEAIVR [189]
EPIDLR [217]
NPVDVK [958]
TNGTGRVR [984]
VGEEDDGEYR [762]
VQAVNSQGK [998]
VTAINK [1000]
YGPGEPSPVSETVVTPEAAPEK [1005]

Tandem Peptides (underline):

AQLLVVGSPPGVPR [82]
DATQITQGER [109]
DLQELGDSDK [137]
DPELR [893]
EGPGEAIVR [189]
EPIDLR [217]
NPVDVK [958]
TNGTGRVR [984]
VGEEDDGEYR [762]
VQAVNSQGK [998]
VTAINK [1000]
YGPGEPSPVSETVVTPEAAPEK [1005]

OGTA248 (SEQ ID No: 45)

Peptide Source: 1D-GE, Renal cell cancer

MGCWGQLLVWFGAAGAILCSPSGSQETFLRSSPLPLASPSQDPKVSAPPSILEPASPLNSPGTEGSWLFSTCGA
SGRHGPTQTQCDGAYAGTSVVVTVGAAQQLRGVQLWRVPGPGQYLIISAYGAAGGKGAKNHLRAHGVFVSAIFSL
GLGESLYILVGQGEDACPGGSPESQLVCLGESRAVEEHAAMDGSEGVFGSRRWAGGGGGGGGATYVFRVRAGEL
EPLLVAAAGGGGRAYLRPRDRGRQTQASPEKLENRSEAPGSGCRGGAAGGGGCWTSRAPSPQAGRSLQEGAEGGQGC
SEAWATLGWAAAGGFGGGGGACTAGGGGGGYRGGDASETDNLWADGEDGVSTFIHPSSSELFLOPLAVTENHGEVEI
RRHLNCHCPLRDCQWQAEQLAECLCPEGMELAVDNVTCDLHKPPGPLVLMVAVVATSTLSLLMVCGLLILVK
QKKWQGLQEMRLPSPELELSKLRTSAIRTPNPNYYCQVGLGPAQSWPLPPGVTEVSPANVTLLRALGHGAFGEVY
EGLVIGLPGDSSPLQVAIKTLPELCSPODELDFLMEALIIISKFRHQNIIVRCVGLSLRATPRLILLELMSSGDMKS
FLRHSRPHLGQPSPLVMRDLLQLAQDIAQGCCHYLEENHFIHRDIAARNCLLSCAGPSRVAKIGDFGMARDIYRAS
YYRRGDRALLPVKMPPEAFLEGIFTSKTDSWSFGVLLWEIFSLGYMPYPCRTNQEVLDDEVVGGGRMDPPRGCPG
PVYRIMTQCWQHEPELRPSFASILERLQYCTQDPDVLNSLLPMELGPTPEEEGTSGLGNRSLECLRPPQPQELSP
EKLKSWGGSPLGPWLSSGLKPLKSRGLQPQNLWNPTYRS

Mass Match Peptides (bold):

Tandem Peptides (underline):

TNQEVLDDEVVGGGR [712]

Peptide Source: iTRAQ, Non-small cell lung cancer

MGCWGQLLVWFGAAGAILCSSPGSQETFLRSSPLPLASPSQDPKVSAPPSILEPASPLNSPGTEGSWLFSTCGA
SGRHGPTQTQCDGAYAGTSVVVTGGAAGQLRGVQLWRVPGPGQYLISAYGAAGGKGAKNHLSRAHGVFVSAIFSL
GLGESLYILVGQQGEDACPGGSPESQLVCLGESRAVEEHAAMDGSEGVPGSRRWAGGGGGGGGATYVFRVRAGEL
EPLLVAAGGGGRAYLRPRDRGRTQASPEKLENRSEAPGSGGRGAAGGGGGWTSRAPSPQAGRSIQEGAEGGQGC
SEAWATLGWAAAGGFGGGGGACTAGGGGGGYRGDASETDNLWADGEDGVSFHPSSEFLQPLAVTENHGEVEI
RRHLNCSHCPLRDCQWQAEQLAECLCPEGMELAVDNVTCMDLHKPPGPLVLMVAVVATSTLSLLMVCVLIILVK
QKKWQGLQEMRLPSPLELELSK**LRTSAIR**TAPNPYYCQVGLGPAQSWPLPPGVTEVSPANVTLLRALGHGAFGEVY
EGLVIGLPGDSSPLQVAIKTLPELCSFQDELDLMEALIISKFRHQNVRCVGLSLRATPRLILLELMSGGDMKS
FLRHSRPHLGQPSPLVMRDLQLAQDIAQGCHYLEENHFIHRDIAARNCLLSCAGPSRVAKIGDFGMARDIYRAS
YYRRGDRALLPVKWMPPPEAFLEGIPTSKTDSWSFGVLLWEIFSLGYMPYPGRTNQEVLDFFVGGGRMDPPRGCPG
FVYRIMTQCQWHEPELRPSFASILERLQYCTQDDPVLNSLLPMELGPTPEEEGTSGLGNRSLECLRPPQPQELSP
EKLKSWGGSPLGPWLSSGLKPLKSRGLQPQNLWNPTYRS

Mass Match Peptides (bold):

LRTSAIR [945]

Tandem Peptides (underline):

LRTSAIR [945]

OGTA249 (SEQ ID No: 46)

Peptide Source: 1D-GE, Ovarian cancer

MSAGGASVPPPPNPAVSFPFPPRVTLPAGPDILRTYSGAFVLCLEILFGGLVWILVASSNVPLPLLQGWVMFVSVTA
FFFSLLFLGMFLSGMVAQIDANWNFLDFAYHFTVFVFYFGAFLLEAAATSLHDLHCNTTITGQPLLSDNQYNINV
AASIFAFMTTACYGCSLGLALRRWRP

Mass Match Peptides (bold):

MSAGGASVPPPPNPAVSFPFPPR [524]

Tandem Peptides (underline):

VTLPAGPDILR [805]

Peptide Source: iTRAQ, Non-small cell lung cancer

MSAGGASVPPPPNPAVSFPFPPR**VTLPAGPDILR**TYSGAFVLCLEILFGGLVWILVASSNVPLPLLQGWVMFVSVTA
FFFSLLFLGMFLSGMVAQIDANWNFLDFAYHFTVFVFYFGAFLLEAAATSLHDLHCNTTITGQPLLSDNQYNINV
AASIFAFMTTACYGCSLGLALRRWRP

Mass Match Peptides (bold):

VTLPAGPDILR [1001]

Tandem Peptides (underline):

VTLPAGPDILR [1001]

Peptide Source: iTRAQ, Renal cell cancer

MSAGGASVPPPPNPAVSFPFPPR**VTLPAGPDILR**TYSGAFVLCLEILFGGLVWILVASSNVPLPLLQGWVMFVSVTA
FFFSLLFLGMFLSGMVAQIDANWNFLDFAYHFTVFVFYFGAFLLEAAATSLHDLHCNTTITGQPLLSDNQYNINV
AASIFAFMTTACYGCSLGLALRRWRP

Mass Match Peptides (bold):

VTLPAGPDILR [1001]

Tandem Peptides (underline):

VTLPAGFDILR [1001]

OGTA257 (SEQ ID No: 47)

Peptide Source: 1D-GE, Pancreatic cancer

MGLSLPKEKGLILCLWSKFCRWFQRRESWAQSRDEQNLLQQKRIWESPLLLAAKDNDVQALNKLKLYEDCKVHQR
GAMGETALHIAALYDNLEAAMVLMEAAPELVFEPMTSELYEGQTALHIAVVNQNMNLVRALLARRASVSARATGT
AFRRSPCNLIYFGEHPLSFAACVNSEEIVRLLEHGCADIRAQDSLGNLTVLHILILQPNKTFACQMYNLLLSYDRH
GDHLQPLDLVPNHQGLTPFKLAGVEGNTVMFQHLMQKRKHTQWYTGPLTSTLYDLTEIDSSGDEQSLELELIITTK
KREARQILDQTPVKELVSLKWKRYGRPYFCMLGAIYLLYIICFTMCCIRPLKPRNTNNRTSPRDNTLLQQKLLQE
AYMTPKDDIRLVGELVTVIGAIILLVEVPDIFRMGVTRFFGQTILGGPFHVLIITYAFMVLVTMVMRLISASGE
VVPMSFALVLGWCNVMYFARGFQMLGPFTIMIQQMIFGDLMRFCWLMMAVILGFASAFYIIFQTEDPEELGHFYD
YPMALFSTFELFLTIIDGPANYNVDLPFMSITYAAFAIIATLLMLNLLIAMMGDTHWRVAHERDELWRAQIVAT
TVMLERKLPRLWPRSGICGREYGLGDRWFLRVEDRQDLNRQRIQRYAQAFHTRGSEDLDKDSVEKLELGCPTSP
HLSLPMPSVSRSTSRSSANWERLRQGTLRDLRDLGIINRGLEDGESWEYQI

Mass Match Peptides (bold):

Tandem Peptides (underline):

LLQEAYMTPK [468]

Peptide Source: iTRAQ, Colorectal cancer

MGLSLPKEKGLILCLWSKFCRWFQRRESWAQSRDEQNLLQQKRIWESPLLLAAKDNDVQALNKLKLYEDCKVHQR
GAMGETALHIAALYDNLEAAMVLMEAAPELVFEPMTSELYEGQTALHIAVVNQNMNLVRALLARRASVSARATGT
AFRRSPCNLIYFGEHPLSFAACVNSEEIVRLLEHGCADIRAQDSLGNLTVLHILILQPNKTFACQMYNLLLSYDRH
GDHLQPLDLVPNHQGLTPFKLAGVEGNTVMFQHLMQKRKHTQWYTGPLTSTLYDLTEIDSSGDEQSLELELIITTK
KREARQILDQTPVKELVSLKWKRYGRPYFCMLGAIYLLYIICFTMCCIRPLKPRNTNNRTSPRDNTLLQQKLLQE
AYMTPKDDIRLVGELVTVIGAIILLVEVPDIFRMGVTRFFGQTILGGPFHVLIITYAFMVLVTMVMRLISASGE
VVPMSFALVLGWCNVMYFARGFQMLGPFTIMIQQMIFGDLMRFCWLMMAVILGFASAFYIIFQTEDPEELGHFYD
YPMALFSTFELFLTIIDGPANYNVDLPFMSITYAAFAIIATLLMLNLLIAMMGDTHWRVAHERDELWRAQIVAT
TVMLERKLPRLWPRSGICGREYGLGDRWFLRVEDRQDLNRQRIQRYAQAFHTRGSEDLDKDSVEKLELGCPTSP
HLSLPMPSVSRSTSRSSANWERLRQGTLRDLRDLGIINRGLEDGESWEYQI

Mass Match Peptides (bold):

QILDQTPVK [962]

Tandem Peptides (underline):

QILDQTPVK [962]

Peptide Source: iTRAQ, Hepatocellular cancer

MGLSLPKEKGLILCLWSKFCRWFQRRESWAQSRDEQNLLQQKRIWESPLLLAAKDNDVQALNKLKLYEDCKVHQR
GAMGETALHIAALYDNLEAAMVLMEAAPELVFEPMTSELYEGQTALHIAVVNQNMNLVRALLARRASVSARATGT
AFRRSPCNLIYFGEHPLSFAACVNSEEIVRLLEHGCADIRAQDSLGNLTVLHILILQPNKTFACQMYNLLLSYDRH
GDHLQPLDLVPNHQGLTPFKLAGVEGNTVMFQHLMQKRKHTQWYTGPLTSTLYDLTEIDSSGDEQSLELELIITTK
KREARQILDQTPVKELVSLKWKRYGRPYFCMLGAIYLLYIICFTMCCIRPLKPRNTNNRTSPRDNTLLQQKLLQE
AYMTPKDDIRLVGELVTVIGAIILLVEVPDIFRMGVTRFFGQTILGGPFHVLIITYAFMVLVTMVMRLISASGE
VVPMSFALVLGWCNVMYFARGFQMLGPFTIMIQQMIFGDLMRFCWLMMAVILGFASAFYIIFQTEDPEELGHFYD
YPMALFSTFELFLTIIDGPANYNVDLPFMSITYAAFAIIATLLMLNLLIAMMGDTHWRVAHERDELWRAQIVAT
TVMLERKLPRLWPRSGICGREYGLGDRWFLRVEDRQDLNRQRIQRYAQAFHTRGSEDLDKDSVEKLELGCPTSP
HLSLPMPSVSRSTSRSSANWERLRQGTLRDLRDLGIINRGLEDGESWEYQI

Mass Match Peptides (bold):

LRQGTLR [944]

Tandem Peptides (underline):

LRQGTLR [944]

Peptide Source: iTRAQ, Non-small cell lung cancer

MGLSLPKEKGLILCLWSKFCRWFQRRESWAQSRDEQNLLQQKRIWESPLLLAAKDNDVQALNKLKLYEDCKVHOR
GAMGETALHIAALYDNLEAAMVLMEEAPELVFEPMTSELYEGQTALHIAVNVQNMNLVRALLARRASVSAR**ATGT**
AFRRSPCNLIYFGEHPLSPAACVNSEEIVRLLEHGADIRAQDSLGNLTVLHILILQPNKTFACQMYNLLLSYDRH
GDHLQPLDLVFNHQGLTPFKLAGVEGNTVMFQHLMOQRKHTQWTYGPLTSTLYDLTEIDSSGDEQSLELEIITTK
KREARQILDQTPVK**ELVSLK**WKRYGRPYFCMLGAIYLLYICFTMCCTYRPLKPRTNNRSPRDNLLQKLLQE
AYMTPKDDIRLVGELVTVIGAIILLVEVPDIFRMGVTRFFGQTILGGPFHVLIITYAFMVLVTMVMRLISASGE
VVPMSFALVLGWCNVMYFARGFQMLGPFTIMIQKMIFGDLMRFCWLMMAVVLGFAAFYIIFQTEDPEELGHFYD
YPMALFSTFELFLTIDGPANYNVDLPFMYSITYAAFAIATLLMLNLLIAMMGDTHWRVAHERDELWRAQIVAT
TMMLERKLPRLWPRSGICGREYGLGDRWFLRVEDRQDLNRQRIQRYAQAFHTRGSEDLKDSVEKLELGCFFSP
HLSLPMPSVSRSTSRSSANWERLRQGTLRDLRGIINRGLEDGESWEYQI

Mass Match Peptides (bold):

ATGTAFRR [884]

ELVSLK [902]

Tandem Peptides (underline):

ATGTAFRR [884]

ELVSLK [902]

Peptide Source: iTRAQ, Ovarian cancer

MGLSLPKEKGLILCLWSKFCRWFQRRESWAQSRDEQNLLQQKRIWESPLLLAAKDNDVQALNKLKLYEDCKVHOR
GAMGETALHIAALYDNLEAAMVLMEEAPELVFEPMTSELYEGQTALHIAVNVQNMNLVRALLARRASVSARATGT
AFRRSPCNLIYFGEHPLSPAACVNSEEIVR**LLIEHGADIR**AQDSLGNLTVLHILILQPNKTFACQMYNLLLSYDRH
GDHLQPLDLVFNHQGLTPFKLAGVEGNTVMFQHLMOQRKHTQWTYGPLTSTLYDLTEIDSSGDEQSLELEIITTK
KREARQILDQTPVKELVSLKWKRYGRPYFCMLGAIYLLYICFTMCCTYRPLKPRTNNRSPRDNLLQKLLQE
AYMTPKDDIRLVGELVTVIGAIILLVEVPDIFRMGVTRFFGQTILGGPFHVLIITYAFMVLVTMVMRLISASGE
VVPMSFALVLGWCNVMYFARGFQMLGPFTIMIQKMIFGDLMRFCWLMMAVVLGFAAFYIIFQTEDPEELGHFYD
YPMALFSTFELFLTIDGPANYNVDLPFMYSITYAAFAIATLLMLNLLIAMMGDTHWRVAHERDELWRAQIVAT
TMMLERKLPRLWPRSGICGREYGLGDRWFLRVEDRQDLNRQRIQRYAQAFHTRGSEDLKDSVEKLELGCFFSP
HLSLPMPSVSRSTSRSSANWERLRQGTLRDLRGIINRGLEDGESWEYQI

Mass Match Peptides (bold):

LLIEHGADIR [936]

Tandem Peptides (underline):

LLIEHGADIR [936]

OGTA271 (SEQ ID No: 48)

Peptide Source: 1D-GE, Breast cancer

MAPEPAPGRMTMVPLVPALVMLGLVAGAHGDSKPVFIK**VPEDQTCLSGGVASFVCCQATGEPKPRITWMKK**GKKVSS
QR**FEVIEFDDGAGSVLR**IQPLRVQRDEAIYECTATNSLGEINTSAK**LSVLEEEQLPPGFPSIDMGPOLK**VVEKAR
TATMLCAAGGNPDPEISWFKDFLPVDPATSNGRIKQLRSGALQIESSEESDQGYECVATNSAGTRYSAFANLYV
RVRRVAPRFSIPSSQEVMPGGSVNLTCAVAVGAPMPYVKWMMGAELTKEDEMPVGRNVLELSNVVRS**SANYTCVA**
ISSLGMIEATAQVTYKALPKPPIDLVTETTATSVTLTWDSGNSEPVTYYGIQYR**AAGTEGPFQEVVDGVATTRY**S
IGGLSPFSEYAFRVLAVNSIGRGPPSEAVRARTGEQAPSSPPRRVQAR**MLSASTMLVQWEPPEENGLVR**GYRVY
YTPDSR**RPPNAWHK**HNTDAGLLTIVGSLLPGITYSRLVLAFTAVGDGPPSPITIQVKTQQGVPAQPADFQAEVESD
TRIQLSWLLPPQERIIMYELVYWAAEDEDQHKVTFDPTSSYTLEDLKPDTLYRFQLAAR**SDMGVGVFTPTIEAR**

TAQSTPSAAPPQK**VMCVSMGSTTVRVSWVPPPADSRNGVITQYSVAYEAVDGEDRGRHVVDGISREHSSWDLVGLE**
KWTEYRVWVR**AHTDVGPGPESSPVLVR****DEDEDVPSGPPRK**VEVEPLNSTAVHVYWKLPVPSK**QHGQIR**GYQVTVVR
LENGEPRGLPIIQDVMLAEAQETTISGLTPETTSVTVAAYTKGDGARSKP KIVTTTGAVPGRPTMMISTTAMN
TALLQWHP**PKELPGELLGYR**LQYCRADARPNTIDFGKDD**QFTVTGLHKGTTYIFRLAAKNR****AGLGEEFEKEIR**
TPEDLPSGFPQNLHVTGLTSTTELAWDFFVLAERNRIISYTVVFR**DINSQOELQNITTDTRFTLTGLKPDTTY**
DIKVRAWTSK**SGGPLSPSIQSR**TMPVEQVFAKNFRVAAAMK**TSVLLSWEVPSYKS**AVPFK**ILYNGQSVEVDGHS**
MRKLIADLQPNTEYSFVLMNRGSSAGGLQHLVSIRTAPDLLPHKPLPASAYIEDGR**FDLSMPHVQDPSLVR**WFYI
VVVPIDRVGGSMLTPRWSTPEELELDELLEAIEQGEEQRRRRQAERLKPVAAQLDVLPEFTTLGDKKNYRGF
YNRPLSPDLSYQCFVLASLKEPMDQKRYASSPYSDIIVVQVTPAQOQEEPEMLWVTGPVLAVILILIVIAILLF
KKRTHSPSSKDEQSIGLK**DSLLAHSSDPVEMRRLNYQTPGMRDHPPIPTDLADNIER**LKANDGLKFSQEYESI
DPGQQFTWENSLVKNPKNRYANVIAYDHSRVILTSIDGVPGSDYINANYIDGYR**KQNAYIATQGPLPETMGDF**
WRMVWEQRTATVMMTRLEEKSRVKCDQYWPARGTETCGLIQVTLTLDVTELATYTVRTFALHKSSESSEKRELRFQ
QFMAWPDHGVPEYPTPILAFRRVK**ACNPLDAGPMVVHCSAGVGRTGCFIVIDAMLERMKHEK****TVDIYGHVTCMR**
SQRNYMVQTEDQYVFIHEALLEAATCGHTEVPARNLYAHIQK**LGQVPPGESVTAMELEFK**LLASSKAHTSRFISA
NLPCNKFKNRLVNIMPYELTRVCLQPIR**GVEGSDYINASF****LDGYRQK****AYIATQGPLAESTEDFWRMLWEHNSTI**
IVMLTKREMGRKCHQYWPASARS**YQYFVVDPM****AEYNNMPQYIL**REFKVTDARDGQSR**TIRQFQFTDWPEQGV**
KTGEGFIDFIGQVHK**TEQFGQDGPITVHCSAGVGR**TGVFITLSIVLERMR**YEGVDMFQTVK**FLRTQRPAMVQT
EDQYQLCYR**AALEYLGSFDHYAT**

Mass Match Peptides (bold):

AAGTEGPFQEVGDVATTR [50]
AALEYLGSFDHYAT [51]
ACNPLDAGPMVVHCSAGVGR [56]
AGLGEEFEK [71]
AHTDVGPGPESSPVLVR [72]
AYIATQGPLAESTEDFWR [98]
DFLPVDPATSNR [117]
DHPPIPTDLADNIER [127]
DINSQOELQNITTDTR [129]
DSLLAHSSDPVEMRR [157]
EHSSWDLVGLEK [196]
ELPGELLGYR [206]
EQFGQDGPITVHCSAGVGR [220]
FDLSMPHVQDPSLVR [246]
FEVIEFDDGAGSVLR [249]
FTLTGLKPDTTYDIK [275]
GPPSEAVR [308]
GSGPLSPSIQSR [315]
GVEGSDYINASF**LDGYR** [326]
HVVDGISR [347]
ILYNGQSVEVDGHSMR [378]
ILYNGQSVEVDGHSMRK [379]
ITWMKK [399]
KLIADLQPNTEYSFVLMNR [424]
KQNAYIATQGPLPETMGDFWR [433]
LENGEPR [455]
LGQVPPGESVTAMELEFK [462]
LIADLQPNTEYSFVLMNR [467]
LNYQTPGMR [475]
LSVLEEEQLPPGFPSIDMGQLK [492]
MLSASTMLVQWEPPEEPNGLVR [518]
MLWEHNSTIIVMLTK [519]
MVWEQR [529]
NGVITQYSVAYEAVDGEDR [537]
QFQFTDWPEQGVK [572]
QHGQIR [578]
QNAYIATQGPLPETMGDFWR [581]
RLNYQTPGMR [606]
RPPNAWHK [609]
SANYTCVAISSLGMIETAQVTVK [619]
SDMGVGVFTPTIEAR [621]

TATMLCAAGGNPDPEISWFK [674]
 TATVVMTR [676]
 TDEDVPSGPPRK [683]
 TGCFIGVIDAMLER [692]
 TEGGFIDFIGQVHK [693]
 TSVLLSWEVPDSYK [732]
 TVDIYGHVTCMR [735]
 VLAVNSIGR [774]
 VMCVSMGSTTVR [785]
 VPEDQTGLSGGVASFVCQATGEPKPR [789]
 VSWVPPPADSR [799]
 YEGVDMFQTVK [844]
 YQYFVVDPMAYNMPQYILR [869]

Tandem Peptides (underline):

AALEYLGSFDHYAT [51]
 DDQHFVTGLHK [111]
 GVEGSDYINASFIDGYR [326]
 SDMGVGVFTPTIEAR [621]
 YEGVDMFQTVK [844]

Peptide Source: 1D-GE, Cervical cancer

MAPEPAPGRMTVPLVPLVMLGLVAGAHGDSKPVFIKVPEDQTGLSGGVASFVCQATGEPKPRITWMKKGKKVSS
 QR**FEVIEFDDGAGSVLR**IQPLRVQRDEAIYECTATNSLGEINTSAKLSVLEEEQLPPGFPSIDMGFQPKVEKAR
 TATMLCAAGGNPDPEISWFK**DFLPVDPATSNGR**IKQLRSGALQIESSEESDQGYECVATNSAGTRYSAKANLYV
 RVRRVAPRFSIPSSQEVMPGGSVNLTCVAVGAPMPYVKKMMGAEEITKEDEMPVGR**NVLELSNVVRS**ANYTCVA
 ISSLGMIEATAQVTVKALPKPPIDLVVTETTATSVTLTWDSGNSEPVITYYGIQYR**AAGTEGPFQEV**DGVATTRY**S**
IGGLSPFSEYAFRVLA**NSIGR**GPPSEAVRARTGEQAPSSPPRRVQARMLASTMLVQWEPPEEPNGLVRGYR**VY**
YTPDSRRPPNAWHKHNTDAGLLTTVGSLLPGITYSRLVLAFTAVGDGPPSPITQVK**TQOGVPAQPADFQAEVESD**
TRIQLSWLLPPQERIIMYELVYWAAEDEDQHKVTFDPTSSYTLDELKPDITLYRFQLAAR**SDMGVGVFTPTIEAR**
 TAQSTPSAPQKVMCMVSMGSTTVR**VSWVPPPADSR**NGVITQYSVAYEAVDGEDRGRHVVDGISREHSSWDLVGL
 K**WTEYR**VWVR**AHTDVGPGPESSPVLVR**T**DE**DVPSGPPRKVEVEPLNSTAVHVYWKLPVPSK**QHGQIR**GYQVTVR
 LENGEPRGLPIQDVMLAAEQETTISGLTPETTYSVTVAAAYTTKGDGARSKPKIVTTGAVPGRPTMMISTTAMN
 TALLQWHPPK**ELPGELLGYR**LQYCR**ADEARNTIDFGKDDQHFVTGLHK**GTTYIFRLAAKNRAGLGEEFEKEIR
 TPEDLPSGFQNLHVTGLTTSTTELAWDPPVLAERNRIISYTVVFRDINSQQELQNTTDTRETLTGLKPDTTY
 DIKVRAWTSKSGSPSPSIQSRTPMEVQVFAKNFRVAAAMKTSVLLSWEVPDSYKSAVFPKILYNGQSVEVDGHS
 MRKLIADLPNTEYSFVLMNR**GSSAGGLQHLVSIR**TAPDLLPHKPLPASAYIEDGR**FDLSMPHVQDPSLVR**WFYI
 VVVPIDRVGGMLTPRWSTPEELEDLEAIEQGGEQRRRRRQAERLKPVAAQLDVLPEFTTLGDKKNYRGF
 YNRPLSPDLQYCFVLASLK**EPMDQKR**YASSPYSDEIVVQVTPAQQQEPEMLWVTGPVLAVILIIILIVIAILLF
 KRKRTHSPSSKDEQSIGLKDSLLAHSSDPVEMRRLNYQTPGMRDHPPIPTDLADNIEERLKANDGLKFSQYESI
 DPGQQFTWNSNLEVNPKPNRYANVIAVDHRSVILTSIDGVPGSDYINANYIDGYRKQNAVYIATQGGLPETMGDF
 WRMVWEQRTATVMMTRLEEKSRVKCDQYWPARGTETCGLIQVTLTDLTVELATYTVRTFALHKSSESSEKRELRFQ
 QFMAWPDHGVPEYPTPIAFLRRVKACNPLDAGPMVHVCSAGVGRGTGCFIVIDAMLERMKHEK**TVDIYGHVTCMR**
 SQRYNMVQTEDQYVFIHEALLEAATCGHTEVPARNLYAHIQKLGQVPPGESVTAMELEFKLLASSKAHTSRFISA
 NLPCKNFKNRLVNIMPYELTRVCLQPIRGVEGSDYINASFIDGYRQKAYIATQGGLAESTEDFWRMLWEHNSTI
 IVMLTKLREMGREKCHQYWPASARYQYFVVDPMAYNMPQYILREFKVTDARDGQSRITRQFQFTDWPEQGV
 KTGEFIDFIGQVHKTEQFGQDGPITVHCSAGVGRGTGFTILSIVLERMRYEGVDMFQTVKTLRTQRPAMVQT
 EDQYQLCYRAALEYLGSFDHYAT

Mass Match Peptides (bold):

AAGTEGPFQEV DGVATTR [50]
 ADEARNTIDFGK [58]
 AHTDVGPGPESSPVLVR [72]
 DDQHFVTGLHK [111]
 DFLPVDPATSNGR [117]
 ELPGELLGYR [206]
 EPMDQKR [218]
 FDLSMPHVQDPSLVR [246]
 FEVIEFDDGAGSVLR [249]

GSSAGGLQHLVSIR [321]
 NVLELSNVVR [558]
 QHGQIR [578]
 RPPNAWHK [609]
 SDMGVGVFTPTIEAR [621]
 TDEDVPSGPPR [682]
 TQQGVPAQPADFQAEVESDTR [725]
 TVDIYGHVTCMR [735]
 VLAVNSIGR [774]
 VSWVPPPADSR [799]
 VYYTPDSR [823]
 WTEYR [836]
 YSIGGLSEFFSEYAFR [872]

Tandem Peptides (underline):

AAGTEGPFQEV DGVATTR [50]
 TDEDVPSGPPR [682]
 VYYTPDSR [823]

Peptide Source: 1D-GE, Colorectal cancer

MAPEPAPGRTMVPLVPALVMLGLVAGAHGDSKPVFIKVPEDQTGLSGGVASFVCQATCEPKPRIITWMKKGKKVSS
 QRFEVIEFDDGAGSVLRIQPLRVQRDEAIYECTATNSLGEINTSAKLSVLEEEQLPPGFPSIDMGPQLKVVEKAR
 TATMLCAAGGNEDPEISWFKDFLPVDPATSNRIKQLRSGALQIESSEESDQKYECAVINSAGTRY**SAPANLYV**
RVRRAVAPRFSIFPSSQEVMPGGSVNLTCAVAGAMPYVKMMGAEEELTKEDEMPVGRNVLELSNVVRSANYTCVA
 ISSLGMIEATAQVTVKALPKPPIDLVTETTATSVTLTWDSGNSEPVYYGIQYRAAGTEGPFQEV DGVATTRY**S**
 IGGLSPFSEYAFRVLAVNSIGRPPSEAVRAR**TGEQAPSSPPR**RVQARMLSASTMLVQWEPPEEPNGLVRGYRVY
 YTPDSRRPPNAWHKHNTDAGLLTTVGSLPGLITYSLRVLAFTAVGDGPPSPTIQVKT**TQQGVPAQPADFQAEVESD**
TRIQLSWLLPPQERIIMYELVYWAAEDEDQHKVTFDPTSSYTLEDLKPDTLYRFQLAAR**SDMGVGVFTPTIEAR**
 TAQSTPSAPPQKVMCSVMGSTTVRVSWVPPPADSRNGVITQYSVAYEAVDGEDRGRHVVDGISREHSSWDLVGL
 KWTEYRVVWRAHTDVGPPESSPVLVR**TDEDVPSGPPR**KVEVEPLNSTAVHVYWKLPVPSKQHGQIRGYQVTYVR
 LENGEPRGLPIIQDVMLAEAQETTISGLTPETTYSVTAAAYTTKGDGARSKPKIVTTTGAVPGRPTMMISTTAMN
 TALLQWHPPKELPGELLGYRLQYCRADARPNTIDFGKDDQHFTVTGLHKGTTYIFRLAAKNRAGLGEEFEKEIR
 TPEDLPSGFPPQNLHVTGLTTSTTELAWDPPVLAERNRIISYTVVFRDINSQQELQNIITDTRFTLTGLKPD
 DTTYDIKVRWTSK**GSGPLSPSIQSR**TMPVEQVFANFRVAAAMKTSVLLSWEVPDSYKSAPVFPKILYNGQSVEVDGHS
 MRKLIADLQNPTEYSFVLMNRGSSAGGLQHLVSIRTPADLLPHKPLPASAYIEDGRFDLSMPHVQDPFLVRWFYI
 VVVPIDRVGSSMLTPRWSTPEELEDLELEAIEQGGEEQRRRRRQAERLKPYVAAQLDVLPEFTTLGDKKNYRGF
 YNRPLSPDLISYQCFVLASLKEPMDQKRYASSPYSDEIVVQVTPAQQQEPEPEMLWVTGPVLAVILILIVIAILLF
 KRKRTHSPSSKDEQSIGLKDSLAAHSSDPVEMRRINLYQTPGMRDHPPITDLDADNLERLKNANDGLKFSQYESI
 DPGQQTWENSNLEVNKPKNRYANVIAYDHSRVILTSIDGVPGSDYINANYIDGYRKQNAIATQGFLPETMGDF
 WRMVWEQRTATVMMTRLEEKSRVKCDQYWPARGTETCGLIQVTLTDTVELATYTVRTFALHKSSESSEKRELRFQ
 QFMAWPDHGVPEYPTPILAFRLRVKACNPLDAGPMVHCSAGVGRTGCFIVIDAMLERMKHEKTVDIYGHVTCMR
 SQRYNMVQTEDQYVFIHEALLEAATCGHTEVPARNLYAHIQKLGQVPPGESVTAMELEFKLLASSKAHTSRFISA
 NLPCNKFKNRLVNIIMPYELTRVCLQPIRGVEGSDYINASFIDGYRQKAYIATQGFLAESTEDFWRLWEHNSTI
 IVMLTKLREMGREKCHQYWPASARYQYFVVDPAEYNNMPQYILREFKVTDARDGQSRITIRQFQFTDWPEQGV
 KTGEFGIDFIGVHKTKEQFGQDGPITVHCSAGVGRTGVFTLSIVLERMRMYEGVVDMEQTVKTLRTQRPAMVQT
 EDQYQLCYRAALEYLGSEFDHYAT

Mass Match Peptides (bold):

GSGPLSPSIQSR [315]
 MAPEPAPGR [509]
 SDMGVGVFTPTIEAR [621]
 TDEDVPSGPPR [682]
 TGEQAPSSPPR [694]
 TQQGVPAQPADFQAEVESDTR [725]

Tandem Peptides (underline):

TDEDVPSGPPR [682]
 TGEQAPSSPPR [694]
 YSAPANLYVR [870]

Peptide Source: 1D-GE, Hepatocellular carcinoma

MAPEPAPGRMTMVLPLVPALVMLGLVAGAHGDSKPVFIKVPEDQTGLSGGVASFVCQATGEPKPRITWMKKGKKVSS
QRFEVIEFDDGAGSVLRITQPLRVQRDEAIYECTATNSLGEINTSAKLSVLEEEQLPPGFPSIDMGPQLKVVEKAR
TATMLCAAGGNPDPEISWFKDFLPVDPATSNRIKQLRSGALQIESSEESDQKYEVCATNSAGTRY**YSAPANLYV**
RVRRVAPRFSIPPSSQEVMPGGSVNLTCVAVGAMPFYVKWMMGAELTKEDEMPVGRNVLELSNVVRSANYTCVA
ISSLGMIETAQVTVKALPKPPIDLVTETTATSVTLTWDSCGNSEPVYYGIQYRAAGTEGPFQEVGDGVATTRY
IGGLSPFSEYAFRLAVNSIGRGPPSEAVRARTGEQAPSSPPRRVQARMLSASTMLVQWEPPEEPNGLVRGYRVY
YTPDSRRPPNAWHKHNTDAGLLTTVGSLLPGITYSLRVLAFTAVGDGPPSPPTIQVKTOQGVPAQPADFQAEVESD
TRIQLSWLLPPQERIIMYELVYWAAEDEDQCHKVTFDPTSSYTLEDLKPDTLYRFQLAARSDMGVGVFTPTIEAR
TAQSTPSAPPQKVMCVMGSGSTTVRVSWVPPADSRNGVITQYSVAYEAVDGEDRGRHVVDGISREHSSWDLVGLE
KWTEYRVVWRAHTDVGPGESSPVLVRTDEDVPSGPPRKVEVEPLNSTAVHVYWKLPVPSKQHGQIRGYQVTYVR
LENGEPRGLPIIQDVMLAEAQETTISGLTPETTYSVTVAAAYTTKGDGARSKPKIVTTTGAVPGRPTMMISTTAMN
TALLQWHPPKELPGELLGYRLQYCRADARPNTIDFGKDDQHFTVTGLHKGTTYIFRLAAKNRAGLGEEFEKEIR
TPEDLPSGFPQNLHVTVGLTTSTTELAWDPVLAERNRIISYTVVFRDINSQOELQNTTDTTRFTLTGLKPDTTY
DIKVRATWSKSGPLSPSIQSRIMPVEQVFAKNFRVAAAMKTSVLLSWEVPDSYKSAPVFKILYNGQSVEVDGHS
MRKLIADLQPNTEYSFVLMNRGSSAGGLQHLVSIPTAPDLLPHKPLPASAYIEDGRFDLSMPHVQDPSLVRWFYI
VVVPIDRVGGSMLTPRWSTPEELEDLELEAIEQGEEQRRRRRQAERLKPVAAQLDVLPEFTFLGDKKNYRGF
YNRLSPDLQSYQCFVLASLKEPMDQKRYASSPYSDIIVVQVTPAQQQEPEMLWVTGPVLAVILIILIVIAILLF
KRKRTHSPSSKDEQSIGLKDSLHSSDPVEMRRLNYQTPGMRDHPPITDLDADNIEERLKANDGLKFSQYESI
DPGQOFTWENSNLVKNPKNRYANVIAYDHSRVILTSIDGVPGSDYINANYIDGYRKQAYIATQGPLPETMGDF
WRMVWEQRTATVMMTRLEEKSRVKCDQYWPARGTETCGLIQVTLTDLVELATYTVRTFALHKSSESSEKRELRF
QFMAWPDHGVPEYPTPIILAFILRRVKACNPLDAGPMVHVCSAGVGRGCFIVIDAMLERMKHEKTVDIYGHVTCMR
SQRYNMVQTEDQYVFIHEALLEAATCGHTEVPARNLYAHIQKLGQVPPGESVTAMELEFKLLASSKAHSTRFISA
NLPCNKFKNRLVNIIMPYELTRVCLQPIRGVEGSDYINASFIDGYRQKAYIATQGPLAESTEDFWRMLWEHNSTI
IVMLTKLREMGREKCHQYWPASARYQYFVVDPAEYNMPQYILREFKVTDARDGQSRITIRQFQFTDWEQGV
KTGEGFIDFIGVHKTEQFGQDGPITVHCSAGVGRGTGVFITLSIVLERMRYEGVVDMFQTVKTLRTQRPAMVQT
EDQYQLCYRAALEYLGSEDFHYAT

Mass Match Peptides (bold):

YSAPANLYVR [870]

Tandem Peptides (underline):

YANVIAYDHSR [840]

Peptide Source: 1D-GE, Lung cancer

MAPEPAPGRMTMVLPLVPALVMLGLVAGAHGDSKPVFIKVPEDQTGLSGGVASFVCQATGEPKPRITWMKKGKKVSS
QR**FEVIEFDDGAGSVLR**ITQPLRVQRDEAIYECTATNSLGEINTSAKLSVLEEEQLPPGFPSIDMGPQLKVVEKAR
TATMLCAAGGNPDPEISWFKDFLPVDPATSNRIKQLRSGALQIESSEESDQKYEVCATNSAGTRY**YSAPANLYV**
RVRRVAPRFSIPPSSQEVMPGGSVNLTCVAVGAMPFYVKWMMGAELTKEDEMPVGRNVLELSNVVRSANYTCVA
ISSLGMIETAQVTVKALPKPPIDLVTETTATSVTLTWDSCGNSEPVYYGIQYRAAGTEGPFQEVGDGVATTRY
IGGLSPFSEYAFRLAVNSIGRGPPSEAVRARTGEQAPSSPPRRVQARMLSASTMLVQWEPPEEPNGLVRGYRVY
YTPDSRRPPNAWHKHNTDAGLLTTVGSLLPGITYSLRVLAFTAVGDGPPSPPTIQVKTOQGVPAQPADFQAEVESD
TRIQLSWLLPPQERIIMYELVYWAAEDEDQCHKVTFDPTSSYTLEDLKPDTLYRFQLAARSDMGVGVFTPTIEAR
TAQSTPSAPPQKVMCVMGSGSTTVRVSWVPPADSRNGVITQYSVAYEAVDGEDRGRHVVDGISREHSSWDLVGLE
KWTEYRVVWRAHTDVGPGESSPVLVRTDEDVPSGPPRKVEVEPLNSTAVHVYWKLPVPSKQHGQIRGYQVTYVR
LENGEPRGLPIIQDVMLAEAQETTISGLTPETTYSVTVAAAYTTKGDGARSKPKIVTTTGAVPGRPTMMISTTAMN
TALLQWHPPKELPGELLGYRLQYCRADARPNTIDFGKDDQHFTVTGLHKGTTYIFRLAAKNRAGLGEEFEKEIR
TPEDLPSGFPQNLHVTVGLTTSTTELAWDPVLAERNRIISYTVVFRDINSQOELQNTTDTTRFTLTGLKPDTTY
DIKVRATWSKSGPLSPSIQSRIMPVEQVFAKNFRVAAAMKTSVLLSWEVPDSYKSAPVFKILYNGQSVEVDGHS
MRKLIADLQPNTEYSFVLMNRGSSAGGLQHLVSIPTAPDLLPHKPLPASAYIEDGRFDLSMPHVQDPSLVRWFYI
VVVPIDRVGGSMLTPRWSTPEELEDLELEAIEQGEEQRRRRRQAERLKPVAAQLDVLPEFTFLGDKKNYRGF
YNRLSPDLQSYQCFVLASLKEPMDQKRYASSPYSDIIVVQVTPAQQQEPEMLWVTGPVLAVILIILIVIAILLF
KRKRTHSPSSKDEQSIGLKDSLHSSDPVEMRRLNYQTPGMRDHPPITDLDADNIEERLKANDGLKFSQYESI
DPGQOFTWENSNLVKNPKNRYANVIAYDHSRVILTSIDGVPGSDYINANYIDGYRKQAYIATQGPLPETMGDF
WRMVWEQRTATVMMTRLEEKSRVKCDQYWPARGTETCGLIQVTLTDLVELATYTVRTFALHKSSESSEKRELRF

QFMAWPDHGVPEYPTPILAFLLRRVKACNPLDAGPMVVHCSAGVGRITGCFIVIDAMLERMKHEK**TVDIYGHVTCMR**
 SQRRYMQVTEQYVFIHEALLEAATCGHTEVPARNLYAHIOK**LGQVPPGESVTAMELEFK**LLASSKAHTSRFISA
 NLPCNKFKNRLVNIMPYELTRVCLQPIR**GVEGSDYINASF**LDGYR**QOKAYIATQGPLAESTEDFWRMLWEHNSTI**
IVMLTKILREMGREKCHQYWPASARYQYFVVDPMAYNMPQYILREFKVTDARDGOSRTIR**QFQFTDWPEQGV**
KTGEGFIDFIGQVHKTKEQFGQDGPITVHCSAGVGRITGVFTLSIVLERMR**YEGVVDMFQTVKTLR****TQRPAMVOT**
EDQYQLCYRAALLEYLGSFDHYAT

Mass Match Peptides (bold):

AAGTEGFFQEVGDVATTR [50]
 ADEARPNITDFCK [58]
 AHTDVGPGPESSPVLVR [72]
 AYIATQGPLAESTEDFWR [98]
 DDQHTVTGLHK [111]
 DHPPIPTDLADNIER [127]
 DINSQQELQNITTDTR [129]
 DSLAHSSDPVEMR [156]
 DSLAHSSDPVEMRR [157]
 EHSSWDLVGLK [196]
 FEVIEFDDGAGSVLR [249]
 GFPSEAVR [308]
 GTTYIFR [324]
 GVEGSDYINASF

Tandem Peptides (underline):

SGPLSPSIQSR [315]
 QFQFTDWPEQGVK [572]
 YANVIAYDHSR [840]
 YEGVVDMFQTVK [844]

Peptide Source: 1D-GE, Osteosarcoma

MAPEPAPGRMTMVPLPALVMLGLVAGAHGDSKPVFIK**VPEDQTGLSGGVASFVCQATGEPKPR**ITWMKKGKKVSS
 QR**FEVIEFDDGAGSVLR**IQPLRVQRDEAIYECTATNSLGEINTSAKLSVLEEEQLPPGFPSIDMGFQLKVVVKAR
 TATMLCAAGGNPDPEISWFKDPLVPDPATSNRIKQLRSGALQIESSESDQGYECVATNSAGTRYSAANLYV
 RVRRAVPRFSIPSSQEVMPGGSVNLTCVAVGAPMPYVKMMGAELTKEDEMPVGRNVLELSNVVRSANYTCVA
 ISSLGMIEATAQVTVKALPKPPIDLVVTETTATSVTLTWDSGNSEPVYTYGIQYR**AAGTEGFFQEVGDVATTRY**
IGGLSPFSEYAFRVLAVNSICRGPPSEAVRARTGEQAPSSPERRVQAR**MLSASTMLVQWEPPEEPNGLVR**GYRVY
 YTPDSR**RPPNAWHK**HNTDAGLLTTVGSLPGITYSLRV**LAETAVGDGPPSEPIQVK****TQQGVFAQPADFQAEVESD**

TRIQLSWLLPPQERIIMYELVYWAAEDEDQQHKVTFDPTSSYTLEDLKPD~~TL~~YRFQLAARSSDMGVGVFTPTIEAR
 TAQSTPSAPPQKVMCVSMGSTTVRVSWVPPADSRNGVITQYSVAYEAVDGEDRGRHVVDGISREHSSWDLVGLE
 KWTEYRVWVRAHTDVGPGPESSPVLVRTDDEDVPSGPPRKVEVEPLNSTAVHVYWKLPVPSKQHGQIRGYQV~~TY~~VR
 LENGEPRLPIIQDVMLAEAQETTISGLTPETTYSVTVAAAYTTKGDGARSKPKIVTTTGAVPGRPTMMISTAMN
 TALLQWHPPKELPGELLGYRLQYCRADearPNTIDFGKDDQHFTVTGLHKGT~~TY~~IFRLAAKNRAGLGEEFEKEIR
 TPEDLPSGFPQNLHVTGLTTSTTELAWDPPVLAERNRIISYTVVFRDINSQELQNTTDT~~TR~~F~~TL~~TGLKPD~~TT~~Y
 DIKVRATWSKSGSPLSPSIQSRTMPVEQVFAKNFRVAAAMKTSVLLSWEVPDSYKSAVPFKILYNGQSVEVDGHS
 MRKLIADLQPNTEYSFVLMNRGSSAGGLOHLVSI~~RT~~APDLLPHKPLPASAYIEDGRFDLSMPHVQDPSLVRWFI
 VVVPI~~DR~~VGGSM~~TP~~RWSTPEELEDLELEAIEQGGEQRRRRRQAERLKPYVAAQLDVL~~PET~~TLGDKKNYRGF
 YNRPLSPDLSYQCFLASLKEPMDQKRYASSPYSD~~IV~~VQVTPAQQQEPEMLWVTGPFVLAVILILIVIAILLF
 KRKRTHSPSSKDEQSIGLKDSLLAHSSDPVEMRRLNYQTPGMRDHPPI~~PT~~DLADNIERL~~KAN~~DGLKFSQEYESI
 DPGQQTWENSLEVNKPKNRYANVIAYDHSRVILTSIDGVPGSDYINANYIDGYRKQ~~NAY~~IATQGGLPETMGDF
 WRMVWEQRTATVMMTRLEEKSRVKCDQYWPARGTETCGLIQVTL~~LD~~TVELATYTVRTFALHKS~~GS~~SEKRELQF
 QFMAWPDHGVPEYPTPILAF~~LR~~VKACNPLDAGPMVVHCSAGVGRTGCFIVIDAMLERMKHEKTVDIYGHVTCMR
 SQ~~RNY~~VMVQTEDQYVFIHEALLEAATCGHTEVPARNLYAHIQKLGQVPPGESVTAMELEFKLLASSKAHTSRFISA
 NLPCNKFKNRLVNIMPYELTRVCLQPIRGVEGSDYINASFLDGYRQQKAYIATQGPLAESTEDFWRMLWEHNSTI
 IVMLTKLREMGREKCHQYWPAERSARYQYFVVDPMAEYNMPQYILREFKVTDARDGQSRTIRQFQFTDWPEQGV
 KTGE~~GF~~IDFIGVHKTEQFGQDGPITVHCSAGVGRTGVFITLSIVLERMRYEGVVDMFQTVKTLRTQRPAMVQT
 EDQYQLCYRAALEYLGSFDHYAT

Mass Match Peptides (bold):

AAGTEGPFQEV~~D~~GVAT~~TR~~ [50]
 AHTDVGPGPESSPVLVR [72]
 AYIATQGPLAESTEDFWR [98]
 DDQHFTVTGLHK [111]
 ELPGELLGYR [206]
 FDLSMPHVQDPSLVR [246]
 FEVIEFDDGAGSVLR [249]
 FTLTGLKPD~~TT~~YDIK [275]
 GYQV~~TY~~VR [331]
 ILYNGQSVEVDGHS~~MR~~ [378]
 LIADLQPNTEYSFVLMNR [467]
 MLSASTMLVQWEPPEEPNGLVR [518]
 NGVITQYSVAYEAVDGEDR [537]
 QHGQIR [578]
 RPPNAWHK [609]
 RRQAER [614]
 RTHSPSSK [616]
 SDMGVGVFTPTIEAR [621]
 TQQGVPAQPADFQAEVESD~~TR~~ [725]
 VPEDQTGLSGGVASFVCQATGEPKPR [789]
 VTFDPTSSYTLEDLKPD~~TL~~YR [803]
 YEGVVDMFQTVK [844]
 YQYFVVDPMAEYNMPQYILR [869]
 YSIGGLSPFSEYAFR [872]

Tandem Peptides (underline):

TQLSWLLPPQER [388]
 NGVITQYSVAYEAVDGEDR [537]
 VLAFTAVGDGPPSPTIQVK [770]

Peptide Source: 1D-GE, Pancreatic cancer

MAPEPAPGR~~TM~~VLVLPALVMLGLVAGAHGDSKPVFIKVPEDQTGLSGGVASFVCQATGEPKPRITWMKKGKKVSS
 QRFEVIEFDDGAGSVLRIQPLRVQRDEAIYECTATNSLGEINTSAKLSVLEEEQLPPGFPSIDMG~~POL~~KVV~~EAR~~
TATMLCAAGGNPDPEISWFKDFLPVDPATSNGR~~IK~~QLRSGALQIESSEESDQGYECVATNSAGTRYSAPANLYV
RVR~~RV~~APRFSI~~PP~~SSQEVMPGGSVNLTCVAVGAMPYVKWMMGAELTKEDEM~~PV~~GRNVLELSNVVRSANYTCVA
 ISSLGMI~~EAT~~QVTVKALPKPPIDLVVTETTATSVTLTWDGNS~~EP~~VTYGIQYRAAGTEGPFQEV~~D~~GVAT~~TR~~YS
IGGLSPFSEYAFRVLAVNSIGRGPPSEAVRARTGEQAPSSP~~RR~~VQARMLSASTMLVQWEPPEEPNGLVRGYRVY
 YTPDSRRPPNAWHKHNTDAGLLTTVGSLLPGITYSLRVLAFTAVGDGPPSPTIQVKTQQGVPAQPADFQAEVESD

TRIQLSWLLPQER**IIMYELVYWAAEDEDQQHK**VTFDPTSSYTLEDLKPDITLYR**FQLAARSDMGVGVFTPTIEAR**
TAQSTPSAPPQKVMCVSMGSTTVR**VSWVPPPADSR**NGVITQYSVAYEAVDGEDRGR**HVVDGISREHSSWDLVGLE**
KWTEYRVVRAHTDVGGPRESSPVLVR**TDEDVPSGPPRKVEVEPLNSTAVHVIWK**LPVPSKQHGQIRGYQVTYVR
 LENGEPRLPIIQDVMLAEAQETTISGLTPETTYSVTVAAYTTKGDGARSKP KIVTTTGAVPGRPTMMISTTAMN
 TALLQWHPPK**ELPGELLGYR**LQYCRADAEARNTIDFGK**DDQHFTVTGLHKGTTYIFR**LAAKNRAGLGEEFEKEIR
 T2EDLPSCGFQNLHVITGLTISTTELAWDPPVLAERNRIISYTVVFRDINS**QQELQNITTDTR**FTLTGLKPDTTY
 DIKVRATWSK**GSGPLSPSIQSR**TMPEQV**FAK**NFRVAAAMK**TSVLLSWEVPDSYK**SAVPFKILYNGQSVEVDGHS
 MRKLIADLQNTHEYSFVLMNRGSSAGGLQHLVSI RTAPDLLPHKPLPASAYIEDGR**FDLSMPHVQDPSLVR**WFYI
 VVVPIDR**VGGSMLTPR**WSTPEELEDLELEAIEQGGEQRRRRRQAERLKPVAAQLDVL PETFTLGDKKNYRGF
 YNRPLSPDLSYQCFVLASLKEPMDQKRYASSPYSDEIVVQVTPAQQQEPEMLWVTGPVLAVILIILIVIAILLF
 KRKR**RTHSPSSK**DEQSIGLK**DSLLAHSSDPVEMRLNYQTPGMRDHPP**IPITDLADNIERLKANDGLKFSQEYESI
 D2GQQTWENSNLVNPKPNR**YANVIAYDHSR**VILTSIDGVPGSYINANYIDCYRKQNYIATQGPLPETMGDF
 WR**MVWEQRTATVMMTR**LEEKSRVKCDQYWPARGTETCGLIQVTLLDTVELATYTVRTFALHKS GSSEKRELR**QF**
QFMAWPDHGVPEYPTPILAFLRVKACNPLDAGPMVVHCSAGVGR**TGCFIVIDAMLER**MKHEKTVDIYGHVTCMR
 SQRNVMQTEDQYVFIHEALLEAATCGHTEVPARNLYAHIQ**KLQVPPGESVTAMELEFK**LLASSKAHSTRFISA
 NLPCKFKNRLVNI MPYELTRVCLQPIR**GVEGSDYINASF**LDGYRQ**KAYIATQGPLAESTEDFWRMLWEHNSTI**
IVMLTKIREMGREKCHQYWPASARSARY**QYFVVDPMAYNMPQYILR**EFKVTDARDGQSRTIRQFQFTDWPEQGV
 KTGEGLDFIGQVHKTK**EQFGQDGPITVHCSAGVGR**TGVFITLSIVLERMR**YEGVVDMFQTVK**TLR**TQRPAMVQT**
EDQYQLCYRAALEYLGSFDHYAT

Mass Match Peptides (bold):

AAGTECPFQEV DGVATTR [50]
 AYIATQGPLAESTEDFWR [98]
 DDQHFTVTGLHK [111]
 DEAIYECTATNSLGEINTSAK [112]
 DFLVPDPATSNR [117]
 DHPPIPITDLADNIER [127]
 DINSQQELQNITTDTR [129]
 DSLAHSSDPVEMR [156]
 DSLAHSSDPVEMR [157]
 EHSSWDLVGLEK [196]
 ELPGELLGYR [206]
 EQFGQDGPITVHCSAGVGR [220]
 FDLSMPHVQDPSLVR [246]
 FEVIEFDDGAGSVLR [249]
 FQLAAR [267]
 GPPSEAVR [308]
 GSGPLSPSIQSR [315]
 GTTYIFR [324]
 GVEGSDYINASF LDGYR [326]
 HNTDAGLLTTVGSLLPGITYSLR [341]
 HVVDGISR [347]
 IIMYELVYWAAEDEDQQHK [372]
 LGQVPPGESVTAMELEFK [462]
 LNYQTPGMR [475]
 MLWEHNSTIIVMLTK [519]
 MVWEQR [529]
 QFQMAWPDHGVPEYPTPILAF LR [571]
 RLNYQTPGMR [606]
 RPPNAWHK [609]
 RTHSPSSK [616]
 SDMGVGVFTPTIEAR [621]
 TAQSTPSAPPQK [672]
 TATMLCAAGGNPD EISWFK [674]
 TATVMMTR [676]
 TDEDVPSGPPRK [683]
 TGCFIVIDAMLER [692]
 TMPVEQVFAK [708]
 TQQGVPAQPADFQAEVESDTR [725]
 TQRPAMVQTEDQYQLCYR [726]
 TSVLLSWEVPDSYK [732]

VEVEPLNSTAVHVYWK [756]
VGGSM LTPR [764]
VSWVPPPADSR [799]
WMMGAEELTK [830]
YANVIAYDHSR [840]
YEGVDMFQTVK [844]
YQYFVVDPM AEYNMPQYILR [869]
YSAPANLYVR [870]
YSIGGLSPFSEYAFR [872]

Tandem Peptides (underline):

AAGTEGPFQ EVDGVATTR [50]
NGVITQYSVAYEAVDGEDR [537]
YANVIAYDHSR [840]
YEGVDMFQTVK [844]
YSAPANLYVR [870]

Peptide Source: 1D-GE, Renal cell cancer

MAPEPAPGRMTMVPLVPALVMLGLVAGAHGDSKPVFIKVPEDQTGLSGGVASFVCQATGEPKPRITWMKKGKKVSS
QR**FEVIEFDDGAGSVLR**IQPLRVQRDEAIYECTATNSLGEINTSAKLSVLEEEQLPPGFPSIDMGPQLKVVEKAR
TATMLCAAGGNPDPEISWFKDFLPVDPATSNRIKQLRSGALQIESSEESDQGYECVATNSAGTRY SAPANLYV
RVRRVAPRF SIPPSSQEVMPGGSVNLTCVAVGAPMPYVKWMMGAEELTKEDEMPVGRNVLELSNVVRSANYTCVA
ISSLGMI EATAQVTVKALPKPPIDLVTETTTATSVTLTWD SGNSEPVTY YGIQYR**AAGTEGPFQ EVDGVATTR**YS
IGGLSPFSEYAFRVLAVNSIGRGPPSEAVRAR**TGEQAPSSPPR**RVQARMLSA STM LVQWEPPEEPNGLVRGYRVY
YTPDSRRPPNAWHKHNTDAGLLTTVGSLPGITYSLRVLAFTAVGDGPPSP TIQVK TQOGVPAQPADFOAEVESD
TRIQLSWLLPQERIMYELVYWAAEDEDQHKVTFDPTSSY TLEDLKPDTLYR**FQLAARSDMGVGVFTPTIEAR**
TAQSTPSAPPQKVMCVSMGSTTVRVSWVPPPADSRNGVITQYSVAYEAVDGEDRGRHVVDGISR**EHSSWDLVGLE**
KWTEYRVVRAHTDVGPGPESSPVLVRTDEDVPSGPPRKVEVEPLNSTAVHVYWKLPVPSKQHGQIRGYQVTTYVR
LENGEPRGLPIIQDVMLAEAEQETTISGLTPETTYSVTVAA YTTKGDGARSKPKIVTTTGAVPGRPTMMISTTAMN
TALLQWHPPKELPGELLGYRLQYCRADARPNTIDFGKDDQHFTVTGLHKGTTYIFRLA AKNRAGLGEEFEKEIR
TPEDLPSGFQNLHVTGLTTSTTELAWDPPVLAERNRIISYTVVFRDINSQQELQNTTDTTRFTTLGLKPDTTY
DIKVRAWTSKSGSPLSPSIQSRTMPVEQVFAKNFRVAAAMKTSVLLSWEVPDSYKSAVPFKILYNGQSVEVDGHS
MRKLIADLQNT EYSFVLMNRGSSAGGLQLHVSIRTAPDLLPHKPLPASAYIEDGRFDLSMPHVQDPSLVRWFYI
VVVPI DRVGGSM LTPRWSTPEELELDELLEAIEQGGEQRRRRRQAERLKPVYAAQLDVLPEFTTLGDKKNYRGF
YNRPLSPDLSYQCFVLASLKEPMDQKRYASSPYSDEIVVQVTPAQQQEPEMLWVTGPVLAVILIIILIVIAILLF
KRKRTHSPSSKDEQSIGLKDSLHSSDPVEMRRLNYQTPGMRDHPPIPITDLADNIERL KANDGLKFSQ EYESI
DPGQQFTWENS NLEV NPKPNRYANVIAYDHSRVILTSIDGVPGSDYINANYIDGYRKQNA YIATQG PLPETMGDF
WRMVWEQRTATVMMTRLEEKSRVKCDQYWPARGTETCGLIQVTLLDTVELATYTVRTFALHKSGSSEKREL RQF
QFMAWPDHGVPEYPTPILAF LRVRKACNPLDAGPMVVECSAGVGRTGCFIVIDAMLERMKHEKTVDIYGHVTCMR
SQ RNYMVQTEDQYVFIHEALLEAATCGHTEVPARNLYAHIQKLGQVPPGESVTAMELEFKLLASSKAH TS RFISA
NLPCNFKPNRLVNIMPYELTRVCLQPIRGVEGSDYINASF LDGYRQQKAYIATQG PLAESTEDFWRMLWEHNSTI
IVMLTKLREMGREKCHQYWP AERSARYQYFVVDPM AEYNMPQYILREFKVT DARDGQSRTIRQFQFTDWPEQGV P
KTGEGFIDFIGVHKTEQFGQDGPITVHCSAGVGRTGVFITLSIVLERMRYEGVDMFQTVKTLRTQR PAMVQT
EDQYQLCYRAALEYLG SFDHYAT

Mass Match Peptides (bold):

AAGTEGPFQ EVDGVATTR [50]
EHSSWDLVGLEK [196]
FEVIEFDDGAGSVLR [249]
FQLAAR [267]
SDMGVGVFTPTIEAR [621]
TGEQAPSSPPR [694]

Tandem Peptides (underline):

TGEQAPSSPPR [694]

Peptide Source: iTRAQ, Colorectal cancer

MAPEPAPGRMTMVPLVPALVMLGLVAGAHGDSKPVFIKVPEDQDTGLSGGVASFVCQATGEPKPRITWMKKGKKVSS
QRFEVIEFDDGAGSVLRIQPLRVQRDEAIYECTATNSLGEINTSAKLSVLEEEQLPPGFPSIDMGPQLKVVEKAR
TATMLCAAGGNPDPEISWFKDFLPVDPATSNGR**IKQLR**SGALQIESSESDQGGKYECVATNSAGTRYSA PANLYV
RVRRVAPRFSIFPSSQEVMPGGSVNLTCVAVGAPMPYVKMMGAEELTKEDEMPVGRNVLELSNVVRSANYTCVA
ISSLMIEATAQVTVKALPKPIDLVVTETTATSVTLTWDSGNSEPVYYGIQYRAAGTEGPFQEVGDGVATTRY
IGGLSPFFSEYAFRVLAVNSIGRGPPSEAVRARTGEQAPSSPPRRVQARMLASASTMLVQWEPPEEPNGLVRGYRVY
YTPDSRRPPNAWHKHTDAGLLTTVGSLLPGITYSRLVLAFTAVGDGPPSPITQVKTQQGVPAQPADFQAEVESD
TRIQLSWLLPPQERIIMYELVYWAAEDEDQQHKVTFDPTSSYTLEDLKPDTLYRFQLAARSDMGVGVFTPTTEAR
TAQSTPSAPPQKVMCVSMGSTTVRVSWVPPPADSRNGVITQYSVAYEAVDGEDRGRHVVDGISREHSSWDLVGL
KWTEYRVVWRAHTDVGPGPESSPVLVRTDEDVPSGPPRKVEVEPLNSTAVHVYWKLPVPSKQHGQIRGYQVTVVR
LENGEPRGLPIIQDVMLAEAEQETTISGLTPETTSVTVAAYTTKGDGARSKPKIVTTTGAVPGRPTMMISTAMN
TALLQWHPPKELPGEELLGYRLQYCRADEARPNTIDFGKDDQHFTVTGLHKGTTYIFRLAAKNRAGLGEFEKEIR
TPEDLPFGFPQNLHVLTGLTTSTELAWDPVLAERNGLIISYTVVFRDINSQQELQNITTDTRFTLTGLKPDTTY
DIKVRAWTSKSGSPLSPSISQSRIMPVEQVFAKNFRVAAAMKTSVLLSWEVPDSYKSAVPFKILYNGQSVEDGHS
MRKLIADLQNPTEYSFVLMNRGSSAGGLQHLVSIRTAPDLLPHKPLPASAYIEDGRFDLSMPHVQDPSLVRWFI
VVVPIDRVGGSMLTPRWSTPEELELDELLEAIEQGCGEEQRRRRRQAERLKPYYAAQLDVLPEFTFLGDKKNYRGF
YNRPLSPDLSYQCFVLASLKEPMDQKRYASSPYSDEIVVQVTPAQQQEPEMLWVTGPVLAVILIILIVIAILLF
KRRKTHSPSSKDEQSTGLKDSLLAHSSDPVEMRRLNYQTPGMRDHPPIITDLADNIERLKANDGLKFSQEYESI
DPGQQTWENSNLEVNKPKNRYANVIAYDHSRVILTSIDGVPGSYINANYIDGYRKQNAVYIATQGFPLPETMGDF
WRMVWEQR**TATVVMTRLEEKSRVKCDQYWPAP**RGTTETCGLIQVTLTLDVELATYTVRTFALHKSSESSEKRELRF
QFMAWPDHGVPEYPTPIALFLRRVKACNPLDAGPMVHVCSAGVGRGTGCFIVIDAMLERMKHEKTVDIYGHVTCMR
SQRYNMVQTEDQYVFIHEALLEAATCGHTEVPARNLYAHIQKLGQVPPGESVTAMELEFKLLASSKAHTSRFISA
NLPCNKFKNRLVNMIMPYELTRVCLQPIRGVEGSDYINASFIDGYRQQKAYIATQCPLESTEDFWRLMWEHNSTI
IVMLTKLREMGREKCHQYWPASARYQYFVVDPMAYNMPQYILREFKVTDARDGQSRITRQFQFTDWPQGV
KTGEGFIDFIGVHKTEQFGQDGPI TVHCSAGVGRGTGVFITLSIVLERMRYEGVDMFQTVKTLRTQRPAMVQT
EDQYQLCYRAALEYLGSEFDHYAT

Mass Match Peptides (bold):

IKQLR [922]
TAQSTPSAPPQK [672]
TATVVMTRLEEK [979]
VKCDQYWPAP [991]

Tandem Peptides (underline):

IKQLR [922]
TAQSTPSAPPQK [672]
TATVVMTRLEEK [979]
VKCDQYWPAP [991]

Peptide Source: iTRAQ, Hepatocellular cancer

MAPEPAPGRMTMVPLVPALVMLGLVAGAHGDSKPVFIKVPEDQDTGLSGGVASFVCQATGEPKPRITWMKKGKKVSS
QRFEVIEFDDGAGSVLRIQPLRVQRDEAIYECTATNSLGEINTSAKLSVLEEEQLPPGFPSIDMGPQLKVVEKAR
TATMLCAAGGNPDPEISWFKDFLPVDPATSNGR**IKQLR**SGALQIESSESDQGGKYECVATNSAGTRYSA PANLYV
RVRRVAPRFSIFPSSQEVMPGGSVNLTCVAVGAPMPYVKMMGAEELTKEDEMPVGRNVLELSNVVRSANYTCVA
ISSLMIEATAQVTVKALPKPIDLVVTETTATSVTLTWDSGNSEPVYYGIQYRAAGTEGPFQEVGDGVATTRY
IGGLSPFFSEYAFRVLAVNSIGRGPPSEAVRARTGEQAPSSPPRRVQARMLASASTMLVQWEPPEEPNGLVRGYRVY
YTPDSRRPPNAWHKHTDAGLLTTVGSLLPGITYSRLVLAFTAVGDGPPSPITQVKTQQGVPAQPADFQAEVESD
TRIQLSWLLPPQERIIMYELVYWAAEDEDQQHKVTFDPTSSYTLEDLKPDTLYRFQLAARSDMGVGVFTPTTEAR
TAQSTPSAPPQKVMCVMGSTTVRVSWVPPPADSRNGVITQYSVAYEAVDGEDRGRHVVDGISREHSSWDLVGL
KWTEYRVVWRAHTDVGPGPESSPVLVRTDEDVPSGPPRKVEVEPLNSTAVHVYWKLPVPSKQHGQIRGYQVTVVR
LENGEPRGLPIIQDVMLAEAEQETTISGLTPETTSVTVAAYTTKGDGARSKPKIVTTTGAVPGRPTMMISTAMN
TALLQWHPPKELPGEELLGYRLQYCRADEARPNTIDFGKDDQHFTVTGLHKGTTYIFRLAAKNRAGLGEFEKEIR
TPEDLPFGFPQNLHVLTGLTTSTELAWDPVLAERNGLIISYTVVFRDINSQQELQNITTDTRFTLTGLKPDTTY
DIKVRAWTSKSGSPLSPSISQSRIMPVEQVFAKNFRVAAAMKTSVLLSWEVPDSYKSAVPFKILYNGQSVEDGHS
MRKLIADLQNPTEYSFVLMNRGSSAGGLQHLVSIRTAPDLLPHKPLPASAYIEDGRFDLSMPHVQDPSLVRWFI
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KTGEGFIDFIGQVHKTKEQFGQDGPITVHCSAGVGRGTGVFITLSIVLERMRYEGVDMFQTVKTLRTQRPAMVQT
EDQYQLCYRAALEYLGSDHYAT

Mass Match Peptides (bold):

IKQLR [922]

Tandem Peptides (underline):

IKQLR [922]

Peptide Source: iTRAQ, Non-small cell lung cancer

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IVMLTKLREMGREKCHQYWPASARYQYFVVDPMAYNMPQYILREFKVTDAEDGQSRTIRQFQFTDWPEQGV
KTGEGFIDFIGQVHKTKEQFGQDGPITVHCSAGVGRGTGVFITLSIVLERMRYEGVDMFQTVKTLRTQRPAMVQT
EDQYQLCYRAALEYLGSDHYAT

Mass Match Peptides (bold):

DSLLAHSSDPVEMR [156]

NRAGLGEEFEKEIR [960]

TAQSTPSAPPQK [672]

TMPVEQVFAK [708]

Tandem Peptides (underline):

DSLLAHSSDPVEMR [156]

NRAGLGEEFEKEIR [960]

TAQSTPSAPPQK [672]

TMPVEQVFAK [708]

Peptide Source: iTRAQ, Renal cell cancer

MAPEPAPGRMTMPLVLPALVMLGLVAGAHGDSKPVFIKVPEDQTLGSGGVASFVCQATGEPKPRITWMKKGKKVSS
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 EDQYQLCYRAALEYLGSEFDHYAT

Mass Match Peptides (bold):

EPMDQKR [218]
 TAQSTPSAPPQK [672]

Tandem Peptides (underline):

EPMDQKR [218]
 TAQSTPSAPPQK [672]

Figure 2

Box Plot data for OGTA066

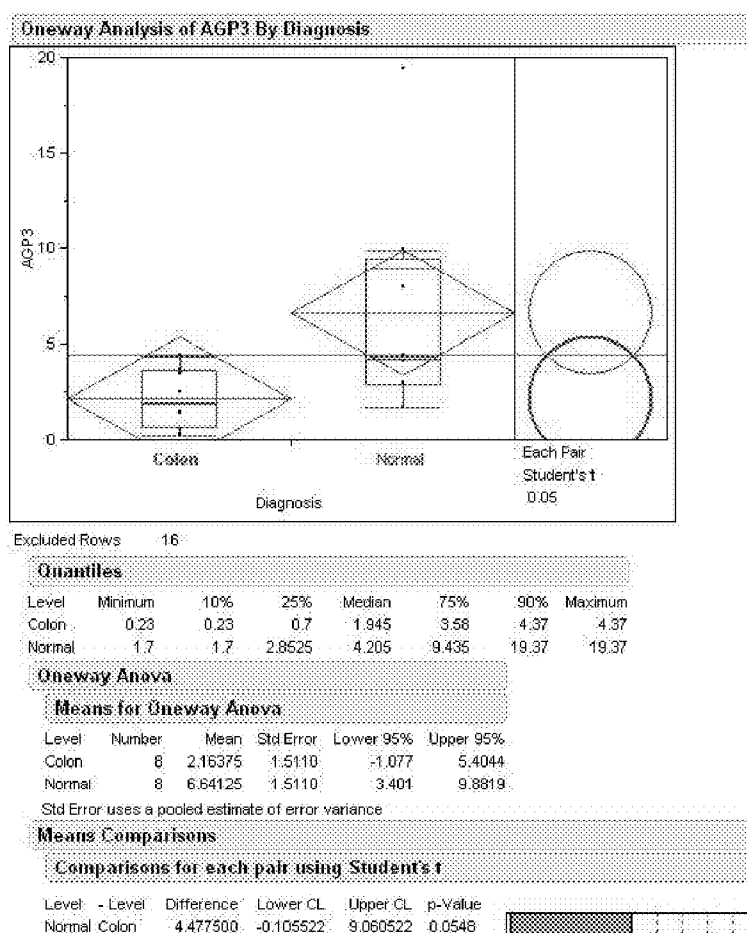
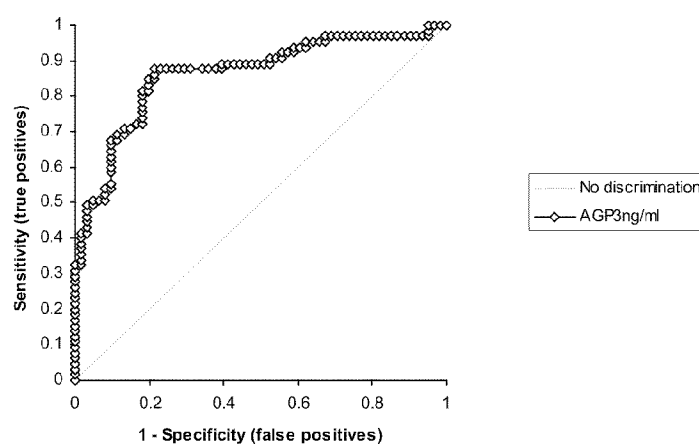


Figure 3

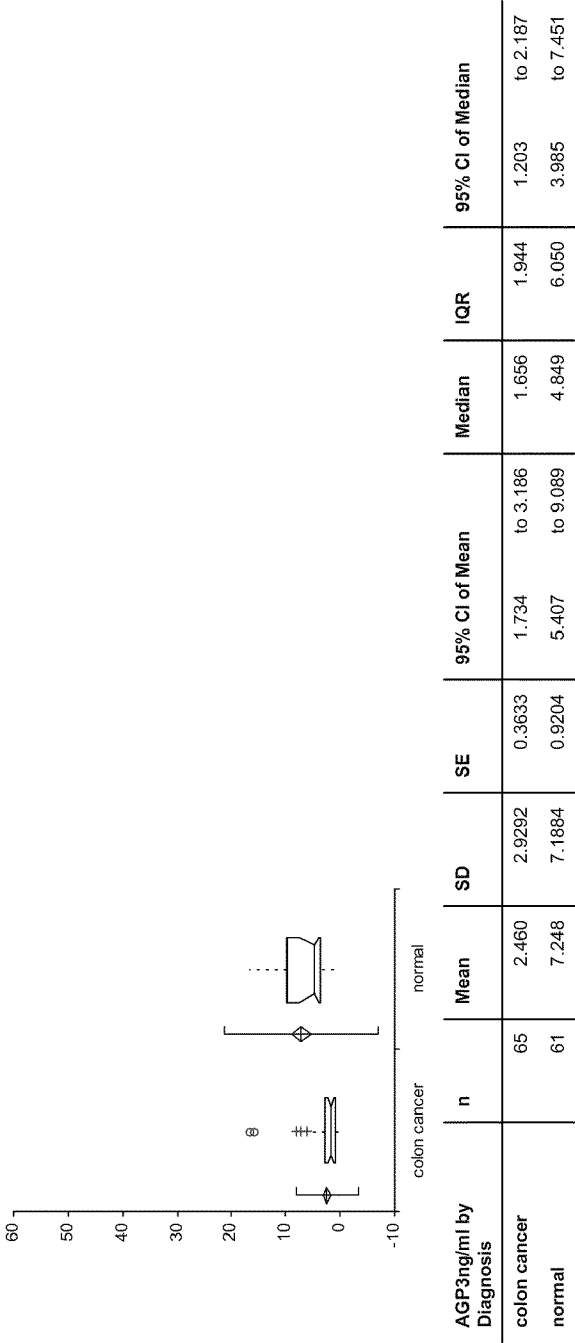
ROC curve data for OGTA066



Curve	Area	SE	p	95% CI of Area	Colon vs Normals = colon cancer
AGP3ng/ml	0.863	0.0334	<0.0001	0.797 to 0.928	have lower values

Figure 4

Box Plot data for OGTA066



PROTEINS

RELATED APPLICATIONS

[0001] The present application is a Continuation of co-pending PCT Application No. PCT/GB2008/050125 filed Feb. 26, 2008, which in turn, claims priority from PCT Application Nos. PCT/EP2008/055537 filed Jun. 5, 2007 and PCT/GB2008/050124 filed Feb. 25, 2008, and U.S. Provisional Application Ser. Nos. 60/903,509 and 60/903,510, both filed Feb. 26, 2007. Applicants claim the benefits of 35 U.S.C. §120 as to the first-referenced PCT application and priority under 35 U.S.C. §119 as to the second- and third-referenced PCT applications, and the said U.S. Provisional applications, and the entire disclosures of all applications are incorporated herein by reference in their entireties.

INTRODUCTION

[0002] The present invention relates to the identification of membrane proteins associated with B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer and retinoblastoma which have utility as markers for B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer and retinoblastoma and breast cancer, cervical cancer, colorectal cancer, gastric cancer, hepatocellular carcinoma, lung cancer, melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer and retinoblastoma metastases and which also form biological targets against which antibodies such as therapeutic antibodies (or other affinity reagents) or other pharmaceutical agents can be made.

BACKGROUND OF THE INVENTION

Acute Lymphocytic Leukaemia

[0003] Each year, about 35,000 new cases of all types of leukaemia are diagnosed in the USA. Of these, about 4,000 will be acute lymphocytic leukaemia (ALL). Although this is a leukaemia that occurs mostly in children, about one-third, or 1300 cases, will occur in adults. About 1,500 people will die of ALL in the USA each year; two-thirds of them will be adults. The risk of ALL is lowest between the ages of 25 and 50 and then begins to pick up.

Acute Lymphocytic Leukaemia Diagnosis

[0004] Diagnostic tests for ALL include blood cell count, bone marrow aspiration, bone marrow biopsy, excisional lymph node biopsy, blood chemistry tests and lumbar puncture. Other lab tests include routine microscopic exam, cytochemistry, flow cytometry, immunocytochemistry, cytogenetics, molecular genetic studies, and gene-expression profiling. Imaging tests such as chest x-ray, computed tomogra-

phy (CT) scans, magnetic resonance imaging (MRI), gallium scans, bone scans, and ultrasound may also be carried out.

Acute Lymphocytic Leukaemia Staging

[0005] Leukaemia involves all the bone marrow and, in many cases, it has also spread to other organs. Lab tests focus on finding out the exact type (and subtype) of leukaemia. This in turn helps predict which treatments will work best and the prognosis for the patient.

[0006] There are 3 subtypes for ALL according to the French-American-British (FAB) classification. The original FAB system was based only on the way the leukaemic cells looked under the microscope after they were routinely processed or cytochemically stained. More recently, doctors have found that cytogenetic studies, flow cytometry, and molecular genetic studies provide more information that is sometimes useful in classifying ALL and predicting the patient's prognosis. Now the subtypes of ALL are: early pre-B ALL, common ALL, pre-B-cell ALL, mature B-cell ALL (Burkitt leukaemia), pre-T-cell ALL and mature T-cell ALL. T-cell ALL has the best prognosis, mature B-cell ALL the worst, and pre-B-cell ALL is intermediate. One of the most important factors that affects outcome is a translocation between chromosomes 9 and 22 (Philadelphia chromosome). People with this translocation (20% to 25%) have a worse outcome than those without it. Another translocation that carries a poor outlook is one between chromosomes 4 and 11, which occurs in about 5% of patients.

Acute Lymphocytic Leukaemia Treatment

[0007] Chemotherapy is the major treatment for ALL. Treatments are given in the following phases: remission induction, consolidation, maintenance therapy and central nervous system (CNS) prophylaxis. Chemotherapeutic agents used for remission induction and consolidation include cyclophosphamide, vincristine, dexamethasone or prednisone, L-asparaginase and doxorubicin (Adriamycin) or daunorubicin. Maintenance therapy consists of methotrexate with 6-mercaptopurine (6-MP), often combined with vincristine and prednisone. CNS prophylaxis involves methotrexate and/or cytarabine. In general, about 80% of patients will respond completely to these treatments. Unfortunately, about half of these patients relapse, so the overall cure rate is around 30%. If leukaemias recur after treatment, they will most often do so in the bone marrow and blood. Occasionally, the brain or spinal fluid will be the first place they recur. If the leukaemia is refractory (which happens in about 15%-20% of cases) then newer or more intensive doses of drugs may be tried, although they are less likely to work. A stem cell transplant may be attempted if the leukaemia can be put into remission. It is possible for a patient with recurrent leukaemia to go into remission again, although it may be only temporary. In this situation, a stem cell transplant is considered after more induction chemotherapy. If the leukaemia is persistent, eventually chemotherapy treatment becomes unhelpful.

[0008] Radiation therapy is sometimes used to treat leukaemia that has spread to the brain and spinal fluid or to the testicles. Radiation to the whole body is often an important part of treatment before bone marrow or peripheral blood stem cell transplantation.

[0009] Clinical trials are being conducted to see whether better outcomes are achieved using a combination of chemotherapy and imatinib mesylate (Gleevec), a drug which tar-

gets cells that have the Philadelphia chromosome (9-22 translocation or bcr-abl gene fusion). Another drug, dasatinib, approved for treatment of ALL, has the same mode of action as imatinib but appears to be more potent and can act against leukaemia cells that have become resistant to imatinib.

Non-Hodgkin's Lymphoma

[0010] Non-Hodgkin's lymphoma (NHL) is a cancer of lymphoid tissue. In the USA, 85% of all cases of non-Hodgkin's lymphoma derive from B lymphocytes (B-cell) and 15% from T lymphocytes (T-cell). There are about 59,000 new cases of NHL in the USA each year, with around 19,000 deaths. This cancer is more common in men than in women and whites are affected more often than African or Asian people. A person's risk of getting NHL during his or her lifetime is 1 in 50. The risk of dying of this disease is about 1 in 100. Since the early 1970s, incidence rates for non-Hodgkin lymphoma have nearly doubled. More recently, incidence rates have stabilized due, perhaps, to the decline in AIDS-related NHL.

B-Cell Lymphomas:

[0011] About 33% of all non-Hodgkin's lymphomas in the USA are diffuse large B-cell lymphomas. About 14% are follicular lymphomas. Chronic lymphocytic leukaemia (CLL) and small lymphocytic lymphoma (SLL) account for 24% of all lymphomas. Only about 2% of lymphomas are mantle cell lymphomas. All marginal zone lymphomas account for about 4% of lymphomas. Primary mediastinal B-cell lymphoma accounts for about 2% of all lymphomas. Burkitt's lymphoma makes up about 1% to 2% of all lymphomas. Lymphoplasmocytic lymphoma (Waldenstrom macroglobulinemia) accounts for 1-2% of lymphomas. Hairy cell leukaemia is rare—about 1,000 people in the USA are diagnosed with this type each year. Although primary central nervous system (CNS) lymphoma was a rare tumour in the past, it has become more common in patients with AIDS.

Non-Hodgkin's Lymphoma Diagnosis

[0012] NHL may cause many different signs and symptoms, depending on where it is found in the body. A biopsy is the only way to tell for sure if cancer is present. Types of biopsy include excisional or incisional biopsy, fine needle aspiration (FNA) biopsy, bone marrow aspiration and biopsy, and lumbar puncture. Lab tests including immunohistochemistry, flow cytometry, cytogenetics, molecular genetic studies and blood tests can also be performed. Imaging tests that may be used include chest x-ray, computed tomography (CT) scan, magnetic resonance imaging (MRI) scan, positron emission tomography (PET) scan, gallium scan, bone scan, and ultrasound.

Non-Hodgkin's Lymphoma Staging

[0013] Survival statistics vary widely by cell type and stage of disease at the time of diagnosis. However, the overall 5-year relative survival rate for people with non-Hodgkin's lymphoma is 60%, and 10-year relative survival is 49%.

[0014] Non-Hodgkin's lymphoma is staged using the Ann Arbor staging system stages I-IV. The International Prognostic Index (IPI) helps predict how quickly the lymphoma might grow and how well a patient might respond to treatment. It is mainly used in patients with fast growing lymphomas. Over

75% of people in the lowest group will live longer than 5 years, whereas only 30% of people in the highest group live 5 years.

Survival Rates for B-Cell Lymphomas:

[0015] Diffuse large B-cell lymphoma can be cured in around 40% to 50% of patients. Follicular lymphomas are not considered curable but are slow growing, and the 5-year survival rate is around 60% to 70%. Over time, about one third of follicular lymphomas change into a fast growing diffuse B-cell lymphoma. Chronic lymphocytic leukaemia (CLL) and small lymphocytic lymphoma (SLL) are not considered curable but depending on the stage and growth rate of the disease, most patients can live well over 10 years with this lymphoma. Only 20% of patients with mantle cell lymphoma survive at least 5 years. Marginal zone lymphomas are often curable. About half of patients with primary mediastinal B-cell lymphoma can be cured. Although Burkitt's lymphoma is a fast growing lymphoma, over half of patients can be cured by intensive chemotherapy. Although lymphoplasmocytic lymphoma (Waldenstrom macroglobulinemia) isn't curable, most patients live longer than 5 years. Hairy cell leukaemia can usually be treated successfully. The outlook for people with primary CNS lymphoma is poor but about 30% to 50% of people can live at least 5 years.

Non-Hodgkin's Lymphoma Treatment

[0016] Surgery is not often used to treat NHL. It has been used to treat lymphomas that start in organs such as the stomach or thyroid, but only if it has not spread beyond these organs. External beam radiation therapy is often the main treatment for early stage lymphomas, and is often used along with chemotherapy. Chemotherapeutic drugs used include a combination of cyclophosphamide, doxorubicin, vincristine and prednisone known as CHOP, chlorambucil, fludarabine, and etoposide. Immunotherapy using either interferon or monoclonal antibodies such as rituximab can also sometimes be used as a treatment. Bone marrow or peripheral blood stem cell transplantation (SCT) is used for patients when standard treatment has not worked.

Treatment of B-Cell Lymphomas:

[0017] The main treatment for diffuse large B-cell lymphoma is chemotherapy with CHOP with the addition of rituximab. Radiation therapy may also be added. Follicular lymphoma has not been shown to be curable by any of the standard treatments. Radiation therapy, chemotherapy and/or monoclonal antibodies can be used, with the point of therapy being to control the disease for as long as possible while causing the fewest side effects. Chronic lymphocytic leukaemia (CLL) and small lymphocytic lymphoma (SLL) are also not considered curable and the treatment is the same as for follicular lymphoma. There is also no curative treatment for mantle cell lymphoma which is often fatal. Radiation therapy and chemotherapy are used to treat extranodal marginal zone B-cell lymphomas. Nodal marginal zone B-cell lymphoma and splenic marginal zone B-cell lymphoma are generally low-grade lymphomas and are treated with either observation or low-intensity chemotherapy. Primary mediastinal B-cell lymphoma is treated like localized diffuse large B-cell lymphoma. Burkitt's lymphoma is a very fast growing lymphoma that is treated intensely with chemotherapy. The main treatment for lymphoplasmocytic lymphoma (Walden-

strom macroglobulinemia) is chemotherapy or rituximab. Hairy cell leukaemia is a slow growing lymphoma that invades the spleen and lymph nodes as well as the blood and can be treated with chemotherapy.

Breast Cancer

[0018] Globally, breast cancer is both the most common cancer (10% of all cancer cases) and the leading cause of cancer death (6% of cancer deaths) in women. Global incidence of breast cancer is over 1 million cases per year, with about 400,000 deaths. Women in North America have the highest rate of breast cancer in the world (over 200,000 new cases per year, with about 40,000 deaths). The chance of developing invasive breast cancer at some time in a woman's life is about 1 in 8. Breast cancer incidence increases with age, rising sharply after age 40. In the USA, about 77% of invasive breast cancers occur in women over age 50. It has been estimated that approximately US\$8.1 billion is spent in the USA each year on treating breast cancer.

Breast Cancer Diagnosis

[0019] Early diagnosis improves the likelihood that treatment will be successful. Screening methods such as mammograms, clinical breast examinations and breast self-examinations are useful in detecting breast cancer. Current diagnostic methods include breast ultrasound, ductogram, full-field digital mammography (FFDM), scintimammography and MRI. A biopsy (fine needle aspiration biopsy, core biopsy or surgical biopsy) is then performed to confirm the presence of breast cancer. Imaging tests such as a chest x-ray, bone scan, CT, MRI and PET are used to detect if the breast cancer has spread.

Breast Cancer Staging

[0020] Breast cancer is staged using the American Joint Committee on Cancer (AJCC) TNM system—Stage 0-Stage IV. Ductal carcinoma in situ (DCIS), a non-invasive cancer which accounts for 20% of new breast cancer cases is Stage 0. Nearly all women diagnosed at this early stage of breast cancer can be cured. Infiltrating (invasive) ductal carcinoma (IDC), which accounts for 80% of invasive breast cancer and infiltrating (invasive) lobular carcinoma (ILC), which accounts for 5% of invasive breast cancers are more severe Stage I-IV cancers and can metastasize.

Breast Cancer Treatment

[0021] Breast-conserving surgery (lumpectomy) or mastectomy are the usual treatments for breast cancer. For stage I or II breast cancer, breast-conserving surgery is as effective as mastectomy. Patients can then undergo reconstructive surgery. Axillary lymph node sampling and removal or sentinel lymph node biopsy (SLNB) is performed to see if the cancer has spread to the lymph nodes.

[0022] Neoadjuvant chemotherapy can be given before surgery to shrink large cancers. Adjuvant chemotherapy after surgery reduces the risk of breast cancer recurrence. Chemotherapy can also be used as the main treatment for women whose cancer has spread outside the breast and underarm area. Chemotherapeutic agents used include anthracyclines (e.g. methotrexate, fluorouracil, doxorubicin, epirubicin), taxanes (e.g. paclitaxel, docetaxel, vinorelbine) and alkylating agents (e.g. cyclophosphamide).

[0023] Radiation therapy (usually external beam radiation but sometimes brachytherapy) is given once chemotherapy is complete.

[0024] Hormone therapy with selective estrogen receptor modulators (e.g. tamoxifen) can be given to women with estrogen receptor positive breast cancers. Taking tamoxifen after surgery for 5 years can reduce recurrence by about 50% in women with early breast cancer. Aromatase inhibitors such as exemestane, letrozole or anastrozole can also be used.

[0025] Women with HER2 positive cancers (about 1/3 of breast cancers) can be given biological response modifiers such as trastuzumab (Herceptin). Clinical trials have shown that adding trastuzumab to chemotherapy lowers the recurrence rate and death rate over chemotherapy alone after surgery in women with HER2 positive early breast cancers.

Breast Cancer Survival by Stage

[0026] Patients diagnosed with breast cancer between 1995 and 1998 had a 5 year relative survival rate of 100% for stage 0 and I, 92% for stage IIA, 81% for stage IIB, 67% for stage IIIA, 54% for stage IIIB and 20% for stage IV.

Cervical Cancer

[0027] Cervical cancer is second only to breast cancer as the most common malignancy in both incidence and mortality and remains a significant public health problem throughout the world. In the USA alone, invasive cervical cancer accounts for approximately 19% of all gynecological cancers. In the USA, about 9,710 cases of invasive cervical cancer are diagnosed each year, with 3,700 deaths. Non-invasive cervical cancer (carcinoma in situ) is about 4 times more common than invasive cervical cancer. Between 1955 and 1992, the number of cervical cancer deaths in the United States dropped by 74%. The main reason for this change is the increased use of the Pap test screening procedure. The death rate from cervical cancer in the USA continues to decline by nearly 4% a year. Half of women diagnosed with this cancer are between the ages of 35 and 55. Cervical cancer occurs most often in Hispanic women; the rate is over twice that in non-Hispanic white women. African-American women develop this cancer about 50% more often than non-Hispanic white women. In many developing countries, where mass screening programs are not widely available, the clinical problem is more serious. Worldwide, the number of new cases is estimated to be 471,000 with a four-year survival rate of only 40% (Munoz et al., 1989, *Epidemiology of Cervical Cancer in: "Human Papillomavirus"*, New York, Oxford Press, pp. 9-39; National Institutes of Health, Consensus Development Conference Statement on Cervical Cancer, Apr. 1-3, 1996). These cases are usually diagnosed at an invasive late stage, rather than as precancers or early cancers.

Cervical Cancer Diagnosis

[0028] Early detection greatly improves the chances of successful treatment and prevents any early cervical cell changes from becoming cancerous. Although the Pap test is the most cost-effective cancer screening test developed to date (Greenberg, M. D., et al., 1995, *Clin Obstet Gynecol* 38(3): 600-9), it is not perfect. One of its limitations is that Pap tests are examined by humans, so an accurate analysis of the hundreds of thousands of cells in each sample is not always possible. It was reported that the mean sensitivity of primary Pap tests is approximately 58% and the accuracy of a repeat test is only

about 66% (Fahey M. T., et al., 1995, *Am. J. Epidemiol.* 141: 680-689). The low sensitivity and poor reproducibility have complicated the management of ASCUS (atypical squamous cells of undetermined significance) and LSIL (low-grade squamous intraepithelial lesion) patients. If an “accelerated repeat Pap test” is recommended for the follow-up of women with primary diagnosis of ASCUS or LSIL, patients will risk delay in diagnosis of potential high-grade lesions. However, if these patients are universally referred to colposcopy, the vast majority of women will be over treated. Only 5-10% of women with ASCUS have high-grade disease upon colposcopy, and more than 80% of LSIL will regress to normal or stay in their current state (Cox, J. T., 2000, *Clinics in Laboratory Medicine*. 20 (2): 303-343, Ostor A. G., 1993, *Int. J. Gynecol. Pathol.* 12 (2): 186-192). New tests can identify HPV's by finding their DNA in the cells. Many doctors are now testing for HPV if the Pap test result is mildly abnormal. However, since the vast majority of HPV infections and the resulting squamous intraepithelial lesions regress spontaneously, especially in young women, HPV testing cannot specifically identify patients whose lesions will persist or progress to invasive carcinoma (Sasieni, P. D., 2000, *J. Am. Med. Womens Assoc.* 55 (4): 216-219, Sasieni, P. D., 2000, *Br. J. Cancer*, 83 (5): 561-565). A vaccine (Gardasil) has been approved for use by FDA and it protects against HPV types 16, 18, 6, and 11. The vaccine does not protect against all cancer-causing types of HPV, so Pap tests are still necessary. Other tests are required to diagnose cervical cancer following the Pap test including a colposcopy and biopsy, and sometimes an endocervical scraping. The biopsy can be either a colposcopic biopsy, an endocervical curettage or a cone biopsy—LEEP (LLETZ) or cold knife cone biopsy. Imaging tests such as a chest x-ray, computed tomography (CT), magnetic resonance imaging (MRI) and positron emission topography (PET) can also be used.

Cervical Cancer Staging

[0029] Cervical cancer is staged with the FIGO (International Federation of Gynecology and Obstetrics) System of Staging—0-IV. The overall (all stages combined) 5-year survival rate for cervical cancer is about 73%.

Cervical Cancer Treatment

[0030] For pre-invasive cancer, cryosurgery, laser surgery or conisation can be used as treatment. For Stage I-IIA cervical cancer, a hysterectomy is the usual treatment. A trachelectomy may be possible in some cases. For recurrent cervical cancer, a pelvic exenteration is usually performed. Radiation therapy (either external beam radiation therapy or brachytherapy) is an option for Stage IB-Stage IV patients. Combining radiation therapy with chemotherapy has been found to be more effective than radiation therapy alone. Chemotherapeutic agents used include cisplatin, paclitaxel, topotecan, ifosfamide, and fluorouracil. Stage IVB cervical cancer is usually not considered curable but a combination of radiation therapy and chemotherapy can help relieve symptoms.

Cervical Cancer Survival by Stage

[0031] Women who were treated more than 10 years ago had 5 year survival rates of above 95% for stage IA, around

90% for stage IB1, around 80-85% for stage IB2, around 75-78% for stage IIA/B, around 47-50% for stage IIIA/B and around 20-30% for stage IV.

Chronic Lymphocytic Leukaemia

[0032] Chronic lymphocytic leukaemia (CLL) is the most common adult leukaemia in the Western Hemisphere, and is generally fatal once the disease progresses. There are probably two different kinds of CLL. One is very slow growing and rarely needs to be treated. People with this kind of CLL survive on average 13 to 15 years. The other kind of CLL is faster growing and is a more serious disease. People with this form of CLL survive only about 6 to 8 years. About 9,800 new cases of CLL are diagnosed each year in the USA, with about 4,600 deaths. CLL affects only adults. The average age of patients is about 70 and it is rarely seen in people under the age of 40.

Chronic Lymphocytic Leukaemia Diagnosis

[0033] Diagnostic tests for chronic lymphocytic leukaemia carried out include blood cell count, bone marrow aspiration, bone marrow biopsy, excisional lymph node biopsy, blood chemistry tests and lumbar puncture. Other lab tests include routine microscopic exam, cytochemistry, flow cytometry, immunocytochemistry, cytogenetics, molecular genetic studies, and fluorescent in situ hybridization (FISH). Imaging tests may also be carried out including chest x-rays, computed tomography (CT) scans, magnetic resonance imaging (MRI) and ultrasound.

Chronic Lymphocytic Leukaemia Staging

[0034] The prognosis of a patient with leukaemia depends on the leukaemia's type or subtype, cellular features determined by lab tests, and results of imaging studies.

[0035] There are 2 different systems for staging CLL. The Rai classification is used more often in the USA, whereas the Binet system is used more widely in Europe.

[0036] The 5 Rai system stages can be separated into low-, intermediate-, and high-risk categories. Stage 0 is considered low risk, stages I and II are considered intermediate risk, and stages III and IV are considered high risk.

[0037] The Binet staging system uses the letters A (least severe), B, and C (most severe) to define the stages. CLL is classified according to the number of affected lymphoid tissue groups and the presence of anaemia or thrombocytopenia.

[0038] Other markers such as chromosome changes, mutational status, ZAP-70 and CD38 status are also used to distinguish between the two different types of CLL.

Chronic Lymphocytic Leukaemia Treatment

[0039] The prognosis for patients with low-risk CLL is very good. Treatment is only considered if there are signs that the leukaemia is progressing. When indicated, initial treatment is usually chemotherapy. Chlorambucil (Leukeran) and fludarabine (Fludara) are the chemotherapy drugs most commonly used to treat CLL.

[0040] Patients with intermediate- and high-risk CLL who do not have any symptoms may not need treatment right away. Some with very high-risk disease may best be treated with early stem cell transplantation. No specific treatment has been shown to improve survival. In general, chemotherapy is used as treatment. Monoclonal antibodies such as rituximab can be used alongside chemotherapy. Alemtuzumab (Campath) is

used in patients with CLL who are no longer responding to standard chemotherapy treatments.

Colorectal Cancer

[0041] Colorectal cancer (CRC) is one of the leading causes of cancer-related morbidity and mortality, responsible for an estimated half a million deaths per year, mostly in Western, well developed countries. In these territories, CRC is the third most common malignancy (estimated number of new cases per annum in USA and EU is approximately 350,000 per year). Estimated healthcare costs related to treatment for colorectal cancer in the United States are more than \$8 billion.

Colorectal Cancer Diagnosis

[0042] Today, the fecal occult blood test and colonoscopy, a highly invasive procedure, are the most frequently used screening and diagnostic methods for colorectal cancer. Other diagnostic tools include Flexible Sigmoidoscopy (allowing the observation of only about half of the colon) and Double Contrast Barium Enema (DCBE, to obtain X-ray images).

Colorectal Cancer Staging

[0043] CRC has four distinct stages: patients with stage I disease have a five-year survival rate of >90%, while those with metastatic stage IV disease have a <5% survival rate according to the US National Institutes of Health (NIH).

Colorectal Cancer Treatment

[0044] Once CRC has been diagnosed, the correct treatment needs to be selected. Surgery is usually the main treatment for rectal cancer, although radiation and chemotherapy will often be given before surgery. Possible side effects of surgery include bleeding from the surgery, deep vein thrombosis and damage to nearby organs during the operation.

[0045] Currently, 60 percent of colorectal cancer patients receive chemotherapy to treat their disease; however, this form of treatment only benefits a few percent of the population, while carrying with it high risks of toxicity, thus demonstrating a need to better define the patient selection criteria.

[0046] Colorectal cancer has a 30 to 40 percent recurrence rate within an average of 18 months after primary diagnosis. As with all cancers, the earlier it is detected the more likely it can be cured, especially as pathologists have recognised that the majority of CRC tumours develop in a series of well-defined stages from benign adenomas.

Colon Cancer Survival by Stage:

[0047] For stage I 93%, for stage HA 85%, for stage IIB 72%, for stage IIIA 83%, for stage IIIB 64%, for stage IIIC 44% and for stage IV 8%.

Gastric Cancer

[0048] Gastric cancer is the second-leading cause of cancer-related deaths in the world, with about 700,000 deaths per year, mostly in less developed countries. In the USA, about 22,000 people are diagnosed with gastric cancer each year, with about 11,000 deaths. This figure is approximately ten

times higher in Japan. Two thirds of people diagnosed with gastric cancer are older than 65.

Gastric Cancer Diagnosis

[0049] Early stage gastric cancer rarely causes symptoms so only about 10-20% of gastric cancers in the USA are found in the early stages, before they have spread to other areas of the body. Studies in the USA have not found mass screening for gastric cancer to be useful because the disease is not that common. Endoscopy followed by a biopsy is the main procedure used to diagnose gastric cancer. Other diagnostic methods include barium upper gastrointestinal radiographs, endoscopic ultrasound, CT scan, PET scan, MRI scan, chest x-ray, laparoscopy, complete blood count (CBC) test and fecal occult blood test.

Gastric Cancer Staging

[0050] Gastric cancer is staged using the American Joint Commission on Cancer (AJCC) TNM system—Stage 0-Stage IV. Patients with stage 0 disease have a 5-year survival rate of >90%, while there is usually no cure for patients with stage IV disease where the 5-year survival rate is only 7%. The overall 5-year relative survival rate of people with gastric cancer in the USA is about 23%. The 5-year survival rate for cancers of the proximal stomach is lower than for cancers in the distal stomach.

Gastric Cancer Treatment

[0051] Surgery is the only way to cure gastric cancer. There are three types of surgery used—endoscopic mucosal resection (only for early stage gastric cancer), subtotal gastrectomy or total gastrectomy. Gastric cancer often spreads to lymph nodes so these must also be removed. If the cancer has extended to the spleen, the spleen is also removed. Surgery for gastric cancer is difficult and complications can occur.

[0052] Chemotherapy may be given as the primary treatment for gastric cancer that has spread to distant organs. Chemotherapy together with external beam radiation therapy may delay cancer recurrence and extend the life span of people with less advanced gastric cancer, especially when the cancer could not be removed completely by surgery. Chemotherapeutic agents used include fluorouracil, doxorubicin, methotrexate, etoposide and cisplatin. More recently, imatinib mesylate (Gleevec) has been trialled in gastrointestinal stromal tumours (GIST), improving progression free survival.

Gastric Cancer Survival by Stage:

[0053] For stage 0 greater than 90%, for stage IA 80% for stage IB 60%, for stage II 34%, for stage IIIA 17%, for stage IIIB 12% and stage IV 7%.

Glioblastoma

[0054] Glioblastoma, also known as glioblastoma multiforme, may develop from a diffuse astrocytoma or an anaplastic astrocytoma but more commonly presents de novo without evidence of a less malignant precursor. Histologically, this tumour is an anaplastic, cellular glioma composed of poorly differentiated, often pleomorphic astrocytic tumour cells with marked nuclear atypia and brisk mitotic activity. Glioblastoma primarily affects the cerebral hemispheres.

CNS tumours are associated with characteristic patterns of altered oncogenes, altered tumour-suppressor genes, and chromosomal abnormalities.

[0055] Glioblastoma accounts for approximately 12% to 15% of all brain tumours (which account for 85% to 90% of all primary central nervous system (CNS) tumours). New cases for CNS tumours in USA are approximately 18,800 (6.6 per 100,000 persons) per year, with around 12,800 (4.7 per 100,000 persons) deaths. This type of cancer accounts for approximately 1.3% of all cancers and 2.2% of all cancer-related deaths in the USA. Worldwide, there are approximately 176,000 new cases of brain and other CNS tumours per year, with an estimated mortality of 128,000. In general, the incidence of primary brain tumours is higher in whites than in blacks, and mortality is higher in males than in females. The peak incidence occurs between the ages of 45 and 70 years.

[0056] Primary brain tumours rarely spread to other areas of the body, but they can spread to other parts of the brain and to the spinal axis. Most patients with central nervous system (CNS) neoplasms do not live long enough to develop metastatic disease.

Glioblastoma Diagnosis

[0057] Computed tomography (CT) and magnetic resonance imaging (MRI) have complementary roles in the diagnosis of CNS neoplasms. Angiography can also be used in diagnosis. In post-therapy imaging, single-photon emission computed tomography (SPECT) and positron emission tomography (PET) may be useful in differentiating tumour recurrence from radiation necrosis. A definite diagnosis is then made by performing a biopsy.

Glioblastoma Staging

[0058] Glioblastomas are among the most aggressively malignant human neoplasms, with a mean total length of disease in patients with primary glioblastoma of less than 1 year. On the WHO classification of nervous system tumours from grade I to grade IV, glioblastoma is classified as grade IV. The 5-year survival rate for patients with glioblastoma aged over 45 is 2% or less.

Glioblastoma Treatment

[0059] The cure rate for glioblastoma is very low with standard local treatment. The first step in most cases is surgical removal by craniotomy of as much of the tumour as is safe without destroying normal function. Glioblastomas are not cured by surgery because cells from the tumour invade deeply the surrounding normal brain tissue. However, surgery reduces the pressure of the tumour against the rest of the brain and can prolong life.

[0060] Radiation therapy (external beam radiation, interstitial radiotherapy, 3D conformal therapy, stereotactic radiosurgery or brachytherapy) can increase the cure rate or prolong disease-free survival. Radiation therapy may also be useful in the treatment of recurrences in patients initially treated with surgery alone. Therapy can involve surgically implanted carmustine-impregnated polymer combined with postoperative external-beam radiation therapy (EBRT). Chemotherapy is usually given along with or following radiation therapy and may prolong survival. Chemotherapeutic agents used include temozolomide, BCNU (carmustine) and cispl-

atin. Growth factor inhibitors erlotinib (Tarceva) and gefitinib (Iressa) have been shown to shrink tumours in some patients.

[0061] Novel biologic therapies under clinical evaluation for patients with brain tumours include dendritic cell vaccination, tyrosine kinase receptor inhibitors, farnesyl transferase inhibitors, viral-based gene therapy, and oncolytic viruses.

Hepatocellular Carcinoma (HCC)

[0062] Hepatocellular carcinoma (HCC) arises from the main cells of the liver (the hepatocytes) and accounts for around 80% of all cases of liver cancer. It is usually confined to the liver and is associated with cirrhosis in 50% to 80% of patients. Hepatocellular carcinoma is about 3 times more common in males than in females. Chronic infection with hepatitis B virus (HBV) or hepatitis C virus (HCV) is a major cause of HCC and is responsible for making liver cancer the most common cancer in many parts of the world. In the United States, hepatitis C infection is responsible for about 50% to 60% of all liver cancers and hepatitis B is responsible for another 20%. Exposure to Aflatoxins is also a cause of HCC, mostly in warmer and tropical countries. Liver cancer accounts for about 5.8% of all cancer cases globally (about 626,000 cases) and 8.9% of deaths per year (about 598,000). It is the 3rd most common cause of cancer-related death in both men and women worldwide. HCC is predominantly found in Asia and Africa, which account for 80% of cases. In the USA, there are approximately 18,500 new cases of HCC and 16,000 deaths per year. About 85% of people diagnosed with liver cancer are between 45 and 85 years of age. About 4% are between 35 and 44 years of age and only 2.4% are younger than 35.

Hepatocellular Carcinoma Diagnosis

[0063] Since symptoms of liver cancer often do not appear until the disease is advanced, only a small number of liver cancers are found in the early stages and can be removed with surgery.

[0064] Many signs and symptoms of liver cancer are relatively nonspecific—that is, they can be caused by other cancers or by non-cancerous diseases. Imaging tests such as ultrasound, computed tomography (CT), magnetic resonance imaging (MRI) and angiography are commonly used to diagnose HCC. Other diagnostic tools include laparoscopy, biopsy, alpha-fetoprotein (AFP) blood test, liver function tests (LFTs), prothrombin time (PT) and tests for hepatitis B and C.

Hepatocellular Carcinoma Staging

[0065] HCC has four stages, stage I to stage IV according to the American Joint Committee on Cancer (AJCC) TNM system. HCC can be classified as localized resectable, localized unresectable or advanced. The overall 5-year relative survival rate for liver cancer is about 9%.

[0066] One reason for this low survival rate is that most patients with liver cancer also have cirrhosis of the liver, which itself can be fatal (people with liver cancer and class C cirrhosis are generally too sick for any treatment and usually die in a few months). The 5 year survival for localized resectable HCC following surgery is between 40% and 70%. For advanced HCC there is no standard treatment and the 5 year

survival rate is less than 5%. Survival continues to drop after diagnosis and treatment so that by 10 years it is less than 2.5%.

Hepatocellular Carcinoma Treatment

[0067] Treatment of liver cancer depends on the size of the tumour and whether the patient has cirrhosis. At this time, surgery, either by resection or liver transplantation, offers the only chance to cure a liver cancer. People without cirrhosis can do well with surgical removal of the tumour.

[0068] However, in many cases, it might not be possible to safely remove a localized liver cancer. Less than 30% of the patients having explorative surgery are able to have their cancer completely removed by surgery. Partial hepatectomy results in a 5-year survival of 30% to 40%. If there is cirrhosis, or a very large tumour, most experts recommend liver transplantation as the main treatment. The 5-year survival for liver transplantation patients is around 70% but the opportunities for liver transplantation are limited.

[0069] Other treatments include radiofrequency ablation (RFA), ethanol ablation, cryosurgery, hepatic artery embolization, chemoembolization or three-dimensional conformal radiation therapy (3DCRT). Chemotherapy can also be used but shrinks fewer than 1 in 5 tumours. This may be improved by hepatic artery infusion (HAI). Chemotherapeutic agents used include Adriamycin, VP-16, Cisplatin, Mitomycin, 5-FU and Leucovorin.

[0070] The prognosis for any treated primary liver cancer patient with progressing, recurring, or relapsing disease is poor. Treatment of liver cancer that returns after initial therapy depends on many factors, including the site of the recurrence, the type of initial treatment, and the functioning of the liver. Patients with localized resectable disease that recurs in the same spot may be eligible for further surgery.

Lung Cancer

[0071] Lung cancer is the most common form of cancer worldwide (accounting for about 12% of cancer cases) and the main cause of death from cancer (accounting for about 18% of deaths). Global incidence of lung cancer is over 1,300,000 per year, with the number of deaths over 1,100,000. In the USA, there are about 170,000 new cases per year (about 13% of all cancers), with about 160,000 deaths (about 28% of cancer deaths). Lung cancer is much more prevalent among men than women. Nearly 70% of people diagnosed with lung cancer are older than 65; fewer than 3% of all cases are found in people under the age of 45. Around 15% of all lung cancers are small cell type (SCLC), which tend to spread widely through the body, while the remaining 85% are non-small cell (NSCLC). It has been estimated that approximately US\$9.6 billion is spent in the USA each year on treating lung cancer.

Lung Cancer Diagnosis

[0072] Lung cancer is a life-threatening disease because it often metastasises even before it can be detected on a chest x-ray. Usually symptoms of lung cancer do not appear until the disease is in an advanced stage. So far, there is no screening test that has been shown to improve a person's chance for a cure. Imaging tests such as a chest x-ray, CT scan, MRI scan or PET scan may be used to detect lung cancer. Tests to confirm the diagnosis are then performed and include sputum

cytology, needle biopsy, bronchoscopy, endobronchial ultrasound and complete blood count (CBC).

Lung Cancer Staging

[0073] Nearly 60% of people diagnosed with lung cancer die within one year of diagnosis; 75% die within 2 years. The 5-year survival rate for people diagnosed with NSCLC is about 15%; for SCLC the 5-year survival rate is about 6%. NSCLC is staged using the American Joint Committee on Cancer (AJCC) TNM system—Stage 0–Stage IV. The 5-year survival rates by stage are as follows: stage I: 47%; stage II: 26%; stage III: 8% and stage IV: 2%. SCLC has a 2-stage system—limited stage and extensive stage. About two thirds of SCLC patients have extensive disease at diagnosis. If SCLC is found very early and is localised to the lung alone, the 5-year survival rate is around 21%, but only 6% of patients fall into this category. Where the cancer has spread, the 5-year survival is around 11%. For patients with extensive disease, the 5-year survival is just 2%.

Lung Cancer Treatment

[0074] Surgery is the only reliable method to cure NSCLC. Types of surgery include lobectomy, pneumonectomy, segmentectomy and video-assisted thoracic surgery (for small tumours). External beam radiation therapy is sometimes used as the primary treatment, especially if the patient's health is too poor to undergo surgery. Radiation therapy can also be used after surgery. Chemotherapy may be given as the primary treatment or as an adjuvant to surgery. Targeted therapy using epidermal growth factor receptor (EGFR) antagonists such as gefitinib or erlotinib can also be given after other treatments have failed. Antiangiogenic drugs, such as bevacizumab, have been found to prolong survival of patients with advanced lung cancer. Photodynamic therapy is also being researched as a treatment for lung cancer.

[0075] The main treatment for SCLC is chemotherapy, either alone or in combination with external beam radiation therapy and very rarely, surgery.

[0076] Chemotherapeutic agents used for NSCLC and SCLC include cisplatin, carboplatin, mitomycin C, ifosfamide, vinblastine, gemcitabine, etoposide, vinorelbine, paclitaxel, docetaxel and irinotecan.

Melanoma

[0077] Cancer of the skin is the most common of all cancers, probably accounting for more than 50% of all cancers. Melanoma accounts for about 4% of skin cancer cases but causes a large majority of skin cancer deaths. Half of all melanomas are found in people under age 57. About 1 of every 30,000 girls aged 15 to 19 will develop melanoma. For boys of this age, the rate is about 1 of every 15,000. In the USA, about 62,000 new melanomas are diagnosed each year, with around 8,000 deaths. The number of new melanomas diagnosed in the United States is increasing. Among white men and women in the United States, incidence rates for melanoma increased sharply at about 6% per year from 1973 until the early 1980s. Since 1981, however, the rate of increase slowed to little less than 3% per year. Since 1973, the mortality rate for melanoma has increased by 50%. More recently, the death rate from melanoma has leveled off for

men and dropped slightly in women. The risk of melanoma is about 20 times higher for whites than for African Americans.

Melanoma Diagnosis

[0078] Excisional biopsy is the preferred diagnostic method but other types of skin biopsy can also be used including incisional biopsy, shave biopsy and punch biopsy. Metastatic melanoma may not be found until long after the original melanoma was removed from the skin. Metastatic melanoma can be diagnosed using a number of methods including fine needle aspiration biopsy, surgical lymph node biopsy and sentinel lymph node mapping and biopsy. Imaging tests such as a chest x-ray, computed tomography (CT), magnetic resonance imaging (MRI), positron emission tomography (PET) and nuclear bone scans can also be used.

Melanoma Staging

[0079] Melanoma is staged using the American Joint Committee on Cancer (AJCC) TNM system—Stage 0-Stage IV. The thickness of the melanoma is measured using the Breslow measurement.

Melanoma Treatment

[0080] Thin melanomas can be completely cured by excision. If the melanoma is on a finger or toe, treatment may involve amputation of the digit. If the melanoma has spread to the lymph nodes, lymph node dissection may be required.

[0081] No current treatment is usually able to cure stage IV melanoma. Although chemotherapy is usually not as effective in melanoma as in some other types of cancer, it may relieve symptoms or extend survival of some patients with stage IV melanoma. Chemotherapy drugs often used to treat melanoma include dacarbazine, carmustine, cisplatin, vinblastine and temozolomide. Recent studies have found that biochemotherapy, combining several chemotherapy drugs with 1 or more immunotherapy drugs may be more effective than a single chemotherapy drug alone. Immunotherapy drugs include interferon-alpha and/or interleukin-2. Both drugs can help shrink metastatic (stage III and IV) melanomas in about 10% to 20% of patients. Interferon-alpha2b given to patients with stage III melanoma following surgery may delay the recurrence of melanoma. Isolated limb perfusion, using Melphalan, is an experimental type of chemotherapy sometimes used to treat metastatic melanomas confined to the arms or legs. Radiation therapy may be used to treat recurrent melanoma and is used as palliation of metastases to the bone and brain.

[0082] A person who has already had melanoma has an increased risk of developing melanoma again. In one study, about 11% of people with melanoma developed a second one within 5 years. And those that developed a second melanoma had a 30% chance of developing a third one in 5 years.

Melanoma Survival by Stage

[0083]

Stage	5-year relative survival rate	10-year relative survival rate
0	97%	—
I	90-95%	80%
IIA	78%	64%

-continued

Stage	5-year relative survival rate	10-year relative survival rate
IIB	63-67%	51-54%
IIC	45%	32%
IIIA	63-70%	57-63%
IIIB	46-53%	38%
IIIC	28%	15-25%
IV	18%	14%

Neuroblastoma

[0084] Neuroblastoma occurs in infants and young children and is rarely found in children older than 10 years. Neuroblastoma is by far the most common cancer in infants and the fourth most common type of cancer in children. There are approximately 650 new cases of neuroblastoma each year in the USA.

Neuroblastoma Diagnosis

[0085] In about 90% of cases, neuroblastoma cells produce enough catecholamines to be detected by blood or urine tests. The 2 catecholamine metabolites most often measured are: homovanillic acid (HVA) and vanillylmandelic acid (VMA). Imaging tests such as a chest x-ray, computed tomography (CT), magnetic resonance imaging (MRI), ultrasound, positron emission tomography (PET), meta-iodobenzylguanidine (MIBG) scan and bone scan can also be performed. A biopsy is needed to confirm the diagnosis. A bone marrow aspiration and biopsy can be performed to see if the disease has spread to the bone marrow (which it does in about half of patients).

[0086] In as many as 6 or 7 of 10 cases, the disease is not diagnosed until it has already metastasised.

Neuroblastoma Staging

[0087] Neuroblastoma is staged using the International Neuroblastoma Staging System (INSS)—Stage 1-Stage 4. Prognostic markers such as age, tumour grade, DNA ploidy, MYCN gene amplifications, cytogenetics, neurotrophin receptors and serum markers are used to calculate a child's chance of cure. These prognostic markers are combined with the stage of the disease to form three risk groups—low, intermediate and high. Low-risk children have a 5-year survival of around 95%. Intermediate-risk children's 5-year survival is around 85% to 90%. The 5-year survival of high-risk children is around 30%.

Neuroblastoma Treatment

[0088] For children at low risk, surgery can often remove the entire tumour and bring about a complete cure. Chemotherapy is given if less than half the tumour can be surgically removed.

[0089] For children at intermediate risk, chemotherapy is usually given before or after surgery to control the disease. Chemotherapeutic agents used include cyclophosphamide, ifosfamide, cisplatin, carboplatin, vincristine, doxorubicin, etoposide, teniposide, topotecan. A second surgery or radiation therapy may also be required. Studies show that in some cases the use of radiation combined with chemotherapy produces better results than chemotherapy alone.

[0090] For children at high risk, when the cancer has spread too far to be completely removed by surgery, very intensive chemotherapy along with blood-forming stem cell transplant (bone marrow or peripheral blood) is used. Some experts estimate that this technique results in a cure in about 25% of children with neuroblastoma who would not be cured with the more standard treatments. Some recent studies offer hope that improved bone marrow transplant (BMT) or peripheral blood stem cell transplant (PBSC) methods may increase the rate to 30% to 60%. Surgery and/or radiation may be part of this treatment regimen. Radiation therapy can help relieve pain caused by advanced neuroblastoma. A highly radioactive form of MIBG is also being used for treating some patients with advanced neuroblastoma. Biologic agents such as 13-cis retinoic acid are often given for 6 months after therapy is completed to reduce the risk of recurrence.

Osteosarcoma

[0091] Osteosarcoma is the most common bone cancer in children, adolescents and young adults (accounting for approximately 5% of childhood tumours) but it is still a rare disease with an annual incidence of 2-3 per million in the general population. There are about 900 new cases of osteosarcoma diagnosed in the United States each year (about 400 of which occur in children and adolescents younger than 20 years old), with approximately 300 deaths each year. Osteosarcoma is a primary malignant tumour of the appendicular skeleton that is characterized by the direct formation of bone or osteoid tissue by the tumour cells. In children and adolescents, more than 50% of these tumours arise from the bones around the knee. Many people with osteosarcoma can be cured but not all and the price of cure even with the most modern treatments is high.

Osteosarcoma Diagnosis

[0092] Diagnostic methods for osteosarcoma include an X-ray, bone scan, CT scan, PET scan and MRI of the affected area. A CT scan of the chest is also conducted to see if the cancer has spread to the lungs. Blood tests can be used to detect serum levels of alkaline phosphatase and/or LDH, which are increased in a considerable number of osteosarcoma patients, although serum levels do not correlate reliably with disease extent. The diagnosis of osteosarcoma must be verified histologically with a core needle biopsy or open biopsy. Micrometastatic disease is present at diagnosis in 80-90% of patients but undetectable with any of present tests.

Osteosarcoma Staging

[0093] There are two staging systems for osteosarcoma: the Enneking system where low-grade tumours are stage I, high-grade tumours are stage II, and metastatic tumours (regardless of grade) are stage III and the American Joint Commission on Cancer (AJCC) system which stages osteosarcoma from IA to IVB.

[0094] There are essentially 2 categories of patients: those who present without clinically detectable metastatic disease (localized osteosarcoma) and the 15-20% of patients who present with clinically detectable metastatic disease (metastatic osteosarcoma). 85% to 90% of metastatic disease is in the lungs.

[0095] Osteosarcoma has one of the lowest survival rates for pediatric cancer. The overall 5-year survival rate for patients with non-metastatic osteosarcoma is over 70%. The

5-year survival rate for patients whose cancers have already metastasised at the time of their diagnosis is about 30%.

Osteosarcoma Treatment

[0096] Once osteosarcoma has been diagnosed, the correct treatment needs to be selected. Successful treatment generally requires the combination of effective systemic chemotherapy and complete resection (amputation, limb preservation, or rotationplasty) of all clinically detectable disease (including resection of all overt metastatic disease). Protective weight bearing is recommended for patients with tumours of weight-bearing bones to prevent pathological fractures that could preclude limb-preserving surgery.

[0097] At least 80% of patients with localized osteosarcoma treated with surgery alone will develop metastatic disease. Randomized clinical trials have established that adjuvant chemotherapy is effective in preventing relapse or recurrence in patients with localized resectable primary tumours. The chemotherapeutic agents used include high-dose methotrexate, doxorubicin, cisplatin, high-dose ifosfamide, etoposide, carboplatin, cyclophosphamide, actinomycin D and bleomycin. Bone-seeking radioactive chemicals are sometimes used to treat osteosarcoma. Samarium-153 may be given in addition to external beam radiation therapy.

[0098] There is no difference in overall survival (OS) between patients initially treated by amputation and those treated with a limb-sparing procedure. In general, more than 80% of patients with extremity osteosarcoma can be treated by a limb-sparing operation and do not require amputation. Complications of limb-salvage surgery include infection and grafts or rods that become loose or broken. Limb-salvage surgery patients may need more surgery during the following 5 years, and some may eventually need an amputation. Limb length inequality is also a major potential problem for young children. Treatment options include extensible prostheses, amputation, and rotationplasty for these children.

[0099] Most recurrences of osteosarcoma develop within 2 to 3 years after treatment completion. Fewer than 30% of patients with localized resectable primary tumours treated with surgery alone can be expected to survive free of relapse. Recurrence of osteosarcoma is most often in the lung.

[0100] The ability to achieve a complete resection of recurrent disease is the most important prognostic factor at first relapse, with a 5-year survival rate of 20% to 45% following complete resection of metastatic pulmonary tumours and 20% following complete resection of metastases at other sites. Repeated resections of pulmonary recurrences can lead to extended disease control and possibly cure for some patients. Survival for patients with unresectable metastatic disease is less than 5%. Resection of metastatic disease followed by observation alone results in low overall and disease-free survival.

Ovarian Cancer

[0101] Ovarian cancer accounts for about 1.9% of cancer cases globally and around 1.8% of deaths. Global incidence of ovarian cancer is around 205,000, predominantly in post-menopausal women in developed countries, with around 125,000 deaths. About 85% to 90% of ovarian cancers are epithelial ovarian carcinomas. About 5% of ovarian cancers are germ cell tumours and a smaller percentage are stromal tumours. Ovarian cancer is the eighth most common cancer among women. In the USA, about 20,200 new cases of ova-

rian cancer are diagnosed each year and it accounts for about 3% of all cancers in women. The risk of developing and dying from ovarian cancer is higher for white women than black women. Around two-thirds of women with ovarian cancer are 55 or older. Ovarian cancer ranks fifth in cancer deaths among women in the USA, accounting for more deaths than any other cancer of the female reproductive system. There are around 15,300 deaths in the USA from ovarian cancer each year. It has been estimated that approximately US\$2.2 billion is spent in the USA each year on treating ovarian cancer.

Ovarian Cancer Diagnosis

[0102] It is currently difficult to diagnose ovarian cancer at an early stage. Imaging tests such as ultrasound, computed tomography and magnetic resonance imaging can confirm whether a pelvic mass is present. Blood tests, including a CA-125 test and a laparoscopy are performed. Ovarian cancer is then confirmed by biopsy.

Ovarian Cancer Staging

[0103] Ovarian cancer is staged using the American Joint Committee on Cancer (AJCC) TNM system—stage I-IV. The FIGO (International Federation of Gynecology and Obstetrics) system is also used. Ovarian cancers are also given a grade from 1-3. About 76% of women with ovarian cancer survive 1 year after diagnosis, and 45% survive longer than 5 years after diagnosis. If diagnosed and treated while the cancer has not spread outside the ovary, the 5-year survival rate is 94%. However, only 19% of all ovarian cancers are found at this early stage.

Ovarian Cancer Treatment

[0104] Surgery for ovarian cancer includes hysterectomy, bilateral salpingectomy, bilateral oophorectomy and omentectomy. Debulking is performed in women in whom the cancer has spread widely throughout their abdomen.

[0105] Intraperitoneal (IP) chemotherapy using a combination therapy using a platinum compound, such as cisplatin or carboplatin, and a taxane, such as paclitaxel or docetaxel, is the standard approach. Tumour recurrence is sometimes treated with additional cycles of a platinum compound and/or a taxane. In other cases, recurrence is treated with other drugs, such as topotecan, anthracyclines such as doxorubicin (Adriamycin) and liposomal doxorubicin (Doxil), gemcitabine, cyclophosphamide, vinorelbine (Navelbine), hexamethylmelamine, ifosfamide, and etoposide. Resistance to currently-available chemotherapeutic agents is a major problem. Although complete clinical response is achieved in 75% of patients after initial treatment, most will develop recurrent disease and require re-treatment.

[0106] External beam radiation therapy can also sometimes be used.

Ovarian Cancer 5-Year Survival by Stage:

[0107] For IA is 92.7%, for stage IB is 85.4%, for stage IC is 84.7%, for stage IIA is 78.6%, for stage IIB is 72.4%, for stage IIC is 64.4%, for stage IIIA is 50.8%, for stage IIIB is 42.4%, for stage IIIC is 31.5% and for stage IV is 17.5%.

Pancreatic Cancer

[0108] Pancreatic cancer is a very difficult cancer to detect and the prognosis for patients is usually very poor. The num-

ber of new cases and deaths per year is almost equal. Global incidence of pancreatic cancer is approximately 230,000 cases (about 2% of all cancer cases), with about 225,000 deaths (3.4% of cancer deaths) per year. It is much more prevalent in the developed world. In the USA, there are about 34,000 new cases per year, with about 32,000 deaths. It has been estimated that approximately US\$1.5 billion is spent in the USA each year on treating pancreatic cancer.

Pancreatic Cancer Diagnosis

[0109] Pancreatic cancer is very difficult to detect and very few pancreatic cancers are found early. Patients usually have no symptoms until the cancer has spread to other organs. There are currently no blood tests or easily available screening tests that can accurately detect early cancers of the pancreas. An endoscopic ultrasound followed by a biopsy is the best way to diagnose pancreatic cancer. Other detection methods include CT, CT-guided needle biopsy, PET, ultrasonography and MRI. Blood levels of CA 19-9 and carcinoembryonic antigen (CEA) may be elevated but by the time blood levels are high enough to be detected, the cancer is no longer in its early stages.

Pancreatic Cancer Staging

[0110] Pancreatic cancer has four stages, stage I to stage IV according to the American Joint Committee on Cancer (AJCC) TNM system. Pancreatic cancer is also divided into resectable, locally advanced (unresectable) and metastatic cancer. For patients with advanced cancers, the overall survival rate is <1% at 5 years with most patients dying within 1 year.

Pancreatic Cancer Treatment

[0111] Surgery is the only method of curing pancreatic cancer. About 10% of pancreatic cancers are contained entirely within the pancreas at the time of diagnosis and attempts to remove the entire cancer by surgery may be successful in some of these patients. The 5-year survival for those undergoing surgery with the intent of completely removing the cancer is about 20%. Potentially curative surgery, usually by pancreaticoduodenectomy (Whipple procedure), is used when it may be possible to remove all of the cancer. Palliative surgery may be performed if the tumour is too widespread to be completely removed. Removing only part of the cancer does not allow patients to live longer. Pancreatic cancer surgery is difficult to perform with a high likelihood of complications.

[0112] External beam radiation therapy combined with chemotherapy can be given before or after surgery and can also be given to patients whose tumours are too widespread to be removed by surgery. The main chemotherapeutic agents which are used are gemcitabine and 5-fluorouracil. Targeted therapy using drugs such as erlotinib and cetuximab may be of benefit to patients with advanced pancreatic cancer.

Prostate Cancer

[0113] Prostate cancer is the third most common cancer in the world amongst men and it accounts for 5.4% of all cancer cases globally and 3.3% of cancer-related deaths. Global incidence of prostate cancer is around 680,000 cases, with about 221,000 deaths. In the USA, prostate cancer is the most common cancer, other than skin cancers, in American men. About 234,460 new cases of prostate cancer are diagnosed in

the USA each year. About 1 man in 6 will be diagnosed with prostate cancer during his lifetime, but only 1 in 34 will die of it. A little over 1.8 million men in the USA are survivors of prostate cancer. The risk of developing prostate cancer rises significantly with age and 60% of cases occur in men over the age of 70. Prostate cancer is the second leading cause of cancer death in American men. Around 27,350 men in the USA die of prostate cancer each year. Prostate cancer accounts for about 10% of cancer-related deaths in men. Modern methods of detection and treatment mean that prostate cancers are now found earlier and treated more effectively. This has led to a yearly drop in death rates of about 3.5% in recent years. Prostate cancer is most common in North America and northwestern Europe. It is less common in Asia, Africa, Central America, and South America. It has been estimated that approximately US\$8.0 billion is spent in the USA each year on treating prostate cancer.

Prostate Cancer Diagnosis

[0114] Prostate cancer can often be found early by testing the amount of prostate-specific antigen (PSA) in the blood. A digital rectal exam (DRE) can also be performed. However, there are potential problems with the current screening methods. Neither the PSA test nor the DRE is 100% accurate. A core needle biopsy is the main method used to diagnose prostate cancer. A transrectal ultrasound (TRUS) may be used during a prostate biopsy.

Prostate Cancer Staging

[0115] Prostate cancers are graded according to the Gleason system, graded from 1-5, which results in the Gleason score, from 1-10. Prostate cancer is staged using the American Joint Committee on Cancer (AJCC) TNM system and combined with the Gleason score to give stages from I-IV. Ninety one percent of all prostate cancers are found in the local and regional stages; the 5-year relative survival rate for these men is nearly 100%. The 5-year relative survival rate for men whose prostate cancers have already spread to distant parts of the body at the time of diagnosis is about 34%.

Prostate Cancer Treatment

[0116] Because prostate cancer often grows very slowly, some men never have treatment and expectant management is recommended. If treatment is required and the cancer is not thought to have spread outside of the gland, a radical prostatectomy can be performed. Transurethral resection of the prostate (TURP) can be performed to relieve symptoms but not to cure prostate cancer.

[0117] External beam radiation therapy (three-dimensional conformal radiation therapy (3DCRT), intensity modulated radiation therapy (IMRT) or conformal proton beam radiation therapy) or brachytherapy can also be used as treatment.

[0118] Cryosurgery is sometimes used to treat localized prostate cancer but as not much is known about the long-term effectiveness of cryosurgery, it is not routinely used as a first treatment for prostate cancer. It can be used for recurrent cancer after other treatments.

[0119] Androgen deprivation therapy (ADT) (orchiectomy or luteinizing hormone-releasing hormone (LHRH) analogs or antagonists) can be used to shrink prostate cancers or make them grow more slowly.

[0120] Chemotherapy is sometimes used if prostate cancer has spread outside of the prostate gland and is hormone

therapy resistant. Chemotherapeutic agents include docetaxel, prednisone, doxorubicin, etoposide, vinblastine, paclitaxel, carboplatin, estramustine, vinorelbine. Like hormone therapy, chemotherapy is unlikely to result in a cure.

Renal Cell Cancer

[0121] The incidence of kidney cancer is much higher in developed countries, being the sixth most common form of cancer in Western Europe. Kidney cancer accounts for about 1.9% of cancer cases globally and 1.5% of deaths. Global incidence of kidney cancer is around 208,000 cases, with over 100,000 deaths. Around 38,900 new cases of kidney cancer are diagnosed in the USA each year, with around 12,800 deaths. It is very uncommon under age 45, and its incidence is highest between the ages of 55 and 84. The rate of people developing kidney cancer has been increasing at about 1.5% per year but the death rate has not been increasing. Renal cell carcinoma accounts for more than 90% of malignant kidney tumours. It has been estimated that approximately US\$1.9 billion is spent in the USA each year on treating kidney cancer.

Renal Cell Cancer Diagnosis

[0122] Many renal cell cancers are found at a late stage; they can become quite large without causing any pain or discomfort. Because the kidney is deep inside the body, small renal cell tumours cannot be seen or felt during a physical exam. There are no simple tests that can detect renal cell cancer early. About 25% of patients with renal cell carcinoma will already have metastatic spread of their cancer when they are diagnosed. Imaging tests such as computed tomography (CT) scans and magnetic resonance imaging (MRI) can find small renal cell carcinomas. However, these imaging tests are relatively expensive and cannot always distinguish benign tumours from small renal cell carcinomas.

[0123] Renal cell cancer can often be diagnosed without the need for a biopsy using a CT scan, MRI, ultrasound, positron emission tomography (PET) scan, intravenous pyelogram (IVP) and/or angiography. Fine needle aspiration biopsy may however be valuable when imaging results are not conclusive enough to warrant removing a kidney.

Renal Cell Cancer Staging

[0124] Renal cell cancers are usually graded on a scale of 1-4. Renal cell cancer is also staged using the American Joint Committee on Cancer (AJCC) TNM system—stage I-IV. The University of California Los Angeles Integrated Staging System can also be used, which divides patients without any tumour spread into three groups—low risk, intermediate risk and high risk. The 5-year cancer-specific survival for the low-risk group is 91%, for the intermediate-risk group is 80%, and for the high-risk group is 55%. Patients with tumour spread are also divided into three groups—low, intermediate and high risk. The 5-year cancer-specific survival for the low-risk group is 32%, for the intermediate-risk group 20% and for the high-risk group 0%.

Renal Cell Cancer Treatment

[0125] Surgery by radical nephrectomy (and sometimes regional lymphadenectomy), partial nephrectomy or laparoscopic nephrectomy is the main treatment for renal cell carcinoma. External beam radiation therapy is sometimes used as the main treatment for renal cell cancer if a person's gen-

eral health is too poor to undergo surgery. Radiation therapy can also be used to palliate symptoms of renal cell cancer. Unfortunately, renal cell carcinomas are not very sensitive to radiation. Using radiation therapy before or after removing the cancer is not routinely recommended because studies have shown no improvement in survival rates.

[0126] Renal cell cancers are very resistant to present forms of chemotherapy, and there is no standard way to treat it with drugs. Some drugs, such as vinblastine, floxuridine, and 5-fluorouracil (5-FU) are mildly effective. A combination of 5-FU and gemcitabine has benefited some patients. A 5-FU-like drug, capecitabine, may also have some benefit.

[0127] Cytokines (interleukin-2 (IL-2) and interferon-alpha) have become one of the standard treatments for metastatic renal cell carcinoma. These cause the cancers to shrink to less than half their original size in about 10% to 20% of patients. Patients who respond to IL-2 tend to have lasting responses. Recent research with a combination of IL-2, interferon, and chemotherapy (using 5-fluorouracil) is also promising and may offer a better chance of partial or complete remission. Cytokine therapy does have severe side effects however.

[0128] Sorafenib (Nexavar) has been shown to slow the progression of the cancer in patients with advanced disease. It acts by blocking both angiogenesis and growth-stimulating molecules in the cancer cell. Sunitinib (Sutent) is another drug that attacks both blood vessel growth and other targets that stimulate cancer cell growth. Promising results have also been seen in studies of this drug with tumours shrinking in about one-third of patients and tumours staying about the same size in another third. Bevacizumab (Avastin) is an angiogenesis inhibitor. This drug is already approved for use against other cancer types and recent studies have shown it may also be effective against renal cell cancer.

Renal Cell Cancer Survival by Stage

[0129]

T stage cancer	5/10-year cancer-specific survival
T1	95%/91%
T2	80%/70%
T3a	66%/53%
T3b	52%/43%
T3c	43%/42%

Retinoblastoma

[0130] Retinoblastoma is the only common type of eye cancer in children. About 4 out of every million children under age 15, or about 250 children, are diagnosed with retinoblastoma each year in the USA. The rate is higher in infants and very young children. About 60% to 75% of children with retinoblastoma have a tumour in only one eye. In about 25% to 40% of cases, both eyes are affected. When both eyes are affected, it is always caused by a gene mutation present at birth.

Retinoblastoma Diagnosis

[0131] Most retinoblastomas are found and treated before they have spread outside the globe of the eye. The most important gene involved in retinoblastoma is the tumour sup-

pressor gene known as Rb. One third of retinoblastoma patients have hereditary retinoblastoma with a germline mutation of the Rb gene which can be detected by testing DNA of blood cells. In the remaining two thirds of retinoblastoma patients, the Rb gene mutation happens during their early life and occurs only in one cell in one eye. An ophthalmologist can diagnose retinoblastoma by examining the retina. Imaging tests such as ultrasound and magnetic resonance imaging (MRI) can also be used.

Retinoblastoma Staging

[0132] The Reese-Ellsworth staging system is used to classify cases of retinoblastoma that have not spread beyond the eye into 5 groups. Well over 90% of children with retinoblastoma that has not spread beyond the eye are cured. The major challenge is preserving their vision and the groups help to determine the likelihood of preserving vision and controlling the tumour. Staging is sometimes based upon the ABC Classification—groups A-E.

Retinoblastoma Treatment

[0133] When tumour occurs in only one eye, it tends to get quite large before it is diagnosed. Vision has often already been destroyed, with no hope of restoration. The usual treatment in this case is enucleation. When retinoblastoma occurs in both eyes, enucleation of both eyes would automatically result in complete blindness. This is the safest treatment if neither eye has useful vision but if there is any chance of preserving useful vision in one or both eyes by using more conservative treatments, these are considered.

[0134] Radiation therapy (external beam radiation therapy or brachytherapy), compared with surgery, has the advantage of possibly preserving vision in the eye. Unfortunately, radiation also has several potential disadvantages. Radiation therapy can damage surrounding normal tissue, which may eventually lead to cataracts and damage to the retina, which would reduce vision. Photocoagulation, thermotherapy or cryotherapy can be used as treatment for small tumours. Chemoreduction may be used to shrink small tumours, which can then be treated more effectively by photocoagulation, cryotherapy, thermotherapy, or brachytherapy to completely kill the tumour.

[0135] Chemotherapy is often used to treat children whose retinoblastoma has spread beyond the eye. Unfortunately, retinoblastomas tend to become resistant to chemotherapy. Retinoblastoma metastases often shrink for a period of time, but usually start growing again within a year. Chemotherapeutic agents used include carboplatin, cisplatin, vincristine, etoposide, teniposide, cyclophosphamide and doxorubicin.

[0136] A group 1 retinoblastoma is very likely to be controlled with chemotherapy, photocoagulation, cryotherapy, thermotherapy, brachytherapy, or external beam radiation therapy while still preserving vision in the eye.

[0137] A group 4 or especially group 5 retinoblastoma is very unlikely to be controlled with chemotherapy or radiation therapy, and even if it were, the vision in the eye would be very poor. Enucleation is usually performed in these cases.

[0138] When the cancer has spread outside of the orbit to the bones and bone marrow, the chances of cure using conventional chemotherapy and surgery are very poor; in these cases, the use of higher doses of chemotherapy with an autologous stem cell transplant can be successful, and more

than 50% of the children can be cured. When the cancer has spread to the brain, the chances of cure even using stem cell transplant are very low.

Therapeutic Challenges

[0139] The major challenges in treatment of the above mentioned cancers are to improve early detection rates, to find new non-invasive markers that can be used to follow disease progression and identify relapse, and to find improved and less toxic therapies, especially for more advanced disease where 5 year survival is still poor. There is a great need to identify targets which are more specific to the cancer cells, e.g. ones which are expressed on the surface of the tumour cells so that they can be attacked by promising new approaches like immunotherapeutics and targeted toxins.

SUMMARY OF THE INVENTION

[0140] The present invention provides methods and compositions for:

- [0141]** therapy of, or
- [0142]** drug development for, or
- [0143]** screening, diagnosis and prognosis for, or
- [0144]** monitoring the effectiveness of treatment for

B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer and retinoblastoma (including patient stratification).

[0145] We have used mass spectrometry to identify peptides generated by gel electrophoresis or tagging with iTRAQ reagents and tryptic digest of membrane proteins extracted from lymphoid, breast, cervical, colorectal, gastric, brain, liver, lung, skin, neuronal, osteoblast, ovarian, pancreatic, prostate, kidney and eye cancer tissue samples. Peptide sequences were compared to existing protein and cDNA databases and the corresponding gene sequences identified. The proteins of the invention have not been previously reported to originate from lymphocytic, breast, cervical, colorectal, gastric, brain, liver, lung, skin, neuronal, osteoblast, ovarian, pancreatic, prostate, kidney or eye cancer cell membranes and represent proteins of new therapeutic and/or diagnostic value.

[0146] Thus, a first aspect of the invention provides methods of treating B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer and retinoblastoma, comprising administering to a patient a therapeutically effective amount of a compound that modulates (e.g., upregulates or downregulates) or complements the expression or the biological activity (or both) of one or more of the proteins of the invention in patients having B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma, in order to ((a) prevent the onset or development of B-cell non-Hodgkin's

lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma; (b) prevent the progression of B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma; or (c) ameliorate the symptoms of B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma.

[0147] Thus according to a second aspect of the invention we provide a method of detecting, diagnosing and/or screening for or monitoring the progression of B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma or of monitoring the effect of an anti-B-cell non-Hodgkin's lymphoma, anti-breast cancer, anti-cervical cancer, anti-colorectal cancer, anti-gastric cancer, anti-glioblastoma, anti-hepatocellular carcinoma, anti-lung cancer, anti-lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), anti-melanoma, anti-neuroblastoma, anti-osteosarcoma, anti-ovarian cancer, anti-pancreatic cancer, anti-prostate cancer, anti-renal cell cancer or anti-retinoblastoma drug or therapy in a subject which comprises detecting the presence or level of the proteins of the invention, or one or more fragments thereof, or the presence or level of nucleic acid encoding the proteins of the invention or the presence or level of the activity of the proteins of the invention or which comprises detecting a change in the level thereof in said subject.

[0148] According to a third aspect of the invention we provide a method of detecting, diagnosing and/or screening for B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma in a candidate subject which comprises detecting the presence of the proteins of the invention, or one or more fragments thereof, or the presence of nucleic acid encoding the proteins of the invention or the presence of the activity of the proteins of the invention in said candidate subject, in which either (a) the presence of an elevated level of the proteins of the invention or said one or more fragments thereof or an elevated level of nucleic acid encoding the proteins of the invention or the presence of an elevated level of the activity of the proteins of the invention in the candidate subject as compared with the level in a healthy subject or (b) the presence of a detectable level of the proteins of the inven-

tion or said one or more fragments thereof or a detectable level of nucleic acid encoding the proteins of the invention or the presence of a detectable level of the activity of the proteins of the invention in the candidate subject as compared with a corresponding undetectable level in a healthy subject indicates the presence of B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma in said subject.

[0149] According to a fourth aspect of the invention we provide a method of monitoring the progression of B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma in a subject or of monitoring the effect of an anti-B-cell non-Hodgkin's lymphoma, anti-breast cancer, anti-cervical cancer, anti-colorectal cancer, anti-gastric cancer, anti-glioblastoma, anti-hepatocellular carcinoma, anti-lung cancer, anti-lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), anti-melanoma, anti-neuroblastoma, anti-osteosarcoma, anti-ovarian cancer, anti-pancreatic cancer, anti-prostate cancer, anti-renal cell cancer or anti-retinoblastoma drug or therapy which comprises detecting the presence of the proteins of the invention, or one or more fragments thereof, or the presence of nucleic acid encoding the proteins of the invention or the presence of the activity of the proteins of the invention in said candidate subject at a first time point and at a later time point, the presence of an elevated or lowered level of the proteins of the invention or said one or more fragments thereof or an elevated or lowered level of nucleic acid encoding the proteins of the invention or the presence of an elevated or lowered level of the activity of the proteins of the invention in the subject at the later time point as compared with the level in the subject at said first time point, indicating the progression or regression of B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma or indicating the effect or non-effect of an anti-B-cell non-Hodgkin's lymphoma, anti-breast cancer, anti-cervical cancer, anti-colorectal cancer, anti-gastric cancer, anti-glioblastoma, anti-hepatocellular carcinoma, anti-lung cancer, anti-lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), anti-melanoma, anti-neuroblastoma, anti-osteosarcoma, anti-ovarian cancer, anti-pancreatic cancer, anti-prostate cancer, anti-renal cell cancer or anti-retinoblastoma drug or therapy in said subject.

[0150] The presence of the proteins of the invention, or one or more fragments thereof, or the presence of nucleic acid encoding the proteins of the invention or the presence of the activity of the proteins of the invention may, for example, be detected by analysis of a biological sample obtained from said subject.

[0151] The method of invention may typically include the step of obtaining a biological sample for analysis from said subject. In one or more aspects the methods of the invention do not include the step of obtaining a biological sample from a subject.

[0152] In one aspect of the invention provides monoclonal and polyclonal antibodies or other affinity reagents such as an Affibodies capable of immunospecific binding to the proteins of the invention and compositions comprising same, for example for use in treatment or prophylaxis, such for the treatment or prophylaxis of cancer, particularly a cancer described herein.

[0153] The biological sample used can be from any source such as a serum sample or a tissue sample, e.g. lymphoid, breast, cervical, colorectal, gastric, brain, liver, lung, skin, neuronal, osteoblast, ovarian, pancreatic, prostate, kidney or eye tissue. For instance, when looking for evidence of metastatic breast cancer, cervical cancer, colorectal cancer, gastric cancer, hepatocellular carcinoma, lung cancer, melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer and retinoblastoma, one would look at major sites of breast cancer, cervical cancer, colorectal cancer, gastric cancer, hepatocellular carcinoma, lung cancer, melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer and retinoblastoma metastasis, e.g. the liver, the lungs and bones for breast cancer; the bladder and the rectum for cervical cancer; the liver, the peritoneal cavity, the pelvis, the retroperitoneum and the lungs for colorectal cancer; the liver, the lungs, the brain and bones for gastric cancer; the lungs and bones for hepatocellular carcinoma; the brain, the liver, the bones and adrenal glands for lung cancer; the lungs, the brain and bones for melanoma; the liver and bones for neuroblastoma; the lungs and other bones for osteosarcoma; the abdomen for ovarian cancer; the liver for pancreatic cancer; the bladder, the rectum and bones for prostate cancer; the lungs, the liver and bones for renal cell cancer and the brain and bones for retinoblastoma.

[0154] Alternatively the presence of the proteins of the invention, or one or more fragments thereof, or the presence of nucleic acid encoding the proteins of the invention or the presence of the activity of the proteins of the invention may be detected by analysis *in situ*.

[0155] In certain embodiments, methods of diagnosis described herein may be at least partly, or wholly, performed *in vitro*.

[0156] Suitably the presence of the proteins of the invention, or one or more fragments thereof, or the presence of nucleic acid encoding the proteins of the invention or the presence of the activity of the proteins of the invention is detected quantitatively.

[0157] For example, quantitatively detecting may comprise:

[0158] (a) contacting a biological sample with an affinity reagent that is specific for the proteins of the invention, said affinity reagent optionally being conjugated to a detectable label; and

[0159] (b) detecting whether binding has occurred between the affinity reagent and at least one species in the sample, said detection being performed either directly or indirectly.

[0160] Alternatively the presence of the proteins of the invention, or one or more fragments thereof, or the presence of nucleic acid encoding the proteins of the invention or the

presence of the activity of the proteins of the invention may be detected quantitatively by means involving use of an imaging technology.

[0161] In another embodiment, the method of the invention involves use of immunohistochemistry on tissue sections in order to determine the presence of the proteins of the invention, or one or more fragments thereof, or the presence of nucleic acid encoding the proteins of the invention or the presence of the activity of the proteins of the invention, and thereby to localise B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma cells.

[0162] In one embodiment the presence of the proteins of the invention or one or more epitope-containing fragments thereof is detected, for example using an affinity reagent capable of specific binding to the proteins of the invention or one or more fragments thereof, such as an antibody.

[0163] In another embodiment the activity of the proteins of the invention is detected.

[0164] According to another aspect of the invention there is provided a method of detecting, diagnosing and/or screening for or monitoring the progression of B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma or of monitoring the effect of an anti-B-cell non-Hodgkin's lymphoma, anti-breast cancer, anti-cervical cancer, anti-colorectal cancer, anti-gastric cancer, anti-glioblastoma, anti-hepatocellular carcinoma, anti-lung cancer, anti-lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), anti-melanoma, anti-neuroblastoma, anti-osteosarcoma, anti-ovarian cancer, anti-pancreatic cancer, anti-prostate cancer, anti-renal cell cancer or anti-retinoblastoma drug or therapy in a subject which comprises detecting the presence or level of antibodies capable of immunospecific binding to the proteins of the invention, or one or more epitope-containing fragments thereof or which comprises detecting a change in the level thereof in said subject.

[0165] According to another aspect of the invention there is also provided a method of detecting, diagnosing and/or screening for B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma in a subject which comprises detecting the presence of antibodies capable of immunospecific binding to the proteins of the invention, or one or more epitope-containing fragments thereof in said subject, in which (a) the presence of an elevated level of antibodies capable of immunospecific binding to the proteins of the invention or said one or more epitope-containing fragments thereof in said subject as compared with the level in a healthy subject or (b) the presence of a detectable level of antibodies capable of immunospecific binding to the proteins of the invention or said one or more epitope-containing frag-

ments thereof in said subject as compared with a corresponding undetectable level in a healthy subject indicates the presence of B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma in said subject.

[0166] One particular method of detecting, diagnosing and/or screening for B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma comprises:

[0167] (a) bringing into contact with a biological sample to be tested the proteins of the invention, or one or more epitope-containing fragments thereof; and

[0168] (b) detecting the presence of antibodies in the subject capable of immunospecific binding to the proteins of the invention, or one or more epitope-containing fragments thereof.

[0169] According to another aspect of the invention there is provided a method of monitoring the progression of B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma or of monitoring the effect of an anti-B-cell non-Hodgkin's lymphoma, anti-breast cancer, anti-cervical cancer, anti-colorectal cancer, anti-gastric cancer, anti-glioblastoma, anti-hepatocellular carcinoma, anti-lung cancer, anti-lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), anti-melanoma, anti-neuroblastoma, anti-osteosarcoma, anti-ovarian cancer, anti-pancreatic cancer, anti-prostate cancer, anti-renal cell cancer or anti-retinoblastoma drug or therapy in a subject which comprises detecting the presence of antibodies capable of immunospecific binding to the proteins of the invention, or one or more epitope-containing fragments thereof in said subject at a first time point and at a later time point, the presence of an elevated or lowered level of antibodies capable of immunospecific binding to the proteins of the invention, or one or more epitope-containing fragments thereof in said subject at the later time point as compared with the level in said subject at said first time point, indicating the progression or regression of B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma or the effect or non-effect of an anti-B-cell non-Hodgkin's lymphoma, anti-breast cancer, anti-cervical cancer, anti-colorectal cancer, anti-gastric cancer, anti-glioblastoma, anti-hepatocellular carcinoma, anti-lung cancer, anti-lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), anti-melanoma, anti-neuroblastoma, anti-osteosarcoma, anti-ovarian cancer, anti-pancreatic cancer, anti-

prostate cancer, anti-renal cell cancer or anti-retinoblastoma drug or therapy in said subject.

[0170] The presence of antibodies capable of immunospecific binding to the proteins of the invention, or one or more epitope-containing fragments thereof is typically detected by analysis of a biological sample obtained from said subject (exemplary biological samples are mentioned above, e.g. the sample is a sample of lymphoid, breast, cervical, colorectal, gastric, brain, liver, lung, skin, neuronal, osteoblast, ovarian, pancreatic, prostate, kidney or eye tissue, or else a sample of blood or saliva).

[0171] The method typically includes the step of obtaining said biological sample for analysis from said subject.

[0172] The antibodies that may be detected include IgA, IgM and IgG antibodies.

[0173] In any of the above methods, the level that may be detected in the candidate subject who has B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma is 2 or more fold higher than the level in the healthy subject.

[0174] Another aspect of the invention is an agent capable of specific binding to the proteins of the invention, or a fragment thereof, or a hybridising agent capable of hybridizing to nucleic acid encoding the proteins of the invention or an agent capable of detecting the activity of the proteins of the invention for use in screening for, detecting and/or diagnosing disease, such as cancer, and especially B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma.

[0175] Another aspect of the invention is the proteins of the invention, or fragments thereof for use in screening for, detecting and/or diagnosing disease such as cancer, and especially B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma.

[0176] Another aspect of the invention is affinity reagents capable of specific binding to the proteins of the invention or fragments thereof, for example an affinity reagent which contains or is conjugated to a detectable label or contains or is conjugated to a therapeutic moiety such as a cytotoxic moiety. The affinity reagent may, for example, be an antibody.

[0177] Another aspect of the invention is hybridizing agents capable of hybridizing to nucleic acid encoding the proteins of the invention, for example, a hybridizing agent which contains or is conjugated to a detectable label. One example of a hybridizing agent is an inhibitory RNA (RNAi). Other examples include anti-sense oligonucleotides and ribozymes.

[0178] The invention also provides kits containing the proteins of the invention and/or one or more fragments thereof or containing one or more aforementioned affinity reagents and/

or hybridizing agents or containing one or more agents capable of detecting the activity of the proteins of the invention together with instructions for their use in an aforementioned method. The kit may further contain reagents capable of detecting and reporting the binding of said affinity reagents and/or hybridizing agents to their binding partners.

[0179] Another aspect of the invention is pharmaceutical compositions comprising a therapeutically effective amount of affinity reagents capable of specific binding to the proteins of the invention or a fragment thereof.

[0180] Another aspect of the invention is a pharmaceutically acceptable diluent or carrier and a pharmaceutical composition comprising one or more affinity reagents or hybridizing reagents as aforesaid and a pharmaceutically acceptable diluent or carrier.

[0181] In one embodiment the cancer to be detected, prevented or treated is B-cell non-Hodgkin's lymphoma.

[0182] In one embodiment the cancer to be detected, prevented or treated is breast cancer.

[0183] In one embodiment the cancer to be detected, prevented or treated is cervical cancer.

[0184] In one embodiment the cancer to be detected, prevented or treated is colorectal cancer.

[0185] In one embodiment the cancer to be detected, prevented or treated is gastric cancer.

[0186] In one embodiment the cancer to be detected, prevented or treated is glioblastoma.

[0187] In one embodiment the cancer to be detected, prevented or treated is hepatocellular carcinoma.

[0188] In one embodiment the cancer to be detected, prevented or treated is lung cancer.

[0189] In one embodiment the cancer to be detected, prevented or treated is lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia).

[0190] In one embodiment the cancer to be detected, prevented or treated is melanoma.

[0191] In one embodiment the cancer to be detected, prevented or treated is neuroblastoma.

[0192] In one embodiment the cancer to be detected, prevented or treated is osteosarcoma.

[0193] In another embodiment the cancer to be detected, prevented or treated is ovarian cancer.

[0194] In another embodiment the cancer to be detected, prevented or treated is pancreatic cancer.

[0195] In another embodiment the cancer to be detected, prevented or treated is prostate cancer.

[0196] In another embodiment the cancer to be detected, prevented or treated is renal cell cancer.

[0197] In another embodiment the cancer to be detected, prevented or treated is retinoblastoma.

[0198] Other aspects of the present invention are set out below and in the claims herein.

BRIEF DESCRIPTION OF THE FIGURES

[0199] FIG. 1 shows the amino acid sequences of the proteins of the invention. The tryptics detected experimentally by mass spectrometry are highlighted—mass match peptides are shown in bold, tandem peptides are underlined.

[0200] FIGS. 2 and 4 show so-called Box Plot data for OGTA066, as described in Examples 3 and 4.

[0201] FIG. 3 shows ROC curve data for OGTA066, as described in Example 4.

DETAILED DESCRIPTION OF THE INVENTION

[0202] The invention encompasses the administration of therapeutic compositions to a mammalian subject to treat or prevent B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer and retinoblastoma.

[0203] The invention also encompasses clinical screening, diagnosis and prognosis in a mammalian subject for identifying patients most likely to respond to a particular therapeutic treatment, for monitoring the results of B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer and retinoblastoma therapy, for drug screening and drug development.

[0204] The mammalian subject may be a non-human mammal, for example a human, such as a human adult, i.e. a human subject at least 21 (more preferably at least 35, at least 50, at least 60, at least 70, or at least 80) years old. For clarity of disclosure, and not by way of limitation, the invention will be described with respect to the analysis of lymphoid, breast, cervical, colorectal, gastric, brain, liver, lung, skin, neuronal, osteoblast, ovarian, pancreatic, prostate, kidney and eye tissue. However, as one skilled in the art will appreciate, the assays and techniques described below can be applied to other types of patient samples, including body fluids (e.g. blood, urine or saliva), a tissue sample from a patient at risk of having B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma (e.g. a biopsy such as a bone marrow, breast, cervical, liver, stomach, brain, lung, skin, bone, ovarian, pancreatic, prostate or kidney biopsy) or homogenate thereof.

[0205] The methods and compositions of the present invention are specially suited for screening, diagnosis and prognosis of a living subject, but may also be used for postmortem diagnosis in a subject, for example, to identify family members at risk of developing the same disease.

[0206] A relevant cancer as used herein refers to B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer and/or retinoblastoma.

Proteins of the Invention

[0207] In one aspect of the invention, one-dimensional electrophoresis or isobaric tags for relative and absolute

quantification (iTRAQ) or other appropriate methods are used to analyse relevant cancer tissue samples from a subject, such as a living subject, in order to measure the expression of the proteins of the invention for screening or diagnosis of a relevant cancer, to determine the prognosis of a patient with same, to monitor the effectiveness of therapy for same, or for drug development in relation to same.

[0208] As used herein, the terms:

[0209] OGTA(s), or

[0210] OGTA according to the invention, or

[0211] OGTA employed in the invention or

[0212] "Proteins of the invention",

relates to "OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 and/or OGTA271" as illustrated in FIG. 1 detected experimentally by 1D gel electrophoresis and iTRAQ analysis of lymphoid, breast, cervical, colorectal, gastric, brain, liver, lung, skin, neuronal, osteoblast, ovarian, pancreatic, prostate, kidney and/or eye tissue samples. These terms are used interchangeably in this specification.

[0213] OGTA002 has been identified in membrane protein extracts of breast, colorectal, liver, skin, pancreatic, lung and kidney tissue samples from breast cancer, colorectal cancer, hepatocellular carcinoma, melanoma, ovarian cancer, pancreatic cancer, lung cancer and kidney cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: P54760, Ephrin type-B receptor 4, was identified.

[0214] Ephrin type-B receptor 4 is known to be abundantly expressed in placenta and in a range of primary tissues and malignant cell lines. It is expressed in fetal, but not adult, brain, and in primitive and myeloid, but not lymphoid, hematopoietic cells. It is a receptor for members of the ephrin-B family. It binds to ephrin-B2. It may have a role in events mediating differentiation and development.

[0215] OGTA009 has been identified in membrane protein extracts of breast, pancreatic, prostate, kidney, colorectal, lung and ovarian tissue samples from breast cancer, pancreatic cancer, prostate cancer, renal cell cancer, colorectal cancer, lung cancer and ovarian cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: O15551, Claudin-3, was identified.

[0216] Claudin-3 plays a major role in tight junction-specific obliteration of the intercellular space, through calcium-independent cell-adhesion activity.

[0217] OGTA016 has been identified in membrane protein extracts of colorectal and lung tissue samples from colorectal cancer and lung cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: P01833, Polymeric-immunoglobulin receptor, was identified.

[0218] Polymeric-immunoglobulin receptor binds polymeric IgA and IgM at the basolateral surface of epithelial cells. The complex is then transported across the cell to be secreted at the apical surface. During this process a cleavage occurs that separates the extracellular (known as the secretory component) from the transmembrane segment.

[0219] OGTA028 has been identified in membrane protein extracts of ovarian, colorectal, kidney, liver and lung samples from ovarian cancer, colorectal cancer, kidney cancer, liver cancer and lung cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: Q5T7N2, FLJ10884, was identified.

[0220] OGTA037 has been identified in membrane protein extracts of gastric, colorectal, lung and ovarian tissue samples from gastric cancer, colorectal cancer, lung cancer and ovarian cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: Q9HA72, Protein FAM26B, was identified.

[0221] OGTA041 has been identified in membrane protein extracts of liver, lung and pancreatic tissue samples from hepatocellular carcinoma, lung cancer and pancreatic cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: P40189, Interleukin-6 receptor subunit beta, was identified.

[0222] Interleukin-6 receptor subunit beta is expressed in all the tissues and cell lines examined. Expression is not restricted to IL6 responsive cells. It is a signal-transducing molecule. The receptor systems for IL6, LIF, OSM, CNTF, IL11, CTF1 and BSF3 can utilize gp130 for initiating signal transmission. It binds to IL6/IL6R (alpha chain) complex, resulting in the formation of high-affinity IL6 binding sites,

and transduces the signal. It does not bind IL6. It may have a role in embryonic development. The type I OSM receptor is capable of transducing OSM-specific signaling events.

[0223] OGTA053 has been identified in membrane protein extracts of pancreatic, colorectal, kidney, liver and lung tissue samples from pancreatic cancer, colorectal cancer, kidney cancer, liver cancer and lung cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: Q9Y4D2, Sn1-specific diacylglycerol lipase alpha, was identified. Sn1-specific diacylglycerol lipase alpha is known to be highly expressed in the brain and pancreas. It catalyses the hydrolysis of diacylglycerol (DAG) to 2-arachidonoyl-glycerol (2-AG), the most abundant endocannabinoid in tissues. It is required for axonal growth during development and for retrograde synaptic signaling at mature synapses.

[0224] OGTA054 has been identified in membrane protein extracts of pancreatic, colorectal and lung tissue samples from pancreatic cancer, colorectal cancer and lung cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: P13164, Interferon-induced transmembrane protein 1, was identified.

[0225] Interferon-induced transmembrane protein 1 is implicated in the control of cell growth. It is a component of a multimeric complex involved in the transduction of antiproliferative and homotypic adhesion signals.

[0226] OGTA066 has been identified in membrane protein extracts of colorectal, pancreatic, kidney and lung tissue samples from colorectal cancer, pancreatic cancer, kidney cancer and lung cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: Q8TD06, Anterior gradient protein 3 homolog, was identified.

[0227] OGTA072 has been identified in membrane protein extracts of colorectal tissue samples from colorectal cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: Q16186, Adhesion-regulating molecule 1, was identified.

[0228] Adhesion-regulating molecule 1 promotes cell adhesion.

[0229] OGTA074 has been identified in membrane protein extracts of colorectal and lung tissue samples from colorectal cancer and lung cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: O00508, Latent TGF-beta binding protein-4, was identified.

[0230] OGTA076 has been identified in membrane protein extracts of lymphoid, colorectal, pancreatic, kidney, liver, lung and ovarian tissue samples from chronic lymphocytic leukaemia, colorectal cancer, pancreatic cancer, kidney cancer, liver cancer, lung cancer and ovarian cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: O60449, Lymphocyte antigen 75, was identified.

[0231] Lymphocyte antigen 75 is known to be predominantly expressed in the spleen, thymus, colon and peripheral blood lymphocytes. It is detected in myeloid and B lymphoid cell lines. It is also expressed in malignant Hodgkin's lymphoma cells called Hodgkin's and Reed-Sternberg (HRS) cells. It acts as an endocytic receptor to direct captured antigens from the extracellular space to a specialized antigen-processing compartment. It causes reduced proliferation of B-lymphocytes.

[0232] OGTA085 has been identified in membrane protein extracts of lung, skin, eye and colorectal tissue samples from lung cancer, melanoma, retinoblastoma and colorectal cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: Q14318, 38 kDa FK506-binding protein homologue, was identified.

[0233] 38 kDa FK506-binding protein homologue is known to be widely expressed, with the highest levels seen in the brain. It has no PPIase/rotamase activity.

[0234] OGTA087 has been identified in membrane protein extracts of lymphoid, breast, colorectal, lung, stomach and ovarian tissue samples from B-cell non-Hodgkin's lymphoma, breast cancer, colorectal cancer, gastric cancer, lung cancer, lymphoid leukaemia and ovarian cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: O94935, KIAA0851 protein, was identified.

[0235] OGTA088 has been identified in membrane protein extracts of breast, gastric, brain, liver, lung, lymphoid, pancreatic, kidney, eye and colorectal tissue samples from breast cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia, pancreatic cancer, renal cell cancer, retinoblastoma and colorectal cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: O15126, Secretory carrier-associated membrane protein 1, was identified.

[0236] Secretory carrier-associated membrane protein 1 is known to be widely expressed, with the highest levels seen in the brain. It functions in post-Golgi recycling pathways. It acts as a recycling carrier to the cell surface.

[0237] OGTA089 has been identified in membrane protein extracts of breast, lung, ovarian and kidney tissue samples from breast cancer, lung cancer, ovarian cancer and kidney cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: Q5T225, Polycystic kidney disease 1-like, was identified.

[0238] OGTA091 has been identified in membrane protein extracts of breast, cervical, lymphoid, stomach, liver, lung, skin, bone, ovarian, pancreatic, prostate, kidney, eye and colorectal tissue samples from breast cancer, cervical cancer, chronic lymphocytic leukaemia, gastric cancer, hepatocellular carcinoma, lung cancer, melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer, retinoblastoma and colorectal cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: O75923, Dysferlin, was identified.

[0239] Dysferlin is known to be highly expressed in skeletal muscle. It is also found in heart, placenta and at lower levels in liver, lung, kidney and pancreas.

[0240] OGTA098 has been identified in membrane protein extracts of breast, cervical, liver, lung, bone, pancreatic, prostate, kidney, colorectal and ovarian tissue samples from breast cancer, cervical cancer, hepatocellular carcinoma, lung cancer, osteosarcoma, pancreatic cancer, prostate cancer, renal cell cancer, colorectal cancer and ovarian cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: O75923, Dysferlin, was identified.

tute (EBI) which are available at <http://www.expasy.com/>), and the following entry: Q14126, Desmoglein-2, was identified.

[0241] Desmoglein-2 is found in all of the tissues tested and carcinomas. It is a component of intercellular desmosome junctions. It is involved in the interaction of plaque proteins and intermediate filaments mediating cell-cell adhesion.

[0242] OGTA101 has been identified in membrane protein extracts of breast, cervical, colorectal, liver, lung, bone, pancreatic, kidney and ovarian tissue samples from breast cancer, cervical cancer, colorectal cancer, gastric cancer, hepatocellular carcinoma, lung cancer, osteosarcoma, pancreatic cancer, kidney cancer and ovarian cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: P23468, Receptor-type tyrosine-protein phosphatase delta, was identified.

[0243] OGTA104 has been identified in membrane protein extracts of breast, liver, ovarian, pancreatic, colorectal, kidney and lung tissue samples from breast cancer, hepatocellular carcinoma, ovarian cancer, pancreatic cancer, colorectal cancer, kidney cancer and lung cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: Q13443, ADAM 9, was identified.

[0244] ADAM 9 is known to be widely expressed. It is expressed in chondrocytes, liver and heart. It is a probable zinc protease. It may mediate cell-cell or cell-matrix interactions. It displays alpha-secretase activity for APP.

[0245] OGTA106 has been identified in membrane protein extracts of cervical, skin, pancreatic and liver tissue samples from cervical cancer, melanoma, pancreatic cancer and liver cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: Q99466, Neurogenic locus notch homologue protein 4, was identified.

[0246] Neurogenic locus notch homologue protein 4 is known to be highly expressed in the heart, moderately expressed in the lung and placenta and at low levels in the liver, skeletal muscle, kidney, pancreas, spleen, lymph node, thymus, bone marrow and fetal liver. No expression was seen in adult brain or peripheral blood leukocytes. It functions as a receptor for membrane-bound ligands Jagged1, Jagged2 and Delta1 to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus. It affects the implementation of differentiation, prolif-

eration and apoptotic programs. It may regulate branching morphogenesis in the developing vascular system.

[0247] OGTA112 has been identified in membrane protein extracts of breast, cervical, lymphoid, liver, pancreatic and kidney tissue samples from breast cancer, cervical cancer, chronic lymphocytic leukaemia, hepatocellular carcinoma, pancreatic cancer and renal cell cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: P48594, Serpin B4, was identified.

[0248] Serpin B4 is known to be predominantly expressed in squamous cells. It may act as a protease inhibitor to modulate the host immune response against tumour cells.

[0249] OGTA113 has been identified in membrane protein extracts of pancreatic, colorectal, kidney, lung and ovarian tissue samples from pancreatic cancer, colorectal cancer, kidney cancer, lung cancer and ovarian cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: Q9BT4, Transmembrane protein 43, was identified.

[0250] OGTA119 has been identified in membrane protein extracts of lymphoid, breast, colorectal, stomach, liver, lung, brain, bone, pancreatic, prostate, kidney and ovarian tissue samples from B-cell non-Hodgkin's lymphoma, breast cancer, colorectal cancer, gastric cancer, hepatocellular carcinoma, lung cancer, lymphoid leukaemia, neuroblastoma, osteosarcoma, pancreatic cancer, prostate cancer, renal cell cancer and ovarian cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: Q6UK14, KIAA1228 protein, was identified.

[0251] OGTA124 has been identified in membrane protein extracts of liver, lung, ovarian, pancreatic, kidney and colorectal tissue samples from hepatocellular carcinoma, lung cancer, ovarian cancer, pancreatic cancer, renal cell cancer and colorectal cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: Q9UP95, Solute carrier family 12 member 4, was identified.

[0252] Solute carrier family 12 member 4 is known to be ubiquitous. Levels are much higher in erythrocytes from patients with Hb SC and Hb SS compared to normal AA erythrocytes. This may contribute to red blood cell dehydra-

tion and to the manifestation of sickle cell disease by increasing the intracellular concentration of HbS. It mediates electroneutral potassium-chloride cotransport when activated by cell swelling. It may contribute to cell volume homeostasis in single cells. It may be involved in the regulation of basolateral Cl⁻ exit in NaCl absorbing epithelia.

[0253] OGTA126 has been identified in membrane protein extracts of breast, colorectal, liver, skin, pancreatic, prostate, kidney and lung tissue samples from breast cancer, colorectal cancer, hepatocellular carcinoma, melanoma, pancreatic cancer, prostate cancer, renal cell cancer and lung cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: Q9H5V8, CUB domain-containing protein 1, was identified.

[0254] CUB domain-containing protein 1 is known to be highly expressed in mitotic cells with low expression during interphase. It is detected at highest levels in skeletal muscle and colon with lower levels in kidney, small intestine, placenta and lung. It is expressed in a number of human tumour cell lines as well as in colorectal cancer, breast carcinoma and lung cancer. It is also expressed in cells with phenotypes reminiscent of mesenchymal stem cells and neural stem cells. It may be involved in cell adhesion and cell matrix association. It may play a role in the regulation of anchorage versus migration or proliferation versus differentiation via its phosphorylation. It may be a novel marker for leukaemia diagnosis and for immature hematopoietic stem cell subsets. It belongs to the tetraspanin web involved in tumour progression and metastasis.

[0255] OGTA156 has been identified in membrane protein extracts of lymphoid, liver, colorectal, kidney, lung and ovarian tissue samples from acute T-cell leukaemia, B-cell non-Hodgkin's lymphoma, chronic lymphocytic leukaemia, hepatocellular carcinoma, colorectal cancer, kidney cancer, lung cancer and ovarian cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: P13612, Integrin alpha-4, was identified. Integrins alpha-4/beta-1 (VLA-4) and alpha-4/beta-7 are receptors for fibronectin. They recognize one or more domains within the alternatively spliced CS-1 and CS-5 regions of fibronectin. They are also receptors for VCAM1. Integrin alpha-4/beta-1 recognizes the sequence Q-I-D-S in VCAM1. Integrin alpha-4/beta-7 is also a receptor for MADCAM1. It recognizes the sequence L-D-T in MADCAM1. On activated endothelial cells integrin VLA-4 triggers homotypic aggregation for most VLA-4-positive leukocyte cell lines. It may also participate in cytolytic T-cell interactions with target cells.

[0256] OGTA159 has been identified in membrane protein extracts of breast, lymphoid, colorectal, liver, skin, pancreatic, eye, kidney and lung tissue samples from breast cancer, chronic lymphocytic leukaemia, colorectal cancer, hepatocellular carcinoma, melanoma, pancreatic cancer, kidney

cancer and lung cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: Q96HY6, Uncharacterized protein C20orf116, was identified.

[0257] OGTA168 has been identified in membrane protein extracts of brain and skin tissue samples from glioblastoma and melanoma patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: Q8WZA4, Collectin placenta 1, was identified.

[0258] OGTA169 has been identified in membrane protein extracts of breast, lymphoid, colorectal, kidney and lung tissue samples from breast cancer, chronic lymphocytic leukaemia, kidney cancer and lung cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: P20702, Integrin alpha-X, was identified.

[0259] Integrin alpha-X is known to be predominantly expressed in monocytes and granulocytes. Integrin alpha-X/beta-2 is a receptor for fibrinogen. It recognizes the sequence G-P-R in fibrinogen. It mediates cell-cell interaction during inflammatory responses. It is especially important in monocyte adhesion and chemotaxis.

[0260] OGTA174 has been identified in membrane protein extracts of lymphoid and lung tissue samples from acute T-cell leukaemia, chronic lymphocytic leukaemia and lung cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: P06127, T-cell surface glycoprotein CD5, was identified.

[0261] T-cell surface glycoprotein CD5 may act as a receptor in regulating T-cell proliferation. CD5 interacts with CD72/LYB-2.

[0262] OGTA176 has been identified in membrane protein extracts of lymphoid, colorectal, kidney and lung tissue samples from B-cell non-Hodgkin's lymphoma, chronic lymphocytic leukaemia, colorectal cancer, kidney cancer and lung cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by

the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: P21854, B-cell differentiation antigen CD72 homolog, was identified.

[0263] B-cell differentiation antigen CD72 is known to be predominantly expressed in pre-B-cells and B-cells but not terminally differentiated plasma cells. It plays a role in B-cell proliferation and differentiation. It associates with CD5.

[0264] OGTA177 has been identified in membrane protein extracts of lymphoid, colorectal, kidney, lung and ovarian tissue samples from chronic lymphocytic leukaemia, colorectal cancer, kidney cancer, lung cancer and ovarian cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: P49961, Ectonucleoside triphosphate diphosphohydrolase 1, was identified.

[0265] Ectonucleoside triphosphate diphosphohydrolase 1 is known to be expressed primarily on activated lymphoid cells. It is also expressed in endothelial tissues. It is present in both placenta and umbilical vein. In the nervous system, it could hydrolyze ATP and other nucleotides to regulate purinergic neurotransmission. It could also be implicated in the prevention of platelet aggregation. It hydrolyses ATP and ADP equally well.

[0266] OGTA197 has been identified in membrane protein extracts of colorectal, liver, lung, skin, bone, ovarian, pancreatic, prostate and kidney tissue samples from colorectal cancer, hepatocellular carcinoma, lung cancer, melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer and retinoblastoma patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: P29317, Ephrin type-A receptor 2, was identified.

[0267] Ephrin type-A receptor 2 is known to be expressed most highly in tissues that contain a high proportion of epithelial cells e.g. skin, intestine, lung, and ovary. It is a receptor for members of the ephrin-A family. It binds to ephrin-A1, -A3, -A4 and -A5.

[0268] OGTA202 has been identified in membrane protein extracts of colorectal and lung tissue samples from colorectal cancer and lung cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: P22223, Cadherin-3, was identified.

[0269] Cadherin-3 is known to be expressed in some normal epithelial tissues and in some carcinoma cell lines. Cadherins are calcium dependent cell adhesion proteins. They preferentially interact with themselves in a homophilic man-

ner in connecting cells; cadherins may thus contribute to the sorting of heterogeneous cell types.

[0270] OGTA203 has been identified in membrane protein extracts of ovarian, kidney and lung tissue samples from ovarian cancer, renal cell cancer and lung cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: P55285, Cadherin-6, was identified.

[0271] Cadherin-6 is known to be highly expressed in brain, cerebellum, and kidney. Lung, pancreas, and gastric mucosa show a weak expression. It is also expressed in certain liver and kidney carcinomas. Cadherins are calcium dependent cell adhesion proteins. They preferentially interact with themselves in a homophilic manner in connecting cells; cadherins may thus contribute to the sorting of heterogeneous cell types.

[0272] OGTA206 has been identified in membrane protein extracts of breast, pancreatic, prostate, colorectal and lung tissue samples from breast cancer, pancreatic cancer, prostate cancer, colorectal cancer and lung cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: O14493, Claudin-4, was identified.

[0273] Claudin-4 plays a major role in tight junction-specific obliteration of the intercellular space.

[0274] OGTA213 has been identified in membrane protein extracts of lung and colorectal tissue samples from lung cancer and colorectal cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: Q14767, Latent-transforming growth factor beta-binding protein 2, was identified.

[0275] Latent-transforming growth factor beta-binding protein 2 is known to be expressed in lung and weakly expressed in heart, placenta, liver and skeletal muscle. It may play an integral structural role in elastic-fiber architectural organization and/or assembly.

[0276] OGTA214 has been identified in membrane protein extracts of ovarian and colorectal tissue samples from ovarian cancer and colorectal cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: Q9H3R2, Mucin-13, was identified. Mucin-13 is known to be highly expressed in epithelial tissues, particu-

larly those of the gastrointestinal and respiratory tracts, such as large intestine and trachea, followed by kidney, small intestine, appendix and stomach. It is an epithelial and hemopoietic transmembrane mucin that may play a role in cell signaling.

[0277] OGTA216 has been identified in membrane protein extracts of breast, pancreatic, colorectal, kidney, liver, lung and ovarian tissue samples from breast cancer, pancreatic cancer, colorectal cancer, kidney cancer, lung cancer and ovarian cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: P55011, Solute carrier family 12 member 2, was identified.

[0278] Solute carrier family 12 member 2 is known to be expressed in many tissues. It is an electrically silent transporter system. It mediates sodium and chloride reabsorption. It plays a vital role in the regulation of ionic balance and cell volume.

[0279] OGTA222 has been identified in membrane protein extracts of lymphoid and colorectal tissue samples from B-cell non-Hodgkin's lymphoma and colorectal cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: P16444, Dipeptidase 1, was identified.

[0280] Dipeptidase 1 hydrolyses a wide range of dipeptides. It is implicated in the renal metabolism of glutathione and its conjugates. It converts leukotriene D4 to leukotriene E4; it may play an important role in the regulation of leukotriene activity.

[0281] OGTA236 has been identified in membrane protein extracts of pancreatic and colorectal tissue samples from pancreatic cancer and colorectal cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: P50443, Sulfate transporter, was identified.

[0282] Sulfate transporter is known to be ubiquitously expressed. It is a sulfate transporter. It may play a role in endochondral bone formation.

[0283] OGTA237 has been identified in membrane protein extracts of lymphoid, prostate, colorectal, kidney and lung tissue samples from B-cell non-Hodgkin's lymphoma, lymphoid leukaemia, prostate cancer, colorectal cancer, kidney cancer and lung cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL

databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: P22455, Fibroblast growth factor receptor 4, was identified.

[0284] Fibroblast growth factor receptor 4 is a receptor for acidic fibroblast growth factor. It does not bind to basic fibroblast growth factor. It binds FGF19.

[0285] OGTA247 has been identified in membrane protein extracts of liver, skin and lung tissue samples from hepatocellular carcinoma, melanoma and lung cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: P32004, Neural cell adhesion molecule L1, was identified.

[0286] Neural cell adhesion molecule L1 is a cell adhesion molecule with an important role in the development of the nervous system. It is involved in neuron-neuron adhesion, neurite fasciculation, outgrowth of neurites, etc. It binds to axonin on neurons.

[0287] OGTA248 has been identified in membrane protein extracts of kidney and lung tissue samples from renal cell cancer and lung cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: P29376, Leukocyte tyrosine kinase receptor, was identified.

[0288] Leukocyte tyrosine kinase receptor is known to be expressed in non-hematopoietic cell lines and T- and B-cell lines. The exact function of this protein is not known. It is probably a receptor with a tyrosine-protein kinase activity.

[0289] OGTA249 has been identified in membrane protein extracts of ovarian, kidney and lung tissue samples from ovarian cancer, kidney cancer and lung cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: Q969L2, Protein MAL2, was identified.

[0290] Protein MAL2 is known to be predominantly expressed in kidney, lung, and liver. It is also found in thyroid gland, stomach and at lower levels in testis and small intestine. It is a member of the machinery of polarized transport. It is required for the indirect transcytotic route at the step of the egress of the transcytosing cargo from perinuclear endosomes in order for it to travel to the apical surface via a raft-dependent pathway.

[0291] OGTA257 has been identified in membrane protein extracts of pancreatic, colorectal, liver, lung and ovarian tissue samples from pancreatic cancer, colorectal cancer, liver

cancer, lung cancer and ovarian cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: Q9H1D0, Transient receptor potential cation channel subfamily V member 6, was identified.

[0292] Transient receptor potential cation channel subfamily V member 6 is known to be expressed at high levels in the gastrointestinal tract, including esophagus, stomach, duodenum, jejunum, ileum and colon, and in pancreas, placenta, prostate and salivary gland. It is expressed at moderate levels in liver, kidney and testis. It is expressed in locally advanced prostate cancer, metastatic and androgen-insensitive prostatic lesions but not detected in healthy prostate tissue and benign prostatic hyperplasia. It is a calcium selective cation channel probably involved in $\text{Ca}(2+)$ uptake in various tissues, including $\text{Ca}(2+)$ reabsorption in intestine. The channel is activated by low internal calcium level, probably including intracellular calcium store depletion, and the current exhibits an inward rectification. Inactivation includes both a rapid $\text{Ca}(2+)$ -dependent and a slower $\text{Ca}(2+)$ -calmodulin-dependent mechanism, the latter may be regulated by phosphorylation. In vitro, is slowly inhibited by $\text{Mg}(2+)$ in a voltage-independent manner. Heteromeric assembly with TRPV5 seems to modify channel properties. TRPV5-TRPV6 heteromultimeric concatemers exhibit voltage-dependent gating.

[0293] OGTA271 has been identified in membrane protein extracts of breast, cervical, colorectal, liver, lung, osteoblast, pancreatic and kidney tissue samples from breast cancer, cervical cancer, colorectal cancer, hepatocellular carcinoma, lung cancer, osteosarcoma, pancreatic cancer and renal cell cancer patients, through the methods and apparatus of the Preferred Technologies described in Examples 1 and 2 (1D gel electrophoresis or iTRAQ together with tryptic digest of membrane protein extracts). Peptide sequences were compared to the SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at <http://www.expasy.com/>), and the following entry: Q5T021, Protein tyrosine phosphatase, receptor type, F, was identified.

[0294] Proteins of the invention are useful as are fragments e.g. antigenic or immunogenic fragments thereof and derivatives thereof. Epitope containing fragments including antigenic or immunogenic fragments will typically be of length 12 amino acids or more e.g. 20 amino acids or more e.g. 50 or 100 amino acids or more. Fragments may be 95% or more of the length of the full protein e.g. 90% or more e.g. 75% or 50% or 25% or 10% or more of the length of the full protein.

[0295] Epitope containing fragments including antigenic or immunogenic fragments will be capable of eliciting a relevant immune response in a patient. DNA encoding proteins of the invention is also useful as are fragments thereof e.g. DNA encoding fragments of proteins of the invention such as immunogenic fragments thereof. Fragments of nucleic acid (e.g. DNA) encoding Proteins of the invention may be 95% or more of the length of the full coding region

e.g. 90% or more e.g. 75% or 50% or 25% or 10% or more of the length of the full coding region. Fragments of nucleic acid (e.g. DNA) may be 36 nucleotides or more e.g. 60 nucleotides or more e.g. 150 or 300 nucleotides or more in length.

[0296] Derivatives of proteins of the invention include variants on the sequence in which one or more (e.g. 1-20 such as 15, or up to 20% such as up to 10% or 5% or 1% by number based on the total length of the protein) deletions, insertions or substitutions have been made. Substitutions may typically be conservative substitutions. Derivatives of proteins of the invention include variants on the sequence which have a sequence identity over the entire length thereof of typically at least 60%, 70%, 80%, 90 or 95%. Derivatives will typically have essentially the same biological function as the protein from which they are derived. Derivatives will typically be comparably antigenic or immunogenic to the protein from which they are derived. Derivatives will typically have either the ligand-binding activity, or the active receptor-complex forming ability, or preferably both, of the protein from which they are derived.

[0297] Tables 1-48 below illustrate the different occurrences of OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 and OGTA271 as detected by 1D gel electrophoresis and mass spectrometry of membrane protein extracts of lymphoid, breast, cervical, colorectal, gastric, brain, liver, lung, skin, neuronal, osteoblast, ovarian, pancreatic, prostate, kidney and eye tissue samples from relevant cancer patients. The first column provides the molecular weight, the second column gives information on the subfractionation protocol used, if any (see Example 1 below), and the last column provides a list of the sequences observed by mass spectrometry and the corresponding SEQ ID Nos.

[0298] Tables 49-93 illustrate the different occurrences of OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA074, OGTA076, OGTA085, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 and OGTA271 as detected by iTRAQ and mass spectrometry of membrane protein extracts of colorectal, kidney, liver, lung and ovarian tissue samples from colorectal cancer, kidney cancer, liver cancer, lung cancer and ovarian cancer patients respectively. The first column provides the samples batch number, the second column gives the iTRAQ experiment number and the last column provides a list of the sequences observed by mass spectrometry and the corresponding SEQ ID Nos.

[0299] OGTA002

TABLE 1a

<u>Breast cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
88475		LNGSSLHLEWSAPLESGGR [473], QPHYSAFGSVGEWLR [585], SQAKPGTPGGTGGPAPQY [646], VDTVAAEHLTR [749]

TABLE 1b

<u>Colorectal cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
	Heparin Binding	DLVEPWVVVR [141], EFLSEASIMGQFEHPNIIR [184], EVPPAVSDIR [237], LETADLK [456], VDTVAAEHLTR [749]
46639	Nucleotide Binding	FPQVVSALDK [263], ILASVQHMK [373], VYIDPFTYEDPNEAVR [818], WTAPEAIAFR [833], YLAEMSYVHR [859]
119837	Nucleotide Binding	FPQVVSALDK [263], GAPCTTPPSAPR [286]

TABLE 1c

<u>Hepatocellular carcinoma</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
88432		VSDFGLSR [796]

TABLE 1d

<u>Melanoma</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
81352		ENGGAHPLLDQR [214], FLEENSSDPTYTSSLGGK [258], FTMLECLSLPR [276], IEEVIGAGEFGEVCR [360], KESCVAIK [413], LPPPPDCPTSLHQLMLDCWQK [479], VDTVAAEHLTR [749]

TABLE 1e

<u>Ovarian cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
69811		VSDFGLSR [796]

TABLE 1f

<u>Pancreatic cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
116302		FPQVVSALDK [263], HGQYLIGHGTK [335], TYEVCDVQR [739]

[0300] OGTA009

TABLE 2a

<u>Breast cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
23489	Vesicles	DFYNPVVPEAQK [119], DFYNPVVPEAQKR [120], STGPGASLGTGYDR [657]
23739	Vesicles	DFYNPVVPEAQK [119]
26156	Vesicles	DFYNPVVPEAQK [119], STGPGASLGTGYDRK [658]
27751	Vesicles	VYDSLLALPQDLQAAR [817]

TABLE 2b

<u>Colorectal cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
20920		DFYNPVVPEAQKR [120], STGPGASLGTGYDR [657]
21129		DFYNPVVPEAQK [119], STGPGASLGTGYDR [657]
21235		STGPGASLGTGYDR [657]
21342		STGPGASLGTGYDR [657]
21450		STGPGASLGTGYDR [657]
21560		STGPGASLGTGYDR [657]
21671		STGPGASLGTGYDR [657]

TABLE 2c

<u>Pancreatic cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
26738		VYDSLLALPQDLQAAR [817]
27019		VYDSLLALPQDLQAAR [817]
27306		STGPGASLGTGYDR [657]

TABLE 2d

<u>Prostate cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
	Digitonin	DFYNPVVPEAQK [120], STGPGASLGTGYDR [657], VVYSAPR [815], VYDSLALPQDLQAAR [817]

TABLE 2e

<u>Renal cell cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
19493		STGPGASLGTGYDR [657]

[0301] OGTA016

TABLE 3

<u>Colorectal cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
	Heparin Binding	ADAAPDEK [57], DGSFSVVITGLR [125]
	Heparin Binding	AFVNCDENSR [68], ASVDSGSSEEQGGSSR [86], DGSFSVVITGLR [125], ILLNPQDK [377], QGHFYGETAAVYVAVEER [574]
	Heparin Binding	ANLTNFPENGTFVFNIAQLSQDDSGR [79], AQYEGR [85], DGSFSVVITGLR [125], EEFVATTESTTETK [171], QGHFYGETAAVYVAVEER [574], VYTVDLGR [821]
	Heparin Binding	DGSFSVVITGLR [125], GSVTFHCALGPEVANVAK [323], ILLNPQDK [377], QGHFYGETAAVYVAVEER [574], VYTVDLGR [821]
	Heparin Binding	DGSFSVVITGLR [125], QGHFYGETAAVYVAVEER [574]
	Heparin Binding	DGSFSVVITGLR [125], DQADGSR [150], IEGEPNLK [371], ILLNPQDK [377], QGHFYGETAAVYVAVEER [574], TDISMSDFENSR [684], VPCHFPCCK [788], VYTVDLGR [821]
70703	Nucleotide Binding	AQYEGR [85], EEFVATTESTTETK [171]
84772	Nucleotide Binding	DGSFSVVITGLR [125], FSSYEK [74], KYWCR [443], QGHFYGETAAVYVAVEER [574]
88695	Nucleotide Binding	DGSFSVVITGLR [125], FSSYEK [74], QGHFYGETAAVYVAVEER [574], YLCGAHSDGQLQEGSPIQAWQLFVNEE STIPR [861]

TABLE 3-continued

<u>Colorectal cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
91099		DFLLQSSSTVAEEAQDGPQEA [116], DGSFSVVITGLR [125], EEFVATTESTTETK [171], QGHFYGETAAVYVAVEER [574], TDISMSDFENSR [684], VYTVDLGR [821]
91554	Nucleotide Binding	ILLNPQDK [377], QGHFYGETAAVYVAVEER [574], RAPAFEGR [597]
93409		EEFVATTESTTETK [171], QGHFYGETAAVYVAVEER [574], QSSGENCDVVNTLGK [588], QSSGENCDVVNTLGKR [589], VLDGFR [776], TDISMSDFENSR [684]
95846		EEFVATTESTTETK [171], QGHFYGETAAVYVAVEER [574], QGHFYGETAAVYVAVEERK [575], QSSGENCDVVNTLGK [588]
107634	Nucleotide Binding	DGSFSVVITGLR [125], EEFVATTESTTETK [171], ILLNPQDK [377], QGHFYGETAAVYVAVEER [574], VYTVDLGR [821]
109842	Nucleotide Binding	ASVDSGSSEEQGGSSR [86], DGSFSVVITGLR [125], EEFVATTESTTETK [171], FSSYEK [74], ILLNPQDK [377], LSLLEEPNGTFTVILNQLTSR [486], QGHFYGETAAVYVAVEER [574], TDISMSDFENSR [684], VYTVDLGR [821]
117144	Nucleotide Binding	ASVDSGSSEEQGGSSR [86], DGSFSVVITGLR [125], GGCITLISSEGYVSSK [97], QGHFYGETAAVYVAVEER [574], TDISMSDFENSR [684]
125678	Nucleotide Binding	EEFVATTESTTETK [171]

[0302] OGTA028

TABLE 4

<u>Ovarian cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
22364		HQVVHK [343], KENITYMKR [412], MSDVSTSVQSK [525], TEFQIINLALQK [687], TFSDLQSLRK [691], VAKPEEMK [743], VLMEIQDLMFEEMR [783]
22505		EADLTEETENLR [166], IDSLDQIEEFSK [358], KENITYMKR [412], VAKPEEMK [743], VFLSIEEFR [761]

TABLE 4-continued

<u>Ovarian cancer</u>	
MW (Da) Subfractionation	Tryptics identified [SEQ ID No]
24585	EITYQGTR [00], KKENITYMK [421], KLPQGESR [425], MDILEER [510], TFSDLQSLR [690], VFLSIEEFR [761], VLMEIQDLMFEEMR [783]
26031	KENITYMKR [412], KKENITYMK [421], KLPQGESR [425], QWSNVFNILR [592], REQLTETDK [602], VLMEIQDLMFEEMR [783]
26256	EEINQGGR [177], FLCEVK [56], KKENITYMK [421], LPQGESR [480], QWSNVFNILR [592], VLMEIQDLMFEEMR [783]
26487	DYVLHMPTLR [165], EEINQGGR [177], IGDDNENLTFK [366], KENITYMKR [412], KKENITYMK [421], LPQGESR [480], NVHLEFTER [557], QWSNVFNILR [592], TEFQIINLALQK [687], VAKPEEMK [743], VLMEIQDLMFEEMR [783], YGIQEK [852]
26724	EEINQGGR [177], IGDDNENLTFK [366], KENITYMKR [412], KKENITYMK [421], LPQGESR [480], QWSNVFNILR [592], TEFQIINLALQK [687], TLHTEELTSK [704], VLMEIQDLMFEEMR [783], YGIQEK [852]
26966	EEIGNLK [175], EIIDENFAELK [197], ELLGNNIP [03], KENITYMK [411], KKENITYMK [421], LPQGESR [480], QWSNVFNILR [592], TLHTEELTSK [704], VLMDEGAVLTLVADLSSATLDISK [782], VLMEIQDLMFEEMR [783]
27470	AGEITSDGLSFLFLK [70], DYVLHMPTLR [165], ELLGNNIP [03], KKENITYMK [421], KLPQGESR [425], YGIQEK [852]
28000	AGEITSDGLSFLFLK [70], KKENITYMK [421]
47275	DVSAIMNK [162], DYVLHMPTLR [165], EIIDENFAELK [197], EITYQGTR [00], HSHTNLSISTGVTK [344], KKENITYMK [421], KLPQGESR [425], KTEEEK [437], LPQGESR [480], LTADLSLDTLDAR [494], REITYQGTR [601], SSHSGVLEIENSVDLSSR [649], SSVINSIR [652], TFSDLQSLR [690], VFLSIEEFR [761], VLMEIQDLMFEEMR [783]
48293	DYVLHMPTLR [165], EIIDENFAELK [197], EITYQGTR [200], HSHTNLSISTGVTK

TABLE 4-continued

<u>Ovarian cancer</u>	
MW (Da) Subfractionation	Tryptics identified [SEQ ID No]
	[344], KLPQGESR [425], KTEEEK [437], LTADLSLDTLDAR [494], MAFDFR [507], SLEMSHDEHKK [639], VFLSIEEFR [761], WSNVFK [832]

[0303] OGTA037

TABLE 5

<u>Gastric cancer</u>	
MW (Da) Subfractionation	Tryptics identified [SEQ ID No]
24774	ENPDNLSDFR [15]

[0304] OGTA041

TABLE 6a

<u>Hepatocellular carcinoma</u>	
MW (Da) Subfractionation	Tryptics identified [SEQ ID No]
90607	DGPEFTFTTPK [124], KPFPEDLK [431]

TABLE 6b

<u>Lung cancer</u>	
MW (Da) Subfractionation	Tryptics identified [SEQ ID No]
122412	DNMLWVEWTTTPR [146], QNCSQHESPDISHFER [582], QVSSVNEEDFVR [591], SHLQNYTVNATK [635]

TABLE 6c

<u>Pancreatic cancer</u>	
MW (Da) Subfractionation	Tryptics identified [SEQ ID No]
104240	HIWPNVPDPSK [336], NYTIFYR [564], SHLQNYTVNATK [635], TNHFTIPK [711]

[0305] OGTA053

TABLE 7

<u>Pancreatic cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
67953		FAPGVTIEEDNCCGCNAIAIR [43], LEEGQATSWSR [452], VLENYNK [780]

[0306] OGTA054

TABLE 8

<u>Pancreatic cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
9213		EEHEVAVLGAPPSTILPR [173]

[0307] OGTA066

TABLE 9a

<u>Colorectal cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
19046		IMFVDPSLTVR [380]
19131		IMFVDPSLTVR [380]
19217		IMFVDPSLTVR [380]
19304		IMFVDPSLTVR [380]

TABLE 9c

<u>Pancreatic cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
24387		IMFVDPSLTVR [380]
24611		IMFVDPSLTVR [380], KPLMVIHLEDQYSQALK [432]

[0308] In one or more aspects of the invention OGTA does not relate to, the example use/methods of diagnosis for colorectal cancer.

[0309] OGTA072

TABLE 10

<u>Colorectal cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
	Heparin Binding	MTTSGALFPSPVPGSR [526], TDQDEHCR [685]

[0310] OGTA074

TABLE 11

<u>Colorectal cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
36031	Nucleotide Binding	EDGYSDASGFGYCFR [169]
	Heparin Binding	EDGYSDASGFGYCFR [169], QGPVGSRR [577], VPEGFTCR [790]

[0311] OGTA076

TABLE 12a

<u>Chronic lymphocytic leukaemia</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
98008	Chloroform Extracted	AANDPFTIVHGNTGK [52], CEHHSLYGAAR [102], CSMLIASNETWKK [108], EFIYLRPFACDTK [183], ELTYSNFHPLLVSGR [08], FCQALGAHLSSFHVDEIK [45], FEQEYLNDLMK [47], GWHFYDDR [328], IPENFFEEESR [385], ISEWPIDDHFTYSR [392], KYFWTGLR [442], LFHLHSQK [460], SPDLQGSQWSDR [644], TPLSYTHWR [718], TPVSTIIMPNEFQQDYDIR [722], VFHRPWR [760], VQCSEQWIPFQNK [793], WVSQHR [838], YFWTGLR [851], YPWHR [866]
223568		AANDPFTIVHGNTGK [52], CSMLIASNETWKK [108], ELTYSNFHPLLVSGR [08], FEQEYLNDLMKK [48], FPVTFGECLYMSAK [65], GWHFYDDR [328], HFVSLCQK [333], IPENFFEEESR [385], ISEWPIDDHFTYSR [392], KVECEHGFR [439], NWEAER [563], SDQALHSFSEAK [623], SPDLQGSQWSDR [644], TPLSYTHWR [718], VFHAER [759], VQCSEQWIPFQNK [793], WVSQHR [838], YPWHR [866]
238644		KVECEHGFR [439], SDQALHSFSEAK [623], TPLSYTHWR [718], VFHAER [759]

TABLE 12b

<u>Colorectal cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
167535		IPENFFEEESR [385], TPVSTIIMPNEFQQDYDIR [722]

TABLE 12c

<u>Pancreatic cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
161314		AANDPFTIVHGNTGK [52], EFIYLRPFACDTK [183], ELTYSNFHPLLVSGR [08], IEMVDYK [362], IPENFFEEESR [385], ISEWPIDDHFTYSR [392], LTYSSR [499], RHGETCYK [604], SPDLQGSWQWSDR [644], TPLSYTHWR [718], VFHAER [759], VFHRPWR [760], VQCSEQWIPFQNK [793], WVSQHR [838], YFWTGLR [851], YPWHR [866], YVCKRK [875]
261976		AFSSDLISIHSLADVEVVVTK [67], CSMLIASNETWKK [108], DGHGTAISNASDVWKK [122], EFIYLRPFACDTK [183], HMATTQDEVHTK [338], IPENFFEEESR [385], ISEWPIDDHFTYSR [392], KYFWTGLR [442], SPDLQGSWQWSDR [644], TPLSYTHWR [718], VFHRPWR [760], VIEEAVYFHQHSILACK [767], VQCSEQWIPFQNK [793], YFWTGLR [851], YPWHR [866], YVCKRK [875]

[0312] OGTA085

TABLE 13a

<u>Lung cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
31005		KMLGNPSR [427], STETALYR [655], TIHAELSK [700], VLAQQGEYSEAIPIRL [773]
64045		TAVDGPDLLEMLTGQER [677], VLAQQGEYSEAIPIRL [773]
69488		TAVDGPDLLEMLTGQER [677], VLAQQGEYSEAIPIRL [773]

TABLE 13b

<u>Melanoma</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
22017		KMLGNPSR [427], MGQPPAEAEQPGALAR [516], STETALYR [655], TAVDGPDLLEMLTGQER [677], VDMTFEEEAQLQLK [748]
22380		STETALYRK [656], TAVDGPDLLEMLTGQER [677], VDMTFEEEAQLQLK [748]

TABLE 13b-continued

<u>Melanoma</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
22505		SCSLVLEHQPDNIK [620], STETALYRK [656], TAVDGPDLLEMLTGQER [677]
22632		SCSLVLEHQPDNIK [620], TAVDGPDLLEMLTGQER [677], VDMTFEEEAQLQLK [748]
27711		ADFVLAANSYDLAIK [60], GQVTVVHLQTSLENGTR [313], KMLGNPSR [427], LDHYR [447], TAVDGPDLLEMLTGQER [677]

TABLE 13c

<u>Retinoblastoma</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
50346		KMLGNPSR [427], MGQPPAEAEQPGALAR [516], VLAQQGEYSEAIPIRL [773]

[0313] OGTA087

TABLE 14a

<u>B-cell non-Hodgkin's lymphoma</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
54163		FVWNGHLLR [279], LGVLVHGQK [464], LHITPEK [466], LSNTSPEPQEMSLER [488], NNFSDGFR [550], YIAPDFHK [854], YKPLPQISK [856]
55443		ATDFDVLSYKK [89], FVWNGHLLR [279], KTMLHLTDIQLQDNK [438], LHITPEK [466], NNFSDGFR [550], QVIINLINQK [590], QYAGTGALK [593], VANHMDGFQR [744], YKPLPQISK [856]
75222		LHITPEK [466], NNFSDGFR [550], QVIINLINQK [590], QYAGTGALK [593], VANHMDGFQR [744], YKPLPQISK [856]

TABLE 14b

Breast cancer		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
52857		ATDFDVLSYKK [89], FVWNGHLLR [279], TNVIQSLAR [714]

TABLE 14c

Colorectal cancer		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
	Heparin Binding	LHITPEK [466], YIAFDPHK [854]

TABLE 14d

Gastric cancer		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
50390		TNVIQSLAR [714]
50979		TNVIQSLAR [714]

TABLE 14e

Lung cancer		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
34397		LSNTSPEFQEMSLER [488], NNFSDGFR [550], YFDWILISR [848], YFDWILISR [849], YIAFDPHK [854], YKPLPQISK [856]
63738		HFDSQVVIYK [332], LHITPEK [466], NNFSDGFR [550], RTHLGLIMDGWNSMIR [615], TNVIQSLAR [714]
66502		GSEKPLEQTFATMVSSLGSGMMR [314], HFDSQVVIYK [332], LHITPEK [466], NNFSDGFR [550], QYAGTGALK [593], VANHMDGFQR [744], YIAFDPHK [854]
69051		ATDFDVLSYK [88], GSEKPLEQTFATMVSSLGSGMMR [314], LEEQDEFK [453], THLGLIMDGWNSMIR [696], VSTEVTIAVK [797]

TABLE 14f

Lymphoid leukaemia, unspecified		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
56356		TNVIQSLAR [714], YKPLPQISK [856]
58422		LSNTSPEFQEMSLER [488], NNFSDGFR [550], THLGLIMDGWNSMIR [696]

TABLE 14g

Ovarian cancer		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
42632		ATDFDVLSYK [89], FVWNGHLLR [279], GSIPVFWQRPNLK [316], HFDSQVVIYK [332], KTMLHLTDIQLQDNK [438], LEEQDEFK [453], RTHLGLIMDGWNSMIR [615], TMLHLTDIQLQDNK [707]

[0314] OGTA088

TABLE 15a

Breast cancer		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
29702		EHALAQAELLK [190], EMQNLSQHGR [211], NVPPGLDEYNPFSDSR [560], RQEELER [612]
29901		DPSVTQVTR [149], EMQNLSQHGR [211], NVPPGLDEYNPFSDSR [560], RQEELER [612]
30103		EHALAQAELLK [190], EMQNLSQHGR [211], NVPPGLDEYNPFSDSR [560], RQEELER [612]
30309		EMQNLSQHGR [211], NVPPGLDEYNPFSDSR [560], RQEELER [612]

TABLE 15b

Gastric cancer		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
29509		EHALAQAELLK [190], EMQNLSQHGR [211]

TABLE 15c

<u>Glioblastoma</u>		
MW (Da)	Subfrac- tionation	Tryptics identified [SEQ ID No]
29544		EHALAQAELLK [190], EMQNLSQHGR [211], KAAELDR [405], MPNVNTQPAIMKPTEHPAYTQIAK [522], NVPPGLDEYNPFSDSR [560], QEELER [566], RQEELER [612], TPPPGGVK [721], TVQTAAANAATAASSAAQNAFK [737], VHGLYR [766]
29779		EHALAQAELLK [190], EMQNLSQHGR [211], NVPPGLDEYNPFSDSR [560], RQEELER [612]
30027		AQQEFATGVMSNK [84], EHALAQAELLK [190], EMQNLSQHGR [211], NVPPGLDEYNPFSDSR [560], RQEELER [612], TVQTAAANAATAASSAAQNAFK [737], VHGLYR [766]

TABLE 15d

<u>Hepatocellular carcinoma</u>		
MW (Da)	Subfrac- tionation	Tryptics identified [SEQ ID No]
26264		DPSVTQVTR [149], EHALAQAELLK [190], EMQNLSQHGR [211], KAAELDRR [406], NVPPGLDEYNPFSDSR [560], RQEELER [612]
26522		EMQNLSQHGR [211], NVPPGLDEYNPFSDSR [560]
27053		EMQNLSQHGR [211], EMQNLSQHGRK [212], NVPPGLDEYNPFSDSR [560], RQEELERK [613]
28538		EHALAQAELLK [190], EMQNLSQHGR [211], MPNVNTQPAIMKPTEHPAYTQIAK [522], NVPPGLDEYNPFSDSR [560]

TABLE 15e

<u>Lung cancer</u>		
MW (Da)	Subfrac- tionation	Tryptics identified [SEQ ID No]
31584		KVHGLYR [441], NVPPGLDEYNPFSDSR [560]
31835		EMQNLSQHGR [211], NVPPGLDEYNPFSDSR [560]
33009		EMQNLSQHGR [211], NVPPGLDEYNPFSDSR [560], QEELER [566]

TABLE 15e-continued

<u>Lung cancer</u>		
MW (Da)	Subfrac- tionation	Tryptics identified [SEQ ID No]
33422		EHALAQAELLK [190], EMQNLSQHGR [211], MPNVNTQPAIMKPTEHPAYTQIAK [522], NVPPGLDEYNPFSDSR [560], RQEELER [612]
33847		EMQNLSQHGR [211], NVPPGLDEYNPFSDSR [560]
34135		AQQEFATGVMSNK [84], EMQNLSQHGR [211], NVPPGLDEYNPFSDSR [560]
35643		EMQNLSQHGR [211], NVPPGLDEYNPFSDSR [560], TPPPGGVK [721], TVQTAAANAATAASSAAQNAFK [737]

TABLE 15f

<u>Lymphoid leukaemia, unspecified</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
28206		EHALAQAELLK [190], EMQNLSQHGR [211], NVPPGLDEYNPFSDSR [560]

TABLE 15

<u>Pancreatic cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
26742		EHALAQAELLK [190], NVPPGLDEYNPFSDSR [560]
31738		EHALAQAELLK [190], EMQNLSQHGR [211], NVPPGLDEYNPFSDSR [560]
32245		EHALAQAELLK [190], EMQNLSQHGR [211], NVPPGLDEYNPFSDSR [560]
34059		DPSVTQVTR [149], EMQNLSQHGR [211], KVHGLYR [441], NVPPGLDEYNPFSDSR [560], TVQTAAANAATAASSAAQNAFK [737]
34270		DPSVTQVTR [149], EMQNLSQHGR [211], NVPPGLDEYNPFSDSR [560]
36671		EHALAQAELLK [190], EMQNLSQHGR [211], KAAELDRR [406], NVPPGLDEYNPFSDSR [560], RQEELER [612]
36974		DPSVTQVTR [149], EHALAQAELLK [190], EMQNLSQHGR [211],

TABLE 15-continued

<u>Pancreatic cancer</u>	
MW (Da)	Tryptics identified Subfractionation[SEQ ID No]
	NVPPGLDEYNPFSDSR [560], RQEELER [612]

TABLE 15h

<u>Renal cell cancer</u>	
MW (Da)	Tryptics identified Subfractionation[SEQ ID No]
30318	EHALAQAECLK [190], EMQNLSQHGR [211], NVPPGLDEYNPFSDSR [560]
33762	EHALAQAECLK [190], EMQNLSQHGR [211], KVHGLYR [441], NVPPGLDEYNPFSDSR [560]

TABLE 15i

<u>Retinoblastoma</u>	
MW (Da)	Tryptics identified Subfractionation [SEQ ID No]
30816	EHALAQAECLK [190], EMQNLSQHGR [211], NVPPGLDEYNPFSDSR [560], RQEELER [612], TVQTAANAATAASSAAQNAFK [737], VHGLYR [766]

[0315] OGTA089

TABLE 16a

<u>Breast cancer</u>	
MW (Da)	Tryptics identified Subfractionation[SEQ ID No]
110512	ADFLIFR [59], EETINKPPIAK [176], ELTLPVDSTTLDGSK [207], GETYTYDWQLITHPR [293], VVEMQGV [809]

TABLE 16b

<u>Lung cancer</u>	
MW (Da)	Tryptics identified Subfractionation[SEQ ID No]
72110	GETYTYDWQLITHPR [293], IQPYTEQSTK [391], VNDSENLGGLTTSGSAEVHK [786]

TABLE 16c

<u>Ovarian cancer</u>	
MW (Da)	Tryptics identified Subfractionation[SEQ ID No]
77125	GETYTYDWQLITHPR [293], NLQSQSSVNVIVK [544]
89348	ADFLIFR [59], EEINKPPIAK [176], GETYTYDWQLITHPR [293], ILDATDQESLELKPTSR [374], IQPYTEQSTK [391], LTPGLYEFK [497], MVFFVQNEPPHQIFK [528], NVSQPEISEGLATTPSTQQVK [562], THSSNSMLVFLK [699]

[0316] OGTA091

TABLE 17a

<u>Breast cancer</u>	
MW (Da)	Tryptics identified Subfractionation [SEQ ID No]
24993 Vesicles	NLVDPFVEVSFAGK [547]
114969	TDVHYR [686]
120658	TDVHYR [686]
124535 PNGase F Deglycosylation	GEGVAYR [291]
142847	GEGVAYR [291]
164389	GEGVAYR [291], NLVDPFVEVSFAGK [547]
165165	GEGVAYR [291], NLVDPFVEVSFAGK [547]
171988	GEGVAYR [291], NLVDPFVEVSFAGK [547], TDVHYR [686]
176984	GEGVAYR [291], TDVHYR [686]
179325	GEGVAYR [291], NLVDPFVEVSFAGK [547]
210126 PNGase F Deglycosylation	TDVHYR [686]
230530 PNGase F Deglycosylation	TDVHYR [686]

TABLE 17b

<u>Cervical cancer</u>	
MW (Da)	Tryptics identified Subfractionation[SEQ ID No]
	GEGVAYR [291], TDVHYR [686]
	GEGVAYR [291], TDVHYR [686]
	TDVHYR [686]

TABLE 17c

<u>Chronic lymphocytic leukaemia</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
223568		FSDVTGK [272], TDVHYR [686]

TABLE 17d

<u>Gastric cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
95956		TDVHYR [686]
125740		TDVHYR [686]
129831		NLVDPFVEVSFAGK [547]
138914		GEGVAYR [291], NLVDPFVEVSFAGK [547], TDVHYR [686]
143975		GEGVAYR [291], TDVHYR [686]

TABLE 17e

<u>Hepatocellular carcinoma</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
98239		GEGVAYR [291]
102119		GEGVAYR [291], NLVDPFVEVSFAGK [547]
106345		GEGVAYR [291], TDVHYR [686]
107073		GEGVAYR [291]
110964		GEGVAYR [291], TDVHYR [686]
114377		GEGVAYR [291]
116037		GEGVAYR [291], TDVHYR [686]
118513		GEGVAYR [291], NLVDPFVEVSFAGK [547], TDVHYR [686]
121636		FFASIGER [250], FHLEYR [254], GEGVAYR [291], IGETVVDLENR [367], IIDWDR [370], IPNPHLGPEER [386], KTDAFR [436], LLSDKPQDFQIR [469], QIFGFESNK [579], SLGGEGNFWR [640], TDALLGEFR [681], TDVHYR [686], VEDLPADDILR [753], VQVIEGR [794], VTAAGQTK [800]
123033		NLVDPFVEVSFAGK [547], TDVHYR [686]
127849		GEGVAYR [291]
128000		TDVHYR [686]

TABLE 17e-continued

<u>Hepatocellular carcinoma</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
133487		AVDEQGWESITIPPER [94], DLSQMEALK [139], DSFSDPYAIVSFLHQSQK [155], EKPAIHHPGFEVQETSR [201], EVLATPSLSASFNAPLLDTK [234], FHLEYR [254], GEGVAYR [291], GSQPSGELLASFELIQR [320], HWVPAEK [348], IETQNQLLGIADR [363], IGETVVDLENR [367], ILDESEDIDLPPPPQR [375], IPNPHLGPEER [386], IYPLPEDPAIMPPE [403], LPGGQWIYMSDNYTDVNGEK [477], LSVFAETYNENETK [491], MDVGTIYR [511], MFELTCTLPLEK [515], MYTHRRR [533], RMEPLEK [607], RPDTSFLWFTSPYK [608], SLGGEGNFWR [640], TDALLGEFR [681], TDVHYR [686], TSLCVLGPGEAPLERK [729], VEDLPADDILR [753], VPAHQVLEFR [787], VQVIEGR [794], VVFQIWDNDK [810], WEDEEWSTDLNR [824], WLLSDPDDFSAGAR [827]
139587		AVDEQGWESITIPPER [94], DLSQMEALK [139], DLSQMEALKR [140], FFASIGER [250], ILDESEDIDLPPPPQR [375], KNPNFDICTLFMEVMLPR [430], LPGGQWIYMSDNYTDVNGEK [477], MFELTCTLPLEK [515], NPNFICTLFMEVMLPR [551], QFHQLAAQGPQECVLR [570], RDLSQMEALK [599], RMEPLEK [607], TANPQWNQNTLPAMFSPMCEK [670], TDAFR [680], TDALLGEFR [681], TQETEDPSVIGEFK [724], TSLCVLGPGEAPLER [728], VEDLPADDILR [753], VVFQIWDNDK [810]
192580		TDVHYR [686]
200565		GEGVAYR [291], TDVHYR [686]
209214		TDVHYR [686]

TABLE 17f

<u>Lung cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
195217		GEGVAYR [291], TDVHYR [686]
202986		GEGVAYR [291], KNLVDPFVEVSFAGK [429], TDVHYR [686]
211353		GEGVAYR [291], KNLVDPFVEVSFAGK [429], TDVHYR [686]

TABLE 17f-continued

<u>Lung cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
220388		GEGVAYR [291], KNLVDPFVEVSFAGK [429], TDVHYR [686]
230173		EYSIEEIEAGR [241], ILDESEDTDLPYPPPPQR [375], IPNPHLGPVEER [386], MEPLEK [513], RMEPLEK [607], SLGGEGNFWNR [640], TDVHYR [686]

TABLE 17g

<u>Melanoma</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
20629		FSDVTGK [272], NLVDPFVEVSFAGK [547]

TABLE 17h

<u>Osteosarcoma</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
151810		NLVDPFVEVSFAGK [547]
159457		TDVHYR [686]
181827		NLVDPFVEVSFAGK [547]

TABLE 17i

<u>Ovarian cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
70973		KNLVDPFVEVSFAGK [429]
74967		KNLVDPFVEVSFAGK [429]
110436		NLVDPFVEVSFAGK [547]
115528		NLVDPFVEVSFAGK [547]
127159		GEGVAYR [291]

TABLE 17j

<u>Pancreatic cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
55323		TDVHYR [686]
70820		GEGVAYR [291]

TABLE 17j-continued

<u>Pancreatic cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
88202		FSDVTGK [272], KNLVDPFVEVSFAGK [429]
100099		GEGVAYR [291]
132648		TDVHYR [686]
133778		TDVHYR [686]
142218		GEGVAYR [291]
142690		NLVDPFVEVSFAGK [547]
154726		GEGVAYR [291], NLVDPFVEVSFAGK [547]
158113		GEGVAYR [291]
168430		GEGVAYR [291], TDVHYR [686]
174222		NLVDPFVEVSFAGK [547]
184505		FSDVTGK [272], TDVHYR [686]
189061		KNLVDPFVEVSFAGK [429]
192682		TDVHYR [686]
208929		GEGVAYR [291], NLVDPFVEVSFAGK [547], TDVHYR [686]
216690		GEGVAYR [291], NLVDPFVEVSFAGK [547], TDVHYR [686]
217481		TDVHYR [686]
222673		TDVHYR [686]
229012		GEGVAYR [291], TDVHYR [686]
230839		GEGVAYR [291], TDVHYR [686]
261976		TDVHYR [686]

TABLE 17k

<u>Prostate cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
		GEGVAYR [291], TDVHYR [686]
		TDVHYR [686]

TABLE 171

<u>Renal cell cancer</u>	
MW (Da)	Tryptics identified Subfractionation[SEQ ID No]
62841	TDVHYR [686]
83490	GEGVAYR [291]
122161	FSDVTGK [272], GEGVAYR [291]
126235	GEGVAYR [291]
135291	GEGVAYR [291]
143822	GEGVAYR [291], TDVHYR [686]
148249	TDVHYR [686]
151721	GEGVAYR [291], TDVHYR [686]
158158	ALGRPGPPFNITPR [76], AVDEQGWESITIPPER [94], CIIWNTR [104], DLAAMDK [132], DLSQMEALK [139], EFNQFAEGK [185], EKPAIHHPGFVQETSR [201], EYSIEIEAGR [241], FHLEYR [254], FSFDDFLGSLQLDLNR [273], GEGVAYR [291], GWMIGFEEHK [329], IETQNQLGIADR [363], IGETVVDLENR [367], IIDWDR [370], ILDESEDTLPPPPQR [375], IYPLPEDPAIPMPPR [403], KLPSRPPPHYPGK [426], LLSDKPQDFQIR [469], MDVGTIYR [511], MYYTHR [531], MYYTHR [532], RMEPLEK [607], SLGEGGNFNWR [640], SYQLANISSPSLVVECGQTVQSCVIR [667], TDALLGEFR [681], TQEETEDPSVIGEFK [724], VEDLPADDILR [753], VQVIEGR [794], WEDEEWSTDLNR [824], WLLLSDPDDFSAGAR [827]
200334	NLVDPFVEVSFAGK [547]
221217	GEGVAYR [291], NLVDPFVEVSFAGK [547], TDVHYR [686]
233732	TDVHYR [686]

[0317] OGTA098

TABLE 18a

<u>Breast cancer</u>	
MW (Da)	Tryptics identified Subfractionation[SEQ ID No]
49867	VVPSFLPVDQGGSLVGR [812]
50576	DGNGEVTDKPKV [123], DMAGQAQAAVALNEEFLLR [142], DNWISVDSVTSEIK [148], DTGEIYTTSVTLDR [159], EETPFLLTGYALDAR [182], NGVGGMAK [536], QUESTSVLLQQSEKK [569],

TABLE 18a-continued

<u>Breast cancer</u>	
MW (Da)	Tryptics identified Subfractionation[SEQ ID No]
	VTQEIVTER [806], VVPSFLPVDQGGSLVGR [812], VYAPASTLVDQPYANEGTVVTER [816], YVQNGTYTVK [876]
115607	ATQFTGATGAIMTTETTK [93], DGNGEVTDKPKV [123], FLDDLGLK [257], IVAISEDYPR [400], QUESTSVLLQQSEK [568], VVPSFLPVDQGGSLVGR [812]

TABLE 18b

<u>Cervical cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
82244	MonoQ Aqueous	DTGEIYTTSVTLDR [159], EEHSSYTLTVEAR [174], IVAISEDYPR [400]

TABLE 18c

<u>Hepatocellular carcinoma</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
83238		ATQFTGATGAIMTTETTK [93], GNNVEKPLELR [304], INATDAEPNTLNSK [381], IVAISEDYPR [400], QUESTSVLLQQSEK [568]
112208		ATQFTGATGAIMTTETTK [93], DNWISVDSVTSEIK [148], DTGEIYTTSVTLDR [159], FLDDLGLK [257], GNNVEKPLELR [304], GQIIGNFQAFDEDTGLPAHAR [311], IVAISEDYPR [400], VATPLPDPMASR [746], VLEGMVEENQVNVETR [778], VTQEIVTER [806], VVPSFLPVDQGGSLVGR [812], WEEHR [825]
134896		ATQFTGATGAIMTTETTK [93]

TABLE 18d

<u>Lung cancer</u>	
MW (Da)	Tryptics identified Subfractionation[SEQ ID No]
	ATQFTGATGAIMTTETTK [93], DTGEIYTTSVTLDR [159], EEHSSYTLTVEAR [174], FLDDLGLK [257], GNNVEKPLELR [304], GQIIGNFQAFDEDTGLPAHAR [311], INATDAEPNTLNSK [381],

TABLE 18d-continued

<u>Lung cancer</u>	
MW (Da)	Subfractionation Tryptics identified [SEQ ID No]
	IWAISEDYPR [400], LPDFESR [476], QESTSVLLQQSEK [568], VATPLPDPMASR [746], VLEGMVEENQVNVETR [778], VTQEIIVTER [806], VVPSFLPVDQGGSLVGR [812]
	DNWISVDSVTSEIK [148], DTGEIYTTSVTLDR [159], EEHSSYTLTVEAR [174], GNNVEKPLELR [304], GQIIGNFQAFDEDTGLPAHAR [311], INATDADEPNTLNSK [381], IWAISEDYPR [400], LPDFESR [476], VLAPASTLQSSYQIPTENSMTAR [772], VLEGMVEENQVNVETR [778], VVPSFLPVDQGGSLVGR [812], VYAPASTLVDQPYANEGTVVVTTER [816], YKPTPIPIK [858]

TABLE 18e

<u>Osteosarcoma</u>	
MW (Da)	Subfractionation Tryptics identified [SEQ ID No]
24158	GITEPPFGIFVFNK [301]
41065	DNWISVDSVTSEIK [148], IWAISEDYPR [400], VLEGMVEENQVNVETR [778]

TABLE 18f

<u>Pancreatic cancer</u>	
MW (Da)	Subfractionation Tryptics identified [SEQ ID No]
47024	ATQFTGATGAIMTTETTK [93], DNGEVTDKPVK [123], EGEDLSKK [187], ESFLAPSSGVQPTLAMPNIAVGQNVTVTER [223], GSSSASIVK [322], VATPLPDPMASR [746], VTQEIIVTER [806], VVPSFLPVDQGGSLVGR [812], VYAPASTLVDQPYANEGTVVVTTER [816]
47767	ATQFTGATGAIMTTETTK [93], DTGEIYTTSVTLDR [159], ESFLAPSSGVQPTLAMPNIAVGQNVTVTER [223], GSSSASIVK [322], VATPLPDPMASR [746], VLAPASTLQSSYQIPTENSMTAR [772], VTQEIIVTER [806], VVPSFLPVDQGGSLVGR [812], VYAPASTLVDQPYANEGTVVVTTER [816], WEEHR [825]
48531	ATQFTGATGAIMTTETTK [93], DNGEVTDKPVK [123], VTQEIIVTER [806], VVPSFLPVDQGGSLVGR [812],

TABLE 18f-continued

<u>Pancreatic cancer</u>	
MW (Da)	Subfractionation Tryptics identified [SEQ ID No]
57915	VYAPASTLVDQPYANEGTVVVTTER [816], WEEHR [825]
	ATQFTGATGAIMTTETTK [93], DNGEVTDKPVK [123], DMAGAQAAVALNEEFLLR [142], DTGELNVTSLDR [160], EEHSSYTLTVEAR [174], EETPPFLLTGYALDAR [182], ESFLAPSSGVQPTLAMPNIAVGQNVTVTER [223], GNNVEKPLELR [304], INATDADEPNTLNSK [381], SSVISIYVSESMDR [653], VTQEIIVTER [806], VVPSFLPVDQGGSLVGR [812], VYAPASTLVDQPYANEGTVVVTTER [816], WEEHR [825]
58846	ATQFTGATGAIMTTETTK [93], DNGEVTDKPVK [123], EGEDLSKK [187], ESFLAPSSGVQPTLAMPNIAVGQNVTVTER [223], IHSDLAEEER [369], INATDADEPNTLNSK [381], VTQEIIVTER [806], VVPSFLPVDQGGSLVGR [812], VYAPASTLVDQPYANEGTVVVTTER [816], WEEHR [825]
119656	DNGEVTDKPVK [123], DMAGAQAAVALNEEFLLR [142], GNNVEKPLELR [304], INATDADEPNTLNSK [381], IWAISEDYPR [400], SEIQFLISDNQGFSCPEK [628], SSVISIYVSESMDR [653]
134980	ATQFTGATGAIMTTETTK [93], DNWISVDSVTSEIK [148], DTGEIYTTSVTLDR [159], EEHSSYTLTVEAR [174], GNNVEKPLELR [304], GQIIGNFQAFDEDTGLPAHAR [311], VTQEIIVTER [806], VYAPASTLVDQPYANEGTVVVTTER [816]
142690	ATQFTGATGAIMTTETTK [93], DTGEIYTTSVTLDR [159], EEHSSYTLTVEAR [174], EETPPFLLTGYALDAR [182], GNNVEKPLELR [304], GQIIGNFQAFDEDTGLPAHAR [311], QESTSVLLQQSEK [568], VLEGMVEENQVNVETR [778]

TABLE 18

<u>Prostate cancer</u>	
MW (Da)	Subfractionation Tryptics identified [SEQ ID No]
	DTGEIYTTSVTLDR [159], FLDDLGLK [257], VATPLPDPMASR [746]

TABLE 18h

<u>Renal cell cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
111421		GNNVEKPLELR [304], IVAISEDYPR [400], LPDFESR [476], VTQEIVTER [806]

[0318] OGTA101

TABLE 19a

<u>Breast cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
24841	Vesicles	QFQFTDWPEQGVPK [572], YQYFVVDPMAYNMPQYILR [869]
24993	Vesicles	AALEYLGSFDHYAT [51], QFQFTDWPEQGVPK [572], YQYFVVDPMAYNMPQYILR [869]
55008		GVEGSDYINASFIDGYR [325], YQYFVVDPMAYNMPQYILR [869]
55921		AALEYLGSFDHYAT [51], QFQFTDWPEQGVPK [572]
56324		QHGQIR [578]
56872		AEPESETSILLSWTTPR [63], EIPSHHPTDPVELR [198], FIKPWESPDEMEDELLEK [255], GFPTIDMGPQLK [295], GPPSEPVLQTSEQAPSSAPR [309], GVEGSDYINASFIDGYR [325], LTQIETGENVTGMELEFK [498], LVNIMPYESTR [503], MLWEHNSTIVVMLTK [520], MVEEVDGR [527], SYSFVLNTR [668], TATMLCAASGNPDPEITWFK [675], TNEDVPSGPPRK [709], TSVLLSWEIPENYNSAMPFK [731], VGFGHEEMVK [763]
105325		TGCFIVIDAMLER [692]

TABLE 19b

<u>Cervical cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
118858	Integral	QHGQIR [578], WTEYR [836]
124604	Integral	WTEYR [836]

TABLE 19c

<u>Colorectal cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
	Heparin Binding	YSAPANLYVR [870]

TABLE 19d

<u>Hepatocellular carcinoma</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
72397		DMEPLTTLEFSEK [143], GFPTIDMGPQLK [295], GPGPYSPSVQFR [306], SGEGFIDFIGQVHK [632], TATMLCAASGNPDPEITWFK [675], YSAPANLYVR [870], YANVIAYDHSR [840]

TABLE 19e

<u>Lung cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
		YSAPANLYVR [870]
77419		FIKPWESPDEMEDELLEK [255], GFPTIDMGPQLK [295], GVEGSDYINASFIDGYR [325], LTQIETGENVTGMELEFK [498], QFQFTDWPEQGVPK [572], SDTIANYELVYK [625], TATMLCAASGNPDPEITWFK [675], TVDIYGHVTLMR [736], VEVEAVNSTSVK [755], YEGVVDIFQTVK [843]
78771		YANVIAYDHSR [840]

TABLE 19f

<u>Osteosarcoma</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
63624		QHGQIR [578], YQYFVVDPMAYNMPQYILR [869]

TABLE 19g

<u>Pancreatic cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
74307		DFLPVDTSNNNGR [118], EIPSHHPTDPVELRR [199], EQFGQDGPISVHCSAGVGR [219], GFPTIDMGPQLK [295], GNSAGGLQHR [305], GVEGSDYINASFIDGYR [325], KRAESDSR [434], LTQIETGENVTGMELEFK [498], LVNIMPYESTR [503], RAESDSRK [595], SDTIANYELVYK [625], SGEGFIDFIGQVHK [632], TGCFIVIDAMLER [692], TVDIYGHVTLMR [736], YANVIAYDHSR [840], YSVAGLSPYSDYEFR [873]

TABLE 19g-continued

<u>Pancreatic cancer</u>	
MW (Da)	Tryptics Subfractionation identified [SEQ ID No]
115291	TGCFIVIDAMLER [692], YQYFVVDPMAEYNMPQYILR [869], YSAPANLYVR [870]
124451	TGCFIVIDAMLER [692], YSAPANLYVR [870]
126215	YSAPANLYVR [870]
129890	YSAPANLYVR [870]

[0319] OGTA104

TABLE 20a

<u>Breast cancer</u>	
MW (Da)	Tryptics Subfractionation identified [SEQ ID No]
78181	EVPIYANR [236], FAVPTYAAK [244], QPQQFPSRPPPPQPK [586]

TABLE 20b

<u>Hepatocellular carcinoma</u>	
MW (Da)	Tryptics Subfractionation identified [SEQ ID No]
63302	DEEEPPSMTQLLR [113], DLLPEDFVVITYNK [134], EVPIYANR [236], KGFGGTAGMAFVGTVCSSR [419], QPGSVPR [584], QPQQFPSRPPPPQPK [586], RDQLWR [600]

TABLE 20c

<u>Ovarian cancer</u>	
MW (Da)	Tryptics Subfractionation identified [SEQ ID No]
49732	EVPIYANR [236], KGFGGTAGMAFVGTVCSSR [419], QPQQFPSRPPPPQPK [586]
50782	DQLWR [152], FAVPTYAAK [244], HVSPVTPPR [346], KGFGGTAGMAFVGTVCSSR [419], QPQQFPSRPPPPQPK [586], SYFRK [666]
54191	FAVPTYAAK [244], FLPGGTLR [260], FPSGTLR [264], QPQQFPSRPPPPQPK [586], SYFRK [666]

TABLE 20d

<u>Pancreatic cancer</u>	
MW (Da)	Tryptics Subfractionation identified [SEQ ID No]
73243	EEMILLANYLDSMYIMLNIR [179], EVPIYANR [236], HVSPVTPPR [346], KGFGGTAGMAFVGTVCSSR [419], QPQQFPSRPPPPQPK [586]

[0320] OGTA106

TABLE 21a

<u>Cervical cancer</u>	
MW (Da)	Tryptics Subfractionation identified [SEQ ID No]
61458	MonoQ Aqueous SLSGVGAGGGTPR [642]

TABLE 21b

<u>Melanoma</u>	
MW (Da)	Tryptics Subfractionation identified [SEQ ID No]
75458	CHIQASGRPQCSCMPGWTGECQLR [103], EQTPLFLAAR [221], ETDLSAGFVVVMGVDLSR [229], GPRPNPAIMR [310], GSPQLDCGPPALQEMPINQGGEGKK [318], TSLAGAGPR [705], TPLHAAVAADAR [717]

TABLE 21c

<u>Pancreatic cancer</u>	
MW (Da)	Tryptics Subfractionation identified [SEQ ID No]
88318	EQTPLFLAAR [221]

[0321] OGTA112

TABLE 22a

<u>Breast cancer</u>	
MW (Da)	Tryptics Subfractionation identified [SEQ ID No]
Triton X114	ETCVDLHLPR [228], FMFDLFQQFR [261], FYQTSVESTDFANAPESR [280], FYQTSVESTDFANAPESRKK [281], KFYQTSVESTDFANAPESR [416], KINSWVESQTNEK [420], LMEWTSLQNM [470], QYNSFNFALEDVQAK [594], TNSILFYGR [713], TYQFLQEYLDIAIK [741], VLHFDQVTENTTEK [781]

TABLE 22b

Cervical cancer		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
133844 MonoQ Aqueous		FMFDLFQQFRK [262], LMEWTSLQNMNR [470], SVQMMR [665], TMGMVNIFNGDADLSGMTWSHGLSVSK [706], VLEIPYK [779]

TABLE 22c

Chronic lymphocytic leukaemia		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
34501		ETCVDLHLPR [228], FMFDLFQQFR [261]

TABLE 22d

Hepatocellular carcinoma		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
26010		AATYHVDR [54], ETCVDLHLPR [228], FMFDLFQQFR [261], INSWVESQTNEK [384], LMEWTSLQNMNR [470], QYNSFNFALLEDVQAK [594], TNSILFYGR [713], VLHFDQVTENTTEK [781]

TABLE 22e

Pancreatic cancer		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
37971		ETCVDLHLPR [228], FMFDLFQQFR [261], FMFDLFQQFRK [262], INSWVESQTNEK [384], LMEWTSLQNMNR [470], QYNSFNFALLEDVQAK [594], SVQMMR [665], TNSILFYGR [713], VLHFDQVTENTTEK [781]
77017		ETCVDLHLPR [228], FMFDLFQQFR [261], INSWVESQTNEK [384], LMEWTSLQNMNR [470], QYNSFNFALLEDVQAK [594], SVQMMR [665]

TABLE 22f

Renal cell cancer		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
34256		INSWVESQTNEK [384], LMEWTSLQNMNR [470], SVQMMR [665], TNSILFYGR [713], VLHFDQVTENTTEK [781]

[0322] OGTA113

TABLE 23

Pancreatic cancer		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
32378		LEDPHVDIIR [449], LVHIIGALR [500], RGDDFFYHSENP [603], SEIINSK [627], TSSQPGFLER [730], YSYNTEWR [874]
32754		LEDPHVDIIR [449], LVHIIGALR [500], RGDDFFYHSENP [603], TSSQPGFLER [730], YPEVGDLR [865], YSYNTEWR [874]
42556		HVEMYQWVETEESR [345], LEDPHVDIIR [449], RGDDFFYHSENP [603], TSSQPGFLER [730], YPEVGDLR [865], YSYNTEWR [874]
43294		HVEMYQWVETEESR [345], LEDPHVDIIR [449], LVHIIGALR [500], RGDDFFYHSENP [603], TSSQPGFLER [730], YSYNTEWR [874]

[0323] OGTA119

TABLE 24a

B-cell non-Hodgkin's lymphoma		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
115552		AQPPEAGPQGLHDLGR [83], DEQHQCSSLGNLK [115], ERPPDHQHSQVK [222], GANTHLSTFSFTK [285], VGNQIFQSR [765]

TABLE 24b

Breast cancer		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
		AEWLNK [64]
70772		ALALLEDEER [75], AQPPEAGPQGLHDLGR [83], FQLNSGPNSTIK [268], ISSNPNPVVQMSVGHK [393],

TABLE 24b-continued

<u>Breast cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
		NLIAFSEDGSDPYVR [542], VGNQIFQSR [765]
98013		AEWLNK [64]
121313		AEWLNK [64]

TABLE 24c

<u>Colorectal cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
96268	Nucleotide Binding	ALALLEDEER [75], AQPPEAGPQGLHDLGR [83], ERPPDHQHSQVK [222], FQLSNSGPNSTIK [268], LEWLTMPNASNLDK [457], NLIAFSEDGSDPYVR [542], RQDLEVEVR [611], TNEPVWEENFTFFIHNPK [710]

TABLE 24d

<u>Gastric cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
56270		VDVGQQPLR [750]

TABLE 24e

<u>Hepatocellular carcinoma</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
59358		ALALLEDEER [75], ERPPDHQHSQVK [222]
60649		ALALLEDEER [75], AQPPEAGPQGLHDLGR [83], RQDLEVEVR [611], VDVGQQPLR [750], VGNQIFQSR [765]
73339		AEWLNK [64], AQPPEAGPQGLHDLGR [83], ERPPDHQHSQVK [222], NLIAFSEDGSDPYVR [542], SDPYGIIR [622], VGNQIFQSR [765], VPLSQLLTSEDMTVSQR [792]
84442		AEWLNK [64]
87814		AQPPEAGPQGLHDLGR [83], DEQHQCSSLGNLK [115], ERPPDHQHSQVK [222], FQLSNSGPNSTIK [268], HWWPFICQFIEK [339], IHFIEAQLQGGK [368], NLIAFSEDGSDPYVR [542],

TABLE 24e-continued

<u>Hepatocellular carcinoma</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
		TNEPVWEENFTFFIHNPK [710], VDVGQQPLR [750]
98646		AEWLNK [64]

TABLE 24f

<u>Lung cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
92181		AQPPEAGPQGLHDLGR [83], ERPPDHQHSQVK [222], HWWPFICQFIEK [339], ITVPLVSEVQIAQLR [398]

TABLE 24g

<u>Lymphoid leukaemia, unspecified</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
85026		ETIEPAVR [230], FQLSNSGPNSTIK [268], GEGPEAGAGGAGGR [290], RQDLEVEVR [611], VDVGQQPLR [750]
86516		AQPPEAGPQGLHDLGR [83], ERPPDHQHSQVK [222], GEGPEAGAGGAGGR [290], HWWPFICQFIEK [339], IHFIEAQLQGGK [368], ISSNPNPVVQMSVGHK [393], NLIAFSEDGSDPYVR [542], RQDLEVEVR [611], VDVGQQPLR [750], VLVALASEELAK [784]

TABLE 24h

<u>Neuroblastoma</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
	Sodium Carbonate Scrub	AEWLNK [64]

TABLE 24i

<u>Osteosarcoma</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
73285		AEWLNK [64]

TABLE 24j

<u>Pancreatic cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
80573		AQPPEAGPQGLHDLGR [83], ERPPDHQHSQVK [222], GEGPEAGAGGAGGR [290], HMWPFICQFIEK [339], IHFIEAQDLQ GK [368], NLIAFSEDGSDPYVR [542], SDPYGIIR [622], VGNQIFQSR [765], VYTENVDK [819]
93931		ALALLEDEER [75], DEQHQC SLGNLK [115], ERPPDHQHSQVK [222], GEGPEAGAGGAGGR [290], ISSNPNPVVQMSVGHK [393], VPLSQLLTSEDMTVSQR [792]

TABLE 24k

<u>Prostate cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
	Digitonin Insoluble, Triton X114, Aqueous	AEWLNK [64]

TABLE 24l

<u>Renal cell cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
76269		AEWLNK [64], AQPPEAGPQGLHDLGR [83], ERPPDHQHSQVK [222], HMWPFICQFIEK [339], SIQIHGTMR [638], TNEPVWEENFTFFIHNPK [710], VDVGQQPLR [750], VYTENVDKR [820]

[0324] OGTA124

TABLE 25a

<u>Hepatocellular carcinoma</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
98003		DLAVFLYHLR [133], EGLAHLIQSCGLGGMR [188], ESSPFLSPLEASR [227], EWGDGIR [240], HGLPSADAPSLK [334], HNSVVLGWPGYGR [340], LDEDLHVK [446], LEEGPPHTK [451], LVLLNMPGPPR [501], MPHFTVVPVDGPR [521], NIAFYPSNHER [539], NLALFEEELDIRPK [541], SIFDPPVFPVCMLGMR [636]

TABLE 25a-continued

<u>Hepatocellular carcinoma</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
116154		ESSPFLSPLEASR [227], EWGDGIR [240], HGLPSADAPSLK [334], LEEGPPHTK [451], NIAFYPSNHER [539], TPNWRPR [720], YIEYQGAEK [855]
126143		EHEEAESGEGTRRR [192], ESSPFLSPLEASR [227], EWGDGIR [240], HNSVVLGWPGYGR [340], LVSYTNLTQGAK [504], MPHFTVVPVDGPR [521], NSEGDENYMEFLEVLTEGLER [553], TFIDTVR [689], YMTETWDPSHAPDNFR [863]
137186		AELDDSDGHGNHR [62], EVITIYS [233], LVSYTNLTQGAK [504], MPHFTVVPVDGPR [521], NIAFYPSNHER [539]

TABLE 25b

<u>Lung cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
153348		DQFDICAK [151], EHEEAESGEGTR [191], EHEEAESGEGTRRR [192], ESSPFLSPLEASR [227], EVITIYS [233], LVLLNMPGPPR [501], LVSYTNLTQGAK [504]

TABLE 25c

<u>Ovarian cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
69811		ESSPFLSPLEASR [227], EVITIYS [233], IQMTWTR [389], LNEVIVTR [472], MHTAVK [517], NIAFYPSNHER [539], NSEGDENYMEFLEVLTEGLER [553], TPNWRPR [720]
74557		ESSPFLSPLEASR [227], GIDYYDR [300], NIAFYPSNHER [539], TFIDTVR [689], TPNWRPR [720]

TABLE 25d

<u>Pancreatic cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
137609		ELVHIKPDQSNVR [209], ESSPFLSPLEASR [227],

TABLE 25d-continued

<u>Pancreatic cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
		HNSVVLGWPYGWR [340], LEEGPPHTK [451], LVSYTNLTQGAK [504], NIAFYPSNHER [539], SIFDPPVFPVCMLGNR [636]

TABLE 25e

<u>Renal cell cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
135833		HNSVVLGWPYGWR [340], IFTVAQMDDNSIQMK [364], LVSYTNLTQGAK [504], MPHFTVVPVDGPR [521], NIAFYPSNHER [539]
154919		ESSPFLSPLEASR [227], HNSVVLGWPYGWR [340], IFTVAQMDDNSIQMKK [365], LVSYTNLTQGAK [504], SIFDPPVFPVCMLGNR [636]

[0325] OGTA126

TABLE 26a

<u>Breast cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
105325		AFMIIQEQ [66], GAAFEIALPR [282], GLPSLTSVSWNISVPR [302], IYVDLSNER [404], MALHLPWFHPR [508]

TABLE 26b

<u>Colorectal cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
104028		ASVSFLNFNLSNCER [87], MALHLPWFHPR [508], VEYYIPGSTTNPEVFK [757]

TABLE 26c

<u>Hepatocellular carcinoma</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
82606		AFMIIQEQ [66], ASVSFLNFNLSNCER [87], EEGVFTVTPDTK [172], LATEEPPPR [444], LWMNVEK

TABLE 26c-continued

<u>Hepatocellular carcinoma</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
		[505], QIGPGESCPDGVTHSISGR [580], TCSSNLTLTSGSK [679]
86381		AFMIIQEQ [66], LATEEPPPR [444]
88432		AFMIIQEQ [66], ASVSFLNFNLSNCER [87], IYVDLSNER [404], LATEEPPPR [444], LWMNVEK [505], MALHLPWFHPR [508], NVSGFSIANR [561], QIGPGESCPDGVTHSISGR [580]
90607		AFMIIQEQ [66], LATEEPPPR [444], NVSGFSIANR [561]

TABLE 26d

<u>Melanoma</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
81352		DQVACLTFK [153], IYVDLSNER [404], KFVPGCFVCLES [415]
87990		AFMIIQEQ [66], DQVACLTFK [153], IYVDLSNER [404], MALHLPWFHPR [508]
102001		AFMIIQEQ [66], ASVSFLNFNLSNCER [87], IYVDLSNER [404], LATEEPPPR [444]

TABLE 26e

<u>Pancreatic cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
57018		QGLTVSFIPYFK [576], QIGPGESCPDGVTHSISGR [580], QPGNMAGNFNLSLQGCQDAQSPGILR [583], VEYYIPGSTTNPEVFK [757]

TABLE 26f

<u>Prostate cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
		AFMIIQEQ [66], EEGVFTVTPDTK [172], IDATVVR [353], IYVDLSNER [404], LWMNVEK [505], TPNWDR [719]
		AFMIIQEQ [66], IYVDLSNER [404], LATEEPPPR [444], TPNWDR [719]

TABLE 26f-continued

<u>Prostate cancer</u>	
MW (Da) Subfractionation [SEQ ID No]	Tryptics identified
	AFMIIEQQR [66], EEGVFTVTPDTK [172], IYVVDLSNER [404], LWMNVEK [505], TPNWDR [719], VEYYIPGSTTNPEVFK [757]

TABLE 26

<u>Renal cell cancer</u>	
MW (Da) Subfractionation [SEQ ID No]	Tryptics identified
125611	KFVPGCFVCLESR [415], LSLVLVPAQK [487], SGVVCQTGR [633]

[0326] OGTA156

TABLE 27a

<u>Acute T-cell leukaemia</u>	
MW (Da) Subfractionation [SEQ ID No]	Tryptics identified
	ADGISSTFSQR [61], ATGFPEPNPR [90], AYIFSIDEK [99], SILQEENR [637], THQAFMR [697], TINFAR [701]
	ADGISSTFSQR [61], ATGFPEPNPR [90], AYIFSIDEK [99], DNQWLGVTLR [147], LPTGGCYGVPPDLR [482], SILQEENR [637], SQHTTEVVGAPQHEQIGK [648], TINFAR [701]
	ATGFPEPNPR [90], AYIFSIDEK [99], SILQEENR [637], THQAFMR [697], TINFAR [701], VTVAIPLK [807]
	ATGFPEPNPR [90], AYIFSIDEK [99], SILQEENR [637], SQHTTEVVGAPQHEQIGK [648], THQAFMR [697]
	ATGFPEPNPR [90], AYIFSIDEK [99], SILQEENR [637]

TABLE 27b

<u>B-cell non-Hodgkin's lymphoma</u>	
MW (Da) Subfractionation [SEQ ID No]	Tryptics identified
112390	ADGISSTFSQR [61], ATGFPEPNPR [90], AYIFSIDEK [99], DNQWLGVTLR [147], EASVHIQLEGRPSILEMDETSALK [167], LPVGLYFIK [484], NIFYIK [540], SDSAVLLR

TABLE 27b-continued

<u>B-cell non-Hodgkin's lymphoma</u>	
MW (Da) Subfractionation [SEQ ID No]	Tryptics identified
	[624], SILQEENR [637], SQHTTEVVGAPQHEQIGK [648], TINFAR [701], TYLAVGSMK [740]
114990	ADGISSTFSQR [61], ATGFPEPNPR [90], AYIFSIDEK [99], DNQWLGVTLR [147], IAPCYQDYVK [351], KAESPFR [407], NIFYIK [540], SDSAVLLR [624], SILQEENR [637], SQHTTEVVGAPQHEQIGK [648], STEEPPLQPILQQK [654], TCLEER [678], THQAFMRK [698], TINFAR [701], TYLAVGSMK [740]

TABLE 27c

<u>Chronic lymphocytic leukaemia</u>	
MW (Da) Subfractionation [SEQ ID No]	Tryptics identified
95173	DNQWLGVTLR [147], ELNILHEMK [205], SQHTTEVVGAPQHEQIGK [648]
168205	EVPGYIVLFYNMSLDVNR [235], ILELEEK [376], SQHTTEVVGAPQHEQIGK [648], STEEPPLQPILQQK [654]

TABLE 27d

<u>Hepatocellular carcinoma</u>	
MW (Da) Subfractionation	Tryptics identified [SEQ ID No]
66260	IEGLQISK [361], VIELNK [768]

[0327] OGTA159

TABLE 28a

<u>Breast cancer</u>	
MW (Da) Subfractionation	Tryptics identified [SEQ ID No]
Unknown	ESPAQAPA [226], VAQPGPLEPEEPR [745]

TABLE 28b

<u>Chronic lymphocytic leukaemia</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
124836		LEEEQK [450]

TABLE 28c

<u>Colorectal cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
42137		AASAGQEPLHNEELAGAGR [53], EEQAQR [180], VAQPGPLEPEEPR [745]
42590		AASAGQEPLHNEELAGAGR [53], VAQPGPLEPEEPR [745]

TABLE 28d

<u>Hepatocellular carcinoma</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
44183		VAQPGPLEPEEPR [745]

TABLE 28e

<u>Melanoma</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
21554		IQDLLAEGTITGVIDDR [387], VVLEDLASQVGLR [811]
21899		RDLGSR [598], VVLEDLASQVGLR [811]

TABLE 28f

<u>Pancreatic cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
33531		AASAGQEPLHNEELAGAGR [53], EHEEYLK [193], VAQPGPLEPEEPR [745]
33932		AASAGQEPLHNEELAGAGR [53], VAQPGPLEPEEPR [745]

[0328] OGTA168

TABLE 29a

<u>Glioblastoma</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
82431	MonoQ/Digitonin	AISTNSELSLTFR [74], ESHWIGLTDSEER [225], GSPGKPGPQGSSGDPGPPGPPGK [317], LQASGDALVDR [485], NDFQNLQQVFLQAK [534], NLITNLQR [543]
99352	MonoQ/Digitonin	GSPGKPGPQGSSGDPGPPGPPGK [317], GSQGGPPTGNK [319], KLGDQGTGK [423], LDTEVANLSVIMEEMK [448], LGDQGTGKK [461], LQASGDALVDR [485], NDFQNLQQVFLQAK [534], SVDDTSQAIQR [661]

TABLE 29b

<u>Melanoma</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
33451		GEPGPPGPAGER [292], LTAVESDLK [495], SVDDTSQAIQR [661]

[0329] OGTA169

TABLE 30a

<u>Breast cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
100968	PNGase F Deglycosylation	FGAALTVLGDVNGDK [252]

TABLE 30b

<u>Chronic lymphocytic leukaemia</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
	Triton X114, Detergent Soluble	AVIFTQVSR [96], DLQSSVTLDLALDPGR [138], ELNDIASKPSQEHIFK [204], ESHVAMHR [224], FQTHFTFEER [269], FQTHFTFEER [270], GAVYLFHGVLPSPISPSHSQR [287], GVQSLVLGAPR [327], IAGSQLSSR [350], IAPPASDPLAHIQK [352], INHLIFR [383], LFHASYGAR [458], LTDVVIGAPGEEENR [496], NFATMMNFVR [535], NLREMLAADAQR [545], QEQDIVFLIDGSGSISSR [567], SLHLTCDSAPVGSQGTWSTSCR [641], VEDFDALK [752], YAVYTVVSSHEQFTK [841]

TABLE 3Ob-continued

<u>Chronic lymphocytic leukaemia</u>	
MW (Da) Subfractionation	Tryptics identified [SEQ ID No]
108778	AVIFTQVSR [96], DVIPMADAAGIIR [161], ESHVAMHR [224], FQTHFTFEEFR [269], GVQSLVLGAPR [327], INHLIFR [383], LFHASYGAR [458], LTDVVIGAPGEEENR [496], NLRPMLAADAQR [545], QEQDIVFLIDGSGSISRR [567], YAVYTVVSSHEQFTK [841]
111501	AVIFTQVSR [96], DVIPMADAAGIIR [161], ELNDIASKPSQEHIFK [204], ESHVAMHR [224], FGAALTVLGDVNGDK [252], FQTHFTFEEFR [269], FQTHFTFEEFR [270], GAVYLFHGVGLGPSISPSHSQR [287], GVQSLVLGAPR [327], IAGSQLSSR [350], INHLIFR [383], LFHASYGAR [458], LTDVVIGAPGEEENR [496], NFATMMNFVR [535], NLRPMLAADAQR [545], NMYLTGLCFLLGPTQLTQR [548], QEQDIVFLIDGSGSISRR [567], YAIGVGLAFQNR [839], YAVYTVVSSHEQFTK [841], YQVNNLGQR [868]
114387	AVIFTQVSR [96], DVIPMADAAGIIR [161], EMMEEANGQIAPENGTQTPSPSEK [210], ESHVAMHR [224], FQTHFTFEEFR [269], FQTHFTFEEFR [270], GGAQITFLATFDVSPK [296], IAGSQLSSR [350], INHLIFR [383], KEGDSLIDYK [409], LFHASYGAR [458], LTDVVIGAPGEEENR [496], NFATMMNFVR [535], NLRPMLAADAQR [545], VEDFDALK [752], YAIGVGLAFQNR [839], YAVYTVVSSHEQFTK [841], YQVNNLGQR [868]
117454	DVIPMADAAGIIR [161], FQTHFTFEEFR [269], GGQVSVCLPR [299], IAGSQLSSR [350], INHLIFR [383], KEGDSLIDYK [409], LFHASYGAR [458], LTDVVIGAPGEEENR [496], NMYLTGLCFLLGPTQLTQR [548], QEQDIVFLIDGSGSISRR [567], YQVNNLGQR [868]
136634	AVIFTQVSR [96], CDVPSFSVQEELDFTLK [100], FQTHFTFEEFR [269], FQTHFTFEEFR [270], GVQSLVLGAPR [327], INHLIFR [383], KEGDSLIDYK [409], LTDVVIGAPGEEENR [496], NFATMMNFVR [535], NLRPMLAADAQR [545], NPVLDCSIAGCLR [552],

TABLE 3Ob-continued

<u>Chronic lymphocytic leukaemia</u>	
MW (Da) Subfractionation	Tryptics identified [SEQ ID No]
	SLHLTCDAPVGSQGTWSTSCR [641], YQHTGK [867]
139470	AVIFTQVSR [96], DSYLGYSTELALWK [158], FQTHFTFEEFR [269], GVQSLVLGAPR [327], INHLIFR [383], KEGDSLIDYK [409], LTDVVIGAPGEEENR [496], NFATMMNFVR [535], NLRPMLAADAQR [545], QEQDIVFLIDGSGSISRR [567]
142364	GGQVSVCLPR [299]
152450	AVIFTQVSR [96], AVISQFQRPSTQFSLMQFSNK [97], DIQNQLK [130], DVIPMADAAGIIR [161], ELNDIASKPSQEHIFK [204], ESHVAMHR [224], FQTHFTFEEFR [269], GNLSFGWVR [303], GVQSLVLGAPR [327], IAPPASDFLAHIQK [352], INHLIFR [383], KEGDSLIDYK [409], LFHASYGAR [458], LFHASYGARR [459], LTDVVIGAPGEEENR [496], NLRPMLAADAQR [545], QEQDIVFLIDGSGSISRR [567], YAVYTVVSSHEQFTK [841], YQVNNLGQR [868]
159984	AVIFTQVSR [96], DIQNQLK [130], DVIPMADAAGIIR [161], ESHVAMHR [224], FQTHFTFEEFR [269], GAVYLFHGVGLGPSISPSHSQR [287], GVQSLVLGAPR [327], INHLIFR [383], KEGDSLIDYK [409], LFHASYGAR [458], LTDVVIGAPGEEENR [496], NLRPMLAADAQR [545], NMYLTGLCFLLGPTQLTQR [548], QEQDIVFLIDGSGSISRR [567], YAVYTVVSSHEQFTK [841], YQVNNLGQR [868]

[0330] OGTA174

TABLE 31a

<u>Acute T-cell leukaemia</u>	
MW (Da) Subfractionation	Tryptics identified [SEQ ID No]
	CQQQLEVLK [107], HLPETEAGR [337], LSQCHELWER [490], LSWYDPDFQAR [493], NSYCKK [554], QGAQWAALCDSSSR [573], SHAENPTASHVDNEYSQPPR [634], TTPPTTRPPPTTTPEPTAPPR [734], VLALLCSGFQPK [771], WEEVCR [826]HLPETEAGR [337], NSYCKK [554], QGAQWAALCDSSSR [573], VLDAGDPTSR [775]VLDAGDPTSR [775]

TABLE 31b

Chronic lymphocytic leukaemia		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
52248		HLPETEAGR [337], LSWYDPDFQAR [493], TQDLENFLCNNLQCGSFLK [723]
53229		LSWYDPDFQAR [493]
70807		AQDPGEPR [81], HLPETEAGR [337], IQNSSCTSLHCFPRK [390], LSWYDPDFQAR [493], SHAENPTASHVDNEYSQPPR [634]
72277		EHQPLPIQWK [194], HLPETEAGR [337], LSQCHELWER [490], LSWYDPDFQAR [493], SHAENPTASHVDNEYSQPPR [634], VLDAGDPTSR [775]
73777		HLPETEAGR [337], LSWYDPDFQAR [493], SHAENPTASHVDNEYSQPPR [634], VLDAGDPTSR [775]

[0331] OGTA176

TABLE 32a

B-cell non-Hodgkin's lymphoma		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
33825		ELAQSQEALQVEQR [202], ETLQSEEQQR [231], ITQLGQSAEDLQGSR [396], ITQLGQSAEDLQGSRR [397], YLQVSQQLQQTNR [862]

TABLE 32b

Chronic lymphocytic leukaemia		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
38233		ELAQSQEALQVEQR [202], ETLQSEEQQR [231], ETLQSEEQRR [232], ITQLGQSAEDLQGSR [396], SEQPTASWR [630], SSLPYICEMTAFR [650], YLQVSQQLQQTNR [862]
39836		ELAQSQEALQVEQR [202], ITQLGQSAEDLQGSR [396]
40663		ELAQSQEALQVEQR [202], ITQLGQSAEDLQGSR [396]

[0332] OGTA177

TABLE 33

Chronic lymphocytic leukaemia		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
81514		FLNLTSEK [259], MESEELADR [514], SLSNYPDFQGAR [643]
81757		SLSNYPDFQGAR [643]
83454		DIQVASNEILR [131], FLNLTSEK [259], SLSNYPDFQGAR [643], SQHQETPVYLGATAGMR [647], YGVLDAGSSHTSLYIYK [853], VTEMMK [801]
83957		DIQVASNEILR [131], SLSNYPDFQGAR [643], SQHQETPVYLGATAGMR [647], VTEMMK [802]
85186		SLSNYPDFQGAR [643]
86534		SQHQETPVYLGATAGMR [647]
86954		DIQVASNEILR [131], SLSNYPDFQGAR [643]

[0333] OGTA197

TABLE 34a

Colorectal cancer		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
93409		QSPEDVYFSK [587], TYVDPHTYEDPNQAVLK [742], WTPPDQSGGR [837], YKPMMIITEYMENGALDK [857]
95846		MQQYTEHFMAAGYTAIEK [523], NGVSGLVTSR [538], VIGAGEFGEVYK [769], WTPPDQSGGR [837], YKPMMIITEYMENGALDK [857]
101142		QSPEDVYFSK [587], TSVTVSDLEPHMNYFTVEAR [733], YKPMMIITEYMENGALDK [857]

TABLE 34b

Hepatocellular carcinoma		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
75736		AINDGFR [73], LPSTSGSEGVPPR [481], TLADFDPR [702], YLANMNYVHR [860], YSEPPHGLTR [871]
82606		AINDGFR [73], EVLDDFAAAGGELGWLTHPYGK [239], IDTIAPDEITVSSDFEAR [359], LPSTSGSEGVPPR [481], RKNQR [605], TYVDPHTYEDPNQAVLK [742],

TABLE 34b-continued

<u>Hepatocellular carcinoma</u>	
MW (Da)	Tryptics identified Subfractionation[SEQ ID No]
	VDFLGEAGIMGQFSHHNIIR [747], VVQMTNDDIK [813], YLANMNYVHR [860], YSEPPHGLTR [871]
84442	AINDGFR [73], FTTEIHPSCVTR [278], IDTIAPDEITVSSDFEAR [359], LPSTSGSEGVPPFR [481], MQQYTEHFMAAGYTAIEK [523], TVVDPHTYEDPNQAVLK [742], VVQMTNDDIKR [814], YKPMMIITEYMENGALDK [857], YLANMNYVHR [860], YSEPPHGLTR [871]
86381	AINDGFR [73], QSPEDVYFSK [587]
88432	AINDGFR [73], LPGHQKR [478], QSPEDVYFSK [587], VIGAGEFGEVYK [769], VSDFGLSR [796], VVQMTNDDIK [813], VVQMTNDDIKR [814], WTAPEAISYR [834], WTAPEAISYRK [835], YKPMMIITEYMENGALDK [857], YSEPPHGLTR [871]
92956	KGDSNSYNVR [417], QSPEDVYFSK [587], RKNQR [605], VIGAGEFGEVYK [769], VVQMTNDDIK [813], WTAPEAISYR [834], YLANMNYVHR [860], YSEPPHGLTR [871]
116695	LPSTSGSEGVPPFR [481], MELQAAR [512], MQQYTEHFMAAGYTAIEK [523], TLADFDPR [702], VYYKK [822], YKPMMIITEYMENGALDK [857]

TABLE 34c

<u>Lung cancer</u>	
MW (Da)	Tryptics identified Subfractionation[SEQ ID No]
	DQVNTVGIPi [154], EVPVAIK [238], FTTEIHPSCVTR [278], IDTIAPDEITVS SDFEAR [359], KKGDSNSYNVR [422], VIGAGEFGEVYK [769], VLEDDPEATYTTSGGK [777], VVQMTNDDIK [813], VVQMTNDDIKR [814], YKPMMIITEYMENGALDK [857]
	KEVPVAIK [414], LPSTSGSEGVPPFR [481], TSVTVSDLEPHMNYTFTVEAR [733], VLEDDPEATYTTSGGK [777], WTPPDQSGGR [837], YEVYTR [845], YLANMNYVHR [860], YSEPPHGLTR [871]

TABLE 34c-continued

<u>Lung cancer</u>	
MW (Da)	Tryptics identified Subfractionation[SEQ ID No]
113648	DGEFSLVLQLVGMLR [121], LPSTSGSEGVPPFR [481], MQQYTEHFMAAGYTAIEK [523], QSPEDVYFSK [587], RKNQR [605], VDFLGEAGIMGQFSHHNIIR [747], VIGAGEFGEVYK [769], VVQMTNDDIK [813], WTAPEAISYRK [835], YKPMMIITEYMENGALDK [857], YLANMNYVHR [860]
116436	AINDGFR [73], FADIVSILDK [242], FTTEIHPSCVTR [278], GDSNSYNVR [288], LPSTSGSEGVPPFR [481], MQQYTEHFMAAGYTAIEK [523], NGVSGLVTSR [538], TASVSINTEPPK [673], TLADFDPR [702], TVSEWLESIK [738], VIGAGEFGEVYK [769], WTPPDQSGGR [837], YEVYTR [845], YKPMMIITEYMENGALDK [857], YLANMNYVHR [860]
122412	LPSTSGSEGVPPFR [481], VYYKK [822], YLANMNYVHR [860], QSPEDVYFSK [587]

TABLE 34d

<u>Melanoma</u>	
MW (Da)	Tryptics identified Subfractionation[SEQ ID No]
78319	APQDPASMPCTRPPSAPHYLTAVGMA K [80], DGEFSLVLQLVGMLR [121], EVPVAIK [238], FADIVSILDK [242], MELQAAR [512], STTSLSVWSIPPPQSSR [660], SVGPLTR [662], TASVSINTEPPK [673], TSVTVSDLEPHMNYTFTVEAR [733], VIGAGEFGEVYK [769], YKPMMIITEYMENGALDK [857], YLANMNYVHR [860]

TABLE 34e

<u>Osteosarcoma</u>	
MW (Da)	Tryptics identified Subfractionation[SEQ ID No]
30076	LPSTSGSEGVPPFR [481], VVQMTNDDIK [813], VVQMTNDDIKR [814], YEVYTR [846], YKPMMIITEYMENGALDK [857], YLANMNYVHR [860]
55008	AINDGFR [73], APQDPASMPCTRPPSAPHYLTAVGMA K [80], DGEFSLVLQLVGMLR [121], IDTIAPDEITVSSDFEAR [359], RKNQR [605],

TABLE 34e-continued

<u>Osteosarcoma</u>	
MW (Da)	Subfractionation Tryptics identified [SEQ ID No]
67385	STTSLSVSWSI PPPQSR [660], SVGPLTR [662], TASVSINQTEPPK [673], TNWVYR [715], TSVTVSDLEPHMNYTFTVEAR [733], TYVDPHTYEDPNQAVLK [742], VLEDDPEATYTTSGGK [777], WTPPQDSGGR [837], YKPMMIITEYMENGALDK [857]
	AINDGFR [73], IDTIAPDEITVSSDFEAR [359], KGDSNSYNVR [417], LPTPMDCPSAIYQLMMQCWQQR [483], MQQYTEHFMAAGYTAIEK [523], NGVSGLVTSR [538], STTSLSVSWSI PPPQSR [660], SVGPLTR [662], TASVSINQTEPPK [673], TLADFDPR [702], TNWVYR [715], TSVTVSDLEPHMNYTFTVEAR [733], TYVDPHTYEDPNQAVLK [742], VDFLGEAGIMGQFSHHNIIR [747], WTPPQDSGGR [837], YSEPPHGLTR [871]
93496	ACFALLWGCALAAAAAQGK [55], AINDGFR [73], FTTEIHPSCVTR [278], IDTIAPDEITVSSDFEAR [359], RKNQR [605], STTSLSVSWSI PPPQSR [660], SVGPLTR [662], TASVSINQTEPPK [673], TNWVYR [715], TYVDPHTYEDPNQAVLK [742], VIGAGEFGEVYK [769], VVQMTNDDIKR [814], YEVYRK [846], YLANMNYVHR [860], YSEPPHGLTR [871]

TABLE 34f

<u>Ovarian cancer</u>	
MW (Da)	Subfractionation Tryptics identified [SEQ ID No]
63557	AINDGFR [73], FTTEIHPSCVTR [278]LPSTSGSEGVPPFR [481], STTSLSVSWSI PPPQSR [660], TASVSINQTEPPK [673], TNWVYR [715], VVQMTNDDIKR [814], WTPPQDSGGR [837], YEVYR [845], YLANMNYVHR [860], YSEPPHGLTR [871]
67618	ACFALLWGCALAAAAAQGK [55], QSPEDVYFSK [587], RKNQR [605], SVGPLTR [662], TASVSINQTEPPK [673], TLADFDPR [702], TSVTVSDLEPHMNYTFTVEAR [733], VDFLGEAGIMGQFSHHNIIR [747], WTPPQDSGGR [837], YKPMMIITEYMENGALDK [857]

TABLE 34f-continued

<u>Ovarian cancer</u>	
MW (Da)	Subfractionation Tryptics identified [SEQ ID No]
69811	FADIVSILDK [242], KGDSNSYNVR [418], RKNQR [605], TASVSINQTEPPK [673], TYVDPHTYEDPNQAVLK [742], VSDFGLSR [796]
79417	ACFALLWGCALAAAAAQGK [55], DGEFSLVQLVGLR [121], IDTIAPDEITVSSDFEAR [359], SVGPLTR [662], TSVTVSDLEPHMNYTFTVEAR [733], TYVDPHTYEDPNQAVLK [742], VIGAGEFGEVYK [769], YKPMMIITEYMENGALDK [857], YLANMNYVHR [860], YSEPPHGLTR [871]

TABLE 34

<u>Pancreatic cancer</u>	
MW (Da)	Subfractionation Tryptics identified [SEQ ID No]
53057	AINDGFR [73], IDTIAPDEITVSSDFEAR [359], LEGVSK [454], LNVEER [474], LPSTSGSEGVPPFR [481], SVGPLTR [662], VIGAGEFGEVYK [769], VVQMTNDDIK [813], YEVYRK [847]
53737	IDTIAPDEITVSSDFEAR [359], LPSTSGSEGVPPFR [481], SEQLKPLK [629], SVGPLTRK [663], YLANMNYVHR [860]
93964	LPSTSGSEGVPPFR [481], TVSEWLESIK [738], WTPPQDSGGR [837], YSEPPHGLTR [871]
102286	VIGAGEFGEVYK [769], VVQMTNDDIKR [814], WTPPQDSGGR [837], YSEPPHGLTR [871]
107693	KGDSNSYNVR [417], QSPEDVYFSK [587], TNWVYR [715], TYVDPHTYEDPNQAVLK [742], VIGAGEFGEVYK [769], VVQMTNDDIKR [814], WTPPQDSGGR [837], YLANMNYVHR [860], YSEPPHGLTR [871]
110489	TASVSINQTEPPK [673], TLADFDPR [702], TYVDPHTYEDPNQAVLK [742], VIGAGEFGEVYK [769], WTPPQDSGGR [837]
113324	FADIVSILDK [242], IDTIAPDEITVSSDFEAR [359], KGDSNSYNVR [417], SVGPLTR [662], TLADFDPR [702], TYVDPHTYEDPNQAVLK [742], VYK [822], WTPPQDSGGR [837], YEVYR [845],

TABLE 34-continued

Pancreatic cancer	
MW (Da)	Subfractionation [SEQ ID No]
	YEVTYRK [846], YLANMNYVHR [860], YSEPPHGLTR [871]
116302	IDTIAPDEITVSSDFEAR [359], TYVDPHTYEDPNQAVLK [742], VVQMTNDDIK [813], WTPPQDSGGR [837], YEVTYR [845], YLANMNYVHR [860], YSEPPHGLTR [871]
116866	ACFALLWGCALAAAAAQGK [55], AINDGFR [73], IDTIAPDEITVSSDFEAR [359], LPSTSGSEGVPPFR [481], STTSLSVSWSIPPPQQSR [660], TYVDPHTYEDPNQAVLK [742], VIGAGEFGEVYK [769], VLEDDPEATYTTSGGK [777], WTAPEAISYR [834], WTPPQDSGGR [837], YKPMMIITEYMENGALDK [857], YLANMNYVHR [860], YSEPPHGLTR [871]
122219	ACFALLWGCALAAAAAQGK [55], AINDGFR [73], IDTIAPDEITVSSDFEAR [359], KGDSNSYNVR [417], LPSTSGSEGVPPFR [481], MQQYTEHFMAAGYTAIEK [523], QSPEDVYFSK [587], STTSLSVSWSIPPPQQSR [660], TNWVYR [715], VIGAGEFGEVYK [769], WTAPEAISYR [834], WTPPQDSGGR [837], YKPMMIITEYMENGALDK [857], YSEPPHGLTR [871]
180074	KGDSNSYNVR [417], KGDSNSYNVR [418], LPSTSGSEGVPPFR [481], MELQAAR [512], QSPEDVYFSK [587], TNWVYR [715], WTAPEAISYR [834], WTPPQDSGGR [837], YEVTYR [845], YSEPPHGLTR [871]
184373	AINDGFR [73], LPSTSGSEGVPPFR [481], QSPEDVYFSK [587], TNWVYR [715], WTAPEAISYR [834], WTPPQDSGGR [837], YEVTYR [845], YLANMNYVHR [860], YSEPPHGLTR [871]
188775	LPSTSGSEGVPPFR [481], TNWVYR [715], VIGAGEFGEVYK [769], VVQMTNDDIK [813], WTAPEAISYR [834], WTPPQDSGGR [837], YLANMNYVHR [860], YSEPPHGLTR [871]

TABLE 34h

Prostate cancer	
MW (Da)	Subfractionation [SEQ ID No]
	LPSTSGSEGVPPFR [481], MELQAAR [512], YEVTYR [845]
	LPSTSGSEGVPPFR [481], NGVSGLVTSR [538], VVQMTNDDIK [813], WTPPQDSGGR [837], YSEPPHGLTR [871]

TABLE 34i

Renal cell cancer	
MW (Da)	Subfractionation [SEQ ID No]
88378	AINDGFR [73], KGDSNSYNVR [418], LPSTSGSEGVPPFR [481], TNWVYR [715], WTAPEAISYR [834], WTPPQDSGGR [837], YSEPPHGLTR [871]
90442	AINDGFR [73], LPSTSGSEGVPPFR [481], SVGPLTR [662], TNWVYR [715], TYVDPHTYEDPNQAVLK [742], VIGAGEFGEVYK [769], VVQMTNDDIKR [814], WTAPEAISYR [834], WTPPQDSGGR [837], YEVTYR [845], YLANMNYVHR [860], YSEPPHGLTR [871]
117578	AINDGFR [73], TNWVYR [715], VIGAGEFGEVYK [769], VVQMTNDDIK [813], VVQMTNDDIKR [814], WTAPEAISYR [834], YLANMNYVHR [860], YSEPPHGLTR [871]
122597	ACFALLWGCALAAAAAQGK [55], TYVDPHTYEDPNQAVLK [742], VIGAGEFGEVYK [769], VVQMTNDDIKR [814], WTAPEAISYR [834], YEVTYR [846], YLANMNYVHR [860], YSEPPHGLTR [871]

[0334] OGTA202

TABLE 35

Colorectal cancer		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
51531	Nucleotide Binding	FTQDTFR [277]

[0335] OGTA203

TABLE 36a

<u>Ovarian cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
69811		DNIVSYNDEGGGEEDTQAFDIGTLR [144], EDAQINTTIGSVTAQDPDAAR [168], RTPTAR [618], TALLNMDR [669], TPESSPPGTPIGR [716], TSGFPAKK [727], VEASNPYVEPR [751]

TABLE 36b

<u>Renal cell cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
82732		IVVEDVDEPPVFSK [402], KNGYNR [428], TSGFPAKK [727],

[0336] OGTA206

TABLE 37a

<u>Breast cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
27751	Vesicles	VYDSSLALPQDLQAAR [817]

TABLE 37b

<u>Pancreatic cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No] ⁹
26738		VYDSSLALPQDLQAAR [817]
27019		VYDSSLALPQDLQAAR [817]

TABLE 37c

<u>Prostate cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
	Digitonin	VYDSSLALPQDLQAAR [817]

[0337] OGTA213

TABLE 38

<u>Lung cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
27644		IVFTPTICK [401]

[0338] OGTA214

TABLE 39

<u>Ovarian cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
65600		QCLIKK [565], SSSNFLNYDLTLR [651]
79331		ISVTVSETFDPEEK [394], SSSNFLNYDLTLR [651]
89348		ISVTVSETFDPEEK [394], SSSNFLNYDLTLR [651]

[0339] OGTA216

TABLE 40a

<u>Breast cancer</u>	
MW (Da)	Tryptics identified [SEQ ID No]
196008	AFYAPVHADDLR [69], EGAQYLMQAAGLGR [186], FQVDLVSENAGR [271], GPIVPLNVADQK [307], IDHRR [356], KDWLQADMR [408], NVGLMICGHVHMGR [555], SEIFNENFGPDFR [626]
248063	DEGPAAAGDGLGRPLGPTPSQSR [114], DVVVSVEYSK [163], EGAQYLMQAAGLGR [186], FQVDLVSENAGR [271], NVGLMICGHVHMGR [556], SEIFNENFGPDFR [626]

TABLE 40b

<u>Colorectal cancer</u>	
MW (Da)	Tryptics identified [SEQ ID No]
Heparin Binding	DAVVTYTAESK [110], DVVVSVEYSK [163], SEIFNENFGPDFR [626]
Heparin Binding	KENIIAFEEIIEPYR [410], SEIFNENFGPDFR [626]
Heparin Binding	KENIIAFEEIIEPYR [410], LNELLK [471], SEIFNENFGPDFR [626]
Heparin Binding	AFYAPVHADDLR [69], EHSSTANIIVMSLPVAR [195], FQVDLVSENAGR [271],

TABLE 40b-continued

<u>Colorectal cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
		SEIFNENFGPDFR [626], SPGWRPAFK [645]
	Heparin Binding	DEGPAAAGDGLGRPLGPTPSQSR [114], GFFGYK [294], KENIIAFEEIIEPYR [410], SEIFNENFGPDFR [626]
	Heparin Binding	FQVDLVSENAGR [271], GGGAYYLISR [298], KENIIAFEEIIEPYR [410], SEIFNENFGPDFR [626]
	Heparin Binding	AAAAAAAAAAAAAGAGAGAK [49], DLPPILLVR [136], DNIYPAFQMFAPK [145], EGAQYLMQAAGLGR [186], EHSSTANIIIVMSLPVAR [195], EPFEDGFANGEESTPTR [216], FQVDLVSENAGR [271], IDFSDIMVLGDINTKPK [354], IDHYR [357], KENIIAFEEIIEPYR [410], SEIFNENFGPDFR [626]
	Heparin Binding	CMLNIWGVMLFIR [106], IDHRR [356], ITDNELELYK [395], SEIFNENFGPDFR [626]
	Heparin Binding	DLPPILLVR [136], NVGLMICGHVHMGPR [555], SEIFNENFGPDFR [626]
	Heparin Binding	AMATLLSK [78], EGAQYLMQAAGLGR [186], GGGAYYLISR [298], GPIVPLNVADQK [307], NVGLMICGHVHMGPRR [556], SPGWRPAFK [645]
121506		DEGPAAAGDGLGRPLGPTPSQSR [114], DLPPILLVR [136], DNIYPAFQMFAPK [145], DWLQADMR [164], EGAQYLMQAAGLGR [186], EPFEDGFANGEESTPTR [216], IDFSDIMVLGDINTKPKK [355], IDHYR [357], KENIIAFEEIIEPYR [410], KSDLDTSKPLSEKPITHK [435], LNELK [471], NVGLMICGHVHMGPRR [556], SEIFNENFGPDFR [626], TFGHNTMDAVPR [688], VELPGTAVPSVPEDAAPASR [754]
125772		DLPPILLVR [136], DWLQADMR [164], EPFEDGFANGEESTPTR [216], DWLQADMR [408], SEIFNENFGPDFR [626], SPGWRPAFK [645], TFGHNTMDAVPR [688], VELPGTAVPSVPEDAAPASR [754]
140688		DLPPILLVR [136], DWLQADMR [164], EGAQYLMQAAGLGR [186], EPFEDGFANGEESTPTR [216], DWLQADMR [408], KSDLDTSKPLSEKPITHK [435], NVGLMICGHVHMGPR [555], TFGHNTMDAVPR [688], VELPGTAVPSVPEDAAPASR [754]

TABLE 40b-continued

<u>Colorectal cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
146522		DLPPILLVR [136], DWLQADMR [164], EGAQYLMQAAGLGR [186], EPFEDGFANGEESTPTR [216], IDHRR [356], DWLQADMR [408], KENIIAFEEIIEPYR [410], KSDLDTSKPLSEKPITHK [435], SEIFNENFGPDFR [626], TFGHNTMDAVPR [688], VELPGTAVPSVPEDAAPASR [754]
167535		DWLQADMR [164], EPFEDGFANGEESTPTR [216], GPIVPLNVADQK [307], IDHRR [356], SEIFNENFGPDFR [626], TFGHNTMDAVPR [688], VELPGTAVPSVPEDAAPASR [754]
175447	Nucleotide Binding	NNEPLR [549], SEIFNENFGPDFR [626], TFGHNTMDAVPR [688], VELPGTAVPSVPEDAAPASR [754]
190098	Nucleotide Binding	DAVVITYAESK [110], EGAQYLMQAAGLGR [186], EMSIDQAK [213], LHEDDK [465], LNELLK [471], RAMATLLSK [596], SEIFNENFGPDFR [626], SPGWRPAFK [645], TFGHNTMDAVPR [688]
218400	Nucleotide Binding	DEGPAAAGDGLGRPLGPTPSQSR [114], EGAQYLMQAAGLGR [186], KENIIAFEEIIEPYR [410], KSDLDTSKPLSEKPITHK [435], SEIFNENFGPDFR [626]
221484		DEGPAAAGDGLGRPLGPTPSQSR [114], EGAQYLMQAAGLGR [186], EPFEDGFANGEESTPTR [216], IDHRR [356], DWLQADMR [408], NVGLMICGHVHMGPRR [556], SEIFNENFGPDFR [626], TFGHNTMDAVPR [688]
255000		EGAQYLMQAAGLGR [186], EPFEDGFANGEESTPTR [216], SEIFNENFGPDFR [626], TFGHNTMDAVPR [688], VELPGTAVPSVPEDAAPASR [754]
301246		DEGPAAAGDGLGRPLGPTPSQSR [114], EGAQYLMQAAGLGR [186], EPFEDGFANGEESTPTR [216], IDHRR [356], IDHYR [357], SEIFNENFGPDFR [626], TFGHNTMDAVPR [688]

TABLE 40c

<u>Pancreatic cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
148609		AFYAPVHADDLR [69], DVVVSVEYSK [163],

TABLE 40c-continued

<u>Pancreatic cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
		GGGAYYLISR [298], NNEPLR [549], SEIFNENFGPDFR [626], VELPGTAVPSVPEDAAPASR [754]
154726		DVVVSVEYSK [163], EPFEDGFANGEESTPTR [216], GPVPLNVADQK [307], NVGLMICGHVHMGP [555], SEIFNENFGPDFR [626]

[0340] OGTA222

TABLE 41a

<u>B-cell non-Hodgkin's lymphoma</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
45662		AVGFGGDFDGVPR [95], TLEQMDVVHR [703]
48028		ALYQLGMR [77], AVGFGGDFDGVPR [95], GALADNLLR [283], MYPETFLYVTSSAGIR [530], NVPDDVLR [559], RTLEQMDVVHR [617], TLEQMDVVHR [703], YPDLIAELLR [864], VPEGLEDVSK [791]
48530		ALYQLGMR [77], AVGFGGDFDGVPR [95], GALADNLLR [283], MYPETFLYVTSSAGIR [530], TLEQMDVVHR [703], VPEGLEDVSK [791]
49042		ALYQLGMR [77], AVGFGGDFDGVPR [95], GALADNLLR [283], MYPETFLYVTSSAGIR [530], TLEQMDVVHR [703], VPEGLEDVSK [791]
66777		ALYQLGMR [77], AVGFGGDFDGVPR [95], GALADNLLR [283], TLEQMDVVHR [703], ATLQLSR [91]
68315		ALYQLGMR [77], AVGFGGDFDGVPR [95], GALADNLLR [283], TLEQMDVVHR [703]
69923		ALYQLGMR [77], ATLQLSR [91], AVGFGGDFDGVPR [95], GALADNLLR [283], TLEQMDVVHR [703]
71607		ALYQLGMR [77], AVGFGGDFDGVPR [95], GALADNLLR [283], TLEQMDVVHR [703], VPEGLEDVSK [791]

TABLE 41b

<u>Colorectal cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
52940		ALYQLGMR [77], AVGFGGDFDGVPR [95], GALADNLLR [283], TLEQMDVVHR [703]
55204		AVGFGGDFDGVPR [95]
58558		AVGFGGDFDGVPR [95], TLEQMDVVHR [703]

[0341] OGTA236

TABLE 42

<u>Pancreatic cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
73411		SVLGVITIVNLR [664]

[0342] OGTA237

TABLE 43a

<u>B-cell non-Hodgkin's lymphoma</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
47536		IADFGLAR [349]
48028		IADFGLAR [349]
48530		IADFGLAR [349]
49565		IADFGLAR [349]
50098		IADFGLAR [349]
51766		IADFGLAR [349]
52346		IADFGLAR [349]

TABLE 43b

<u>Lymphoid leukaemia, unspecified</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
52041		IADFGLAR [349]
52618		IADFGLAR [349]
55054		IADFGLAR [349]

TABLE 43c

Prostate cancer		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
		IADFGLAR [349]
		IADFGLAR [349]

[0343] OGTA247

TABLE 44a

Hepatocellular carcinoma		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
102119		DATQITQGPR [109], EDTQVDSEARPMK [170], GYNVTYWR [330], STIEKK [659], YDIEFEDK [842], YFIEDGR [850]
114377		DATQITQGPR [109], FFPYANGTLGIR [251], PHILFK [253], GYNVTYWR [330], LGTAMSHEIR [463], LSPYVHYTFR [489], STIEKK [659], VSWSPAEDHNAPIEK [798], VTFTCQASFDPQLQPSITWR [804], VTYQNHNK [808], WLRPSGMPADR [828], WMDWNAPQVQYR [829], YDIEFEDK [842]
116037		DATQITQGPR [109], EPIDLR [217], FQGIYR [266], LDCQVQGRPQPEVTWR [445], LGTAMSHEIR [463], YFIEDGR [850]
118513		AQLLVVGSPGPVPR [82], ATNSMIDR [92], DATQITQGPR [109], EGPGEAIVR [189], FFPYANGTLGIR [251], LGTAMSHEIR [463], LSPYVHYTFR [489], VTYQNHNK [808], WLRPSGMPADR [828], YFIEDGR [850]
121636		DATQITQGPR [109], EPIDLR [217], PHILFK [253], FQGIYR [266], YDIEFEDK [842], YFIEDGR [850]
123033		AQLLVVGSPGPVPR [82], CEASGKPEVQFR [101], DATQITQGPR [109], EGPGEAIVR [189], FFPYANGTLGIR [251], LSPYVHYTFR [489], VGEEDDGEYR [762], VQWRPQGTR [795], YFIEDGR [850]
128000		AQLLVVGSPGPVPR [82], DATQITQGPR [109], LGTAMSHEIR [463], LSPYVHYTFR [489], YFIEDGR [850]
200565		CEASGKPEVQFR [101], EPIDLR [217], INGIPVEELAK [382],

TABLE 44a-continued

Hepatocellular carcinoma		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
		VSWSPAEDHNAPIEK [798], WLRPSGMPADR [828]
209214		ATNSMIDR [92], DATQITQGPR [109], EGPGEAIVR [189], EPIDLR [217], GALILSNVQPSDTMTVQCEAR [284], HQMAVK [342]
218613		AQLLVVGSPGPVPR [82], CEASGKPEVQFR [101], DLQELGDSK [137], FFPYANGTLGIR [251], LGTAMSHEIR [463], WLRPSGMPADR [828]

TABLE 44b

Melanoma		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
146479		AQLLVVGSPGPVPR [82], CEASGKPEVQFR [101], CLAENSLGSAR [105], DATQITQGPR [109], DGVHFKPK [126], EGPGEAIVR [189], EPIDLR [217], FQGIYR [266], GQLSFNLR [312], INGIPVEELAK [382], LGTAMSHEIR [463], LSPYVHYTFR [489], LVLSDLHLLTQSQVR [502], VGEEDDGEYR [762], VSWSPAEDHNAPIEK [798], WLRPSGMPADR [828], WMDWNAPQVQYR [829], WRPVDLAQVK [831], YFIEDGR [850]
152349		AQLLVVGSPGPVPR [82], CLAENSLGSAR [105], DATQITQGPR [109], DGVHFKPK [126], EGPGEAIVR [189], EPIDLR [217], FQGIYR [266], LGTAMSHEIR [463], LSPYVHYTFR [489], LVLSDLHLLTQSQVR [502], WLRPSGMPADR [828], WMDWNAPQVQYR [829], WRPVDLAQVK [831], YFIEDGR [850]
163936		AFGAPVPSVQWLDEDGTTVLQDER [65], AQLLVVGSPGPVPR [82], CEASGKPEVQFR [101], FQGIYR [266], GQLSFNLR [312], LGTAMSHEIR [463], LVLSDLHLLTQSQVR [502], VSWSPAEDHNAPIEK [798], WLRPSGMPADR [828], WMDWNAPQVQYR [829], WRPVDLAQVK [831], YFIEDGR [850]
172991		AFGAPVPSVQWLDEDGTTVLQDER [65], AQLLVVGSPGPVPR [82], CEASGKPEVQFR [101], CLAENSLGSAR [105],

TABLE 44b-continued

<u>Melanoma</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
193221		DHVVVPANTTSVILSGLRPYSSYHLEV QAFNGR [128], EELGVTVYQSPHSGSFTITGNNSNFAQ R [178], EGPGEAIVR [189], EPIDLR [217], FHILFK [253], FQGIYR [266], GQLSFNLR [312], LVLSDLHLLTQSQVR [502], VGEEDDGEYR [762], VQWRPQGR [795], VSWSPAEDHNAPIEK [798], WLRPSGPMMPADR [828], WMDWNAPQVQYR [829], WRPVDLAQVK [831], YFIEDGR [850]
		AFGAPVPSVQWLDEGTTVLQDER [65], AQLLVVGSPPGVPR [82], FFPYANGTLGIR [251], FHILFK [253], FQGIYR [266], GALILSNVQPSDTMTQCEAR [284], GEGNETTNMVTWKPLR [289], GQLSFNLR [312], INGIPVEELAK [382], LGTAMSHEIR [463], LVLSDLHLLTQSQVR [502], WLRPSGPMMPADR [828], WMDWNAPQVQYR [829], WRPVDLAQVK [831]

[0344] OGTA248

TABLE 45

<u>Renal cell cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
34832		TNQEVLDFVVGGR [712]

[0345] OGTA249

TABLE 46

<u>Ovarian cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
		VTLPAGPDLLR [805] MSAGGASVPPPNPAVSFPFPR [524]

[0346] OGTA257

TABLE 47

<u>Pancreatic cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
176135		LLQEAYMTPK [468]

[0347] OGTA271

TABLE 48a

<u>Breast cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
24841	Vesicles	AHTDVGPGEPPSVLVR [72], AYIATQGPLAESTEDFWR [98], DHPPIPIDLADNIER [127], DSL LAHSSDPVEMRR [157], GVEGSDYINASF LDGYR [326], LGQVPPGESVTAMELEFK [462], LIADLPQNTYFSFVLMNR [467], MLWEHNSTIIIVMLTK [519], QFQFTDWPEQGVK [572], QNAIYATQGPLPETMGDFWR [581], SDMGVGVFTPTTEAR [621], YEGVVDMPQTVK [844], YQYFVVDPMAEYNMPQYILR [869]
24993	Vesicles	AALEYLGSFDHYAT [51], AYIATQGPLAESTEDFWR [98], DHPPIPIDLADNIER [127], DINSQELQNITDTR [129], DSL LAHSSDPVEMRR [157], FDLSMPHVQDPSLVR [246], GVEGSDYINASF LDGYR [326], HVVDGISR [347], ITWMKK [399], KQNAIYATQGPLPETMGDFWR [433], LGQVPPGESVTAMELEFK [462], LIADLPQNTYFSFVLMNR [467], LSVLEEEQLPPGFSIDMGFQK [492], MLSASTMLVQWEPPEEPNGLVR [518], MLWEHNSTIIIVMLTK [519], NGVITQYSVAYEAVDGEDR [537], QFQFTDWPEQGVK [572], TGEFGIDFIGQVHK [693], VPEDQTGLSGGVASFCQATGEPKPR [789], YQYFVVDPMAEYNMPQYILR [869]
55008		MVWEQR [529], YQYFVVDPMAEYNMPQYILR [869]
55921		AALEYLGSFDHYAT [51], AYIATQGPLAESTEDFWR [98], DFLPVDPATSNR [117], DHPPIPIDLADNIER [127], EHSSWDLVLEK [196], GVEGSDYINASF LDGYR [326], HVVDGISR [347], ILYNGQSV EVDGHSR [379], KLIADLPQNTYFSFVLMNR [424], LENGEPR [455], LGQVPPGESVTAMELEFK [462], LNYQTPGMR [475], MLWEHNSTIIIVMLTK [519], MVWEQR [529], NGVITQYSVAYEAVDGEDR [537], QFQFTDWPEQGVK [572], RLNYQTPGMR [606], TGEFGIDFIGQVHK [693], YEGVVDMPQTVK [844]
56324		DFLPVDPATSNR [117], DHPPIPIDLADNIER [127], ILYNGQSV EVDGHSR [378], LNYQTPGMR [475], MLWEHNSTIIIVMLTK [519], QHQQIR [578], RLNYQTPGMR [606], TDEDVPSGPPRK [683], TVDIYGHVTCMR [735], VMCVSMGSTTVR [785], YEGVVDMPQTVK [844]

TABLE 48a-continued

<u>Breast cancer</u>		
MW (Da)	Subfraction-ation	Tryptics identified [SEQ ID No]
56872		AGLGEEFEK [71], AYIATQGFLAESTEDFWR [98], DHPPIPTDLADNIER [127], FDLSMPHVQDPSLVR [246], FTLTGLKPDTTYDIK [275], GSGPLSPSIQSR [315], GVEGSDYINASFLLDGYR [326], LNYQTPGMR [475], MVWEQR [529], RPPNAWHK [609], SDMGVGVFTPTIEAR [621], TVDIYGHVTCMR [735], VLAVNSIGR [774]
105325		AAGTEGPFQEVGDVATTR [50], ACNPLDAGPMVVHCSAGVGR [56], AYIATQGFLAESTEDFWR [98], DFLPVDPATSNR [117], DINSQQELQNIITTDTR [129], FDLSMPHVQDPSLVR [246], FEVIEFDDGAGSVLR [249], FTLTGLKPDTTYDIK [275], GPPSEAVR [308], GSGPLSPSIQSR [315], ILYNGQSVVDGHSR [378], MVWEQR [529], RPPNAWHK [609], SANYTCVAISSLGMIEATAQVTVK [619], SDMGVGVFTPTIEAR [621], TATMLCAAGGNPDPEISWFK [674], TATVMMTR [676], TDEDVPSGPPRK [683], TGCFIVIDAMLER [692], TGEFIDFIGQVHK [693], TSVLLSWEVPDSYK [732], VSWVPPADSR [799]
109891		AAGTEGPFQEVGDVATTR [50], ACNPLDAGPMVVHCSAGVGR [56], AYIATQGFLAESTEDFWR [98], DDQHFTVTGLHK [111], ELPGELLYR [206], EQFGQDGPIVHCSAGVGR [220], FEVIEFDDGAGSVLR [249], ILYNGQSVVDGHSR [379], KQNYAIATQGPLPETMGDFWR [433], SDMGVGVFTPTIEAR [621], YEGVDMFQTVK [844]

TABLE 48b

<u>Cervical cancer</u>		
MW (Da)	Subfraction-ation	Tryptics identified [SEQ ID No]
118858	Integral	AAGTEGPFQEVGDVATTR [50], AHTDVGPGESESPVLVR [72], DDQHFTVTGLHK [111], DFLPVDPATSNR [117], ELPGELLYR [206], EPMDQKR [218], FEVIEFDDGAGSVLR [249], GSSAGGLQHLVSIR [321], QHGGIR [578], RPPNAWHK [609], TDEDVPSGPPR [682], TQQGVPAQPADFQAEVESDTR [725],

TABLE 48b-continued

<u>Cervical cancer</u>		
MW (Da)	Subfraction-ation	Tryptics identified [SEQ ID No]
124604	Integral	TVDIYGHVTCMR [735], VSWVPPADSR [799], WTEYR [836], YSIGGLSPFSEYAFR [872]
		AAGTEGPFQEVGDVATTR [50], ADEARPNTIDFGK [58], AHTDVGPGESESPVLVR [72], DDQHFTVTGLHK [111], ELPGELLYR [206], EPMDQKR [218], FDLSMPHVQDPSLVR [246], FEVIEFDDGAGSVLR [249], GSSAGGLQHLVSIR [321], NVLELSNVVR [558], RPPNAWHK [609], SDMGVGVFTPTIEAR [621], TQQGVPAQPADFQAEVESDTR [725], VLAVNSIGR [774], VSWVPPADSR [799], VYTPDSR [823], WTEYR [836], YSIGGLSPFSEYAFR [872]

TABLE 48c

<u>Colorectal cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
	Heparin Binding	GSGPLSPSIQSR [315], MAPEPAPGR [509], SDMGVGVFTPTIEAR [621], TDEDVPSGPPR [682], TGEQAPSSPPR [694], TQQGVPAQPADFQAEVESDTR [725], YSAPANLYVR [870]

TABLE 48d

<u>Hepatocellular carcinoma</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
72397		YANVIAYDHSR [840], YSAPANLYVR [870]

TABLE 48e

<u>Lung cancer</u>		
MW (Da)	Subfraction-ation	Tryptics identified [SEQ ID No]
		AAGTEGPFQEVGDVATTR [50], ADEARPNTIDFGK [58], AHTDVGPGESESPVLVR [72], DSSLAHSSDPVEMR [156], EHSWDLVGLK [196], FEVIEFDDGAGSVLR [249], GSGPLSPSIQSR [315], GTTYIFR [324],

TABLE 48e-continued

<u>Lung cancer</u>		
MW (Da)	Subfraction- ation	Tryptics identified [SEQ ID No]
		ILYNGQSVEVDGHSR [378], ILYNGQSVEVDGHSR [379], KLIADLQPNTEYSFVLMNR [424], KQAYIATQGPLPETMGDFWR [433], SGALQIESSEESDQK [631], TAPDLLPHKPLPASAYIEDGR [671], TATMLCAAGGNPDPEISWFK [674], TMPVEQVFAK [708], TQQGVPAQPADFQAEVESDTR [725], TORPAMVQTEDQYQLCYR [726], TVDIYGHVTCMR [735], YEGVDMFQTVK [844], YSAPANLYVR [870]
77419		AYIATQGPLAESTEDFWR [98], DDQHFTVTGLHK [111], GPPSEAVR [308], GVEGSDYINASFLDGYR [326], IIMYELVYWAAEDEDQCHK [372], KQAYIATQGPLPETMGDFWR [433], LGQVPPGESVTAMELEFK [462], QFQFTDWPEQGVK [572], RTHSPSSK [616], YEGVDMFQTVK [844]
78771		DHPPIPITDLADNIER [127], DINSQQELQNITTDTR [129], DSLLAHSSDPVEMRR [157], EHSSWDLVGLEK [196], GVEGSDYINASFLDGYR [326], ILYNGQSVEVDGHSR [379], LGQVPPGESVTAMELEFK [462], MLSASTMLVQWEPPEEPNGLVR [518], MLWEHNSTIIVMLTK [519], MVWEQR [529], QNAYIATQGPLPETMGDFWR [581], TAPDLLPHKPLPASAYIEDGR [671], TGEQAPSSPPRR [695], YANVIAYDHSR [840], YEGVDMFQTVK [844]

TABLE 48f

<u>Osteosarcoma</u>		
MW (Da)	Subfrac- tionation	Tryptics identified [SEQ ID No]
63624		AAGTEGPFQEVGDVATTR [50], AHTDVGPGEPPSVLVR [72], AYIATQGPLAESTEDFWR [98], DDQHFTVTGLHK [111], ELPGELLGYR [206], FDLSMPHVQDPSLVR [246], FEVIEFDDGAGSVLR [249], FTLTGLKPDITYDIK [275], GYQVTVYR [331], ILYNGQSVEVDGHSR [378], IQLSWLLPQER [388], LIADLQPNTEYSFVLMNR [467], MLSASTMLVQWEPPEEPNGLVR [518], NGVITQYSVAYEAVDGEDR [537], QHQQIR [578], RPPNAWHK [609], RRAER [614], RTHSPSSK [616], SDMGVGVFTPTIEAR [621], TQQGVPAQPADFQAEVESDTR [725],

TABLE 48f-continued

<u>Osteosarcoma</u>		
MW (Da)	Subfrac- tionation	Tryptics identified [SEQ ID No]
		VLAFTAVGDGPPSPTIQVK [770], VPEDQTGLSGGVASFVCQATGEPKPR [789], VTFDPTSSYTLEDLKPDTLYR [803], YEGVDMFQTVK [844], YQYFVVDPMAYNMPQYILR [869], YSIGGLSPFSEYAFR [872]

TABLE 48

<u>Pancreatic cancer</u>		
MW (Da)	Subfraction- ation	Tryptics identified [SEQ ID No]
73243		DDQHFTVTGLHK [111], DSLLAHSSDPVEMRR [157], GVEGSDYINASFLDGYR [326], LGQVPPGESVTAMELEFK [462], RLNYQTPGMR [606], TATMLCAAGGNPDPEISWFK [674], TMPVEQVFAK [708], VGSMLTPR [764], YEGVDMFQTVK [844]
74307		AYIATQGPLAESTEDFWR [98], DEAIYECTATNSLGEINTSAK [112], DSLLAHSSDPVEMRR [157], FDLSMPHVQDPSLVR [246], GPPSEAVR [308], GVEGSDYINASFLDGYR [326], IIMYELVYWAAEDEDQCHK [372], LNYQTPGMR [475], MVWEQR [529], SDMGVGVFTPTIEAR [621], TAQSTPSAPPQK [672], TDEDVPSGPPRK [683], TGCFFIVIDAMLER [692], YANVIAYDHSR [840], YEGVDMFQTVK [844], YSIGGLSPFSEYAFR [872]
115291		AAGTEGPFQEVGDVATTR [50], DINSQQELQNITTDTR [129], DSLLAHSSDPVEMRR [157], EHSSWDLVGLEK [196], EQFGQDGPITVHCSAGVGR [220], FQLAAR [267], LNYQTPGMR [475], RPPNAWHK [609], RTHSPSSK [616], SDMGVGVFTPTIEAR [621], TDEDVPSGPPRK [683], TGCFFIVIDAMLER [692], TQQGVPAQPADFQAEVESDTR [725], YEGVDMFQTVK [844], YQYFVVDPMAYNMPQYILR [869], YSAPANLYVR [870]
124451		DDQHFTVTGLHK [111], DEAIYECTATNSLGEINTSAK [112], DFLPVDPATSNR [117], DHPPIPITDLADNIER [127], FDLSMPHVQDPSLVR [246], HNTDAGLLTTVGSLLPITYSLR [341], LNYQTPGMR [475], MLWEHNSTIIVMLTK [519], QFQFMAWPDHGVPEYTPILAFR [571], RLNYQTPGMR [606],

TABLE 48-continued

<u>Pancreatic cancer</u>		
MW (Da)	Subfraction- ation	Tryptics identified [SEQ ID No]
		RTHSPSSK [616], TATVVMTR [676], TGCFIVIDAMLER [692], TQRPAMVQTEDQYQLCYR [726], TSVLLSWEVPDSYK [732], VEVEPLNSTAVHVYWK [756], YEGVDMFQTVK [844], YSAPANLYVR [870]
126215		DDQHFTVTGLHK [111], DSLLAHSSDPVEMR [156], EHSSWDLVGLEK [196], ELPGELLGYR [206], GTTYIFR [324], LNYQTPGMR [475], MVWEQR [529], TATVVMTR [676], VGGSMTPR [764], WMMGAEELTK [830], YSAPANLYVR [870]
129890		AAGTEGPFQEVGDVATTR [50], DSLLAHSSDPVEMR [156], ELPGELLGYR [206], FEVIEFDDGAGSVLR [249], GPPSEAVR [308], GSGPLSPSIQSR [315], HVVVGISR [347], LNYQTPGMR [475], NGVITQYSVAYEAVDGEDR [537], RLNYQTPGMR [606], RTHSPSSK [616], VSWVPPPADSR [799], YEGVDMFQTVK [844], YSAPANLYVR [870], YSIGGLSPFSEYAFR [872]

TABLE 48h

<u>Renal cell cancer</u>		
MW (Da)	Subfractionation	Tryptics identified [SEQ ID No]
135833		AAGTEGPFQEVGDVATTR [50], EHSSWDLVGLEK [196], FEVIEFDDGAGSVLR [249], FQLAAR [267], SDMGVGVFTPTIEAR [621], TGEQAPSSPPR [694]

[0348] OGTA002

TABLE 49a

<u>Colorectal cancer, iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	AELRGLK [880], TLRLGPLSK [983]
Samples 2	Experiment 1	ILASVQHMK [373]
Samples 2	Experiment 2	ILASVQHMK [373]

TABLE 49b

<u>Kidney cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	ILASVQHMK [373]

TABLE 49c

<u>Liver cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	EIDVSYVK [899]

TABLE 49d

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	AELRGLK [880], KCAQLTVNLTR [927]
Samples 2	Experiment 1	QPHYSAFSGVGEWLRAIK [964]

[0349] OGTA009

TABLE 50a

<u>Colorectal cancer, iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	STGPGASLGTGYDR [657]
Samples 1	Experiment 2	DFYNPVVPEAQK [119]
Samples 2	Experiment 1	VYDSSLALPQDLQAAR [817]
Samples 2	Experiment 2	VYDSSLALPQDLQAAR [817]
Samples 2	Experiment 3	VYDSSLALPQDLQAAR [817]
Samples 2	Experiment 4	VYDSSLALPQDLQAAR [817]

TABLE 50b

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	VYDSSLALPQDLQAAR [817]
Samples 2	Experiment 1	VYDSSLALPQDLQAAR [817]
Samples 2	Experiment 2	VYDSSLALPQDLQAAR [817]

TABLE 50c

<u>Ovarian cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	DFYNPVVPEAQK [119]
Samples 1	Experiment 2	DFYNPVVPEAQK [119]

[0350] OGTA016

TABLE 51a

<u>Colorectal cancer, iTRA</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	ADAAPDEK [57], AFVNCDENSR [68], ASVDSGSSEEQGGSSR [86], LSDAGQYLCQAGDDNSNKK [947], NADLQVLKPEPELVYEDLR [955], QSSGENCDVVNTLGK [588], VYTVDLGR [821]
Samples 1	Experiment 2	ADAAPDEK [57]
Samples 2	Experiment 1	ADAAPDEK [57], ASVDSGSSEEQGGSSR [86]
Samples 2	Experiment 2	AAGSRDVS LAKADAAPDEK [877]
Samples 2	Experiment 3	ADAAPDEK [57], IIEGEPNLK [371], ILLNPQDK [377], VYTVDLGR [821]
Samples 2	Experiment 4	ASVDSGSSEEQGGSSR [86]
Samples 2	Experiment 5	ASVDSGSSEEQGGSSR [86]
Samples 2	Experiment 6	ASVDSGSSEEQGGSSR [86], IIEGEPNLK [371], ILLNPQDK [377], QSSGENCDVVNTLGK [588]

TABLE 51b

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	ADAAPDEK [57], ASVDSGSSEEQGGSSR [86], ILLNPQDK [377]
Samples 2	Experiment 1	IIEGEPNLK [371]
Samples 2	Experiment 2	ESKSIK [907], TVTINCPFK [987]

[0351] OGTA028

TABLE 52a

<u>Colorectal cancer, iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	AEDIIK [879], DIAPVLDLK [890]
Samples 2	Experiment 1	DIAPVLDLK [890]
Samples 2	Experiment 2	DIAPVLDLK [890], EEINQGGR [177], IDEKR [919]
Samples 2	Experiment 3	DIAPVLDLK [890], SSVKELLLK [973]
Samples 2	Experiment 4	DIAPVLDLK [890]
Samples 2	Experiment 5	DIAPVLDLK [890]
Samples 2	Experiment 6	DIAPVLDLK [890]

TABLE 52b

<u>Kidney cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	DIAPVLDLK [890], EEINQGGR [177]
Samples 1	Experiment 2	DIAPVLDLK [890], EEINQGGR [177]
Samples 1	Experiment 3	DIAPVLDLK [890]

TABLE 52c

<u>Liver cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	VKTTSLTEKK [992]
Samples 1	Experiment 2	DIAPVLDLK [890], WSNVFK [832]

TABLE 52d

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	DIAPVLDLK [890], LKNKEEVLLK [933], VLLEK [995]
Samples 1	Experiment 2	DIAPVLDLK [890]
Samples 2	Experiment 1	DIAPVLDLK [890]
Samples 2	Experiment 2	DIAPVLDLK [890]
Samples 2	Experiment 3	DIAPVLDLK [890]

TABLE 52d-continued

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 2	Experiment 4	DIAPVLDLK [890], DVLPQK [897]
Samples 2	Experiment 5	DIAPVLDLK [890], EEINQGG [177]

TABLE 52e

<u>Small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	DIAPVLDLK [890]
Samples 1	Experiment 2	DIAPVLDLK [890], EEINQGG [177]

TABLE 52f

<u>Ovarian cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	DIAPVLDLK [890]
Samples 1	Experiment 2	DIAPVLDLK [890]
Samples 1	Experiment 3	DIAPVLDLK [890]
Samples 1	Experiment 4	DIAPVLDLK [890]

[0352] OGTA037

TABLE 53a

<u>Colorectal cancer, iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	VLAANNVR [993]

TABLE 53b

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	VLAANNVR [993]

TABLE 53c

<u>Ovarian cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	VLAANNVR [993]

[0353] OGTA041

TABLE 54

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	LTWTNPSIK [950]
Samples 2	Experiment 1	LTWTNPSIK [950]

[0354] OGTA053

TABLE 55a

<u>Colorectal cancer, iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	VVISIR [1002]
Samples 2	Experiment 1	TELLAADSLSK [980]
Samples 2	Experiment 2	VVISIR [1002]
Samples 2	Experiment 3	IRTSTPTGHGASPAK [924]
Samples 2	Experiment 4	TELLAADSLSK [980]
Samples 2	Experiment 5	IRTSTPTGHGASPAK [924], TELLAADSLSK [980]

TABLE 55b

<u>Kidney cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	TELLAADSLSK [980]
Samples 1	Experiment 2	IRTSTPTGHGASPAK [924], TELLAADSLSK [980]
Samples 1	Experiment 3	IRTSTPTGHGASPAK [924]

TABLE 55c

<u>Liver cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	IRTSTPTGHGASPAK [924]

TABLE 55d

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	IRTSTPTGHGASPAK [924], TELLAADSLSK [980]
Samples 1	Experiment 2	GTLSPKDALTDLTGDAER [916], IRTSTPTGHGASPAK [924], TELLAADSLSK [980]
Samples 2	Experiment 1	IRTSTPTGHGASPAK [924]
Samples 2	Experiment 2	IRTSTPTGHGASPAK [924], TELLAADSLSK [980]

TABLE 55e

<u>Small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	TELLAADSLSK [980]
Samples 1	Experiment 2	TELLAADSLSK [980]

[0355] OGTA054

TABLE 56a

<u>Colorectal cancer, iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	EEHEVAVLGAPPSTILPR [173], MVGDTVGAQAYASTAK [954]
Samples 2	Experiment 1	MVGDTVGAQAYASTAK [954]

TABLE 56b

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	MVGDTVGAQAYASTAK [954]
Samples 1	Experiment 2	MVGDTVGAQAYASTAK [954]

[0356] OGTA066

TABLE 57a

<u>Colorectal cancer iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	IMFVDPSLTVR [380] [3]
Samples 1	Experiment 2	IMFVDPSLTVR [380] [3]
Samples 2	Experiment 1	IMFVDPSLTVR [380] [3]

TABLE 57a-continued

<u>Colorectal cancer iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 2	Experiment 2	DLPLLIENMK [135] [2], IMFVDPSLTVR [380] [3]
Samples 2	Experiment 3	IMFVDPSLTVR [380] [3]
Samples 2	Experiment 4	DLPLLIENMK [135] [2], IMFVDPSLTVR [380] [3]
Samples 2	Experiment 5	IMFVDPSLTVR [380] [3]

TABLE 57b

<u>Kidney cancer iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	DLPLLIENMK [135] [2]

TABLE 57c

<u>Non-small cell lung cancer iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	DLPLLIENMK [135] [2], IMFVDPSLTVR [380] [3], NLSPDGQYVPR [546] [5]
Samples 2	Experiment 1	IMFVDPSLTVR [380] [3]
Samples 2	Experiment 2	IMFVDPSLTVR [380] [3]
Samples 2	Experiment 3	IMFVDPSLTVR [380] [3]
Samples 2	Experiment 4	IMFVDPSLTVR [380] [3]

[0357] OGTA074

TABLE 58

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	CLNPVPAVPSPSPSVRK [888]

[0358] OGTA076

TABLE 59a

<u>Colorectal cancer iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	EGIAK [898] [14], IIPK [921] [28], LALK [929] [35], LNPK [941] [40]

TABLE 59a-continued

<u>Colorectal cancer iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 2	EGIAK [898] [14], LALK [929] [35]
Samples 1	Experiment 3	EGIAK [898] [14], IIPK [921] [28], LALK [929] [35]
Samples 1	Experiment 4	LNPK [941] [40]

TABLE 59b

<u>Kidney cancer iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	EGIAK [898] [14], LALK [929] [35], LNPK [941] [40], YLNNLYK [1006] [66]
Samples 1	Experiment 2	LALK [929] [35]

TABLE 59c

<u>Liver cancer iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	YLNNLYK [1006] [66]

TABLE 59d

<u>Non-small cell lung cancer iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	YLNNLYK [1006] [66]
Samples 1	Experiment 2	LALK [929] [35]
Samples 2	Experiment 1	IIPK [921] [28], LALK [929] [35], YLNNLYK [1006] [66]
Samples 2	Experiment 2	YLNNLYK [1006] [66]

TABLE 59e

<u>Small cell lung cancer iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	EGIAK [898] [14]
Samples 1	Experiment 2	EGIAK [898] [14]

TABLE 59f

<u>Ovarian cancer iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	LALK [929] [35]
Samples 1	Experiment 2	LALK [929] [35], YLNNLYK [1006] [66]
Samples 1	Experiment 3	LALK [929] [35]

[0359] OGTA085

TABLE 60a

<u>Colorectal cancer, iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	KMLGNPSR [427]

TABLE 60b

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	KMLGNPSR [427]

[0360] OGTA088

TABLE 61a

<u>Colorectal cancer, iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	RQEELERK [613]

TABLE 61b

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	RQEELERK [613]

[0361] OGTA089

TABLE 62a

<u>Kidney cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	GHEVAAMLK [913]

TABLE 62b

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	LLHGQNGSVPNGQTPLK [935]

TABLE 62c

<u>Ovarian cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	NNLVEIILDINVSQALTER [956]

[0362] OGTA091

TABLE 63a

<u>Colorectal cancer, iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	IYIVR [926]
Samples 2	Experiment 1	KRSAPTSR [928]

TABLE 63b

<u>Kidney cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	LLSDK [938], RMEPLEK [607]
Samples 1	Experiment 2	FSDVTGKIK [912], IGETVVVDLENR [367], RRDLSQMEALK [966]

TABLE 63c

<u>Liver cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	VVFQIWDNDK [810]

TABLE 63d

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	IPNPHLGPVEER [386], IYIVR [926], TAIEILAWGLR [976]

TABLE 63d-continued

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 2	FSDVTGK [272], VTAAGQTK [800]
Samples 2	Experiment 1	RRDLSQMEALK [966]

TABLE 63e

<u>Small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	LLSDK [938]

TABLE 63f

<u>Ovarian cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	VTAAGQTKRTR [999]
Samples 1	Experiment 2	VPAHQVLFSSRR [997], VTAAGQTKRTR [999]

[0363] OGTA098

TABLE 64a

<u>Colorectal cancer, iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	SLQEANAER [970], TLAEVCLGQK [982]
Samples 2	Experiment 1	INATDAEPNTLNK [381], SLQEANAER [970]

TABLE 64b

<u>Kidney cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	SLQEANAER [970]

TABLE 64c

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	INATDAEPNTLNK [381]
Samples 1	Experiment 2	NPIAK [957]
Samples 2	Experiment 1	NPIAK [957]

TABLE 64d

<u>Small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	NPIAK [957], TARATGASR [977]

TABLE 64c

<u>Ovarian cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	NPIAK [957]

[0364] OGTA101

TABLE 65a

<u>Colorectal cancer, iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	LSARNK [946]
Samples 2	Experiment 1	IKQLR [922]
Samples 2	Experiment 2	LASSKAHTSR [930]

TABLE 65b

<u>Kidney cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	ILYDDGKMVEEVDGR [923]

TABLE 65c

<u>Liver cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	IKQLR [922]

TABLE 65d

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	ELREVR [901], LTVLR [949], MRYEGVVDIFQTVK [952], VEVEAVNSTSVK [755]
Samples 1	Experiment 2	LASSKAHTSR [930], LTVLR [949]

TABLE 65d-continued

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 2	Experiment 1	GNSAGGLQHRVTAK [914], LSARNK [946]
Samples 2	Experiment 2	TVDIYGHVTLMR [736]

TABLE 65e

<u>Ovarian cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	YEGVVDIFQTVK [843]

[0365] OGTA104

TABLE 66a

<u>Colorectal cancer, iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	FPSGTLR [264], NQTAVR [959]
Samples 2	Experiment 1	LQCEVQEIPIVFGIVPAIIQTPSR [943]
Samples 2	Experiment 2	FPSGTLR [264]

TABLE 66b

<u>Kidney cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	FLITRRR [910]

TABLE 66c

<u>Liver cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	SQTYESDGK [972]

TABLE 66d

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	FLITRRR [910]
Samples 1	Experiment 2	CGVSNKDIEK [887], FLITRRR [910]

TABLE 66e

<u>Ovarian cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	FLITRRR [910]

[0366] OGTA106

TABLE 67

<u>Liver cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	EVCQLLLR [908]

[0367] OGTA112

TABLE 68

<u>Kidney cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	LFGEK [932]

[0368] OGTA113

TABLE 69a

<u>Colorectal cancer, iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	LLSDPNYGVHLPVK [939]
Samples 2	Experiment 1	YPEVGDLR [865]
Samples 2	Experiment 2	LEDPHVDIIR [931]

TABLE 69b

<u>Kidney cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	LEDPHVDIIR [449]

TABLE 69c

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	YPEVGDLR [865], YSYNTWR [874]

TABLE 69d

<u>Ovarian cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	LEDPHVDIIR [449]

[0369] OGTA119

TABLE 70a

<u>Colorectal cancer, iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	ALALLEDEER [75], GEGPEAGAGGAGGR [290]
Samples 2	Experiment 1	VLTDIK [996]
Samples 2	Experiment 2	MTPPSRAEAGVRR [953]

TABLE 70b

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	AEWLNK [64], DTYLK [896]
Samples 1	Experiment 2	GEGPEAGAGGAGGR [290]
Samples 2	Experiment 1	DTYLK [896]

TABLE 70c

<u>Ovarian cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	ALALLEDEER [75]
Samples 1	Experiment 2	ALALLEDEER [75]

[0370] OGTA124

TABLE 71a

<u>Colorectal cancer, iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	LLQAIK [937]

TABLE 71b

<u>Kidney cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	IFTVAQMDDNSIQMKK [365], LDEDLHVK [446]

TABLE 71c

<u>Liver cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	EWGDGIR [240]

TABLE 71d

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	LDEDLHVK [446]
Samples 1	Experiment 2	LDEDLHVK [446]

TABLE 71e

<u>Ovarian cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	EREAQLVK [905]

[0371] OGTA126

TABLE 72

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	IGTFCSNGTVSRIK [1007], LLVPKDR [940], LWMNVEK [505]
Samples 2	Experiment 1	LLVPKDR [940]

[0372] OGTA156

TABLE 73a

<u>Colorectal cancer, iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	DIMKKTINFAR [891]

TABLE 73b

<u>Kidney cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	DIMKKTINFAR [891], HSRVTVAIPLK [918]

TABLE 73c

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	HSRVTVAIPLK [918]
Samples 2	Experiment 1	HSRVTVAIPLK [918], TYLAVGSMK [740]

TABLE 73d

<u>Ovarian cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	DIMKKTINFAR [891]

[0373] OGTA159

TABLE 74a

<u>Kidney cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	RDLGSRLQAQR [965]
Samples 1	Experiment 2	RDLGSRLQAQR [965]

TABLE 74b

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	RDLGSRLQAQR [965]
Samples 1	Experiment 2	RDLGSRLQAQR [965]

[0374] OGTA169

TABLE 75a

<u>Colorectal cancer, iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	GGQVSVCPPLPR [299], NRSLSRVR [961]
Samples 2	Experiment 1	GGQVSVCPPLPR [299]
Samples 2	Experiment 2	TSKTTFQLELPVK [985]

TABLE 75b

<u>Kidney cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	AVLGDR [885]

TABLE 75c

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	GGQVSVCP LPR [299]
Samples 2	Experiment 1	TSKTTFQLELPVK [985]
Samples 2	Experiment 2	GGQVSVCP LPR [299], LTDVVIGAPGEEENR [496], YFTASLPFEK [1004]

[0375] OGTA174

TABLE 76

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	LSQCHELWER [490]

[0376] OGTA176

TABLE 77a

<u>Colorectal cancer, iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	AVTSPAVGR [886]
Samples 1	Experiment 2	AVTSPAVGR [886]

TABLE 77b

<u>Kidney cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	AVTSPAVGR [886]

TABLE 77c

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	AVTSPAVGR [886]

TABLE 77d

<u>Small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	AVTSPAVGR [886]
Samples 1	Experiment 2	AVTSPAVGR [886]

[0377] OGTA177

TABLE 78a

<u>Colorectal cancer, iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	VLDVVER [994], VVNVSDLYK [1003]
Samples 2	Experiment 1	AREVIPR [883]
Samples 2	Experiment 2	DIQVASNEILR [131], SQHQETPVYLGATAGMRLLR [971]
Samples 2	Experiment 3	GPGISK [915], SQHQETPVYLGATAGMRLLR [971]

TABLE 78b

<u>Kidney cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	DIQVASNEILR [131], GPGISK [915], SLSNYPDFQGAR [643], VLDVVER [994]

TABLE 78c

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	DIQVASNEILR [131], DPCFHPGYK [892], SLSNYPDFQGAR [643], SQHQETPVYLGATAGMR [647]
Samples 1	Experiment 2	EVIPR [909], SLSNYPDFQGAR [643]
Samples 2	Experiment 1	FLNLTSEKVSQEK [911]

TABLE 78d

<u>Small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	AREVIPR [883]

TABLE 78e

<u>Ovarian cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	GPGISK [915]

[0378] OGTA197

TABLE 79a

<u>Colorectal cancer, iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	LNVEERSVGPLTR [942]
Samples 2	Experiment 1	NGVSGGLVTSR [538], TASVSINQTEPPK [673]
Samples 2	Experiment 2	NGVSGGLVTSR [538]

TABLE 79b

<u>Kidney cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	LPGHQKR [478], NGVSGGLVTSR [538], TASVSINQTEPPK [673]

TABLE 79c

<u>Liver cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	TASVSINQTEPPK [673]

TABLE 79d

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	TASVSINQTEPPK [673]
Samples 1	Experiment 2	DGEFSVLQLVGMLR [121], LNVEERSVGPLTR [942]
Samples 2	Experiment 1	NGVSGGLVTSR [538]

TABLE 79e

<u>Small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	SVGPLTRK [663], TASVSINQTEPPK [673]
Samples 1	Experiment 2	NGVSGGLVTSR [538], SVGPLTRK [663], TASVSINQTEPPK [673]

[0379] OGTA202

TABLE 80a

<u>Colorectal cancer, iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	STGTISVISSGLDREK [975]
Samples 2	Experiment 1	EQLTVIR [904], ISYRILR [925]

TABLE 80b

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	EQLTVIR [904]
Samples 1	Experiment 2	EQLTVIR [904]
Samples 2	Experiment 1	EQLTVIR [904]

[0380] OGTA203

TABLE 81a

<u>Kidney cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	LLDFEK [934], TGRPVEPESEFIK [981]

TABLE 81b

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	VEASNYPVEPRFLYLGPFK [989]

[0381] OGTA206

TABLE 82a

<u>Colorectal cancer, iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	VYDSSLALPQDLQAAR [817]
Samples 2	Experiment 1	SAAASNYV [968], VYDSSLALPQDLQAAR [817]
Samples 2	Experiment 2	VYDSSLALPQDLQAAR [817]
Samples 2	Experiment 3	VYDSSLALPQDLQAAR [817]
Samples 2	Experiment 4	VYDSSLALPQDLQAAR [817]

TABLE 82b

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	VYDSLLALPQDLQAAR [817]
Samples 2	Experiment 1	VYDSLLALPQDLQAAR [817]
Samples 2	Experiment 2	VYDSLLALPQDLQAAR [817]

[0382] OGTA213

TABLE 83a

<u>Colorectal cancer, iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	RSSAAGEGTLAR [967]
Samples 2	Experiment 1	RSSAAGEGTLAR [967]
Samples 2	Experiment 2	RSSAAGEGTLAR [967]

TABLE 83b

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	RSSAAGEGTLAR [967]
Samples 1	Experiment 2	RSSAAGEGTLAR [967]
Samples 2	Experiment 1	RSSAAGEGTLAR [967]

[0383] OGTA214

TABLE 84

<u>Colorectal cancer, iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	DSQMNPYSR [895], HIEEENLIDEDFQNLK [917], SDLQRPNPQSPFCVASSLK [969], STGFTNLGAEGSVFPAK [974]
Samples 1	Experiment 2	STGFTNLGAEGSVFPAK [974]
Samples 2	Experiment 1	HIEEENLIDEDFQNLK [917]
Samples 2	Experiment 2	VFPK [990]

[0384] OGTA216

TABLE 85a

<u>Colorectal cancer, iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	AAAAAAAAAAAAAGAGAGAK [49], AFYAPVHADDLR [69], GGGAYYLISR [298],

TABLE 85a-continued

<u>Colorectal cancer, iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
		GPIVPLNVADQK [307], ITDNELELYK [395]
Samples 1	Experiment 2	DLPPILLVR [136], EGAQYLMQAAGLGR [186]
Samples 2	Experiment 1	AMATLLSK [78], EGAQYLMQAAGLGR [186]
Samples 2	Experiment 2	DLPPILLVR [136]
Samples 2	Experiment 3	QTPADGEASGESEPAK [1008]

TABLE 85b

<u>Kidney cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	RAMATLLSK [596]
Samples 1	Experiment 2	RAMATLLSK [596], SPGWRPAFK [645]

TABLE 85c

<u>Liver cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	IFQALCK [920]
Samples 1	Experiment 2	SPGWRPAFK [645]

TABLE 85d

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	AMATLLSK [78], DCKIRVFIGGK [889], TATQPLLK [978]
Samples 1	Experiment 2	EMSIDQAK [213], LHEDDK [465]
Samples 2	Experiment 1	EQDIADK [903]
Samples 2	Experiment 2	DLPPILLVR [136]

TABLE 85e

<u>Small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	LSGVEDHVK [948]

TABLE 85f

<u>Ovarian cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	AMATLLSK [78]

[0385] OGTA222

TABLE 86a

<u>Colorectal cancer, iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	AGFVGQGFWSVYTPCDTQNK [881], ATLQLSR [91], AVGFGGDFDGVPR [95], GALADNLLR [283], NVPDDVLR [559], TLEQMDVVHR [703]
Samples 1	Experiment 2	AGFVGQGFWSVYTPCDTQNK [881], ALYQLGMR [77], AVGFGGDFDGVPR [95], DSPVIDGHNDLPWQLDMFNRR [894], GALADNLLR [283], TLEQMDVVHR [703], VASLIGVEGGHSIDSSLGVLRL [988], VPEGLEDVSK [791], YPDLIAELLR [864]
Samples 2	Experiment 1	AVGFGGDFDGVPR [95]

TABLE 86b

<u>Kidney cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	AVGFGGDFDGVPR [95], VPEGLEDVSK [791]
Samples 1	Experiment 2	ALYQLGMR [77], AVGFGGDFDGVPR [95], GALADNLLR [283], NVPDDVLR [559], VPEGLEDVSK [791], YPDLIAELLR [864]
Samples 1	Experiment 3	AVGFGGDFDGVPR [95]

TABLE 86c

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	ANLSQVADHLDHIK [882]
Samples 1	Experiment 2	VPEGLEDVSK [791]

[0386] OGTA236

TABLE 87

<u>Colorectal cancer, iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	ELNEHFVSK [900]

[0387] OGTA237

TABLE 88a

<u>Colorectal cancer, iTRAQ</u>		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	QLVEALDK [963]

TABLE 88b

<u>Kidney cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	AEAFGMDPARPDQASTVAVK [878]

TABLE 88c

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	TSNGRLPVK [986]

TABLE 88d

<u>Small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	LVLGK [951]

[0388] OGTA247

TABLE 89a

6/27 Non-small cell lung cancer, iTRAQ		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	TNGTGRVR [984], WRPVDLAQVK [831]
Samples 1	Experiment 2	ERMFR [906]

TABLE 89b

Small cell lung cancer, iTRAQ		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	DATQITQGPR [109], DLQELGDSK [137], DPELR [893], EGPGEAIVR [189], NPVDVK [958], TNGTGRVR [984], VGEEDDGEYR [762], VTAINK [1000], YGPGEPSPVSETVVTPEAAPEK [1005]
Samples 1	Experiment 2	AQLLVGSPGPVPR [82], DATQITQGPR [109], DPELR [893], EPIDLR [217], NPVDVK [958], TNGTGRVR [984], VGEEDDGEYR [762], VQAVNSQGK [998], VTAINK [1000], YGPGEPSPVSETVVTPEAAPEK [1005]

[0389] OGTA248

TABLE 90

Non-small cell lung cancer, iTRAQ		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	LRTSAIR [945]

[0390] OGTA249

TABLE 91a

Kidney cancer, iTRAQ		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	VTLPAGPDILR [1001]

TABLE 91b

Non-small cell lung cancer, iTRAQ		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	VTLPAGPDILR [1001]
Samples 2	Experiment 1	VTLPAGPDILR [1001]
Samples 2	Experiment 2	VTLPAGPDILR [1001]
Samples 2	Experiment 3	VTLPAGPDILR [1001]

[0391] OGTA257

TABLE 92a

Colorectal cancer, iTRAQ		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	QILDTPVK [962]

TABLE 92b

Liver cancer, iTRAQ		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	LRQGTLR [944]

TABLE 92c

Non-small cell lung cancer, iTRAQ		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	ATGTAFRR [884], ELVSLK [902]

TABLE 92d

Ovarian cancer, iTRAQ		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	LLIEHGADIR [936]

[0392] OGTA271

TABLE 93a

Colorectal cancer, iTRAQ		
Samples batch no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	IKQLR [922], TAQSTPSAPPQK [672], TATVMMTRLEEK [979]
Samples 1	Experiment 2	VKCDQYWPAP [991]

TABLE 93b

<u>Kidney cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	TAQSTPSAPPQK [672]
Samples 1	Experiment 2	EPMDQKR [218]

TABLE 93c

<u>Liver cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	IKIQLR [922]

TABLE 93d

<u>Non-small cell lung cancer, iTRAQ</u>		
Sample no.	Experiment no.	Tryptics identified [SEQ ID No]
Samples 1	Experiment 1	NRAGLGEEFEKEIR [960], TAQSTPSAPPQK [672]
Samples 2	Experiment 1	DSLLAHSSDPVEMR [156], TMPVEQVFAK [708]

[0393] For proteins of the invention the detected level obtained upon analyzing tissue from subjects having a relevant cancer relative to the detected level obtained upon analyzing tissue from subjects free from said cancers will depend upon the particular analytical protocol and detection technique that is used. Accordingly, the present invention contemplates that each laboratory will establish a reference range in subjects free from said cancers according to the analytical protocol and detection technique in use, as is conventional in the diagnostic art. For example, at least one control positive tissue sample from a subject known to have a relevant cancer or at least one control negative tissue sample from a subject known to be free from said cancer (and more preferably both positive and negative control samples) are included in each batch of test samples analysed.

[0394] Proteins of the invention can be used for detection, prognosis, diagnosis, or monitoring of a relevant cancer or for drug development. In one embodiment of the invention, tissue from a subject (e.g., a subject suspected of having a relevant cancer) is analysed by 1D electrophoresis or iTRAQ for detection of a protein according to the invention. An increased abundance of a protein according to the invention in the tissue from the subject relative to tissue from a subject or subjects free from said cancer (e.g., a control sample) or a previously determined reference range indicates the presence of a relevant cancer.

[0395] In particular, OGTA002 can be used for detection, prognosis, diagnosis, or monitoring of breast cancer, colorectal cancer, hepatocellular carcinoma, lung cancer, melanoma, ovarian cancer, pancreatic cancer and renal cell cancer.

[0396] In particular, OGTA009 can be used for detection, prognosis, diagnosis, or monitoring of breast cancer, colorec-

tal cancer, lung cancer, ovarian cancer, pancreatic cancer, prostate cancer and renal cell cancer.

[0397] In particular, OGTA016 can be used for detection, prognosis, diagnosis, or monitoring of colorectal cancer and lung cancer.

[0398] In particular, OGTA028 can be used for detection, prognosis, diagnosis, or monitoring of colorectal cancer, hepatocellular carcinoma, lung cancer, ovarian cancer and renal cell cancer.

[0399] In particular, OGTA037 can be used for detection, prognosis, diagnosis, or monitoring of colorectal cancer, lung cancer, gastric cancer and ovarian cancer.

[0400] In particular, OGTA041 can be used for detection, prognosis, diagnosis, or monitoring of hepatocellular carcinoma, lung cancer and pancreatic cancer.

[0401] In particular, OGTA053 can be used for detection, prognosis, diagnosis, or monitoring of colorectal cancer, hepatocellular carcinoma, lung cancer, pancreatic cancer and renal cell cancer.

[0402] In particular, OGTA054 can be used for detection, prognosis, diagnosis, or monitoring of colorectal cancer, lung cancer and pancreatic cancer.

[0403] In particular, OGTA066 can be used for detection, prognosis, diagnosis, or monitoring of colorectal cancer, lung cancer, pancreatic cancer and renal cell cancer.

[0404] In particular, OGTA072 can be used for detection, prognosis, diagnosis, or monitoring of colorectal cancer.

[0405] In particular, OGTA074 can be used for detection, prognosis, diagnosis, or monitoring of colorectal cancer and lung cancer.

[0406] In particular, OGTA076 can be used for detection, prognosis, diagnosis, or monitoring of chronic lymphocytic leukaemia, colorectal cancer, hepatocellular carcinoma, lung cancer, ovarian cancer, pancreatic cancer and renal cell cancer.

[0407] In particular, OGTA085 can be used for detection, prognosis, diagnosis, or monitoring of colorectal cancer, lung cancer, melanoma and retinoblastoma.

[0408] In particular, OGTA087 can be used for detection, prognosis, diagnosis, or monitoring of B-cell non-Hodgkin's lymphoma, breast cancer, colorectal cancer, gastric cancer, lung cancer, lymphoid leukaemia and ovarian cancer.

[0409] In particular, OGTA088 can be used for detection, prognosis, diagnosis, or monitoring of breast cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia, pancreatic cancer, renal cell cancer and retinoblastoma.

[0410] In particular, OGTA089 can be used for detection, prognosis, diagnosis, or monitoring of breast cancer, lung cancer, ovarian cancer and renal cell cancer.

[0411] In particular, OGTA091 can be used for detection, prognosis, diagnosis, or monitoring of breast cancer, cervical cancer, chronic lymphocytic leukaemia, colorectal cancer, gastric cancer, hepatocellular carcinoma, lung cancer, melanoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer and renal cell cancer.

[0412] In particular, OGTA098 can be used for detection, prognosis, diagnosis, or monitoring of breast cancer, cervical cancer, colorectal cancer, hepatocellular carcinoma, lung cancer, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer and renal cell cancer.

[0413] In particular, OGTA101 can be used for detection, prognosis, diagnosis, or monitoring of breast cancer, cervical

cancer, colorectal cancer, hepatocellular carcinoma, lung cancer, osteosarcoma, ovarian cancer, pancreatic cancer and renal cell cancer.

[0414] In particular, OGTA104 can be used for detection, prognosis, diagnosis, or monitoring of breast cancer, colorectal cancer, hepatocellular carcinoma, lung cancer, ovarian cancer, pancreatic cancer and renal cell cancer.

[0415] In particular, OGTA106 can be used for detection, prognosis, diagnosis, or monitoring of cervical cancer, hepatocellular carcinoma, melanoma and pancreatic cancer.

[0416] In particular, OGTA112 can be used for detection, prognosis, diagnosis, or monitoring of breast cancer, cervical cancer, chronic lymphocytic leukaemia, hepatocellular carcinoma, pancreatic cancer and renal cell cancer.

[0417] In particular, OGTA113 can be used for detection, prognosis, diagnosis, or monitoring of colorectal cancer, lung cancer, ovarian cancer, pancreatic cancer and renal cell cancer.

[0418] In particular, OGTA119 can be used for detection, prognosis, diagnosis, or monitoring of B-cell non-Hodgkin's lymphoma, breast cancer, colorectal cancer, gastric cancer, hepatocellular carcinoma, lung cancer, lymphoid leukaemia, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer and renal cell cancer.

[0419] In particular, OGTA124 can be used for detection, prognosis, diagnosis, or monitoring of colorectal cancer, hepatocellular carcinoma, lung cancer, ovarian cancer, pancreatic cancer and renal cell cancer.

[0420] In particular, OGTA126 can be used for detection, prognosis, diagnosis, or monitoring of breast cancer, colorectal cancer, hepatocellular carcinoma, lung cancer, melanoma, pancreatic cancer, prostate cancer and renal cell cancer.

[0421] In particular, OGTA156 can be used for detection, prognosis, diagnosis, or monitoring of acute T-cell leukaemia, B-cell non-Hodgkin's lymphoma, chronic lymphocytic leukaemia, colorectal cancer, hepatocellular carcinoma, lung cancer, ovarian cancer and renal cell cancer.

[0422] In particular, OGTA159 can be used for detection, prognosis, diagnosis, or monitoring of breast cancer, chronic lymphocytic leukaemia, colorectal cancer, hepatocellular carcinoma, lung cancer, melanoma, pancreatic cancer and renal cell cancer.

[0423] In particular, OGTA168 can be used for detection, prognosis, diagnosis, or monitoring of glioblastoma and melanoma.

[0424] In particular, OGTA169 can be used for detection, prognosis, diagnosis, or monitoring of breast cancer, chronic lymphocytic leukaemia, colorectal cancer, lung cancer and renal cell cancer.

[0425] In particular, OGTA174 can be used for detection, prognosis, diagnosis, or monitoring of acute T-cell leukaemia, chronic lymphocytic leukaemia and lung cancer.

[0426] In particular, OGTA176 can be used for detection, prognosis, diagnosis, or monitoring of B-cell non-Hodgkin's lymphoma, chronic lymphocytic leukaemia, colorectal cancer, lung cancer and renal cell cancer.

[0427] In particular, OGTA177 can be used for detection, prognosis, diagnosis, or monitoring of chronic lymphocytic leukaemia, colorectal cancer, lung cancer, ovarian cancer and renal cell cancer.

[0428] In particular, OGTA197 can be used for detection, prognosis, diagnosis, or monitoring of colorectal cancer,

hepatocellular carcinoma, lung cancer, melanoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer and renal cell cancer.

[0429] In particular, OGTA202 can be used for detection, prognosis, diagnosis, or monitoring of colorectal cancer and lung cancer.

[0430] In particular, OGTA203 can be used for detection, prognosis, diagnosis, or monitoring of lung cancer, ovarian cancer and renal cell cancer.

[0431] In particular, OGTA206 can be used for detection, prognosis, diagnosis, or monitoring of breast cancer, colorectal cancer, lung cancer, pancreatic cancer and prostate cancer.

[0432] In particular, OGTA213 can be used for detection, prognosis, diagnosis, or monitoring of colorectal cancer and lung cancer.

[0433] In particular, OGTA214 can be used for detection, prognosis, diagnosis, or monitoring of colorectal cancer and ovarian cancer.

[0434] In particular, OGTA216 can be used for detection, prognosis, diagnosis, or monitoring of breast cancer, colorectal cancer, hepatocellular carcinoma, lung cancer, ovarian cancer, pancreatic cancer and renal cell cancer.

[0435] In particular, OGTA222 can be used for detection, prognosis, diagnosis, or monitoring of B-cell non-Hodgkin's lymphoma, colorectal cancer, lung cancer and renal cell cancer.

[0436] In particular, OGTA236 can be used for detection, prognosis, diagnosis, or monitoring of colorectal cancer and pancreatic cancer.

[0437] In particular, OGTA237 can be used for detection, prognosis, diagnosis, or monitoring of B-cell non-Hodgkin's lymphoma, colorectal cancer, lung cancer, lymphoid leukaemia, prostate cancer and renal cell cancer.

[0438] In particular, OGTA247 can be used for detection, prognosis, diagnosis, or monitoring of hepatocellular carcinoma, lung cancer and melanoma.

[0439] In particular, OGTA248 can be used for detection, prognosis, diagnosis, or monitoring of lung cancer and renal cell cancer.

[0440] In particular, OGTA249 can be used for detection, prognosis, diagnosis, or monitoring of gastric cancer, lung cancer, ovarian cancer and renal cell cancer.

[0441] In particular, OGTA257 can be used for detection, prognosis, diagnosis, or monitoring of colorectal cancer, hepatocellular carcinoma, lung cancer, ovarian cancer and pancreatic cancer.

[0442] In particular, OGTA271 can be used for detection, prognosis, diagnosis, or monitoring of breast cancer, cervical cancer, colorectal cancer, hepatocellular carcinoma, lung cancer, osteosarcoma, pancreatic cancer and renal cell cancer.

[0443] In one or more aspects of the invention:

OGTA002 may, in particular, be characterized as an isoform having a MW substantially as recited (e.g. $\pm 10\%$, particularly $\pm 5\%$ of the value) in column 1 of any of the rows of Tables 1a-1f

OGTA009 may, in particular, be characterized as an isoform having a MW substantially as recited (e.g. $\pm 10\%$, particularly $\pm 5\%$ of the value) in column 1 of any of the rows of Tables 2a-2e

OGTA016 may, in particular, be characterized as an isoform having a MW substantially as recited (e.g. $\pm 10\%$, such as $\pm 5\%$ of the value) in column 1 of any of the rows of Table

OGTA203 may, in particular, be characterized as an isoform having a MW substantially as recited (e.g. $\pm 10\%$, particularly $\pm 5\%$ of the value) in column 1 of any of the rows of Tables 36a-36b

OGTA206 may, in particular, be characterized as an isoform having a MW substantially as recited (e.g. $\pm 10\%$, particularly $\pm 5\%$ of the value) in column 1 of any of the rows of Tables 37a-37c

OGTA213 may, in particular, be characterized as an isoform having a MW substantially as recited (e.g. $\pm 10\%$, such as $\pm 5\%$ of the value) in column 1 of any of the rows of Table 38

OGTA214 may, in particular, be characterized as an isoform having a MW substantially as recited (e.g. $\pm 10\%$, particularly $\pm 5\%$ of the value) in column 1 of any of the rows of Table 39

OGTA216 may, in particular, be characterized as an isoform having a MW substantially as recited (e.g. $\pm 10\%$, particularly $\pm 5\%$ of the value) in column 1 of any of the rows of Tables 40a-40b

OGTA222 may, in particular, be characterized as an isoform having a MW substantially as recited (e.g. $\pm 10\%$, particularly $\pm 5\%$ of the value) in column 1 of any of the rows of Tables 41a-41b

OGTA236 may, in particular, be characterized as an isoform having a MW substantially as recited (e.g. $\pm 10\%$, such as $\pm 5\%$ of the value) in column 1 of any of the rows of Table 42

OGTA237 may, in particular, be characterized as an isoform having a MW substantially as recited (e.g. $\pm 10\%$, particularly $\pm 5\%$ of the value) in column 1 of any of the rows of Tables 43a-43c

OGTA247 may, in particular, be characterized as an isoform having a MW substantially as recited (e.g. $\pm 10\%$, particularly $\pm 5\%$ of the value) in column 1 of any of the rows of Tables 44a-44b

OGTA248 may, in particular, be characterized as an isoform having a MW substantially as recited (e.g. $\pm 10\%$, such as $\pm 5\%$ of the value) in column 1 of any of the rows of Table 45

OGTA249 may, in particular, be characterized as an isoform having a MW substantially as recited (e.g. $\pm 10\%$, particularly $\pm 5\%$ of the value) in column 1 of any of the rows of Table 46.

OGTA257 may, in particular, be characterized as an isoform having a MW substantially as recited (e.g. $\pm 10\%$, such as $\pm 5\%$ of the value) in column 1 of any of the rows of Table 47

OGTA271 may, in particular, be characterized as an isoform having a MW substantially as recited (e.g. $\pm 10\%$, particularly $\pm 5\%$ of the value) in column 1 of any of the rows of Tables 48a-48h

[0444] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA002:

[0445] for breast cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 1a;

[0446] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 1b and Table 49a;

[0447] for hepatocellular carcinoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 1c and Table 49c;

[0448] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 49d;

[0449] for melanoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 1d;

[0450] for ovarian cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 1e;

[0451] for pancreatic cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 1f;

[0452] for renal cell cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 49b.

[0453] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA009:

[0454] for breast cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 2a;

[0455] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 2b and Table 50a;

[0456] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 50b;

[0457] for ovarian cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 50c;

[0458] for pancreatic cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 2c;

[0459] for prostate cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 2d;

[0460] for renal cell cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 2e;

[0461] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA016:

[0462] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 3 and Table 51a;

[0463] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 51b.

[0464] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA028:

[0465] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 52a;

[0466] for hepatocellular carcinoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 52c;

- [0467] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 52d and Table 52e;
- [0468] for ovarian cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 4 and Table 52f;
- [0469] for renal cell cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 52b.
- [0470] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA037:
- [0471] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 53a;
- [0472] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 53b;
- [0473] for gastric cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 5;
- [0474] for ovarian cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 53c.
- [0475] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA041:
- [0476] for hepatocellular carcinoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 6a;
- [0477] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 6b and Table 54;
- [0478] for pancreatic cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 6c.
- [0479] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA053:
- [0480] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 55a;
- [0481] for hepatocellular carcinoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 55c;
- [0482] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 55d and Table 55e;
- [0483] for pancreatic cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 7;
- [0484] for renal cell cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 55b.
- [0485] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA054:
- [0486] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 56a;
- [0487] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 56b;
- [0488] for pancreatic cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 8.
- [0489] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA066:
- [0490] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 9a and Table 57a;
- [0491] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 57c;
- [0492] for pancreatic cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 9b;
- [0493] for renal cell cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 57b.
- [0494] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA072:
- [0495] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 10.
- [0496] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA074:
- [0497] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 11;
- [0498] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 58.
- [0499] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA076:
- [0500] for chronic lymphocytic leukaemia applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 12a;
- [0501] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 12b and Table 59a;
- [0502] for hepatocellular carcinoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 59c;
- [0503] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 59d and Table 59e;
- [0504] for ovarian cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 59f;
- [0505] for pancreatic cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 12c;
- [0506] for renal cell cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 59b.

[0507] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA085:

[0508] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 60a;

[0509] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 13a and Table 60b;

[0510] for melanoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 13b;

[0511] for retinoblastoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 13c.

[0512] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA087:

[0513] for B-cell non-Hodgkin's lymphoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 14a;

[0514] for breast cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 14b;

[0515] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 14c;

[0516] for gastric cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 14d;

[0517] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 14e;

[0518] for lymphoid leukaemia applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 14f;

[0519] for ovarian cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 14g.

[0520] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA088:

[0521] for breast cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 15a;

[0522] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 61a;

[0523] for gastric cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 15b;

[0524] for glioblastoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 15c;

[0525] for hepatocellular carcinoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 15d;

[0526] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 15e and Table 61b;

[0527] for lymphoid leukaemia applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 15f;

[0528] for pancreatic cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 15g;

[0529] for renal cell cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 15h;

[0530] for retinoblastoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 15i.

[0531] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA089:

[0532] for breast cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 16a;

[0533] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 16b and Table 62b;

[0534] for ovarian cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 16c and Table 62c;

[0535] for renal cell cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 62a.

[0536] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA091:

[0537] for breast cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 17a;

[0538] for cervical cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 17b;

[0539] for chronic lymphocytic leukaemia applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 17c;

[0540] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 63a;

[0541] for gastric cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 17d;

[0542] for hepatocellular carcinoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 17e and Table 63c;

[0543] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 17f, Table 63d and Table 63e;

[0544] for melanoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 17g;

[0545] for osteosarcoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 17h;

[0546] for ovarian cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 17i and Table 63f;

[0547] for pancreatic cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 17j;

- [0548] for prostate cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 17k;
- [0549] for renal cell cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 17l and Table 63b.
- [0550] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA098:
- [0551] for breast cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 18a;
- [0552] for cervical cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 18b;
- [0553] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 64a;
- [0554] for hepatocellular carcinoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 18c;
- [0555] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 18d, Table 64c and Table 64d;
- [0556] for osteosarcoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 18e;
- [0557] for ovarian cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 64e;
- [0558] for pancreatic cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 18f;
- [0559] for prostate cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 18g;
- [0560] for renal cell cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 18h and Table 64b.
- [0561] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA101:
- [0562] for breast cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 19a;
- [0563] for cervical cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 19b;
- [0564] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 19c and Table 65a;
- [0565] for hepatocellular carcinoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 19d and Table 65c;
- [0566] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 19e and Table 65d;
- [0567] for osteosarcoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 19f;
- [0568] for ovarian cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 65e;
- [0569] for pancreatic cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 19g;
- [0570] for renal cell cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 65b.
- [0571] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA104:
- [0572] for breast cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 20a;
- [0573] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 66a;
- [0574] for hepatocellular carcinoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 20b and Table 66c;
- [0575] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 66d;
- [0576] for ovarian cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 20c and Table 66e;
- [0577] for pancreatic cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 20d;
- [0578] for renal cell cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 66b.
- [0579] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA106:
- [0580] for cervical cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 21a;
- [0581] for hepatocellular carcinoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 67;
- [0582] for melanoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 21b;
- [0583] for pancreatic cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 21c.
- [0584] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA112:
- [0585] for breast cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 22a;
- [0586] for cervical cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 22b;
- [0587] for chronic lymphocytic leukaemia applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 22c;

- [0588] for hepatocellular carcinoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 22d;
- [0589] for pancreatic cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 22e;
- [0590] for renal cell cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 22f and Table 68.
- [0591] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA113:
- [0592] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 69a;
- [0593] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 69c;
- [0594] for ovarian cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 69d;
- [0595] for pancreatic cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 23;
- [0596] for renal cell cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 69b.
- [0597] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA119:
- [0598] for B-cell non-Hodgkin's lymphoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 24a;
- [0599] for breast cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 24b;
- [0600] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 24c and Table 70a;
- [0601] for gastric cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 24d;
- [0602] for hepatocellular carcinoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 24e;
- [0603] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 24f and Table 70b;
- [0604] for lymphoid leukaemia applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 24g;
- [0605] for neuroblastoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 24h;
- [0606] for osteosarcoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 24i;
- [0607] for ovarian cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 70c;
- [0608] for pancreatic cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 24j;
- [0609] for prostate cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 24k;
- [0610] for renal cell cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 24l.
- [0611] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA124:
- [0612] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 71a;
- [0613] for hepatocellular carcinoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 25a and Table 71c;
- [0614] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 25b and Table 71d;
- [0615] for ovarian cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 25c and Table 71e;
- [0616] for pancreatic cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 25d;
- [0617] for renal cell cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 25e and Table 71b.
- [0618] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA126:
- [0619] for breast cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 26a;
- [0620] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 26b;
- [0621] for hepatocellular carcinoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 26c;
- [0622] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 72;
- [0623] for melanoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 26d;
- [0624] for pancreatic cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 26e;
- [0625] for prostate cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 26f;
- [0626] for renal cell cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 26g.

[0627] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA156:

[0628] for acute T-cell leukaemia applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 27a;

[0629] for B-cell non-Hodgkin's lymphoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 27b;

[0630] for chronic lymphocytic leukaemia applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 27c;

[0631] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 73a;

[0632] for hepatocellular carcinoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 27d;

[0633] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 73c;

[0634] for ovarian cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 73d;

[0635] for renal cell cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 73b.

[0636] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA159:

[0637] for breast cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 28a;

[0638] for chronic lymphocytic leukaemia applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 28b;

[0639] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 28c;

[0640] for hepatocellular carcinoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 28d;

[0641] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 74b;

[0642] for melanoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 28e;

[0643] for pancreatic cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 28f;

[0644] for renal cell cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 74a.

[0645] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA168:

[0646] for glioblastoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 29a;

[0647] for melanoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 29b.

[0648] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA169:

[0649] for breast cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 30a;

[0650] for chronic lymphocytic leukaemia applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 30b;

[0651] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 75a;

[0652] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 75c;

[0653] for renal cell cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 75b.

[0654] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA174:

[0655] for acute T-cell leukaemia applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 31a;

[0656] for chronic lymphocytic leukaemia applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 31b;

[0657] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 76.

[0658] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA176:

[0659] for B-cell non-Hodgkin's lymphoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 32a:

[0660] for chronic lymphocytic leukaemia applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 32b:

[0661] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 77a;

[0662] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 77c and Table 77d:

[0663] for renal cell cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 77b.

[0664] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA177:

[0665] for chronic lymphocytic leukaemia applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 33:

[0666] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 78a;

- [0667] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 78c and Table 78d;
- [0668] for ovarian cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 78e;
- [0669] for renal cell cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 78b;
- [0670] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA197:
- [0671] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 34a and Table 79a;
- [0672] for hepatocellular carcinoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 34b and Table 79c;
- [0673] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 34c, Table 79d and Table 79e;
- [0674] for melanoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 34d;
- [0675] for osteosarcoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 34e;
- [0676] for ovarian cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 34f;
- [0677] for pancreatic cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 34g;
- [0678] for prostate cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 34h;
- [0679] for renal cell cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 34i and Table 79b.
- [0680] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA0202:
- [0681] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 35 and Table 80a;
- [0682] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 80b.
- [0683] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA203:
- [0684] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 81b;
- [0685] for ovarian cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 36a;
- [0686] for renal cell cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 36b and Table 81a.
- [0687] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA206:
- [0688] for breast cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 37a;
- [0689] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 82a;
- [0690] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 82b;
- [0691] for pancreatic cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 37b;
- [0692] for prostate cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 37c.
- [0693] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA213:
- [0694] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 83a;
- [0695] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 38 and Table 83b.
- [0696] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA214:
- [0697] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 84;
- [0698] for ovarian cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 39.
- [0699] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA216:
- [0700] for breast cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 40a;
- [0701] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 40b and Table 85a;
- [0702] for hepatocellular carcinoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 85c;
- [0703] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 85d and Table 85e;
- [0704] for ovarian cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 85f;
- [0705] for pancreatic cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 40c;
- [0706] for renal cell cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 85b.

[0707] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA222:

[0708] for B-cell non-Hodgkin's lymphoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 41a;

[0709] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 41b and Table 86a;

[0710] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 86c;

[0711] for renal cell applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 86b.

[0712] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA236:

[0713] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 87;

[0714] for pancreatic cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 42.

[0715] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA237:

[0716] for B-cell non-Hodgkin's lymphoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 43a;

[0717] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 88a;

[0718] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 88c and table 88d;

[0719] for lymphoid leukaemia applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 43b;

[0720] for prostate cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 43c;

[0721] for renal cell cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 88b.

[0722] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA247:

[0723] for hepatocellular carcinoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 44a;

[0724] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 89a and Table 89b;

[0725] for melanoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 44b.

[0726] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA248:

[0727] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 90.

[0728] for renal cell cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 45.

[0729] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA249:

[0730] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 91b;

[0731] for ovarian cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 46;

[0732] for renal cell cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 91a.

[0733] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA257:

[0734] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 92a;

[0735] for hepatocellular carcinoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 92b;

[0736] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 92c;

[0737] for ovarian cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 92d;

[0738] for pancreatic cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 47.

[0739] In relation to fragments, immunogenic fragments or antigenic fragments of OGTA271:

[0740] for breast cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 48a;

[0741] for cervical cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 48b;

[0742] for colorectal cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 48c and Table 93a;

[0743] for hepatocellular carcinoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 48d and table 93c;

[0744] for lung cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 48e and Table 93d;

[0745] for osteosarcoma applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 48f;

[0746] for pancreatic cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 48g;

[0747] for renal cell cancer applications: for example these comprise one or more of the sequences identified as tryptic sequences in the 3rd column of Table 48f and table 93b.

[0748] The present invention additionally provides: (a) preparations comprising an isolated OGTA according to the invention; (b) preparations comprising one or more fragments of an OGTA according to the invention; and (c) antibodies or other affinity reagents that bind to an OGTA according to the invention, to fragments thereof, or both. As used herein, OGTA(s) are “isolated” when they are present in preparations that are substantially free of contaminating proteins, i.e., preparations in which less than 10% by weight (for example less than 5%, such as less than 1%) of the total protein present is contaminating protein(s). A contaminating protein is a protein having a significantly different amino acid sequence from that of an isolated OGTA according to the invention, as determined by mass spectral analysis. As used herein, a “significantly different” sequence is one that permits the contaminating protein to be resolved from an OGTA of the invention by mass spectral analysis, performed according to the Reference Protocols.

[0749] An OGTA according to the invention can be assayed by any method known to those skilled in the art, including but not limited to, the Preferred Technologies described herein in Examples 1 and 2, kinase assays, enzyme assays, binding assays and other functional assays, immunoassays, and western blotting. In one embodiment, the OGTAs according to the invention are separated on 1-D gels by virtue of their MW and visualized by staining the gel. In one embodiment, OGTA(s) are stained with a fluorescent dye and imaged with a fluorescence scanner. Sypro Red (Molecular Probes, Inc., Eugene, Oreg.) is a suitable dye for this purpose. A preferred fluorescent dye is disclosed in U.S. application Ser. No. 09/412,168, filed on Oct. 5, 1999, which is incorporated herein by reference in its entirety. In another embodiment, OGTA(s) are analysed using isobaric tags for relative and absolute quantification (iTRAQ).

[0750] Alternatively, OGTAs according to the invention can be detected in an immunoassay. In one embodiment, an immunoassay is performed by contacting a sample from a subject to be tested with an anti-OGTA002, anti-OGTA009, anti-OGTA016, anti-OGTA028, anti-OGTA037, anti-OGTA041, anti-OGTA053, anti-OGTA054, anti-OGTA066, anti-OGTA072, anti-OGTA074, anti-OGTA076, anti-OGTA085, anti-OGTA087, anti-OGTA088, anti-OGTA089, anti-OGTA091, anti-OGTA098, anti-OGTA101, anti-OGTA104, anti-OGTA106, anti-OGTA112, anti-OGTA113, anti-OGTA119, anti-OGTA124, anti-OGTA126, anti-OGTA156, anti-OGTA159, anti-OGTA168, anti-OGTA169, anti-OGTA174, anti-OGTA176, anti-OGTA177, anti-OGTA197, anti-OGTA202, anti-OGTA203, anti-OGTA206, anti-OGTA213, anti-OGTA214, anti-OGTA216, anti-OGTA222, anti-OGTA236, anti-OGTA237, anti-OGTA247, anti-OGTA248, anti-OGTA249, anti-OGTA257 or anti-OGTA271 antibody (or other affinity reagent) under conditions such that immunospecific binding can occur if the relevant OGTA is present, and detecting or measuring the amount of any immunospecific binding by the affinity reagent. Anti-OGTA002, anti-OGTA009, anti-OGTA016, anti-OGTA028, anti-OGTA037, anti-OGTA041, anti-OGTA053, anti-OGTA054, anti-OGTA066, anti-OGTA072, anti-OGTA074, anti-OGTA076, anti-OGTA085, anti-OGTA087, anti-OGTA088, anti-OGTA089, anti-OGTA091,

anti-OGTA098, anti-OGTA101, anti-OGTA104, anti-OGTA106, anti-OGTA112, anti-OGTA113, anti-OGTA119, anti-OGTA124, anti-OGTA126, anti-OGTA156, anti-OGTA159, anti-OGTA168, anti-OGTA169, anti-OGTA174, anti-OGTA176, anti-OGTA177, anti-OGTA197, anti-OGTA202, anti-OGTA203, anti-OGTA206, anti-OGTA213, anti-OGTA214, anti-OGTA216, anti-OGTA222, anti-OGTA236, anti-OGTA237, anti-OGTA247, anti-OGTA248, anti-OGTA249, anti-OGTA257 and anti-OGTA271 affinity reagents can be produced by the methods and techniques taught herein.

[0751] Proteins according to the invention may be detected by virtue of the detection of a fragment thereof e.g. an immunogenic or antigenic fragment thereof. Fragments may have a length of at least 10, more typically at least 20 amino acids e.g. at least 50 or 100 amino acids e.g. at least 200 or 500 amino acids e.g. at least 1000 amino acids e.g. at least 1500 amino acids e.g. at least 2000 amino acids.

[0752] In one embodiment one or more for example 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47 or 48 proteins according to the invention are detected using an appropriate array analysis.

[0753] In one embodiment, binding of antibody (or other affinity reagent) in tissue sections can be used to detect aberrant OGTA(s) localization or an aberrant level of OGTA(s). In a specific embodiment, an antibody (or other affinity reagent) to an OGTA according to the invention can be used to assay a patient tissue (e.g., a lymphoid, breast, cervical, colorectal, gastric, brain, liver, lung, skin, neuronal, osteoblast, ovarian, pancreatic, prostate, kidney or eye tissue) for the level of OGTA(s) where an aberrant level of OGTA(s) is indicative of a relevant cancer. As used herein, an “aberrant level” means a level that is increased compared with the level in a subject free from said cancer or a reference level. This embodiment may be suitable for detecting elevated levels of OGTA066 in cancer tissue, such as colorectal cancer, kidney cancer, lung cancer and/or pancreatic cancer tissue.

[0754] Any suitable immunoassay can be used, including, without limitation, competitive and non-competitive assay systems using techniques such as western blots, radioimmunoassays, ELISA (enzyme linked immunosorbent assay), “sandwich” immunoassays, immunoprecipitation assays, precipitin reactions, gel diffusion precipitin reactions, immunodiffusion assays, agglutination assays, complement-fixation assays, immunoradiometric assays, fluorescent immunoassays and protein A immunoassays.

[0755] For example, a protein according to the invention can be detected in a fluid sample (e.g., blood, urine, or saliva) by means of a two-step sandwich assay. In the first step, a capture reagent (e.g., an anti-OGTA002, anti-OGTA009, anti-OGTA016, anti-OGTA028, anti-OGTA037, anti-OGTA041, anti-OGTA053, anti-OGTA054, anti-OGTA066, anti-OGTA072, anti-OGTA074, anti-OGTA076, anti-OGTA085, anti-OGTA087, anti-OGTA088, anti-OGTA089, anti-OGTA091, anti-OGTA098, anti-OGTA101, anti-OGTA104, anti-OGTA106, anti-OGTA112, anti-OGTA113, anti-OGTA119, anti-OGTA124, anti-OGTA126, anti-OGTA156, anti-OGTA159, anti-OGTA168, anti-OGTA169, anti-OGTA174, anti-OGTA176, anti-OGTA177, anti-OGTA197, anti-OGTA202, anti-OGTA203, anti-OGTA206, anti-OGTA213, anti-OGTA214, anti-OGTA216, anti-OGTA222, anti-OGTA236, anti-OGTA237, anti-OGTA247, anti-OGTA248, anti-OGTA249, anti-OGTA257 or anti-

OGTA271 antibody or other affinity reagent) is used to capture the relevant OGTA(s). The capture reagent can optionally be immobilized on a solid phase. In the second step, a directly or indirectly labeled detection reagent is used to detect the captured OGTA(s). In one embodiment, the detection reagent is a lectin. Any lectin can be used for this purpose that preferentially binds to an OGTA according to the invention rather than to other isoforms that have the same core protein as an OGTA according to the invention or to other proteins that share the antigenic determinant recognized by the antibody. In one embodiment, the chosen lectin binds an OGTA according to the invention with at least 2-fold greater affinity, more for example at least 5-fold greater affinity, still more preferably at least 10-fold greater affinity, than to said other isoforms that have the same core protein as an OGTA according to the invention or to said other proteins that share the antigenic determinant recognized by the affinity reagent.

[0756] Whilst not wishing to be bound by theory it is thought that in patients with a relevant cancer such as colorectal cancer, kidney cancer, lung cancer and/or pancreatic cancer that the levels of OGTA066 are reduced in fluid samples such as serum samples in comparison to a subject free of said cancer. This is thought to be because the protein seems to be recruited to the cancerous tissue and thus the levels found in the cancerous tissue are higher in patients with the relevant cancer than subjects free from same.

[0757] Based on the present description, a lectin that is suitable for detecting an OGTA according to the invention can readily be identified by methods well known in the art, for instance upon testing one or more lectins enumerated in Table I on pages 158-159 of Sumar et al., *Lectins as Indicators of Disease-Associated Glycoforms*, In: Gabius H-J & Gabius S (eds.), 1993, *Lectins and Glycobiology*, at pp. 158-174 (which is incorporated herein by reference in its entirety). In an alternative embodiment, the detection reagent is an antibody (or other affinity reagent), e.g. an antibody that immunospecifically detects other post-translational modifications, such as an antibody that immunospecifically binds to phosphorylated amino acids. Examples of such antibodies include those that bind to phosphotyrosine (BD Transduction Laboratories, catalog nos.: P11230-050/P11230-150; P11120; P38820; P39020), those that bind to phosphoserine (Zymed Laboratories Inc., South San Francisco, Calif., catalog no. 61-8100) and those that bind to phosphothreonine (Zymed Laboratories Inc., South San Francisco, Calif., catalogue nos. 71-8200, 13-9200).

[0758] If desired, a gene encoding a protein according to the invention a related gene, or related nucleic acid sequences or subsequences, including complementary sequences, can also be used in hybridization assays. A nucleotide encoding a protein according to the invention, or subsequences thereof comprising at least 8 nucleotides, for example at least 12 nucleotides, and most preferably at least 15 nucleotides can be used as a hybridization probe. Hybridization assays can be used for detection, prognosis, diagnosis, or monitoring of conditions, disorders, or disease states, associated with aberrant expression of the gene encoding a protein according to the invention, or for differential diagnosis of subjects with signs or symptoms suggestive of a relevant cancer. In particular, such a hybridization assay can be carried out by a method comprising contacting a subject's sample containing nucleic acid with a nucleic acid probe capable of hybridizing to a DNA or RNA that encodes a protein according to the inven-

tion under conditions such that hybridization can occur, and detecting or measuring any resulting hybridization.

[0759] Hence nucleic acid encoding OGTA(s) (e.g. DNA or more suitably RNA) may be detected, for example, using a hybridizing agent capable of hybridizing to nucleic acid encoding OGTA.

[0760] One such exemplary method comprises:

[0761] (a) contacting one or more oligonucleotide probes comprising 10 or more consecutive nucleotides complementary to a nucleotide sequence encoding OGTA, with an RNA obtained from a biological sample from the subject or with cDNA copied from the RNA, wherein said contacting occurs under conditions that permit hybridization of the probe to the nucleotide sequence if present;

[0762] (b) detecting hybridization, if any, between the probe and the nucleotide sequence; and

[0763] (c) comparing the hybridization, if any, detected in step (b) with the hybridization detected in a control sample, or with a previously determined reference range.

[0764] Thus in one aspect the analysis for differential expression of the gene or proteins in performed using microarrays comprising probes sets, allowing simultaneous analysis in relation to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47 or 48 proteins according to the invention. This technology is well known in the relevant field.

[0765] The invention also provides diagnostic kits, comprising an anti-OGTA002, anti-OGTA009, anti-OGTA016, anti-OGTA028, anti-OGTA037, anti-OGTA041, anti-OGTA053, anti-OGTA054, anti-OGTA066, anti-OGTA072, anti-OGTA074, anti-OGTA076, anti-OGTA085, anti-OGTA087, anti-OGTA088, anti-OGTA089, anti-OGTA091, anti-OGTA098, anti-OGTA101, anti-OGTA104, anti-OGTA106, anti-OGTA112, anti-OGTA113, anti-OGTA119, anti-OGTA124, anti-OGTA126, anti-OGTA156, anti-OGTA159, anti-OGTA168, anti-OGTA169, anti-OGTA174, anti-OGTA176, anti-OGTA177, anti-OGTA197, anti-OGTA202, anti-OGTA203, anti-OGTA206, anti-OGTA213, anti-OGTA214, anti-OGTA216, anti-OGTA222, anti-OGTA236, anti-OGTA237, anti-OGTA247, anti-OGTA248, anti-OGTA249, anti-OGTA257 or anti-OGTA271 antibody (or other affinity reagent).

[0766] In addition, such a kit may optionally comprise one or more of the following: (1) instructions for using the anti-OGTA002, anti-OGTA009, anti-OGTA016, anti-OGTA028, anti-OGTA037, anti-OGTA041, anti-OGTA053, anti-OGTA054, anti-OGTA066, anti-OGTA072, anti-OGTA074, anti-OGTA076, anti-OGTA085, anti-OGTA087, anti-OGTA088, anti-OGTA089, anti-OGTA091, anti-OGTA098, anti-OGTA101, anti-OGTA104, anti-OGTA106, anti-OGTA112, anti-OGTA113, anti-OGTA119, anti-OGTA124, anti-OGTA126, anti-OGTA156, anti-OGTA159, anti-OGTA168, anti-OGTA169, anti-OGTA174, anti-OGTA176, anti-OGTA177, anti-OGTA197, anti-OGTA202, anti-OGTA203, anti-OGTA206, anti-OGTA213, anti-OGTA214, anti-OGTA216, anti-OGTA222, anti-OGTA236, anti-OGTA237, anti-OGTA247, anti-OGTA248, anti-OGTA249, anti-OGTA257 or anti-OGTA271 affinity reagent for diagnosis, prognosis, therapeutic monitoring or any combination of these applications; (2) a labeled binding partner to the affinity reagent; (3) a solid phase (such as a reagent strip) upon which

the anti-OGTA002, anti-OGTA009, anti-OGTA016, anti-OGTA028, anti-OGTA037, anti-OGTA041, anti-OGTA053, anti-OGTA054, anti-OGTA066, anti-OGTA072, anti-OGTA074, anti-OGTA076, anti-OGTA085, anti-OGTA087, anti-OGTA088, anti-OGTA089, anti-OGTA091, anti-OGTA098, anti-OGTA101, anti-OGTA104, anti-OGTA106, anti-OGTA112, anti-OGTA113, anti-OGTA119, anti-OGTA124, anti-OGTA126, anti-OGTA156, anti-OGTA159, anti-OGTA168, anti-OGTA169, anti-OGTA174, anti-OGTA176, anti-OGTA177, anti-OGTA197, anti-OGTA202, anti-OGTA203, anti-OGTA206, anti-OGTA213, anti-OGTA214, anti-OGTA216, anti-OGTA222, anti-OGTA236, anti-OGTA237, anti-OGTA247, anti-OGTA248, anti-OGTA249, anti-OGTA257 or anti-OGTA271 affinity reagent is immobilized; and (4) a label or insert indicating regulatory approval for diagnostic, prognostic or therapeutic use or any combination thereof.

[0767] If no labeled binding partner to the affinity reagent is provided, the anti-OGTA002, anti-OGTA009, anti-OGTA016, anti-OGTA028, anti-OGTA037, anti-OGTA041, anti-OGTA053, anti-OGTA054, anti-OGTA066, anti-OGTA072, anti-OGTA074, anti-OGTA076, anti-OGTA085, anti-OGTA087, anti-OGTA088, anti-OGTA089, anti-OGTA091, anti-OGTA098, anti-OGTA101, anti-OGTA104, anti-OGTA106, anti-OGTA112, anti-OGTA113, anti-OGTA119, anti-OGTA124, anti-OGTA126, anti-OGTA156, anti-OGTA159, anti-OGTA168, anti-OGTA169, anti-OGTA174, anti-OGTA176, anti-OGTA177, anti-OGTA197, anti-OGTA202, anti-OGTA203, anti-OGTA206, anti-OGTA213, anti-OGTA214, anti-OGTA216, anti-OGTA222, anti-OGTA236, anti-OGTA237, anti-OGTA247, anti-OGTA248, anti-OGTA249, anti-OGTA257 or anti-OGTA271 affinity reagent itself can be labeled with a detectable marker, e.g. a chemiluminescent, enzymatic, fluorescent, or radioactive moiety.

[0768] The invention also provides a kit comprising a nucleic acid probe capable of hybridizing to RNA encoding a protein according to the invention. In a specific embodiment, a kit comprises in one or more containers a pair of primers (e.g. each in the size range of 6-30 nucleotides, more preferably 10-30 nucleotides and still more preferably 10-20 nucleotides) that under appropriate reaction conditions can prime amplification of at least a portion of a nucleic acid encoding a protein according to the invention, such as by polymerase chain reaction (see, e.g., Innis et al., 1990, PCR Protocols, Academic Press, Inc., San Diego, Calif.), ligase chain reaction (see EP 320,308) use of Q β replicase, cyclic probe reaction, or other methods known in the art.

[0769] A kit can optionally further comprise a predetermined amount of an OGTA according to the invention or a nucleic acid encoding same, e.g. for use as a standard or control.

Use in Clinical Studies

[0770] The diagnostic methods and compositions of the present invention can assist in monitoring a clinical study, e.g. to evaluate drugs for therapy of a relevant cancer. In one embodiment, candidate molecules are tested for their ability to restore levels of a protein(s) according to the invention in a subject having a relevant cancer to levels found in subjects free from said cancer or, in a treated subject, to preserve said levels at or near non-B-cell non-Hodgkin's lymphoma, non-breast cancer, non-cervical cancer, non-colorectal cancer, non-gastric cancer, non-glioblastoma, non-hepatocellular

carcinoma, non-lung cancer, non-lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), non-melanoma, non-neuroblastoma, non-osteosarcoma, non-ovarian cancer, non-pancreatic cancer, non-prostate cancer, non-renal cell cancer or non-retinoblastoma values.

[0771] In another embodiment, the methods and compositions of the present invention are used to screen candidates for a clinical study to identify individuals having a relevant cancer; such individuals can then be excluded from the study or can be placed in a separate cohort for treatment or analysis.

Production of Proteins of the Invention and Corresponding Nucleic Acid

[0772] A DNA of the present invention can be obtained by isolation as a cDNA fragment from cDNA libraries using as starter materials commercial mRNAs and determining and identifying the nucleotide sequences thereof. That is, specifically, clones are randomly isolated from cDNA libraries, which are prepared according to Ohara et al's method (DNA Research Vol. 4, 53-59 (1997)). Next, through hybridization, duplicated clones (which appear repeatedly) are removed and then in vitro transcription and translation are carried out. Nucleotide sequences of both termini of clones, for which products of 50 kDa or more are confirmed, are determined. Furthermore, databases of known genes are searched for homology using the thus obtained terminal nucleotide sequences as queries. The entire nucleotide sequence of a clone revealed to be novel as a result is determined. In addition to the above screening method, the 5' and 3' terminal sequences of cDNA are related to a human genome sequence. Then an unknown long-chain gene is confirmed in a region between the sequences, and the full-length of the cDNA is analyzed. In this way, an unknown gene that is unable to be obtained by a conventional cloning method that depends on known genes can be systematically cloned.

[0773] Moreover, all of the regions of a human-derived gene containing a DNA of the present invention can also be prepared using a PCR method such as RACE while paying sufficient attention to prevent artificial errors from taking place in short fragments or obtained sequences. As described above, clones having DNA of the present invention can be obtained.

[0774] In another means for cloning DNA of the present invention, a synthetic DNA primer having an appropriate nucleotide sequence of a portion of a polypeptide of the present invention is produced, followed by amplification by the PCR method using an appropriate library.

[0775] Alternatively, selection can be carried out by hybridization of the DNA of the present invention with a DNA that has been incorporated into an appropriate vector and labeled with a DNA fragment or a synthetic DNA encoding some or all of the regions of the polypeptide of the present invention. Hybridization can be carried out by, for example, the method described in Current Protocols in Molecular Biology (edited by Frederick M. Ausubel et al., 1987). DNA of the present invention may be any DNA, as long as they contain nucleotide sequences encoding the polypeptides of the present invention as described above. Such a DNA may be a cDNA identified and isolated from cDNA libraries or the like that are derived from lymphoid, breast, cervical, colorectal, gastric, brain, liver, lung, skin, neuronal, osteoblast, ovarian, pancreatic, prostate, kidney or eye tissue. Such a DNA may also be a synthetic DNA or the like. Vectors for use in library

construction may be any of bacteriophages, plasmids, cosmids, phagemids, or the like. Furthermore, by the use of a total RNA fraction or a mRNA fraction prepared from the above cells and/or tissues, amplification can be carried out by a direct reverse transcription coupled polymerase chain reaction (hereinafter abbreviated as "RT-PCR method").

[0776] DNA encoding the above polypeptides consisting of amino acid sequences that are substantially identical to the amino acid sequences of OGTA(s) according to the invention or DNA encoding the above polypeptides consisting of amino acid sequences derived from the amino acid sequences of OGTA(s) by deletion, substitution, or addition of one or more amino acids composing a portion of the amino acid sequence can be easily produced by an appropriate combination of, for example, a site-directed mutagenesis method, a gene homologous recombination method, a primer elongation method, and the PCR method known by persons skilled in the art. In addition, at this time, a possible method for causing a polypeptide to have substantially equivalent biological activity is substitution of homologous amino acids (e.g. polar and nonpolar amino acids, hydrophobic and hydrophilic amino acids, positively-charged and negatively charged amino acids, and aromatic amino acids) among amino acids composing the polypeptide. Furthermore, to maintain substantially equivalent biological activity, amino acids within functional domains contained in each polypeptide of the present invention are for example conserved.

[0777] Furthermore, examples of DNA of the present invention include DNA comprising nucleotide sequences that encode the amino acid sequences of an OGTA according to the invention and DNA hybridizing under stringent conditions to the DNA and encoding polypeptides (proteins) having biological activity (functions) equivalent to the functions of the polypeptides consisting of the amino acid sequence of an OGTA according to the invention. Under such conditions, an example of such DNA capable of hybridizing to DNA comprising the nucleotide sequences that encode the amino acid sequence of a protein according to the invention is DNA comprising nucleotide sequences that have a degree of overall mean homology with the entire nucleotide sequence of the DNA, such as approximately 80% or more, for example approximately 90% or more, and more preferably approximately 95% or more. Hybridization can be carried out according to a method known in the art such as a method described in Current Protocols in Molecular Biology (edited by Frederick M. Ausubel et al., 1987) or a method according thereto. Here, "stringent conditions" are, for example, conditions of approximately "1*SSC, 0.1% SDS, and 37° C., more stringent conditions of approximately "0.5*SSC, 0.1% SDS, and 42° C., or even more stringent conditions of approximately "0.2*SSC, 0.1% SDS, and 65° C. With more stringent hybridization conditions, the isolation of a DNA having high homology with a probe sequence can be expected. The above combinations of SSC, SDS, and temperature conditions are given for illustrative purposes. Stringency similar to the above can be achieved by persons skilled in the art using an appropriate combination of the above factors or other factors (for example, probe concentration, probe length, and reaction time for hybridization) for determination of hybridization stringency.

[0778] A cloned DNA of the present invention can be directly used or used, if desired, after digestion with a restriction enzyme or addition of a linker, depending on purposes. The DNA may have ATG as a translation initiation codon at

the 5' terminal side and have TAA, TGA, or TAG as a translation termination codon at the 3' terminal side. These translation initiation and translation termination codons can also be added using an appropriate synthetic DNA adapter.

[0779] In methods of the invention the OGTA employed is, for example provided in isolated form, such as a form where the polypeptide has been purified to at least to some extent. The polypeptide may be provided in substantially pure form, that is to say free, to a substantial extent, from other proteins. The polypeptide can also be produced using recombinant methods, synthetically produced or produced by a combination of these methods. OGTA(s) according to the invention can be easily prepared by any method known by persons skilled in the art, which involves producing an expression vector containing a DNA of the present invention or a gene containing a DNA of the present invention, culturing a transformant transformed using the expression vector, generating and accumulating a polypeptide of the present invention or a recombinant protein containing the polypeptide, and then collecting the resultant.

[0780] Recombinant OGTA polypeptide may be prepared by processes well known in the art from genetically engineered host cells comprising expression systems. Accordingly, the present invention also relates to expression systems which comprise an OGTA polypeptide or nucleic acid, to host cells which are genetically engineered with such expression systems and to the production of OGTA polypeptide by recombinant techniques. For recombinant polypeptide production, host cells can be genetically engineered to incorporate expression systems or portions thereof for nucleic acids. Such incorporation can be performed using methods well known in the art, such as, calcium phosphate transfection, DEAD-dextran mediated transfection, transfection, microinjection, cationic lipid-mediated transfection, electroporation, transduction, scrape loading, ballistic introduction or infection (see e.g. Davis et al., Basic Methods in Molecular Biology, 1986 and Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbour laboratory Press, Cold Spring Harbour, N.Y., 1989).

[0781] As host cells, for example, bacteria of the genus *Escherichia*, *Streptococci*, *Staphylococci*, *Streptomyces*, bacteria of the genus *Bacillus*, yeast, *Aspergillus* cells, insect cells, insects, and animal cells are used. Specific examples of bacteria of the genus *Escherichia*, which are used herein, include *Escherichia coli* K12 and DH1 (Proc. Natl. Acad. Sci. U.S.A., Vol. 60, 160 (1968)), JM103 (Nucleic Acids Research, Vol. 9, 309 (1981)), JA221 (Journal of Molecular Biology, Vol. 120, 517 (1978)), and HB101 (Journal of Molecular Biology, Vol. 41, 459 (1969)). As bacteria of the genus *Bacillus*, for example, *Bacillus subtilis* MI114 (Gene, Vol. 24, 255 (1983)) and 207-21 (Journal of Biochemistry, Vol. 95, 87 (1984)) are used. As yeast, for example, *Saccharomyces cerevisiae* AH22, AH22R—, NA87-11A, DKD-5D, and 20B-12, *Schizosaccharomyces pombe* NCYC1913 and NCYC2036, and *Pichia pastoris* are used. As insect cells, for example, *Drosophila* S2 and *Spodoptera* Sf9 cells are used. As animal cells, for example, COS-7 and Vero monkey cells, CHO Chinese hamster cells (hereinafter abbreviated as CHO cells), dhfr-gene-deficient CHO cells, mouse L cells, mouse AtT-20 cells, mouse myeloma cells, rat GH3 cells, human FL cells, COS, HeLa, C127,3T3, HEK 293, BHK and Bowes melanoma cells are used.

[0782] Cell-free translation systems can also be employed to produce recombinant polypeptides (e.g. rabbit reticulocyte

lysate, wheat germ lysate, SP6/T7 in vitro T&T and RTS 100 *E. Coli* HY transcription and translation kits from Roche Diagnostics Ltd., Lewes, UK and the TNT Quick coupled Transcription/Translation System from Promega UK, Southampton, UK). The expression vector can be produced according to a method known in the art. For example, the vector can be produced by (1) excising a DNA fragment containing a DNA of the present invention or a gene containing a DNA of the present invention and (2) ligating the DNA fragment downstream of the promoter in an appropriate expression vector. A wide variety of expression systems can be used, such as and without limitation, chromosomal, episomal and virus-derived systems, e.g. plasmids derived from *Escherichia coli* (e.g. pBR322, pBR325, pUC18, and pUC118), plasmids derived from *Bacillus subtilis* (e.g. pUB110, pTP5, and pC194), from bacteriophage, from transposons, from yeast episomes (e.g. pSH19 and pSH15), from insertion elements, from yeast chromosomal elements, from viruses such as baculoviruses, papova viruses such as SV40, vaccinia viruses, adenoviruses, fowl pox viruses, pseudorabies viruses and retroviruses, and vectors derived from combinations thereof, such as those derived from plasmid and bacteriophage (such as [lambda] phage) genetic elements, such as cosmids and phagemids. The expression systems may contain control regions that regulate as well as engender expression. Promoters to be used in the present invention may be any promoters as long as they are appropriate for hosts to be used for gene expression. For example, when a host is *Escherichia coli*, a trp promoter, a lac promoter, a recA promoter, a pL promoter, an lpp promoter, and the like are preferred. When a host is *Bacillus subtilis*, an SPO1 promoter, an SPO2 promoter, a penP promoter, and the like are preferred. When a host is yeast, a PHO5 promoter, a PGK promoter, a GAP promoter, an ADH promoter, and the like are preferred. When an animal cell is used as a host, examples of promoters for use in this case include an SRa promoter, an SV40 promoter, an LTR promoter, a CMV promoter, and an HSV-TK promoter. Generally, any system or vector that is able to maintain, propagate or express a nucleic acid to produce a polypeptide in a host may be used.

[0783] The appropriate nucleic acid sequence may be inserted into an expression system by any variety of well known and routine techniques, such as those set forth in Sambrook et al., supra. Appropriate secretion signals may be incorporated into the OGTA polypeptide to allow secretion of the translated protein into the lumen of the endoplasmic reticulum, the periplasmic space or the extracellular environment. These signals may be endogenous to the OGTA polypeptide or they may be heterologous signals. Transformation of the host cells can be carried out according to methods known in the art. For example, the following documents can be referred to: Proc. Natl. Acad. Sci. U.S.A., Vol. 69, 2110 (1972); Gene, Vol. 17, 107 (1982); Molecular & General Genetics, Vol. 168, 111 (1979); Methods in Enzymology, Vol. 194, 182-187 (1991); Proc. Natl. Acad. Sci. U.S.A., Vol. 75, 1929 (1978); Cell Technology, separate volume 8, New Cell Technology, Experimental Protocol. 263-267 (1995) (issued by Shujunsha); and Virology, Vol. 52, 456 (1973). The thus obtained transformant transformed with an expression vector containing a DNA of the present invention or a gene containing a DNA of the present invention can be cultured according to a method known in the art. For example, when hosts are bacteria of the genus *Escherichia*, the bacteria are generally cultured at approximately 15° C. to 43° C. for approximately

3 to 24 hours. If necessary, aeration or agitation can also be added. When hosts are bacteria of the genus *Bacillus*, the bacteria are generally cultured at approximately 30° C. to 40° C. for approximately 6 to 24 hours. If necessary, aeration or agitation can also be added. When transformants whose hosts are yeast are cultured, culture is generally carried out at approximately 20° C. to 35° C. for approximately 24 to 72 hours using media with pH adjusted to be approximately 5 to 8. If necessary, aeration or agitation can also be added. When transformants whose hosts are animal cells are cultured, the cells are generally cultured at approximately 30° C. to 40° C. for approximately 15 to 60 hours using media with the pH adjusted to be approximately 6 to 8. If necessary, aeration or agitation can also be added.

[0784] If an OGTA(s) polypeptide is to be expressed for use in cell-based screening assays, it is preferred that the polypeptide be produced at the cell surface. In this event, the cells may be harvested prior to use in the screening assay. If the OGTA polypeptide is secreted into the medium, the medium can be recovered in order to isolate said polypeptide. If produced intracellularly, the cells must first be lysed before the OGTA polypeptide is recovered. OGTA polypeptide can be recovered and purified from recombinant cell cultures or from other biological sources by well known methods including, ammonium sulphate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, affinity chromatography, hydrophobic interaction chromatography, hydroxylapatite chromatography, molecular sieving chromatography, centrifugation methods, electrophoresis methods and lectin chromatography. In one embodiment, a combination of these methods is used. In another embodiment, high performance liquid chromatography is used. In a further embodiment, an antibody which specifically binds to an OGTA polypeptide according to the invention can be used to deplete a sample comprising an relevant OGTA polypeptide of said polypeptide or to purify said polypeptide.

[0785] To separate and purify a polypeptide or a protein of the present invention from the culture products, for example, after culture, microbial bodies or cells are collected by a known method, they are suspended in an appropriate buffer, the microbial bodies or the cells are disrupted by, for example, ultrasonic waves, lysozymes, and/or freeze-thawing, the resultant is then subjected to centrifugation or filtration, and then a crude extract of the protein can be obtained. The buffer may also contain a protein denaturation agent such as urea or guanidine hydrochloride or a surfactant such as Triton X-100™. When the protein is secreted in a culture solution, microbial bodies or cells and a supernatant are separated by a known method after the completion of culture and then the supernatant is collected. The protein contained in the thus obtained culture supernatant or the extract can be purified by an appropriate combination of known separation and purification methods. The thus obtained polypeptide (protein) of the present invention can be converted into a salt by a known method or a method according thereto. Conversely, when the polypeptide (protein) of the present invention is obtained in the form of a salt, it can be converted into a free protein or peptide or another salt by a known method or a method according thereto. Moreover, an appropriate protein modification enzyme such as trypsin or chymotrypsin is caused to act on a protein produced by a recombinant before or after purification, so that modification can be arbitrarily added or a polypeptide can be partially removed. The presence of a

polypeptide (protein) of the present invention or a salt thereof can be measured by various binding assays, enzyme immunoassays using specific antibodies, and the like.

[0786] Techniques well known in the art, may be used for refolding to regenerate native or active conformations of the OGTA polypeptide when the polypeptide has been denatured during isolation and or purification. In the context of the present invention, OGTA polypeptide can be obtained from a biological sample from any source, such as and without limitation, a blood sample or tissue sample, e.g. lymphoid, breast, cervical, colorectal, gastric, brain, liver, lung, skin, neuronal, osteoblast, ovarian, pancreatic, prostate, kidney or eye tissue sample. OGTA polypeptide may be in the form of a “mature protein” or may be part of a larger protein such as a fusion protein. It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, a pre-, pro- or prepro-protein sequence, or a sequence which aids in purification such as an affinity tag, for example, but without limitation, multiple histidine residues, a FLAG tag, HA tag or myc tag.

[0787] An additional sequence that may provide stability during recombinant production may also be used. Such sequences may be optionally removed as required by incorporating a cleavable sequence as an additional sequence or part thereof. Thus, an OGTA polypeptide may be fused to other moieties including other polypeptides or proteins (for example, glutathione S-transferase and protein A). Such a fusion protein can be cleaved using an appropriate protease, and then separated into each protein. Such additional sequences and affinity tags are well known in the art. In addition to the above, features known in the art, such as an enhancer, a splicing signal, a polyA addition signal, a selection marker, and an SV40 replication origin can be added to an expression vector, if desired.

[0788] In one embodiment one or more proteins according to the invention or fragments thereof, for example one or more sequences described herein may be fused with a heterologous fusion partner such as the surface protein, known as protein D from *Haemophilus Influenza* B, a non-structural protein from influenzae virus such as NS1, the S antigen from Hepatitis B or a protein known as LYTA such as the C terminal thereof.

Production of Affinity Reagents to the Proteins of the Invention

[0789] According to those in the art, there are three main types of immunoaffinity reagent—monoclonal antibodies, phage display antibodies and smaller antibody-derived molecules such as Affibodies, Domain Antibodies (dAbs), Nanobodies or UniBodies. In general in applications according to the present invention where the use of antibodies is stated, other affinity reagents (e.g. Affibodies, domain antibodies, Nanobodies or UniBodies) may be employed. Such substances may be said to be capable of immunospecific binding to the proteins of the invention. Where appropriate the term “affinity agent” shall be construed to embrace immunoaffinity reagents and other substances capable of specific binding to the proteins of the invention including but not limited to ligands, lectins, streptavidins, antibody mimetics and synthetic binding agents.

Production of Antibodies to the Proteins of the Invention

[0790] According to the invention OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053,

OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271, an analog of any of same, a related protein or a fragment or derivative of any of the foregoing may be used as an immunogen to generate antibodies which immunospecifically bind such an immunogen. Such immunogens can be isolated by any convenient means, including the methods described above. The term “antibody” as used herein refers to a peptide or polypeptide derived from, modeled after or substantially encoded by an immunoglobulin gene or immunoglobulin genes, or fragments thereof, capable of specifically binding an antigen or epitope. See, e.g. *Fundamental Immunology*, 3rd Edition, W. E. Paul, ed., Raven Press, N.Y. (1993); Wilson (1994) *J. Immunol. Methods* 175:267-273; Yarmush (1992) *J. Biochem. Biophys. Methods* 25:85-97. The term antibody includes antigen-binding portions, i.e., “antigen binding sites,” (e.g., fragments, subsequences, complementarity determining regions (CDRs)) that retain capacity to bind antigen, including (i) a Fab fragment, a monovalent fragment consisting of the VL, VH, CL and CH1 domains; (ii) a F(ab')₂ fragment, a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region; (iii) a Fd fragment consisting of the VH and CH1 domains; (iv) a Fv fragment consisting of the VL and VH domains of a single arm of an antibody, (v) a dAb fragment (Ward et al., (1989) *Nature* 341:544-546), which consists of a VH domain; and (vi) an isolated complementarity determining region (CDR). Single chain antibodies are also included by reference in the term “antibody.” Antibodies of the invention include, but are not limited to polyclonal, monoclonal, bispecific, humanized or chimeric antibodies, single chain antibodies, Fab fragments and F(ab')₂ fragments, fragments produced by a Fab expression library, anti-idiotypic (anti-Id) antibodies, and epitope-binding fragments of any of the above. The immunoglobulin molecules of the invention can be of any class (e.g., IgG, IgE, IgM, IgD and IgA) or subclass of immunoglobulin molecule.

[0791] The term “specifically binds” (or “immunospecifically binds”) is not intended to indicate that an antibody binds exclusively to its intended target. Rather, an antibody “specifically binds” if its affinity for its intended target is about 5-fold greater when compared to its affinity for a non-target molecule. For example the affinity of the antibody will be at least about 5 fold, for example 10 fold, such as 25-fold, particularly 50-fold, and especially 100-fold or more, greater for a target molecule than its affinity for a non-target molecule. In some embodiments, specific binding between an antibody or other binding agent and an antigen means a binding affinity of at least 10^6 M^{-1} . Antibodies may bind with affinities of at least about 10^7 M^{-1} , such as between about 10^8 M^{-1} to about 10^9 M^{-1} , about 10^9 M^{-1} to about 10^{10} M^{-1} , or about 10^{10} M^{-1} to about 10^{11} M^{-1} .

[0792] Affinity is calculated as $K_d = k_{off}/k_{on}$ (k_{off} is the dissociation rate constant, k_{on} is the association rate constant and K_d is the equilibrium constant. Affinity can be determined at equilibrium by measuring the fraction bound (r) of labeled ligand at various concentrations (c). The data are graphed using the Scatchard equation: $r/c = K(n-r)$:

[0793] where

[0794] r =moles of bound ligand/mole of receptor at equilibrium;

[0795] c =free ligand concentration at equilibrium;

[0796] K =equilibrium association constant; and

[0797] n =number of ligand binding sites per receptor molecule

[0798] By graphical analysis, r/c is plotted on the Y-axis versus r on the X-axis thus producing a Scatchard plot. The affinity is the negative slope of the line. k_{off} can be determined by competing bound labeled ligand with unlabeled excess ligand (see, e.g., U.S. Pat. No. 6,316,409). The affinity of a targeting agent for its target molecule is for example at least about 1×10^{-6} moles/liter, is more preferably at least about 1×10^{-7} moles/liter, is even more preferably at least about 1×10^{-8} moles/liter, is yet even more preferably at least about 1×10^{-9} moles/liter, and is most preferably at least about 1×10^{-10} moles/liter. Antibody affinity measurement by Scatchard analysis is well known in the art. See, e.g., van Erp et al., *J. Immunoassay* 12: 425-43, 1991; Nelson and Griswold, *Comput. Methods Programs Biomed.* 27: 65-8, 1988.

[0799] In one embodiment, antibodies that recognize gene products of genes encoding a protein of the invention are publicly available. In another embodiment, methods known to those skilled in the art are used to produce antibodies that recognize OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271, an analog thereof, a related polypeptide, or a fragment or derivative of any of the foregoing. One skilled in the art will recognize that many procedures are available for the production of antibodies, for example, as described in *Antibodies*, A Laboratory Manual, Ed Harlow and David Lane, Cold Spring Harbor Laboratory (1988), Cold Spring Harbor, N.Y. One skilled in the art will also appreciate that binding fragments or Fab fragments which mimic antibodies can also be prepared from genetic information by various procedures (*Antibody Engineering: A Practical Approach* (Borrebaeck, C., ed.), 1995, Oxford University Press, Oxford; *J. Immunol.* 149, 3914-3920 (1992)).

[0800] In one embodiment of the invention, antibodies to a specific domain of an OGTA according to the invention are produced. In a specific embodiment, hydrophilic fragments of protein according to the invention are used as immunogens for antibody production.

[0801] In the production of antibodies, screening for the desired antibody can be accomplished by techniques known in the art, e.g. ELISA (enzyme-linked immunosorbent assay). For example, to select antibodies which recognize a specific domain of a protein according to the invention, one may assay generated hybridomas for a product which binds to an OGTA fragment containing such domain. For selection of an antibody that specifically binds a first OGTA homolog but which does not specifically bind to (or binds less avidly to) a second OGTA homolog, one can select on the basis of positive binding to the first OGTA homolog and a lack of binding to (or reduced binding to) the second OGTA homolog. Similarly,

for selection of an antibody that specifically binds an OGTA according to the invention but which does not specifically bind to (or binds less avidly to) a different isoform of the same protein (such as a different glycoform having the same core peptide as an OGTA according to the invention, one can select on the basis of positive binding to an OGTA according to the invention and a lack of binding to (or reduced binding to) the different isoform (e.g., a different glycoform). Thus, the present invention provides an antibody (for example a monoclonal antibody) that binds with greater affinity (for example at least 2-fold, such as at least 5-fold, particularly at least 10-fold greater affinity) to OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 than to a different isoform or isoforms (e.g., glycoforms) of same.

[0802] Polyclonal antibodies which may be used in the methods of the invention are heterogeneous populations of antibody molecules derived from the sera of immunized animals. Unfractionated immune serum can also be used. Various procedures known in the art may be used for the production of polyclonal antibodies to OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271, a fragment thereof, a related polypeptide, or a fragment of an OGTA related polypeptide. For example, one way is to purify polypeptides of interest or to synthesize the polypeptides of interest using, e.g., solid phase peptide synthesis methods well known in the art. See, e.g., *Guide to Protein Purification*, Murray P. Deutcher, ed., *Meth. Enzymol.* Vol 182 (1990); *Solid Phase Peptide Synthesis*, Greg B. Fields ed., *Meth. Enzymol.* Vol 289 (1997); Kiso et al., *Chem. Pharm. Bull.* (Tokyo) 38: 1192-99, 1990; Mostafavi et al., *Biomed. Pept. Proteins Nucleic Acids* 1: 255-60, 1995; Fujiwara et al., *Chem. Pharm. Bull.* (Tokyo) 44: 1326-31, 1996. The selected polypeptides may then be used to immunize by injection various host animals, including but not limited to rabbits, mice, rats, etc., to generate polyclonal or monoclonal antibodies. The Preferred Technology described herein in Example 1 provides isolated OGTA suitable for such immunization. If an OGTA is purified by gel electrophoresis, it can be used for immunization with or without prior extraction from the polyacrylamide gel. Various adjuvants (i.e. immunostimulants) may be used to enhance the immunological response, depending on the host species, including, but not limited to, complete or incomplete Freund's adjuvant, a mineral gel such as aluminum hydroxide, surface active substance such as lysolecithin, pluronic polyol, a polyanion, a peptide, an oil emulsion, keyhole limpet hemocyanin, dinitrophenol, and an adjuvant such as BCG (bacille Calmette-

Guerin) or *corynebacterium parvum*. Additional adjuvants are also well known in the art.

[0803] For preparation of monoclonal antibodies (mAbs) directed toward proteins of the invention, a fragment thereof, a related polypeptide, or a fragment of a related polypeptide, any technique which provides for the production of antibody molecules by continuous cell lines in culture may be used. For example, the hybridoma technique originally developed by Kohler and Milstein (1975, *Nature* 256:495-497), as well as the trioma technique, the human B-cell hybridoma technique (Kozbor et al., 1983, *Immunology Today* 4:72), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole et al., 1985, in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96). Such antibodies may be of any immunoglobulin class including IgG, IgM, IgE, IgA, IgD and any subclass thereof. The hybridoma producing the mAbs of the invention may be cultivated in vitro or in vivo. In an additional embodiment of the invention, monoclonal antibodies can be produced in germ-free animals utilizing known technology (PCT/US90/02545, incorporated herein by reference).

[0804] The monoclonal antibodies include but are not limited to human monoclonal antibodies and chimeric monoclonal antibodies (e.g., human-mouse chimeras). A chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a human immunoglobulin constant region and a variable region derived from a murine mAb. (See, e.g., Cabilly et al., U.S. Pat. No. 4,816,567; and Boss et al., U.S. Pat. No. 4,816,397, which are incorporated herein by reference in their entirety.) Humanized antibodies are antibody molecules from non-human species having one or more complementarity determining regions (CDRs) from the non-human species and a framework region from a human immunoglobulin molecule. (See, e.g., Queen, U.S. Pat. No. 5,585,089, which is incorporated herein by reference in its entirety.)

[0805] Chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT Publication No. WO 87/02671; European Patent Application 184,187; European Patent Application 171,496; European Patent Application 173,494; PCT Publication No. WO 86/01533; U.S. Pat. No. 4,816,567; European Patent Application 125,023; Better et al., 1988, *Science* 240:1041-1043; Liu et al., 1987, *Proc. Natl. Acad. Sci. USA* 84:3439-3443; Liu et al., 1987, *J. Immunol.* 139:3521-3526; Sun et al., 1987, *Proc. Natl. Acad. Sci. USA* 84:214-218; Nishimura et al., 1987, *Canc. Res.* 47:999-1005; Wood et al., 1985, *Nature* 314:446-449; and Shaw et al., 1988, *J. Natl. Cancer Inst.* 80:1553-1559; Morrison, 1985, *Science* 229:1202-1207; Oi et al., 1986, *Bio/Techniques* 4:214; U.S. Pat. No. 5,225,539; Jones et al., 1986, *Nature* 321:552-525; Verhoeyan et al. (1988) *Science* 239:1534; and Beidler et al., 1988, *J. Immunol.* 141:4053-4060.

[0806] Completely human antibodies are for example desirable for therapeutic treatment of human subjects.

[0807] Antibodies can be produced using transgenic mice which are incapable of expressing endogenous immunoglobulin heavy and light chain genes, but which can express human heavy and light chain genes. The transgenic mice are immunized in the normal fashion with a selected antigen, e.g., all or a portion of a protein according to the invention. Monoclonal antibodies directed against the antigen can be obtained using conventional hybridoma technology. The human

immunoglobulin transgenes harbored by the transgenic mice rearrange during B cell differentiation, and subsequently undergo class switching and somatic mutation. Thus, using such a technique, it is possible to produce useful (including therapeutically useful) IgG, IgA, IgM and IgE antibodies. For an overview of this technology for producing human antibodies, see Lonberg and Huszar (1995, *Int. Rev. Immunol.* 13:65-93). For a detailed discussion of this technology for producing human antibodies and human monoclonal antibodies and protocols for producing such antibodies, see, e.g., U.S. Pat. No. 5,625,126; U.S. Pat. No. 5,633,425; U.S. Pat. No. 5,569,825; U.S. Pat. No. 5,661,016; and U.S. Pat. No. 5,545,806. In addition, companies such as Abgenix, Inc. (Freemont, Calif.) and Genpharm (San Jose, Calif.) can be engaged to provide human antibodies directed against a selected antigen using technology similar to that described above.

[0808] Completely human antibodies which recognize a selected epitope can be generated using a technique referred to as "guided selection." In this approach a selected non-human monoclonal antibody, e.g., a mouse antibody, is used to guide the selection of a completely human antibody recognizing the same epitope. (Jespers et al. (1994) *Bio/technology* 12:899-903).

[0809] The antibodies of the present invention can also be generated by the use of phage display technology to produce and screen libraries of polypeptides for binding to a selected target. See, e.g., Cwirla et al., *Proc. Natl. Acad. Sci. USA* 87, 6378-82, 1990; Devlin et al., *Science* 249, 404-6, 1990; Scott and Smith, *Science* 249, 386-88, 1990; and Ladner et al., U.S. Pat. No. 5,571,698. A basic concept of phage display methods is the establishment of a physical association between DNA encoding a polypeptide to be screened and the polypeptide. This physical association is provided by the phage particle, which displays a polypeptide as part of a capsid enclosing the phage genome which encodes the polypeptide. The establishment of a physical association between polypeptides and their genetic material allows simultaneous mass screening of very large numbers of phage bearing different polypeptides. Phage displaying a polypeptide with affinity to a target bind to the target and these phage are enriched by affinity screening to the target. The identity of polypeptides displayed from these phage can be determined from their respective genomes. Using these methods a polypeptide identified as having a binding affinity for a desired target can then be synthesized in bulk by conventional means. See, e.g., U.S. Pat. No. 6,057,098, which is hereby incorporated in its entirety, including all tables, figures, and claims. In particular, such phage can be utilized to display antigen binding domains expressed from a repertoire or combinatorial antibody library (e.g., human or murine). Phage expressing an antigen binding domain that binds the antigen of interest can be selected or identified with antigen, e.g., using labeled antigen or antigen bound or captured to a solid surface or bead. Phage used in these methods are typically filamentous phage including fd and M13 binding domains expressed from phage with Fab, Fv or disulfide stabilized Fv antibody domains recombinantly fused to either the phage gene III or gene VIII protein. Phage display methods that can be used to make the antibodies of the present invention include those disclosed in Brinkman et al., *J. Immunol. Methods* 182:41-50 (1995); Ames et al., *J. Immunol. Methods* 184:177-186 (1995); Kettleborough et al., *Eur. J. Immunol.* 24:952-958 (1994); Persic et al., *Gene* 187 9-18 (1997); Burton et al., *Advances in Immunology* 57:191-280 (1994); PCT Application No. PCT/GB91/01134; PCT Publi-

cations WO 90/02809; WO 91/10737; WO 92/01047; WO 92/18619; WO 93/11236; WO 95/15982; WO 95/20401; and U.S. Pat. Nos. 5,698,426; 5,223,409; 5,403,484; 5,580,717; 5,427,908; 5,750,753; 5,821,047; 5,571,698; 5,427,908; 5,516,637; 5,780,225; 5,658,727; 5,733,743 and 5,969,108; each of which is incorporated herein by reference in its entirety.

[0810] As described in the above references, after phage selection, the antibody coding regions from the phage can be isolated and used to generate whole antibodies, including human antibodies, or any other desired antigen binding fragment, and expressed in any desired host, including mammalian cells, insect cells, plant cells, yeast, and bacteria, e.g., as described in detail below. For example, techniques to recombinantly produce Fab, Fab' and F(ab')₂ fragments can also be employed using methods known in the art such as those disclosed in PCT publication WO 92/22324; Mullinax et al., *BioTechniques* 12(6):864-869 (1992); and Sawai et al., *AJRI* 34:26-34 (1995); and Better et al., *Science* 240:1041-1043 (1988) (said references incorporated by reference in their entireties).

[0811] Examples of techniques which can be used to produce single-chain Fvs and antibodies include those described in U.S. Pat. Nos. 4,946,778 and 5,258,498; Huston et al., *Methods in Enzymology* 203:46-88 (1991); Shu et al., *PNAS* 90:7995-7999 (1993); and Skerra et al., *Science* 240:1038-1040 (1988).

[0812] The invention further provides for the use of bispecific antibodies, which can be made by methods known in the art. Traditional production of full length bispecific antibodies is based on the coexpression of two immunoglobulin heavy chain-light chain pairs, where the two chains have different specificities (Milstein et al., 1983, *Nature* 305:537-539). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of 10 different antibody molecules, of which only one has the correct bispecific structure. Purification of the correct molecule, which is usually done by affinity chromatography steps, is rather cumbersome, and the product yields are low. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker et al., 1991, *EMBO J.* 10:3655-3659.

[0813] According to a different and more preferred approach, antibody variable domains with the desired binding specificities (antibody-antigen combining sites) are fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light chain binding, present in at least one of the fusions. DNAs encoding the immunoglobulin heavy chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. This provides for great flexibility in adjusting the mutual proportions of the three polypeptide fragments in embodiments when unequal ratios of the three polypeptide chains used in the construction provide the optimum yields. It is, however, possible to insert the coding sequences for two or all three polypeptide chains in one expression vector when the expression of at least two polypeptide chains in equal ratios results in high yields or when the ratios are of no particular significance.

[0814] In a preferred embodiment of this approach, the bispecific antibodies are composed of a hybrid immunoglobulin heavy chain with a first binding specificity in one arm, and a hybrid immunoglobulin heavy chain-light chain pair (providing a second binding specificity) in the other arm. It was found that this asymmetric structure facilitates the separation of the desired bispecific compound from unwanted immunoglobulin chain combinations, as the presence of an immunoglobulin light chain in only one half of the bispecific molecule provides for a facile way of separation. This approach is disclosed in WO 94/04690 published Mar. 3, 1994. For further details for generating bispecific antibodies see, for example, Suresh et al., *Methods in Enzymology*, 1986, 121:210.

[0815] The invention provides functionally active fragments, derivatives or analogs of anti-OGTA002, anti-OGTA009, anti-OGTA016, anti-OGTA028, anti-OGTA037, anti-OGTA041, anti-OGTA053, anti-OGTA054, anti-OGTA066, anti-OGTA072, anti-OGTA074, anti-OGTA076, anti-OGTA085, anti-OGTA087, anti-OGTA088, anti-OGTA089, anti-OGTA091, anti-OGTA098, anti-OGTA101, anti-OGTA104, anti-OGTA106, anti-OGTA112, anti-OGTA113, anti-OGTA119, anti-OGTA124, anti-OGTA126, anti-OGTA156, anti-OGTA159, anti-OGTA168, anti-OGTA169, anti-OGTA174, anti-OGTA176, anti-OGTA177, anti-OGTA197, anti-OGTA202, anti-OGTA203, anti-OGTA206, anti-OGTA213, anti-OGTA214, anti-OGTA216, anti-OGTA222, anti-OGTA236, anti-OGTA237, anti-OGTA247, anti-OGTA248, anti-OGTA249, anti-OGTA257 or anti-OGTA271 immunoglobulin molecules.

[0816] Functionally active means that the fragment, derivative or analog is able to elicit anti-anti-idiotypic antibodies (i.e., tertiary antibodies) that recognize the same antigen that is recognized by the antibody from which the fragment, derivative or analog is derived. Specifically, in a preferred embodiment the antigenicity of the idiotype of the immunoglobulin molecule may be enhanced by deletion of framework and CDR sequences that are C-terminal to the CDR sequence that specifically recognizes the antigen. To determine which CDR sequences bind the antigen, synthetic peptides containing the CDR sequences can be used in binding assays with the antigen by any binding assay method known in the art.

[0817] The present invention provides antibody fragments such as, but not limited to, F(ab')₂ fragments and Fab fragments. Antibody fragments which recognize specific epitopes may be generated by known techniques. F(ab')₂ fragments consist of the variable region, the light chain constant region and the CH1 domain of the heavy chain and are generated by pepsin digestion of the antibody molecule. Fab fragments are generated by reducing the disulfide bridges of the F(ab')₂ fragments. The invention also provides heavy chain and light chain dimers of the antibodies of the invention, or any minimal fragment thereof such as Fvs or single chain antibodies (SCAs) (e.g., as described in U.S. Pat. No. 4,946,778; Bird, 1988, *Science* 242:423-42; Huston et al., 1988, *Proc. Natl. Acad. Sci. USA* 85:5879-5883; and Ward et al., 1989, *Nature* 334:544-54), or any other molecule with the same specificity as the antibody of the invention. Single chain antibodies are formed by linking the heavy and light chain fragments of the Fv region via an amino acid bridge, resulting in a single chain polypeptide. Techniques for the assembly of functional Fv fragments in *E. coli* may be used (Skerra et al., 1988, *Science* 242:1038-1041).

[0818] In other embodiments, the invention provides fusion proteins of the immunoglobulins of the invention (or functionally active fragments thereof), for example in which the immunoglobulin is fused via a covalent bond (e.g., a peptide bond), at either the N-terminus or the C-terminus to an amino acid sequence of another protein (or portion thereof, for example at least 10, 20 or 50 amino acid portion of the protein) that is not the immunoglobulin. For example the immunoglobulin, or fragment thereof, is covalently linked to the other protein at the N-terminus of the constant domain. As stated above, such fusion proteins may facilitate purification, increase half-life in vivo, and enhance the delivery of an antigen across an epithelial barrier to the immune system.

[0819] The immunoglobulins of the invention include analogs and derivatives that are modified, i.e., by the covalent attachment of any type of molecule as long as such covalent attachment does not impair immunospecific binding. For example, but not by way of limitation, the derivatives and analogs of the immunoglobulins include those that have been further modified, e.g., by glycosylation, acetylation, pegylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to a cellular ligand or other protein, etc. Any of numerous chemical modifications may be carried out by known techniques, including, but not limited to specific chemical cleavage, acetylation, formylation, etc. Additionally, the analog or derivative may contain one or more non-classical amino acids.

[0820] The foregoing antibodies can be used in methods known in the art relating to the localization and activity of an OGTA, e.g., for imaging this protein, measuring levels thereof in appropriate physiological samples, in diagnostic methods, etc.

Production of Affibodies to the Proteins of the Invention

[0821] Affibody molecules represent a new class of affinity proteins based on a 58-amino acid residue protein domain, derived from one of the IgG-binding domains of staphylococcal protein A. This three helix bundle domain has been used as a scaffold for the construction of combinatorial phagemid libraries, from which Affibody variants that target the desired molecules can be selected using phage display technology (Nord K, Gunneriusson E, Ringdahl J, Stahl S, Uhlen M, Nygren P A, Binding proteins selected from combinatorial libraries of an α -helical bacterial receptor domain, *Nat Biotechnol* 1997; 15:772-7. Ronmark J, Gronlund H, Uhlen M, Nygren P A, Human immunoglobulin A (IgA)-specific ligands from combinatorial engineering of protein A, *Eur J Biochem* 2002; 269:2647-55). The simple, robust structure of Affibody molecules in combination with their low molecular weight (6 kDa), make them suitable for a wide variety of applications, for instance, as detection reagents (Ronmark J, Hansson M, Nguyen T, et al, Construction and characterization of affibody-Fc chimeras produced in *Escherichia coli*, *J Immunol Methods* 2002; 261:199-211) and to inhibit receptor interactions (Sandstrom K, Xu Z, Forsberg G, Nygren P A, Inhibition of the CD28-CD80 co-stimulation signal by a CD28-binding Affibody ligand developed by combinatorial protein engineering, *Protein Eng* 2003; 16:691-7). Further details of Affibodies and methods of production thereof may be obtained by reference to U.S. Pat. No. 5,831,012 which is herein incorporated by reference in its entirety.

[0822] Labelled Affibodies or the like may also be useful in imaging applications for determining abundance of Isoforms.

Production of Domain Antibodies to the Proteins of the Invention

[0823] References to antibodies herein embrace references to Domain Antibodies. Domain Antibodies (dAbs) are the smallest functional binding units of antibodies, corresponding to the variable regions of either the heavy (V_H) or light (V_L) chains of human antibodies. Domain Antibodies have a molecular weight of approximately 13 kDa. Domantis has developed a series of large and highly functional libraries of fully human V_H and V_L dAbs (more than ten billion different sequences in each library), and uses these libraries to select dAbs that are specific to therapeutic targets. In contrast to many conventional antibodies, Domain Antibodies are well expressed in bacterial, yeast, and mammalian cell systems. Further details of domain antibodies and methods of production thereof may be obtained by reference to U.S. Pat. Nos. 6,291,158; 6,582,915; 6,593,081; 6,172,197; 6,696,245; US Serial No. 2004/0110941; European patent application No. 1433846 and European Patents 0368684 & 0616640; WO05/035572, WO04/101790, WO04/081026, WO04/058821, WO04/003019 and WO03/002609, each of which is herein incorporated by reference in its entirety.

Production of Nanobodies to the Proteins of the Invention

[0824] Nanobodies are antibody-derived therapeutic proteins that contain the unique structural and functional properties of naturally-occurring heavy-chain antibodies. These heavy-chain antibodies contain a single variable domain (V_{HH}) and two constant domains (C_{H2} and C_{H3}). Importantly, the cloned and isolated V_{HH} domain is a perfectly stable polypeptide harbouring the full antigen-binding capacity of the original heavy-chain antibody. Nanobodies have a high homology with the VH domains of human antibodies and can be further humanised without any loss of activity. Importantly, Nanobodies have a low immunogenic potential, which has been confirmed in primate studies with Nanobody lead compounds.

[0825] Nanobodies combine the advantages of conventional antibodies with important features of small molecule drugs. Like conventional antibodies, Nanobodies show high target specificity, high affinity for their target and low inherent toxicity. However, like small molecule drugs they can inhibit enzymes and readily access receptor clefts. Furthermore, Nanobodies are extremely stable, can be administered by means other than injection (see e.g. WO 04/041867, which is herein incorporated by reference in its entirety) and are easy to manufacture. Other advantages of Nanobodies include recognising uncommon or hidden epitopes as a result of their small size, binding into cavities or active sites of protein targets with high affinity and selectivity due to their unique 3-dimensional, drug format flexibility, tailoring of half-life and ease and speed of drug discovery.

[0826] Nanobodies are encoded by single genes and are efficiently produced in almost all prokaryotic and eukaryotic hosts e.g. *E. coli* (see e.g. U.S. Pat. No. 6,765,087, which is herein incorporated by reference in its entirety), moulds (for example *Aspergillus* or *Trichoderma*) and yeast (for example *Saccharomyces*, *Kluyveromyces*, *Hansenula* or *Pichia*) (see e.g. U.S. Pat. No. 6,838,254, which is herein incorporated by reference in its entirety). The production process is scalable

and multi-kilogram quantities of Nanobodies have been produced. Because Nanobodies exhibit a superior stability compared with conventional antibodies, they can be formulated as a long shelf-life, ready-to-use solution.

[0827] The Nanoclone method (see e.g. WO 06/079372, which is herein incorporated by reference in its entirety) is a proprietary method for generating Nanobodies against a desired target, based on automated high-throughout selection of B-cells.

Production of UniBodies to the Proteins of the Invention

[0828] UniBody is a new proprietary antibody technology that creates a stable, smaller antibody format with an anticipated longer therapeutic window than current small antibody formats. IgG4 antibodies are considered inert and thus do not interact with the immune system. Genmab modified fully human IgG4 antibodies by eliminating the hinge region of the antibody. Unlike the full size IgG4 antibody, the half molecule fragment is very stable and is termed a UniBody. Halving the IgG4 molecule left only one area on the UniBody that can bind to disease targets and the UniBody therefore binds univalently to only one site on target cells. This univalent binding does not stimulate cancer cells to grow like bivalent antibodies might and opens the door for treatment of some types of cancer which ordinary antibodies cannot treat.

[0829] The UniBody is about half the size of a regular IgG4 antibody. This small size can be a great benefit when treating some forms of cancer, allowing for better distribution of the molecule over larger solid tumors and potentially increasing efficacy.

[0830] Fabs typically do not have a very long half-life. UniBodies, however, were cleared at a similar rate to whole IgG4 antibodies and were able to bind as well as whole antibodies and antibody fragments in pre-clinical studies. Other antibodies primarily work by killing the targeted cells whereas UniBodies only inhibit or silence the cells.

[0831] Further details of UniBodies may be obtained by reference to patent WO2007/059782, which is herein incorporated by reference in its entirety.

Expression of Affinity Reagents

Expression of Antibodies

[0832] The antibodies of the invention can be produced by any method known in the art for the synthesis of antibodies, in particular, by chemical synthesis or by recombinant expression, and are for example produced by recombinant expression techniques.

[0833] Recombinant expression of antibodies, or fragments, derivatives or analogs thereof, requires construction of a nucleic acid that encodes the antibody. If the nucleotide sequence of the antibody is known, a nucleic acid encoding the antibody may be assembled from chemically synthesized oligonucleotides (e.g., as described in Kutmeier et al., 1994, *Bio Techniques* 17:242), which, briefly, involves the synthesis of overlapping oligonucleotides containing portions of the sequence encoding antibody, annealing and ligation of those oligonucleotides, and then amplification of the ligated oligonucleotides by PCR.

[0834] Alternatively, the nucleic acid encoding the antibody may be obtained by cloning the antibody. If a clone containing the nucleic acid encoding the particular antibody is not available, but the sequence of the antibody molecule is known, a nucleic acid encoding the antibody may be obtained

from a suitable source (e.g., an antibody cDNA library, or cDNA library generated from any tissue or cells expressing the antibody) by PCR amplification using synthetic primers hybridizable to the 3' and 5' ends of the sequence or by cloning using an oligonucleotide probe specific for the particular gene sequence.

[0835] If an antibody molecule that specifically recognizes a particular antigen is not available (or a source for a cDNA library for cloning a nucleic acid encoding such an antibody), antibodies specific for a particular antigen may be generated by any method known in the art, for example, by immunizing an animal, such as a rabbit, to generate polyclonal antibodies or, more preferably, by generating monoclonal antibodies. Alternatively, a clone encoding at least the Fab portion of the antibody may be obtained by screening Fab expression libraries (e.g., as described in Huse et al., 1989, *Science* 246:1275-1281) for clones of Fab fragments that bind the specific antigen or by screening antibody libraries (See, e.g., Clackson et al., 1991, *Nature* 352:624; Hane et al., 1997 *Proc. Natl. Acad. Sci. USA* 94:4937).

[0836] Once a nucleic acid encoding at least the variable domain of the antibody molecule is obtained, it may be introduced into a vector containing the nucleotide sequence encoding the constant region of the antibody molecule (see, e.g., PCT Publication WO 86/05807; PCT Publication WO 89/01036; and U.S. Pat. No. 5,122,464). Vectors containing the complete light or heavy chain for co-expression with the nucleic acid to allow the expression of a complete antibody molecule are also available. Then, the nucleic acid encoding the antibody can be used to introduce the nucleotide substitution(s) or deletion(s) necessary to substitute (or delete) the one or more variable region cysteine residues participating in an intrachain disulfide bond with an amino acid residue that does not contain a sulfhydryl group. Such modifications can be carried out by any method known in the art for the introduction of specific mutations or deletions in a nucleotide sequence, for example, but not limited to, chemical mutagenesis, in vitro site directed mutagenesis (Hutchinson et al., 1978, *J. Biol. Chem.* 253:6551), PCT based methods, etc.

[0837] In addition, techniques developed for the production of "chimeric antibodies" (Morrison et al., 1984, *Proc. Natl. Acad. Sci.* 81:851-855; Neuberger et al., 1984, *Nature* 312: 604-608; Takeda et al., 1985, *Nature* 314:452-454) by splicing genes from a mouse antibody molecule of appropriate antigen specificity together with genes from a human antibody molecule of appropriate biological activity can be used. As described supra, a chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a variable region derived from a murine mAb and a human antibody constant region, e.g., humanized antibodies.

[0838] Once a nucleic acid encoding an antibody molecule of the invention has been obtained, the vector for the production of the antibody molecule may be produced by recombinant DNA technology using techniques well known in the art. Thus, methods for preparing the proteins of the invention by expressing nucleic acid containing the antibody molecule sequences are described herein. Methods which are well known to those skilled in the art can be used to construct expression vectors containing antibody molecule coding sequences and appropriate transcriptional and translational control signals. These methods include, for example, in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. See, for example, the techniques

described in Sambrook et al. (1990, Molecular Cloning, A Laboratory Manual, 2nd Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.) and Ausubel et al. (eds., 1998, Current Protocols in Molecular Biology, John Wiley & Sons, NY).

[0839] The expression vector is transferred to a host cell by conventional techniques and the transfected cells are then cultured by conventional techniques to produce an antibody of the invention.

[0840] The host cells used to express a recombinant antibody of the invention may be either bacterial cells such as *Escherichia coli*, or, for example, eukaryotic cells, especially for the expression of whole recombinant antibody molecule. In particular, mammalian cells such as Chinese hamster ovary cells (CHO), in conjunction with a vector such as the major intermediate early gene promoter element from human cytomegalovirus are an effective expression system for antibodies (Foecking et al., 1986, Gene 45:101; Cockett et al., 1990, Bio/Technology 8:2).

[0841] A variety of host-expression vector systems may be utilized to express an antibody molecule of the invention. Such host-expression systems represent vehicles by which the coding sequences of interest may be produced and subsequently purified, but also represent cells which may, when transformed or transfected with the appropriate nucleotide coding sequences, express the antibody molecule of the invention in situ. These include but are not limited to microorganisms such as bacteria (e.g., *E. coli*, *B. subtilis*) transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors containing antibody coding sequences; yeast (e.g., *Saccharomyces*, *Pichia*) transformed with recombinant yeast expression vectors containing antibody coding sequences; insect cell systems infected with recombinant virus expression vectors (e.g., baculovirus) containing the antibody coding sequences; plant cell systems infected with recombinant virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or transformed with recombinant plasmid expression vectors (e.g., Ti plasmid) containing antibody coding sequences; or mammalian cell systems (e.g., COS, CHO, BHK, 293, 3T3 cells) harboring recombinant expression constructs containing promoters derived from the genome of mammalian cells (e.g., metallothionein promoter) or from mammalian viruses (e.g., the adenovirus late promoter; the vaccinia virus 7.5K promoter).

[0842] In bacterial systems, a number of expression vectors may be advantageously selected depending upon the use intended for the antibody molecule being expressed. For example, when a large quantity of such a protein is to be produced, for example for the generation of pharmaceutical compositions comprising an antibody molecule, vectors which direct the expression of high levels of fusion protein products that are readily purified may be desirable. Such vectors include, but are not limited, to the *E. coli* expression vector pUR278 (Ruther et al., 1983, EMBO J. 2:1791), in which the antibody coding sequence may be ligated individually into the vector in frame with the lac Z coding region so that a fusion protein is produced; pIN vectors (Inouye & Inouye, 1985, *Nucleic Acids Res.* 13:3101-3109; Van Heeke & Schuster, 1989, *J. Biol. Chem.* 264:5503-5509); and the like. pGEX vectors may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption and binding to a

matrix glutathione-agarose beads followed by elution in the presence of free glutathione. The pGEX vectors are designed to include thrombin or factor Xa protease cleavage sites so that the cloned target gene product can be released from the GST moiety.

[0843] In an insect system, *Autographa californica* nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes. The virus grows in *Spodoptera frugiperda* cells. The antibody coding sequence may be cloned individually into non-essential regions (for example the polyhedrin gene) of the virus and placed under control of an AcNPV promoter (for example the polyhedrin promoter). In mammalian host cells, a number of viral-based expression systems (e.g., an adenovirus expression system) may be utilized.

[0844] As discussed above, a host cell strain may be chosen which modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Such modifications (e.g., glycosylation) and processing (e.g., cleavage) of protein products may be important for the function of the protein.

[0845] For long-term, high-yield production of recombinant antibodies, stable expression is preferred. For example, cell lines that stably express an antibody of interest can be produced by transfecting the cells with an expression vector comprising the nucleotide sequence of the antibody and the nucleotide sequence of a selectable (e.g., neomycin or hygromycin), and selecting for expression of the selectable marker. Such engineered cell lines may be particularly useful in screening and evaluation of compounds that interact directly or indirectly with the antibody molecule.

[0846] The expression levels of the antibody molecule can be increased by vector amplification (for a review, see Bebbington and Hentschel, The use of vectors based on gene amplification for the expression of cloned genes in mammalian cells in DNA cloning, Vol. 3. (Academic Press, New York, 1987)). When a marker in the vector system expressing antibody is amplifiable, increase in the level of inhibitor present in culture of host cell will increase the number of copies of the marker gene. Since the amplified region is associated with the antibody gene, production of the antibody will also increase (Crouse et al., 1983, *Mol. Cell. Biol.* 3:257).

[0847] The host cell may be co-transfected with two expression vectors of the invention, the first vector encoding a heavy chain derived polypeptide and the second vector encoding a light chain derived polypeptide. The two vectors may contain identical selectable markers which enable equal expression of heavy and light chain polypeptides. Alternatively, a single vector may be used which encodes both heavy and light chain polypeptides. In such situations, the light chain should be placed before the heavy chain to avoid an excess of toxic free heavy chain (Proudfoot, 1986, *Nature* 322:52; Kohler, 1980, *Proc. Natl. Acad. Sci. USA* 77:2197). The coding sequences for the heavy and light chains may comprise cDNA or genomic DNA.

[0848] Once an antibody molecule of the invention has been recombinantly expressed, it may be purified by any method known in the art for purification of an antibody molecule, for example, by chromatography (e.g., ion exchange chromatography, affinity chromatography such as with protein A or specific antigen, and sizing column chromatography), centrifugation, differential solubility, or by any other standard technique for the purification of proteins.

[0849] Alternatively, any fusion protein may be readily purified by utilizing an antibody specific for the fusion pro-

tein being expressed. For example, a system described by Janknecht et al. allows for the ready purification of non-denatured fusion proteins expressed in human cell lines (Janknecht et al., 1991, Proc. Natl. Acad. Sci. USA 88:8972-897). In this system, the gene of interest is subcloned into a vaccinia recombination plasmid such that the open reading frame of the gene is translationally fused to an amino-terminal tag consisting of six histidine residues. The tag serves as a matrix binding domain for the fusion protein. Extracts from cells infected with recombinant vaccinia virus are loaded onto Ni²⁺ nitriloacetic acid-agarose columns and histidine-tagged proteins are selectively eluted with imidazole-containing buffers.

[0850] The antibodies that are generated by these methods may then be selected by first screening for affinity and specificity with the purified polypeptide of interest and, if required, comparing the results to the affinity and specificity of the antibodies with polypeptides that are desired to be excluded from binding. The screening procedure can involve immobilization of the purified polypeptides in separate wells of microtiter plates. The solution containing a potential antibody or groups of antibodies is then placed into the respective microtiter wells and incubated for about 30 min to 2 h. The microtiter wells are then washed and a labeled secondary antibody (for example, an anti-mouse antibody conjugated to alkaline phosphatase if the raised antibodies are mouse antibodies) is added to the wells and incubated for about 30 min and then washed. Substrate is added to the wells and a color reaction will appear where antibody to the immobilized polypeptide(s) is present.

[0851] The antibodies so identified may then be further analyzed for affinity and specificity in the assay design selected. In the development of immunoassays for a target protein, the purified target protein acts as a standard with which to judge the sensitivity and specificity of the immunoassay using the antibodies that have been selected. Because the binding affinity of various antibodies may differ, certain antibody pairs (e.g., in sandwich assays) may interfere with one another sterically, etc., assay performance of an antibody may be a more important measure than absolute affinity and specificity of an antibody.

[0852] Those skilled in the art will recognise that many approaches can be taken in producing antibodies or binding fragments and screening and selecting for affinity and specificity for the various polypeptides, but these approaches do not change the scope of the invention.

[0853] For some applications (including therapeutica applications), antibodies (particularly monoclonal antibodies) may suitably be human or humanized animal (e.g. mouse) antibodies. Animal antibodies may be raised in animals using the human protein (e.g. OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271) as immunogen. Humanisation typically involves grafting CDRs identified thereby into human framework regions. Nor-

mally some subsequent retromutation to optimize the conformation of chains is required. Such processes are known to persons skilled in the art.

Expression of Affibodies

[0854] The construction of affibodies has been described elsewhere (Ronnmark J, Gronlund H, Uhle' n, M., Nygren P. A°, Human immunoglobulin A (IgA)-specific ligands from combinatorial engineering of protein A, 2002, Eur. J. Biochem. 269, 2647-2655), including the construction of affibody phage display libraries (Nord, K., Nilsson, J., Nilsson, B., Uhle' n, M. & Nygren, P. A, A combinatorial library of an a-helical bacterial receptor domain, 1995, Protein Eng. 8, 601-608. Nord, K., Gunneriusson, E., Ringdahl, J., Sta° hl, S., Uhle' n, M. & Nygren, P. A°, Binding proteins selected from combinatorial libraries of an a-helical bacterial receptor domain, 1997, Nat. Biotechnol. 15, 772-777.)

[0855] The biosensor analyses to investigate the optimal affibody variants using biosensor binding studies has also been described elsewhere (Ronnmark J, Gronlund H, Uhle' n, M., Nygren P. A°, Human immunoglobulin A (IgA)-specific ligands from combinatorial engineering of protein A, 2002, Eur. J. Biochem. 269, 2647-2655).

Affinity Reagent Modifications

[0856] In a preferred embodiment, anti-OGTA002, anti-OGTA009, anti-OGTA016, anti-OGTA028, anti-OGTA037, anti-OGTA041, anti-OGTA053, anti-OGTA054, anti-OGTA066, anti-OGTA072, anti-OGTA074, anti-OGTA076, anti-OGTA085, anti-OGTA087, anti-OGTA088, anti-OGTA089, anti-OGTA091, anti-OGTA098, anti-OGTA101, anti-OGTA104, anti-OGTA106, anti-OGTA112, anti-OGTA113, anti-OGTA119, anti-OGTA124, anti-OGTA126, anti-OGTA156, anti-OGTA159, anti-OGTA168, anti-OGTA169, anti-OGTA174, anti-OGTA176, anti-OGTA177, anti-OGTA197, anti-OGTA202, anti-OGTA203, anti-OGTA206, anti-OGTA213, anti-OGTA214, anti-OGTA216, anti-OGTA222, anti-OGTA236, anti-OGTA237, anti-OGTA247, anti-OGTA248, anti-OGTA249, anti-OGTA257 and/or anti-OGTA271 affinity reagents such as antibodies or fragments thereof are conjugated to a diagnostic or therapeutic moiety.

[0857] Anti-OGTA002, anti-OGTA009, anti-OGTA016, anti-OGTA028, anti-OGTA037, anti-OGTA041, anti-OGTA053, anti-OGTA054, anti-OGTA066, anti-OGTA072, anti-OGTA074, anti-OGTA076, anti-OGTA085, anti-OGTA087, anti-OGTA088, anti-OGTA089, anti-OGTA091, anti-OGTA098, anti-OGTA101, anti-OGTA104, anti-OGTA106, anti-OGTA112, anti-OGTA113, anti-OGTA119, anti-OGTA124, anti-OGTA126, anti-OGTA156, anti-OGTA159, anti-OGTA168, anti-OGTA169, anti-OGTA174, anti-OGTA176, anti-OGTA177, anti-OGTA197, anti-OGTA202, anti-OGTA203, anti-OGTA206, anti-OGTA213, anti-OGTA214, anti-OGTA216, anti-OGTA222, anti-OGTA236, anti-OGTA237, anti-OGTA247, anti-OGTA248, anti-OGTA249, anti-OGTA257 or anti-OGTA271 antibodies or fragments thereof can be conjugated to a therapeutic agent or drug moiety to modify a given biological response. The therapeutic agent or drug moiety is not to be construed as limited to classical chemical therapeutic agents. For example, the drug moiety may be a protein or polypeptide possessing a desired biological activity. Such proteins may include, for example, a toxin such as abrin, ricin A, pseudomonas exo-

toxin, or diphtheria toxin; a protein such as tumour necrosis factor, -interferon, -interferon, nerve growth factor, platelet derived growth factor, tissue plasminogen activator, a thrombotic agent or an anti-angiogenic agent, e.g., angiostatin or endostatin; or, a biological response modifier such as a lymphokine, interleukin-1 (IL-1), interleukin-2 (IL-2), interleukin-6 (IL-6), granulocyte macrophage colony stimulating factor (GM-CSF), granulocyte colony stimulating factor (G-CSF), nerve growth factor (NGF) or other growth factor

[0858] The antibodies can be used for diagnosis or to determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, radioactive nuclides, positron emitting metals (for use in positron emission tomography), and nonradioactive paramagnetic metal ions. See generally U.S. Pat. No. 4,741,900 for metal ions which can be conjugated to antibodies for use as diagnostics according to the present invention. Suitable enzymes include horseradish peroxidase, alkaline phosphatase, beta-galactosidase, or acetylcholinesterase; suitable prosthetic groups include streptavidin, avidin and biotin; suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride and phycoerythrin; suitable luminescent materials include luminol; suitable bioluminescent materials include luciferase, luciferin, and aequorin; and suitable radioactive nuclides include ^{125}I , ^{131}I , ^{111}In and ^{99}Tc . ^{68}Ga may also be employed.

[0859] Techniques for conjugating such therapeutic moiety to antibodies are well known, see, e.g., Arnon et al., "Monoclonal Antibodies For Immunotargeting Of Drugs In Cancer Therapy", in *Monoclonal Antibodies And Cancer Therapy*, Reisfeld et al. (eds.), pp. 243-56 (Alan R. Liss, Inc. 1985); Hellstrom et al., "Antibodies For Drug Delivery", in *Controlled Drug Delivery* (2nd Ed.), Robinson et al. (eds.), pp. 623-53 (Marcel Dekker, Inc. 1987); Thorpe, "Antibody Carriers Of Cytotoxic Agents In Cancer Therapy: A Review", in *Monoclonal Antibodies '84: Biological And Clinical Applications*, Pinchera et al. (eds.), pp. 475-506 (1985); "Analysis, Results, And Future Prospective Of The Therapeutic Use Of Radiolabeled Antibody In Cancer Therapy", in *Monoclonal Antibodies For Cancer Detection And Therapy*, Baldwin et al. (eds.), pp. 303-16 (Academic Press 1985), and Thorpe et al., "The Preparation And Cytotoxic Properties Of Antibody-Toxin Conjugates", *Immunol. Rev.*, 62:119-58 (1982).

[0860] Alternatively, an antibody can be conjugated to a second antibody to form an antibody heteroconjugate as described by Segal in U.S. Pat. No. 4,676,980.

[0861] An antibody with or without a therapeutic moiety conjugated to it can be used as a therapeutic that is administered alone or in combination with cytotoxic factor(s) and/or cytokine(s).

[0862] The invention also provides for fully human, or humanised antibodies that induce antibody-directed cell-mediated cytotoxicity (ADCC). A fully human antibody is one in which the protein sequences are encoded by naturally occurring human immunoglobulin sequences, either from isolated antibody-producing human B-lymphocytes, or from transgenic murine B-lymphocytes of mice in which the murine immunoglobulin coding chromosomal regions have been replaced by orthologous human sequences. Transgenic antibodies of the latter type include, but are not restricted to,

HuMab (Medarex, Inc, CA) and Xenomouse (Abgenix Inc., CA). A humanised antibody is one in which the constant region of a non-human antibody molecule of appropriate antigen specificity, is replaced by the constant region of a human antibody, preferably of the IgG subtype, with appropriate effector functions (Morrison et al., 1984, *Proc. Natl. Acad. Sci.* 81:851-855; Neuberger et al., 1984, *Nature* 312: 604-608; Takeda et al., 1985, *Nature* 314:452-454). Appropriate effector functions include ADCC, which is a natural process by which fully-human antibodies or humanized antibodies, when bound to targets on the surface of cancer cells, switch on the cell killing properties of lymphocytes that are part of the normal immune system. These active lymphocytes, called Natural Killer (NK) cells, use a cytotoxic process to destroy living cells to which the antibodies are bound. ADCC activity may be detected and quantified by measuring release of Europium (Eu3+) from Eu3+ labelled, living cells in the presence of an antigen-specific antibody and peripheral blood mononuclear cells extracted from an immunocompetent, living human subject. The ADCC process is described in detail in Janeway Jr. C. A. et al., *Immunobiology*, 5th ed., 2001, Garland Publishing, ISBN 0-8153-3642-X; Pier G. B. et al., *Immunology, Infection, and Immunity*, 2004, p. 246-5; Albanell J. et al., *Advances in Experimental Medicine and Biology*, 2003, 532:p. 2153-68 and Weng, W.-K. et al., *Journal of Clinical Oncology*, 2003, 21:p. 3940-3947. Suitable methods for the detection and quantification of ADCC can be found in Blomberg et al., *Journal of Immunological Methods*, 1986, 86:p. 225-9; Blomberg et al., *Journal of Immunological Methods*, 1986, 21; 92:p. 117-23 and Patel & Boyd, *Journal of Immunological Methods*, 1995, 184:p. 29-38.

[0863] ADCC typically involves activation of NK cells and is dependent on the recognition of antibody-coated cells by Fc receptors on the surface of the NK cell. The Fc receptors recognize the Fc (crystalline) portion of antibodies such as IgG, bound specifically to the surface of a target cell. The Fc receptor that triggers activation of the NK cell is called CD16 or FcγRIIIa. Once the FcγRIIIa receptor is bound to the IgG Fc, the NK cell releases cytokines such as IFN-γ, and cytotoxic granules containing perforin and granzymes that enter the target cell and promote cell death by triggering apoptosis.

[0864] The induction of antibody-dependent cellular cytotoxicity (ADCC) by an antibody can be enhanced by modifications that alter interactions between the antibody constant region (Fc) and various receptors that are present on the surface of cells of the immune system. Such modifications include the reduction or absence of alpha1,6-linked fucose moieties in the complex oligosaccharide chains that are normally added to the Fc of antibodies during natural or recombinant synthesis in mammalian cells. In a preferred embodiment, non-fucosylated anti-OGTA002, anti-OGTA009, anti-OGTA016, anti-OGTA028, anti-OGTA037, anti-OGTA041, anti-OGTA053, anti-OGTA054, anti-OGTA066, anti-OGTA072, anti-OGTA074, anti-OGTA076, anti-OGTA085, anti-OGTA087, anti-OGTA088, anti-OGTA089, anti-OGTA091, anti-OGTA098, anti-OGTA101, anti-OGTA104, anti-OGTA106, anti-OGTA112, anti-OGTA113, anti-OGTA119, anti-OGTA124, anti-OGTA126, anti-OGTA156, anti-OGTA159, anti-OGTA168, anti-OGTA169, anti-OGTA174, anti-OGTA176, anti-OGTA177, anti-OGTA197, anti-OGTA202, anti-OGTA203, anti-OGTA206, anti-OGTA213, anti-OGTA214, anti-OGTA216, anti-OGTA222, anti-OGTA236, anti-OGTA237, anti-OGTA247, anti-OGTA248, anti-OGTA249, anti-OGTA257 or anti-

OGTA271 affinity reagents such as antibodies or fragments thereof are produced for the purpose of enhancing their ability to induce the ADCC response.

[0865] Techniques for reducing or ablating alpha 1,6-linked fucose moieties in the oligosaccharide chains of the Fc are well established. In one example, the recombinant antibody is synthesized in a cell line that is impaired in its ability to add fucose in an alpha 1,6 linkage to the innermost N-acetylglucosamine of the N-linked biantennary complex-type Fc oligosaccharides. Such cell lines include, but are not limited to, the rat hybridoma YB2/0, which expresses a reduced level of the alpha 1,6-fucosyltransferase gene, FUT8. Preferably, the antibody is synthesized in a cell line that is incapable of adding alpha 1,6-linked fucosyl moieties to complex oligosaccharide chains, due to the deletion of both copies of the FUT8 gene. Such cell lines include, but are not limited to, FUT8-/- CHO/DG44 cell lines. Techniques for synthesizing partially fucosylated, or non-fucosylated antibodies and affinity reagents are described in Shinkawa et al., *J. Biol. Chem.* 278:3466-34735 (2003); Yamane-Ohnuki et al., *Biotechnology and Bioengineering* 87: 614-22 (2004) and in WO00/61739 A1, WO02/31140 A1 and WO03/085107 A1. In a second example, the fucosylation of a recombinant antibody is reduced or abolished by synthesis in a cell line that has been genetically engineered to overexpress a glycoprotein-modifying glycosyl transferase at a level that maximizes the production of complex N-linked oligosaccharides carrying bisecting N-acetylglucosamine. For example, the antibody is synthesized in a Chinese Hamster Ovary cell line expressing the enzyme N-acetyl glucosamine transferase III (GnT III). Cell lines stably transfected with suitable glycoprotein-modifying glycosyl transferases, and methods of synthesizing antibodies using these cells are described in WO9954342.

[0866] A non-fucosylated antibody or affinity reagent can be used as a therapeutic that is administered alone or in combination with cytotoxic factor(s) and/or cytokine(s).

[0867] In a further modification, the amino acid sequences of the antibody Fc are altered in a way that enhances ADCC activation, without affecting ligand affinity. Examples of such modifications are described in Lazar et al., *Proceedings of the National Academy of Sciences* 2006, 103:p. 4005-4010; WO03074679 and WO2007039818. In these examples, substitution of amino acids in the antibody Fc, such as aspartate for serine at position 239, and isoleucine for glutamate at position 332, altered the binding affinity of an antibody for Fc receptors, leading to an increase in ADCC activation.

[0868] An antibody reagent with enhanced ADCC activation due to amino acid substitutions can be used as a therapeutic that is administered alone or in combination with cytotoxic factor(s) and/or cytokine(s).

Therapeutic Use of the Proteins of the Invention

[0869] The invention provides for treatment or prevention of various diseases and disorders by administration of a therapeutic compound. Such compounds include but are not limited to: OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214,

OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or

[0870] OGTA271, analogs thereof, related polypeptides and derivatives (including fragments) thereof; antibodies (or other affinity reagents) to the foregoing; nucleic acids encoding an OGTA, analogs of the latter or a related polypeptides and fragments thereof; antisense nucleic acids to a gene encoding an OGTA, analogs of the latter or a related polypeptides and fragments thereof; and modulator (e.g., agonists and antagonists) of a gene encoding an OGTA or a related polypeptide. An important feature of the present invention is the identification of genes encoding OGTA(s) involved in a relevant cancer. B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer and retinoblastoma can be treated (e.g. to ameliorate symptoms or to retard onset or progression) or prevented by administration of a therapeutic compound that reduces function or expression of an OGTA in the serum or tissue of subjects having said cancer.

[0871] In one embodiment, one or more antibodies (or other affinity reagents) each specifically binding to a relevant OGTA are administered alone or in combination with one or more additional therapeutic compounds or treatments.

[0872] In one embodiment a biological product such as an antibody (or other affinity reagent) is allogeneic to the subject to which it is administered. In another embodiment, a human OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 or a related polypeptide, a nucleotide sequence encoding any of the aforementioned moieties, or an antibody (or other affinity reagent) to a human OGTA or a related polypeptide, is administered to a human subject for therapy (e.g. to ameliorate symptoms or to retard onset or progression) or prophylaxis.

[0873] Without being limited by theory, it is conceived that the therapeutic activity of antibodies (or other affinity reagents) which specifically bind to the proteins of the invention may be achieved through the phenomenon of Antibody-Dependent Cell-mediated Cytotoxicity (ADCC) (see e.g. Janeway Jr. C. A. et al., *Immunobiology*, 5th ed., 2001, Garland Publishing, ISBN 0-8153-3642-X; Pier G. B. et al., *Immunology, Infection, and Immunity*, 2004, p. 246-5; Albanell J. et al., *Advances in Experimental Medicine and Biology*, 2003, 532:p. 2153-68 and Weng, W.-K. et al., *Journal of Clinical Oncology*, 2003, 21:p 3940-3947).

Treatment and Prevention and/or Diagnosis of B-Cell Non-Hodgkin's Lymphoma, Breast Cancer, Cervical Cancer, Colorectal Cancer, Gastric Cancer, Glioblastoma, Hepatocellular Carcinoma, Lung Cancer, Lymphoid Leukaemia (Particularly Acute T-Cell Leukaemia and Chronic Lymphocytic Leukaemia), Melanoma, Neuroblastoma, Osteosarcoma, Ovarian Cancer, Pancreatic Cancer, Prostate Cancer, Renal Cell Cancer and Retinoblastoma

[0874] Relevant cancers are treated or prevented by administration to a subject, suspected of having or known to have or to be at risk of developing said cancer, of a compound that modulates (i.e., increases or decreases) the level or activity (i.e., function or expression) of an OGTA according to the invention that is differentially present in the serum or tissue of subjects having a relevant cancer listed herein compared with serum or tissue of subjects free from said cancer.

[0875] In one embodiment, the cancer/cancers is/are treated or prevented by administering to a subject suspected having or known to have or to be at risk of developing a relevant cancer a compound that upregulates (i.e., increases) the level or activity (i.e., function or expression) of an OGTA according to the invention that are decreased in the serum or tissue of subjects having a relevant cancer. Examples of such a compound include, but are not limited to, OGTA antisense oligonucleotides, ribozymes, antibodies (or other affinity reagents) directed against the proteins of the invention, and compounds that inhibit the enzymatic activity of the proteins of the invention. Other useful compounds e.g. OGTA antagonists and small molecule OGTA antagonists, can be identified using in vitro assays.

[0876] A relevant cancer/cancers is/are also treated or prevented by administration to a subject suspected of having or known to have said cancer or to be at risk of developing said cancer of a compound that downregulates the level or activity (i.e. function) of an OGTA that are increased in the serum or tissue of subjects having said cancer. Examples of such a compound include but are not limited to: OGTAs according to the invention, OGTA fragments and OGTA-related polypeptides; nucleic acids encoding an OGTA, an OGTA fragment and an OGTA-related polypeptide (e.g. for use in gene therapy); and, for those OGTA or OGTA-related polypeptides with enzymatic activity, compounds or molecules known to modulate that enzymatic activity. Other compounds that can be used, e.g. OGTA agonists, can be identified using in vitro assays.

[0877] In one embodiment, therapy or prophylaxis is tailored to the needs of an individual subject. Thus, in specific embodiments, compounds that promote the level or function of an OGTA according to the invention are therapeutically or prophylactically administered to a subject suspected of having or known to have a relevant cancer, in whom the levels or functions of an OGTA according to the invention are absent or are decreased relative to a control or normal reference range. In further embodiments, compounds that promote the level or function of an OGTA according to the invention are therapeutically or prophylactically administered to a subject suspected of having or known to have a relevant cancer in whom the levels or functions of an OGTA according to the invention are increased relative to a control or to a reference range. In further embodiments, compounds are employed that decrease the level or function of an OGTA according to the invention, for example in subjects in whom said levels or functions are increased relative to a control or to a reference range.

[0878] In further embodiments, compounds that decrease the level or function of OGTA according to the invention are therapeutically or prophylactically administered to a subject suspected of having or known to have a relevant cancer in whom said levels or functions are increased relative to a control or to a reference range.

[0879] In further embodiments, compounds that decrease the level or function of an OGTA according to the invention are therapeutically or prophylactically administered to a sub-

ject suspected of having or known to have a relevant cancer in whom said levels or functions are decreased relative to a control or to a reference range.

[0880] The change in OGTA function or level due to the administration of such compounds can be readily detected, e.g., by obtaining a sample (e.g., blood or urine) and assaying in vitro the levels or activities of an OGTA according to the invention, or the levels of mRNAs encoding same, or any combination of the foregoing. Such assays can be performed before and after the administration of the compound as described herein.

[0881] The compounds of the invention include but are not limited to any compound, e.g., a small organic molecule, protein, peptide, antibody (or other affinity reagent), nucleic acid, etc. that restores the relevant OGTAs profile towards normal. The compounds of the invention may be given in combination with any other chemotherapy drugs.

[0882] In accordance with the present invention, test samples of lymphoid, breast, cervical, colorectal, gastric, brain, liver, lung, skin, neuronal, osteoblast, ovarian, pancreatic, prostate, kidney or eye tissue, serum, plasma or urine obtained from a subject suspected of having or known to have a relevant cancer can be used for diagnosis or monitoring. In one embodiment, a change in the abundance of an OGTA according to the invention in a test sample relative to a control sample (from a subject or subjects free from said cancer or a previously determined reference range indicates the presence of the relevant cancer.

[0883] In another embodiment, the relative abundance of an OGTA according to the invention in a test sample compared to a control sample or a previously determined reference range indicates a subtype of the relevant cancer (e.g. pre-T-cell or mature T-cell acute lymphocytic leukaemia, diffuse large B-cell lymphoma, inflammatory breast cancer, squamous cell cervical carcinoma, T-cell chronic lymphocytic leukaemia, familial or sporadic colorectal cancer, gastrointestinal stromal tumours, fibrolamellar hepatocellular carcinoma, squamous cell lung carcinoma, ganglioneuroblastoma or familial neuroblastoma, parosteal or periosteal osteosarcoma, malignant papillary serous adenocarcinoma, endocrine tumours of the pancreas or bilateral, multifocal retinoblastoma or unilateral, unifocal retinoblastoma). In yet another embodiment, the relative abundance of OGTA(s) in a test sample relative to a control sample or a previously determined reference range indicates the degree or severity of the relevant cancer (e.g., the likelihood for metastasis). In any of the aforesaid methods, detection of OGTA(s) may optionally be combined with detection of one or more of additional biomarkers for a relevant cancer. Any suitable method in the art can be employed to measure the level of OGTA(s), including but not limited to the Preferred Technologies described in Examples 1 and 2 described herein, kinase assays, immunoassays to detect and/or visualize OGTA(s) (e.g., Western blot, immunoprecipitation followed by sodium dodecyl sulfate polyacrylamide gel electrophoresis, immunocytochemistry, etc.). In a further embodiment, a change in the abundance of mRNA encoding an OGTA according to the invention in a test sample relative to a control sample or a previously determined reference range indicates the presence of a relevant cancer. Any suitable hybridization assay can be used to detect expression of an OGTA according to the invention by detecting and/or visualizing mRNA encoding an OGTA according to the invention (e.g., Northern assays, dot blots, in situ hybridization, etc.).

[0884] In another embodiment of the invention, labeled antibodies (or other affinity reagents), derivatives and analogs thereof, which specifically bind to an OGTA according to the invention can be used for diagnostic purposes to detect, diagnose, or monitor a relevant cancer. For example a relevant cancer is detected in an animal, such as in a mammal and particularly in a human.

Screening Assays

[0885] The invention provides methods for identifying agents (e.g., candidate compounds or test compounds) that bind to an OGTA according to the invention or have a stimulatory or inhibitory effect on the expression or activity of an OGTA according to the invention. The invention also provides methods of identifying agents, candidate compounds or test compounds that bind to an OGTA according to the invention or a related polypeptide or an fusion protein or have a stimulatory or inhibitory effect on the expression or activity of any of the aforementioned moieties. Examples of agents, candidate compounds or test compounds include, but are not limited to, nucleic acids (e.g., DNA and RNA), carbohydrates, lipids, proteins, peptides, peptidomimetics, small molecules and other drugs. Agents can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the "one-bead one-compound" library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptide libraries, while the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam, 1997, *Anticancer Drug Des.* 12:145; U.S. Pat. No. 5,738,996; and U.S. Pat. No. 5,807,683, each of which is incorporated herein in its entirety by reference).

[0886] Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt et al., 1993, *Proc. Natl. Acad. Sci. USA* 90:6909; Erb et al., 1994, *Proc. Natl. Acad. Sci. USA* 91:11422; Zuckermann et al., 1994, *J. Med. Chem.* 37:2678; Cho et al., 1993, *Science* 261:1303; Carrell et al., 1994, *Angew. Chem. Int. Ed. Engl.* 33:2059; Carell et al., 1994, *Angew. Chem. Int. Ed. Engl.* 33:2061; and Gallop et al., 1994, *J. Med. Chem.* 37:1233, each of which is incorporated herein in its entirety by reference.

[0887] Libraries of compounds may be presented, e.g., presented in solution (e.g., Houghten, 1992, *Bio/Techniques* 13:412-421), or on beads (Lam, 1991, *Nature* 354:82-84), chips (Fodor, 1993, *Nature* 364:555-556), bacteria (U.S. Pat. No. 5,223,409), spores (U.S. Pat. Nos. 5,571,698; 5,403,484; and 5,223,409), plasmids (Cull et al., 1992, *Proc. Natl. Acad. Sci. USA* 89:1865-1869) or phage (Scott and Smith, 1990, *Science* 249:386-390; Devlin, 1990, *Science* 249:404-406; Cwirla et al., 1990, *Proc. Natl. Acad. Sci. USA* 87:6378-6382; and Felici, 1991, *J. Mol. Biol.* 222:301-310), each of which is incorporated herein in its entirety by reference.

[0888] In one embodiment, agents that interact with (i.e., bind to) OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197,

OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271, a fragment (e.g. a functionally active fragment) thereof, a related polypeptide, a fragment of a related polypeptide, or an OGTA fusion protein are identified in a cell-based assay system.

[0889] In accordance with this embodiment, cells expressing OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271, a fragment thereof, a related polypeptide, a fragment of a related polypeptide, or an OGTA fusion protein are contacted with a candidate compound or a control compound and the ability of the candidate compound to interact with an OGTA according to the invention is determined. If desired, this assay may be used to screen a plurality (e.g. a library) of candidate compounds. The cell, for example, can be of prokaryotic origin (e.g., *E. coli*) or eukaryotic origin (e.g., yeast or mammalian). Further, the cells can express OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271, a fragment thereof, a related polypeptide, a fragment of a related polypeptide, or an OGTA fusion protein endogenously or be genetically engineered to express one or more of the same. In certain instances, OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271, a fragment thereof, a related polypeptide, a fragment of a related polypeptide, or an OGTA fusion protein or the candidate compound is labeled, for example with a radioactive label (such as ³²P, ³⁵S, and ¹²⁵I) or a fluorescent label (such as fluorescein isothiocyanate, rhodamine, phycoerythrin, phycocyanin, allophycocyanin, o-phthaldehyde or fluorescamine) to enable detection of an interaction between a relevant OGTA according to the invention and a candidate compound. The ability of the candidate compound to interact directly or indirectly with OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177,

OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271, a fragment thereof, a related polypeptide, a fragment of a related polypeptide, or an OGTA fusion protein can be determined by methods known to those of skill in the art. For example, the interaction between a candidate compound and OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271, a related polypeptide, a fragment of a related polypeptide, or an OGTA fusion protein can be determined by flow cytometry, a scintillation assay, immunoprecipitation or western blot analysis.

[0890] In another embodiment, agents that interact with (i.e., bind to) OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271, a fragment (e.g., a functionally active fragment) thereof, a related polypeptide, or an OGTA fusion protein are identified in a cell-free assay system. In accordance with this embodiment, a native or recombinant OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 or fragment thereof, or a native or recombinant related polypeptide or fragment thereof, or an OGTA fusion protein or fragment thereof, is contacted with a candidate compound or a control compound and the ability of the candidate compound to interact with OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 or the related polypeptide, or the fusion protein is determined. If desired, this assay may be used to screen a plurality (e.g. a library) of candidate compounds.

[0891] In one embodiment, OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076,

OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271, a fragment thereof, a related polypeptide, a fragment of a related polypeptide, or an OGTA fusion protein is first immobilized, by, for example, contacting the relevant entity with an immobilized antibody (or other affinity reagent) which specifically recognizes and binds it, or by contacting a purified preparation of OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271, a fragment thereof, a related polypeptide, a fragment of a related polypeptide, or an OGTA fusion protein with a surface designed to bind proteins.

[0892] OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271, a fragment thereof, a related polypeptide, a fragment of a related polypeptide, or an OGTA fusion protein may be partially or completely purified (e.g., partially or completely free of other polypeptides) or part of a cell lysate. Further, OGTA's of the invention, a fragment thereof, a related polypeptide, a fragment of a related polypeptide may be a fusion protein comprising OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 or a biologically active portion thereof, or a related polypeptide and a domain such as glutathionine-S-transferase.

[0893] Alternatively, an OGTA according to the invention, a fragment thereof, a related polypeptide, fragment of a related polypeptide or an OGTA fusion protein can be biotinylated using techniques well known to those of skill in the art (e.g., biotinylation kit, Pierce Chemicals; Rockford, Ill.). The ability of the candidate compound to interact with an OGTA according to the invention, a fragment thereof, a related polypeptide, a fragment of a related polypeptide, or an OGTA fusion protein can be determined by methods known to those of skill in the art.

[0894] In another embodiment, a cell-based assay system is used to identify agents that bind to or modulate the activity of a protein, such as an enzyme, or a biologically active portion thereof, which is responsible for the production or degradation of an OGTA according to the invention is responsible for the post-translational modification of same. In a primary screen, a plurality (e.g., a library) of compounds are contacted with cells that naturally or recombinantly express: (i) OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271, an isoform of any of the aforementioned, a homolog thereof, an a related polypeptide, an OGTA fusion protein, or a biologically active fragment of any of the foregoing; and (ii) a protein that is responsible for processing of OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271, isoform of any of the aforementioned, an OGTA homolog, a related polypeptide, an OGTA fusion protein, or fragment in order to identify compounds that modulate the production, degradation, or post-translational modification of the same. If desired, compounds identified in the primary screen can then be assayed in a secondary screen against cells naturally or recombinantly expressing a protein according to the invention. The ability of the candidate compound to modulate the production, degradation or post-translational modification of OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271, isoform, homolog, a related polypeptide, or OGTA fusion protein can be determined by methods known to those of skill in the art, including without limitation, flow cytometry, a scintillation assay, immunoprecipitation and western blot analysis.

[0895] In another embodiment, agents that competitively interact with (i.e., bind to) OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237,

OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271, a fragment thereof, a related polypeptide, a fragment of a related polypeptide, or an OGTA fusion protein are identified in a competitive binding assay.

[0896] In accordance with this embodiment, cells expressing an OGTA according to the invention, a fragment thereof, a related polypeptide, a fragment of a related polypeptide, or an OGTA fusion protein are contacted with a candidate compound and a compound known to interact with the same (any of the aforementioned); the ability of the candidate compound to preferentially interact with OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271, a fragment thereof, a related polypeptide, fragment of a related polypeptide, or an OGTA fusion protein is then determined.

[0897] Alternatively, agents that preferentially interact with (i.e., bind to) an OGTA according to the invention, a fragment thereof, a related polypeptide or fragment of a related polypeptide are identified in a cell-free assay system by contacting OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271, a fragment thereof, a related polypeptide, a fragment of a related polypeptide, or an OGTA fusion protein with a candidate compound and a compound known to interact with an OGTA according to the invention, a related polypeptide or the OGTA fusion protein.

[0898] As stated above, the ability of the candidate compound to interact with an OGTA according to the invention, a fragment thereof, a related polypeptide, a fragment of a related polypeptide, or an OGTA fusion protein can be determined by methods known to those of skill in the art. These assays, whether cell-based or cell-free, can be used to screen a plurality (e.g., a library) of candidate compounds.

[0899] In another embodiment, agents that modulate (i.e., upregulate or downregulate) the expression or activity of an OGTA according to the invention or a related polypeptide are identified by contacting cells (e.g., cells of prokaryotic origin or eukaryotic origin) expressing OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271, or a related polypeptide with a candidate com-

pound or a control compound (e.g., phosphate buffered saline (PBS)) and determining the expression of OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271, a related polypeptide, or an OGTA fusion protein, mRNA encoding an OGTA according to the invention, or mRNA encoding OGTA according to the invention or a related polypeptide.

[0900] The level of expression of OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271, a related polypeptide, mRNA encoding an OGTA according to the invention, or mRNA encoding an OGTA related polypeptide in the presence of the candidate compound is compared to the level of expression in the absence of the candidate compound (e.g., in the presence of a control compound). The candidate compound can then be identified as a modulator of the expression of OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271, or a related polypeptide based on this comparison. For example, when expression of an OGTA according to the invention or mRNA is significantly greater in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of expression of OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271, or mRNA. Alternatively, when expression of OGTA according to the invention or mRNA is significantly less in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of the expression of OGTA according to the invention or mRNA. The level of expression of OGTA according to the invention or the mRNA that encodes it can be determined by methods known to those of skill in the art. For example, mRNA expression can be assessed by

Northern blot analysis or RT-PCR, and protein levels can be assessed by western blot analysis.

[0901] In another embodiment, agents that modulate the activity of an OGTA according to the invention or a related polypeptide are identified by contacting a preparation containing OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 or a related polypeptide or cells (e.g., prokaryotic or eukaryotic cells) expressing any of the aforementioned with a test compound or a control compound and determining the ability of the test compound to modulate (e.g., stimulate or inhibit) the activity of an OGTA according to the invention or a related polypeptide. The activity of OGTA according to the invention or a related polypeptide can be assessed by detecting induction of a cellular signal transduction pathway of OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 or a related polypeptide (e.g., intracellular Ca^{2+} , diacylglycerol, IP3, etc.), detecting catalytic or enzymatic activity of the target on a suitable substrate, detecting the induction of a reporter gene (e.g., a regulatory element that is responsive to an OGTA according to the invention or a related polypeptide and is operably linked to a nucleic acid encoding a detectable marker, e.g., luciferase), or detecting a cellular response, for example, cellular differentiation, or cell proliferation. Based on the present description, techniques known to those of skill in the art can be used for measuring these activities (see, e.g., U.S. Pat. No. 5,401,639, which is incorporated herein by reference).

[0902] The candidate compound can then be identified as a modulator of the activity of an OGTA according to the invention or a related polypeptide by comparing the effects of the candidate compound to the control compound. Suitable control compounds include phosphate buffered saline (PBS) and normal saline (NS).

[0903] In another embodiment, agents that modulate (i.e., upregulate or downregulate) the expression, activity or both the expression and activity of an OGTA according to the invention or a related polypeptide are identified in an animal model. Examples of suitable animals include, but are not limited to, mice, rats, rabbits, monkeys, guinea pigs, dogs and cats. For example, the animal used represent a model of a relevant cancer (e.g. xenografts of acute T-cell leukaemia cell lines such as HSB-2 in SCID mice, Morland et al, Cell Biophys. 1994; 24-25:315-29; xenografts of B-cell non-Hodgkin's lymphoma cell lines such as SU-DHL-4 and OCI-Ly8 in SCID mice, Schmidt-Wolf et al, J Exp Med. 1991 Jul. 1; 174(1):139-49; xenografts of breast cancer cell lines such as MCF-7 (Ozzello L, Sordat M., Eur J Cancer. 1980; 16:553-

559) and MCF10AT (Miller et al., J Natl Cancer Inst. 1993; 85:1725-1732) in nude or SCID mice; xenografts of cervical cancer cell lines such as CaSki in nude mice; xenografts of chronic lymphocytic leukaemia cell lines such as WSU-CLL in SCID mice, Mohammad et al, Leukaemia. 1996 January; 10(1):130-7; xenografts of human colorectal cancer cell lines such as MDA-MB-345 in oestrogen-deprived SCID mice, Eccles et al. 1994 Cell Biophysics 24/25, 279; xenografts of gastric cell lines such as AZ-521 in nude mice; xenografts of glioblastoma cell lines such as U87MG in nude mice, Abernathy et al., Neurosurgery 1988 May; 22(5):877-81; xenografts of hepatocellular carcinoma cell lines such as MHCC97 in nude mice, Tian et al., Br J 5 Cancer 1999 November; 81(5):814-21; xenografts of non small cell lung cancer cell lines such as A549 and H460 and xenografts of small cell lung cancer cell lines such as NCI-H345; xenografts of melanoma cell lines such as MV3 in nude mice, van Muijen et al, Int J Cancer 1991 Apr. 22; 48(1):85-91; xenografts of neuroblastoma cell lines such as SK—N—SH in nude mice, Helson et al, Cancer Res. 1975 September; 35(9):2594-9; xenografts of human osteosarcoma cell lines such as HuO9 in nude mice, Kimura et al., Clin Exp Metastasis 2002; 19(6):477-85; xenografts of ovarian cancer cell lines such as IGR0V1 in nude mice, Benard et al, Cancer Res. 1985 October; 45(10):4970-9; xenografts of pancreatic cancer cell lines such as MIA PaCa-2 in nude mice, Marincola et al., J Surg Res 1989 December; 47(6):520-9; xenografts of prostate cancer cell lines such as CWR-22 in nude mice, Pretlow et al, J Natl Cancer Inst. 1993 Mar. 3; 85(5):394-8; xenografts of renal cell cancer cell lines such as LABA21 in immune compromised mice, Zisman et al, Cancer Research 63, 4952-4959, Aug. 15, 2003, or xenografts of retinoblastoma cell lines such as Y79). These can be utilized to test compounds that modulate levels of an OGTA according to the invention, since the pathology exhibited in these models is similar to that of a relevant cancer. In accordance with this embodiment, the test compound or a control compound is administered (e.g., orally, rectally or parenterally such as intraperitoneally or intravenously) to a suitable animal and the effect on the expression, activity or both expression and activity of OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 or a related polypeptide is determined. Changes in the expression of the same can be assessed by the methods outlined above.

[0904] In yet another embodiment, OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 or a related polypeptide is used as a “bait protein” in a two-hybrid assay or three hybrid assay to identify other

proteins that bind to or interact with an OGTA according to the invention or a related polypeptide (see, e.g., U.S. Pat. No. 5,283,317; Zervos et al. (1993) Cell 72:223-232; Madura et al. (1993) J. Biol. Chem. 268:12046-12054; Bartel et al. (1993) Bio/Techniques 14:920-924; Iwabuchi et al. (1993) Oncogene 8:1693-1696; and PCT Publication No. WO 94/10300). As those skilled in the art will appreciate, such binding proteins are also likely to be involved in the propagation of signals by OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 as, for example, upstream or downstream elements of a signaling pathway involving same.

[0905] This invention provides novel agents identified by screening assays and uses thereof for treatments as described herein. In addition, the invention also provides the use of an agent which interacts with, or modulates the activity of, an OGTA according to the invention in the manufacture of a medicament for the treatment and/or diagnosis of a relevant cancer.

Vaccine Therapy

[0906] Another aspect of the invention is an immunogenic composition, suitably a vaccine composition, comprising OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 or an epitope containing fragment thereof, or nucleic acid encoding OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 or a fragment thereof optionally together with an immunostimulant.

[0907] There is also provided a method of raising an immune response which comprises administering to a subject such compositions and a method for treating or preventing a relevant cancer which comprises administering to a subject in need thereof a therapeutically effective amount of such compositions and such compositions for use in preventing or treating a relevant cancer.

[0908] Thus, OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098,

OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 and OGTA271 may be useful as antigenic material, and may be used in the production of vaccines for treatment or prophylaxis of B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer and retinoblastoma. Such material can be "antigenic" and/or "immunogenic". Generally, "antigenic" is taken to mean that the protein is capable of being used to raise antibodies (or other affinity reagents) or indeed is capable of inducing an antibody response in a subject or experimental animal. "Immunogenic" is taken to mean that the protein is capable of eliciting a protective immune response in a subject or experimental animal. Thus, in the latter case, the protein may be capable of not only generating an antibody response but, in addition, non-antibody based immune responses. "Immunogenic" also embraces whether the protein may elicit an immune-like response in an in-vitro setting e.g. a T-cell proliferation assay.

[0909] The immune response may require appropriate formulation or presentation of the immunogen and may require the presence of one or more excipients such as one or more adjuvant components. Nevertheless the invention extends to such composition which may form a key component of a final vaccine.

[0910] The skilled person will appreciate that homologues or derivatives of OGTA according to the invention will also find use as antigenic/immunogenic material and for other applications according to the invention. Thus, for instance proteins which include one or more additions, deletions, substitutions or the like are encompassed by the present invention. In addition, it may be possible to replace one amino acid with another of similar "type". For instance, replacing one hydrophobic amino acid with another. One can use a program such as the CLUSTAL program to compare amino acid sequences. This program compares amino acid sequences and finds the optimal alignment by inserting spaces in either sequence as appropriate. It is possible to calculate amino acid identity or similarity (identity plus conservation of amino acid type) for an optimal alignment. A program like BLASTx will align the longest stretch of similar sequences and assign a value to the fit. It is thus possible to obtain a comparison where several regions of similarity are found, each having a different score. Both types of analysis are contemplated in the present invention.

[0911] In the case of homologues and derivatives, the degree of identity with a protein as described herein is less important than that the homologue or derivative should retain its antigenicity and/or immunogenicity. However, suitably, homologues or derivatives having at least 60% similarity (as discussed above) or identity with the proteins or polypeptides described herein are provided. Preferably, homologues or derivatives having at least 70% similarity or identity, more preferably at least 80% similarity or identity are provided. Most preferably, homologues or derivatives having at least 90% or even 95% similarity or identity are provided.

[0912] In an alternative approach, the homologues or derivatives could be fusion proteins, incorporating moieties which render purification easier, for example by effectively tagging the desired protein or polypeptide. It may be necessary to remove the "tag" or it may be the case that the fusion protein itself retains sufficient antigenicity to be useful.

[0913] It is well known that it is possible to screen an antigenic protein or polypeptide to identify epitopic regions, i.e. those regions which are responsible for the protein or polypeptide's antigenicity or immunogenicity. Methods well known to the skilled person can be used to test fragments and/or homologues and/or derivatives for antigenicity. Thus, the fragments of the present invention should include one or more such epitopic regions or be sufficiently similar to such regions to retain their antigenic/immunogenic properties. Thus, for fragments according to the present invention the degree of identity is perhaps irrelevant, since they may be 100% identical to a particular part of a protein or polypeptide, homologue or derivative as described herein. The key issue, once again, is that the fragment retains the antigenic/immunogenic properties of the protein from which it is derived.

[0914] What is important for homologues, derivatives and fragments is that they possess at least a degree of the antigenicity/immunogenicity of the protein or polypeptide from which they are derived. Thus, in an additional aspect of the invention, there is provided antigenic/or immunogenic fragments of OGTA according to the invention, or of homologues or derivatives thereof.

[0915] OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 and OGTA271, or antigenic fragments thereof, can be provided alone, as a purified or isolated preparation. They may be provided as part of a mixture with one or more other proteins of the invention, or antigenic fragments thereof. In a further aspect, therefore, the invention provides an antigen composition comprising an OGTA according to the invention and/or one or more antigenic fragments thereof. Such a composition can be used for the detection and/or diagnosis of a relevant cancer.

[0916] The antigenic OGTA according to the invention, antigenic fragment thereof or antigen composition of the invention can be used to induce an immune response against a relevant cancer.

[0917] In one aspect, the present invention provides a method of detecting and/or diagnosing a relevant cancer which comprises:

bringing into contact with a sample to be tested an antigenic OGTA according to the invention (including one or more of same), or an antigenic fragment thereof, or an antigen composition of the invention; and
detecting the presence of antibodies (or other affinity reagents) to a relevant cancer.

[0918] In particular, the protein, antigenic fragment thereof or antigen composition of the present invention can be used to detect IgA, IgM or IgG antibodies. Suitably, the sample to be tested will be a biological sample, e.g. a sample of blood, tissue or saliva.

[0919] In a further aspect, the invention provides the use of an antigenic OGTA according to the invention, an antigenic fragment thereof or an antigen composition of the invention in medicine.

[0920] In a further aspect, the present invention provides a composition capable of eliciting an immune response in a subject, which composition comprises OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271, an antigenic fragment thereof, or an antigen composition of the invention. Suitably, the composition will be a vaccine composition, optionally comprising one or more suitable adjuvants. Such a vaccine composition may be either a prophylactic or therapeutic vaccine composition.

[0921] Vaccine compositions according to the invention may be either a prophylactic or therapeutic vaccine composition.

[0922] The vaccine compositions of the invention can include one or more adjuvants (immunostimulants). Examples well-known in the art include inorganic gels, such as aluminium hydroxide, and water-in-oil emulsions, such as incomplete Freund's adjuvant. Other useful adjuvants will be well known to the skilled person.

[0923] Such preparations may include other vehicles.

[0924] In another embodiment, a preparation of oligonucleotides comprising 10 or more consecutive nucleotides complementary to a nucleotide sequence encoding an OGTA or an OGTA peptide fragments is used as vaccines for the treatment of a relevant cancer. Such preparations may include adjuvants or other vehicles.

[0925] Suitable adjuvants for use in vaccine compositions for the treatment of cancer include: 3De-O-acylated monophosphoryl lipid A (known as 3D-MPL or simply MPL see WO92/116556), a saponin, for example QS21 or QS7, and TLR4 agonists such as a CpG containing molecule, for example as disclosed in WO95/26204.

[0926] The adjuvants employed may be a combination of components, for example MPL and QS21 or MPL, QS21 and a CpG containing moiety.

[0927] Adjuvants may be formulated as oil-in-water emulsions or liposomal formulations.

[0928] In yet further aspects, the present invention provides:

(a) the use of OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271, an antigenic fragment thereof, or an antigen composition of the invention in the preparation of an immunogenic composition, preferably a vaccine;

(b) the use of such an immunogenic composition in inducing an immune response in a subject; and

(c) a method for the treatment or prophylaxis of B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma in a subject, or of vaccinating a subject against said cancer(s) which comprises the step of administering to the subject an effective amount of OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271, at least one antigenic fragment thereof or an antigen composition of the invention, such as a vaccine.

[0929] In a specific embodiment, a preparation of OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 or peptide fragments thereof is used as a vaccine for the treatment of a relevant cancer. Such preparations may include adjuvants or other vehicles.

[0930] The invention also extends to use of a vaccine as described herein for use in prophylaxis or treatment of an appropriate cancer as described herein.

[0931] In another embodiment, a preparation of oligonucleotides comprising 10 or more consecutive nucleotides complementary to a nucleotide sequence encoding OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 and OGTA271, antigenic fragments thereof or can be provided as a kit for use in the *in vitro* detection and/or diagnosis of a relevant cancer. Thus, in a still further aspect, the present invention provides a kit for use in the detection and/or diagnosis of a relevant cancer, which kit comprises an antigenic OGTA according to the invention, an antigenic fragment thereof or an antigenic composition of the present invention.

Identification of Compounds that Inhibit the Proteins of the Invention to Treat B-Cell Non-Hodgkin's Lymphoma, Breast Cancer, Cervical Cancer, Colorectal Cancer, Gastric Cancer, Glioblastoma, Hepatocellular Carcinoma, Lung Cancer,

Lymphoid Leukaemia (Particularly Acute T-Cell Leukaemia and Chronic Lymphocytic Leukaemia), Melanoma, Neuroblastoma, Osteosarcoma, Ovarian Cancer, Pancreatic Cancer, Prostate Cancer, Renal Cell Cancer and Retinoblastoma

[0932] In one embodiment of the invention, B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma is treated or prevented by administration of a compound that antagonizes (inhibits) the level(s) and/or function(s) of OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 which are elevated in the serum or tissue of subjects having B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer and retinoblastoma.

[0933] Compounds useful for this purpose include but are not limited to anti-OGTA002, anti-OGTA009, anti-OGTA016, anti-OGTA028, anti-OGTA037, anti-OGTA041, anti-OGTA053, anti-OGTA054, anti-OGTA066, anti-OGTA072, anti-OGTA074, anti-OGTA076, anti-OGTA085, anti-OGTA087, anti-OGTA088, anti-OGTA089, anti-OGTA091, anti-OGTA098, anti-OGTA101, anti-OGTA104, anti-OGTA106, anti-OGTA112, anti-OGTA113, anti-OGTA119, anti-OGTA124, anti-OGTA126, anti-OGTA156, anti-OGTA159, anti-OGTA168, anti-OGTA169, anti-OGTA174, anti-OGTA176, anti-OGTA177, anti-OGTA197, anti-OGTA202, anti-OGTA203, anti-OGTA206, anti-OGTA213, anti-OGTA214, anti-OGTA216, anti-OGTA222, anti-OGTA236, anti-OGTA237, anti-OGTA247, anti-OGTA248, anti-OGTA249, anti-OGTA257 or anti-OGTA271 antibodies (or other affinity reagents, and fragments and derivatives containing the binding region thereof), OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248,

OGTA249, OGTA257 or OGTA271 antisense or ribozyme nucleic acids, and nucleic acids encoding dysfunctional OGTAAs that are used to "knockout" endogenous OGTA function by homologous recombination (see, e.g., Capecchi, 1989, *Science* 244:1288-1292). Other compounds that inhibit OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 function can be identified by use of known in vitro assays, e.g., assays for the ability of a test compound to inhibit binding of an OGTA according to the invention to another protein or a binding partner, or to inhibit a known OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 function. Such inhibition may, for example be assayed in vitro or in cell culture, but genetic assays may also be employed. The Preferred Technologies described in Examples 1 and 2 can also be used to detect levels of an OGTA according to the invention before and after the administration of the compound. Preferably, suitable in vitro or in vivo assays are utilized to determine the effect of a specific compound and whether its administration is indicated for treatment of the affected tissue.

[0934] In a specific embodiment, a compound that inhibits OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 function is administered therapeutically or prophylactically to a subject in whom an increased serum or tissue level or functional activity of OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 (e.g., greater than the normal level or desired level) is detected as compared with serum or tissue of subjects free from B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung

cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer and retinoblastoma or a predetermined reference range.

[0935] Methods standard in the art can be employed to measure the increase in the level or function of an OGTA according to the invention, as outlined above.

[0936] In one embodiment OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 inhibitor compositions include small molecules, i.e. molecules of 1000 daltons or less. Such small molecules can be identified by the screening methods described herein.

Assays for Therapeutic or Prophylactic Compounds

[0937] The present invention also provides assays for use in drug discovery in order to identify or verify the efficacy of compounds for treatment or prevention of a relevant cancer. Test compounds can be assayed for their ability to restore levels of an OGTA according to the invention in a subject having a relevant cancer towards levels found in subjects free from B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer and retinoblastoma (as appropriate) or to produce similar changes in experimental animal models of said cancers.

[0938] Compounds able to restore OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 levels in a subject having B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma towards levels found in subjects free from B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer and retinoblastoma or to produce similar changes in experimental animal models of said cancer can be used as lead compounds for further drug discovery, or used therapeutically.

[0939] OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 expression can be assayed by the Preferred Technologies described in Examples 1 and 2, immunoassays, gel electrophoresis followed by visualization, detection of OGTA activity, or any other method taught herein or known to those skilled in the art. Such assays can be used to screen candidate drugs, in clinical monitoring or in drug development, where abundance of OGTA(s) can serve as a surrogate marker for clinical disease.

[0940] In various specific embodiments, in vitro assays can be carried out with cells representative of cell types involved in a subject's disorder, to determine if a compound has a desired effect upon such cell types.

[0941] Compounds for use in therapy can be tested in suitable animal model systems prior to testing in humans, including but not limited to rats, mice, chicken, cows, monkeys, rabbits, etc. For in vivo testing, prior to administration to humans, any animal model system known in the art may be used. Examples of animal models of B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer and retinoblastoma include, but are not limited to, xenografts of acute T-cell leukaemia cell lines such as HSB-2 in SCID mice, Morland et al, Cell Biophys. 1994; 24-25:315-29; xenografts of B-cell non-Hodgkin's lymphoma cell lines such as SU-DHL-4 and OCI-Ly8 in SCID mice, Schmidt-Wolf et al, J Exp Med. 1991 Jul. 1; 174(1):139-49; xenografts of breast cancer cell lines such as MCF-7 (Ozzello L, Sordat M., Eur J Cancer. 1980; 16:553-559) and MCF10AT (Miller et al., J Natl Cancer Inst. 1993; 85:1725-1732) in nude or SCID mice; xenografts of cervical cancer cell lines such as CaSki in nude mice; xenografts of chronic lymphocytic leukaemia cell lines such as WSU-CLL in SCID mice, Mohammad et al, Leukaemia. 1996 January; 10(1):130-7; xenografts of human colorectal cancer cell lines such as MDA-MB-345 in oestrogen-deprived SCID mice, Eccles et al. 1994 Cell Biophysics 24/25, 279; xenografts of gastric cell lines such as AZ-521 in nude mice; xenografts of glioblastoma cell lines such as U87MG in nude mice, Abernathey et al., Neurosurgery 1988 May; 22(5): 877-81; xenografts of hepatocellular carcinoma cell lines such as MHCC97 in nude mice, Tian et al., Br J Cancer 1999 November; 81(5):814-21; xenografts of non small cell lung cancer cell lines such as A549 and H460 and xenografts of small cell lung cancer cell lines such as NCI-H345; xenografts of melanoma cell lines such as MV3 in nude mice, van Muijen et al, Int J Cancer 1991 Apr. 22; 48(1):85-91; xenografts of neuroblastoma cell lines such as SK-N-SH in nude mice, Helson et al, Cancer Res. 1975 September; 35(9):2594-9; xenografts of human osteosarcoma cell lines such as HuO9 in nude mice, Kimura et al., Clin Exp Metastasis 2002; 19(6):477-85; xenografts of ovarian cancer cell

lines such as IGROV1 in nude mice, Benard et al, Cancer Res. 1985 October; 45(10):4970-9; xenografts of pancreatic cancer cell lines such as MIA PaCa-2 in nude mice, Marincola et al., J Surg Res 1989 December; 47(6):520-9; xenografts of prostate cancer cell lines such as CWR-22 in nude mice, Pretlow et al, J Natl Cancer Inst. 1993 Mar. 3; 85(5):394-8; xenografts of renal cell cancer cell lines such as LABA21 in immune compromised mice, Zisman et al, Cancer Research 63, 4952-4959, Aug. 15, 2003, or xenografts of retinoblastoma cell lines such as Y79. These can be utilized to test compounds that modulate levels of an OGTA according to the invention, since the pathology exhibited in these models is similar to that of B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer and retinoblastoma.

[0942] It is also apparent to the skilled artisan that based upon the present disclosure, transgenic animals can be produced with "knock-out" mutations of the gene or genes encoding OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271. A "knock-out" mutation of a gene is a mutation that causes the mutated gene to not be expressed, or expressed in an aberrant form or at a low level, such that the activity associated with the gene product is nearly or entirely absent. Preferably, the transgenic animal is a mammal; more preferably, the transgenic animal is a mouse.

[0943] In one embodiment, test compounds that modulate the expression of OGTA's according to the invention are identified in non-human animals (e.g., mice, rats, monkeys, rabbits, and guinea pigs), preferably non-human animal models for B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma, expressing OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271. In accordance with this embodiment, a test compound or a control compound is administered to the animals, and the effect of the test compound on expression of an OGTA according to the invention is determined. A test compound that alters the expression of an OGTA according to the invention can be identified by comparing the level of an OGTA

according to the invention (or mRNA(s) encoding the same) in an animal or group of animals treated with a test compound with the level of an OGTA according to the invention or mRNA(s) in an animal or group of animals treated with a control compound. Techniques known to those of skill in the art can be used to determine the mRNA and protein levels, for example, in situ hybridization. The animals may or may not be sacrificed to assay the effects of a test compound.

[0944] In another embodiment, test compounds that modulate the activity of an OGTA according to the invention or a biologically active portion thereof are identified in non-human animals (e.g., mice, rats, monkeys, rabbits, and guinea pigs), preferably non-human animal models for B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma, expressing an OGTA according to the invention. In accordance with this embodiment, a test compound or a control compound is administered to the animals, and the effect of a test compound on the activity of OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 is determined. A test compound that alters the activity of an OGTA according to the invention can be identified by assaying animals treated with a control compound and animals treated with the test compound. The activity of OGTA according to the invention can be assessed by detecting induction of a cellular second messenger of OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 (e.g., intracellular Ca^{2+} , diacylglycerol, IP3, etc.), detecting catalytic or enzymatic activity of an OGTA according to the invention or binding partner thereof, detecting the induction of a reporter gene (e.g., a regulatory element that is responsive to OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 operably linked to a nucleic acid encoding a detectable marker, such as luciferase or green fluorescent protein), or detecting a cellular response (e.g., cellular differ-

entiation or cell proliferation). Techniques known to those of skill in the art can be utilized to detect changes in the activity of an OGTA according to the invention (see, e.g., U.S. Pat. No. 5,401,639, which is incorporated herein by reference).

[0945] In yet another embodiment, test compounds that modulate the level or expression of an OGTA according to the invention are identified in human subjects having a relevant cancer, for example those having severe B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma.

[0946] In accordance with this embodiment, a test compound or a control compound is administered to the human subject, and the effect of a test compound on OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 expression is determined by analyzing the expression of an OGTA according to the invention or the mRNA encoding the same in a biological sample (e.g., serum, plasma, or urine). A test compound that alters the expression of an OGTA according to the invention can be identified by comparing the level of an OGTA according to the invention or mRNA encoding the same in a subject or group of subjects treated with a control compound to that in a subject or group of subjects treated with a test compound. Alternatively, alterations in the expression of an OGTA according to the invention can be identified by comparing the level of OGTA or mRNA encoding the same in a subject or group of subjects before and after the administration of a test compound.

[0947] Techniques known to those of skill in the art can be used to obtain the biological sample and analyze the mRNA or protein expression. For example, the Preferred Technologies described in Examples 1 and 2 described herein can be used to assess changes in the level of OGTA.

[0948] In another embodiment, test compounds that modulate the activity of OGTA are identified in human subjects having B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma, (preferably those with severe B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma). In this embodiment, a test compound or a control compound is administered to the human subject, and the effect of a test compound on the activity of the OGTA is

determined. A test compound that alters the activity of the relevant OGTA can be identified by comparing biological samples from subjects treated with a control compound to samples from subjects treated with the test compound. Alternatively, alterations in the activity of a relevant OGTA can be identified by comparing the activity of a relevant OGTA in a subject or group of subjects before and after the administration of a test compound. The activity of a relevant OGTA can be assessed by detecting in a biological sample (e.g., serum, plasma, or urine) induction of a cellular signal transduction pathway of an OGTA according to the invention (e.g., intracellular Ca^{2+} , diacylglycerol, IP3, etc.), catalytic or enzymatic activity of the OGTA or a binding partner thereof, or a cellular response, for example, cellular differentiation, or cell proliferation. Techniques known to those of skill in the art can be used to detect changes in the induction of a second messenger of OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 or changes in a cellular response. For example, RT-PCR can be used to detect changes in the induction of a cellular second messenger.

[0949] In one embodiment, a test compound that changes the level or expression of an OGTA according to the invention towards levels detected in control subjects (e.g., humans free from B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer and retinoblastoma) is selected for further testing or therapeutic use. In another preferred embodiment, a test compound that changes the activity of the relevant OGTA towards the activity found in control subjects (e.g., humans free from B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer and retinoblastoma) is selected for further testing or therapeutic use.

[0950] In another embodiment, test compounds that reduce the severity of one or more symptoms associated with a relevant cancer are identified in human subjects having a relevant cancer. In accordance with this embodiment, a test compound or a control compound is administered to the subjects, and the effect of a test compound on one or more symptoms of a relevant cancer is determined. A test compound that reduces one or more symptoms can be identified by comparing the subjects treated with a control compound to the subjects treated with the test compound. Techniques known to physicians familiar with a relevant cancer can be used to determine whether a test compound reduces one or more symptoms associated with a relevant cancer. For example, a test com-

pound that reduces tumour burden in a subject having a relevant cancer will be beneficial for subjects having B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma.

[0951] In a preferred embodiment, a test compound that reduces the severity of one or more symptoms associated with B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma in a human having B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma is selected for further testing or therapeutic use.

Therapeutic and Prophylactic Compositions and their Use

[0952] The invention provides methods of treatment (and prophylaxis) comprising administering to a subject an effective amount of a compound of the invention. In a preferred aspect, the compound is substantially purified (e.g., substantially free from substances that limit its effect or produce undesired side-effects). The subject is preferably an animal, including but not limited to animals such as cows, pigs, horses, chickens, cats, dogs, etc., and is preferably a mammal, and most preferably human. In a specific embodiment, a non-human mammal is the subject.

[0953] Formulations and methods of administration that can be employed when the compound comprises a nucleic acid are described above; additional appropriate formulations and routes of administration are described below.

[0954] Various delivery systems are known and can be used to administer a compound of the invention, e.g., encapsulation in liposomes, microparticles, microcapsules, recombinant cells capable of expressing the compound, receptor-mediated endocytosis (see, e.g., Wu and Wu, 1987, *J. Biol. Chem.* 262:4429-4432), construction of a nucleic acid as part of a retroviral or other vector, etc. Methods of introduction can be enteral or parenteral and include but are not limited to intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal, epidural, and oral routes. The compounds may be administered by any convenient route, for example by infusion or bolus injection, by absorption through epithelial or mucocutaneous linings (e.g., oral mucosa, rectal and intestinal mucosa, etc.) and may be administered together with other biologically active agents. Administration can be systemic or local. In addition, it may be desirable to introduce the pharmaceutical compositions of the invention into the central nervous system by any suitable route, including intraventricular and intrathecal injection; intraventricular injection may be facilitated by an intraventricular catheter, for example, attached to a reservoir, such as an Ommaya reservoir. Pulmonary administration can also be employed, e.g., by use of an inhaler or nebulizer, and formulation with an aerosolizing agent.

[0955] In a specific embodiment, it may be desirable to administer the pharmaceutical compositions of the invention locally to the area in need of treatment; this may be achieved, for example, and not by way of limitation, by local infusion during surgery, topical application, e.g., by injection, by means of a catheter, or by means of an implant, said implant being of a porous, non-porous, or gelatinous material, including membranes, such as sialastic membranes, or fibers. In one embodiment, administration can be by direct injection into lymphoid, breast, cervical, colorectal, gastric, brain, liver, lung, skin, neuronal, osteoblast, ovarian, pancreatic, prostate, kidney and eye tissue or at the site (or former site) of a malignant tumour or neoplastic or pre-neoplastic tissue.

[0956] In another embodiment, the compound can be delivered in a vesicle, in particular a liposome (see Langer, 1990, *Science* 249:1527-1533; Treat et al., in *Liposomes in the Therapy of Infectious Disease and Cancer*, Lopez-Berestein and Fidler (eds.), Liss, New York, pp. 353-365 (1989); Lopez-Berestein, *ibid.*, pp. 317-327; see generally *ibid.*).

[0957] In yet another embodiment, the compound can be delivered in a controlled release system. In one embodiment, a pump may be used (see Langer, *supra*; Sefton, 1987, *CRC Crit. Ref. Biomed. Eng.* 14:201; Buchwald et al., 1980, *Surgery* 88:507; Saudek et al., 1989, *N. Engl. J. Med.* 321:574). In another embodiment, polymeric materials can be used (see *Medical Applications of Controlled Release*, Langer and Wise (eds.), CRC Pres., Boca Raton, Fla. (1974); *Controlled Drug Bioavailability, Drug Product Design and Performance*, Smolen and Ball (eds.), Wiley, New York (1984); Ranger and Peppas, J., 1983, *Macromol. Sci. Rev. Macromol. Chem.* 23:61; see also Levy et al., 1985, *Science* 228:190; During et al., 1989, *Ann. Neurol.* 25:351; Howard et al., 1989, *J. Neurosurg.* 71:105). In yet another embodiment, a controlled release system can be placed in proximity of the therapeutic target, e.g. the breast, cervix, colon, stomach, brain, liver, lung, skin, bone, ovary, pancreas, prostate, kidney or eye, thus requiring only a fraction of the systemic dose (see, e.g., Goodson, in *Medical Applications of Controlled Release*, *supra*, vol. 2, pp. 115-138 (1984)).

[0958] Other controlled release systems are discussed in the review by Langer (1990, *Science* 249:1527-1533).

[0959] In a specific embodiment where the compound of the invention is a nucleic acid encoding a protein, the nucleic acid can be administered *in vivo* to promote expression of its encoded protein, by constructing it as part of an appropriate nucleic acid expression vector and administering it so that it becomes intracellular, e.g., by use of a retroviral vector (see U.S. Pat. No. 4,980,286), or by direct injection, or by use of microparticle bombardment (e.g., a gene gun; Biolistic, Dupont), or coating with lipids or cell-surface receptors or transfecting agents, or by administering it in linkage to a homeobox-like peptide which is known to enter the nucleus (see e.g., Joliet et al., 1991, *Proc. Natl. Acad. Sci. USA* 88:1864-1868), etc. Alternatively, a nucleic acid can be introduced intracellularly and incorporated within host cell DNA for expression, by homologous recombination.

[0960] The present invention also provides pharmaceutical compositions. Such compositions comprise a therapeutically effective amount of a compound, and a pharmaceutically acceptable carrier. In a specific embodiment, the term "pharmaceutically acceptable" means approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopeia or other generally recognized pharmacopeia for use in animals, and more particularly in humans.

The term "carrier" refers to a diluent, adjuvant, excipient, or vehicle with which the therapeutic is administered. Such pharmaceutical carriers can be sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. Water may be a suitable carrier when the pharmaceutical composition is administered intravenously. Saline solutions and aqueous dextrose and glycerol solutions can also be employed as liquid carriers, particularly for injectable solutions. Suitable pharmaceutical excipients include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium stearate, glycerol monostearate, talc, sodium chloride, dried skim milk, glycerol, propylene, glycol, water, ethanol and the like. The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. These compositions can take the form of solutions, suspensions, emulsion, tablets, pills, capsules, powders, sustained-release formulations and the like. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, etc. Examples of suitable pharmaceutical carriers are described in "Remington's Pharmaceutical Sciences" by E. W. Martin. Such compositions will contain a therapeutically effective amount of the compound, preferably in purified form, together with a suitable amount of carrier so as to provide the form for proper administration to the subject. The formulation should suit the mode of administration.

[0961] In one embodiment, the composition is formulated in accordance with routine procedures as a pharmaceutical composition adapted for intravenous administration to human beings. Typically, compositions for intravenous administration are solutions in sterile isotonic aqueous buffer. Where necessary, the composition may also include a solubilizing agent and a local anesthetic such as lidocaine to ease pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water free concentrate in a hermetically sealed container such as an ampoule or sachette indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water or saline. Where the composition is administered by injection, an ampoule of sterile water for injection or saline can be provided so that the ingredients may be mixed prior to administration.

[0962] The compounds of the invention can be formulated as neutral or salt forms. Pharmaceutically acceptable salts include those formed with free amino groups such as those derived from hydrochloric, phosphoric, acetic, oxalic, tartaric acids, etc., and those formed with free carboxyl groups such as those derived from sodium, potassium, ammonium, calcium, ferric hydroxides, isopropylamine, triethylamine, 2-ethylamino ethanol, histidine, procaine, etc.

[0963] The amount of the compound of the invention which will be effective in the treatment of B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma

can be determined by standard clinical techniques. In addition, in vitro assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of the practitioner and each subject's circumstances. However, suitable dosage ranges for intravenous administration are generally about 20-500 micrograms of active compound per kilogram body weight. Suitable dosage ranges for intranasal administration are generally about 0.01 pg/kg body weight to 1 mg/kg body weight or more such as 10 or 100 mg/kg. Effective doses may be extrapolated from dose-response curves derived from in vitro or animal model test systems.

[0964] Suppositories generally contain active ingredient in the range of 0.5% to 10% by weight; oral formulations preferably contain 10% to 95% active ingredient.

[0965] The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects (a) approval by the agency of manufacture, use or sale for human administration, (b) directions for use, or both.

Determining Abundance of the Proteins of the Invention by Imaging Technology

[0966] An advantage of determining abundance of OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 by imaging technology may be that such a method is non-invasive (save that reagents may need to be administered) and there is no need to extract a sample from the subject.

[0967] Suitable imaging technologies include positron emission tomography (PET) and single photon emission computed tomography (SPECT). Visualisation of an OGTA using such techniques requires incorporation or binding of a suitable label e.g. a radiotracer such as ^{18}F , ^{11}C or ^{123}I (see e.g. NeuroRx—The Journal of the American Society for Experimental NeuroTherapeutics (2005) 2(2), 348-360 and idem pages 361-371 for further details of the techniques). Radiotracers or other labels may be incorporated into OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 by administration to the subject (e.g. by injection) of a suitably labelled specific ligand. Alternatively they may be incorporated into a binding

affinity reagent (antibody, Affibody etc.) specific for an OGTA which may be administered to the subject (e.g. by injection). For discussion of use of Affibodies for imaging see e.g. Orlova A, Magnusson M, Eriksson TL, Nilsson M, Larsson B, Hoiden-Guthenberg I, Widstrom C, Carlsson J, Tolmachev V, Stahl S, Nilsson FY, Tumour imaging using a picomolar affinity HER2 binding affibody molecule, *Cancer Res.* 2006 Apr. 15; 66(8):4339-48).

Diagnosis and Treatment of B-Cell Non-Hodgkin's Lymphoma, Breast Cancer, Cervical Cancer, Colorectal Cancer, Gastric Cancer, Glioblastoma, Hepatocellular Carcinoma, Lung Cancer, Lymphoid Leukaemia (Particularly Acute T-Cell Leukaemia and Chronic Lymphocytic Leukaemia), Melanoma, Neuroblastoma, Osteosarcoma, Ovarian Cancer, Pancreatic Cancer, Prostate Cancer, Renal Cell Cancer and Retinoblastoma Using Immunohistochemistry

[0968] Immunohistochemistry is an excellent detection technique and may therefore be very useful in the diagnosis and treatment of a relevant cancer. Immunohistochemistry may be used to detect, diagnose, or monitor a relevant cancer through the localization of OGTA antigens in tissue sections by the use of labeled antibodies (or other affinity reagents), derivatives and analogs thereof, which specifically bind to the proteins of the invention, as specific reagents through antigen-antibody interactions that are visualized by a marker such as fluorescent dye, enzyme, radioactive element or colloidal gold.

[0969] The advancement of monoclonal antibody technology has been of great significance in assuring the place of immunohistochemistry in the modern accurate microscopic diagnosis of human neoplasms. The identification of disseminated neoplastically transformed cells by immunohistochemistry allows for a clearer picture of cancer invasion and metastasis, as well as the evolution of the tumour cell associated immunophenotype towards increased malignancy. Future antineoplastic therapeutical approaches may include a variety of individualized immunotherapies, specific for the particular immunophenotypical pattern associated with each individual patient's neoplastic disease. For further discussion see e.g. Bodey B, The significance of immunohistochemistry in the diagnosis and therapy of neoplasms, *Expert Opin Biol Ther.* 2002 April; 2(4):371-93.

[0970] Preferred features of each aspect of the invention are as for each of the other aspects *mutatis mutandis*. The prior art documents mentioned herein are incorporated to the fullest extent permitted by law.

Example 1

Identification of Membrane Proteins Expressed in B-Cell Non-Hodgkin's Lymphoma, Breast Cancer, Cervical Cancer, Colorectal Cancer, Gastric Cancer, Glioblastoma, Hepatocellular Carcinoma, Lung Cancer, Lymphoid Leukaemia (Particularly Acute T-Cell Leukaemia and Chronic Lymphocytic Leukaemia), Melanoma, Neuroblastoma, Osteosarcoma, Ovarian Cancer, Pancreatic Cancer, Prostate Cancer, Renal Cell Cancer and Retinoblastoma Blood and Tissue Samples

[0971] Using the following Reference Protocol, membrane proteins extracted from B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and

chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer and retinoblastoma tissue samples were separated by 1D gel and analysed.

1.1 Materials and Methods

1.1.1—Plasma Membrane Fractionation

[0972] The cells recovered from a B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer and retinoblastoma were lysed and submitted to centrifugation at 1000 G. The supernatant was taken, and it was subsequently centrifuged at 3000 G. Once again, the supernatant was taken, and it was then centrifuged at 100 000 G.

[0973] The resulting pellet was recovered and put on 15-60% sucrose gradient.

[0974] A Western blot was used to identify sub cellular markers, and the Plasma Membrane fractions were pooled.

[0975] The pooled solution was either run directly on 1D gels (see section 1.1.4 below), or further fractionated into heparin binding and nucleotide binding fractions as described below.

1.1.2—Plasma Membrane Heparin-Binding Fraction

[0976] The pooled solution from 1.1.1 above was applied to a Heparin column, eluted from column and run on 1D gels (see section 1.1.4 below).

1.1.3—Plasma Nucleotide-Binding Fraction

[0977] The pooled solution from 1.1.1 above was applied to a Cibacrom Blue 3GA column, eluted from column and run on 1D gels (see section 1.1.4 below).

1.1.4—1D Gel Technology

[0978] Protein or membrane pellets were solubilised in 1D sample buffer (1-2 µg/µl). The sample buffer and protein mixture was then heated to 95° C. for 3 min.

[0979] A 9-16% acrylamide gradient gel was cast with a stacking gel and a stacking comb according to the procedure described in Ausubel F. M. et al., eds., 1989, *Current Protocols in Molecular Biology*, Vol. II, Green Publishing Associates, Inc., and John Wiley & Sons, Inc., New York, section 10.2, incorporated herein by reference in its entirety.

[0980] 30-50 micrograms of the protein mixtures obtained from detergent and the molecular weight standards (66, 45, 31, 21, 14 kDa) were added to the stacking gel wells using a 10 microlitre pipette tip and the samples run at 40 mA for 5 hours.

[0981] The plates were then prised open, the gel placed in a tray of fixer (10% acetic acid, 40% ethanol, 50% water) and shaken overnight. Following this, the gel was primed by 30 minutes shaking in a primer solution (7.5% acetic acid (75 ml), 0.05% SDS (5 ml of 10%)). The gel was then incubated with a fluorescent dye (7.5% acetic acid, 0.06% OGS in-house dye (600 µl)) with shaking for 3 hrs. Sypro Red (Molecular Probes, Inc., Eugene, Oreg.) is a suitable dye for this purpose. A preferred fluorescent dye is disclosed in U.S.

application Ser. No. 09/412,168, filed on Oct. 5, 1999, which is incorporated herein by reference in its entirety.

[0982] A computer-readable output was produced by imaging the fluorescently stained gels with an Apollo 3 scanner (Oxford Glycosciences, Oxford, UK). This scanner is developed from the scanner described in WO 96/36882 and in the Ph.D. thesis of David A. Basiji, entitled "Development of a High-throughput Fluorescence Scanner Employing Internal Reflection Optics and Phase-sensitive Detection (Total Internal Reflection, Electrophoresis)", University of Washington (1997), Volume 58/12-B of Dissertation Abstracts International, page 6686, the contents of each of which are incorporated herein by reference. The latest embodiment of this instrument includes the following improvements: The gel is transported through the scanner on a precision lead-screw drive system. This is preferable to laying the glass plate on the belt-driven system that is defined in the Basiji thesis as it provides a reproducible means of accurately transporting the gel past the imaging optics.

[0983] The gel is secured into the scanner against three alignment stops that rigidly hold the glass plate in a known position. By doing this in conjunction with the above precision transport system and the fact that the gel is bound to the glass plate, the absolute position of the gel can be predicted and recorded. This ensures that accurate co-ordinates of each feature on the gel can be communicated to the cutting robot for excision. This cutting robot has an identical mounting arrangement for the glass plate to preserve the positional accuracy.

[0984] The carrier that holds the gel in place has integral fluorescent markers (Designated M1, M2, M3) that are used to correct the image geometry and are a quality control feature to confirm that the scanning has been performed correctly.

[0985] The optical components of the system have been inverted. The laser, mirror, waveguide and other optical components are now above the glass plate being scanned. The embodiment of the Basiji thesis has these underneath. The glass plate is therefore mounted onto the scanner gel side down, so that the optical path remains through the glass plate. By doing this, any particles of gel that may break away from the glass plate will fall onto the base of the instrument rather than into the optics.

[0986] In scanning the gels, they were removed from the stain, rinsed with water and allowed to air dry briefly and imaged on the Apollo 3. After imaging, the gels were sealed in polyethylene bags containing a small volume of staining solution, and then stored at 4° C.

[0987] Apparent molecular weights were calculated by interpolation from a set of known molecular weight markers run alongside the samples.

1.1.5—Recovery and Analysis of Selected Proteins

[0988] Proteins were robotically excised from the gels by the process described in U.S. Pat. No. 6,064,754, Sections 5.4 and 5.6, 5.7, 5.8 (incorporated herein by reference), as is applicable to 1D-electrophoresis, with modification to the robotic cutter as follows: the cutter begins at the top of the lane, and cuts a gel disc 1.7 mm in diameter from the left edge of the lane. The cutter then moves 2 mm to the right, and 0.7 mm down and cuts a further disc. This is then repeated. The cutter then moves back to a position directly underneath the first gel cut, but offset by 2.2 mm downwards, and the pattern of three diagonal cuts are repeated. This is continued for the whole length of the gel.

[0989] NOTE: If the lane is observed to broaden significantly then a correction can be made also sideways i.e. instead of returning to a position directly underneath a previous gel cut, the cut can be offset slightly to the left (on the left of the lane) and/or the right (on the right of the lane). The proteins contained within the gel fragments were processed to generate tryptic peptides; partial amino acid sequences of these peptides were determined by mass spectroscopy as described in WO98/53323 and application Ser. No. 09/094,996, filed Jun. 15, 1998.

[0990] Proteins were processed to generate tryptic digest peptides. Tryptic peptides were analyzed by mass spectrometry using a PerSeptive Biosystems Voyager-DETM STR Matrix-Assisted Laser Desorption Ionization Time-of-Flight (MALDI-TOF) mass spectrometer, and selected tryptic peptides were analyzed by tandem mass spectrometry (MS/MS) using a Micromass Quadrupole Time-of-Flight (Q-TOF) mass spectrometer (Micromass, Altrincham, U.K.) equipped with a Nanoflow™ electrospray Z-spray source. For partial amino acid sequencing and identification of OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 and OGTA271, uninterpreted tandem mass spectra of tryptic peptides were searched using the SEQUEST search program (Eng et al., 1994, J. Am. Soc. Mass Spectrom. 5:976-989), version v.C.1. Criteria for database identification included: the cleavage specificity of trypsin; the detection of a suite of a, b and y ions in peptides returned from the database, and a mass increment for all Cys residues to account for carbamidomethylation. The database searched was a database constructed of protein entries in the non-redundant database held by the National Centre for Biotechnology Information (NCBI) which is accessible at <http://www.ncbi.nlm.nih.gov/>. Following identification of proteins through spectral-spectral correlation using the SEQUEST program, masses detected in MALDI-TOF mass spectra were assigned to tryptic digest peptides within the proteins identified. In cases where no amino acid sequences could be identified through searching with uninterpreted MS/MS spectra of tryptic digest peptides using the SEQUEST program, tandem mass spectra of the peptides were interpreted manually, using methods known in the art. (In the case of interpretation of low-energy fragmentation mass spectra of peptide ions see Gaskell et al., 1992, Rapid Commun. Mass Spectrom. 6:658-662).

1.1.6—Discrimination of B-Cell Non-Hodgkin's Lymphoma, Breast Cancer, Cervical Cancer, Colorectal Cancer, Gastric Cancer, Glioblastoma, Hepatocellular Carcinoma, Lung Cancer, Lymphoid Leukaemia (Particularly Acute T-Cell Leukaemia and Chronic Lymphocytic Leukaemia), Melanoma, Neuroblastoma, Osteosarcoma, Ovarian Cancer, Pancreatic Cancer, Prostate Cancer, Renal Cell Cancer and Retinoblastoma Associated Proteins

[0991] The process to identify OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112,

OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 and OGTA271 uses the peptide sequences obtained experimentally by mass spectrometry described above of naturally occurring human proteins to identify and organise coding exons in the published human genome sequence.

[0992] Recent dramatic advances in defining the chemical sequence of the human genome have led to the near completion of this immense task (Venter, J. C. et al. (2001). The sequence of the human genome. *Science* 16: 1304-51; International Human Genome Sequencing Consortium. (2001). Initial sequencing and analysis of the human genome *Nature* 409: 860-921). There is little doubt that this sequence information will have a substantial impact on our understanding of many biological processes, including molecular evolution, comparative genomics, pathogenic mechanisms and molecular medicine. For the full medical value inherent in the sequence of the human genome to be realised, the genome needs to be 'organised' and annotated. By this, is meant at least the following three things: (i) The assembly of the sequences of the individual portions of the genome into a coherent, continuous sequence for each chromosome. (ii) The unambiguous identification of those regions of each chromosome that contain genes. (iii) Determination of the fine structure of the genes and the properties of its mRNA and protein products. While the definition of a 'gene' is an increasingly complex issue (H Pearson: What is a gene? *Nature* (2006) 24: 399-401), what is of immediate interest for drug discovery and development is a catalogue of those genes that encode functional, expressed proteins. A subset of these genes will be involved in the molecular basis of most if not all pathologies. Therefore an important and immediate goal for the pharmaceutical industry is to identify all such genes in the human genome and describe their fine structure.

Processing and Integration of Peptide Masses, Peptide Signatures, ESTs and Public Domain Genomic Sequence Data to Form OGAP® Database

[0993] Discrete genetic units (exons, transcripts and genes) were identified using the following sequential steps:

1. A 'virtual transcriptome' is generated, containing the tryptic peptides which map to the human genome by combining the gene identifications available from Ensembl and various gene prediction programs. This also incorporates SNP data (from dbSNP) and all alternate splicing of gene identifications. Known contaminants were also added to the virtual transcriptome.
2. All tandem spectra in the OGeS Mass Spectrometry Database are interpreted in order to produce a peptide that can be mapped to one in the virtual transcriptome. A set of automated spectral interpretation algorithms were used to produce the peptide identifications.
3. The set of all mass-matched peptides in the OGeS Mass Spectrometry Database is generated by searching all peptides from transcripts hit by the tandem peptides using a tolerance based on the mass accuracy of the mass spectrometer, typically 20 ppm.
4. All tandem and mass-matched peptides are combined in the form of "protein clusters". This is done using a recursive process which groups sequences into clusters based on com-

mon peptide hits. Biological sequences are considered to belong to the same cluster if they share one or more tandem or mass-matched peptide.

5. After initial filtering to screen out incorrectly identified peptides, the resulting clusters are then mapped on the human genome.

6. The protein clusters are then aggregated into regions that define preliminary gene boundaries using their proximity and the co-observation of peptides within protein clusters. Proximity is defined as the peptide being within 80,000 nucleotides on the same strand of the same chromosome. Various elimination rules, based on cluster observation scoring and multiple mapping to the genome are used to refine the output. The resulting 'confirmed genes' are those which best account for the peptides and masses observed by mass spectrometry in each cluster. Nominal co-ordinates for the gene are also an output of this stage.

7. The best set of transcripts for each confirmed gene are created from the protein clusters, peptides, ESTs, candidate exons and molecular weight of the original protein spot.

8. Each identified transcript was linked to the sample providing the observed peptides.

9. Use of an application for viewing and mining the data. The result of steps 1-8 was a database containing genes, each of which consisted of a number of exons and one or more transcripts. An application was written to display and search this integrated genome/proteome data. Any features (OMIM disease locus, InterPro etc.) that had been mapped to the same Golden Path co-ordinate system by Ensembl could be cross-referenced to these genes by coincidence of location and fine structure.

[0994] The process was used to generate approximately 1 million peptide sequences to identify protein-coding genes and their exons resulted in the identification of protein sequences for 18083 genes across 67 different tissues and 57 diseases including 2,025 genes in acute T-cell leukaemia, 501 genes in B-cell non-Hodgkin's lymphoma, 4,713 genes in breast cancer, 1,371 genes in cervical cancer, 2,424 genes in chronic lymphocytic leukaemia, 949 genes in colorectal cancer, 524 genes in gastric cancer, 1,544 genes in glioblastoma, 1,782 genes in hepatocellular carcinoma, 978 genes in lung cancer, 373 genes in lymphoid leukaemia (unspecified), 1,764 genes in melanoma, 1,391 genes in neuroblastoma, 1,324 genes in osteosarcoma, 1,033 genes in ovarian cancer, 2,961 genes in pancreatic cancer, 3,307 genes in prostate cancer, 1005 genes in renal cell cancer and 1,783 genes in retinoblastoma, illustrated here by OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 and OGTA271 isolated and identified from B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer and retinoblastoma samples. Following comparison of the experi-

mentally determined sequences with sequences in the OGAP® database, OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 and OGTA271 showed a high degree of specificity to B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer and retinoblastoma indicative of the prognostic and diagnostic nature.

1.2 Results

[0995] These experiments identified OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 and OGTA271, as further described herein.

[0996] The full-length OGTA002 was detected in the plasma membrane of breast cancer, colorectal cancer, hepatocellular carcinoma, melanoma, ovarian cancer and pancreatic cancer samples. The full-length OGTA009 was detected in the plasma membrane of breast cancer, colorectal cancer, pancreatic cancer, prostate cancer and renal cell cancer samples. The full-length OGTA016 was detected in the plasma membrane of colorectal cancer samples. The full-length OGTA028 was detected in the plasma membrane of ovarian cancer samples. The full-length OGTA037 was detected in the plasma membrane of gastric cancer samples. The full-length OGTA041 was detected in the plasma membrane of hepatocellular carcinoma, lung cancer and pancreatic cancer samples. The full-length OGTA053 was detected in the plasma membrane of pancreatic cancer samples. The full-length OGTA054 was detected in the plasma membrane of pancreatic cancer samples. The full-length OGTA066 was detected in the plasma membrane of colorectal cancer and pancreatic cancer samples. The full-length OGTA072 was detected in the plasma membrane of colorectal cancer samples. The full-length OGTA074 was detected in the plasma membrane of colorectal cancer samples. The full-length OGTA076 was detected in the plasma membrane of chronic lymphocytic leukaemia, colorectal cancer and pancreatic cancer samples. The full-length OGTA085 was detected in the plasma membrane of lung cancer, melanoma and retinoblastoma samples. The full-length OGTA087 was detected in the plasma membrane of B-cell non-Hodgkin's lymphoma, breast cancer, colorectal cancer, gastric cancer, lung cancer, lymphoid leukaemia and ovarian cancer samples. The full-length OGTA088 was detected in the plasma membrane of breast cancer, gastric cancer, glioblas-

toma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia, pancreatic cancer, renal cell cancer and retinoblastoma samples. The full-length OGTA089 was detected in the plasma membrane of breast cancer, lung cancer and ovarian cancer samples. The full-length OGTA091 was detected in the plasma membrane of breast cancer, cervical cancer, chronic lymphocytic leukaemia, gastric cancer, hepatocellular carcinoma, lung cancer, melanoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer and renal cell cancer samples. The full-length OGTA098 was detected in the plasma membrane of breast cancer, cervical cancer, hepatocellular carcinoma, lung cancer, osteosarcoma, pancreatic cancer, prostate cancer and renal cell cancer samples. The full-length OGTA101 was detected in the plasma membrane of breast cancer, cervical cancer, colorectal cancer, hepatocellular carcinoma, lung cancer, osteosarcoma and pancreatic cancer samples. The full-length OGTA104 was detected in the plasma membrane of breast cancer, hepatocellular carcinoma, ovarian cancer and pancreatic cancer samples. The full-length OGTA106 was detected in the plasma membrane of cervical cancer, melanoma and pancreatic cancer samples. The full-length OGTA112 was detected in the plasma membrane of breast cancer, cervical cancer, chronic lymphocytic leukaemia, hepatocellular carcinoma, pancreatic cancer and renal cell cancer samples. The full-length OGTA113 was detected in the plasma membrane of pancreatic cancer samples. The full-length OGTA119 was detected in the plasma membrane of B-cell non-Hodgkin's lymphoma, breast cancer, colorectal cancer, gastric cancer, hepatocellular carcinoma, lung cancer, lymphoid leukaemia, neuroblastoma, osteosarcoma, pancreatic cancer, prostate cancer and renal cell cancer samples. The full-length OGTA124 was detected in the plasma membrane of hepatocellular carcinoma, lung cancer, ovarian cancer, pancreatic cancer and renal cell cancer samples. The full-length OGTA126 was detected in the plasma membrane of breast cancer, colorectal cancer, hepatocellular carcinoma, melanoma, pancreatic cancer, prostate cancer and renal cell cancer samples. The full-length OGTA156 was detected in the plasma membrane of acute T-cell leukaemia, B-cell non-Hodgkin's lymphoma, chronic lymphocytic leukaemia and hepatocellular carcinoma samples. The full-length OGTA159 was detected in the plasma membrane of breast cancer, chronic lymphocytic leukaemia, colorectal cancer, hepatocellular carcinoma, melanoma and pancreatic cancer samples. The full-length OGTA168 was detected in the plasma membrane of glioblastoma and melanoma samples. The full-length OGTA169 was detected in the plasma membrane of breast cancer and chronic lymphocytic leukaemia samples. The full-length OGTA174 was detected in the plasma membrane of acute T-cell leukaemia and chronic lymphocytic leukaemia samples. The full-length OGTA176 was detected in the plasma membrane of B-cell non-Hodgkin's lymphoma and chronic lymphocytic leukaemia samples. The full-length OGTA177 was detected in the plasma membrane of chronic lymphocytic leukaemia samples. The full-length OGTA197 was detected in the plasma membrane of colorectal cancer, hepatocellular carcinoma, lung cancer, melanoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer and renal cell cancer samples. The full-length OGTA202 was detected in the plasma membrane of colorectal cancer samples. The full-length OGTA203 was detected in the plasma membrane of ovarian cancer and renal cell cancer samples. The full-length OGTA206 was detected in the

plasma membrane of breast cancer, pancreatic cancer and prostate cancer samples. The full-length OGTA213 was detected in the plasma membrane of lung cancer samples. The full-length OGTA214 was detected in the plasma membrane of ovarian cancer samples. The full-length OGTA216 was detected in the plasma membrane of breast cancer, colorectal cancer and pancreatic cancer samples. The full-length OGTA222 was detected in the plasma membrane of B-cell non-Hodgkin's lymphoma and colorectal cancer samples. The full-length OGTA236 was detected in the plasma membrane of pancreatic cancer samples. The full-length OGTA237 was detected in the plasma membrane of B-cell non-Hodgkin's lymphoma, lymphoid leukaemia and prostate cancer samples. The full-length OGTA247 was detected in the plasma membrane of hepatocellular carcinoma and melanoma samples. The full-length OGTA248 was detected in the plasma membrane of renal cell cancer samples. The full-length OGTA249 was detected in the plasma membrane of ovarian cancer samples. The full-length OGTA257 was detected in the plasma membrane of pancreatic cancer samples. The full-length OGTA271 was detected in the plasma membrane of breast cancer, cervical cancer, colorectal cancer, hepatocellular carcinoma, lung cancer, osteosarcoma, pancreatic cancer and renal cell cancer samples.

Example 2

Identification of Membrane Proteins Expressed in Colorectal Cancer, Kidney Cancer, Liver Cancer, Lung Cancer or Ovarian Cancer Blood and Tissue Samples Using Isotope Tagging for Absolute and Relative Quantitation (iTRAQ)

[0997] Using the following Reference Protocol, membrane proteins extracted from colorectal cancer, kidney cancer, liver cancer, lung cancer and ovarian cancer tissue and normal adjacent colorectal and lung tissue samples were digested, labelled with Isotope Tagging for Absolute & Relative Quantitation reagents (iTRAQ; Applied Biosystems, Foster City, Calif., USA) and resulting peptides sequenced by tandem mass spectrometry.

2.1 Materials and Methods

2.1.1—Plasma Membrane Fractionation

[0998] The cells recovered from a colorectal cancer, kidney cancer, liver cancer, lung cancer or ovarian cancer or normal adjacent colorectal, kidney, liver, lung or ovarian tissue were lysed and submitted to centrifugation at 1000 G. The supernatant was taken, and it was subsequently centrifuged at 3000 G. Once again, the supernatant was taken, and it was then centrifuged at 100 000 G.

[0999] The resulting pellet was recovered and put on 15-60% sucrose gradient.

[1000] A Western blot was used to identify sub cellular markers, and the Plasma Membrane fractions were pooled.

[1001] The pooled solution was then analysed directly by iTRAQ (see section 2.1.2 below).

2.1.2—iTRAQ Methodology

[1002] Membrane protein pellets from colorectal cancer, kidney cancer, liver cancer, lung cancer or ovarian cancer and normal adjacent colorectal, kidney, liver, lung or ovarian tissue were solubilised in sample buffer (2-4 µg/µl in 0.5% SDS) by the addition of buffer and then heating to 95° C. for 3 min.

[1003] To a volume of each protein solution equating to 50 µg, 150 µl of 0.5M triethylammonium bicarbonate (TEAB) solution was added. To each sample, 3 µl of 50 mM tris-(2-carboxyethyl)phosphine was added and the mixture was incubated at 60° C. for 1 hour. 1 µl of cysteine blocking reagent, 200 mM methyl methanethiosulphonate (MMTS) in isopropanol, was then added. After incubation at room temperature for 10 minutes, 15 µl of 1 µg/µl trypsin was added to each sample followed by incubation at 37° C. overnight.

[1004] The digested samples were dried under a vacuum and re-constituted with 30 µl of 0.5M TEAB solution. 70 µl ethanol was added to each of the four iTRAQ reagents (114/115/116/117) and one reagent added to each of the four samples analysed (two colorectal cancer, kidney cancer, liver cancer, lung cancer or ovarian cancer samples and two corresponding normal adjacent tissue samples) and left at room temperature for 1 hour. The specific reagent added to each sample was recorded. The four labeled samples were combined & vortexed.

[1005] The combined sample was reduced to dryness under a vacuum and de-salted by loading onto a C18 spin column, washing with aqueous solvent and then eluting with 70% acetonitrile. The sample fraction was again reduced to dryness and then re-dissolved in 40 µl of solvent A (97.9 water, 2% acetonitrile, 0.1% formic acid) prior to ion exchange fractionation.

2.1.3—Fractionation and Analysis of Labeled Peptides

[1006] The sample was fractionated by strong cation exchange chromatography using an Agilent 1200 chromatograph (Agilent, Santa Clara, Calif., USA). Samples were eluted off an Agilent Zorbax Bio-SCXII column (3.5 µm; 50×0.8 mm) using a 200 min gradient of 0-100 mM sodium acetate over 20 minutes and then to 1M over 10 minutes. 1 minute fractions were collected over the 30 minute run.

[1007] Each fraction was analysed by liquid chromatography/mass spectrometry using an Agilent 1200 chromatograph fitted with a Zorbax 300SB-C18 (150 mm×75 µm) and an Agilent 6510 quadrupole—time-of-flight instrument (Agilent, Santa Clara, Calif., USA). Peptides were eluted with a 300n1/min gradient increasing from 15% to 45% acetonitrile in 60 minutes. Data was acquired in auto MS/MS mode such that up to 3 precursor ions above the intensity threshold were selected and product ion spectra accumulated to facilitate the sequencing of the labeled peptides. Raw was processed to create peak lists using Spectrum Mill software (Agilent, Santa Clara, Calif., USA).

2.1.4—Amino Acid Sequence Analysis of Labeled Peptides

[1008] For partial amino acid sequencing and identification of OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA074, OGTA076, OGTA085, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 and OGTA271, uninterpreted tandem mass spectra of tryptic peptides were searched using the SEQUEST search program (Eng et al., 1994, J. Am. Soc. Mass Spectrom. 5:976-989). Criteria for database identification included: the cleavage

specificity of trypsin; the detection of a suite of a, b and y ions in peptides returned from the database, and a mass increment for all cysteine residues to account for modification with methyl methanethiosulphonate and the addition of iTRAQ labels to free amines (N-terminus & lysine). The data was searched through IPI Human v3.23 (www.ebi.ac.uk/IPI/IPI-human.html).

2.1.5—Discrimination of Colorectal Cancer, Kidney Cancer, Liver Cancer, Lung Cancer and Ovarian Cancer Associated Proteins

[1009] The process described in Example 1 section 1.1.6 was employed to discriminate the colorectal cancer, kidney cancer, liver cancer, lung cancer and ovarian cancer associated proteins in the experimental samples.

2.2 Results

[1010] These experiments identified OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA066, OGTA074, OGTA076, OGTA085, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA216, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 and OGTA271, as further described herein.

[1011] The full-length OGTA002 was detected in the plasma membrane of colorectal cancer, hepatocellular carcinoma, lung cancer and renal cell cancer samples. The full-length OGTA009 was detected in the plasma membrane of colorectal cancer, lung cancer and ovarian cancer samples. The full-length OGTA016 was detected in the plasma membrane of colorectal cancer and lung cancer samples. The full-length OGTA028 was detected in the plasma membrane of colorectal cancer, hepatocellular carcinoma, lung cancer, ovarian cancer and renal cell cancer samples. The full-length OGTA037 was detected in the plasma membrane of colorectal cancer, lung cancer and ovarian cancer samples. The full-length OGTA041 was detected in the plasma membrane of lung cancer samples. The full-length OGTA053 was detected in the plasma membrane of colorectal cancer, hepatocellular carcinoma, lung cancer and renal cell cancer samples. The full-length OGTA054 was detected in the plasma membrane of colorectal cancer and lung cancer samples. The full-length OGTA066 was detected in the plasma membrane of colorectal cancer, lung cancer and renal cell cancer samples. The full-length OGTA074 was detected in the plasma membrane of lung cancer samples. The full-length OGTA076 was detected in the plasma membrane of colorectal cancer, hepatocellular carcinoma, lung cancer, ovarian cancer and renal cell cancer samples. The full-length OGTA085 was detected in the plasma membrane of colorectal cancer and lung cancer samples. The full-length OGTA088 was detected in the plasma membrane of colorectal cancer and lung cancer samples. The full-length OGTA089 was detected in the plasma membrane of lung cancer, ovarian cancer and renal cell cancer samples. The full-length OGTA091 was detected in the plasma membrane of breast colorectal cancer, hepatocellular carcinoma, lung cancer, ovarian cancer and renal cell cancer samples. The full-length OGTA098 was detected in the plasma membrane of colorectal cancer, lung cancer, ova-

rian cancer and renal cell cancer samples. The full-length OGTA101 was detected in the plasma membrane of colorectal cancer, hepatocellular carcinoma, lung cancer, ovarian cancer and renal cell cancer samples. The full-length OGTA104 was detected in the plasma membrane of colorectal cancer, hepatocellular carcinoma, lung cancer, ovarian cancer and renal cell cancer samples. The full-length OGTA106 was detected in the plasma membrane of hepatocellular carcinoma samples. The full-length OGTA112 was detected in the plasma membrane of renal cell cancer samples. The full-length OGTA113 was detected in the plasma membrane of colorectal cancer, lung cancer, ovarian cancer and renal cell cancer samples. The full-length OGTA119 was detected in the plasma membrane of colorectal cancer, lung cancer, and ovarian cancer samples. The full-length OGTA124 was detected in the plasma membrane of colorectal cancer, hepatocellular carcinoma, lung cancer, ovarian cancer and renal cell cancer samples. The full-length OGTA126 was detected in the plasma membrane of lung cancer samples. The full-length OGTA156 was detected in the plasma membrane of colorectal cancer, lung cancer, ovarian cancer and renal cell cancer samples. The full-length OGTA159 was detected in the plasma membrane of lung cancer and renal cell cancer samples. The full-length OGTA169 was detected in the plasma membrane of colorectal cancer, lung cancer and renal cell cancer samples. The full-length OGTA174 was detected in the plasma membrane of lung cancer samples. The full-length OGTA176 was detected in the plasma membrane of colorectal cancer, lung cancer and renal cell cancer samples. The full-length OGTA177 was detected in the plasma membrane of colorectal cancer, lung cancer, ovarian cancer and renal cell cancer samples. The full-length OGTA197 was detected in the plasma membrane of colorectal cancer, hepatocellular carcinoma, lung cancer and renal cell cancer samples. The full-length OGTA202 was detected in the plasma membrane of colorectal cancer and lung cancer samples. The full-length OGTA203 was detected in the plasma membrane of lung cancer and renal cell cancer samples. The full-length OGTA206 was detected in the plasma membrane of colorectal cancer and lung cancer samples. The full-length OGTA213 was detected in the plasma membrane of colorectal cancer and lung cancer samples. The full-length OGTA214 was detected in the plasma membrane of colorectal cancer samples. The full-length OGTA216 was detected in the plasma membrane of colorectal cancer, hepatocellular carcinoma, lung cancer, ovarian cancer and renal cell cancer samples. The full-length OGTA222 was detected in the plasma membrane of colorectal cancer, lung cancer and renal cell cancer samples. The full-length OGTA236 was detected in the plasma membrane of colorectal cancer samples. The full-length OGTA237 was detected in the plasma membrane of colorectal cancer, lung cancer and renal cell cancer samples. The full-length OGTA247 was detected in the plasma membrane of lung cancer samples. The full-length OGTA248 was detected in the plasma membrane of lung cancer and renal cell cancer samples. The full-length OGTA249 was detected in the plasma membrane of lung cancer and renal cell cancer samples. The full-length OGTA257 was detected in the plasma membrane of colorectal cancer, hepatocellular carcinoma, lung cancer and ovarian cancer samples. The full-length OGTA271 was detected in the plasma membrane of colorectal cancer, hepatocellular carcinoma, lung cancer and renal cell cancer samples.

Example 3

Evaluation of Colorectal Cancer Marker Proteins in Sandwich ELISA

[1012] Using the following Reference Protocol, colorectal cancer marker proteins, including OGTA066 were evaluated in a sandwich ELISA.

3.1 Materials and Methods

[1013] Antibodies for the sandwich ELISAs were developed at Biosite. Biotinylated antibody (primary antibody) was diluted into assay buffer (10 mM Tris, 150 mM NaCl, 1% BSA) to 2 ug/ml and added to 384 well neutravidin coated plate (Pierce Chemical Company, Rockford Ill.) and allowed to incubate at room temperature for 1 hour. Wells were then washed with wash buffer (20 mM Borate, 150 mM NaCl, 0.2% Tween 20). Samples and standards were added and allowed to incubate at room temperature for 1 hour. Wells again were washed. An antibody conjugated to fluorescein (secondary antibody) was diluted into assay buffer to 2 ug/ml and was then added to the plate and allowed to incubate at room temperature for 1 hour. Wells again were washed. Anti-fluorescein antibody conjugated to alkaline phosphatase, diluted 1/2338 into assay buffer, was added and allowed to incubate at room temperature for 1 hour. Final wash was then performed. Finally substrate (Promega Attophos Product#S1011, Promega Corporation, Madison, Wis.) was added and the plate was read immediately. All additions were 10 ul/well. The plate was washed 3 times between each addition and final wash was 9 times prior to the addition of substrate. Standards were prepared by spiking specific antigen into a normal serum patient pool. Reading was performed using a Tecan Spectrafluor plus (Tecan Inc, Mannheim, Switzerland) in kinetic mode for 6 read cycles with excitation filter of 430 nm and an emission filter 570 nm emission. Slope of RFU/seconds was determined. Final Box and ROC results were analyzed using Analyse-it General+Clinical Laboratory 1.73 (Analyse-it Software Ltd., Leeds England).

3.2 Results

[1014] These experiments identified proteins of particular interest including, but not limited to, OGTA066 (SEQ ID No: 9).

[1015] FIG. 2 shows Box plot data for OGTA066. The vertical axis on this graph is concentration of OGTA066 in ng/ml. These data show decreased concentration of OGTA066 in colorectal cancer samples compared to normal samples, with an almost significant p value, thereby indicating that OGTA066 discriminates well between colorectal cancer and normal, making it a good potential marker for colorectal cancer.

Example 4

Evaluation of Colorectal Cancer Marker Proteins in Multiplex Assay Using Luminex Technology

[1016] Using the following Reference Protocol, OGTA066 was evaluated in a multiplex assay using the Luminex technology.

4.1 Materials and Methods

[1017] Each primary antibody was conjugated to a unique Luminex magnetic microsphere (Mug beads, Luminex Cor-

poration, Austin, Tex.). Mag bead cocktail (50 ul) was added to a 96 black well round bottom Costar plate (Corning Incorporated, Corning N.Y.). Using a 96 well magnetic ring stand, the Mag beads were pulled down for 1 minute and washed with wash/assay buffer (PBS with 1% BSA and 0.02% Tween 20). 50 ul of sample or standard was added along with an additional 50 ul of wash/assay buffer and allowed to incubate on a shaker for 1 hour at room temperature. Plate was placed on magnetic ring stand and allowed to sit for 1 minute. Mag beads were then washed again. Biotin labeled antibody was then added at 50 ul per well with an additional 50 ul of wash/assay buffer and allowed to incubate on a shaker for 1 hour at room temperature. The plate again was placed on a magnetic stand and the Mag beads were washed. Streptavidin-RPE (Prozyme, San Leandro, Calif., Phycolin, Code# PJ31S) was diluted to 1 ug/ml in wash/assay buffer and 50 ul was added to each well along with an additional 50 ul of wash/assay buffer and allowed to incubate on a shaker for 1 hour at room temperature. Final wash was performed and the beads were re-suspended with 100 ul of wash/assay buffer and each well was then read in a Luminex 200 reader using Xponent software 3.0. All reagent dilutions were made in wash/assay buffer. Biotin-antibody varied for each assay to optimal concentration. Initial Mag bead amounts added were approximately 50,000 for each assay. Magnetic beads were allowed 1 minute pull down time prior to each wash. Each wash step was 3 times washed with 100 ul of wash/assay buffer. Assay standard curves were made in a normal donor patient serum pool. Luminex reader and Mag beads were used and prepared according to manufacturer guidelines. Standard curves were calculated using a 5 parameter log-logistic fit and each sample concentration was determined from this curve fit.

[1018] Final Box and ROC results were analyzed using Analyse-it General+Clinical Laboratory 1.73 (Analyse-it Software Ltd., Leeds England).

4.2 Results

[1019] Experiments using 61 normal samples and 65 colorectal cancer samples resulted in further evidence for some of the proteins of interest identified in Example 3 above, including, but not limited to, OGTA066. FIG. 4 shows Box plot data for OGTA066. FIG. 3 shows ROC curve data for OGTA066.

[1020] The ROC curves plot sensitivity (true positives) against 1-specificity (false positives). The area under the ROC curve is a measure of the probability that the measured marker level will allow correct identification of a disease or condition. An area of greater than 0.5 indicates that the marker can discriminate between disease and normal. This is the case in the data shown in FIG. 3, with OGTA066 having a high area under the curve and a very low p value therefore indicating that OGTA066 is a good potential marker to discriminate between colorectal cancer and normal.

[1021] The vertical axes on the box plot in FIG. 4 is concentration of the OGTA066 in ng/ml. FIG. 4 shows lower concentration in serum samples of OGTA066 in colorectal cancer samples than in normal samples. OGTA066 shows good discrimination between colorectal cancer and normal, indicating it may be useful as a marker for colorectal cancer.

[1022] All references referred to in this application, including patent and patent applications, are incorporated herein by reference to the fullest extent possible.

[1023] Throughout the specification and the claims which follow, unless the context requires otherwise, the word 'comprise', and variations such as 'comprises' and 'comprising', will be understood to imply the inclusion of a stated integer, step, group of integers or group of steps but not to the exclusion of any other integer, step, group of integers or group of steps.

[1024] The application of which this description and claims form part may be used as a basis for priority in respect of any subsequent application. The claims of such subsequent application may be directed to any feature or combination of features described herein. They may take the form of product, composition, process, or use claims and may include, by way of example and without limitation, the following claims:

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 1008

<210> SEQ ID NO 1

<211> LENGTH: 987

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<222> LOCATION: (1)..(987)

<223> OTHER INFORMATION: Designated OGTA002 = Swissprot Accession No. P54760, Ephrin type-B receptor 4

<400> SEQUENCE: 1

Met Glu Leu Arg Val Leu Leu Cys Trp Ala Ser Leu Ala Ala Ala Leu
1 5 10 15

Glu Glu Thr Leu Leu Asn Thr Lys Leu Glu Thr Ala Asp Leu Lys Trp
20 25 30

Val Thr Phe Pro Gln Val Asp Gly Gln Trp Glu Glu Leu Ser Gly Leu
35 40 45

Asp Glu Glu Gln His Ser Val Arg Thr Tyr Glu Val Cys Asp Val Gln
50 55 60

Arg Ala Pro Gly Gln Ala His Trp Leu Arg Thr Gly Trp Val Pro Arg
65 70 75 80

Arg Gly Ala Val His Val Tyr Ala Thr Leu Arg Phe Thr Met Leu Glu
85 90 95

Cys Leu Ser Leu Pro Arg Ala Gly Arg Ser Cys Lys Glu Thr Phe Thr
100 105 110

Val Phe Tyr Tyr Glu Ser Asp Ala Asp Thr Ala Thr Ala Leu Thr Pro
115 120 125

Ala Trp Met Glu Asn Pro Tyr Ile Lys Val Asp Thr Val Ala Ala Glu
130 135 140

His Leu Thr Arg Lys Arg Pro Gly Ala Glu Ala Thr Gly Lys Val Asn
145 150 155 160

Val Lys Thr Leu Arg Leu Gly Pro Leu Ser Lys Ala Gly Phe Tyr Leu
165 170 175

Ala Phe Gln Asp Gln Gly Ala Cys Met Ala Leu Leu Ser Leu His Leu
180 185 190

Phe Tyr Lys Lys Cys Ala Gln Leu Thr Val Asn Leu Thr Arg Phe Pro
195 200 205

Glu Thr Val Pro Arg Glu Leu Val Val Pro Val Ala Gly Ser Cys Val
210 215 220

Val Asp Ala Val Pro Ala Pro Gly Pro Ser Pro Ser Leu Tyr Cys Arg
225 230 235 240

Glu Asp Gly Gln Trp Ala Glu Gln Pro Val Thr Gly Cys Ser Cys Ala
245 250 255

Pro Gly Phe Glu Ala Ala Glu Gly Asn Thr Lys Cys Arg Ala Cys Ala

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260							265					270				
Gln	Gly	Thr	Phe	Lys	Pro	Leu	Ser	Gly	Glu	Gly	Ser	Cys	Gln	Pro	Cys	
		275					280					285				
Pro	Ala	Asn	Ser	His	Ser	Asn	Thr	Ile	Gly	Ser	Ala	Val	Cys	Gln	Cys	
		290				295					300					
Arg	Val	Gly	Tyr	Phe	Arg	Ala	Arg	Thr	Asp	Pro	Arg	Gly	Ala	Pro	Cys	
305					310					315					320	
Thr	Thr	Pro	Pro	Ser	Ala	Pro	Arg	Ser	Val	Val	Ser	Arg	Leu	Asn	Gly	
				325					330					335		
Ser	Ser	Leu	His	Leu	Glu	Trp	Ser	Ala	Pro	Leu	Glu	Ser	Gly	Gly	Arg	
			340					345					350			
Glu	Asp	Leu	Thr	Tyr	Ala	Leu	Arg	Cys	Arg	Glu	Cys	Arg	Pro	Gly	Gly	
		355					360					365				
Ser	Cys	Ala	Pro	Cys	Gly	Gly	Asp	Leu	Thr	Phe	Asp	Pro	Gly	Pro	Arg	
		370				375					380					
Asp	Leu	Val	Glu	Pro	Trp	Val	Val	Val	Arg	Gly	Leu	Arg	Pro	Asp	Phe	
385					390					395					400	
Thr	Tyr	Thr	Phe	Glu	Val	Thr	Ala	Leu	Asn	Gly	Val	Ser	Ser	Leu	Ala	
				405					410					415		
Thr	Gly	Pro	Val	Pro	Phe	Glu	Pro	Val	Asn	Val	Thr	Thr	Asp	Arg	Glu	
			420					425					430			
Val	Pro	Pro	Ala	Val	Ser	Asp	Ile	Arg	Val	Thr	Arg	Ser	Ser	Pro	Ser	
			435				440					445				
Ser	Leu	Ser	Leu	Ala	Trp	Ala	Val	Pro	Arg	Ala	Pro	Ser	Gly	Ala	Val	
		450				455					460					
Leu	Asp	Tyr	Glu	Val	Lys	Tyr	His	Glu	Lys	Gly	Ala	Glu	Gly	Pro	Ser	
465					470					475					480	
Ser	Val	Arg	Phe	Leu	Lys	Thr	Ser	Glu	Asn	Arg	Ala	Glu	Leu	Arg	Gly	
				485					490					495		
Leu	Lys	Arg	Gly	Ala	Ser	Tyr	Leu	Val	Gln	Val	Arg	Ala	Arg	Ser	Glu	
			500					505					510			
Ala	Gly	Tyr	Gly	Pro	Phe	Gly	Gln	Glu	His	His	Ser	Gln	Thr	Gln	Leu	
			515				520					525				
Asp	Glu	Ser	Glu	Gly	Trp	Arg	Glu	Gln	Leu	Ala	Leu	Ile	Ala	Gly	Thr	
		530				535					540					
Ala	Val	Val	Gly	Val	Val	Leu	Val	Leu	Val	Val	Ile	Val	Val	Ala	Val	
545					550					555					560	
Leu	Cys	Leu	Arg	Lys	Gln	Ser	Asn	Gly	Arg	Glu	Ala	Glu	Tyr	Ser	Asp	
				565					570					575		
Lys	His	Gly	Gln	Tyr	Leu	Ile	Gly	His	Gly	Thr	Lys	Val	Tyr	Ile	Asp	
			580					585					590			
Pro	Phe	Thr	Tyr	Glu	Asp	Pro	Asn	Glu	Ala	Val	Arg	Glu	Phe	Ala	Lys	
			595				600					605				
Glu	Ile	Asp	Val	Ser	Tyr	Val	Lys	Ile	Glu	Glu	Val	Ile	Gly	Ala	Gly	
			610				615				620					
Glu	Phe	Gly	Glu	Val	Cys	Arg	Gly	Arg	Leu	Lys	Ala	Pro	Gly	Lys	Lys	
625					630					635					640	
Glu	Ser	Cys	Val	Ala	Ile	Lys	Thr	Leu	Lys	Gly	Gly	Tyr	Thr	Glu	Arg	
				645					650					655		
Gln	Arg	Arg	Glu	Phe	Leu	Ser	Glu	Ala	Ser	Ile	Met	Gly	Gln	Phe	Glu	
			660					665					670			

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His Pro Asn Ile Ile Arg Leu Glu Gly Val Val Thr Asn Ser Met Pro
 675                      680                      685

Val Met Ile Leu Thr Glu Phe Met Glu Asn Gly Ala Leu Asp Ser Phe
 690                      695                      700

Leu Arg Leu Asn Asp Gly Gln Phe Thr Val Ile Gln Leu Val Gly Met
 705                      710                      715                      720

Leu Arg Gly Ile Ala Ser Gly Met Arg Tyr Leu Ala Glu Met Ser Tyr
 725                      730                      735

Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu
 740                      745                      750

Val Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Phe Leu Glu Glu Asn
 755                      760                      765

Ser Ser Asp Pro Thr Tyr Thr Ser Ser Leu Gly Gly Lys Ile Pro Ile
 770                      775                      780

Arg Trp Thr Ala Pro Glu Ala Ile Ala Phe Arg Lys Phe Thr Ser Ala
 785                      790                      795                      800

Ser Asp Ala Trp Ser Tyr Gly Ile Val Met Trp Glu Val Met Ser Phe
 805                      810                      815

Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp Val Ile Asn Ala
 820                      825                      830

Ile Glu Gln Asp Tyr Arg Leu Pro Pro Pro Asp Cys Pro Thr Ser
 835                      840                      845

Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Asp Arg Asn Ala Arg
 850                      855                      860

Pro Arg Phe Pro Gln Val Val Ser Ala Leu Asp Lys Met Ile Arg Asn
 865                      870                      875                      880

Pro Ala Ser Leu Lys Ile Val Ala Arg Glu Asn Gly Gly Ala Ser His
 885                      890                      895

Pro Leu Leu Asp Gln Arg Gln Pro His Tyr Ser Ala Phe Gly Ser Val
 900                      905                      910

Gly Glu Trp Leu Arg Ala Ile Lys Met Gly Arg Tyr Glu Glu Ser Phe
 915                      920                      925

Ala Ala Ala Gly Phe Gly Ser Phe Glu Leu Val Ser Gln Ile Ser Ala
 930                      935                      940

Glu Asp Leu Leu Arg Ile Gly Val Thr Leu Ala Gly His Gln Lys Lys
 945                      950                      955                      960

Ile Leu Ala Ser Val Gln His Met Lys Ser Gln Ala Lys Pro Gly Thr
 965                      970                      975

Pro Gly Gly Thr Gly Gly Pro Ala Pro Gln Tyr
 980                      985

<210> SEQ ID NO 2
<211> LENGTH: 220
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(220)
<223> OTHER INFORMATION: OGTA009 = Swiss Prot Accession No. 015551,
        claudin-3

<400> SEQUENCE: 2

Met Ser Met Gly Leu Glu Ile Thr Gly Thr Ala Leu Ala Val Leu Gly
 1                      5                      10                      15

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Trp Leu Gly Thr Ile Val Cys Cys Ala Leu Pro Met Trp Arg Val Ser
 20 25 30
 Ala Phe Ile Gly Ser Asn Ile Ile Thr Ser Gln Asn Ile Trp Glu Gly
 35 40 45
 Leu Trp Met Asn Cys Val Val Gln Ser Thr Gly Gln Met Gln Cys Lys
 50 55 60
 Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala Arg
 65 70 75 80
 Ala Leu Ile Val Val Ala Ile Leu Leu Ala Phe Gly Leu Leu Val
 85 90 95
 Ala Leu Val Gly Ala Gln Cys Thr Asn Cys Val Gln Asp Asp Thr Ala
 100 105 110
 Lys Ala Lys Ile Thr Ile Val Ala Gly Val Leu Phe Leu Leu Ala Ala
 115 120 125
 Leu Leu Thr Leu Val Pro Val Ser Trp Ser Ala Asn Thr Ile Ile Arg
 130 135 140
 Asp Phe Tyr Asn Pro Val Val Pro Glu Ala Gln Lys Arg Glu Met Gly
 145 150 155 160
 Ala Gly Leu Tyr Val Gly Trp Ala Ala Ala Leu Gln Leu Leu Gly
 165 170 175
 Gly Ala Leu Leu Cys Cys Ser Cys Pro Pro Arg Glu Lys Lys Tyr Thr
 180 185 190
 Ala Thr Lys Val Val Tyr Ser Ala Pro Arg Ser Thr Gly Pro Gly Ala
 195 200 205
 Ser Leu Gly Thr Gly Tyr Asp Arg Lys Asp Tyr Val
 210 215 220

<210> SEQ ID NO 3
 <211> LENGTH: 764
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapiens
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (1)..(764)
 <223> OTHER INFORMATION: OGTA016 = Swiss Prot Accession No. P01833,
 Polymeric-immunoglobulin receptor

<400> SEQUENCE: 3

Met Leu Leu Phe Val Leu Thr Cys Leu Leu Ala Val Phe Pro Ala Ile
 1 5 10 15
 Ser Thr Lys Ser Pro Ile Phe Gly Pro Glu Glu Val Asn Ser Val Glu
 20 25 30
 Gly Asn Ser Val Ser Ile Thr Cys Tyr Tyr Pro Pro Thr Ser Val Asn
 35 40 45
 Arg His Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala Arg Gly Gly Cys
 50 55 60
 Ile Thr Leu Ile Ser Ser Glu Gly Tyr Val Ser Ser Lys Tyr Ala Gly
 65 70 75 80
 Arg Ala Asn Leu Thr Asn Phe Pro Glu Asn Gly Thr Phe Val Val Asn
 85 90 95
 Ile Ala Gln Leu Ser Gln Asp Asp Ser Gly Arg Tyr Lys Cys Gly Leu
 100 105 110
 Gly Ile Asn Ser Arg Gly Leu Ser Phe Asp Val Ser Leu Glu Val Ser
 115 120 125

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Gln Gly Pro Gly Leu Leu Asn Asp Thr Lys Val Tyr Thr Val Asp Leu	130	135	140
Gly Arg Thr Val Thr Ile Asn Cys Pro Phe Lys Thr Glu Asn Ala Gln	145	150	155
Lys Arg Lys Ser Leu Tyr Lys Gln Ile Gly Leu Tyr Pro Val Leu Val	165	170	175
Ile Asp Ser Ser Gly Tyr Val Asn Pro Asn Tyr Thr Gly Arg Ile Arg	180	185	190
Leu Asp Ile Gln Gly Thr Gly Gln Leu Leu Phe Ser Val Val Ile Asn	195	200	205
Gln Leu Arg Leu Ser Asp Ala Gly Gln Tyr Leu Cys Gln Ala Gly Asp	210	215	220
Asp Ser Asn Ser Asn Lys Lys Asn Ala Asp Leu Gln Val Leu Lys Pro	225	230	235
Glu Pro Glu Leu Val Tyr Glu Asp Leu Arg Gly Ser Val Thr Phe His	245	250	255
Cys Ala Leu Gly Pro Glu Val Ala Asn Val Ala Lys Phe Leu Cys Arg	260	265	270
Gln Ser Ser Gly Glu Asn Cys Asp Val Val Val Asn Thr Leu Gly Lys	275	280	285
Arg Ala Pro Ala Phe Glu Gly Arg Ile Leu Leu Asn Pro Gln Asp Lys	290	295	300
Asp Gly Ser Phe Ser Val Val Ile Thr Gly Leu Arg Lys Glu Asp Ala	305	310	315
Gly Arg Tyr Leu Cys Gly Ala His Ser Asp Gly Gln Leu Gln Glu Gly	325	330	335
Ser Pro Ile Gln Ala Trp Gln Leu Phe Val Asn Glu Glu Ser Thr Ile	340	345	350
Pro Arg Ser Pro Thr Val Val Lys Gly Val Ala Gly Ser Ser Val Ala	355	360	365
Val Leu Cys Pro Tyr Asn Arg Lys Glu Ser Lys Ser Ile Lys Tyr Trp	370	375	380
Cys Leu Trp Glu Gly Ala Gln Asn Gly Arg Cys Pro Leu Leu Val Asp	385	390	395
Ser Glu Gly Trp Val Lys Ala Gln Tyr Glu Gly Arg Leu Ser Leu Leu	405	410	415
Glu Glu Pro Gly Asn Gly Thr Phe Thr Val Ile Leu Asn Gln Leu Thr	420	425	430
Ser Arg Asp Ala Gly Phe Tyr Trp Cys Leu Thr Asn Gly Asp Thr Leu	435	440	445
Trp Arg Thr Thr Val Glu Ile Lys Ile Ile Glu Gly Glu Pro Asn Leu	450	455	460
Lys Val Pro Gly Asn Val Thr Ala Val Leu Gly Glu Thr Leu Lys Val	465	470	475
Pro Cys His Phe Pro Cys Lys Phe Ser Ser Tyr Glu Lys Tyr Trp Cys	485	490	495
Lys Trp Asn Asn Thr Gly Cys Gln Ala Leu Pro Ser Gln Asp Glu Gly	500	505	510
Pro Ser Lys Ala Phe Val Asn Cys Asp Glu Asn Ser Arg Leu Val Ser	515	520	525

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<210> SEQ ID NO 4
<211> LENGTH: 865
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(865)
<223> OTHER INFORMATION: OGTA028 = Swiss Prot Accession No. Q5T7N2,
FLJ10884
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Met	Ser	Asp	Val	Ser	Thr	Ser	Val	Gln	Ser	Lys	Phe	Ala	Arg	Leu	Ala
1				5					10					15	
Lys	Lys	Lys	Glu	Asn	Ile	Thr	Tyr	Met	Lys	Arg	Glu	Gln	Leu	Thr	Glu
			20					25					30		
Thr	Asp	Lys	Asp	Ile	Ala	Pro	Val	Leu	Asp	Leu	Lys	Cys	Lys	Asp	Val
		35					40					45			
Ser	Ala	Ile	Met	Asn	Lys	Phe	Lys	Val	Leu	Met	Glu	Ile	Gln	Asp	Leu
	50					55					60				
Met	Phe	Glu	Glu	Met	Arg	Glu	Thr	Leu	Lys	Asn	Asp	Leu	Lys	Ala	Val
65					70					75				80	
Leu	Gly	Gly	Lys	Ala	Thr	Ile	Pro	Glu	Val	Lys	Asn	Ser	Glu	Asn	Ser
			85					90						95	

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Ser	Ser	Arg	Thr	Glu	Phe	Gln	Gln	Ile	Ile	Asn	Leu	Ala	Leu	Gln	Lys
			100					105					110		
Thr	Gly	Met	Val	Gly	Lys	Ile	Glu	Gly	Glu	Asn	Ser	Lys	Ile	Gly	Asp
		115					120					125			
Asp	Asn	Glu	Asn	Leu	Thr	Phe	Lys	Leu	Glu	Val	Asn	Glu	Leu	Ser	Gly
	130					135					140				
Lys	Leu	Asp	Asn	Thr	Asn	Glu	Tyr	Asn	Ser	Asn	Asp	Gly	Lys	Lys	Leu
145					150					155					160
Pro	Gln	Gly	Glu	Ser	Arg	Ser	Tyr	Glu	Val	Met	Gly	Ser	Met	Glu	Glu
				165					170					175	
Thr	Leu	Cys	Asn	Ile	Asp	Asp	Arg	Asp	Gly	Asn	Arg	Asn	Val	His	Leu
		180					185						190		
Glu	Phe	Thr	Glu	Arg	Glu	Ser	Arg	Lys	Asp	Gly	Glu	Asp	Glu	Phe	Val
		195					200					205			
Lys	Glu	Met	Arg	Glu	Glu	Arg	Lys	Phe	Gln	Lys	Leu	Lys	Asn	Lys	Glu
	210					215					220				
Glu	Val	Leu	Lys	Ala	Ser	Arg	Glu	Glu	Lys	Val	Leu	Met	Asp	Glu	Gly
225					230					235					240
Ala	Val	Leu	Thr	Leu	Val	Ala	Asp	Leu	Ser	Ser	Ala	Thr	Leu	Asp	Ile
			245						250					255	
Ser	Lys	Gln	Trp	Ser	Asn	Val	Phe	Asn	Ile	Leu	Arg	Glu	Asn	Asp	Phe
		260					265						270		
Glu	Pro	Lys	Phe	Leu	Cys	Glu	Val	Lys	Leu	Ala	Phe	Lys	Cys	Asp	Gly
		275					280					285			
Glu	Ile	Lys	Thr	Phe	Ser	Asp	Leu	Gln	Ser	Leu	Arg	Lys	Phe	Ala	Ser
	290					295					300				
Gln	Lys	Ser	Ser	Val	Lys	Glu	Leu	Leu	Lys	Asp	Val	Leu	Pro	Gln	Lys
305					310					315					320
Glu	Glu	Ile	Asn	Gln	Gly	Gly	Arg	Lys	Tyr	Gly	Ile	Gln	Glu	Lys	Arg
			325						330					335	
Asp	Lys	Thr	Leu	Ile	Asp	Ser	Lys	His	Arg	Ala	Gly	Glu	Ile	Thr	Ser
		340					345						350		
Asp	Gly	Leu	Ser	Phe	Leu	Phe	Leu	Lys	Glu	Val	Lys	Val	Ala	Lys	Pro
		355				360					365				
Glu	Glu	Met	Lys	Asn	Leu	Glu	Thr	Gln	Glu	Glu	Glu	Phe	Ser	Glu	Leu
	370					375					380				
Glu	Glu	Leu	Asp	Glu	Glu	Ala	Ser	Gly	Met	Glu	Asp	Asp	Glu	Asp	Thr
385					390					395					400
Ser	Gly	Leu	Glu	Glu	Glu	Glu	Glu	Glu	Pro	Ser	Gly	Leu	Glu	Glu	Glu
			405						410					415	
Glu	Glu	Glu	Glu	Ala	Ser	Gly	Leu	Glu	Glu	Asp	Glu	Ala	Ser	Gly	Leu
			420					425				430			
Glu	Glu	Glu	Glu	Glu	Gln	Thr	Ser	Glu	Gln	Asp	Ser	Thr	Phe	Gln	Gly
			435				440					445			
His	Thr	Leu	Val	Asp	Ala	Lys	His	Glu	Val	Glu	Ile	Thr	Ser	Asp	Gly
	450					455					460				
Met	Glu	Thr	Thr	Phe	Ile	Asp	Ser	Val	Glu	Asp	Ser	Glu	Ser	Glu	Glu
465					470					475					480
Glu	Glu	Glu	Gly	Lys	Ser	Ser	Glu	Thr	Gly	Lys	Val	Lys	Thr	Thr	Ser
			485						490					495	
Leu	Thr	Glu	Lys	Lys	Ala	Ser	Arg	Arg	Gln	Lys	Glu	Ile	Pro	Phe	Ser

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500					505					510						
Tyr	Leu	Val	Gly	Asp	Ser	Gly	Lys	Lys	Lys	Leu	Val	Lys	His	Gln	Val	
515					520					525						
Val	His	Lys	Thr	Gln	Glu	Glu	Glu	Thr	Ala	Val	Pro	Thr	Ser	Gln		
530					535					540						
Gly	Thr	Gly	Thr	Pro	Cys	Leu	Thr	Leu	Cys	Leu	Ala	Ser	Pro	Ser	Lys	
545					550					555					560	
Ser	Leu	Glu	Met	Ser	His	Asp	Glu	His	Lys	Lys	His	Ser	His	Thr	Asn	
565					570					575						
Leu	Ser	Ile	Ser	Thr	Gly	Val	Thr	Lys	Leu	Lys	Lys	Thr	Glu	Glu	Lys	
580					585					590						
Lys	His	Arg	Thr	Leu	His	Thr	Glu	Glu	Leu	Thr	Ser	Lys	Glu	Ala	Asp	
595					600					605						
Leu	Thr	Glu	Glu	Thr	Glu	Glu	Asn	Leu	Arg	Ser	Ser	Val	Ile	Asn	Ser	
610					615					620						
Ile	Arg	Glu	Ile	Lys	Glu	Glu	Ile	Gly	Asn	Leu	Lys	Ser	Ser	His	Ser	
625					630					635					640	
Gly	Val	Leu	Glu	Ile	Glu	Asn	Ser	Val	Asp	Asp	Leu	Ser	Ser	Arg	Met	
645					650					655						
Asp	Ile	Leu	Glu	Glu	Arg	Ile	Asp	Ser	Leu	Glu	Asp	Gln	Ile	Glu	Glu	
660					665					670						
Phe	Ser	Lys	Asp	Thr	Met	Gln	Met	Thr	Lys	Gln	Ile	Ile	Ser	Lys	Glu	
675					680					685						
Arg	Gln	Arg	Asp	Ile	Glu	Glu	Arg	Ser	Arg	Ser	Cys	Asn	Ile	Arg	Leu	
690					695					700						
Ile	Gly	Ile	Pro	Glu	Lys	Glu	Ser	Tyr	Glu	Asn	Arg	Ala	Glu	Asp	Ile	
705					710					715					720	
Ile	Lys	Glu	Ile	Ile	Asp	Glu	Asn	Phe	Ala	Glu	Leu	Lys	Lys	Gly	Ser	
725					730					735						
Ser	Leu	Glu	Ile	Val	Ser	Ala	Cys	Arg	Val	Pro	Ser	Lys	Ile	Asp	Glu	
740					745					750						
Lys	Arg	Leu	Thr	Pro	Arg	His	Ile	Leu	Val	Lys	Phe	Trp	Asn	Ser	Ser	
755					760					765						
Asp	Lys	Glu	Lys	Ile	Ile	Arg	Ala	Ser	Arg	Glu	Arg	Arg	Glu	Ile	Thr	
770					775					780						
Tyr	Gln	Gly	Thr	Arg	Ile	Arg	Leu	Thr	Ala	Asp	Leu	Ser	Leu	Asp	Thr	
785					790					795					800	
Leu	Asp	Ala	Arg	Ser	Lys	Trp	Ser	Asn	Val	Phe	Lys	Val	Leu	Leu	Glu	
805					810					815						
Lys	Gly	Phe	Asn	Pro	Arg	Ile	Leu	Tyr	Pro	Ala	Lys	Met	Ala	Phe	Asp	
820					825					830						
Phe	Arg	Gly	Lys	Thr	Lys	Val	Phe	Leu	Ser	Ile	Glu	Glu	Phe	Arg	Asp	
835					840					845						
Tyr	Val	Leu	His	Met	Pro	Thr	Leu	Arg	Glu	Leu	Leu	Gly	Asn	Asn	Ile	
850					855					860						
Pro																
865																

<210> SEQ ID NO 5

<211> LENGTH: 323

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

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<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(323)
<223> OTHER INFORMATION: OGTA037 = Swiss Prot Accession No. Q9HA72,
Protein FAM26B

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<400> SEQUENCE: 5

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Met Ala Ala Leu Ile Ala Glu Asn Phe Arg Phe Leu Ser Leu Phe Phe
 1             5             10             15

Lys Ser Lys Asp Val Met Ile Phe Asn Gly Leu Val Ala Leu Gly Thr
 20             25             30

Val Gly Ser Gln Glu Leu Phe Ser Val Val Ala Phe His Cys Pro Cys
 35             40             45

Ser Pro Ala Arg Asn Tyr Leu Tyr Gly Leu Ala Ala Ile Gly Val Pro
 50             55             60

Ala Leu Val Leu Phe Ile Ile Gly Ile Ile Leu Asn Asn His Thr Trp
 65             70             75             80

Asn Leu Val Ala Glu Cys Gln His Arg Arg Thr Lys Asn Cys Ser Ala
 85             90             95

Ala Pro Thr Phe Leu Leu Leu Ser Ser Ile Leu Gly Arg Ala Ala Val
100            105            110

Ala Pro Val Thr Trp Ser Val Ile Ser Leu Leu Arg Gly Glu Ala Tyr
115            120            125

Val Cys Ala Leu Ser Glu Phe Val Asp Pro Ser Ser Leu Thr Ala Arg
130            135            140

Glu Glu His Phe Pro Ser Ala His Ala Thr Glu Ile Leu Ala Arg Phe
145            150            155            160

Pro Cys Lys Glu Asn Pro Asp Asn Leu Ser Asp Phe Arg Glu Glu Val
165            170            175

Ser Arg Arg Leu Arg Tyr Glu Ser Gln Leu Phe Gly Trp Leu Leu Ile
180            185            190

Gly Val Val Ala Ile Leu Val Phe Leu Thr Lys Cys Leu Lys His Tyr
195            200            205

Cys Ser Pro Leu Ser Tyr Arg Gln Glu Ala Tyr Trp Ala Gln Tyr Arg
210            215            220

Ala Asn Glu Asp Gln Leu Phe Gln Arg Thr Ala Glu Val His Ser Arg
225            230            235            240

Val Leu Ala Ala Asn Asn Val Arg Arg Phe Phe Gly Phe Val Ala Leu
245            250            255

Asn Lys Asp Asp Glu Glu Leu Ile Ala Asn Phe Pro Val Glu Gly Thr
260            265            270

Gln Pro Arg Pro Gln Trp Asn Ala Ile Thr Gly Val Tyr Leu Tyr Arg
275            280            285

Glu Asn Gln Gly Leu Pro Leu Tyr Ser Arg Leu His Lys Trp Ala Gln
290            295            300

Gly Leu Ala Gly Asn Gly Ala Ala Pro Asp Asn Val Glu Met Ala Leu
305            310            315            320

Leu Pro Ser

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<210> SEQ ID NO 6
<211> LENGTH: 918
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens
<220> FEATURE:

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<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(918)
<223> OTHER INFORMATION: OGTA041 = Swiss Prot Accession No. P40189,
Interleukin-6 receptor subunit beta

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<400> SEQUENCE: 6

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Met Leu Thr Leu Gln Thr Trp Val Val Gln Ala Leu Phe Ile Phe Leu
1          5          10          15
Thr Thr Glu Ser Thr Gly Glu Leu Leu Asp Pro Cys Gly Tyr Ile Ser
20          25          30
Pro Glu Ser Pro Val Val Gln Leu His Ser Asn Phe Thr Ala Val Cys
35          40          45
Val Leu Lys Glu Lys Cys Met Asp Tyr Phe His Val Asn Ala Asn Tyr
50          55          60
Ile Val Trp Lys Thr Asn His Phe Thr Ile Pro Lys Glu Gln Tyr Thr
65          70          75          80
Ile Ile Asn Arg Thr Ala Ser Ser Val Thr Phe Thr Asp Ile Ala Ser
85          90          95
Leu Asn Ile Gln Leu Thr Cys Asn Ile Leu Thr Phe Gly Gln Leu Glu
100         105         110
Gln Asn Val Tyr Gly Ile Thr Ile Ile Ser Gly Leu Pro Pro Glu Lys
115         120         125
Pro Lys Asn Leu Ser Cys Ile Val Asn Glu Gly Lys Lys Met Arg Cys
130         135         140
Glu Trp Asp Gly Gly Arg Glu Thr His Leu Glu Thr Asn Phe Thr Leu
145         150         155         160
Lys Ser Glu Trp Ala Thr His Lys Phe Ala Asp Cys Lys Ala Lys Arg
165         170         175
Asp Thr Pro Thr Ser Cys Thr Val Asp Tyr Ser Thr Val Tyr Phe Val
180         185         190
Asn Ile Glu Val Trp Val Glu Ala Glu Asn Ala Leu Gly Lys Val Thr
195         200         205
Ser Asp His Ile Asn Phe Asp Pro Val Tyr Lys Val Lys Pro Asn Pro
210         215         220
Pro His Asn Leu Ser Val Ile Asn Ser Glu Glu Leu Ser Ser Ile Leu
225         230         235         240
Lys Leu Thr Trp Thr Asn Pro Ser Ile Lys Ser Val Ile Ile Leu Lys
245         250         255
Tyr Asn Ile Gln Tyr Arg Thr Lys Asp Ala Ser Thr Trp Ser Gln Ile
260         265         270
Pro Pro Glu Asp Thr Ala Ser Thr Arg Ser Ser Phe Thr Val Gln Asp
275         280         285
Leu Lys Pro Phe Thr Glu Tyr Val Phe Arg Ile Arg Cys Met Lys Glu
290         295         300
Asp Gly Lys Gly Tyr Trp Ser Asp Trp Ser Glu Glu Ala Ser Gly Ile
305         310         315         320
Thr Tyr Glu Asp Arg Pro Ser Lys Ala Pro Ser Phe Trp Tyr Lys Ile
325         330         335
Asp Pro Ser His Thr Gln Gly Tyr Arg Thr Val Gln Leu Val Trp Lys
340         345         350
Thr Leu Pro Pro Phe Glu Ala Asn Gly Lys Ile Leu Asp Tyr Glu Val
355         360         365

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Thr	Leu	Thr	Arg	Trp	Lys	Ser	His	Leu	Gln	Asn	Tyr	Thr	Val	Asn	Ala
370						375					380				
Thr	Lys	Leu	Thr	Val	Asn	Leu	Thr	Asn	Asp	Arg	Tyr	Leu	Ala	Thr	Leu
385					390					395					400
Thr	Val	Arg	Asn	Leu	Val	Gly	Lys	Ser	Asp	Ala	Ala	Val	Leu	Thr	Ile
			405						410					415	
Pro	Ala	Cys	Asp	Phe	Gln	Ala	Thr	His	Pro	Val	Met	Asp	Leu	Lys	Ala
			420					425					430		
Phe	Pro	Lys	Asp	Asn	Met	Leu	Trp	Val	Glu	Trp	Thr	Thr	Pro	Arg	Glu
		435					440					445			
Ser	Val	Lys	Lys	Tyr	Ile	Leu	Glu	Trp	Cys	Val	Leu	Ser	Asp	Lys	Ala
	450					455					460				
Pro	Cys	Ile	Thr	Asp	Trp	Gln	Gln	Glu	Asp	Gly	Thr	Val	His	Arg	Thr
465					470					475					480
Tyr	Leu	Arg	Gly	Asn	Leu	Ala	Glu	Ser	Lys	Cys	Tyr	Leu	Ile	Thr	Val
				485					490					495	
Thr	Pro	Val	Tyr	Ala	Asp	Gly	Pro	Gly	Ser	Pro	Glu	Ser	Ile	Lys	Ala
			500					505					510		
Tyr	Leu	Lys	Gln	Ala	Pro	Pro	Ser	Lys	Gly	Pro	Thr	Val	Arg	Thr	Lys
		515					520					525			
Lys	Val	Gly	Lys	Asn	Glu	Ala	Val	Leu	Glu	Trp	Asp	Gln	Leu	Pro	Val
	530					535					540				
Asp	Val	Gln	Asn	Gly	Phe	Ile	Arg	Asn	Tyr	Thr	Ile	Phe	Tyr	Arg	Thr
545					550					555					560
Ile	Ile	Gly	Asn	Glu	Thr	Ala	Val	Asn	Val	Asp	Ser	Ser	His	Thr	Glu
			565						570					575	
Tyr	Thr	Leu	Ser	Ser	Leu	Thr	Ser	Asp	Thr	Leu	Tyr	Met	Val	Arg	Met
			580					585					590		
Ala	Ala	Tyr	Thr	Asp	Glu	Gly	Gly	Lys	Asp	Gly	Pro	Glu	Phe	Thr	Phe
		595					600					605			
Thr	Thr	Pro	Lys	Phe	Ala	Gln	Gly	Glu	Ile	Glu	Ala	Ile	Val	Val	Pro
	610					615					620				
Val	Cys	Leu	Ala	Phe	Leu	Leu	Thr	Thr	Leu	Leu	Gly	Val	Leu	Phe	Cys
625					630					635					640
Phe	Asn	Lys	Arg	Asp	Leu	Ile	Lys	Lys	His	Ile	Trp	Pro	Asn	Val	Pro
			645						650					655	
Asp	Pro	Ser	Lys	Ser	His	Ile	Ala	Gln	Trp	Ser	Pro	His	Thr	Pro	Pro
		660						665					670		
Arg	His	Asn	Phe	Asn	Ser	Lys	Asp	Gln	Met	Tyr	Ser	Asp	Gly	Asn	Phe
		675					680					685			
Thr	Asp	Val	Ser	Val	Val	Glu	Ile	Glu	Ala	Asn	Asp	Lys	Lys	Pro	Phe
	690					695					700				
Pro	Glu	Asp	Leu	Lys	Ser	Leu	Asp	Leu	Phe	Lys	Lys	Glu	Lys	Ile	Asn
705					710					715					720
Thr	Glu	Gly	His	Ser	Ser	Gly	Ile	Gly	Gly	Ser	Ser	Cys	Met	Ser	Ser
			725						730					735	
Ser	Arg	Pro	Ser	Ile	Ser	Ser	Ser	Asp	Glu	Asn	Glu	Ser	Ser	Gln	Asn
			740					745					750		
Thr	Ser	Ser	Thr	Val	Gln	Tyr	Ser	Thr	Val	Val	His	Ser	Gly	Tyr	Arg
		755					760					765			
His	Gln	Val	Pro	Ser	Val	Gln	Val	Phe	Ser	Arg	Ser	Glu	Ser	Thr	Gln

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770	775	780
Pro Leu Leu Asp Ser	Glu Glu Arg Pro Glu Asp	Leu Gln Leu Val Asp
785	790	795 800
His Val Asp Gly Gly	Asp Gly Ile Leu Pro Arg	Gln Gln Tyr Phe Lys
	805	810 815
Gln Asn Cys Ser Gln	His Glu Ser Ser Pro Asp	Ile Ser His Phe Glu
	820	825 830
Arg Ser Lys Gln Val	Ser Ser Val Asn Glu Glu Asp	Phe Val Arg Leu
	835	840 845
Lys Gln Gln Ile Ser	Asp His Ile Ser Gln Ser Cys	Gly Ser Gly Gln
	850	855 860
Met Lys Met Phe Gln	Glu Val Ser Ala Ala Asp	Ala Phe Gly Pro Gly
	865	870 875 880
Thr Glu Gly Gln Val	Glu Arg Phe Glu Thr Val Gly	Met Glu Ala Ala
	885	890 895
Thr Asp Glu Gly Met	Pro Lys Ser Tyr Leu Pro Gln	Thr Val Arg Gln
	900	905 910
Gly Gly Tyr Met Pro Gln		
	915	
<210> SEQ ID NO 7		
<211> LENGTH: 1042		
<212> TYPE: PRT		
<213> ORGANISM: Homo Sapiens		
<220> FEATURE:		
<221> NAME/KEY: MISC_FEATURE		
<222> LOCATION: (1)..(1042)		
<223> OTHER INFORMATION: OGTA053 = Swiss Prot Accession No. Q9Y4D2,		
Sn1-specific diacylglycerol lipase alpha		
<400> SEQUENCE: 7		
Met Pro Gly Ile Val Val	Phe Arg Arg Arg Trp Ser Val Gly Ser Asp	
1	5 10	15
Asp Leu Val Leu Pro Ala	Ile Phe Leu Phe Leu Leu His Thr Thr Trp	
	20 25	30
Phe Val Ile Leu Ser Val	Val Leu Phe Gly Leu Val Tyr Asn Pro His	
	35 40	45
Glu Ala Cys Ser Leu Asn	Leu Val Asp His Gly Arg Gly Tyr Leu Gly	
	50 55	60
Ile Leu Leu Ser Cys Met	Ile Ala Glu Met Ala Ile Ile Trp Leu Ser	
	65 70	75 80
Met Arg Gly Gly Ile Leu	Tyr Thr Glu Pro Arg Asp Ser Met Gln Tyr	
	85 90	95
Val Leu Tyr Val Arg Leu	Ala Ile Leu Val Ile Glu Phe Ile Tyr Ala	
	100 105	110
Ile Val Gly Ile Val Trp	Leu Thr Gln Tyr Tyr Thr Ser Cys Asn Asp	
	115 120	125
Leu Thr Ala Lys Asn Val	Thr Leu Gly Met Val Val Cys Asn Trp Val	
	130 135	140
Val Ile Leu Ser Val Cys	Ile Thr Val Leu Cys Val Phe Asp Pro Thr	
	145 150	155 160
Gly Arg Thr Phe Val Lys	Leu Arg Ala Thr Lys Arg Arg Gln Arg Asn	
	165 170	175
Leu Arg Thr Tyr Asn Leu	Arg His Arg Leu Glu Glu Gly Gln Ala Thr	

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180							185				190				
Ser	Trp	Ser	Arg	Arg	Leu	Lys	Val	Phe	Leu	Cys	Cys	Thr	Arg	Thr	Lys
		195					200					205			
Asp	Ser	Gln	Ser	Asp	Ala	Tyr	Ser	Glu	Ile	Ala	Tyr	Leu	Phe	Ala	Glu
	210					215					220				
Phe	Phe	Arg	Asp	Leu	Asp	Ile	Val	Pro	Ser	Asp	Ile	Ile	Ala	Gly	Leu
225					230					235					240
Val	Leu	Leu	Arg	Gln	Arg	Gln	Arg	Ala	Lys	Arg	Asn	Ala	Val	Leu	Asp
				245					250					255	
Glu	Ala	Asn	Asn	Asp	Ile	Leu	Ala	Phe	Leu	Ser	Gly	Met	Pro	Val	Thr
			260					265					270		
Arg	Asn	Thr	Lys	Tyr	Leu	Asp	Leu	Lys	Asn	Ser	Gln	Glu	Met	Leu	Arg
		275					280					285			
Tyr	Lys	Glu	Val	Cys	Tyr	Tyr	Met	Leu	Phe	Ala	Leu	Ala	Ala	Tyr	Gly
	290					295					300				
Trp	Pro	Met	Tyr	Leu	Met	Arg	Lys	Pro	Ala	Cys	Gly	Leu	Cys	Gln	Leu
305					310					315					320
Ala	Arg	Ser	Cys	Ser	Cys	Cys	Leu	Cys	Pro	Ala	Arg	Pro	Arg	Phe	Ala
				325					330					335	
Pro	Gly	Val	Thr	Ile	Glu	Glu	Asp	Asn	Cys	Cys	Gly	Cys	Asn	Ala	Ile
			340					345					350		
Ala	Ile	Arg	Arg	His	Phe	Leu	Asp	Glu	Asn	Met	Thr	Ala	Val	Asp	Ile
		355					360					365			
Val	Tyr	Thr	Ser	Cys	His	Asp	Ala	Val	Tyr	Glu	Thr	Pro	Phe	Tyr	Val
	370					375					380				
Ala	Val	Asp	His	Asp	Lys	Lys	Lys	Val	Val	Ile	Ser	Ile	Arg	Gly	Thr
385					390					395					400
Leu	Ser	Pro	Lys	Asp	Ala	Leu	Thr	Asp	Leu	Thr	Gly	Asp	Ala	Glu	Arg
				405					410					415	
Leu	Pro	Val	Glu	Gly	His	His	Gly	Thr	Trp	Leu	Gly	His	Lys	Gly	Met
			420					425					430		
Val	Leu	Ser	Ala	Glu	Tyr	Ile	Lys	Lys	Lys	Leu	Glu	Gln	Glu	Met	Val
		435					440					445			
Leu	Ser	Gln	Ala	Phe	Gly	Arg	Asp	Leu	Gly	Arg	Gly	Thr	Lys	His	Tyr
	450					455					460				
Gly	Leu	Ile	Val	Val	Gly	His	Ser	Leu	Gly	Ala	Gly	Thr	Ala	Ala	Ile
465					470					475					480
Leu	Ser	Phe	Leu	Leu	Arg	Pro	Gln	Tyr	Pro	Thr	Leu	Lys	Cys	Phe	Ala
				485					490					495	
Tyr	Ser	Pro	Pro	Gly	Gly	Leu	Leu	Ser	Glu	Asp	Ala	Met	Glu	Tyr	Ser
			500					505					510		
Lys	Glu	Phe	Val	Thr	Ala	Val	Val	Leu	Gly	Lys	Asp	Leu	Val	Pro	Arg
		515					520					525			
Ile	Gly	Leu	Ser	Gln	Leu	Glu	Gly	Phe	Arg	Arg	Gln	Leu	Leu	Asp	Val
	530					535					540				
Leu	Gln	Arg	Ser	Thr	Lys	Pro	Lys	Trp	Arg	Ile	Ile	Val	Gly	Ala	Thr
545					550					555					560
Lys	Cys	Ile	Pro	Lys	Ser	Glu	Leu	Pro	Glu	Glu	Val	Glu	Val	Thr	Thr
				565					570					575	
Leu	Ala	Ser	Thr	Arg	Leu	Trp	Thr	His	Pro	Ser	Asp	Leu	Thr	Ile	Ala
			580					585					590		

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Leu	Ser	Ala	Ser	Thr	Pro	Leu	Tyr	Pro	Pro	Gly	Arg	Ile	Ile	His	Val
595							600					605			
Val	His	Asn	His	Pro	Ala	Glu	Gln	Cys	Cys	Cys	Cys	Glu	Gln	Glu	Glu
610						615					620				
Pro	Thr	Tyr	Phe	Ala	Ile	Trp	Gly	Asp	Asn	Lys	Ala	Phe	Asn	Glu	Val
625					630					635					640
Ile	Ile	Ser	Pro	Ala	Met	Leu	His	Glu	His	Leu	Pro	Tyr	Val	Val	Met
				645					650					655	
Glu	Gly	Leu	Asn	Lys	Val	Leu	Glu	Asn	Tyr	Asn	Lys	Gly	Lys	Thr	Ala
		660						665					670		
Leu	Leu	Ser	Ala	Ala	Lys	Val	Met	Val	Ser	Pro	Thr	Glu	Val	Asp	Leu
		675					680						685		
Thr	Pro	Glu	Leu	Ile	Phe	Gln	Gln	Gln	Pro	Leu	Pro	Thr	Gly	Pro	Pro
		690				695						700			
Met	Pro	Thr	Gly	Leu	Ala	Leu	Glu	Leu	Pro	Thr	Ala	Asp	His	Arg	Asn
705					710					715					720
Ser	Ser	Val	Arg	Ser	Lys	Ser	Gln	Ser	Glu	Met	Ser	Leu	Glu	Gly	Phe
				725					730					735	
Ser	Glu	Gly	Arg	Leu	Leu	Ser	Pro	Val	Val	Ala	Ala	Ala	Ala	Arg	Gln
			740					745					750		
Asp	Pro	Val	Glu	Leu	Leu	Leu	Leu	Ser	Thr	Gln	Glu	Arg	Leu	Ala	Ala
		755					760					765			
Glu	Leu	Gln	Ala	Arg	Arg	Ala	Pro	Leu	Ala	Thr	Met	Glu	Ser	Leu	Ser
		770				775					780				
Asp	Thr	Glu	Ser	Leu	Tyr	Ser	Phe	Asp	Ser	Arg	Arg	Ser	Ser	Gly	Phe
785					790					795					800
Arg	Ser	Ile	Arg	Gly	Ser	Pro	Ser	Leu	His	Ala	Val	Leu	Glu	Arg	Asp
				805					810					815	
Glu	Gly	His	Leu	Phe	Tyr	Ile	Asp	Pro	Ala	Ile	Pro	Glu	Glu	Asn	Pro
			820					825					830		
Ser	Leu	Ser	Ser	Arg	Thr	Glu	Leu	Leu	Ala	Ala	Asp	Ser	Leu	Ser	Lys
			835				840					845			
His	Ser	Gln	Asp	Thr	Gln	Pro	Leu	Glu	Ala	Ala	Leu	Gly	Ser	Gly	Gly
		850				855					860				
Val	Thr	Pro	Glu	Arg	Pro	Pro	Ser	Ala	Ala	Ala	Asn	Asp	Glu	Glu	Glu
865					870					875					880
Glu	Val	Gly	Gly	Gly	Gly	Gly	Gly	Pro	Ala	Ser	Arg	Gly	Glu	Leu	Ala
			885						890					895	
Leu	His	Asn	Gly	Arg	Leu	Gly	Asp	Ser	Pro	Ser	Pro	Gln	Val	Leu	Glu
			900					905					910		
Phe	Ala	Glu	Phe	Ile	Asp	Ser	Leu	Phe	Asn	Leu	Asp	Ser	Lys	Ser	Ser
			915				920					925			
Ser	Phe	Gln	Asp	Leu	Tyr	Cys	Met	Val	Val	Pro	Glu	Ser	Pro	Thr	Ser
					935						940				
Asp	Tyr	Ala	Glu	Gly	Pro	Lys	Ser	Pro	Ser	Gln	Gln	Glu	Ile	Leu	Leu
945					950					955					960
Arg	Ala	Gln	Phe	Glu	Pro	Asn	Leu	Val	Pro	Lys	Pro	Pro	Arg	Leu	Phe
				965					970					975	
Ala	Gly	Ser	Ala	Asp	Pro	Ser	Ser	Gly	Ile	Ser	Leu	Ser	Pro	Ser	Phe
			980					985					990		

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Pro Leu Ser Ser Ser Gly Glu Leu Met Asp Leu Thr Pro Thr Gly Leu
   995                      1000                      1005

```

```

Ser Ser Gln Glu Cys Leu Ala Ala Asp Lys Ile Arg Thr Ser Thr
   1010                      1015                      1020

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```

Pro Thr Gly His Gly Ala Ser Pro Ala Lys Gln Asp Glu Leu Val
   1025                      1030                      1035

```

```

Ile Ser Ala Arg
   1040

```

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<210> SEQ ID NO 8
<211> LENGTH: 125
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(125)
<223> OTHER INFORMATION: OGTA054 = Swiss Prot Accession No. P13164,
Interferon-induced transmembrane protein 1

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<400> SEQUENCE: 8

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```

Met His Lys Glu Glu His Glu Val Ala Val Leu Gly Ala Pro Pro Ser
  1                      5                      10                      15

```

```

Thr Ile Leu Pro Arg Ser Thr Val Ile Asn Ile His Ser Glu Thr Ser
   20                      25                      30

```

```

Val Pro Asp His Val Val Trp Ser Leu Phe Asn Thr Leu Phe Leu Asn
   35                      40                      45

```

```

Trp Cys Cys Leu Gly Phe Ile Ala Phe Ala Tyr Ser Val Lys Ser Arg
   50                      55                      60

```

```

Asp Arg Lys Met Val Gly Asp Val Thr Gly Ala Gln Ala Tyr Ala Ser
   65                      70                      75                      80

```

```

Thr Ala Lys Cys Leu Asn Ile Trp Ala Leu Ile Leu Gly Ile Leu Met
   85                      90                      95

```

```

Thr Ile Gly Phe Ile Leu Leu Val Phe Gly Ser Val Thr Val Tyr
   100                      105                      110

```

```

His Ile Met Leu Gln Ile Ile Gln Glu Lys Arg Gly Tyr
   115                      120                      125

```

```

<210> SEQ ID NO 9
<211> LENGTH: 166
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(166)
<223> OTHER INFORMATION: OGTA066 = Swiss Prot Accession No. Q8TD06,
Anterior gradient protein 3 homolog

```

```

<400> SEQUENCE: 9

```

```

Met Met Leu His Ser Ala Leu Gly Leu Cys Leu Leu Val Thr Val
  1                      5                      10                      15

```

```

Ser Ser Asn Leu Ala Ile Ala Ile Lys Lys Glu Lys Arg Pro Pro Gln
   20                      25                      30

```

```

Thr Leu Ser Arg Gly Trp Gly Asp Asp Ile Thr Trp Val Gln Thr Tyr
   35                      40                      45

```

```

Glu Glu Gly Leu Phe Tyr Ala Gln Lys Ser Lys Lys Pro Leu Met Val
   50                      55                      60

```

```

Ile His His Leu Glu Asp Cys Gln Tyr Ser Gln Ala Leu Lys Lys Val
   65                      70                      75                      80

```

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```

Phe Ala Gln Asn Glu Glu Ile Gln Glu Met Ala Gln Asn Lys Phe Ile
      85                      90                      95

Met Leu Asn Leu Met His Glu Thr Thr Asp Lys Asn Leu Ser Pro Asp
      100                    105                    110

Gly Gln Tyr Val Pro Arg Ile Met Phe Val Asp Pro Ser Leu Thr Val
      115                    120                    125

Arg Ala Asp Ile Ala Gly Arg Tyr Ser Asn Arg Leu Tyr Thr Tyr Glu
      130                    135                    140

Pro Arg Asp Leu Pro Leu Leu Ile Glu Asn Met Lys Lys Ala Leu Arg
      145                    150                    155                    160

Leu Ile Gln Ser Glu Leu
      165

<210> SEQ ID NO 10
<211> LENGTH: 407
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(407)
<223> OTHER INFORMATION: OGTA072 = Swiss Prot Accession No. Q16186,
      Adhesion-regulating molecule 1

<400> SEQUENCE: 10

Met Thr Thr Ser Gly Ala Leu Phe Pro Ser Leu Val Pro Gly Ser Arg
1      5                      10                      15

Gly Ala Ser Asn Lys Tyr Leu Val Glu Phe Arg Ala Gly Lys Met Ser
      20                    25                      30

Leu Lys Gly Thr Thr Val Thr Pro Asp Lys Arg Lys Gly Leu Val Tyr
      35                    40                      45

Ile Gln Gln Thr Asp Asp Ser Leu Ile His Phe Cys Trp Lys Asp Arg
      50                    55                      60

Thr Ser Gly Asn Val Glu Asp Asp Leu Ile Ile Phe Pro Asp Asp Cys
      65                    70                      75                      80

Glu Phe Lys Arg Val Pro Gln Cys Pro Ser Gly Arg Val Tyr Val Leu
      85                    90                      95

Lys Phe Lys Ala Gly Ser Lys Arg Leu Phe Phe Trp Met Gln Glu Pro
      100                   105                   110

Lys Thr Asp Gln Asp Glu Glu His Cys Arg Lys Val Asn Glu Tyr Leu
      115                   120                   125

Asn Asn Pro Pro Met Pro Gly Ala Leu Gly Ala Ser Gly Ser Ser Gly
      130                   135                   140

His Glu Leu Ser Ala Leu Gly Gly Glu Gly Gly Leu Gln Ser Leu Leu
      145                   150                   155                   160

Gly Asn Met Ser His Ser Gln Leu Met Gln Leu Ile Gly Pro Ala Gly
      165                   170                   175

Leu Gly Gly Leu Gly Gly Leu Gly Ala Leu Thr Gly Pro Gly Leu Ala
      180                   185                   190

Ser Leu Leu Gly Ser Ser Gly Pro Pro Gly Ser Ser Ser Ser Ser
      195                   200                   205

Ser Arg Ser Gln Ser Ala Ala Val Thr Pro Ser Ser Thr Thr Ser Ser
      210                   215                   220

Thr Arg Ala Thr Pro Ala Pro Ser Ala Pro Ala Ala Ala Ser Ala Thr
      225                   230                   235                   240

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Ser Pro Ser Pro Ala Pro Ser Ser Gly Asn Gly Ala Ser Thr Ala Ala
      245                      250                      255

Ser Pro Thr Gln Pro Ile Gln Leu Ser Asp Leu Gln Ser Ile Leu Ala
      260                      265                      270

Thr Met Asn Val Pro Ala Gly Pro Ala Gly Gly Gln Gln Val Asp Leu
      275                      280                      285

Ala Ser Val Leu Thr Pro Glu Ile Met Ala Pro Ile Leu Ala Asn Ala
      290                      295                      300

Asp Val Gln Glu Arg Leu Leu Pro Tyr Leu Pro Ser Gly Glu Ser Leu
      305                      310                      315

Pro Gln Thr Ala Asp Glu Ile Gln Asn Thr Leu Thr Ser Pro Gln Phe
      325                      330                      335

Gln Gln Ala Leu Gly Met Phe Ser Ala Ala Leu Ala Ser Gly Gln Leu
      340                      345                      350

Gly Pro Leu Met Cys Gln Phe Gly Leu Pro Ala Glu Ala Val Glu Ala
      355                      360                      365

Ala Asn Lys Gly Asp Val Glu Ala Phe Ala Lys Ala Met Gln Asn Asn
      370                      375                      380

Ala Lys Pro Glu Gln Lys Glu Gly Asp Thr Lys Asp Lys Lys Asp Glu
      385                      390                      395                      400

Glu Glu Asp Met Ser Leu Asp
      405

```

```

<210> SEQ ID NO 11
<211> LENGTH: 1587
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(1587)
<223> OTHER INFORMATION: OGTA074 = Swiss Prot Accession No. 000508,
Latent TGF-beta binding protein-4

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<400> SEQUENCE: 11

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```

Met Gly Asp Val Lys Ala Leu Leu Phe Val Ala Ala Ala Arg Ala Arg
1      5      10      15

Arg Leu Gly Gly Ala Ala Ala Ser Glu Ser Leu Ala Val Ser Glu Ala
      20      25      30

Phe Cys Arg Val Arg Ser Cys Gln Pro Lys Lys Cys Ala Gly Pro Gln
      35      40      45

Arg Cys Leu Asn Pro Val Pro Ala Val Pro Ser Pro Ser Pro Ser Val
      50      55      60

Arg Lys Arg Gln Val Ser Leu Asn Trp Gln Pro Leu Thr Leu Gln Glu
      65      70      75      80

Ala Arg Ala Leu Leu Lys Arg Arg Arg Pro Arg Gly Pro Gly Gly Arg
      85      90      95

Gly Leu Leu Arg Arg Arg Pro Pro Gln Arg Ala Pro Ala Gly Lys Ala
      100     105     110

Pro Val Leu Cys Pro Leu Ile Cys His Asn Gly Gly Val Cys Val Lys
      115     120     125

Pro Asp Arg Cys Leu Cys Pro Pro Asp Phe Ala Gly Lys Phe Cys Gln
      130     135     140

Leu His Ser Ser Gly Ala Arg Pro Pro Ala Pro Ala Val Pro Gly Leu
      145     150     155     160

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Thr	Arg	Ser	Val	Tyr	Thr	Met	Pro	Leu	Ala	Asn	His	Arg	Asp	Asp	Glu
			165						170					175	
His	Gly	Val	Ala	Ser	Met	Val	Ser	Val	His	Val	Glu	His	Pro	Gln	Glu
		180						185					190		
Ala	Ser	Val	Val	Val	His	Gln	Val	Glu	Arg	Val	Ser	Gly	Pro	Trp	Glu
		195					200					205			
Glu	Ala	Asp	Ala	Glu	Ala	Val	Ala	Arg	Ala	Glu	Ala	Ala	Ala	Arg	Ala
	210					215					220				
Glu	Ala	Ala	Ala	Pro	Tyr	Thr	Val	Leu	Ala	Gln	Ser	Ala	Pro	Arg	Glu
225				230						235					240
Asp	Gly	Tyr	Ser	Asp	Ala	Ser	Gly	Phe	Gly	Tyr	Cys	Phe	Arg	Glu	Leu
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Arg	Gly	Gly	Glu	Cys	Ala	Ser	Pro	Leu	Pro	Gly	Leu	Arg	Thr	Gln	Glu
			260					265					270		
Val	Cys	Cys	Arg	Gly	Ala	Gly	Leu	Ala	Trp	Gly	Val	His	Asp	Cys	Gln
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Leu	Cys	Ser	Glu	Arg	Leu	Gly	Asn	Ser	Glu	Arg	Val	Ser	Ala	Pro	Asp
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Gly	Pro	Cys	Pro	Thr	Gly	Phe	Glu	Arg	Val	Asn	Gly	Ser	Cys	Glu	Asp
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Val	Asp	Glu	Cys	Ala	Thr	Gly	Gly	Arg	Cys	Gln	His	Gly	Glu	Cys	Ala
			325					330						335	
Asn	Thr	Arg	Gly	Gly	Tyr	Thr	Cys	Val	Cys	Pro	Asp	Gly	Phe	Leu	Leu
		340						345					350		
Asp	Ser	Ser	Arg	Ser	Ser	Cys	Ile	Ser	Gln	His	Val	Ile	Ser	Glu	Ala
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Lys	Gly	Pro	Cys	Phe	Arg	Val	Leu	Arg	Asp	Gly	Gly	Cys	Ser	Leu	Pro
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Ile	Leu	Arg	Asn	Ile	Thr	Lys	Gln	Ile	Cys	Cys	Cys	Ser	Arg	Val	Gly
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Lys	Ala	Trp	Gly	Arg	Gly	Cys	Gln	Leu	Cys	Pro	Pro	Phe	Gly	Ser	Glu
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Gly	Phe	Arg	Glu	Ile	Cys	Pro	Ala	Gly	Pro	Gly	Tyr	His	Tyr	Ser	Ala
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Ser	Asp	Leu	Arg	Tyr	Asn	Thr	Arg	Pro	Leu	Gly	Gln	Glu	Pro	Pro	Arg
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Val	Ser	Leu	Ser	Gln	Pro	Arg	Thr	Leu	Pro	Ala	Thr	Ser	Arg	Pro	Ser
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Ala	Gly	Phe	Leu	Pro	Thr	His	Arg	Leu	Glu	Pro	Arg	Pro	Glu	Pro	Arg
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Pro	Asp	Pro	Arg	Pro	Gly	Pro	Glu	Leu	Pro	Leu	Pro	Ser	Ile	Pro	Ala
			485					490						495	
Trp	Thr	Gly	Pro	Glu	Ile	Pro	Glu	Ser	Gly	Pro	Ser	Ser	Gly	Met	Cys
		500						505					510		
Gln	Arg	Asn	Pro	Gln	Val	Cys	Gly	Pro	Gly	Arg	Cys	Ile	Ser	Arg	Pro
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Ser	Gly	Tyr	Thr	Cys	Ala	Cys	Asp	Ser	Gly	Phe	Arg	Leu	Ser	Pro	Gln
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Gly	Thr	Arg	Cys	Ile	Asp	Val	Asp	Glu	Cys	Arg	Arg	Val	Pro	Pro	Pro
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Cys	Ala	Pro	Gly	Arg	Cys	Glu	Asn	Ser	Pro	Gly	Ser	Phe	Arg	Cys	Val	565	570	575
Cys	Gly	Pro	Gly	Phe	Arg	Ala	Gly	Pro	Arg	Ala	Ala	Glu	Cys	Leu	Asp	580	585	590
Val	Asp	Glu	Cys	His	Arg	Val	Pro	Pro	Pro	Cys	Asp	Leu	Gly	Arg	Cys	595	600	605
Glu	Asn	Thr	Pro	Gly	Ser	Phe	Leu	Cys	Val	Cys	Pro	Ala	Gly	Tyr	Gln	610	615	620
Ala	Ala	Pro	His	Gly	Ala	Ser	Cys	Gln	Asp	Val	Asp	Glu	Cys	Thr	Gln	625	630	635
Ser	Pro	Gly	Leu	Cys	Gly	Arg	Gly	Ala	Cys	Lys	Asn	Leu	Pro	Gly	Ser	645	650	655
Phe	Arg	Cys	Val	Cys	Pro	Ala	Gly	Phe	Arg	Gly	Ser	Ala	Cys	Glu	Glu	660	665	670
Asp	Val	Asp	Glu	Cys	Ala	Gln	Glu	Pro	Pro	Pro	Cys	Gly	Pro	Gly	Arg	675	680	685
Cys	Asp	Asn	Thr	Ala	Gly	Ser	Phe	His	Cys	Ala	Cys	Pro	Ala	Gly	Phe	690	695	700
Arg	Ser	Arg	Gly	Pro	Gly	Ala	Pro	Cys	Gln	Asp	Val	Asp	Glu	Cys	Ala	705	710	715
Arg	Ser	Pro	Pro	Pro	Cys	Thr	Tyr	Gly	Arg	Cys	Glu	Asn	Thr	Glu	Gly	725	730	735
Ser	Phe	Gln	Cys	Val	Cys	Pro	Met	Gly	Phe	Gln	Pro	Asn	Thr	Ala	Gly	740	745	750
Ser	Glu	Cys	Glu	Asp	Val	Asp	Glu	Cys	Glu	Asn	His	Leu	Ala	Cys	Pro	755	760	765
Gly	Gln	Glu	Cys	Val	Asn	Ser	Pro	Gly	Ser	Phe	Gln	Cys	Arg	Thr	Cys	770	775	780
Pro	Ser	Gly	His	His	Leu	His	Arg	Gly	Arg	Cys	Thr	Asp	Val	Asp	Glu	785	790	795
Cys	Ser	Ser	Gly	Ala	Pro	Pro	Cys	Gly	Pro	His	Gly	His	Cys	Thr	Asn	805	810	815
Thr	Glu	Gly	Ser	Phe	Arg	Cys	Ser	Cys	Ala	Pro	Gly	Tyr	Arg	Ala	Pro	820	825	830
Ser	Gly	Arg	Pro	Gly	Pro	Cys	Ala	Asp	Val	Asn	Glu	Cys	Leu	Glu	Gly	835	840	845
Asp	Phe	Cys	Phe	Pro	His	Gly	Glu	Cys	Leu	Asn	Thr	Asp	Gly	Ser	Phe	850	855	860
Ala	Cys	Thr	Cys	Ala	Pro	Gly	Tyr	Arg	Pro	Gly	Pro	Arg	Gly	Ala	Ser	865	870	875
Cys	Leu	Asp	Val	Asp	Glu	Cys	Ser	Glu	Glu	Asp	Leu	Cys	Gln	Ser	Gly	885	890	895
Ile	Cys	Thr	Asn	Thr	Asp	Gly	Ser	Phe	Glu	Cys	Ile	Cys	Pro	Pro	Gly	900	905	910
His	Arg	Ala	Gly	Pro	Asp	Leu	Ala	Ser	Cys	Leu	Asp	Val	Asp	Glu	Cys	915	920	925
Arg	Glu	Arg	Gly	Pro	Ala	Leu	Cys	Gly	Ser	Gln	Arg	Cys	Glu	Asn	Ser	930	935	940
Pro	Gly	Ser	Tyr	Arg	Cys	Val	Arg	Asp	Cys	Asp	Pro	Gly	Tyr	His	Ala	945	950	955
Gly	Pro	Glu	Gly	Thr	Cys	Asp	Asp	Val	Asp	Glu	Cys	Gln	Glu	Tyr	Gly			

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Arg	Cys	Thr	Pro	Ala	Cys	Asp	Pro	Gly	Tyr	Gln	Pro	Thr	Pro	Gly	Gly
			995					1000					1005		
Gly	Cys	Gln	Asp	Val	Asp	Glu	Cys	Arg	Asn	Arg	Ser	Phe	Cys	Gly	
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Leu	Cys	Glu	Asn	Val	Glu	Gly	Ser	Phe	Leu	Cys	Val	Cys	Pro	Asn	
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Ser	Pro	Glu	Glu	Phe	Asp	Pro	Met	Thr	Gly	Arg	Cys	Val	Pro	Pro	
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Ala	Ser	Pro	Val	Leu	Pro	Ala	Arg	Pro	Pro	Pro	Pro	Pro	Leu	Pro	
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Tyr	Leu	Ala	Pro	Ser	Gly	Asp	Leu	Ser	Leu	Arg	Arg	Asp	Val	Asp	
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Val	Asn	Thr	Ala	Pro	Gly	Tyr	Ser	Cys	Tyr	Cys	Ser	Asn	Gly	Tyr	
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Ala	Asp	Glu	Glu	Pro	Ala	Cys	Glu	Gly	Gly	Arg	Cys	Val	Asn	Thr	
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Gly	Ser	Gln	Arg	Arg	Cys	Val	Ser	Asn	Glu	Ser	Gln	Ser	Leu	Asp	
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Cys	Ser	His	Pro	Arg	Leu	Asp	Arg	Gln	Ala	Thr	Tyr	Thr	Glu	Cys	
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Cys	Cys	Leu	Tyr	Gly	Glu	Ala	Trp	Gly	Met	Asp	Cys	Ala	Leu	Cys	
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Pro Ala  Gln Asp Ser Asp Asp  Phe Glu Ala Leu Cys  Asn Val Leu
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Arg Pro  Pro Ala Tyr Ser Pro  Pro Arg Pro Gly Gly  Phe Gly Leu
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Pro Tyr  Glu Tyr Gly Pro  Asp  Leu Gly Pro Pro  Tyr  Gln Gly Leu
1385                      1390                      1395

Pro Tyr  Gly Pro Glu Leu Tyr  Pro Pro Pro Ala  Leu  Pro Tyr Asp
1400                      1405                      1410

Pro Tyr  Pro Pro Pro Pro  Gly  Pro Phe Ala Arg Arg  Glu Ala Pro
1415                      1420                      1425

Tyr Gly  Ala Pro Arg Phe  Asp  Met Pro Asp Phe  Glu  Asp Asp Gly
1430                      1435                      1440

Gly Pro  Tyr Gly Glu Ser  Glu  Ala Pro Ala Pro  Pro  Gly Pro Gly
1445                      1450                      1455

Thr Arg  Trp Pro Tyr Arg  Ser  Arg Asp Thr Arg Arg  Ser Phe Pro
1460                      1465                      1470

Glu Pro  Glu Glu Pro Pro  Glu  Gly Gly Ser Tyr  Ala  Gly Ser Leu
1475                      1480                      1485

Ala Glu  Pro Tyr Glu Glu  Leu  Glu Ala Glu Glu  Cys  Gly Ile Leu
1490                      1495                      1500

Asp Gly  Cys Thr Asn Gly Arg  Cys Val Arg Val Pro  Glu Gly Phe
1505                      1510                      1515

Thr Cys  Arg Cys Phe Asp  Gly  Tyr Arg Leu Asp Met  Thr Arg Met
1520                      1525                      1530

Ala Cys  Val Asp Ile Asn Glu  Cys Asp Glu Ala Glu  Ala Ala Ser
1535                      1540                      1545

Pro Leu  Cys Val Asn Ala Arg  Cys Leu Asn Thr Asp  Gly Ser Phe
1550                      1555                      1560

Arg Cys  Ile Cys Arg Pro  Gly  Phe Ala Pro Thr His  Gln Pro His
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His Cys  Ala Pro Ala Arg Pro  Arg Ala
1580                      1585

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<210> SEQ ID NO 12
<211> LENGTH: 1722
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(1722)
<223> OTHER INFORMATION: OGTA076 = Swiss Prot Accession No. 060449,
    Lymphocyte antigen 75

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<400> SEQUENCE: 12

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20     25     30

Asn Asp Pro Phe Thr Ile Val His Gly Asn Thr Gly Lys Cys Ile Lys
35     40     45

Pro Val Tyr Gly Trp Ile Val Ala Asp Asp Cys Asp Glu Thr Glu Asp
50     55     60

Lys Leu Trp Lys Trp Val Ser Gln His Arg Leu Phe His Leu His Ser
65     70     75     80

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Gln	Lys	Cys	Leu	Gly	Leu	Asp	Ile	Thr	Lys	Ser	Val	Asn	Glu	Leu	Arg	85	90	95
Met	Phe	Ser	Cys	Asp	Ser	Ser	Ala	Met	Leu	Trp	Trp	Lys	Cys	Glu	His	100	105	110
His	Ser	Leu	Tyr	Gly	Ala	Ala	Arg	Tyr	Arg	Leu	Ala	Leu	Lys	Asp	Gly	115	120	125
His	Gly	Thr	Ala	Ile	Ser	Asn	Ala	Ser	Asp	Val	Trp	Lys	Lys	Gly	Gly	130	135	140
Ser	Glu	Glu	Ser	Leu	Cys	Asp	Gln	Pro	Tyr	His	Glu	Ile	Tyr	Thr	Arg	145	150	155
Asp	Gly	Asn	Ser	Tyr	Gly	Arg	Pro	Cys	Glu	Phe	Pro	Phe	Leu	Ile	Asp	165	170	175
Gly	Thr	Trp	His	His	Asp	Cys	Ile	Leu	Asp	Glu	Asp	His	Ser	Gly	Pro	180	185	190
Trp	Cys	Ala	Thr	Thr	Leu	Asn	Tyr	Glu	Tyr	Asp	Arg	Lys	Trp	Gly	Ile	195	200	205
Cys	Leu	Lys	Pro	Glu	Asn	Gly	Cys	Glu	Asp	Asn	Trp	Glu	Lys	Asn	Glu	210	215	220
Gln	Phe	Gly	Ser	Cys	Tyr	Gln	Phe	Asn	Thr	Gln	Thr	Ala	Leu	Ser	Trp	225	230	235
Lys	Glu	Ala	Tyr	Val	Ser	Cys	Gln	Asn	Gln	Gly	Ala	Asp	Leu	Leu	Ser	245	250	255
Ile	Asn	Ser	Ala	Ala	Glu	Leu	Thr	Tyr	Leu	Lys	Glu	Lys	Glu	Gly	Ile	260	265	270
Ala	Lys	Ile	Phe	Trp	Ile	Gly	Leu	Asn	Gln	Leu	Tyr	Ser	Ala	Arg	Gly	275	280	285
Trp	Glu	Trp	Ser	Asp	His	Lys	Pro	Leu	Asn	Phe	Leu	Asn	Trp	Asp	Pro	290	295	300
Asp	Arg	Pro	Ser	Ala	Pro	Thr	Ile	Gly	Gly	Ser	Ser	Cys	Ala	Arg	Met	305	310	315
Asp	Ala	Glu	Ser	Gly	Leu	Trp	Gln	Ser	Phe	Ser	Cys	Glu	Ala	Gln	Leu	325	330	335
Pro	Tyr	Val	Cys	Arg	Lys	Pro	Leu	Asn	Thr	Val	Glu	Leu	Thr	Asp		340	345	350
Val	Trp	Thr	Tyr	Ser	Asp	Thr	Arg	Cys	Asp	Ala	Gly	Trp	Leu	Pro	Asn	355	360	365
Asn	Gly	Phe	Cys	Tyr	Leu	Leu	Val	Asn	Glu	Ser	Asn	Ser	Trp	Asp	Lys	370	375	380
Ala	His	Ala	Lys	Cys	Lys	Ala	Phe	Ser	Ser	Asp	Leu	Ile	Ser	Ile	His	385	390	395
Ser	Leu	Ala	Asp	Val	Glu	Val	Val	Val	Thr	Lys	Leu	His	Asn	Glu	Asp	405	410	415
Ile	Lys	Glu	Glu	Val	Trp	Ile	Gly	Leu	Lys	Asn	Ile	Asn	Ile	Pro	Thr	420	425	430
Leu	Phe	Gln	Trp	Ser	Asp	Gly	Thr	Glu	Val	Thr	Leu	Thr	Tyr	Trp	Asp	435	440	445
Glu	Asn	Glu	Pro	Asn	Val	Pro	Tyr	Asn	Lys	Thr	Pro	Asn	Cys	Val	Ser	450	455	460
Tyr	Leu	Gly	Glu	Leu	Gly	Gln	Trp	Lys	Val	Gln	Ser	Cys	Glu	Glu	Lys	465	470	475

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Leu	Lys	Tyr	Val	Cys	Lys	Arg	Lys	Gly	Glu	Lys	Leu	Asn	Asp	Ala	Ser
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Ser	Asp	Lys	Met	Cys	Pro	Pro	Asp	Glu	Gly	Trp	Lys	Arg	His	Gly	Glu
			500					505					510		
Thr	Cys	Tyr	Lys	Ile	Tyr	Glu	Asp	Glu	Val	Pro	Phe	Gly	Thr	Asn	Cys
		515					520					525			
Asn	Leu	Thr	Ile	Thr	Ser	Arg	Phe	Glu	Gln	Glu	Tyr	Leu	Asn	Asp	Leu
	530					535					540				
Met	Lys	Lys	Tyr	Asp	Lys	Ser	Leu	Arg	Lys	Tyr	Phe	Trp	Thr	Gly	Leu
545					550					555					560
Arg	Asp	Val	Asp	Ser	Cys	Gly	Glu	Tyr	Asn	Trp	Ala	Thr	Val	Gly	Gly
				565					570					575	
Arg	Arg	Arg	Ala	Val	Thr	Phe	Ser	Asn	Trp	Asn	Phe	Leu	Glu	Pro	Ala
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Ser	Pro	Gly	Gly	Cys	Val	Ala	Met	Ser	Thr	Gly	Lys	Ser	Val	Gly	Lys
		595					600					605			
Trp	Glu	Val	Lys	Asp	Cys	Arg	Ser	Phe	Lys	Ala	Leu	Ser	Ile	Cys	Lys
	610					615					620				
Lys	Met	Ser	Gly	Pro	Leu	Gly	Pro	Glu	Glu	Ala	Ser	Pro	Lys	Pro	Asp
625					630					635					640
Asp	Pro	Cys	Pro	Glu	Gly	Trp	Gln	Ser	Phe	Pro	Ala	Ser	Leu	Ser	Cys
				645					650					655	
Tyr	Lys	Val	Phe	His	Ala	Glu	Arg	Ile	Val	Arg	Lys	Arg	Asn	Trp	Glu
			660					665					670		
Glu	Ala	Glu	Arg	Phe	Cys	Gln	Ala	Leu	Gly	Ala	His	Leu	Ser	Ser	Phe
		675				680						685			
Ser	His	Val	Asp	Glu	Ile	Lys	Glu	Phe	Leu	His	Phe	Leu	Thr	Asp	Gln
		690				695					700				
Phe	Ser	Gly	Gln	His	Trp	Leu	Trp	Ile	Gly	Leu	Asn	Lys	Arg	Ser	Pro
705					710					715					720
Asp	Leu	Gln	Gly	Ser	Trp	Gln	Trp	Ser	Asp	Arg	Thr	Pro	Val	Ser	Thr
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Ile	Ile	Met	Pro	Asn	Glu	Phe	Gln	Gln	Asp	Tyr	Asp	Ile	Arg	Asp	Cys
		740						745					750		
Ala	Ala	Val	Lys	Val	Phe	His	Arg	Pro	Trp	Arg	Arg	Gly	Trp	His	Phe
		755					760					765			
Tyr	Asp	Asp	Arg	Glu	Phe	Ile	Tyr	Leu	Arg	Pro	Phe	Ala	Cys	Asp	Thr
	770					775					780				
Lys	Leu	Glu	Trp	Val	Cys	Gln	Ile	Pro	Lys	Gly	Arg	Thr	Pro	Lys	Thr
785					790					795					800
Pro	Asp	Trp	Tyr	Asn	Pro	Asp	Arg	Ala	Gly	Ile	His	Gly	Pro	Pro	Leu
				805					810					815	
Ile	Ile	Glu	Gly	Ser	Glu	Tyr	Trp	Phe	Val	Ala	Asp	Leu	His	Leu	Asn
			820					825					830		
Tyr	Glu	Glu	Ala	Val	Leu	Tyr	Cys	Ala	Ser	Asn	His	Ser	Phe	Leu	Ala
		835					840					845			
Thr	Ile	Thr	Ser	Phe	Val	Gly	Leu	Lys	Ala	Ile	Lys	Asn	Lys	Ile	Ala
		850				855					860				
Asn	Ile	Ser	Gly	Asp	Gly	Gln	Lys	Trp	Trp	Ile	Arg	Ile	Ser	Glu	Trp
865					870					875					880
Pro	Ile	Asp	Asp	His	Phe	Thr	Tyr	Ser	Arg	Tyr	Pro	Trp	His	Arg	Phe

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885					890					895					
Pro	Val	Thr	Phe	Gly	Glu	Glu	Cys	Leu	Tyr	Met	Ser	Ala	Lys	Thr	Trp
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Leu	Ile	Asp	Leu	Gly	Lys	Pro	Thr	Asp	Cys	Ser	Thr	Lys	Leu	Pro	Phe
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Ser	Ala	Ala	Lys	Val	Gln	Cys	Ser	Glu	Gln	Trp	Ile	Pro	Phe	Gln	Asn
		945					950					955			960
Lys	Cys	Phe	Leu	Lys	Ile	Lys	Pro	Val	Ser	Leu	Thr	Phe	Ser	Gln	Ala
			965					970						975	
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			980					985					990		
Gln	Ile	Glu	Gln	Asp	Phe	Ile	Thr	Ser	Leu	Leu	Pro	Asp	Met	Glu	Ala
		995					1000					1005			
Thr	Leu	Trp	Ile	Gly	Leu	Arg	Trp	Thr	Ala	Tyr	Glu	Lys	Ile	Asn	
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Gln	Thr	Leu	Gln	Asn	Ala	Ser	Glu	Thr	Val	Lys	Tyr	Leu	Asn	Asn	
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Ile	Cys	Tyr	Tyr	Ser	Gly	Asn	Glu	Thr	Glu	Lys	Glu	Val	Lys	Pro	
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Val	Asp	Ser	Val	Lys	Cys	Pro	Ser	Pro	Val	Leu	Asn	Thr	Pro	Trp	
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Ile	Pro	Phe	Gln	Asn	Cys	Cys	Tyr	Asn	Phe	Ile	Ile	Thr	Lys	Asn	
	1250					1255					1260				
Arg	His	Met	Ala	Thr	Thr	Gln	Asp	Glu	Val	His	Thr	Lys	Cys	Gln	
	1265					1270					1275				

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Lys	Leu	Asn	Pro	Lys	Ser	His	Ile	Leu	Ser	Ile	Arg	Asp	Glu	Lys
1280						1285						1290		
Glu	Asn	Asn	Phe	Val	Leu	Glu	Gln	Leu	Leu	Tyr	Phe	Asn	Tyr	Met
1295						1300						1305		
Ala	Ser	Trp	Val	Met	Leu	Gly	Ile	Thr	Tyr	Arg	Asn	Asn	Ser	Leu
1310						1315						1320		
Met	Trp	Phe	Asp	Lys	Thr	Pro	Leu	Ser	Tyr	Thr	His	Trp	Arg	Ala
1325						1330						1335		
Gly	Arg	Pro	Thr	Ile	Lys	Asn	Glu	Lys	Phe	Leu	Ala	Gly	Leu	Ser
1340						1345						1350		
Thr	Asp	Gly	Phe	Trp	Asp	Ile	Gln	Thr	Phe	Lys	Val	Ile	Glu	Glu
1355						1360						1365		
Ala	Val	Tyr	Phe	His	Gln	His	Ser	Ile	Leu	Ala	Cys	Lys	Ile	Glu
1370						1375						1380		
Met	Val	Asp	Tyr	Lys	Glu	Glu	His	Asn	Thr	Thr	Leu	Pro	Gln	Phe
1385						1390						1395		
Met	Pro	Tyr	Glu	Asp	Gly	Ile	Tyr	Ser	Val	Ile	Gln	Lys	Lys	Val
1400						1405						1410		
Thr	Trp	Tyr	Glu	Ala	Leu	Asn	Met	Cys	Ser	Gln	Ser	Gly	Gly	His
1415						1420						1425		
Leu	Ala	Ser	Val	His	Asn	Gln	Asn	Gly	Gln	Leu	Phe	Leu	Glu	Asp
1430						1435						1440		
Ile	Val	Lys	Arg	Asp	Gly	Phe	Pro	Leu	Trp	Val	Gly	Leu	Ser	Ser
1445						1450						1455		
His	Asp	Gly	Ser	Glu	Ser	Ser	Phe	Glu	Trp	Ser	Asp	Gly	Ser	Thr
1460						1465						1470		
Phe	Asp	Tyr	Ile	Pro	Trp	Lys	Gly	Gln	Thr	Ser	Pro	Gly	Asn	Cys
1475						1480						1485		
Val	Leu	Leu	Asp	Pro	Lys	Gly	Thr	Trp	Lys	His	Glu	Lys	Cys	Asn
1490						1495						1500		
Ser	Val	Lys	Asp	Gly	Ala	Ile	Cys	Tyr	Lys	Pro	Thr	Lys	Ser	Lys
1505						1510						1515		
Lys	Leu	Ser	Arg	Leu	Thr	Tyr	Ser	Ser	Arg	Cys	Pro	Ala	Ala	Lys
1520						1525						1530		
Glu	Asn	Gly	Ser	Arg	Trp	Ile	Gln	Tyr	Lys	Gly	His	Cys	Tyr	Lys
1535						1540						1545		
Ser	Asp	Gln	Ala	Leu	His	Ser	Phe	Ser	Glu	Ala	Lys	Lys	Leu	Cys
1550						1555						1560		
Ser	Lys	His	Asp	His	Ser	Ala	Thr	Ile	Val	Ser	Ile	Lys	Asp	Glu
1565						1570						1575		
Asp	Glu	Asn	Lys	Phe	Val	Ser	Arg	Leu	Met	Arg	Glu	Asn	Asn	Asn
1580						1585						1590		
Ile	Thr	Met	Arg	Val	Trp	Leu	Gly	Leu	Ser	Gln	His	Ser	Val	Asp
1595						1600						1605		
Gln	Ser	Trp	Ser	Trp	Leu	Asp	Gly	Ser	Glu	Val	Thr	Phe	Val	Lys
1610						1615						1620		
Trp	Glu	Asn	Lys	Ser	Lys	Ser	Gly	Val	Gly	Arg	Cys	Ser	Met	Leu
1625						1630						1635		
Ile	Ala	Ser	Asn	Glu	Thr	Trp	Lys	Lys	Val	Glu	Cys	Glu	His	Gly
1640						1645						1650		

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Phe Gly  Arg Val Val Cys Lys  Val Pro Leu Gly Pro  Asp Tyr Thr
1655                      1660                      1665

Ala Ile  Ala Ile Ile Val Ala  Thr Leu Ser Ile Leu  Val Leu Met
1670                      1675                      1680

Gly Gly  Leu Ile Trp Phe Leu  Phe Gln Arg His Arg  Leu His Leu
1685                      1690                      1695

Ala Gly  Phe Ser Ser Val Arg  Tyr Ala Gln Gly Val  Asn Glu Asp
1700                      1705                      1710

Glu Ile  Met Leu Pro Ser Phe  His Asp
1715                      1720

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<210> SEQ ID NO 13
<211> LENGTH: 355
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(355)
<223> OTHER INFORMATION: OGTA085 = Swiss Prot Accession No. Q14318,
38 kDa FK506-binding protein homologue

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<400> SEQUENCE: 13

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Met Gly Gln Pro Pro Ala Glu Glu Ala Glu Gln Pro Gly Ala Leu Ala
1      5      10      15

Arg Glu Phe Leu Ala Ala Met Glu Pro Glu Pro Ala Pro Ala Pro Ala
20     25     30

Pro Glu Glu Trp Leu Asp Ile Leu Gly Asn Gly Leu Leu Arg Lys Lys
35     40     45

Thr Leu Val Pro Gly Pro Pro Gly Ser Ser Arg Pro Val Lys Gly Gln
50     55     60

Val Val Thr Val His Leu Gln Thr Ser Leu Glu Asn Gly Thr Arg Val
65     70     75     80

Gln Glu Glu Pro Glu Leu Val Phe Thr Leu Gly Asp Cys Asp Val Ile
85     90     95

Gln Ala Leu Asp Leu Ser Val Pro Leu Met Asp Val Gly Glu Thr Ala
100    105    110

Met Val Thr Ala Asp Ser Lys Tyr Cys Tyr Gly Pro Gln Gly Arg Ser
115    120    125

Pro Tyr Ile Pro Pro His Ala Ala Leu Cys Leu Glu Val Thr Leu Lys
130    135    140

Thr Ala Val Asp Gly Pro Asp Leu Glu Met Leu Thr Gly Gln Glu Arg
145    150    155    160

Val Ala Leu Ala Asn Arg Lys Arg Glu Cys Gly Asn Ala His Tyr Gln
165    170    175

Arg Ala Asp Phe Val Leu Ala Ala Asn Ser Tyr Asp Leu Ala Ile Lys
180    185    190

Ala Ile Thr Ser Ser Ala Lys Val Asp Met Thr Phe Glu Glu Glu Ala
195    200    205

Gln Leu Leu Gln Leu Lys Val Lys Cys Leu Asn Asn Leu Ala Ala Ser
210    215    220

Gln Leu Lys Leu Asp His Tyr Arg Ala Ala Leu Arg Ser Cys Ser Leu
225    230    235    240

Val Leu Glu His Gln Pro Asp Asn Ile Lys Ala Leu Phe Arg Lys Gly
245    250    255

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Lys Val Leu Ala Gln Gln Gly Glu Tyr Ser Glu Ala Ile Pro Ile Leu
 260 265 270
 Arg Ala Ala Leu Lys Leu Glu Pro Ser Asn Lys Thr Ile His Ala Glu
 275 280 285
 Leu Ser Lys Leu Val Lys Lys His Ala Ala Gln Arg Ser Thr Glu Thr
 290 295 300
 Ala Leu Tyr Arg Lys Met Leu Gly Asn Pro Ser Arg Leu Pro Ala Lys
 305 310 315 320
 Cys Pro Gly Lys Gly Ala Trp Ser Ile Pro Trp Lys Trp Leu Phe Gly
 325 330 335
 Ala Thr Ala Val Ala Leu Gly Gly Val Ala Leu Ser Val Val Ile Ala
 340 345 350
 Ala Arg Asn
 355

<210> SEQ ID NO 14
 <211> LENGTH: 587
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapiens
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (1)..(587)
 <223> OTHER INFORMATION: OGTA087 = Swiss Prot Accession No. 094935,
 KIAA0851 protein

<400> SEQUENCE: 14

Met Ala Thr Ala Ala Tyr Glu Gln Leu Lys Leu His Ile Thr Pro Glu
 1 5 10 15
 Lys Phe Tyr Val Glu Ala Cys Asp Asp Gly Ala Asp Asp Val Leu Thr
 20 25 30
 Ile Asp Arg Val Ser Thr Glu Val Thr Leu Ala Val Lys Lys Asp Val
 35 40 45
 Pro Pro Ser Ala Val Thr Arg Pro Ile Phe Gly Ile Leu Gly Thr Ile
 50 55 60
 His Leu Val Ala Gly Asn Tyr Leu Ile Val Ile Thr Lys Lys Ile Lys
 65 70 75 80
 Val Gly Glu Phe Phe Ser His Val Val Trp Lys Ala Thr Asp Phe Asp
 85 90 95
 Val Leu Ser Tyr Lys Lys Thr Met Leu His Leu Thr Asp Ile Gln Leu
 100 105 110
 Gln Asp Asn Lys Thr Phe Leu Ala Met Leu Asn His Val Leu Asn Val
 115 120 125
 Asp Gly Phe Tyr Phe Ser Thr Thr Tyr Asp Leu Thr His Thr Leu Gln
 130 135 140
 Arg Leu Ser Asn Thr Ser Pro Glu Phe Gln Glu Met Ser Leu Leu Glu
 145 150 155 160
 Arg Ala Asp Gln Arg Phe Val Trp Asn Gly His Leu Leu Arg Glu Leu
 165 170 175
 Ser Ala Gln Pro Glu Val His Arg Phe Ala Leu Pro Val Leu His Gly
 180 185 190
 Phe Ile Thr Met His Ser Cys Ser Ile Asn Gly Lys Tyr Phe Asp Trp
 195 200 205
 Ile Leu Ile Ser Arg Arg Ser Cys Phe Arg Ala Gly Val Arg Tyr Tyr
 210 215 220

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Val	Arg	Gly	Ile	Asp	Ser	Glu	Gly	His	Ala	Ala	Asn	Phe	Val	Glu	Thr	225	230	235	240
Glu	Gln	Ile	Val	His	Tyr	Asn	Gly	Ser	Lys	Ala	Ser	Phe	Val	Gln	Thr	245	250	255	
Arg	Gly	Ser	Ile	Pro	Val	Phe	Trp	Ser	Gln	Arg	Pro	Asn	Leu	Lys	Tyr	260	265	270	
Lys	Pro	Leu	Pro	Gln	Ile	Ser	Lys	Val	Ala	Asn	His	Met	Asp	Gly	Phe	275	280	285	
Gln	Arg	His	Phe	Asp	Ser	Gln	Val	Ile	Ile	Tyr	Gly	Lys	Gln	Val	Ile	290	295	300	
Ile	Asn	Leu	Ile	Asn	Gln	Lys	Gly	Ser	Glu	Lys	Pro	Leu	Glu	Gln	Thr	305	310	315	320
Phe	Ala	Thr	Met	Val	Ser	Ser	Leu	Gly	Ser	Gly	Met	Met	Arg	Tyr	Ile	325	330	335	
Ala	Phe	Asp	Phe	His	Lys	Glu	Cys	Lys	Asn	Met	Arg	Trp	Asp	Arg	Leu	340	345	350	
Ser	Ile	Leu	Leu	Asp	Gln	Val	Ala	Glu	Met	Gln	Asp	Glu	Leu	Ser	Tyr	355	360	365	
Phe	Leu	Val	Asp	Ser	Ala	Gly	Gln	Val	Val	Ala	Asn	Gln	Glu	Gly	Val	370	375	380	
Phe	Arg	Ser	Asn	Cys	Met	Asp	Cys	Leu	Asp	Arg	Thr	Asn	Val	Ile	Gln	385	390	395	400
Ser	Leu	Leu	Ala	Arg	Arg	Ser	Leu	Gln	Ala	Gln	Leu	Gln	Arg	Leu	Gly	405	410	415	
Val	Leu	His	Val	Gly	Gln	Lys	Leu	Glu	Glu	Gln	Asp	Glu	Phe	Glu	Lys	420	425	430	
Ile	Tyr	Lys	Asn	Ala	Trp	Ala	Asp	Asn	Ala	Asn	Ala	Cys	Ala	Lys	Gln	435	440	445	
Tyr	Ala	Gly	Thr	Gly	Ala	Leu	Lys	Thr	Asp	Phe	Thr	Arg	Thr	Gly	Lys	450	455	460	
Arg	Thr	His	Leu	Gly	Leu	Ile	Met	Asp	Gly	Trp	Asn	Ser	Met	Ile	Arg	465	470	475	480
Tyr	Tyr	Lys	Asn	Asn	Phe	Ser	Asp	Gly	Phe	Arg	Gln	Asp	Ser	Ile	Asp	485	490	495	
Leu	Phe	Leu	Gly	Asn	Tyr	Ser	Val	Asp	Glu	Leu	Glu	Ser	His	Ser	Pro	500	505	510	
Leu	Ser	Val	Pro	Arg	Asp	Trp	Lys	Phe	Leu	Ala	Leu	Pro	Ile	Ile	Met	515	520	525	
Val	Val	Ala	Phe	Ser	Met	Cys	Ile	Ile	Cys	Leu	Leu	Met	Ala	Gly	Asp	530	535	540	
Thr	Trp	Thr	Glu	Thr	Leu	Ala	Tyr	Val	Leu	Phe	Trp	Gly	Val	Ala	Ser	545	550	555	560
Ile	Gly	Thr	Phe	Phe	Ile	Ile	Leu	Tyr	Asn	Gly	Lys	Asp	Phe	Val	Asp	565	570	575	
Ala	Pro	Arg	Leu	Val	Gln	Lys	Glu	Lys	Ile	Asp						580	585		

<210> SEQ ID NO 15

<211> LENGTH: 338

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

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<222> LOCATION: (1)..(338)
 <223> OTHER INFORMATION: OGTA088 = Swiss Prot Accession No. 015126,
 Secretory carrier-associated membrane protein 1

<400> SEQUENCE: 15

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Met Ser Asp Phe Asp Ser Asn Pro Phe Ala Asp Pro Asp Leu Asn Asn
 1           5           10           15

Pro Phe Lys Asp Pro Ser Val Thr Gln Val Thr Arg Asn Val Pro Pro
      20           25           30

Gly Leu Asp Glu Tyr Asn Pro Phe Ser Asp Ser Arg Thr Pro Pro Pro
      35           40           45

Gly Gly Val Lys Met Pro Asn Val Pro Asn Thr Gln Pro Ala Ile Met
 50           55           60

Lys Pro Thr Glu Glu His Pro Ala Tyr Thr Gln Ile Ala Lys Glu His
65           70           75           80

Ala Leu Ala Gln Ala Glu Leu Leu Lys Arg Gln Glu Glu Leu Glu Arg
      85           90           95

Lys Ala Ala Glu Leu Asp Arg Arg Glu Arg Glu Met Gln Asn Leu Ser
      100          105          110

Gln His Gly Arg Lys Asn Asn Trp Pro Pro Leu Pro Ser Asn Phe Pro
      115          120          125

Val Gly Pro Cys Phe Tyr Gln Asp Phe Ser Val Asp Ile Pro Val Glu
      130          135          140

Phe Gln Lys Thr Val Lys Leu Met Tyr Tyr Leu Trp Met Phe His Ala
145          150          155          160

Val Thr Leu Phe Leu Asn Ile Phe Gly Cys Leu Ala Trp Phe Cys Val
      165          170          175

Asp Ser Ala Arg Ala Val Asp Phe Gly Leu Ser Ile Leu Trp Phe Leu
      180          185          190

Leu Phe Thr Pro Cys Ser Phe Val Cys Trp Tyr Arg Pro Leu Tyr Gly
      195          200          205

Ala Phe Arg Ser Asp Ser Ser Phe Arg Phe Phe Val Phe Phe Phe Val
      210          215          220

Tyr Ile Cys Gln Phe Ala Val His Val Leu Gln Ala Ala Gly Phe His
225          230          235          240

Asn Trp Gly Asn Cys Gly Trp Ile Ser Ser Leu Thr Gly Leu Asn Gln
      245          250          255

Asn Ile Pro Val Gly Ile Met Met Ile Ile Ile Ala Ala Leu Phe Thr
      260          265          270

Ala Ser Ala Val Ile Ser Leu Val Met Phe Lys Lys Val His Gly Leu
      275          280          285

Tyr Arg Thr Thr Gly Ala Ser Phe Glu Lys Ala Gln Gln Glu Phe Ala
      290          295          300

Thr Gly Val Met Ser Asn Lys Thr Val Gln Thr Ala Ala Ala Asn Ala
305          310          315          320

Ala Ser Thr Ala Ala Ser Ser Ala Ala Gln Asn Ala Phe Lys Gly Asn
      325          330          335

Gln Ile

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<210> SEQ ID NO 16
 <211> LENGTH: 1058
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapiens

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<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(1058)
<223> OTHER INFORMATION: OGTA089 = Swiss Prot Accession No. Q5T225,
    Polycystic kidney disease 1-like

<400> SEQUENCE: 16

Met Glu Lys Arg Leu Gly Val Lys Pro Asn Pro Ala Ser Trp Ile Leu
 1             5             10             15

Ser Gly Tyr Tyr Trp Gln Thr Ser Ala Lys Trp Leu Arg Ser Leu Tyr
      20             25             30

Leu Phe Tyr Thr Cys Phe Cys Phe Ser Val Leu Trp Leu Ser Thr Asp
      35             40             45

Ala Ser Glu Ser Arg Cys Gln Gln Gly Lys Thr Gln Phe Gly Val Gly
 50             55             60

Leu Arg Ser Gly Gly Glu Asn His Leu Trp Leu Leu Glu Gly Thr Pro
65             70             75             80

Ser Leu Gln Ser Cys Trp Ala Ala Cys Cys Gln Asp Ser Ala Cys His
      85             90             95

Val Phe Trp Trp Leu Glu Gly Met Cys Ile Gln Ala Asp Cys Ser Arg
      100            105            110

Pro Gln Ser Cys Arg Ala Phe Arg Thr His Ser Ser Asn Ser Met Leu
      115            120            125

Val Phe Leu Lys Lys Phe Gln Thr Ala Asp Asp Leu Gly Phe Leu Pro
      130            135            140

Glu Asp Asp Val Pro His Leu Leu Gly Leu Gly Trp Asn Trp Ala Ser
145            150            155            160

Trp Arg Gln Ser Pro Pro Arg Ala Ala Leu Arg Pro Ala Val Ser Ser
      165            170            175

Ser Asp Gln Gln Ser Leu Ile Arg Lys Leu Gln Lys Arg Gly Ser Pro
      180            185            190

Ser Asp Val Val Thr Pro Ile Val Thr Gln His Ser Lys Val Asn Asp
      195            200            205

Ser Asn Glu Leu Gly Gly Leu Thr Thr Ser Gly Ser Ala Glu Val His
      210            215            220

Lys Ala Ile Thr Ile Ser Ser Pro Leu Thr Thr Asp Leu Thr Ala Glu
225            230            235            240

Leu Ser Gly Gly Pro Lys Asn Val Ser Val Gln Pro Glu Ile Ser Glu
      245            250            255

Gly Leu Ala Thr Thr Pro Ser Thr Gln Gln Val Lys Ser Ser Glu Lys
      260            265            270

Thr Gln Ile Ala Val Pro Gln Pro Val Ala Pro Ser Tyr Ser Tyr Ala
      275            280            285

Thr Pro Thr Pro Gln Ala Ser Phe Gln Ser Thr Ser Ala Pro Tyr Pro
      290            295            300

Val Ile Lys Glu Leu Val Val Ser Ala Gly Glu Ser Val Gln Ile Thr
305            310            315            320

Leu Pro Lys Asn Glu Val Gln Leu Asn Ala Tyr Val Leu Gln Glu Pro
      325            330            335

Pro Lys Gly Glu Thr Tyr Thr Tyr Asp Trp Gln Leu Ile Thr His Pro
      340            345            350

Arg Asp Tyr Ser Gly Glu Met Glu Gly Lys His Ser Gln Ile Leu Lys
      355            360            365

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Leu	Ser	Lys	Leu	Thr	Pro	Gly	Leu	Tyr	Glu	Phe	Lys	Val	Ile	Val	Glu	370	375	380	
Gly	Gln	Asn	Ala	His	Gly	Glu	Gly	Tyr	Val	Asn	Val	Thr	Val	Lys	Pro	385	390	395	400
Glu	Pro	Arg	Lys	Asn	Arg	Pro	Pro	Ile	Ala	Ile	Val	Ser	Pro	Gln	Phe	405	410	415	
Gln	Glu	Ile	Ser	Leu	Pro	Thr	Thr	Ser	Thr	Val	Ile	Asp	Gly	Ser	Gln	420	425	430	
Ser	Thr	Asp	Asp	Asp	Lys	Ile	Val	Gln	Tyr	His	Trp	Glu	Glu	Leu	Lys	435	440	445	
Gly	Pro	Leu	Arg	Glu	Glu	Lys	Ile	Ser	Glu	Asp	Thr	Ala	Ile	Leu	Lys	450	455	460	
Leu	Ser	Lys	Leu	Val	Pro	Gly	Asn	Tyr	Thr	Phe	Ser	Leu	Thr	Val	Val	465	470	475	480
Asp	Ser	Asp	Gly	Ala	Thr	Asn	Ser	Thr	Thr	Ala	Asn	Leu	Thr	Val	Asn	485	490	495	
Lys	Ala	Val	Asp	Tyr	Pro	Pro	Val	Ala	Asn	Ala	Gly	Pro	Asn	Gln	Val	500	505	510	
Ile	Thr	Leu	Pro	Gln	Asn	Ser	Ile	Thr	Leu	Phe	Gly	Asn	Gln	Ser	Thr	515	520	525	
Asp	Asp	His	Gly	Ile	Thr	Ser	Tyr	Glu	Trp	Ser	Leu	Ser	Pro	Ser	Ser	530	535	540	
Lys	Gly	Lys	Val	Val	Glu	Met	Gln	Gly	Val	Arg	Thr	Pro	Thr	Leu	Gln	545	550	555	560
Leu	Ser	Ala	Met	Gln	Glu	Gly	Asp	Tyr	Thr	Tyr	Gln	Leu	Thr	Val	Thr	565	570	575	
Asp	Thr	Ile	Gly	Gln	Gln	Ala	Thr	Ala	Gln	Val	Thr	Val	Ile	Val	Gln	580	585	590	
Pro	Glu	Asn	Asn	Lys	Pro	Pro	Gln	Ala	Asp	Ala	Gly	Pro	Asp	Lys	Glu	595	600	605	
Leu	Thr	Leu	Pro	Val	Asp	Ser	Thr	Thr	Leu	Asp	Gly	Ser	Lys	Ser	Ser	610	615	620	
Asp	Asp	Gln	Lys	Ile	Ile	Ser	Tyr	Leu	Trp	Glu	Lys	Thr	Gln	Gly	Pro	625	630	635	640
Asp	Gly	Val	Gln	Leu	Glu	Asn	Ala	Asn	Ser	Ser	Val	Ala	Thr	Val	Thr	645	650	655	
Gly	Leu	Gln	Val	Gly	Thr	Tyr	Val	Phe	Thr	Leu	Thr	Val	Lys	Asp	Glu	660	665	670	
Arg	Asn	Leu	Gln	Ser	Gln	Ser	Ser	Val	Asn	Val	Ile	Val	Lys	Glu	Glu	675	680	685	
Ile	Asn	Lys	Pro	Pro	Ile	Ala	Lys	Ile	Thr	Gly	Asn	Val	Val	Ile	Thr	690	695	700	
Leu	Pro	Thr	Ser	Thr	Ala	Glu	Leu	Asp	Gly	Ser	Lys	Ser	Ser	Asp	Asp	705	710	715	720
Lys	Gly	Ile	Val	Ser	Tyr	Leu	Trp	Thr	Arg	Asp	Glu	Gly	Ser	Pro	Ala	725	730	735	
Ala	Gly	Glu	Val	Leu	Asn	His	Ser	Asp	His	His	Pro	Ile	Leu	Phe	Leu	740	745	750	
Ser	Asn	Leu	Val	Glu	Gly	Thr	Tyr	Thr	Phe	His	Leu	Lys	Val	Thr	Asp	755	760	765	

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Ala Lys Gly Glu Ser Asp Thr Asp Arg Thr Thr Val Glu Val Lys Pro
 770 775 780
 Asp Pro Arg Lys Asn Asn Leu Val Glu Ile Ile Leu Asp Ile Asn Val
 785 790 795 800
 Ser Gln Leu Thr Glu Arg Leu Lys Gly Met Phe Ile Arg Gln Ile Gly
 805 810 815
 Val Leu Leu Gly Val Leu Asp Ser Asp Ile Ile Val Gln Lys Ile Gln
 820 825 830
 Pro Tyr Thr Glu Gln Ser Thr Lys Met Val Phe Phe Val Gln Asn Glu
 835 840 845
 Pro Pro His Gln Ile Phe Lys Gly His Glu Val Ala Ala Met Leu Lys
 850 855 860
 Ser Glu Leu Arg Lys Gln Lys Ala Asp Phe Leu Ile Phe Arg Ala Leu
 865 870 875 880
 Glu Val Asn Thr Val Thr Cys Gln Leu Asn Cys Ser Asp His Gly His
 885 890 895
 Cys Asp Ser Phe Thr Lys Arg Cys Ile Cys Asp Pro Phe Trp Met Glu
 900 905 910
 Asn Phe Ile Lys Val Gln Leu Arg Asp Gly Asp Ser Asn Cys Ala Leu
 915 920 925
 Thr Ile Leu Ile Phe Leu Ala Glu Trp Ser Val Leu Tyr Val Ile Ile
 930 935 940
 Ala Thr Phe Val Ile Val Val Ala Leu Gly Ile Leu Ser Trp Thr Val
 945 950 955 960
 Ile Cys Cys Cys Lys Arg Gln Lys Gly Lys Pro Lys Arg Lys Ser Lys
 965 970 975
 Tyr Lys Ile Leu Asp Ala Thr Asp Gln Glu Ser Leu Glu Leu Lys Pro
 980 985 990
 Thr Ser Arg Ala Gly Ile Lys Gln Lys Gly Leu Leu Leu Ser Ser Ser
 995 1000 1005
 Leu Met His Ser Glu Ser Glu Leu Asp Ser Asp Asp Ala Ile Phe
 1010 1015 1020
 Thr Trp Pro Asp Arg Glu Lys Gly Lys Leu Leu His Gly Gln Asn
 1025 1030 1035
 Gly Ser Val Pro Asn Gly Gln Thr Pro Leu Lys Ala Arg Ser Pro
 1040 1045 1050
 Arg Glu Glu Ile Leu
 1055

<210> SEQ ID NO 17
 <211> LENGTH: 2080
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapiens
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (1)..(2080)
 <223> OTHER INFORMATION: OGTA091 = Swiss Prot Accession No. 075923,
 Dysferlin

<400> SEQUENCE: 17

Met Leu Arg Val Phe Ile Leu Tyr Ala Glu Asn Val His Thr Pro Asp
 1 5 10 15
 Thr Asp Ile Ser Asp Ala Tyr Cys Ser Ala Val Phe Ala Gly Val Lys
 20 25 30

-continued

Lys	Arg	Thr	Lys	Val	Ile	Lys	Asn	Ser	Val	Asn	Pro	Val	Trp	Asn	Glu
	35						40					45			
Gly	Phe	Glu	Trp	Asp	Leu	Lys	Gly	Ile	Pro	Leu	Asp	Gln	Gly	Ser	Glu
	50					55					60				
Leu	His	Val	Val	Val	Lys	Asp	His	Glu	Thr	Met	Gly	Arg	Asn	Arg	Phe
65					70					75					80
Leu	Gly	Glu	Ala	Lys	Val	Pro	Leu	Arg	Glu	Val	Leu	Ala	Thr	Pro	Ser
				85					90					95	
Leu	Ser	Ala	Ser	Phe	Asn	Ala	Pro	Leu	Leu	Asp	Thr	Lys	Lys	Gln	Pro
		100						105					110		
Thr	Gly	Ala	Ser	Leu	Val	Leu	Gln	Val	Ser	Tyr	Thr	Pro	Leu	Pro	Gly
	115					120						125			
Ala	Val	Pro	Leu	Phe	Pro	Pro	Pro	Thr	Pro	Leu	Glu	Pro	Ser	Pro	Thr
	130					135					140				
Leu	Pro	Asp	Leu	Asp	Val	Val	Ala	Asp	Thr	Gly	Gly	Glu	Glu	Asp	Thr
145					150					155					160
Glu	Asp	Gln	Gly	Leu	Thr	Gly	Asp	Glu	Ala	Glu	Pro	Phe	Leu	Asp	Gln
				165				170						175	
Ser	Gly	Gly	Pro	Gly	Ala	Pro	Thr	Thr	Pro	Arg	Lys	Leu	Pro	Ser	Arg
			180					185					190		
Pro	Pro	Pro	His	Tyr	Pro	Gly	Ile	Lys	Arg	Lys	Arg	Ser	Ala	Pro	Thr
		195				200						205			
Ser	Arg	Lys	Leu	Leu	Ser	Asp	Lys	Pro	Gln	Asp	Phe	Gln	Ile	Arg	Val
	210					215					220				
Gln	Val	Ile	Glu	Gly	Arg	Gln	Leu	Pro	Gly	Val	Asn	Ile	Lys	Pro	Val
225					230					235					240
Val	Lys	Val	Thr	Ala	Ala	Gly	Gln	Thr	Lys	Arg	Thr	Arg	Ile	His	Lys
				245					250					255	
Gly	Asn	Ser	Pro	Leu	Phe	Asn	Glu	Thr	Leu	Phe	Phe	Asn	Leu	Phe	Asp
			260					265					270		
Ser	Pro	Gly	Glu	Leu	Phe	Asp	Glu	Pro	Ile	Phe	Ile	Thr	Val	Val	Asp
		275					280					285			
Ser	Arg	Ser	Leu	Arg	Thr	Asp	Ala	Leu	Leu	Gly	Glu	Phe	Arg	Met	Asp
	290					295					300				
Val	Gly	Thr	Ile	Tyr	Arg	Glu	Pro	Arg	His	Ala	Tyr	Leu	Arg	Lys	Trp
305					310					315					320
Leu	Leu	Leu	Ser	Asp	Pro	Asp	Asp	Phe	Ser	Ala	Gly	Ala	Arg	Gly	Tyr
				325					330					335	
Leu	Lys	Thr	Ser	Leu	Cys	Val	Leu	Gly	Pro	Gly	Asp	Glu	Ala	Pro	Leu
			340					345					350		
Glu	Arg	Lys	Asp	Pro	Ser	Glu	Asp	Lys	Glu	Asp	Ile	Glu	Ser	Asn	Leu
		355					360					365			
Leu	Arg	Pro	Thr	Gly	Val	Ala	Leu	Arg	Gly	Ala	His	Phe	Cys	Leu	Lys
	370					375					380				
Val	Phe	Arg	Ala	Glu	Asp	Leu	Pro	Gln	Met	Asp	Asp	Ala	Val	Met	Asp
385					390					395					400
Asn	Val	Lys	Gln	Ile	Phe	Gly	Phe	Glu	Ser	Asn	Lys	Lys	Asn	Leu	Val
			405					410						415	
Asp	Pro	Phe	Val	Glu	Val	Ser	Phe	Ala	Gly	Lys	Met	Leu	Cys	Ser	Lys
		420						425					430		
Ile	Leu	Glu	Lys	Thr	Ala	Asn	Pro	Gln	Trp	Asn	Gln	Asn	Ile	Thr	Leu

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435					440					445				
Pro	Ala	Met	Phe	Pro	Ser	Met	Cys	Glu	Lys	Met	Arg	Ile	Arg	Ile
450						455					460			
Asp	Trp	Asp	Arg	Leu	Thr	His	Asn	Asp	Ile	Val	Ala	Thr	Thr	Tyr
465					470					475				480
Ser	Met	Ser	Lys	Ile	Ser	Ala	Pro	Gly	Gly	Glu	Ile	Glu	Glu	Glu
				485					490					495
Ala	Gly	Ala	Val	Lys	Pro	Ser	Lys	Ala	Ser	Asp	Leu	Asp	Asp	Tyr
			500					505					510	Leu
Gly	Phe	Leu	Pro	Thr	Phe	Gly	Pro	Cys	Tyr	Ile	Asn	Leu	Tyr	Gly
		515					520					525		Ser
Pro	Arg	Glu	Phe	Thr	Gly	Phe	Pro	Asp	Pro	Tyr	Thr	Glu	Leu	Asn
	530					535					540			Thr
Gly	Lys	Gly	Glu	Gly	Val	Ala	Tyr	Arg	Gly	Arg	Leu	Leu	Leu	Ser
545					550					555				560
Glu	Thr	Lys	Leu	Val	Glu	His	Ser	Glu	Gln	Lys	Val	Glu	Asp	Leu
				565					570					575
Ala	Asp	Asp	Ile	Leu	Arg	Val	Glu	Lys	Tyr	Leu	Arg	Arg	Arg	Lys
			580					585					590	Tyr
Ser	Leu	Phe	Ala	Ala	Phe	Tyr	Ser	Ala	Thr	Met	Leu	Gln	Asp	Val
		595					600					605		Asp
Asp	Ala	Ile	Gln	Phe	Glu	Val	Ser	Ile	Gly	Asn	Tyr	Gly	Asn	Lys
	610					615					620			Phe
Asp	Met	Thr	Cys	Leu	Pro	Leu	Ala	Ser	Thr	Thr	Gln	Tyr	Ser	Arg
625					630					635				640
Val	Phe	Asp	Gly	Cys	His	Tyr	Tyr	Tyr	Leu	Pro	Trp	Gly	Asn	Val
				645					650					655
Pro	Val	Val	Val	Leu	Ser	Ser	Tyr	Trp	Glu	Asp	Ile	Ser	His	Arg
			660					665					670	Ile
Glu	Thr	Gln	Asn	Gln	Leu	Leu	Gly	Ile	Ala	Asp	Arg	Leu	Glu	Ala
		675					680					685		Gly
Leu	Glu	Gln	Val	His	Leu	Ala	Leu	Lys	Ala	Gln	Cys	Ser	Thr	Glu
	690					695					700			Asp
Val	Asp	Ser	Leu	Val	Ala	Gln	Leu	Thr	Asp	Glu	Leu	Ile	Ala	Gly
705					710					715				720
Ser	Gln	Pro	Leu	Gly	Asp	Ile	His	Glu	Thr	Pro	Ser	Ala	Thr	His
				725					730					735
Asp	Gln	Tyr	Leu	Tyr	Gln	Leu	Arg	Thr	His	His	Leu	Ser	Gln	Ile
			740					745					750	Thr
Glu	Ala	Ala	Leu	Ala	Leu	Lys	Leu	Gly	His	Ser	Glu	Leu	Pro	Ala
		755					760					765		Ala
Leu	Glu	Gln	Ala	Glu	Asp	Trp	Leu	Leu	Arg	Leu	Arg	Ala	Leu	Ala
		770				775					780			Glu
Glu	Pro	Gln	Asn	Ser	Leu	Pro	Asp	Ile	Val	Ile	Trp	Met	Leu	Gln
785					790					795				800
Asp	Lys	Arg	Val	Ala	Tyr	Gln	Arg	Val	Pro	Ala	His	Gln	Val	Leu
				805					810					815
Ser	Arg	Arg	Gly	Ala	Asn	Tyr	Cys	Gly	Lys	Asn	Cys	Gly	Lys	Leu
			820					825					830	Gln
Thr	Ile	Phe	Leu	Lys	Tyr	Pro	Met	Glu	Lys	Val	Pro	Gly	Ala	Arg
		835					840					845		Met

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Pro	Val	Gln	Ile	Arg	Val	Lys	Leu	Trp	Phe	Gly	Leu	Ser	Val	Asp	Glu
850						855					860				
Lys	Glu	Phe	Asn	Gln	Phe	Ala	Glu	Gly	Lys	Leu	Ser	Val	Phe	Ala	Glu
865					870					875					880
Thr	Tyr	Glu	Asn	Glu	Thr	Lys	Leu	Ala	Leu	Val	Gly	Asn	Trp	Gly	Thr
			885						890					895	
Thr	Gly	Leu	Thr	Tyr	Pro	Lys	Phe	Ser	Asp	Val	Thr	Gly	Lys	Ile	Lys
		900						905					910		
Leu	Pro	Lys	Asp	Ser	Phe	Arg	Pro	Ser	Ala	Gly	Trp	Thr	Trp	Ala	Gly
	915						920					925			
Asp	Trp	Phe	Val	Cys	Pro	Glu	Lys	Thr	Leu	Leu	His	Asp	Met	Asp	Ala
930						935					940				
Gly	His	Leu	Ser	Phe	Val	Glu	Glu	Val	Phe	Glu	Asn	Gln	Thr	Arg	Leu
945					950					955					960
Pro	Gly	Gly	Gln	Trp	Ile	Tyr	Met	Ser	Asp	Asn	Tyr	Thr	Asp	Val	Asn
			965						970					975	
Gly	Glu	Lys	Val	Leu	Pro	Lys	Asp	Asp	Ile	Glu	Cys	Pro	Leu	Gly	Trp
		980					985						990		
Lys	Trp	Glu	Asp	Glu	Glu	Trp	Ser	Thr	Asp	Leu	Asn	Arg	Ala	Val	Asp
	995						1000					1005			
Glu	Gln	Gly	Trp	Glu	Tyr	Ser	Ile	Thr	Ile	Pro	Pro	Glu	Arg	Lys	
1010						1015					1020				
Pro	Lys	His	Trp	Val	Pro	Ala	Glu	Lys	Met	Tyr	Tyr	Thr	His	Arg	
1025						1030						1035			
Arg	Arg	Arg	Trp	Val	Arg	Leu	Arg	Arg	Arg	Asp	Leu	Ser	Gln	Met	
1040						1045						1050			
Glu	Ala	Leu	Lys	Arg	His	Arg	Gln	Ala	Glu	Ala	Glu	Gly	Glu	Gly	
1055						1060						1065			
Trp	Glu	Tyr	Ala	Ser	Leu	Phe	Gly	Trp	Lys	Phe	His	Leu	Glu	Tyr	
1070						1075					1080				
Arg	Lys	Thr	Asp	Ala	Phe	Arg	Arg	Arg	Arg	Trp	Arg	Arg	Arg	Met	
1085						1090					1095				
Glu	Pro	Leu	Glu	Lys	Thr	Gly	Pro	Ala	Ala	Val	Phe	Ala	Leu	Glu	
1100						1105					1110				
Gly	Ala	Leu	Gly	Gly	Val	Met	Asp	Asp	Lys	Ser	Glu	Asp	Ser	Met	
1115						1120					1125				
Ser	Val	Ser	Thr	Leu	Ser	Phe	Gly	Val	Asn	Arg	Pro	Thr	Ile	Ser	
1130						1135					1140				
Cys	Ile	Phe	Asp	Tyr	Gly	Asn	Arg	Tyr	His	Leu	Arg	Cys	Tyr	Met	
1145						1150					1155				
Tyr	Gln	Ala	Arg	Asp	Leu	Ala	Ala	Met	Asp	Lys	Asp	Ser	Phe	Ser	
1160						1165					1170				
Asp	Pro	Tyr	Ala	Ile	Val	Ser	Phe	Leu	His	Gln	Ser	Gln	Lys	Thr	
1175						1180					1185				
Val	Val	Val	Lys	Asn	Thr	Leu	Asn	Pro	Thr	Trp	Asp	Gln	Thr	Leu	
1190						1195					1200				
Ile	Phe	Tyr	Glu	Ile	Glu	Ile	Phe	Gly	Glu	Pro	Ala	Thr	Val	Ala	
1205						1210					1215				
Glu	Gln	Pro	Pro	Ser	Ile	Val	Val	Glu	Leu	Tyr	Asp	His	Asp	Thr	
1220						1225					1230				

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Tyr Gly	Ala Asp	Glu Phe	Met	Gly Arg	Cys Ile	Cys	Gln Pro	Ser	
1235			1240			1245			
Leu Glu	Arg Met	Pro Arg	Leu	Ala Trp	Phe Pro	Leu	Thr Arg	Gly	
1250			1255			1260			
Ser Gln	Pro Ser	Gly Glu	Leu	Leu Ala	Ser Phe	Glu	Leu Ile	Gln	
1265			1270			1275			
Arg Glu	Lys Pro	Ala Ile	His	His Ile	Pro Gly	Phe	Glu Val	Gln	
1280			1285			1290			
Glu Thr	Ser Arg	Ile Leu	Asp	Glu Ser	Glu Asp	Thr	Asp Leu	Pro	
1295			1300			1305			
Tyr Pro	Pro Pro	Gln Arg	Glu	Ala Asn	Ile Tyr	Met	Val Pro	Gln	
1310			1315			1320			
Asn Ile	Lys Pro	Ala Leu	Gln	Arg Thr	Ala Ile	Glu	Ile Leu	Ala	
1325			1330			1335			
Trp Gly	Leu Arg	Asn Met	Lys	Ser Tyr	Gln Leu	Ala	Asn Ile	Ser	
1340			1345			1350			
Ser Pro	Ser Leu	Val Val	Glu	Cys Gly	Gly Gln	Thr	Val Gln	Ser	
1355			1360			1365			
Cys Val	Ile Arg	Asn Leu	Arg	Lys Asn	Pro Asn	Phe	Asp Ile	Cys	
1370			1375			1380			
Thr Leu	Phe Met	Glu Val	Met	Leu Pro	Arg Glu	Glu	Leu Tyr	Cys	
1385			1390			1395			
Pro Pro	Ile Thr	Val Lys	Val	Ile Asp	Asn Arg	Gln	Phe Gly	Arg	
1400			1405			1410			
Arg Pro	Val Val	Gly Gln	Cys	Thr Ile	Arg Ser	Leu	Glu Ser	Phe	
1415			1420			1425			
Leu Cys	Asp Pro	Tyr Ser	Ala	Glu Ser	Pro Ser	Pro	Gln Gly	Gly	
1430			1435			1440			
Pro Asp	Asp Val	Ser Leu	Leu	Ser Pro	Gly Glu	Asp	Val Leu	Ile	
1445			1450			1455			
Asp Ile	Asp Asp	Lys Glu	Pro	Leu Ile	Pro Ile	Gln	Glu Glu	Glu	
1460			1465			1470			
Phe Ile	Asp Trp	Trp Ser	Lys	Phe Phe	Ala Ser	Ile	Gly Glu	Arg	
1475			1480			1485			
Glu Lys	Cys Gly	Ser Tyr	Leu	Glu Lys	Asp Phe	Asp	Thr Leu	Lys	
1490			1495			1500			
Val Tyr	Asp Thr	Gln Leu	Glu	Asn Val	Glu Ala	Phe	Glu Gly	Leu	
1505			1510			1515			
Ser Asp	Phe Cys	Asn Thr	Phe	Lys Leu	Tyr Arg	Gly	Lys Thr	Gln	
1520			1525			1530			
Glu Glu	Thr Glu	Asp Pro	Ser	Val Ile	Gly Glu	Phe	Lys Gly	Leu	
1535			1540			1545			
Phe Lys	Ile Tyr	Pro Leu	Pro	Glu Asp	Pro Ala	Ile	Pro Met	Pro	
1550			1555			1560			
Pro Arg	Gln Phe	His Gln	Leu	Ala Ala	Gln Gly	Pro	Gln Glu	Cys	
1565			1570			1575			
Leu Val	Arg Ile	Tyr Ile	Val	Arg Ala	Phe Gly	Leu	Gln Pro	Lys	
1580			1585			1590			
Asp Pro	Asn Gly	Lys Cys	Asp	Pro Tyr	Ile Lys	Ile	Ser Ile	Gly	
1595			1600			1605			
Lys Lys	Ser Val	Ser Asp	Gln	Asp Asn	Tyr Ile	Pro	Cys Thr	Leu	

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1610	1615	1620
Glu Pro Val Phe Gly Lys Met Phe Glu Leu Thr Cys Thr Leu Pro		
1625	1630	1635
Leu Glu Lys Asp Leu Lys Ile Thr Leu Tyr Asp Tyr Asp Leu Leu		
1640	1645	1650
Ser Lys Asp Glu Lys Ile Gly Glu Thr Val Val Asp Leu Glu Asn		
1655	1660	1665
Arg Leu Leu Ser Lys Phe Gly Ala Arg Cys Gly Leu Pro Gln Thr		
1670	1675	1680
Tyr Cys Val Ser Gly Pro Asn Gln Trp Arg Asp Gln Leu Arg Pro		
1685	1690	1695
Ser Gln Leu Leu His Leu Phe Cys Gln Gln His Arg Val Lys Ala		
1700	1705	1710
Pro Val Tyr Arg Thr Asp Arg Val Met Phe Gln Asp Lys Glu Tyr		
1715	1720	1725
Ser Ile Glu Glu Ile Glu Ala Gly Arg Ile Pro Asn Pro His Leu		
1730	1735	1740
Gly Pro Val Glu Glu Arg Leu Ala Leu His Val Leu Gln Gln Gln		
1745	1750	1755
Gly Leu Val Pro Glu His Val Glu Ser Arg Pro Leu Tyr Ser Pro		
1760	1765	1770
Leu Gln Pro Asp Ile Glu Gln Gly Lys Leu Gln Met Trp Val Asp		
1775	1780	1785
Leu Phe Pro Lys Ala Leu Gly Arg Pro Gly Pro Pro Phe Asn Ile		
1790	1795	1800
Thr Pro Arg Arg Ala Arg Arg Phe Phe Leu Arg Cys Ile Ile Trp		
1805	1810	1815
Asn Thr Arg Asp Val Ile Leu Asp Asp Leu Ser Leu Thr Gly Glu		
1820	1825	1830
Lys Met Ser Asp Ile Tyr Val Lys Gly Trp Met Ile Gly Phe Glu		
1835	1840	1845
Glu His Lys Gln Lys Thr Asp Val His Tyr Arg Ser Leu Gly Gly		
1850	1855	1860
Glu Gly Asn Phe Asn Trp Arg Phe Ile Phe Pro Phe Asp Tyr Leu		
1865	1870	1875
Pro Ala Glu Gln Val Cys Thr Ile Ala Lys Lys Asp Ala Phe Trp		
1880	1885	1890
Arg Leu Asp Lys Thr Glu Ser Lys Ile Pro Ala Arg Val Val Phe		
1895	1900	1905
Gln Ile Trp Asp Asn Asp Lys Phe Ser Phe Asp Asp Phe Leu Gly		
1910	1915	1920
Ser Leu Gln Leu Asp Leu Asn Arg Met Pro Lys Pro Ala Lys Thr		
1925	1930	1935
Ala Lys Lys Cys Ser Leu Asp Gln Leu Asp Asp Ala Phe His Pro		
1940	1945	1950
Glu Trp Phe Val Ser Leu Phe Glu Gln Lys Thr Val Lys Gly Trp		
1955	1960	1965
Trp Pro Cys Val Ala Glu Glu Gly Glu Lys Lys Ile Leu Ala Gly		
1970	1975	1980
Lys Leu Glu Met Thr Leu Glu Ile Val Ala Glu Ser Glu His Glu		
1985	1990	1995

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Glu Arg Pro Ala Gly Gln Gly Arg Asp Glu Pro Asn Met Asn Pro
 2000 2005 2010
 Lys Leu Glu Asp Pro Arg Arg Pro Asp Thr Ser Phe Leu Trp Phe
 2015 2020 2025
 Thr Ser Pro Tyr Lys Thr Met Lys Phe Ile Leu Trp Arg Arg Phe
 2030 2035 2040
 Arg Trp Ala Ile Ile Leu Phe Ile Ile Leu Phe Ile Leu Leu Leu
 2045 2050 2055
 Phe Leu Ala Ile Phe Ile Tyr Ala Phe Pro Asn Tyr Ala Ala Met
 2060 2065 2070
 Lys Leu Val Lys Pro Phe Ser
 2075 2080

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 <222> LOCATION: (1)..(1117)
 <223> OTHER INFORMATION: OGTA098 = Swiss Prot Accession No. Q14126,
 Desmoglein-2

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 Phe Asn Val Gly Ser Gly Leu His Leu Gln Val Leu Ser Thr Arg Asn
 20 25 30
 Glu Asn Lys Leu Leu Pro Lys His Pro His Leu Val Arg Gln Lys Arg
 35 40 45
 Ala Trp Ile Thr Ala Pro Val Ala Leu Arg Glu Gly Glu Asp Leu Ser
 50 55 60
 Lys Lys Asn Pro Ile Ala Lys Ile His Ser Asp Leu Ala Glu Glu Arg
 65 70 75 80
 Gly Leu Lys Ile Thr Tyr Lys Tyr Thr Gly Lys Gly Ile Thr Glu Pro
 85 90 95
 Pro Phe Gly Ile Phe Val Phe Asn Lys Asp Thr Gly Glu Leu Asn Val
 100 105 110
 Thr Ser Ile Leu Asp Arg Glu Glu Thr Pro Phe Phe Leu Leu Thr Gly
 115 120 125
 Tyr Ala Leu Asp Ala Arg Gly Asn Asn Val Glu Lys Pro Leu Glu Leu
 130 135 140
 Arg Ile Lys Val Leu Asp Ile Asn Asp Asn Glu Pro Val Phe Thr Gln
 145 150 155 160
 Asp Val Phe Val Gly Ser Val Glu Glu Leu Ser Ala Ala His Thr Leu
 165 170 175
 Val Met Lys Ile Asn Ala Thr Asp Ala Asp Glu Pro Asn Thr Leu Asn
 180 185 190
 Ser Lys Ile Ser Tyr Arg Ile Val Ser Leu Glu Pro Ala Tyr Pro Pro
 195 200 205
 Val Phe Tyr Leu Asn Lys Asp Thr Gly Glu Ile Tyr Thr Thr Ser Val
 210 215 220
 Thr Leu Asp Arg Glu Glu His Ser Ser Tyr Thr Leu Thr Val Glu Ala
 225 230 235 240

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Arg	Asp	Gly	Asn	Gly	Glu	Val	Thr	Asp	Lys	Pro	Val	Lys	Gln	Ala	Gln	245	250	255
Val	Gln	Ile	Arg	Ile	Leu	Asp	Val	Asn	Asp	Asn	Ile	Pro	Val	Val	Glu	260	265	270
Asn	Lys	Val	Leu	Glu	Gly	Met	Val	Glu	Glu	Asn	Gln	Val	Asn	Val	Glu	275	280	285
Val	Thr	Arg	Ile	Lys	Val	Phe	Asp	Ala	Asp	Glu	Ile	Gly	Ser	Asp	Asn	290	295	300
Trp	Leu	Ala	Asn	Phe	Thr	Phe	Ala	Ser	Gly	Asn	Glu	Gly	Gly	Tyr	Phe	305	310	315
His	Ile	Glu	Thr	Asp	Ala	Gln	Thr	Asn	Glu	Gly	Ile	Val	Thr	Leu	Ile	325	330	335
Lys	Glu	Val	Asp	Tyr	Glu	Glu	Met	Lys	Asn	Leu	Asp	Phe	Ser	Val	Ile	340	345	350
Val	Ala	Asn	Lys	Ala	Ala	Phe	His	Lys	Ser	Ile	Arg	Ser	Lys	Tyr	Lys	355	360	365
Pro	Thr	Pro	Ile	Pro	Ile	Lys	Val	Lys	Val	Lys	Asn	Val	Lys	Glu	Gly	370	375	380
Ile	His	Phe	Lys	Ser	Ser	Val	Ile	Ser	Ile	Tyr	Val	Ser	Glu	Ser	Met	385	390	395
Asp	Arg	Ser	Ser	Lys	Gly	Gln	Ile	Ile	Gly	Asn	Phe	Gln	Ala	Phe	Asp	405	410	415
Glu	Asp	Thr	Gly	Leu	Pro	Ala	His	Ala	Arg	Tyr	Val	Lys	Leu	Glu	Asp	420	425	430
Arg	Asp	Asn	Trp	Ile	Ser	Val	Asp	Ser	Val	Thr	Ser	Glu	Ile	Lys	Leu	435	440	445
Ala	Lys	Leu	Pro	Asp	Phe	Glu	Ser	Arg	Tyr	Val	Gln	Asn	Gly	Thr	Tyr	450	455	460
Thr	Val	Lys	Ile	Val	Ala	Ile	Ser	Glu	Asp	Tyr	Pro	Arg	Lys	Thr	Ile	465	470	475
Thr	Gly	Thr	Val	Leu	Ile	Asn	Val	Glu	Asp	Ile	Asn	Asp	Asn	Cys	Pro	485	490	495
Thr	Leu	Ile	Glu	Pro	Val	Gln	Thr	Ile	Cys	His	Asp	Ala	Glu	Tyr	Val	500	505	510
Asn	Val	Thr	Ala	Glu	Asp	Leu	Asp	Gly	His	Pro	Asn	Ser	Gly	Pro	Phe	515	520	525
Ser	Phe	Ser	Val	Ile	Asp	Lys	Pro	Pro	Gly	Met	Ala	Glu	Lys	Trp	Lys	530	535	540
Ile	Ala	Arg	Gln	Glu	Ser	Thr	Ser	Val	Leu	Leu	Gln	Gln	Ser	Glu	Lys	545	550	555
Lys	Leu	Gly	Arg	Ser	Glu	Ile	Gln	Phe	Leu	Ile	Ser	Asp	Asn	Gln	Gly	565	570	575
Phe	Ser	Cys	Pro	Glu	Lys	Gln	Val	Leu	Thr	Leu	Thr	Val	Cys	Glu	Val	580	585	590
Leu	His	Gly	Ser	Gly	Cys	Arg	Glu	Ala	Gln	His	Asp	Ser	Tyr	Val	Gly	595	600	605
Leu	Gly	Pro	Ala	Ala	Ile	Ala	Leu	Met	Ile	Leu	Ala	Phe	Leu	Leu	Leu	610	615	620
Leu	Leu	Val	Pro	Leu	Leu	Leu	Met	Cys	His	Cys	Gly	Lys	Gly	Ala		625	630	635

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Lys	Ala	Phe	Thr	Pro	Ile	Pro	Gly	Thr	Ile	Glu	Met	Leu	His	Pro	Trp	645	650	655
Asn	Asn	Glu	Gly	Ala	Pro	Pro	Glu	Asp	Lys	Val	Val	Pro	Ser	Phe	Leu	660	665	670
Pro	Val	Asp	Gln	Gly	Gly	Ser	Leu	Val	Gly	Arg	Asn	Gly	Val	Gly	Gly	675	680	685
Met	Ala	Lys	Glu	Ala	Thr	Met	Lys	Gly	Ser	Ser	Ser	Ala	Ser	Ile	Val	690	695	700
Lys	Gly	Gln	His	Glu	Met	Ser	Glu	Met	Asp	Gly	Arg	Trp	Glu	Glu	His	705	710	715
Arg	Ser	Leu	Leu	Ser	Gly	Arg	Ala	Thr	Gln	Phe	Thr	Gly	Ala	Thr	Gly	725	730	735
Ala	Ile	Met	Thr	Thr	Glu	Thr	Thr	Lys	Thr	Ala	Arg	Ala	Thr	Gly	Ala	740	745	750
Ser	Arg	Asp	Met	Ala	Gly	Ala	Gln	Ala	Ala	Ala	Val	Ala	Leu	Asn	Glu	755	760	765
Glu	Phe	Leu	Arg	Asn	Tyr	Phe	Thr	Asp	Lys	Ala	Ala	Ser	Tyr	Thr	Glu	770	775	780
Glu	Asp	Glu	Asn	His	Thr	Ala	Lys	Asp	Cys	Leu	Leu	Val	Tyr	Ser	Gln	785	790	795
Glu	Glu	Thr	Glu	Ser	Leu	Asn	Ala	Ser	Ile	Gly	Cys	Cys	Ser	Phe	Ile	805	810	815
Glu	Gly	Glu	Leu	Asp	Asp	Arg	Phe	Leu	Asp	Asp	Leu	Gly	Leu	Lys	Phe	820	825	830
Lys	Thr	Leu	Ala	Glu	Val	Cys	Leu	Gly	Gln	Lys	Ile	Asp	Ile	Asn	Lys	835	840	845
Glu	Ile	Glu	Gln	Arg	Gln	Lys	Pro	Ala	Thr	Glu	Thr	Ser	Met	Asn	Thr	850	855	860
Ala	Ser	His	Ser	Leu	Cys	Glu	Gln	Thr	Met	Val	Asn	Ser	Glu	Asn	Thr	865	870	875
Tyr	Ser	Ser	Gly	Ser	Ser	Phe	Pro	Val	Pro	Lys	Ser	Leu	Gln	Glu	Ala	885	890	895
Asn	Ala	Glu	Lys	Val	Thr	Gln	Glu	Ile	Val	Thr	Glu	Arg	Ser	Val	Ser	900	905	910
Ser	Arg	Gln	Ala	Gln	Lys	Val	Ala	Thr	Pro	Leu	Pro	Asp	Pro	Met	Ala	915	920	925
Ser	Arg	Asn	Val	Ile	Ala	Thr	Glu	Thr	Ser	Tyr	Val	Thr	Gly	Ser	Thr	930	935	940
Met	Pro	Pro	Thr	Thr	Val	Ile	Leu	Gly	Pro	Ser	Gln	Pro	Gln	Ser	Leu	945	950	955
Ile	Val	Thr	Glu	Arg	Val	Tyr	Ala	Pro	Ala	Ser	Thr	Leu	Val	Asp	Gln	965	970	975
Pro	Tyr	Ala	Asn	Glu	Gly	Thr	Val	Val	Val	Thr	Glu	Arg	Val	Ile	Gln	980	985	990
Pro	His	Gly	Gly	Gly	Ser	Asn	Pro	Leu	Glu	Gly	Thr	Gln	His	Leu	Gln	995	1000	1005
Asp	Val	Pro	Tyr	Val	Met	Val	Arg	Glu	Arg	Glu	Ser	Phe	Leu	Ala		1010	1015	1020
Pro	Ser	Ser	Gly	Val	Gln	Pro	Thr	Leu	Ala	Met	Pro	Asn	Ile	Ala		1025	1030	1035
Val	Gly	Gln	Asn	Val	Thr	Val	Thr	Glu	Arg	Val	Leu	Ala	Pro	Ala				

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1040	1045	1050
Ser Thr Leu Gln Ser Ser Tyr Gln Ile Pro Thr Glu Asn Ser Met		
1055	1060	1065
Thr Ala Arg Asn Thr Thr Val Ser Gly Ala Gly Val Pro Gly Pro		
1070	1075	1080
Leu Pro Asp Phe Gly Leu Glu Glu Ser Gly His Ser Asn Ser Thr		
1085	1090	1095
Ile Thr Thr Ser Ser Thr Arg Val Thr Lys His Ser Thr Val Gln		
1100	1105	1110
His Ser Tyr Ser		
1115		

<210> SEQ ID NO 19
 <211> LENGTH: 1912
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapiens
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (1)..(1912)
 <223> OTHER INFORMATION: OGTA101 = Swiss Prot Accession No. P23468,
 Receptor-type tyrosine-protein phosphatase delta

<400> SEQUENCE: 19

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Gln Thr Gly Val Ser Gly Gly Val Ala Ser Phe Ile Cys Gln Ala Thr		
	35	40 45
Gly Asp Pro Arg Pro Lys Ile Val Trp Asn Lys Lys Gly Lys Lys Val		
	50	55 60
Ser Asn Gln Arg Phe Glu Val Ile Glu Phe Asp Asp Gly Ser Gly Ser		
	65	70 75 80
Val Leu Arg Ile Gln Pro Leu Arg Thr Pro Arg Asp Glu Ala Ile Tyr		
	85	90 95
Glu Cys Val Ala Ser Asn Asn Val Gly Glu Ile Ser Val Ser Thr Arg		
	100	105 110
Leu Thr Val Leu Arg Glu Asp Gln Ile Pro Arg Gly Phe Pro Thr Ile		
	115	120 125
Asp Met Gly Pro Gln Leu Lys Val Val Glu Arg Thr Arg Thr Ala Thr		
	130	135 140
Met Leu Cys Ala Ala Ser Gly Asn Pro Asp Pro Glu Ile Thr Trp Phe		
	145	150 155 160
Lys Asp Phe Leu Pro Val Asp Thr Ser Asn Asn Asn Gly Arg Ile Lys		
	165	170 175
Gln Leu Arg Ser Glu Ser Ile Gly Gly Thr Pro Ile Arg Gly Ala Leu		
	180	185 190
Gln Ile Glu Gln Ser Glu Glu Ser Asp Gln Gly Lys Tyr Glu Cys Val		
	195	200 205
Ala Thr Asn Ser Ala Gly Thr Arg Tyr Ser Ala Pro Ala Asn Leu Tyr		
	210	215 220
Val Arg Glu Leu Arg Glu Val Arg Arg Val Pro Pro Arg Phe Ser Ile		
	225	230 235 240
Pro Pro Thr Asn His Glu Ile Met Pro Gly Gly Ser Val Asn Ile Thr		

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245								250					255				
Cys	Val	Ala	Val	Gly	Ser	Pro	Met	Pro	Tyr	Val	Lys	Trp	Met	Leu	Gly		
260				265				270									
Ala	Glu	Asp	Leu	Thr	Pro	Glu	Asp	Asp	Met	Pro	Ile	Gly	Arg	Asn	Val		
275				280				285									
Leu	Glu	Leu	Asn	Asp	Val	Arg	Gln	Ser	Ala	Asn	Tyr	Thr	Cys	Val	Ala		
290				295				300									
Met	Ser	Thr	Leu	Gly	Val	Ile	Glu	Ala	Ile	Ala	Gln	Ile	Thr	Val	Lys		
305				310				315									
Ala	Leu	Pro	Lys	Pro	Pro	Gly	Thr	Pro	Val	Val	Thr	Glu	Ser	Thr	Ala		
325				330				335									
Thr	Ser	Ile	Thr	Leu	Thr	Trp	Asp	Ser	Gly	Asn	Pro	Glu	Pro	Val	Ser		
340				345				350									
Tyr	Tyr	Ile	Ile	Gln	His	Lys	Pro	Lys	Asn	Ser	Glu	Glu	Leu	Tyr	Lys		
355				360				365									
Glu	Ile	Asp	Gly	Val	Ala	Thr	Thr	Arg	Tyr	Ser	Val	Ala	Gly	Leu	Ser		
370				375				380									
Pro	Tyr	Ser	Asp	Tyr	Glu	Phe	Arg	Val	Val	Ala	Val	Asn	Asn	Ile	Gly		
385				390				395				400					
Arg	Gly	Pro	Pro	Ser	Glu	Pro	Val	Leu	Thr	Gln	Thr	Ser	Glu	Gln	Ala		
405				410				415									
Pro	Ser	Ser	Ala	Pro	Arg	Asp	Val	Gln	Ala	Arg	Met	Leu	Ser	Ser	Thr		
420				425				430									
Thr	Ile	Leu	Val	Gln	Trp	Lys	Glu	Pro	Glu	Glu	Pro	Asn	Gly	Gln	Ile		
435				440				445									
Gln	Gly	Tyr	Arg	Val	Tyr	Tyr	Thr	Met	Asp	Pro	Thr	Gln	His	Val	Asn		
450				455				460									
Asn	Trp	Met	Lys	His	Asn	Val	Ala	Asp	Ser	Gln	Ile	Thr	Thr	Ile	Gly		
465				470				475				480					
Asn	Leu	Val	Pro	Gln	Lys	Thr	Tyr	Ser	Val	Lys	Val	Leu	Ala	Phe	Thr		
485				490				495									
Ser	Ile	Gly	Asp	Gly	Pro	Leu	Ser	Ser	Asp	Ile	Gln	Val	Ile	Thr	Gln		
500				505				510									
Thr	Gly	Val	Pro	Gly	Gln	Pro	Leu	Asn	Phe	Lys	Ala	Glu	Pro	Glu	Ser		
515				520				525									
Glu	Thr	Ser	Ile	Leu	Leu	Ser	Trp	Thr	Pro	Pro	Arg	Ser	Asp	Thr	Ile		
530				535				540									
Ala	Asn	Tyr	Glu	Leu	Val	Tyr	Lys	Asp	Gly	Glu	His	Gly	Glu	Glu	Gln		
545				550				555				560					
Arg	Ile	Thr	Ile	Glu	Pro	Gly	Thr	Ser	Tyr	Arg	Leu	Gln	Gly	Leu	Lys		
565				570				575									
Pro	Asn	Ser	Leu	Tyr	Tyr	Phe	Arg	Leu	Ala	Ala	Arg	Ser	Pro	Gln	Gly		
580				585				590									
Leu	Gly	Ala	Ser	Thr	Ala	Glu	Ile	Ser	Ala	Arg	Thr	Met	Gln	Ser	Lys		
595				600				605									
Pro	Ser	Ala	Pro	Pro	Gln	Asp	Ile	Ser	Cys	Thr	Ser	Pro	Ser	Ser	Thr		
610				615				620									
Ser	Ile	Leu	Val	Ser	Trp	Gln	Pro	Pro	Pro	Val	Glu	Lys	Gln	Asn	Gly		
625				630				635				640					
Ile	Ile	Thr	Glu	Tyr	Ser	Ile	Lys	Tyr	Thr	Ala	Val	Asp	Gly	Glu	Asp		
645				650				655									

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Asp	Lys	Pro	His	Glu	Ile	Leu	Gly	Ile	Pro	Ser	Asp	Thr	Thr	Lys	Tyr	660	665	670
Leu	Leu	Glu	Gln	Leu	Glu	Lys	Trp	Thr	Glu	Tyr	Arg	Ile	Thr	Val	Thr	675	680	685
Ala	His	Thr	Asp	Val	Gly	Pro	Gly	Pro	Glu	Ser	Leu	Ser	Val	Leu	Ile	690	695	700
Arg	Thr	Asn	Glu	Asp	Val	Pro	Ser	Gly	Pro	Pro	Arg	Lys	Val	Glu	Val	705	710	715
Glu	Ala	Val	Asn	Ser	Thr	Ser	Val	Lys	Val	Ser	Trp	Arg	Ser	Pro	Val	725	730	735
Pro	Asn	Lys	Gln	His	Gly	Gln	Ile	Arg	Gly	Tyr	Gln	Val	His	Tyr	Val	740	745	750
Arg	Met	Glu	Asn	Gly	Glu	Pro	Lys	Gly	Gln	Pro	Met	Leu	Lys	Asp	Val	755	760	765
Met	Leu	Ala	Asp	Ala	Gln	Trp	Glu	Phe	Asp	Asp	Thr	Thr	Glu	His	Asp	770	775	780
Met	Ile	Ile	Ser	Gly	Leu	Gln	Pro	Glu	Thr	Ser	Tyr	Ser	Leu	Thr	Val	785	790	795
Thr	Ala	Tyr	Thr	Thr	Lys	Gly	Asp	Gly	Ala	Arg	Ser	Lys	Pro	Lys	Leu	805	810	815
Val	Ser	Thr	Thr	Gly	Ala	Val	Pro	Gly	Lys	Pro	Arg	Leu	Val	Ile	Asn	820	825	830
His	Thr	Gln	Met	Asn	Thr	Ala	Leu	Ile	Gln	Trp	His	Pro	Pro	Val	Asp	835	840	845
Thr	Phe	Gly	Pro	Leu	Gln	Gly	Tyr	Arg	Leu	Lys	Phe	Gly	Arg	Lys	Asp	850	855	860
Met	Glu	Pro	Leu	Thr	Thr	Leu	Glu	Phe	Ser	Glu	Lys	Glu	Asp	His	Phe	865	870	875
Thr	Ala	Thr	Asp	Ile	His	Lys	Gly	Ala	Ser	Tyr	Val	Phe	Arg	Leu	Ser	885	890	895
Ala	Arg	Asn	Lys	Val	Gly	Phe	Gly	Glu	Glu	Met	Val	Lys	Glu	Ile	Ser	900	905	910
Ile	Pro	Glu	Glu	Val	Pro	Thr	Gly	Phe	Pro	Gln	Asn	Leu	His	Ser	Glu	915	920	925
Gly	Thr	Ser	Thr	Ser	Val	Gln	Leu	Ser	Trp	Gln	Pro	Pro	Val	Leu		930	935	940
Ala	Glu	Arg	Asn	Gly	Ile	Ile	Thr	Lys	Tyr	Thr	Leu	Leu	Tyr	Arg	Asp	945	950	955
Ile	Asn	Ile	Pro	Leu	Leu	Pro	Met	Glu	Gln	Leu	Ile	Val	Pro	Ala	Asp	965	970	975
Thr	Thr	Met	Thr	Leu	Thr	Gly	Leu	Lys	Pro	Asp	Thr	Thr	Tyr	Asp	Val	980	985	990
Lys	Val	Arg	Ala	His	Thr	Ser	Lys	Gly	Pro	Gly	Pro	Tyr	Ser	Pro	Ser	995	1000	1005
Val	Gln	Phe	Arg	Thr	Leu	Pro	Val	Asp	Gln	Val	Phe	Ala	Lys	Asn		1010	1015	1020
Phe	His	Val	Lys	Ala	Val	Met	Lys	Thr	Ser	Val	Leu	Leu	Ser	Trp		1025	1030	1035
Glu	Ile	Pro	Glu	Asn	Tyr	Asn	Ser	Ala	Met	Pro	Phe	Lys	Ile	Leu		1040	1045	1050

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Tyr	Asp	Asp	Gly	Lys	Met	Val	Glu	Glu	Val	Asp	Gly	Arg	Ala	Thr
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Gln	Lys	Leu	Ile	Val	Asn	Leu	Lys	Pro	Glu	Lys	Ser	Tyr	Ser	Phe
1070						1075					1080			
Val	Leu	Thr	Asn	Arg	Gly	Asn	Ser	Ala	Gly	Gly	Leu	Gln	His	Arg
1085						1090					1095			
Val	Thr	Ala	Lys	Thr	Ala	Pro	Asp	Val	Leu	Arg	Thr	Lys	Pro	Ala
1100						1105					1110			
Phe	Ile	Gly	Lys	Thr	Asn	Leu	Asp	Gly	Met	Ile	Thr	Val	Gln	Leu
1115						1120					1125			
Pro	Glu	Val	Pro	Ala	Asn	Glu	Asn	Ile	Lys	Gly	Tyr	Tyr	Ile	Ile
1130						1135					1140			
Ile	Val	Pro	Leu	Lys	Lys	Ser	Arg	Gly	Lys	Phe	Ile	Lys	Pro	Trp
1145						1150					1155			
Glu	Ser	Pro	Asp	Glu	Met	Glu	Leu	Asp	Glu	Leu	Leu	Lys	Glu	Ile
1160						1165					1170			
Ser	Arg	Lys	Arg	Arg	Ser	Ile	Arg	Tyr	Gly	Arg	Glu	Val	Glu	Leu
1175						1180					1185			
Lys	Pro	Tyr	Ile	Ala	Ala	His	Phe	Asp	Val	Leu	Pro	Thr	Glu	Phe
1190						1195					1200			
Thr	Leu	Gly	Asp	Asp	Lys	His	Tyr	Gly	Gly	Phe	Thr	Asn	Lys	Gln
1205						1210					1215			
Leu	Gln	Ser	Gly	Gln	Glu	Tyr	Val	Phe	Phe	Val	Leu	Ala	Val	Met
1220						1225					1230			
Glu	His	Ala	Glu	Ser	Lys	Met	Tyr	Ala	Thr	Ser	Pro	Tyr	Ser	Asp
1235						1240					1245			
Pro	Val	Val	Ser	Met	Asp	Leu	Asp	Pro	Gln	Pro	Ile	Thr	Asp	Glu
1250						1255					1260			
Glu	Glu	Gly	Leu	Ile	Trp	Val	Val	Gly	Pro	Val	Leu	Ala	Val	Val
1265						1270					1275			
Phe	Ile	Ile	Cys	Ile	Val	Ile	Ala	Ile	Leu	Leu	Tyr	Lys	Arg	Lys
1280						1285					1290			
Arg	Ala	Glu	Ser	Asp	Ser	Arg	Lys	Ser	Ser	Ile	Pro	Asn	Asn	Lys
1295						1300					1305			
Glu	Ile	Pro	Ser	His	His	Pro	Thr	Asp	Pro	Val	Glu	Leu	Arg	Arg
1310						1315					1320			
Leu	Asn	Phe	Gln	Thr	Pro	Gly	Met	Ala	Ser	His	Pro	Pro	Ile	Pro
1325						1330					1335			
Ile	Leu	Glu	Leu	Ala	Asp	His	Ile	Glu	Arg	Leu	Lys	Ala	Asn	Asp
1340						1345					1350			
Asn	Leu	Lys	Phe	Ser	Gln	Glu	Tyr	Glu	Ser	Ile	Asp	Pro	Gly	Gln
1355						1360					1365			
Gln	Phe	Thr	Trp	Glu	His	Ser	Asn	Leu	Glu	Val	Asn	Lys	Pro	Lys
1370						1375					1380			
Asn	Arg	Tyr	Ala	Asn	Val	Ile	Ala	Tyr	Asp	His	Ser	Arg	Val	Leu
1385						1390					1395			
Leu	Ser	Ala	Ile	Glu	Gly	Ile	Pro	Gly	Ser	Asp	Tyr	Val	Asn	Ala
1400						1405					1410			
Asn	Tyr	Ile	Asp	Gly	Tyr	Arg	Lys	Gln	Asn	Ala	Tyr	Ile	Ala	Thr
1415						1420					1425			
Gln	Gly	Ser	Leu	Pro	Glu	Thr	Phe	Gly	Asp	Phe	Trp	Arg	Met	Ile

1430						1435						1440					
Trp	Glu	Gln	Arg	Ser	Ala	Thr	Val	Val	Met	Met	Thr	Lys	Leu	Glu			
1445						1450						1455					
Glu	Arg	Ser	Arg	Val	Lys	Cys	Asp	Gln	Tyr	Trp	Pro	Ser	Arg	Gly			
1460						1465						1470					
Thr	Glu	Thr	His	Gly	Leu	Val	Gln	Val	Thr	Leu	Leu	Asp	Thr	Val			
1475						1480						1485					
Glu	Leu	Ala	Thr	Tyr	Cys	Val	Arg	Thr	Phe	Ala	Leu	Tyr	Lys	Asn			
1490						1495						1500					
Gly	Ser	Ser	Glu	Lys	Arg	Glu	Val	Arg	Gln	Phe	Gln	Phe	Thr	Ala			
1505						1510						1515					
Trp	Pro	Asp	His	Gly	Val	Pro	Glu	His	Pro	Thr	Pro	Phe	Leu	Ala			
1520						1525						1530					
Phe	Leu	Arg	Arg	Val	Lys	Thr	Cys	Asn	Pro	Pro	Asp	Ala	Gly	Pro			
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Met	Val	Val	His	Cys	Ser	Ala	Gly	Val	Gly	Arg	Thr	Gly	Cys	Phe			
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Ile	Val	Ile	Asp	Ala	Met	Leu	Glu	Arg	Ile	Lys	His	Glu	Lys	Thr			
1565						1570						1575					
Val	Asp	Ile	Tyr	Gly	His	Val	Thr	Leu	Met	Arg	Ala	Gln	Arg	Asn			
1580						1585						1590					
Tyr	Met	Val	Gln	Thr	Glu	Asp	Gln	Tyr	Ile	Phe	Ile	His	Asp	Ala			
1595						1600						1605					
Leu	Leu	Glu	Ala	Val	Thr	Cys	Gly	Asn	Thr	Glu	Val	Pro	Ala	Arg			
1610						1615						1620					
Asn	Leu	Tyr	Ala	Tyr	Ile	Gln	Lys	Leu	Thr	Gln	Ile	Glu	Thr	Gly			
1625						1630						1635					
Glu	Asn	Val	Thr	Gly	Met	Glu	Leu	Glu	Phe	Lys	Arg	Leu	Ala	Ser			
1640						1645						1650					
Ser	Lys	Ala	His	Thr	Ser	Arg	Phe	Ile	Ser	Ala	Asn	Leu	Pro	Cys			
1655						1660						1665					
Asn	Lys	Phe	Lys	Asn	Arg	Leu	Val	Asn	Ile	Met	Pro	Tyr	Glu	Ser			
1670						1675						1680					
Thr	Arg	Val	Cys	Leu	Gln	Pro	Ile	Arg	Gly	Val	Glu	Gly	Ser	Asp			
1685						1690						1695					
Tyr	Ile	Asn	Ala	Ser	Phe	Ile	Asp	Gly	Tyr	Arg	Gln	Gln	Lys	Ala			
1700						1705						1710					
Tyr	Ile	Ala	Thr	Gln	Gly	Pro	Leu	Ala	Glu	Thr	Thr	Glu	Asp	Phe			
1715						1720						1725					
Trp	Arg	Met	Leu	Trp	Glu	His	Asn	Ser	Thr	Ile	Val	Val	Met	Leu			
1730						1735						1740					
Thr	Lys	Leu	Arg	Glu	Met	Gly	Arg	Glu	Lys	Cys	His	Gln	Tyr	Trp			
1745						1750						1755					
Pro	Ala	Glu	Arg	Ser	Ala	Arg	Tyr	Gln	Tyr	Phe	Val	Val	Asp	Pro			
1760						1765						1770					
Met	Ala	Glu	Tyr	Asn	Met	Pro	Gln	Tyr	Ile	Leu	Arg	Glu	Phe	Lys			
1775						1780						1785					
Val	Thr	Asp	Ala	Arg	Asp	Gly	Gln	Ser	Arg	Thr	Val	Arg	Gln	Phe			
1790						1795						1800					
Gln	Phe	Thr	Asp	Trp	Pro	Glu	Gln	Gly	Val	Pro	Lys	Ser	Gly	Glu			
1805						1810						1815					

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Gly Phe Ile Asp Phe Ile Gly Gln Val His Lys Thr Lys Glu Gln
 1820 1825 1830
 Phe Gly Gln Asp Gly Pro Ile Ser Val His Cys Ser Ala Gly Val
 1835 1840 1845
 Gly Arg Thr Gly Val Phe Ile Thr Leu Ser Ile Val Leu Glu Arg
 1850 1855 1860
 Met Arg Tyr Glu Gly Val Val Asp Ile Phe Gln Thr Val Lys Met
 1865 1870 1875
 Leu Arg Thr Gln Arg Pro Ala Met Val Gln Thr Glu Asp Gln Tyr
 1880 1885 1890
 Gln Phe Ser Tyr Arg Ala Ala Leu Glu Tyr Leu Gly Ser Phe Asp
 1895 1900 1905
 His Tyr Ala Thr
 1910

<210> SEQ ID NO 20
 <211> LENGTH: 819
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapiens
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (1)..(819)
 <223> OTHER INFORMATION: OGTA104 = Swiss Prot Accession No. Q13443,
 ADAM 9

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 Gly Phe Gln Gln Thr Ser His Leu Ser Ser Tyr Glu Ile Ile Thr Pro
 35 40 45
 Trp Arg Leu Thr Arg Glu Arg Arg Glu Ala Pro Arg Pro Tyr Ser Lys
 50 55 60
 Gln Val Ser Tyr Val Ile Gln Ala Glu Gly Lys Glu His Ile Ile His
 65 70 75 80
 Leu Glu Arg Asn Lys Asp Leu Leu Pro Glu Asp Phe Val Val Tyr Thr
 85 90 95
 Tyr Asn Lys Glu Gly Thr Leu Ile Thr Asp His Pro Asn Ile Gln Asn
 100 105 110
 His Cys His Tyr Arg Gly Tyr Val Glu Gly Val His Asn Ser Ser Ile
 115 120 125
 Ala Leu Ser Asp Cys Phe Gly Leu Arg Gly Leu Leu His Leu Glu Asn
 130 135 140
 Ala Ser Tyr Gly Ile Glu Pro Leu Gln Asn Ser Ser His Phe Glu His
 145 150 155 160
 Ile Ile Tyr Arg Met Asp Asp Val Tyr Lys Glu Pro Leu Lys Cys Gly
 165 170 175
 Val Ser Asn Lys Asp Ile Glu Lys Glu Thr Ala Lys Asp Glu Glu Glu
 180 185 190
 Glu Pro Pro Ser Met Thr Gln Leu Leu Arg Arg Arg Arg Ala Val Leu
 195 200 205
 Pro Gln Thr Arg Tyr Val Glu Leu Phe Ile Val Val Asp Lys Glu Arg
 210 215 220

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Tyr	Asp	Met	Met	Gly	Arg	Asn	Gln	Thr	Ala	Val	Arg	Glu	Glu	Met	Ile
225					230					235					240
Leu	Leu	Ala	Asn	Tyr	Leu	Asp	Ser	Met	Tyr	Ile	Met	Leu	Asn	Ile	Arg
			245						250					255	
Ile	Val	Leu	Val	Gly	Leu	Glu	Ile	Trp	Thr	Asn	Gly	Asn	Leu	Ile	Asn
		260						265					270		
Ile	Val	Gly	Gly	Ala	Gly	Asp	Val	Leu	Gly	Asn	Phe	Val	Gln	Trp	Arg
		275				280						285			
Glu	Lys	Phe	Leu	Ile	Thr	Arg	Arg	Arg	His	Asp	Ser	Ala	Gln	Leu	Val
290						295					300				
Leu	Lys	Lys	Gly	Phe	Gly	Gly	Thr	Ala	Gly	Met	Ala	Phe	Val	Gly	Thr
305				310						315					320
Val	Cys	Ser	Arg	Ser	His	Ala	Gly	Gly	Ile	Asn	Val	Phe	Gly	Gln	Ile
				325					330					335	
Thr	Val	Glu	Thr	Phe	Ala	Ser	Ile	Val	Ala	His	Glu	Leu	Gly	His	Asn
		340						345					350		
Leu	Gly	Met	Asn	His	Asp	Asp	Gly	Arg	Asp	Cys	Ser	Cys	Gly	Ala	Lys
355						360						365			
Ser	Cys	Ile	Met	Asn	Ser	Gly	Ala	Ser	Gly	Ser	Arg	Asn	Phe	Ser	Ser
370					375						380				
Cys	Ser	Ala	Glu	Asp	Phe	Glu	Lys	Leu	Thr	Leu	Asn	Lys	Gly	Gly	Asn
385				390						395					400
Cys	Leu	Leu	Asn	Ile	Pro	Lys	Pro	Asp	Glu	Ala	Tyr	Ser	Ala	Pro	Ser
			405						410					415	
Cys	Gly	Asn	Lys	Leu	Val	Asp	Ala	Gly	Glu	Glu	Cys	Asp	Cys	Gly	Thr
		420					425						430		
Pro	Lys	Glu	Cys	Glu	Leu	Asp	Pro	Cys	Cys	Glu	Gly	Ser	Thr	Cys	Lys
	435					440						445			
Leu	Lys	Ser	Phe	Ala	Glu	Cys	Ala	Tyr	Gly	Asp	Cys	Cys	Lys	Asp	Cys
450					455					460					
Arg	Phe	Leu	Pro	Gly	Gly	Thr	Leu	Cys	Arg	Gly	Lys	Thr	Ser	Glu	Cys
465				470						475					480
Asp	Val	Pro	Glu	Tyr	Cys	Asn	Gly	Ser	Ser	Gln	Phe	Cys	Gln	Pro	Asp
			485					490						495	
Val	Phe	Ile	Gln	Asn	Gly	Tyr	Pro	Cys	Gln	Asn	Asn	Lys	Ala	Tyr	Cys
		500					505						510		
Tyr	Asn	Gly	Met	Cys	Gln	Tyr	Tyr	Asp	Ala	Gln	Cys	Gln	Val	Ile	Phe
	515					520						525			
Gly	Ser	Lys	Ala	Lys	Ala	Ala	Pro	Lys	Asp	Cys	Phe	Ile	Glu	Val	Asn
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Ser	Lys	Gly	Asp	Arg	Phe	Gly	Asn	Cys	Gly	Phe	Ser	Gly	Asn	Glu	Tyr
545				550					555						560
Lys	Lys	Cys	Ala	Thr	Gly	Asn	Ala	Leu	Cys	Gly	Lys	Leu	Gln	Cys	Glu
			565					570						575	
Asn	Val	Gln	Glu	Ile	Pro	Val	Phe	Gly	Ile	Val	Pro	Ala	Ile	Ile	Gln
		580					585						590		
Thr	Pro	Ser	Arg	Gly	Thr	Lys	Cys	Trp	Gly	Val	Asp	Phe	Gln	Leu	Gly
	595					600						605			
Ser	Asp	Val	Pro	Asp	Pro	Gly	Met	Val	Asn	Glu	Gly	Thr	Lys	Cys	Gly
610					615						620				

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Ala Gly Lys Ile Cys Arg Asn Phe Gln Cys Val Asp Ala Ser Val Leu
625 630 635 640

Asn Tyr Asp Cys Asp Val Gln Lys Lys Cys His Gly His Gly Val Cys
645 650 655

Asn Ser Asn Lys Asn Cys His Cys Glu Asn Gly Trp Ala Pro Pro Asn
660 665 670

Cys Glu Thr Lys Gly Tyr Gly Gly Ser Val Asp Ser Gly Pro Thr Tyr
675 680 685

Asn Glu Met Asn Thr Ala Leu Arg Asp Gly Leu Leu Val Phe Phe Phe
690 695 700

Leu Ile Val Pro Leu Ile Val Cys Ala Ile Phe Ile Phe Ile Lys Arg
705 710 715 720

Asp Gln Leu Trp Arg Ser Tyr Phe Arg Lys Lys Arg Ser Gln Thr Tyr
725 730 735

Glu Ser Asp Gly Lys Asn Gln Ala Asn Pro Ser Arg Gln Pro Gly Ser
740 745 750

Val Pro Arg His Val Ser Pro Val Thr Pro Pro Arg Glu Val Pro Ile
755 760 765

Tyr Ala Asn Arg Phe Ala Val Pro Thr Tyr Ala Ala Lys Gln Pro Gln
770 775 780

Gln Phe Pro Ser Arg Pro Pro Pro Pro Gln Pro Lys Val Ser Ser Gln
785 790 795 800

Gly Asn Leu Ile Pro Ala Arg Pro Ala Pro Ala Pro Pro Leu Tyr Ser
805 810 815

Ser Leu Thr

<210> SEQ ID NO 21
<211> LENGTH: 2003
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(2003)
<223> OTHER INFORMATION: OGTA106 = Swiss Prot Accession No. Q99466,
Neurogenic locus notch homologue protein 4

<400> SEQUENCE: 21

Met Gln Pro Pro Ser Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu
1 5 10 15

Cys Val Ser Val Val Arg Pro Arg Gly Leu Leu Cys Gly Ser Phe Pro
20 25 30

Glu Pro Cys Ala Asn Gly Gly Thr Cys Leu Ser Leu Ser Leu Gly Gln
35 40 45

Gly Thr Cys Gln Cys Ala Pro Gly Phe Leu Gly Glu Thr Cys Gln Phe
50 55 60

Pro Asp Pro Cys Gln Asn Ala Gln Leu Cys Gln Asn Gly Gly Ser Cys
65 70 75 80

Gln Ala Leu Leu Pro Ala Pro Leu Gly Leu Pro Ser Ser Pro Ser Pro
85 90 95

Leu Thr Pro Ser Phe Leu Cys Thr Cys Leu Pro Gly Phe Thr Gly Glu
100 105 110

Arg Cys Gln Ala Lys Leu Glu Asp Pro Cys Pro Pro Ser Phe Cys Ser
115 120 125

Lys Arg Gly Arg Cys His Ile Gln Ala Ser Gly Arg Pro Gln Cys Ser

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130					135					140					
Cys 145	Met	Pro	Gly	Trp	Thr 150	Gly	Glu	Gln	Cys	Gln 155	Leu	Arg	Asp	Phe	Cys 160
Ser	Ala	Asn	Pro	Cys 165	Val	Asn	Gly	Gly	Val 170	Cys	Leu	Ala	Thr	Tyr 175	Pro
Gln	Ile	Gln	Cys 180	His	Cys	Pro	Pro	Gly 185	Phe	Glu	Gly	His 190	Ala	Cys	Glu
Arg	Asp	Val 195	Asn	Glu	Cys	Phe	Gln 200	Asp	Pro	Gly	Pro 205	Cys	Pro	Lys	Gly
Thr	Ser 210	Cys	His	Asn	Thr 215	Leu	Gly	Ser	Phe	Gln 220	Cys	Leu	Cys	Pro	Val
Gly 225	Gln	Glu	Gly	Pro 230	Arg	Cys	Glu	Leu	Arg 235	Ala	Gly	Pro	Cys	Pro	Pro 240
Arg	Gly	Cys	Ser 245	Asn	Gly	Gly	Thr	Cys	Gln 250	Leu	Met	Pro	Glu 255	Lys	Asp
Ser	Thr	Phe 260	His	Leu	Cys	Leu	Cys 265	Pro	Pro	Gly	Phe	Ile 270	Gly	Pro	Asp
Cys	Glu 275	Val	Asn	Pro	Asp	Asn 280	Cys	Val	Ser	His	Gln 285	Cys	Gln	Asn	Gly
Gly 290	Thr	Cys	Gln	Asp	Gly 295	Leu	Asp	Thr	Tyr	Thr 300	Cys	Leu	Cys	Pro	Glu
Thr 305	Trp	Thr	Gly	Trp 310	Asp	Cys	Ser	Glu	Asp 315	Val	Asp	Glu	Cys	Glu	Thr 320
Gln	Gly	Pro	Pro 325	His	Cys	Arg	Asn	Gly 330	Gly	Thr	Cys	Gln	Asn 335	Ser	Ala
Gly	Ser	Phe 340	His	Cys	Val	Cys	Val 345	Ser	Gly	Trp	Gly	Gly 350	Thr	Ser	Cys
Glu	Glu 355	Asn	Leu	Asp	Asp	Cys	Ile 360	Ala	Ala	Thr	Cys 365	Ala	Pro	Gly	Ser
Thr 370	Cys	Ile	Asp	Arg	Val 375	Gly	Ser	Phe	Ser	Cys 380	Leu	Cys	Pro	Pro	Gly
Arg 385	Thr	Gly	Leu	Leu 390	Cys	His	Leu	Glu	Asp 395	Met	Cys	Leu	Ser	Gln	Pro 400
Cys	His	Gly	Asp 405	Ala	Gln	Cys	Ser	Thr	Asn 410	Pro	Leu	Thr	Gly 415	Ser	Thr
Leu	Cys	Leu 420	Cys	Gln	Pro	Gly	Tyr 425	Ser	Gly	Pro	Thr	Cys 430	His	Gln	Asp
Leu	Asp 435	Glu	Cys	Leu	Met	Ala 440	Gln	Gly	Pro	Ser	Pro 445	Cys	Glu	His	
Gly 450	Gly	Ser	Cys	Leu	Asn 455	Thr	Pro	Gly	Ser	Phe 460	Asn	Cys	Leu	Cys	Pro
Pro 465	Gly	Tyr	Thr	Gly 470	Ser	Arg	Cys	Glu	Ala 475	Asp	His	Asn	Glu	Cys	Leu 480
Ser	Gln	Pro	Cys 485	His	Pro	Gly	Ser	Thr	Cys 490	Leu	Asp	Leu	Leu	Ala	Thr 495
Phe	His	Cys 500	Leu	Cys	Pro	Pro	Gly	Leu 505	Glu	Gly	Gln	Leu 510	Cys	Glu	Val
Glu	Thr 515	Asn	Glu	Cys	Ala	Ser	Ala 520	Pro	Cys	Leu	Asn 525	His	Ala	Asp	Cys
His	Asp 530	Leu	Leu	Asn	Gly 535	Phe	Gln	Cys	Ile	Cys 540	Leu	Pro	Gly	Phe	Ser

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Gly	Thr	Arg	Cys	Glu	Glu	Asp	Ile	Asp	Glu	Cys	Arg	Ser	Ser	Pro	Cys	545	550	555	560
Ala	Asn	Gly	Gly	Gln	Cys	Gln	Asp	Gln	Pro	Gly	Ala	Phe	His	Cys	Lys	565	570	575	
Cys	Leu	Pro	Gly	Phe	Glu	Gly	Pro	Arg	Cys	Gln	Thr	Glu	Val	Asp	Glu	580	585	590	
Cys	Leu	Ser	Asp	Pro	Cys	Pro	Val	Gly	Ala	Ser	Cys	Leu	Asp	Leu	Pro	595	600	605	
Gly	Ala	Phe	Phe	Cys	Leu	Cys	Pro	Ser	Gly	Phe	Thr	Gly	Gln	Leu	Cys	610	615	620	
Glu	Val	Pro	Leu	Cys	Ala	Pro	Asn	Leu	Cys	Gln	Pro	Lys	Gln	Ile	Cys	625	630	635	640
Lys	Asp	Gln	Lys	Asp	Lys	Ala	Asn	Cys	Leu	Cys	Pro	Asp	Gly	Ser	Pro	645	650	655	
Gly	Cys	Ala	Pro	Pro	Glu	Asp	Asn	Cys	Thr	Cys	His	His	Gly	His	Cys	660	665	670	
Gln	Arg	Ser	Ser	Cys	Val	Cys	Asp	Val	Gly	Trp	Thr	Gly	Pro	Glu	Cys	675	680	685	
Glu	Ala	Glu	Leu	Gly	Gly	Cys	Ile	Ser	Ala	Pro	Cys	Ala	His	Gly	Gly	690	695	700	
Thr	Cys	Tyr	Pro	Gln	Pro	Ser	Gly	Tyr	Asn	Cys	Thr	Cys	Pro	Thr	Gly	705	710	715	720
Tyr	Thr	Gly	Pro	Thr	Cys	Ser	Glu	Glu	Met	Thr	Ala	Cys	His	Ser	Gly	725	730	735	
Pro	Cys	Leu	Asn	Gly	Gly	Ser	Cys	Asn	Pro	Ser	Pro	Gly	Gly	Tyr	Tyr	740	745	750	
Cys	Thr	Cys	Pro	Pro	Ser	His	Thr	Gly	Pro	Gln	Cys	Gln	Thr	Ser	Thr	755	760	765	
Asp	Tyr	Cys	Val	Ser	Ala	Pro	Cys	Phe	Asn	Gly	Gly	Thr	Cys	Val	Asn	770	775	780	
Arg	Pro	Gly	Thr	Phe	Ser	Cys	Leu	Cys	Ala	Met	Gly	Phe	Gln	Gly	Pro	785	790	795	800
Arg	Cys	Glu	Gly	Lys	Leu	Arg	Pro	Ser	Cys	Ala	Asp	Ser	Pro	Cys	Arg	805	810	815	
Asn	Arg	Ala	Thr	Cys	Gln	Asp	Ser	Pro	Gln	Gly	Pro	Arg	Cys	Leu	Cys	820	825	830	
Pro	Thr	Gly	Tyr	Thr	Gly	Gly	Ser	Cys	Gln	Thr	Leu	Met	Asp	Leu	Cys	835	840	845	
Ala	Gln	Lys	Pro	Cys	Pro	Arg	Asn	Ser	His	Cys	Leu	Gln	Thr	Gly	Pro	850	855	860	
Ser	Phe	His	Cys	Leu	Cys	Leu	Gln	Gly	Trp	Thr	Gly	Pro	Leu	Cys	Asn	865	870	875	880
Leu	Pro	Leu	Ser	Ser	Cys	Gln	Lys	Ala	Ala	Leu	Ser	Gln	Gly	Ile	Asp	885	890	895	
Val	Ser	Ser	Leu	Cys	His	Asn	Gly	Gly	Leu	Cys	Val	Asp	Ser	Gly	Pro	900	905	910	
Ser	Tyr	Phe	Cys	His	Cys	Pro	Pro	Gly	Phe	Gln	Gly	Ser	Leu	Cys	Gln	915	920	925	
Asp	His	Val	Asn	Pro	Cys	Glu	Ser	Arg	Pro	Cys	Gln	Asn	Gly	Ala	Thr	930	935	940	

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Cys Met Ala Gln Pro Ser Gly Tyr Leu Cys Gln Cys Ala Pro Gly Tyr	
945	950 955 960
Asp Gly Gln Asn Cys Ser Lys Glu Leu Asp Ala Cys Gln Ser Gln Pro	
	965 970 975
Cys His Asn His Gly Thr Cys Thr Pro Lys Pro Gly Gly Phe His Cys	
	980 985 990
Ala Cys Pro Pro Gly Phe Val Gly Leu Arg Cys Glu Gly Asp Val Asp	
	995 1000 1005
Glu Cys Leu Asp Gln Pro Cys His Pro Thr Gly Thr Ala Ala Cys	
	1010 1015 1020
His Ser Leu Ala Asn Ala Phe Tyr Cys Gln Cys Leu Pro Gly His	
	1025 1030 1035
Thr Gly Gln Trp Cys Glu Val Glu Ile Asp Pro Cys His Ser Gln	
	1040 1045 1050
Pro Cys Phe His Gly Gly Thr Cys Glu Ala Thr Ala Gly Ser Pro	
	1055 1060 1065
Leu Gly Phe Ile Cys His Cys Pro Lys Gly Phe Glu Gly Pro Thr	
	1070 1075 1080
Cys Ser His Arg Ala Pro Ser Cys Gly Phe His His Cys His His	
	1085 1090 1095
Gly Gly Leu Cys Leu Pro Ser Pro Lys Pro Gly Phe Pro Pro Arg	
	1100 1105 1110
Cys Ala Cys Leu Ser Gly Tyr Gly Gly Pro Asp Cys Leu Thr Pro	
	1115 1120 1125
Pro Ala Pro Lys Gly Cys Gly Pro Pro Ser Pro Cys Leu Tyr Asn	
	1130 1135 1140
Gly Ser Cys Ser Glu Thr Thr Gly Leu Gly Gly Pro Gly Phe Arg	
	1145 1150 1155
Cys Ser Cys Pro His Ser Ser Pro Gly Pro Arg Cys Gln Lys Pro	
	1160 1165 1170
Gly Ala Lys Gly Cys Glu Gly Arg Ser Gly Asp Gly Ala Cys Asp	
	1175 1180 1185
Ala Gly Cys Ser Gly Pro Gly Gly Asn Trp Asp Gly Gly Asp Cys	
	1190 1195 1200
Ser Leu Gly Val Pro Asp Pro Trp Lys Gly Cys Pro Ser His Ser	
	1205 1210 1215
Arg Cys Trp Leu Leu Phe Arg Asp Gly Gln Cys His Pro Gln Cys	
	1220 1225 1230
Asp Ser Glu Glu Cys Leu Phe Asp Gly Tyr Asp Cys Glu Thr Pro	
	1235 1240 1245
Pro Ala Cys Thr Pro Ala Tyr Asp Gln Tyr Cys His Asp His Phe	
	1250 1255 1260
His Asn Gly His Cys Glu Lys Gly Cys Asn Thr Ala Glu Cys Gly	
	1265 1270 1275
Trp Asp Gly Gly Asp Cys Arg Pro Glu Asp Gly Asp Pro Glu Trp	
	1280 1285 1290
Gly Pro Ser Leu Ala Leu Leu Val Val Leu Ser Pro Pro Ala Leu	
	1295 1300 1305
Asp Gln Gln Leu Phe Ala Leu Ala Arg Val Leu Ser Leu Thr Leu	
	1310 1315 1320
Arg Val Gly Leu Trp Val Arg Lys Asp Arg Asp Gly Arg Asp Met	

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1325					1330					1335				
Val Tyr	Pro Tyr	Pro Gly	Ala	Arg	Ala Glu	Glu Lys	Leu Gly	Gly						
1340			1345			1350								
Thr Arg	Asp Pro	Thr Tyr	Gln	Glu Arg	Ala Ala	Pro	Gln Thr	Gln						
1355			1360			1365								
Pro Leu	Gly Lys	Glu Thr	Asp	Ser	Leu Ser	Ala Gly	Phe Val	Val						
1370			1375			1380								
Val Met	Gly Val	Asp Leu	Ser	Arg	Cys Gly	Pro Asp	His Pro	Ala						
1385			1390			1395								
Ser Arg	Cys Pro	Trp Asp	Pro	Gly	Leu Leu	Leu Arg	Phe Leu	Ala						
1400			1405			1410								
Ala Met	Ala Ala	Val Gly	Ala	Leu	Glu Pro	Leu Leu	Pro Gly	Pro						
1415			1420			1425								
Leu Leu	Ala Val	His Pro	His	Ala	Gly Thr	Ala Pro	Pro Ala	Asn						
1430			1435			1440								
Gln Leu	Pro Trp	Pro Val	Leu	Cys	Ser Pro	Val Ala	Gly Val	Ile						
1445			1450			1455								
Leu Leu	Ala Leu	Gly Ala	Leu	Leu	Val Leu	Gln Leu	Ile Arg	Arg						
1460			1465			1470								
Arg Arg	Arg Glu	His Gly	Ala	Leu	Trp Leu	Pro Pro	Gly Phe	Thr						
1475			1480			1485								
Arg Arg	Pro Arg	Thr Gln	Ser	Ala	Pro His	Arg Arg	Arg Pro	Pro						
1490			1495			1500								
Leu Gly	Glu Asp	Ser Ile	Gly	Leu	Lys Ala	Leu Lys	Pro Lys	Ala						
1505			1510			1515								
Glu Val	Asp Glu	Asp Gly	Val	Val	Met Cys	Ser Gly	Pro Glu	Glu						
1520			1525			1530								
Gly Glu	Glu Val	Gly Gln	Ala	Glu	Glu Thr	Gly Pro	Pro Ser	Thr						
1535			1540			1545								
Cys Gln	Leu Trp	Ser Leu	Ser	Gly	Gly Cys	Gly Ala	Leu Pro	Gln						
1550			1555			1560								
Ala Ala	Met Leu	Thr Pro	Pro	Gln	Glu Ser	Glu Met	Glu Ala	Pro						
1565			1570			1575								
Asp Leu	Asp Thr	Arg Gly	Pro	Asp	Gly Val	Thr Pro	Leu Met	Ser						
1580			1585			1590								
Ala Val	Cys Cys	Gly Glu	Val	Gln	Ser Gly	Thr Phe	Gln Gly	Ala						
1595			1600			1605								
Trp Leu	Gly Cys	Pro Glu	Pro	Trp	Glu Pro	Leu Leu	Asp Gly	Gly						
1610			1615			1620								
Ala Cys	Pro Gln	Ala His	Thr	Val	Gly Thr	Gly Glu	Thr Pro	Leu						
1625			1630			1635								
His Leu	Ala Ala	Arg Phe	Ser	Arg	Pro Thr	Ala Ala	Arg Arg	Leu						
1640			1645			1650								
Leu Glu	Ala Gly	Ala Asn	Pro	Asn	Gln Pro	Asp Arg	Ala Gly	Arg						
1655			1660			1665								
Thr Pro	Leu His	Ala Ala	Val	Ala	Ala Asp	Ala Arg	Glu Val	Cys						
1670			1675			1680								
Gln Leu	Leu Leu	Arg Ser	Arg	Gln	Thr Ala	Val Asp	Ala Arg	Thr						
1685			1690			1695								
Glu Asp	Gly Thr	Thr Pro	Leu	Met	Leu Ala	Ala Arg	Leu Ala	Val						
1700			1705			1710								

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Glu Asp Leu Val Glu Glu Leu Ile Ala Ala Gln Ala Asp Val Gly
 1715 1720 1725
 Ala Arg Asp Lys Trp Gly Lys Thr Ala Leu His Trp Ala Ala Ala
 1730 1735 1740
 Val Asn Asn Ala Arg Ala Ala Arg Ser Leu Leu Gln Ala Gly Ala
 1745 1750 1755
 Asp Lys Asp Ala Gln Asp Asn Arg Glu Gln Thr Pro Leu Phe Leu
 1760 1765 1770
 Ala Ala Arg Glu Gly Ala Val Glu Val Ala Gln Leu Leu Leu Gly
 1775 1780 1785
 Leu Gly Ala Ala Arg Glu Leu Arg Asp Gln Ala Gly Leu Ala Pro
 1790 1795 1800
 Ala Asp Val Ala His Gln Arg Asn His Trp Asp Leu Leu Thr Leu
 1805 1810 1815
 Leu Glu Gly Ala Gly Pro Pro Glu Ala Arg His Lys Ala Thr Pro
 1820 1825 1830
 Gly Arg Glu Ala Gly Pro Phe Pro Arg Ala Arg Thr Val Ser Val
 1835 1840 1845
 Ser Val Pro Pro His Gly Gly Gly Ala Leu Pro Arg Cys Arg Thr
 1850 1855 1860
 Leu Ser Ala Gly Ala Gly Pro Arg Gly Gly Gly Ala Cys Leu Gln
 1865 1870 1875
 Ala Arg Thr Trp Ser Val Asp Leu Ala Ala Arg Gly Gly Gly Ala
 1880 1885 1890
 Tyr Ser His Cys Arg Ser Leu Ser Gly Val Gly Ala Gly Gly Gly
 1895 1900 1905
 Pro Thr Pro Arg Gly Arg Arg Phe Ser Ala Gly Met Arg Gly Pro
 1910 1915 1920
 Arg Pro Asn Pro Ala Ile Met Arg Gly Arg Tyr Gly Val Ala Ala
 1925 1930 1935
 Gly Arg Gly Gly Arg Val Ser Thr Asp Asp Trp Pro Cys Asp Trp
 1940 1945 1950
 Val Ala Leu Gly Ala Cys Gly Ser Ala Ser Asn Ile Pro Ile Pro
 1955 1960 1965
 Pro Pro Cys Leu Thr Pro Ser Pro Glu Arg Gly Ser Pro Gln Leu
 1970 1975 1980
 Asp Cys Gly Pro Pro Ala Leu Gln Glu Met Pro Ile Asn Gln Gly
 1985 1990 1995
 Gly Glu Gly Lys Lys
 2000

<210> SEQ ID NO 22
 <211> LENGTH: 390
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapiens
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (1)..(390)
 <223> OTHER INFORMATION: OGTA112 = Swiss Prot Accession No. P48594,
 Serpin B4

<400> SEQUENCE: 22

Met Asn Ser Leu Ser Glu Ala Asn Thr Lys Phe Met Phe Asp Leu Phe
 1 5 10 15

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Gln Gln Phe Arg Lys Ser Lys Glu Asn Asn Ile Phe Tyr Ser Pro Ile
 20 25 30
 Ser Ile Thr Ser Ala Leu Gly Met Val Leu Leu Gly Ala Lys Asp Asn
 35 40 45
 Thr Ala Gln Gln Ile Ser Lys Val Leu His Phe Asp Gln Val Thr Glu
 50 55 60
 Asn Thr Thr Glu Lys Ala Ala Thr Tyr His Val Asp Arg Ser Gly Asn
 65 70 75 80
 Val His His Gln Phe Gln Lys Leu Leu Thr Glu Phe Asn Lys Ser Thr
 85 90 95
 Asp Ala Tyr Glu Leu Lys Ile Ala Asn Lys Leu Phe Gly Glu Lys Thr
 100 105 110
 Tyr Gln Phe Leu Gln Glu Tyr Leu Asp Ala Ile Lys Lys Phe Tyr Gln
 115 120 125
 Thr Ser Val Glu Ser Thr Asp Phe Ala Asn Ala Pro Glu Glu Ser Arg
 130 135 140
 Lys Lys Ile Asn Ser Trp Val Glu Ser Gln Thr Asn Glu Lys Ile Lys
 145 150 155 160
 Asn Leu Phe Pro Asp Gly Thr Ile Gly Asn Asp Thr Thr Leu Val Leu
 165 170 175
 Val Asn Ala Ile Tyr Phe Lys Gly Gln Trp Glu Asn Lys Phe Lys Lys
 180 185 190
 Glu Asn Thr Lys Glu Glu Lys Phe Trp Pro Asn Lys Asn Thr Tyr Lys
 195 200 205
 Ser Val Gln Met Met Arg Gln Tyr Asn Ser Phe Asn Phe Ala Leu Leu
 210 215 220
 Glu Asp Val Gln Ala Lys Val Leu Glu Ile Pro Tyr Lys Gly Lys Asp
 225 230 235 240
 Leu Ser Met Ile Val Leu Leu Pro Asn Glu Ile Asp Gly Leu Gln Lys
 245 250 255
 Leu Glu Glu Lys Leu Thr Ala Glu Lys Leu Met Glu Trp Thr Ser Leu
 260 265 270
 Gln Asn Met Arg Glu Thr Cys Val Asp Leu His Leu Pro Arg Phe Lys
 275 280 285
 Met Glu Glu Ser Tyr Asp Leu Lys Asp Thr Leu Arg Thr Met Gly Met
 290 295 300
 Val Asn Ile Phe Asn Gly Asp Ala Asp Leu Ser Gly Met Thr Trp Ser
 305 310 315 320
 His Gly Leu Ser Val Ser Lys Val Leu His Lys Ala Phe Val Glu Val
 325 330 335
 Thr Glu Glu Gly Val Glu Ala Ala Ala Thr Ala Val Val Val Val
 340 345 350
 Glu Leu Ser Ser Pro Ser Thr Asn Glu Glu Phe Cys Cys Asn His Pro
 355 360 365
 Phe Leu Phe Phe Ile Arg Gln Asn Lys Thr Asn Ser Ile Leu Phe Tyr
 370 375 380
 Gly Arg Phe Ser Ser Pro
 385 390

<210> SEQ ID NO 23

<211> LENGTH: 400

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<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(400)
<223> OTHER INFORMATION: OGTA113 = Swiss Prot Accession No. Q9BTV4,
    Transmembrane protein 43

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<400> SEQUENCE: 23

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Met Ala Ala Asn Tyr Ser Ser Thr Ser Thr Arg Arg Glu His Val Lys
 1          5          10          15

Val Lys Thr Ser Ser Gln Pro Gly Phe Leu Glu Arg Leu Ser Glu Thr
20          25          30

Ser Gly Gly Met Phe Val Gly Leu Met Ala Phe Leu Leu Ser Phe Tyr
35          40          45

Leu Ile Phe Thr Asn Glu Gly Arg Ala Leu Lys Thr Ala Thr Ser Leu
50          55          60

Ala Glu Gly Leu Ser Leu Val Val Ser Pro Asp Ser Ile His Ser Val
65          70          75          80

Ala Pro Glu Asn Glu Gly Arg Leu Val His Ile Ile Gly Ala Leu Arg
      85          90          95

Thr Ser Lys Leu Leu Ser Asp Pro Asn Tyr Gly Val His Leu Pro Ala
      100          105          110

Val Lys Leu Arg Arg His Val Glu Met Tyr Gln Trp Val Glu Thr Glu
      115          120          125

Glu Ser Arg Glu Tyr Thr Glu Asp Gly Gln Val Lys Lys Glu Thr Arg
      130          135          140

Tyr Ser Tyr Asn Thr Glu Trp Arg Ser Glu Ile Ile Asn Ser Lys Asn
      145          150          155          160

Phe Asp Arg Glu Ile Gly His Lys Asn Pro Ser Ala Met Ala Val Glu
      165          170          175

Ser Phe Met Ala Thr Ala Pro Phe Val Gln Ile Gly Arg Phe Phe Leu
      180          185          190

Ser Ser Gly Leu Ile Asp Lys Val Asp Asn Phe Lys Ser Leu Ser Leu
      195          200          205

Ser Lys Leu Glu Asp Pro His Val Asp Ile Ile Arg Arg Gly Asp Phe
      210          215          220

Phe Tyr His Ser Glu Asn Pro Lys Tyr Pro Glu Val Gly Asp Leu Arg
      225          230          235          240

Val Ser Phe Ser Tyr Ala Gly Leu Ser Gly Asp Asp Pro Asp Leu Gly
      245          250          255

Pro Ala His Val Val Thr Val Ile Ala Arg Gln Arg Gly Asp Gln Leu
      260          265          270

Val Pro Phe Ser Thr Lys Ser Gly Asp Thr Leu Leu Leu Leu His His
      275          280          285

Gly Asp Phe Ser Ala Glu Glu Val Phe His Arg Glu Leu Arg Ser Asn
      290          295          300

Ser Met Lys Thr Trp Gly Leu Arg Ala Ala Gly Trp Met Ala Met Phe
      305          310          315          320

Met Gly Leu Asn Leu Met Thr Arg Ile Leu Tyr Thr Leu Val Asp Trp
      325          330          335

Phe Pro Val Phe Arg Asp Leu Val Asn Ile Gly Leu Lys Ala Phe Ala
      340          345          350

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Phe Cys Val Ala Thr Ser Leu Thr Leu Leu Thr Val Ala Ala Gly Trp
355 360 365

Leu Phe Tyr Arg Pro Leu Trp Ala Leu Leu Ile Ala Gly Leu Ala Leu
370 375 380

Val Pro Ile Leu Val Ala Arg Thr Arg Val Pro Ala Lys Lys Leu Glu
385 390 395 400

<210> SEQ ID NO 24

<211> LENGTH: 893

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<222> LOCATION: (1)..(893)

<223> OTHER INFORMATION: OGTA119 = Swiss Prot Accession No. Q6UKI4,
KIAA1228 protein

<400> SEQUENCE: 24

Met Thr Pro Pro Ser Arg Ala Glu Ala Gly Val Arg Arg Ser Arg Val
1 5 10 15

Pro Ser Glu Gly Arg Trp Arg Gly Ala Glu Pro Pro Gly Ile Ser Ala
20 25 30

Ser Thr Gln Pro Ala Ser Ala Gly Arg Ala Ala Arg His Cys Gly Ala
35 40 45

Met Ser Gly Ala Arg Gly Glu Gly Pro Glu Ala Gly Ala Gly Gly Ala
50 55 60

Gly Gly Arg Ala Ala Pro Glu Asn Pro Gly Gly Val Leu Ser Val Glu
65 70 75 80

Leu Pro Gly Leu Leu Ala Gln Leu Ala Arg Ser Phe Ala Leu Leu Leu
85 90 95

Pro Val Tyr Ala Leu Gly Tyr Leu Gly Leu Ser Phe Ser Trp Val Leu
100 105 110

Leu Ala Leu Ala Leu Leu Ala Trp Cys Arg Arg Ser Arg Gly Leu Lys
115 120 125

Ala Leu Arg Leu Cys Arg Ala Leu Ala Leu Leu Glu Asp Glu Glu Arg
130 135 140

Val Val Arg Leu Gly Val Arg Ala Cys Asp Leu Pro Ala Trp Val His
145 150 155 160

Phe Pro Asp Thr Glu Arg Ala Glu Trp Leu Asn Lys Thr Val Lys His
165 170 175

Met Trp Pro Phe Ile Cys Gln Phe Ile Glu Lys Leu Phe Arg Glu Thr
180 185 190

Ile Glu Pro Ala Val Arg Gly Ala Asn Thr His Leu Ser Thr Phe Ser
195 200 205

Phe Thr Lys Val Asp Val Gly Gln Gln Pro Leu Arg Ile Asn Gly Val
210 215 220

Lys Val Tyr Thr Glu Asn Val Asp Lys Arg Gln Ile Ile Leu Asp Leu
225 230 235 240

Gln Ile Ser Phe Val Gly Asn Cys Glu Ile Asp Leu Glu Ile Lys Arg
245 250 255

Tyr Phe Cys Arg Ala Gly Val Lys Ser Ile Gln Ile His Gly Thr Met
260 265 270

Arg Val Ile Leu Glu Pro Leu Ile Gly Asp Met Pro Leu Val Gly Ala
275 280 285

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Leu	Ser	Ile	Phe	Phe	Leu	Arg	Lys	Pro	Leu	Leu	Glu	Ile	Asn	Trp	Thr
290						295					300				
Gly	Leu	Thr	Asn	Leu	Leu	Asp	Val	Pro	Gly	Leu	Asn	Gly	Leu	Ser	Asp
305					310					315					320
Thr	Ile	Ile	Leu	Asp	Ile	Ile	Ser	Asn	Tyr	Leu	Val	Leu	Pro	Asn	Arg
				325					330					335	
Ile	Thr	Val	Pro	Leu	Val	Ser	Glu	Val	Gln	Ile	Ala	Gln	Leu	Arg	Phe
			340					345						350	
Pro	Val	Pro	Lys	Gly	Val	Leu	Arg	Ile	His	Phe	Ile	Glu	Ala	Gln	Asp
		355					360					365			
Leu	Gln	Gly	Lys	Asp	Thr	Tyr	Leu	Lys	Gly	Leu	Val	Lys	Gly	Lys	Ser
	370					375					380				
Asp	Pro	Tyr	Gly	Ile	Ile	Arg	Val	Gly	Asn	Gln	Ile	Phe	Gln	Ser	Arg
385					390					395					400
Val	Ile	Lys	Glu	Asn	Leu	Ser	Pro	Lys	Trp	Asn	Glu	Val	Tyr	Glu	Ala
				405					410					415	
Leu	Val	Tyr	Glu	His	Pro	Gly	Gln	Glu	Leu	Glu	Ile	Glu	Leu	Phe	Asp
			420					425					430		
Glu	Asp	Pro	Asp	Lys	Asp	Asp	Phe	Leu	Gly	Ser	Leu	Met	Ile	Asp	Leu
		435					440					445			
Ile	Glu	Val	Glu	Lys	Glu	Arg	Leu	Leu	Asp	Glu	Trp	Phe	Thr	Leu	Asp
	450					455					460				
Glu	Val	Pro	Lys	Gly	Lys	Leu	His	Leu	Arg	Leu	Glu	Trp	Leu	Thr	Leu
465					470					475					480
Met	Pro	Asn	Ala	Ser	Asn	Leu	Asp	Lys	Val	Leu	Thr	Asp	Ile	Lys	Ala
				485					490					495	
Asp	Lys	Asp	Gln	Ala	Asn	Asp	Gly	Leu	Ser	Ser	Ala	Leu	Leu	Ile	Leu
			500					505					510		
Tyr	Leu	Asp	Ser	Ala	Arg	Asn	Leu	Pro	Ser	Gly	Lys	Lys	Ile	Ser	Ser
		515				520						525			
Asn	Pro	Asn	Pro	Val	Val	Gln	Met	Ser	Val	Gly	His	Lys	Ala	Gln	Glu
						535					540				
Ser	Lys	Ile	Arg	Tyr	Lys	Thr	Asn	Glu	Pro	Val	Trp	Glu	Glu	Asn	Phe
545					550					555					560
Thr	Phe	Phe	Ile	His	Asn	Pro	Lys	Arg	Gln	Asp	Leu	Glu	Val	Glu	Val
				565					570					575	
Arg	Asp	Glu	Gln	His	Gln	Cys	Ser	Leu	Gly	Asn	Leu	Lys	Val	Pro	Leu
				580				585					590		
Ser	Gln	Leu	Leu	Thr	Ser	Glu	Asp	Met	Thr	Val	Ser	Gln	Arg	Phe	Gln
		595					600					605			
Leu	Ser	Asn	Ser	Gly	Pro	Asn	Ser	Thr	Ile	Lys	Met	Lys	Ile	Ala	Leu
		610				615					620				
Arg	Val	Leu	His	Leu	Glu	Lys	Arg	Glu	Arg	Pro	Pro	Asp	His	Gln	His
625					630					635					640
Ser	Ala	Gln	Val	Lys	Arg	Pro	Ser	Val	Ser	Lys	Glu	Gly	Arg	Lys	Thr
				645					650					655	
Ser	Ile	Lys	Ser	His	Met	Ser	Gly	Ser	Pro	Gly	Pro	Gly	Gly	Ser	Asn
			660					665					670		
Thr	Ala	Pro	Ser	Thr	Pro	Val	Ile	Gly	Gly	Ser	Asp	Lys	Pro	Gly	Met
		675					680					685			
Glu	Glu	Lys	Ala	Gln	Pro	Pro	Glu	Ala	Gly	Pro	Gln	Gly	Leu	His	Asp

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690	695	700
Leu Gly Arg Ser Ser	Ser Ser Leu Leu Ala Ser	Pro Gly His Ile Ser
705	710	715 720
Val Lys Glu Pro Thr	Pro Ser Ile Ala Ser Asp	Ile Ser Leu Pro Ile
	725	730 735
Ala Thr Gln Glu Leu Arg	Gln Arg Leu Arg Gln Leu Glu Asn Gly Thr	
	740	745 750
Thr Leu Gly Gln Ser Pro	Leu Gly Gln Ile Gln Leu Thr Ile Arg His	
	755	760 765
Ser Ser Gln Arg Asn Lys	Leu Ile Val Val Val His Ala Cys Arg Asn	
	770	775 780
Leu Ile Ala Phe Ser Glu	Asp Gly Ser Asp Pro Tyr Val Arg Met Tyr	
	785	790 795 800
Leu Leu Pro Asp Lys	Arg Arg Ser Gly Arg Arg Lys Thr His Val Ser	
	805	810 815
Lys Lys Thr Leu Asn Pro	Val Phe Asp Gln Ser Phe Asp Phe Ser Val	
	820	825 830
Ser Leu Pro Glu Val Gln	Arg Arg Thr Leu Asp Val Ala Val Lys Asn	
	835	840 845
Ser Gly Gly Phe Leu Ser	Lys Asp Lys Gly Leu Leu Gly Lys Val Leu	
	850	855 860
Val Ala Leu Ala Ser Glu	Glu Leu Ala Lys Gly Trp Thr Gln Trp Tyr	
	865	870 875 880
Asp Leu Thr Glu Asp Gly	Thr Arg Pro Gln Ala Met Thr	
	885	890

<210> SEQ ID NO 25
 <211> LENGTH: 1085
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapiens
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (1)..(1085)
 <223> OTHER INFORMATION: OGTA124 = Swiss Prot Accession No. Q9UP95,
 Solute carrier family 12 member 4

<400> SEQUENCE: 25

Met Pro His Phe Thr Val Val Pro Val Asp Gly Pro Arg Arg Gly Asp
1 5 10 15
Tyr Asp Asn Leu Glu Gly Leu Ser Trp Val Asp Tyr Gly Glu Arg Ala
20 25 30
Glu Leu Asp Asp Ser Asp Gly His Gly Asn His Arg Glu Ser Ser Pro
35 40 45
Phe Leu Ser Pro Leu Glu Ala Ser Arg Gly Ile Asp Tyr Tyr Asp Arg
50 55 60
Asn Leu Ala Leu Phe Glu Glu Glu Leu Asp Ile Arg Pro Lys Val Ser
65 70 75 80
Ser Leu Leu Gly Lys Leu Val Ser Tyr Thr Asn Leu Thr Gln Gly Ala
85 90 95
Lys Glu His Glu Glu Ala Glu Ser Gly Glu Gly Thr Arg Arg Arg Ala
100 105 110
Ala Glu Ala Pro Ser Met Gly Thr Leu Met Gly Val Tyr Leu Pro Cys
115 120 125
Leu Gln Asn Ile Phe Gly Val Ile Leu Phe Leu Arg Leu Thr Trp Met

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130					135					140					
Val 145	Gly	Thr	Ala	Gly	Val 150	Leu	Gln	Ala	Leu	Leu 155	Ile	Val	Leu	Ile	Cys 160
Cys	Cys	Cys	Thr	Leu 165	Leu	Thr	Ala	Ile	Ser 170	Met	Ser	Ala	Ile	Ala	Thr
Asn	Gly	Val	Val	Pro 180	Ala	Gly	Gly	Ser 185	Tyr	Phe	Met	Ile	Ser 190	Arg	Ser
Leu	Gly	Pro	Glu	Phe 195	Gly	Gly	Ala 200	Val	Gly	Leu	Cys	Phe 205	Tyr	Leu	Gly
Thr	Thr	Phe	Ala	Ala 210	Ala	Met 215	Tyr	Ile	Leu	Gly	Ala 220	Ile	Glu	Ile	Leu
Leu 225	Thr	Tyr	Ile	Ala 230	Pro	Ala	Ala	Ile	Phe 235	Tyr	Pro	Ser	Gly	Ala 240	
His	Asp	Thr	Ser	Asn 245	Ala	Thr	Leu	Asn	Asn 250	Met	Arg	Val	Tyr	Gly 255	Thr
Ile	Phe	Leu	Thr	Phe 260	Met	Thr	Leu	Val 265	Val	Phe	Val	Gly	Val 270	Lys	Tyr
Val	Asn	Lys	Phe	Ala 275	Ser	Leu	Phe 280	Leu	Ala	Cys	Val	Ile 285	Ile	Ser	Ile
Leu	Ser	Ile	Tyr	Ala 290	Gly	Gly 295	Ile	Lys	Ser	Ile 300	Phe	Asp	Pro	Pro	Val
Phe 305	Pro	Val	Cys	Met 310	Leu	Gly	Asn	Arg	Thr	Leu 315	Ser	Arg	Asp	Gln	Phe 320
Asp	Ile	Cys	Ala	Lys 325	Thr	Ala	Val	Val 330	Asn	Glu	Thr	Val	Ala 335	Thr	
Gln	Leu	Trp	Ser	Phe 340	Phe	Cys	His 345	Ser	Pro	Asn	Leu	Thr 350	Thr	Asp	Ser
Cys	Asp	Pro	Tyr	Phe 355	Met	Leu	Asn 360	Asn	Val	Thr	Glu	Ile 365	Pro	Gly	Ile
Pro	Gly	Ala	Ala	Ala 370	Gly	Val 375	Leu	Gln	Glu	Asn 380	Leu	Trp	Ser	Ala	Tyr
Leu 385	Glu	Lys	Gly	Asp 390	Ile	Val	Glu	Lys	His 395	Gly	Leu	Pro	Ser	Ala	Asp 400
Ala	Pro	Ser	Leu	Lys 405	Glu	Ser	Leu	Pro 410	Leu	Tyr	Val	Val	Ala 415	Asp	Ile
Ala	Thr	Ser	Phe	Thr 420	Val	Leu	Val	Gly 425	Ile	Phe	Phe	Pro	Ser 430	Val	Thr
Gly	Ile	Met	Ala	Gly 435	Ser	Asn	Arg 440	Ser	Gly	Asp	Leu	Arg 445	Asp	Ala	Gln
Lys	Ser	Ile	Pro	Val 450	Gly	Thr 455	Ile	Leu	Ala	Ile 460	Ile	Thr	Thr	Ser	Leu
Val 465	Tyr	Phe	Ser	Ser 470	Val	Leu	Phe	Gly	Ala 475	Cys	Ile	Glu	Gly	Val 480	
Val	Leu	Arg	Asp	Lys 485	Tyr	Gly	Asp	Gly 490	Val	Ser	Arg	Asn	Leu	Val 495	Val
Gly	Thr	Leu	Ala	Trp 500	Pro	Ser	Pro	Trp 505	Val	Ile	Val	Ile 510	Gly	Ser	Phe
Phe	Ser	Thr	Cys	Gly 515	Ala	Gly	Leu 520	Gln	Ser	Leu	Thr	Gly 525	Ala	Pro	Arg
Leu	Leu	Gln	Ala	Ile 530	Ala	Lys 535	Asp	Asn	Ile	Ile 540	Pro	Phe	Leu	Arg	Val

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Phe	Gly	His	Gly	Lys	Val	Asn	Gly	Glu	Pro	Thr	Trp	Ala	Leu	Leu	Leu
545					550					555					560
Thr	Ala	Leu	Ile	Ala	Glu	Leu	Gly	Ile	Leu	Ile	Ala	Ser	Leu	Asp	Met
			565						570					575	
Val	Ala	Pro	Ile	Leu	Ser	Met	Phe	Phe	Leu	Met	Cys	Tyr	Leu	Phe	Val
			580					585					590		
Asn	Leu	Ala	Cys	Ala	Val	Gln	Thr	Leu	Leu	Arg	Thr	Pro	Asn	Trp	Arg
	595					600						605			
Pro	Arg	Phe	Lys	Tyr	Tyr	His	Trp	Ala	Leu	Ser	Phe	Leu	Gly	Met	Ser
	610					615					620				
Leu	Cys	Leu	Ala	Leu	Met	Phe	Val	Ser	Ser	Trp	Tyr	Tyr	Ala	Leu	Val
625					630					635					640
Ala	Met	Leu	Ile	Ala	Gly	Met	Ile	Tyr	Lys	Tyr	Ile	Glu	Tyr	Gln	Gly
			645						650					655	
Ala	Glu	Lys	Glu	Trp	Gly	Asp	Gly	Ile	Arg	Gly	Leu	Ser	Leu	Ser	Ala
			660				665						670		
Ala	Arg	Tyr	Ala	Leu	Leu	Arg	Leu	Glu	Glu	Gly	Pro	Pro	His	Thr	Lys
	675					680						685			
Asn	Trp	Arg	Pro	Gln	Leu	Leu	Val	Leu	Leu	Lys	Leu	Asp	Glu	Asp	Leu
	690				695						700				
His	Val	Lys	Tyr	Pro	Arg	Leu	Leu	Thr	Phe	Ala	Ser	Gln	Leu	Lys	Ala
705					710				715						720
Gly	Lys	Gly	Leu	Thr	Ile	Val	Gly	Ser	Val	Ile	Gln	Gly	Ser	Phe	Leu
			725						730					735	
Glu	Ser	Tyr	Gly	Glu	Ala	Gln	Ala	Ala	Glu	Gln	Thr	Ile	Lys	Asn	Met
			740				745						750		
Met	Glu	Ile	Glu	Lys	Val	Lys	Gly	Phe	Cys	Gln	Val	Val	Val	Ala	Ser
	755					760					765				
Lys	Val	Arg	Glu	Gly	Leu	Ala	His	Leu	Ile	Gln	Ser	Cys	Gly	Leu	Gly
	770				775						780				
Gly	Met	Arg	His	Asn	Ser	Val	Val	Leu	Gly	Trp	Pro	Tyr	Gly	Trp	Arg
785				790					795						800
Gln	Ser	Glu	Asp	Pro	Arg	Ala	Trp	Lys	Thr	Phe	Ile	Asp	Thr	Val	Arg
			805					810						815	
Cys	Thr	Thr	Ala	Ala	His	Leu	Ala	Leu	Leu	Val	Pro	Lys	Asn	Ile	Ala
			820				825						830		
Phe	Tyr	Pro	Ser	Asn	His	Glu	Arg	Tyr	Leu	Glu	Gly	His	Ile	Asp	Val
	835					840					845				
Trp	Trp	Ile	Val	His	Asp	Gly	Gly	Met	Leu	Met	Leu	Leu	Pro	Phe	Leu
	850				855						860				
Leu	Arg	Gln	His	Lys	Val	Trp	Arg	Lys	Cys	Arg	Met	Arg	Ile	Phe	Thr
865				870					875						880
Val	Ala	Gln	Met	Asp	Asn	Ser	Ile	Gln	Met	Lys	Lys	Asp	Leu	Ala	
			885				890						895		
Val	Phe	Leu	Tyr	His	Leu	Arg	Leu	Glu	Ala	Glu	Val	Glu	Val	Val	Glu
			900				905						910		
Met	His	Asn	Ser	Asp	Ile	Ser	Ala	Tyr	Thr	Tyr	Glu	Arg	Thr	Leu	Met
	915					920						925			
Met	Glu	Gln	Arg	Ser	Gln	Met	Leu	Arg	Gln	Met	Arg	Leu	Thr	Lys	Thr
	930				935						940				

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Glu Arg Glu Arg Glu Ala Gln Leu Val Lys Asp Arg His Ser Ala Leu
 945 950 955 960
 Arg Leu Glu Ser Leu Tyr Ser Asp Glu Glu Asp Glu Ser Ala Val Gly
 965 970 975
 Ala Asp Lys Ile Gln Met Thr Trp Thr Arg Asp Lys Tyr Met Thr Glu
 980 985 990
 Thr Trp Asp Pro Ser His Ala Pro Asp Asn Phe Arg Glu Leu Val His
 995 1000 1005
 Ile Lys Pro Asp Gln Ser Asn Val Arg Arg Met His Thr Ala Val
 1010 1015 1020
 Lys Leu Asn Glu Val Ile Val Thr Arg Ser His Asp Ala Arg Leu
 1025 1030 1035
 Val Leu Leu Asn Met Pro Gly Pro Pro Arg Asn Ser Glu Gly Asp
 1040 1045 1050
 Glu Asn Tyr Met Glu Phe Leu Glu Val Leu Thr Glu Gly Leu Glu
 1055 1060 1065
 Arg Val Leu Leu Val Arg Gly Gly Gly Arg Glu Val Ile Thr Ile
 1070 1075 1080
 Tyr Ser
 1085

<210> SEQ ID NO 26
 <211> LENGTH: 836
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapiens
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (1)..(836)
 <223> OTHER INFORMATION: OGTA126 = Swiss Prot Accession No. Q9H5V8,
 CUB domain-containing protein 1

<400> SEQUENCE: 26

Met Ala Gly Leu Asn Cys Gly Val Ser Ile Ala Leu Leu Gly Val Leu
 1 5 10 15
 Leu Leu Gly Ala Ala Arg Leu Pro Arg Gly Ala Glu Ala Phe Glu Ile
 20 25 30
 Ala Leu Pro Arg Glu Ser Asn Ile Thr Val Leu Ile Lys Leu Gly Thr
 35 40 45
 Pro Thr Leu Leu Ala Lys Pro Cys Tyr Ile Val Ile Ser Lys Arg His
 50 55 60
 Ile Thr Met Leu Ser Ile Lys Ser Gly Glu Arg Ile Val Phe Thr Phe
 65 70 75 80
 Ser Cys Gln Ser Pro Glu Asn His Phe Val Ile Glu Ile Gln Lys Asn
 85 90 95
 Ile Asp Cys Met Ser Gly Pro Cys Pro Phe Gly Glu Val Gln Leu Gln
 100 105 110
 Pro Ser Thr Ser Leu Leu Pro Thr Leu Asn Arg Thr Phe Ile Trp Asp
 115 120 125
 Val Lys Ala His Lys Ser Ile Gly Leu Glu Leu Gln Phe Ser Ile Pro
 130 135 140
 Arg Leu Arg Gln Ile Gly Pro Gly Glu Ser Cys Pro Asp Gly Val Thr
 145 150 155 160
 His Ser Ile Ser Gly Arg Ile Asp Ala Thr Val Val Arg Ile Gly Thr
 165 170 175

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Phe	Cys	Ser	Asn	Gly	Thr	Val	Ser	Arg	Ile	Lys	Met	Gln	Glu	Gly	Val	180	185	190
Lys	Met	Ala	Leu	His	Leu	Pro	Trp	Phe	His	Pro	Arg	Asn	Val	Ser	Gly	195	200	205
Phe	Ser	Ile	Ala	Asn	Arg	Ser	Ser	Ile	Lys	Arg	Leu	Cys	Ile	Ile	Glu	210	215	220
Ser	Val	Phe	Glu	Gly	Glu	Gly	Ser	Ala	Thr	Leu	Met	Ser	Ala	Asn	Tyr	225	230	235
Pro	Glu	Gly	Phe	Pro	Glu	Asp	Glu	Leu	Met	Thr	Trp	Gln	Phe	Val	Val	245	250	255
Pro	Ala	His	Leu	Arg	Ala	Ser	Val	Ser	Phe	Leu	Asn	Phe	Asn	Leu	Ser	260	265	270
Asn	Cys	Glu	Arg	Lys	Glu	Glu	Arg	Val	Glu	Tyr	Tyr	Ile	Pro	Gly	Ser	275	280	285
Thr	Thr	Asn	Pro	Glu	Val	Phe	Lys	Leu	Glu	Asp	Lys	Gln	Pro	Gly	Asn	290	295	300
Met	Ala	Gly	Asn	Phe	Asn	Leu	Ser	Leu	Gln	Gly	Cys	Asp	Gln	Asp	Ala	305	310	315
Gln	Ser	Pro	Gly	Ile	Leu	Arg	Leu	Gln	Phe	Gln	Val	Leu	Val	Gln	His	325	330	335
Pro	Gln	Asn	Glu	Ser	Asn	Lys	Ile	Tyr	Val	Val	Asp	Leu	Ser	Asn	Glu	340	345	350
Arg	Ala	Met	Ser	Leu	Thr	Ile	Glu	Pro	Arg	Pro	Val	Lys	Gln	Ser	Arg	355	360	365
Lys	Phe	Val	Pro	Gly	Cys	Phe	Val	Cys	Leu	Glu	Ser	Arg	Thr	Cys	Ser	370	375	380
Ser	Asn	Leu	Thr	Leu	Thr	Ser	Gly	Ser	Lys	His	Lys	Ile	Ser	Phe	Leu	385	390	395
Cys	Asp	Asp	Leu	Thr	Arg	Leu	Trp	Met	Asn	Val	Glu	Lys	Thr	Ile	Ser	405	410	415
Cys	Thr	Asp	His	Arg	Tyr	Cys	Gln	Arg	Lys	Ser	Tyr	Ser	Leu	Gln	Val	420	425	430
Pro	Ser	Asp	Ile	Leu	His	Leu	Pro	Val	Glu	Leu	His	Asp	Phe	Ser	Trp	435	440	445
Lys	Leu	Leu	Val	Pro	Lys	Asp	Arg	Leu	Ser	Leu	Val	Leu	Val	Pro	Ala	450	455	460
Gln	Lys	Leu	Gln	Gln	His	Thr	His	Glu	Lys	Pro	Cys	Asn	Thr	Ser	Phe	465	470	475
Ser	Tyr	Leu	Val	Ala	Ser	Ala	Ile	Pro	Ser	Gln	Asp	Leu	Tyr	Phe	Gly	485	490	495
Ser	Phe	Cys	Pro	Gly	Gly	Ser	Ile	Lys	Gln	Ile	Gln	Val	Lys	Gln	Asn	500	505	510
Ile	Ser	Val	Thr	Leu	Arg	Thr	Phe	Ala	Pro	Ser	Phe	Arg	Gln	Glu	Ala	515	520	525
Ser	Arg	Gln	Gly	Leu	Thr	Val	Ser	Phe	Ile	Pro	Tyr	Phe	Lys	Glu	Glu	530	535	540
Gly	Val	Phe	Thr	Val	Thr	Pro	Asp	Thr	Lys	Ser	Lys	Val	Tyr	Leu	Arg	545	550	555
Thr	Pro	Asn	Trp	Asp	Arg	Gly	Leu	Pro	Ser	Leu	Thr	Ser	Val	Ser	Trp	565	570	575
Asn	Ile	Ser	Val	Pro	Arg	Asp	Gln	Val	Ala	Cys	Leu	Thr	Phe	Phe	Lys			

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580	585	590
Glu Arg Ser Gly Val Val Cys Gln Thr Gly Arg Ala Phe Met Ile Ile		
595	600	605
Gln Glu Gln Arg Thr Arg Ala Glu Glu Ile Phe Ser Leu Asp Glu Asp		
610	615	620
Val Leu Pro Lys Pro Ser Phe His His His Ser Phe Trp Val Asn Ile		
625	630	635
Ser Asn Cys Ser Pro Thr Ser Gly Lys Gln Leu Asp Leu Leu Phe Ser		
645	650	655
Val Thr Leu Thr Pro Arg Thr Val Asp Leu Thr Val Ile Leu Ile Ala		
660	665	670
Ala Val Gly Gly Gly Val Leu Leu Leu Ser Ala Leu Gly Leu Ile Ile		
675	680	685
Cys Cys Val Lys Lys Lys Lys Lys Lys Thr Asn Lys Gly Pro Ala Val		
690	695	700
Gly Ile Tyr Asn Gly Asn Ile Asn Thr Glu Met Pro Arg Gln Pro Lys		
705	710	715
Lys Phe Gln Lys Gly Arg Lys Asp Asn Asp Ser His Val Tyr Ala Val		
725	730	735
Ile Glu Asp Thr Met Val Tyr Gly His Leu Leu Gln Asp Ser Ser Gly		
740	745	750
Ser Phe Leu Gln Pro Glu Val Asp Thr Tyr Arg Pro Phe Gln Gly Thr		
755	760	765
Met Gly Val Cys Pro Pro Ser Pro Pro Thr Ile Cys Ser Arg Ala Pro		
770	775	780
Thr Ala Lys Leu Ala Thr Glu Glu Pro Pro Pro Arg Ser Pro Pro Glu		
785	790	795
Ser Glu Ser Glu Pro Tyr Thr Phe Ser His Pro Asn Asn Gly Asp Val		
805	810	815
Ser Ser Lys Asp Thr Asp Ile Pro Leu Leu Ser Thr Gln Glu Pro Met		
820	825	830
Glu Pro Ala Glu		
835		

<210> SEQ ID NO 27
 <211> LENGTH: 1038
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapiens
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (1)..(1038)
 <223> OTHER INFORMATION: OGTA156 = Swiss Prot Accession No. P13612,
 Integrin alpha-4

<400> SEQUENCE: 27

Met Phe Pro Thr Glu Ser Ala Trp Leu Gly Lys Arg Gly Ala Asn Pro
1 5 10 15
Gly Pro Glu Ala Ala Val Arg Glu Thr Val Met Leu Leu Leu Cys Leu
20 25 30
Gly Val Pro Thr Gly Arg Pro Tyr Asn Val Asp Thr Glu Ser Ala Leu
35 40 45
Leu Tyr Gln Gly Pro His Asn Thr Leu Phe Gly Tyr Ser Val Val Leu
50 55 60
His Ser His Gly Ala Asn Arg Trp Leu Leu Val Gly Ala Pro Thr Ala

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65	70				75				80			
Asn Trp Leu Ala	Asn Ala Ser Val Ile	Asn Pro Gly Ala Ile	Tyr Arg	85	90	95						
Cys Arg Ile Gly	Lys Asn Pro Gly Gln Thr	Cys Glu Gln Leu Gln Leu		100	105	110						
Gly Ser Pro Asn Gly	Glu Pro Cys Gly Lys Thr	Cys Leu Glu Glu Arg		115	120	125						
Asp Asn Gln Trp Leu	Gly Val Thr Leu Ser Arg	Gln Pro Gly Glu Asn		130	135	140						
Gly Ser Ile Val Thr	Cys Gly His Arg Trp Lys	Asn Ile Phe Tyr Ile		145	150	155						
Lys Asn Glu Asn Lys	Leu Pro Thr Gly Gly Cys Tyr	Gly Val Pro Pro		165	170	175						
Asp Leu Arg Thr	Glu Leu Ser Lys Arg Ile Ala	Pro Cys Tyr Gln Asp		180	185	190						
Tyr Val Lys Lys Phe	Gly Glu Asn Phe Ala Ser	Cys Gln Ala Gly Ile		195	200	205						
Ser Ser Phe Tyr Thr	Lys Asp Leu Ile Val Met	Gly Ala Pro Gly Ser		210	215	220						
Ser Tyr Trp Thr Gly	Ser Leu Phe Val Tyr Asn	Ile Thr Thr Asn Lys		225	230	235						
Tyr Lys Ala Phe Leu	Asp Lys Gln Asn Gln Val	Lys Phe Gly Ser Tyr		245	250	255						
Leu Gly Tyr Ser Val	Gly Ala Gly His Phe Arg	Ser Gln His Thr Thr		260	265	270						
Glu Val Val Gly Gly	Ala Pro Gln His Glu Gln	Ile Gly Lys Ala Tyr		275	280	285						
Ile Phe Ser Ile Asp	Glu Lys Glu Leu Asn Ile	Leu His Glu Met Lys		290	295	300						
Gly Lys Lys Leu Gly	Ser Tyr Phe Gly Ala Ser	Val Cys Ala Val Asp		305	310	315						
Leu Asn Ala Asp Gly	Phe Ser Asp Leu Leu Val	Gly Ala Pro Met Gln		325	330	335						
Ser Thr Ile Arg Glu	Glu Gly Arg Val Phe Val	Tyr Ile Asn Ser Gly		340	345	350						
Ser Gly Ala Val Met	Asn Ala Met Glu Thr Asn	Leu Val Gly Ser Asp		355	360	365						
Lys Tyr Ala Ala Arg	Phe Gly Glu Ser Ile Val	Asn Leu Gly Asp Ile		370	375	380						
Asp Asn Asp Gly Phe	Glu Asp Val Ala Ile Gly	Ala Pro Gln Glu Asp		385	390	395						
Asp Leu Gln Gly Ala	Ile Tyr Ile Tyr Asn Gly	Arg Ala Asp Gly Ile		405	410	415						
Ser Ser Thr Phe Ser	Gln Arg Ile Glu Gly Leu	Gln Ile Ser Lys Ser		420	425	430						
Leu Ser Met Phe Gly	Gln Ser Ile Ser Gly Gln	Ile Asp Ala Asp Asn		435	440	445						
Asn Gly Tyr Val Asp	Val Ala Val Gly Ala Phe	Arg Ser Asp Ser Ala		450	455	460						
Val Leu Leu Arg Thr	Arg Pro Val Val Ile Val	Asp Ala Ser Leu Ser		465	470	475						

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His	Pro	Glu	Ser	Val	Asn	Arg	Thr	Lys	Phe	Asp	Cys	Val	Glu	Asn	Gly	485	490	495
Trp	Pro	Ser	Val	Cys	Ile	Asp	Leu	Thr	Leu	Cys	Phe	Ser	Tyr	Lys	Gly	500	505	510
Lys	Glu	Val	Pro	Gly	Tyr	Ile	Val	Leu	Phe	Tyr	Asn	Met	Ser	Leu	Asp	515	520	525
Val	Asn	Arg	Lys	Ala	Glu	Ser	Pro	Pro	Arg	Phe	Tyr	Phe	Ser	Ser	Asn	530	535	540
Gly	Thr	Ser	Asp	Val	Ile	Thr	Gly	Ser	Ile	Gln	Val	Ser	Ser	Arg	Glu	545	550	555
Ala	Asn	Cys	Arg	Thr	His	Gln	Ala	Phe	Met	Arg	Lys	Asp	Val	Arg	Asp	565	570	575
Ile	Leu	Thr	Pro	Ile	Gln	Ile	Glu	Ala	Ala	Tyr	His	Leu	Gly	Pro	His	580	585	590
Val	Ile	Ser	Lys	Arg	Ser	Thr	Glu	Glu	Phe	Pro	Pro	Leu	Gln	Pro	Ile	595	600	605
Leu	Gln	Gln	Lys	Lys	Glu	Lys	Asp	Ile	Met	Lys	Lys	Thr	Ile	Asn	Phe	610	615	620
Ala	Arg	Phe	Cys	Ala	His	Glu	Asn	Cys	Ser	Ala	Asp	Leu	Gln	Val	Ser	625	630	635
Ala	Lys	Ile	Gly	Phe	Leu	Lys	Pro	His	Glu	Asn	Lys	Thr	Tyr	Leu	Ala	645	650	655
Val	Gly	Ser	Met	Lys	Thr	Leu	Met	Leu	Asn	Val	Ser	Leu	Phe	Asn	Ala	660	665	670
Gly	Asp	Asp	Ala	Tyr	Glu	Thr	Thr	Leu	His	Val	Lys	Leu	Pro	Val	Gly	675	680	685
Leu	Tyr	Phe	Ile	Lys	Ile	Leu	Glu	Leu	Glu	Glu	Lys	Gln	Ile	Asn	Cys	690	695	700
Glu	Val	Thr	Asp	Asn	Ser	Gly	Val	Val	Gln	Leu	Asp	Cys	Ser	Ile	Gly	705	710	715
Tyr	Ile	Tyr	Val	Asp	His	Leu	Ser	Arg	Ile	Asp	Ile	Ser	Phe	Leu	Leu	725	730	735
Asp	Val	Ser	Ser	Leu	Ser	Arg	Ala	Glu	Glu	Asp	Leu	Ser	Ile	Thr	Val	740	745	750
His	Ala	Thr	Cys	Glu	Asn	Glu	Glu	Glu	Met	Asp	Asn	Leu	Lys	His	Ser	755	760	765
Arg	Val	Thr	Val	Ala	Ile	Pro	Leu	Lys	Tyr	Glu	Val	Lys	Leu	Thr	Val	770	775	780
His	Gly	Phe	Val	Asn	Pro	Thr	Ser	Phe	Val	Tyr	Gly	Ser	Asn	Asp	Glu	785	790	795
Asn	Glu	Pro	Glu	Thr	Cys	Met	Val	Glu	Lys	Met	Asn	Leu	Thr	Phe	His	805	810	815
Val	Ile	Asn	Thr	Gly	Asn	Ser	Met	Ala	Pro	Asn	Val	Ser	Val	Glu	Ile	820	825	830
Met	Val	Pro	Asn	Ser	Phe	Ser	Pro	Gln	Thr	Asp	Lys	Leu	Phe	Asn	Ile	835	840	845
Leu	Asp	Val	Gln	Thr	Thr	Thr	Gly	Glu	Cys	His	Phe	Glu	Asn	Tyr	Gln	850	855	860
Arg	Val	Cys	Ala	Leu	Glu	Gln	Gln	Lys	Ser	Ala	Met	Gln	Thr	Leu	Lys	865	870	875

```
<210> SEQ ID NO 28
<211> LENGTH: 314
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(314)
<223> OTHER INFORMATION: OGTA159 = Swiss Prot Accession No. Q96HY6,
Uncharacterized protein C20orf116
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Met	Val	Ala	Pro	Val	Trp	Tyr	Leu	Val	Ala	Ala	Ala	Leu	Leu	Val	Gly
1			5					10						15	
Phe	Ile	Leu	Phe	Leu	Thr	Arg	Ser	Arg	Gly	Arg	Ala	Ala	Ser	Ala	Gly
			20					25					30		
Gln	Glu	Pro	Leu	His	Asn	Glu	Glu	Leu	Ala	Gly	Ala	Gly	Arg	Val	Ala
		35				40						45			
Gln	Pro	Gly	Pro	Leu	Glu	Pro	Glu	Glu	Pro	Arg	Ala	Gly	Gly	Arg	Pro
	50					55					60				
Arg	Arg	Arg	Arg	Asp	Leu	Gly	Ser	Arg	Leu	Gln	Ala	Gln	Arg	Arg	Ala
65				70						75					80
Gln	Arg	Val	Ala	Trp	Ala	Glu	Ala	Asp	Glu	Asn	Glu	Glu	Glu	Ala	Val
			85					90						95	
Ile	Leu	Ala	Gln	Glu	Glu	Glu	Gly	Val	Glu	Lys	Pro	Ala	Glu	Thr	His
			100					105					110		
Leu	Ser	Gly	Lys	Ile	Gly	Ala	Lys	Lys	Leu	Arg	Lys	Leu	Glu	Glu	Lys
		115					120					125			
Gln	Ala	Arg	Lys	Ala	Gln	Arg	Glu	Ala	Glu	Glu	Ala	Glu	Arg	Glu	Glu
	130					135					140				
Arg	Lys	Arg	Leu	Glu	Ser	Gln	Arg	Glu	Ala	Glu	Trp	Lys	Lys	Glu	Glu
145				150						155				160	
Glu	Arg	Leu	Arg	Leu	Glu	Glu	Glu	Gln	Lys	Glu	Glu	Glu	Glu	Arg	Lys
			165						170					175	

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Ala Arg Glu Glu Gln Ala Gln Arg Glu His Glu Glu Tyr Leu Lys Leu
180 185 190

Lys Glu Ala Phe Val Val Glu Glu Glu Gly Val Gly Glu Thr Met Thr
195 200 205

Glu Glu Gln Ser Gln Ser Phe Leu Thr Glu Phe Ile Asn Tyr Ile Lys
210 215 220

Gln Ser Lys Val Val Leu Leu Glu Asp Leu Ala Ser Gln Val Gly Leu
225 230 235 240

Arg Thr Gln Asp Thr Ile Asn Arg Ile Gln Asp Leu Leu Ala Glu Gly
245 250 255

Thr Ile Thr Gly Val Ile Asp Asp Arg Gly Lys Phe Ile Tyr Ile Thr
260 265 270

Pro Glu Glu Leu Ala Ala Val Ala Asn Phe Ile Arg Gln Arg Gly Arg
275 280 285

Val Ser Ile Ala Glu Leu Ala Gln Ala Ser Asn Ser Leu Ile Ala Trp
290 295 300

Gly Arg Glu Ser Pro Ala Gln Ala Pro Ala
305 310

<210> SEQ ID NO 29
<211> LENGTH: 742
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(742)
<223> OTHER INFORMATION: OGTA168 = Swiss Prot Accession No. Q8WZA4,
Collectin placenta 1

<400> SEQUENCE: 29

Met Lys Asp Asp Phe Ala Glu Glu Glu Glu Val Gln Ser Phe Gly Tyr
1 5 10 15

Lys Arg Phe Gly Ile Gln Glu Gly Thr Gln Cys Thr Lys Cys Lys Asn
20 25 30

Asn Trp Ala Leu Lys Phe Ser Ile Ile Leu Leu Tyr Ile Leu Cys Ala
35 40 45

Leu Leu Thr Ile Thr Val Ala Ile Leu Gly Tyr Lys Val Val Glu Lys
50 55 60

Met Asp Asn Val Thr Gly Gly Met Glu Thr Ser Arg Gln Thr Tyr Asp
65 70 75 80

Asp Lys Leu Thr Ala Val Glu Ser Asp Leu Lys Lys Leu Gly Asp Gln
85 90 95

Thr Gly Lys Lys Ala Ile Ser Thr Asn Ser Glu Leu Ser Thr Phe Arg
100 105 110

Ser Asp Ile Leu Asp Leu Arg Gln Gln Leu Arg Glu Ile Thr Glu Lys
115 120 125

Thr Ser Lys Asn Lys Asp Thr Leu Glu Lys Leu Gln Ala Ser Gly Asp
130 135 140

Ala Leu Val Asp Arg Gln Ser Gln Leu Lys Glu Thr Leu Glu Asn Asn
145 150 155 160

Ser Phe Leu Ile Thr Thr Val Asn Lys Thr Leu Gln Ala Tyr Asn Gly
165 170 175

Tyr Val Thr Asn Leu Gln Gln Asp Thr Ser Val Leu Gln Gly Asn Leu
180 185 190

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Gln	Asn	Gln	Met	Tyr	Ser	His	Asn	Val	Val	Ile	Met	Asn	Leu	Asn	Asn
	195						200					205			
Leu	Asn	Leu	Thr	Gln	Val	Gln	Gln	Arg	Asn	Leu	Ile	Thr	Asn	Leu	Gln
	210					215				220					
Arg	Ser	Val	Asp	Asp	Thr	Ser	Gln	Ala	Ile	Gln	Arg	Ile	Lys	Asn	Asp
225					230					235				240	
Phe	Gln	Asn	Leu	Gln	Gln	Val	Phe	Leu	Gln	Ala	Lys	Lys	Asp	Thr	Asp
			245						250					255	
Trp	Leu	Lys	Glu	Lys	Val	Gln	Ser	Leu	Gln	Thr	Leu	Ala	Ala	Asn	Asn
		260						265					270		
Ser	Ala	Leu	Ala	Lys	Ala	Asn	Asn	Asp	Thr	Leu	Glu	Asp	Met	Asn	Ser
		275					280					285			
Gln	Leu	Asn	Ser	Phe	Thr	Gly	Gln	Met	Glu	Asn	Ile	Thr	Thr	Ile	Ser
	290					295					300				
Gln	Ala	Asn	Glu	Gln	Asn	Leu	Lys	Asp	Leu	Gln	Asp	Leu	His	Lys	Asp
305					310					315				320	
Ala	Glu	Asn	Arg	Thr	Ala	Ile	Lys	Phe	Asn	Gln	Leu	Glu	Glu	Arg	Phe
				325					330					335	
Gln	Leu	Phe	Glu	Thr	Asp	Ile	Val	Asn	Ile	Ile	Ser	Asn	Ile	Ser	Tyr
		340						345					350		
Thr	Ala	His	His	Leu	Arg	Thr	Leu	Thr	Ser	Asn	Leu	Asn	Glu	Val	Arg
		355					360					365			
Thr	Thr	Cys	Thr	Asp	Thr	Leu	Thr	Lys	His	Thr	Asp	Asp	Leu	Thr	Ser
	370					375					380				
Leu	Asn	Asn	Thr	Leu	Ala	Asn	Ile	Arg	Leu	Asp	Ser	Val	Ser	Leu	Arg
385					390					395				400	
Met	Gln	Gln	Asp	Leu	Met	Arg	Ser	Arg	Leu	Asp	Thr	Glu	Val	Ala	Asn
				405					410					415	
Leu	Ser	Val	Ile	Met	Glu	Glu	Met	Lys	Leu	Val	Asp	Ser	Lys	His	Gly
		420						425					430		
Gln	Leu	Ile	Lys	Asn	Phe	Thr	Ile	Leu	Gln	Gly	Pro	Pro	Gly	Pro	Arg
	435						440					445			
Gly	Pro	Arg	Gly	Asp	Arg	Gly	Ser	Gln	Gly	Pro	Pro	Gly	Pro	Thr	Gly
	450					455					460				
Asn	Lys	Gly	Gln	Lys	Gly	Glu	Lys	Gly	Glu	Pro	Gly	Pro	Pro	Gly	Pro
465					470					475				480	
Ala	Gly	Glu	Arg	Gly	Pro	Ile	Gly	Pro	Ala	Gly	Pro	Pro	Gly	Glu	Arg
				485					490					495	
Gly	Gly	Lys	Gly	Ser	Lys	Gly	Ser	Gln	Gly	Pro	Lys	Gly	Ser	Arg	Gly
		500						505					510		
Ser	Pro	Gly	Lys	Pro	Gly	Pro	Gln	Gly	Ser	Ser	Gly	Asp	Pro	Gly	Pro
		515					520					525			
Pro	Gly	Pro	Pro	Gly	Lys	Glu	Gly	Leu	Pro	Gly	Pro	Gln	Gly	Pro	Pro
	530					535					540				
Gly	Phe	Gln	Gly	Leu	Gln	Gly	Thr	Val	Gly	Glu	Pro	Gly	Val	Pro	Gly
545					550					555				560	
Pro	Arg	Gly	Leu	Pro	Gly	Leu	Pro	Gly	Val	Pro	Gly	Met	Pro	Gly	Pro
				565					570					575	
Lys	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Pro	Ser	Gly	Ala	Val	Val	Pro	Leu
		580						585					590		
Ala	Leu	Gln	Asn	Glu	Pro	Thr	Pro	Ala	Pro	Glu	Asp	Asn	Gly	Cys	Pro

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595	600	605
Pro His Trp Lys Asn Phe Thr Asp Lys Cys Tyr Tyr Phe Ser Val Glu 610 615 620		
Lys Glu Ile Phe Glu Asp Ala Lys Leu Phe Cys Glu Asp Lys Ser Ser 625 630 635 640		
His Leu Val Phe Ile Asn Thr Arg Glu Glu Gln Gln Trp Ile Lys Lys 645 650 655		
Gln Met Val Gly Arg Glu Ser His Trp Ile Gly Leu Thr Asp Ser Glu 660 665 670		
Arg Glu Asn Glu Trp Lys Trp Leu Asp Gly Thr Ser Pro Asp Tyr Lys 675 680 685		
Asn Trp Lys Ala Gly Gln Pro Asp Asn Trp Gly His Gly His Gly Pro 690 695 700		
Gly Glu Asp Cys Ala Gly Leu Ile Tyr Ala Gly Gln Trp Asn Asp Phe 705 710 715 720		
Gln Cys Glu Asp Val Asn Asn Phe Ile Cys Glu Lys Asp Arg Glu Thr 725 730 735		
Val Leu Ser Ser Ala Leu 740		
 <210> SEQ ID NO 30 <211> LENGTH: 1163 <212> TYPE: PRT <213> ORGANISM: Homo Sapiens <220> FEATURE: <221> NAME/KEY: MISC_FEATURE <222> LOCATION: (1)..(1163) <223> OTHER INFORMATION: OGTA169 = Swiss Prot Accession No. P20702, Integrin alpha-X		
 <400> SEQUENCE: 30		
Met Thr Arg Thr Arg Ala Ala Leu Leu Leu Phe Thr Ala Leu Ala Thr 1 5 10 15		
Ser Leu Gly Phe Asn Leu Asp Thr Glu Glu Leu Thr Ala Phe Arg Val 20 25 30		
Asp Ser Ala Gly Phe Gly Asp Ser Val Val Gln Tyr Ala Asn Ser Trp 35 40 45		
Val Val Val Gly Ala Pro Gln Lys Ile Thr Ala Ala Asn Gln Thr Gly 50 55 60		
Gly Leu Tyr Gln Cys Gly Tyr Ser Thr Gly Ala Cys Glu Pro Ile Gly 65 70 75 80		
Leu Gln Val Pro Pro Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu 85 90 95		
Ala Ser Thr Thr Ser Pro Ser Gln Leu Leu Ala Cys Gly Pro Thr Val 100 105 110		
His His Glu Cys Gly Arg Asn Met Tyr Leu Thr Gly Leu Cys Phe Leu 115 120 125		
Leu Gly Pro Thr Gln Leu Thr Gln Arg Leu Pro Val Ser Arg Gln Glu 130 135 140		
Cys Pro Arg Gln Glu Gln Asp Ile Val Phe Leu Ile Asp Gly Ser Gly 145 150 155 160		
Ser Ile Ser Ser Arg Asn Phe Ala Thr Met Met Asn Phe Val Arg Ala 165 170 175		
Val Ile Ser Gln Phe Gln Arg Pro Ser Thr Gln Phe Ser Leu Met Gln		

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180							185				190				
Phe	Ser	Asn	Lys	Phe	Gln	Thr	His	Phe	Thr	Phe	Glu	Glu	Phe	Arg	Arg
		195					200					205			
Thr	Ser	Asn	Pro	Leu	Ser	Leu	Leu	Ala	Ser	Val	His	Gln	Leu	Gln	Gly
	210					215					220				
Phe	Thr	Tyr	Thr	Ala	Thr	Ala	Ile	Gln	Asn	Val	Val	His	Arg	Leu	Phe
225					230					235					240
His	Ala	Ser	Tyr	Gly	Ala	Arg	Arg	Asp	Ala	Thr	Lys	Ile	Leu	Ile	Val
				245					250					255	
Ile	Thr	Asp	Gly	Lys	Lys	Glu	Gly	Asp	Ser	Leu	Asp	Tyr	Lys	Asp	Val
			260					265					270		
Ile	Pro	Met	Ala	Asp	Ala	Ala	Gly	Ile	Ile	Arg	Tyr	Ala	Ile	Gly	Val
		275					280					285			
Gly	Leu	Ala	Phe	Gln	Asn	Arg	Asn	Ser	Trp	Lys	Glu	Leu	Asn	Asp	Ile
	290					295					300				
Ala	Ser	Lys	Pro	Ser	Gln	Glu	His	Ile	Phe	Lys	Val	Glu	Asp	Phe	Asp
305					310					315					320
Ala	Leu	Lys	Asp	Ile	Gln	Asn	Gln	Leu	Lys	Glu	Lys	Ile	Phe	Ala	Ile
				325					330					335	
Glu	Gly	Thr	Glu	Thr	Thr	Ser	Ser	Ser	Phe	Glu	Leu	Glu	Met	Ala	
			340					345				350			
Gln	Glu	Gly	Phe	Ser	Ala	Val	Phe	Thr	Pro	Asp	Gly	Pro	Val	Leu	Gly
		355					360					365			
Ala	Val	Gly	Ser	Phe	Thr	Trp	Ser	Gly	Gly	Ala	Phe	Leu	Tyr	Pro	Pro
	370					375					380				
Asn	Met	Ser	Pro	Thr	Phe	Ile	Asn	Met	Ser	Gln	Glu	Asn	Val	Asp	Met
385					390					395					400
Arg	Asp	Ser	Tyr	Leu	Gly	Tyr	Ser	Thr	Glu	Leu	Ala	Leu	Trp	Lys	Gly
				405					410					415	
Val	Gln	Ser	Leu	Val	Leu	Gly	Ala	Pro	Arg	Tyr	Gln	His	Thr	Gly	Lys
			420					425					430		
Ala	Val	Ile	Phe	Thr	Gln	Val	Ser	Arg	Gln	Trp	Arg	Met	Lys	Ala	Glu
		435					440					445			
Val	Thr	Gly	Thr	Gln	Ile	Gly	Ser	Tyr	Phe	Gly	Ala	Ser	Leu	Cys	Ser
	450					455					460				
Val	Asp	Val	Asp	Thr	Asp	Gly	Ser	Thr	Asp	Leu	Val	Leu	Ile	Gly	Ala
465					470					475					480
Pro	His	Tyr	Tyr	Glu	Gln	Thr	Arg	Gly	Gly	Gln	Val	Ser	Val	Cys	Pro
				485					490					495	
Leu	Pro	Arg	Gly	Trp	Arg	Arg	Trp	Trp	Cys	Asp	Ala	Val	Leu	Tyr	Gly
			500					505					510		
Glu	Gln	Gly	His	Pro	Trp	Gly	Arg	Phe	Gly	Ala	Ala	Leu	Thr	Val	Leu
		515					520					525			
Gly	Asp	Val	Asn	Gly	Asp	Lys	Leu	Thr	Asp	Val	Val	Ile	Gly	Ala	Pro
	530					535					540				
Gly	Glu	Glu	Glu	Asn	Arg	Gly	Ala	Val	Tyr	Leu	Phe	His	Gly	Val	Leu
545					550					555					560
Gly	Pro	Ser	Ile	Ser	Pro	Ser	His	Ser	Gln	Arg	Ile	Ala	Gly	Ser	Gln
				565					570					575	
Leu	Ser	Ser	Arg	Leu	Gln	Tyr	Phe	Gly	Gln	Ala	Leu	Ser	Gly	Gly	Gln
			580					585					590		

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Asp	Leu	Thr	Gln	Asp	Gly	Leu	Val	Asp	Leu	Ala	Val	Gly	Ala	Arg	Gly	595	600	605
Gln	Val	Leu	Leu	Leu	Arg	Thr	Arg	Pro	Val	Leu	Trp	Val	Gly	Val	Ser	610	615	620
Met	Gln	Phe	Ile	Pro	Ala	Glu	Ile	Pro	Arg	Ser	Ala	Phe	Glu	Cys	Arg	625	630	635
Glu	Gln	Val	Val	Ser	Glu	Gln	Thr	Leu	Val	Gln	Ser	Asn	Ile	Cys	Leu	645	650	655
Tyr	Ile	Asp	Lys	Arg	Ser	Lys	Asn	Leu	Leu	Gly	Ser	Arg	Asp	Leu	Gln	660	665	670
Ser	Ser	Val	Thr	Leu	Asp	Leu	Ala	Leu	Asp	Pro	Gly	Arg	Leu	Ser	Pro	675	680	685
Arg	Ala	Thr	Phe	Gln	Glu	Thr	Lys	Asn	Arg	Ser	Leu	Ser	Arg	Val	Arg	690	695	700
Val	Leu	Gly	Leu	Lys	Ala	His	Cys	Glu	Asn	Phe	Asn	Leu	Leu	Leu	Pro	705	710	715
Ser	Cys	Val	Glu	Asp	Ser	Val	Thr	Pro	Ile	Thr	Leu	Arg	Leu	Asn	Phe	725	730	735
Thr	Leu	Val	Gly	Lys	Pro	Leu	Leu	Ala	Phe	Arg	Asn	Leu	Arg	Pro	Met	740	745	750
Leu	Ala	Ala	Asp	Ala	Gln	Arg	Tyr	Phe	Thr	Ala	Ser	Leu	Pro	Phe	Glu	755	760	765
Lys	Asn	Cys	Gly	Ala	Asp	His	Ile	Cys	Gln	Asp	Asn	Leu	Gly	Ile	Ser	770	775	780
Phe	Ser	Phe	Pro	Gly	Leu	Lys	Ser	Leu	Leu	Val	Gly	Ser	Asn	Leu	Glu	785	790	795
Leu	Asn	Ala	Glu	Val	Met	Val	Trp	Asn	Asp	Gly	Glu	Asp	Ser	Tyr	Gly	805	810	815
Thr	Thr	Ile	Thr	Phe	Ser	His	Pro	Ala	Gly	Leu	Ser	Tyr	Arg	Tyr	Val	820	825	830
Ala	Glu	Gly	Gln	Lys	Gln	Gly	Gln	Leu	Arg	Ser	Leu	His	Leu	Thr	Cys	835	840	845
Asp	Ser	Ala	Pro	Val	Gly	Ser	Gln	Gly	Thr	Trp	Ser	Thr	Ser	Cys	Arg	850	855	860
Ile	Asn	His	Leu	Ile	Phe	Arg	Gly	Gly	Ala	Gln	Ile	Thr	Phe	Leu	Ala	865	870	875
Thr	Phe	Asp	Val	Ser	Pro	Lys	Ala	Val	Leu	Gly	Asp	Arg	Leu	Leu	Leu	885	890	895
Thr	Ala	Asn	Val	Ser	Ser	Glu	Asn	Asn	Thr	Pro	Arg	Thr	Ser	Lys	Thr	900	905	910
Thr	Phe	Gln	Leu	Glu	Leu	Pro	Val	Lys	Tyr	Ala	Val	Tyr	Thr	Val	Val	915	920	925
Ser	Ser	His	Glu	Gln	Phe	Thr	Lys	Tyr	Leu	Asn	Phe	Ser	Glu	Ser	Glu	930	935	940
Glu	Lys	Glu	Ser	His	Val	Ala	Met	His	Arg	Tyr	Gln	Val	Asn	Asn	Leu	945	950	955
Gly	Gln	Arg	Asp	Leu	Pro	Val	Ser	Ile	Asn	Phe	Trp	Val	Pro	Val	Glu	965	970	975
Leu	Asn	Gln	Glu	Ala	Val	Trp	Met	Asp	Val	Glu	Val	Ser	His	Pro	Gln	980	985	990

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[illegible]

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<210> SEQ ID NO 31
<211> LENGTH: 495
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(495)
<223> OTHER INFORMATION: OGTA174 = Swiss Prot Accession No. P06127,
T-cell surface glycoprotein CD5
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<400> SEQUENCE: 31

Met	Pro	Met	Gly	Ser	Leu	Gln	Pro	Leu	Ala	Thr	Leu	Tyr	Leu	Leu	Gly
1				5					10					15	
Met	Leu	Val	Ala	Ser	Cys	Leu	Gly	Arg	Leu	Ser	Trp	Tyr	Asp	Pro	Asp
			20					25					30		
Phe	Gln	Ala	Arg	Leu	Thr	Arg	Ser	Asn	Ser	Lys	Cys	Gln	Gly	Gln	Leu
		35					40					45			
Glu	Val	Tyr	Leu	Lys	Asp	Gly	Trp	His	Met	Val	Cys	Ser	Gln	Ser	Trp
	50					55					60				
Gly	Arg	Ser	Ser	Lys	Gln	Trp	Glu	Asp	Pro	Ser	Gln	Ala	Ser	Lys	Val
65					70					75					80
Cys	Gln	Arg	Leu	Asn	Cys	Gly	Val	Pro	Leu	Ser	Leu	Gly	Pro	Phe	Leu
				85					90					95	
Val	Thr	Tyr	Thr	Pro	Gln	Ser	Ser	Ile	Ile	Cys	Tyr	Gly	Gln	Leu	Gly
			100					105					110		
Ser	Phe	Ser	Asn	Cys	Ser	His	Ser	Arg	Asn	Asp	Met	Cys	His	Ser	Leu
		115					120					125			
Gly	Leu	Thr	Cys	Leu	Glu	Pro	Gln	Lys	Thr	Thr	Pro	Pro	Thr	Thr	Arg
	130					135					140				

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Pro	Pro	Pro	Thr	Thr	Thr	Pro	Glu	Pro	Thr	Ala	Pro	Pro	Arg	Leu	Gln
145					150					155					160
Leu	Val	Ala	Gln	Ser	Gly	Gly	Gln	His	Cys	Ala	Gly	Val	Val	Glu	Phe
			165						170					175	
Tyr	Ser	Gly	Ser	Leu	Gly	Gly	Thr	Ile	Ser	Tyr	Glu	Ala	Gln	Asp	Lys
		180						185						190	
Thr	Gln	Asp	Leu	Glu	Asn	Phe	Leu	Cys	Asn	Asn	Leu	Gln	Cys	Gly	Ser
		195					200					205			
Phe	Leu	Lys	His	Leu	Pro	Glu	Thr	Glu	Ala	Gly	Arg	Ala	Gln	Asp	Pro
	210					215					220				
Gly	Glu	Pro	Arg	Glu	His	Gln	Pro	Leu	Pro	Ile	Gln	Trp	Lys	Ile	Gln
225					230					235					240
Asn	Ser	Ser	Cys	Thr	Ser	Leu	Glu	His	Cys	Phe	Arg	Lys	Ile	Lys	Pro
			245						250					255	
Gln	Lys	Ser	Gly	Arg	Val	Leu	Ala	Leu	Leu	Cys	Ser	Gly	Phe	Gln	Pro
			260					265						270	
Lys	Val	Gln	Ser	Arg	Leu	Val	Gly	Gly	Ser	Ser	Ile	Cys	Glu	Gly	Thr
		275					280					285			
Val	Glu	Val	Arg	Gln	Gly	Ala	Gln	Trp	Ala	Ala	Leu	Cys	Asp	Ser	Ser
	290					295					300				
Ser	Ala	Arg	Ser	Ser	Leu	Arg	Trp	Glu	Glu	Val	Cys	Arg	Glu	Gln	Gln
305					310					315					320
Cys	Gly	Ser	Val	Asn	Ser	Tyr	Arg	Val	Leu	Asp	Ala	Gly	Asp	Pro	Thr
			325						330					335	
Ser	Arg	Gly	Leu	Phe	Cys	Pro	His	Gln	Lys	Leu	Ser	Gln	Cys	His	Glu
			340					345					350		
Leu	Trp	Glu	Arg	Asn	Ser	Tyr	Cys	Lys	Lys	Val	Phe	Val	Thr	Cys	Gln
	355						360					365			
Asp	Pro	Asn	Pro	Ala	Gly	Leu	Ala	Ala	Gly	Thr	Val	Ala	Ser	Ile	Ile
	370					375					380				
Leu	Ala	Leu	Val	Leu	Leu	Val	Val	Leu	Leu	Val	Val	Cys	Gly	Pro	Leu
385				390						395					400
Ala	Tyr	Lys	Lys	Leu	Val	Lys	Lys	Phe	Arg	Gln	Lys	Lys	Gln	Arg	Gln
			405					410						415	
Trp	Ile	Gly	Pro	Thr	Gly	Met	Asn	Gln	Asn	Met	Ser	Phe	His	Arg	Asn
		420					425						430		
His	Thr	Ala	Thr	Val	Arg	Ser	His	Ala	Glu	Asn	Pro	Thr	Ala	Ser	His
		435					440					445			
Val	Asp	Asn	Glu	Tyr	Ser	Gln	Pro	Pro	Arg	Asn	Ser	Arg	Leu	Ser	Ala
	450					455					460				
Tyr	Pro	Ala	Leu	Glu	Gly	Val	Leu	His	Arg	Ser	Ser	Met	Gln	Pro	Asp
465				470					475					480	
Asn	Ser	Ser	Asp	Ser	Asp	Tyr	Asp	Leu	His	Gly	Ala	Gln	Arg	Leu	
			485					490						495	

<210> SEQ ID NO 32

<211> LENGTH: 359

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<222> LOCATION: (1)..(359)

 <223> OTHER INFORMATION: OGTA176 = Swiss Prot Accession No. P21854,
 B-cell differentiation antigen CD72 homolog

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<400> SEQUENCE: 32

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Met Ala Glu Ala Ile Thr Tyr Ala Asp Leu Arg Phe Val Lys Ala Pro
 1           5           10           15
Leu Lys Lys Ser Ile Ser Ser Arg Leu Gly Gln Asp Pro Gly Ala Asp
 20           25           30
Asp Asp Gly Glu Ile Thr Tyr Glu Asn Val Gln Val Pro Ala Val Leu
 35           40           45
Gly Val Pro Ser Ser Leu Ala Ser Ser Val Leu Gly Asp Lys Ala Ala
 50           55           60
Val Lys Ser Glu Gln Pro Thr Ala Ser Trp Arg Ala Val Thr Ser Pro
 65           70           75           80
Ala Val Gly Arg Ile Leu Pro Cys Arg Thr Thr Cys Leu Arg Tyr Leu
 85           90           95
Leu Leu Gly Leu Leu Leu Thr Cys Leu Leu Leu Gly Val Thr Ala Ile
100           105           110
Cys Leu Gly Val Arg Tyr Leu Gln Val Ser Gln Gln Leu Gln Gln Thr
115           120           125
Asn Arg Val Leu Glu Val Thr Asn Ser Ser Leu Arg Gln Gln Leu Arg
130           135           140
Leu Lys Ile Thr Gln Leu Gly Gln Ser Ala Glu Asp Leu Gln Gly Ser
145           150           155           160
Arg Arg Glu Leu Ala Gln Ser Gln Glu Ala Leu Gln Val Glu Gln Arg
165           170           175
Ala His Gln Ala Ala Glu Gly Gln Leu Gln Ala Cys Gln Ala Asp Arg
180           185           190
Gln Lys Thr Lys Glu Thr Leu Gln Ser Glu Glu Gln Gln Arg Arg Ala
195           200           205
Leu Glu Gln Lys Leu Ser Asn Met Glu Asn Arg Leu Lys Pro Phe Phe
210           215           220
Thr Cys Gly Ser Ala Asp Thr Cys Cys Pro Ser Gly Trp Ile Met His
225           230           235           240
Gln Lys Ser Cys Phe Tyr Ile Ser Leu Thr Ser Lys Asn Trp Gln Glu
245           250           255
Ser Gln Lys Gln Cys Glu Thr Leu Ser Ser Lys Leu Ala Thr Phe Ser
260           265           270
Glu Ile Tyr Pro Gln Ser His Ser Tyr Tyr Phe Leu Asn Ser Leu Leu
275           280           285
Pro Asn Gly Gly Ser Gly Asn Ser Tyr Trp Thr Gly Leu Ser Ser Asn
290           295           300
Lys Asp Trp Lys Leu Thr Asp Asp Thr Gln Arg Thr Arg Thr Tyr Ala
305           310           315           320
Gln Ser Ser Lys Cys Asn Lys Val His Lys Thr Trp Ser Trp Trp Thr
325           330           335
Leu Glu Ser Glu Ser Cys Arg Ser Ser Leu Pro Tyr Ile Cys Glu Met
340           345           350
Thr Ala Phe Arg Phe Pro Asp
355

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<210> SEQ ID NO 33

<211> LENGTH: 510

<212> TYPE: PRT

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<213> ORGANISM: Homo Sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(510)
<223> OTHER INFORMATION: OGTA177 = Swiss Prot Accession No. P49961,
    Ectonucleoside triphosphate diphosphohydrolase 1

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<400> SEQUENCE: 33

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Met Glu Asp Thr Lys Glu Ser Asn Val Lys Thr Phe Cys Ser Lys Asn
 1             5             10             15

Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile Ala Leu
 20             25             30

Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys
 35             40             45

Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
 50             55             60

Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
 65             70             75             80

Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln
 85             90             95

Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala
100             105             110

Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu
115             120             125

Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu
130             135             140

Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro
145             150             155             160

Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala
165             170             175

Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys
180             185             190

Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
195             200             205

Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val
210             215             220

Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
225             230             235             240

Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr
245             250             255

Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
260             265             270

Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys
275             280             285

Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg
290             295             300

Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly
305             310             315             320

Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser
325             330             335

Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro
340             345             350

Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys

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355	360	365
Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu		
370	375	380
Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser		
385	390	395 400
Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly		
405	410	415
Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp		
420	425	430
Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala		
435	440	445
Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala		
450	455	460
Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val Phe Leu		
465	470	475 480
Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile Gly Leu		
485	490	495
Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val		
500	505	510

<210> SEQ ID NO 34
 <211> LENGTH: 976
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapiens
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (1)..(976)
 <223> OTHER INFORMATION: OGTA197 = Swiss Prot Accession No. P29317,
 Ephrin type-A receptor 2

<400> SEQUENCE: 34

Met Glu Leu Gln Ala Ala Arg Ala Cys Phe Ala Leu Leu Trp Gly Cys
1 5 10 15
Ala Leu Ala Ala Ala Ala Ala Ala Gln Gly Lys Glu Val Val Leu Leu
20 25 30
Asp Phe Ala Ala Ala Gly Gly Glu Leu Gly Trp Leu Thr His Pro Tyr
35 40 45
Gly Lys Gly Trp Asp Leu Met Gln Asn Ile Met Asn Asp Met Pro Ile
50 55 60
Tyr Met Tyr Ser Val Cys Asn Val Met Ser Gly Asp Gln Asp Asn Trp
65 70 75 80
Leu Arg Thr Asn Trp Val Tyr Arg Gly Glu Ala Glu Arg Asn Asn Phe
85 90 95
Glu Leu Asn Phe Thr Val Arg Asp Cys Asn Ser Phe Pro Gly Gly Ala
100 105 110
Ser Ser Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Ala Glu Ser Asp Leu
115 120 125
Asp Tyr Gly Thr Asn Phe Gln Lys Arg Leu Phe Thr Lys Ile Asp Thr
130 135 140
Ile Ala Pro Asp Glu Ile Thr Val Ser Ser Asp Phe Glu Ala Arg His
145 150 155 160
Val Lys Leu Asn Val Glu Glu Arg Ser Val Gly Pro Leu Thr Arg Lys
165 170 175
Gly Phe Tyr Leu Ala Phe Gln Asp Ile Gly Ala Cys Val Ala Leu Leu

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180						185						190					
Ser	Val	Arg	Val	Tyr	Tyr	Lys	Lys	Cys	Pro	Glu	Leu	Leu	Gln	Gly	Leu		
		195					200					205					
Ala	His	Phe	Pro	Glu	Thr	Ile	Ala	Gly	Ser	Asp	Ala	Pro	Ser	Leu	Ala		
	210					215					220						
Thr	Val	Ala	Gly	Thr	Cys	Val	Asp	His	Ala	Val	Val	Pro	Pro	Gly	Gly		
225					230					235				240			
Glu	Glu	Pro	Arg	Met	His	Cys	Ala	Val	Asp	Gly	Glu	Trp	Leu	Val	Pro		
				245					250					255			
Ile	Gly	Gln	Cys	Leu	Cys	Gln	Ala	Gly	Tyr	Glu	Lys	Val	Glu	Asp	Ala		
			260					265					270				
Cys	Gln	Ala	Cys	Ser	Pro	Gly	Phe	Phe	Lys	Phe	Glu	Ala	Ser	Glu	Ser		
		275					280					285					
Pro	Cys	Leu	Glu	Cys	Pro	Glu	His	Thr	Leu	Pro	Ser	Pro	Glu	Gly	Ala		
	290					295					300						
Thr	Ser	Cys	Glu	Cys	Glu	Glu	Gly	Phe	Phe	Arg	Ala	Pro	Gln	Asp	Pro		
305					310					315				320			
Ala	Ser	Met	Pro	Cys	Thr	Arg	Pro	Pro	Ser	Ala	Pro	His	Tyr	Leu	Thr		
				325					330					335			
Ala	Val	Gly	Met	Gly	Ala	Lys	Val	Glu	Leu	Arg	Trp	Thr	Pro	Pro	Gln		
			340					345					350				
Asp	Ser	Gly	Gly	Arg	Glu	Asp	Ile	Val	Tyr	Ser	Val	Thr	Cys	Glu	Gln		
		355					360					365					
Cys	Trp	Pro	Glu	Ser	Gly	Glu	Cys	Gly	Pro	Cys	Glu	Ala	Ser	Val	Arg		
	370					375					380						
Tyr	Ser	Glu	Pro	Pro	His	Gly	Leu	Thr	Arg	Thr	Ser	Val	Thr	Val	Ser		
385					390					395				400			
Asp	Leu	Glu	Pro	His	Met	Asn	Tyr	Thr	Phe	Thr	Val	Glu	Ala	Arg	Asn		
				405					410					415			
Gly	Val	Ser	Gly	Leu	Val	Thr	Ser	Arg	Ser	Phe	Arg	Thr	Ala	Ser	Val		
			420					425					430				
Ser	Ile	Asn	Gln	Thr	Glu	Pro	Pro	Lys	Val	Arg	Leu	Glu	Gly	Arg	Ser		
		435					440					445					
Thr	Thr	Ser	Leu	Ser	Val	Ser	Trp	Ser	Ile	Pro	Pro	Pro	Gln	Gln	Ser		
	450					455					460						
Arg	Val	Trp	Lys	Tyr	Glu	Val	Thr	Tyr	Arg	Lys	Lys	Gly	Asp	Ser	Asn		
465					470					475				480			
Ser	Tyr	Asn	Val	Arg	Arg	Thr	Glu	Gly	Phe	Ser	Val	Thr	Leu	Asp	Asp		
				485					490					495			
Leu	Ala	Pro	Asp	Thr	Thr	Tyr	Leu	Val	Gln	Val	Gln	Ala	Leu	Thr	Gln		
			500					505					510				
Glu	Gly	Gln	Gly	Ala	Gly	Ser	Lys	Val	His	Glu	Phe	Gln	Thr	Leu	Ser		
		515					520					525					
Pro	Glu	Gly	Ser	Gly	Asn	Leu	Ala	Val	Ile	Gly	Gly	Val	Ala	Val	Gly		
	530					535					540						
Val	Val	Leu	Leu	Leu	Val	Leu	Ala	Gly	Val	Gly	Phe	Phe	Ile	His	Arg		
545					550					555				560			
Arg	Arg	Lys	Asn	Gln	Arg	Ala	Arg	Gln	Ser	Pro	Glu	Asp	Val	Tyr	Phe		
				565					570					575			
Ser	Lys	Ser	Glu	Gln	Leu	Lys	Pro	Leu	Lys	Thr	Tyr	Val	Asp	Pro	His		
			580					585					590				

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Thr Tyr Glu Asp Pro Asn Gln Ala Val Leu Lys Phe Thr Thr Glu Ile
 595 600 605
 His Pro Ser Cys Val Thr Arg Gln Lys Val Ile Gly Ala Gly Glu Phe
 610 615 620
 Gly Glu Val Tyr Lys Gly Met Leu Lys Thr Ser Ser Gly Lys Lys Glu
 625 630 635 640
 Val Pro Val Ala Ile Lys Thr Leu Lys Ala Gly Tyr Thr Glu Lys Gln
 645 650 655
 Arg Val Asp Phe Leu Gly Glu Ala Gly Ile Met Gly Gln Phe Ser His
 660 665 670
 His Asn Ile Ile Arg Leu Glu Gly Val Ile Ser Lys Tyr Lys Pro Met
 675 680 685
 Met Ile Ile Thr Glu Tyr Met Glu Asn Gly Ala Leu Asp Lys Phe Leu
 690 695 700
 Arg Glu Lys Asp Gly Glu Phe Ser Val Leu Gln Leu Val Gly Met Leu
 705 710 715 720
 Arg Gly Ile Ala Ala Gly Met Lys Tyr Leu Ala Asn Met Asn Tyr Val
 725 730 735
 His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val
 740 745 750
 Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro
 755 760 765
 Glu Ala Thr Tyr Thr Thr Ser Gly Gly Lys Ile Pro Ile Arg Trp Thr
 770 775 780
 Ala Pro Glu Ala Ile Ser Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val
 785 790 795 800
 Trp Ser Phe Gly Ile Val Met Trp Glu Val Met Thr Tyr Gly Glu Arg
 805 810 815
 Pro Tyr Trp Glu Leu Ser Asn His Glu Val Met Lys Ala Ile Asn Asp
 820 825 830
 Gly Phe Arg Leu Pro Thr Pro Met Asp Cys Pro Ser Ala Ile Tyr Gln
 835 840 845
 Leu Met Met Gln Cys Trp Gln Gln Glu Arg Ala Arg Arg Pro Lys Phe
 850 855 860
 Ala Asp Ile Val Ser Ile Leu Asp Lys Leu Ile Arg Ala Pro Asp Ser
 865 870 875 880
 Leu Lys Thr Leu Ala Asp Phe Asp Pro Arg Val Ser Ile Arg Leu Pro
 885 890 895
 Ser Thr Ser Gly Ser Glu Gly Val Pro Phe Arg Thr Val Ser Glu Trp
 900 905 910
 Leu Glu Ser Ile Lys Met Gln Gln Tyr Thr Glu His Phe Met Ala Ala
 915 920 925
 Gly Tyr Thr Ala Ile Glu Lys Val Val Gln Met Thr Asn Asp Asp Ile
 930 935 940
 Lys Arg Ile Gly Val Arg Leu Pro Gly His Gln Lys Arg Ile Ala Tyr
 945 950 955 960
 Ser Leu Leu Gly Leu Lys Asp Gln Val Asn Thr Val Gly Ile Pro Ile
 965 970 975

<210> SEQ ID NO 35

<211> LENGTH: 829

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<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(829)
<223> OTHER INFORMATION: OGTA202 = Swiss Prot Accession No. P22223,
Cadherin-3

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<400> SEQUENCE: 35

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Met Gly Leu Pro Arg Gly Pro Leu Ala Ser Leu Leu Leu Leu Gln Val
 1          5          10          15

Cys Trp Leu Gln Cys Ala Ala Ser Glu Pro Cys Arg Ala Val Phe Arg
 20          25          30

Glu Ala Glu Val Thr Leu Glu Ala Gly Gly Ala Glu Gln Glu Pro Gly
 35          40          45

Gln Ala Leu Gly Lys Val Phe Met Gly Cys Pro Gly Gln Glu Pro Ala
 50          55          60

Leu Phe Ser Thr Asp Asn Asp Asp Phe Thr Val Arg Asn Gly Glu Thr
 65          70          75          80

Val Gln Glu Arg Arg Ser Leu Lys Glu Arg Asn Pro Leu Lys Ile Phe
 85          90          95

Pro Ser Lys Arg Ile Leu Arg Arg His Lys Arg Asp Trp Val Val Ala
100          105          110

Pro Ile Ser Val Pro Glu Asn Gly Lys Gly Pro Phe Pro Gln Arg Leu
115          120          125

Asn Gln Leu Lys Ser Asn Lys Asp Arg Asp Thr Lys Ile Phe Tyr Ser
130          135          140

Ile Thr Gly Pro Gly Ala Asp Ser Pro Pro Glu Gly Val Phe Ala Val
145          150          155          160

Glu Lys Glu Thr Gly Trp Leu Leu Leu Asn Lys Pro Leu Asp Arg Glu
165          170          175

Glu Ile Ala Lys Tyr Glu Leu Phe Gly His Ala Val Ser Glu Asn Gly
180          185          190

Ala Ser Val Glu Asp Pro Met Asn Ile Ser Ile Ile Val Thr Asp Gln
195          200          205

Asn Asp His Lys Pro Lys Phe Thr Gln Asp Thr Phe Arg Gly Ser Val
210          215          220

Leu Glu Gly Val Leu Pro Gly Thr Ser Val Met Gln Val Thr Ala Thr
225          230          235          240

Asp Glu Asp Asp Ala Ile Tyr Thr Tyr Asn Gly Val Val Ala Tyr Ser
245          250          255

Ile His Ser Gln Glu Pro Lys Asp Pro His Asp Leu Met Phe Thr Ile
260          265          270

His Arg Ser Thr Gly Thr Ile Ser Val Ile Ser Ser Gly Leu Asp Arg
275          280          285

Glu Lys Val Pro Glu Tyr Thr Leu Thr Ile Gln Ala Thr Asp Met Asp
290          295          300

Gly Asp Gly Ser Thr Thr Thr Ala Val Ala Val Val Glu Ile Leu Asp
305          310          315          320

Ala Asn Asp Asn Ala Pro Met Phe Asp Pro Gln Lys Tyr Glu Ala His
325          330          335

Val Pro Glu Asn Ala Val Gly His Glu Val Gln Arg Leu Thr Val Thr
340          345          350

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Asp	Leu	Asp	Ala	Pro	Asn	Ser	Pro	Ala	Trp	Arg	Ala	Thr	Tyr	Leu	Ile
	355						360					365			
Met	Gly	Gly	Asp	Asp	Gly	Asp	His	Phe	Thr	Ile	Thr	Thr	His	Pro	Glu
	370					375					380				
Ser	Asn	Gln	Gly	Ile	Leu	Thr	Thr	Arg	Lys	Gly	Leu	Asp	Phe	Glu	Ala
385					390					395					400
Lys	Asn	Gln	His	Thr	Leu	Tyr	Val	Glu	Val	Thr	Asn	Glu	Ala	Pro	Phe
			405						410					415	
Val	Leu	Lys	Leu	Pro	Thr	Ser	Thr	Ala	Thr	Ile	Val	Val	His	Val	Glu
			420					425					430		
Asp	Val	Asn	Glu	Ala	Pro	Val	Phe	Val	Pro	Pro	Ser	Lys	Val	Val	Glu
			435				440					445			
Val	Gln	Glu	Gly	Ile	Pro	Thr	Gly	Glu	Pro	Val	Cys	Val	Tyr	Thr	Ala
	450					455					460				
Glu	Asp	Pro	Asp	Lys	Glu	Asn	Gln	Lys	Ile	Ser	Tyr	Arg	Ile	Leu	Arg
465					470					475					480
Asp	Pro	Ala	Gly	Trp	Leu	Ala	Met	Asp	Pro	Asp	Ser	Gly	Gln	Val	Thr
			485						490					495	
Ala	Val	Gly	Thr	Leu	Asp	Arg	Glu	Asp	Glu	Gln	Phe	Val	Arg	Asn	Asn
			500					505					510		
Ile	Tyr	Glu	Val	Met	Val	Leu	Ala	Met	Asp	Asn	Gly	Ser	Pro	Pro	Thr
	515						520					525			
Thr	Gly	Thr	Gly	Thr	Leu	Leu	Leu	Thr	Leu	Ile	Asp	Val	Asn	Asp	His
	530				535						540				
Gly	Pro	Val	Pro	Glu	Pro	Arg	Gln	Ile	Thr	Ile	Cys	Asn	Gln	Ser	Pro
545					550					555					560
Val	Arg	His	Val	Leu	Asn	Ile	Thr	Asp	Lys	Asp	Leu	Ser	Pro	His	Thr
			565						570					575	
Ser	Pro	Phe	Gln	Ala	Gln	Leu	Thr	Asp	Asp	Ser	Asp	Ile	Tyr	Trp	Thr
		580						585					590		
Ala	Glu	Val	Asn	Glu	Glu	Gly	Asp	Thr	Val	Val	Leu	Ser	Leu	Lys	Lys
		595					600					605			
Phe	Leu	Lys	Gln	Asp	Thr	Tyr	Asp	Val	His	Leu	Ser	Leu	Ser	Asp	His
	610				615						620				
Gly	Asn	Lys	Glu	Gln	Leu	Thr	Val	Ile	Arg	Ala	Thr	Val	Cys	Asp	Cys
625					630				635						640
His	Gly	His	Val	Glu	Thr	Cys	Pro	Gly	Pro	Trp	Lys	Gly	Gly	Phe	Ile
			645					650						655	
Leu	Pro	Val	Leu	Gly	Ala	Val	Leu	Ala	Leu	Leu	Phe	Leu	Leu	Leu	Val
		660					665						670		
Leu	Leu	Leu	Leu	Val	Arg	Lys	Lys	Arg	Lys	Ile	Lys	Glu	Pro	Leu	Leu
	675					680						685			
Leu	Pro	Glu	Asp	Asp	Thr	Arg	Asp	Asn	Val	Phe	Tyr	Tyr	Gly	Glu	Glu
	690					695					700				
Gly	Gly	Gly	Glu	Glu	Asp	Gln	Asp	Tyr	Asp	Ile	Thr	Gln	Leu	His	Arg
705					710					715					720
Gly	Leu	Glu	Ala	Arg	Pro	Glu	Val	Val	Leu	Arg	Asn	Asp	Val	Ala	Pro
			725						730					735	
Thr	Ile	Ile	Pro	Thr	Pro	Met	Tyr	Arg	Pro	Arg	Pro	Ala	Asn	Pro	Asp
			740					745					750		
Glu	Ile	Gly	Asn	Phe	Ile	Ile	Glu	Asn	Leu	Lys	Ala	Ala	Asn	Thr	Asp

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755	760	765
Pro Thr Ala Pro Pro Tyr Asp Thr Leu Leu Val Phe Asp Tyr Glu Gly		
770	775	780
Ser Gly Ser Asp Ala Ala Ser Leu Ser Ser Leu Thr Ser Ser Ala Ser		
785	790	795 800
Asp Gln Asp Gln Asp Tyr Asp Tyr Leu Asn Glu Trp Gly Ser Arg Phe		
	805 810	815
Lys Lys Leu Ala Asp Met Tyr Gly Gly Gly Glu Asp Asp		
	820 825	

<210> SEQ ID NO 36
 <211> LENGTH: 790
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapiens
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (1)..(790)
 <223> OTHER INFORMATION: OGTA203 = Swiss Prot Accession No. P55285,
 Cadherin-6

<400> SEQUENCE: 36

Met Arg Thr Tyr Arg Tyr Phe Leu Leu Leu Phe Trp Val Gly Gln Pro		
1	5	10 15
Tyr Pro Thr Leu Ser Thr Pro Leu Ser Lys Arg Thr Ser Gly Phe Pro		
	20	25 30
Ala Lys Lys Arg Ala Leu Glu Leu Ser Gly Asn Ser Lys Asn Glu Leu		
	35	40 45
Asn Arg Ser Lys Arg Ser Trp Met Trp Asn Gln Phe Phe Leu Leu Glu		
	50	55 60
Glu Tyr Thr Gly Ser Asp Tyr Gln Tyr Val Gly Lys Leu His Ser Asp		
	65	70 75 80
Gln Asp Arg Gly Asp Gly Ser Leu Lys Tyr Ile Leu Ser Gly Asp Gly		
	85	90 95
Ala Gly Asp Leu Phe Ile Ile Asn Glu Asn Thr Gly Asp Ile Gln Ala		
	100	105 110
Thr Lys Arg Leu Asp Arg Glu Glu Lys Pro Val Tyr Ile Leu Arg Ala		
	115	120 125
Gln Ala Ile Asn Arg Arg Thr Gly Arg Pro Val Glu Pro Glu Ser Glu		
	130	135 140
Phe Ile Ile Lys Ile His Asp Ile Asn Asp Asn Glu Pro Ile Phe Thr		
	145	150 155 160
Lys Glu Val Tyr Thr Ala Thr Val Pro Glu Met Ser Asp Val Gly Thr		
	165	170 175
Phe Val Val Gln Val Thr Ala Thr Asp Ala Asp Asp Pro Thr Tyr Gly		
	180	185 190
Asn Ser Ala Lys Val Val Tyr Ser Ile Leu Gln Gly Gln Pro Tyr Phe		
	195	200 205
Ser Val Glu Ser Glu Thr Gly Ile Ile Lys Thr Ala Leu Leu Asn Met		
	210	215 220
Asp Arg Glu Asn Arg Glu Gln Tyr Gln Val Val Ile Gln Ala Lys Asp		
	225	230 235 240
Met Gly Gly Gln Met Gly Gly Leu Ser Gly Thr Thr Thr Val Asn Ile		
	245	250 255
Thr Leu Thr Asp Val Asn Asp Asn Pro Pro Arg Phe Pro Gln Ser Thr		

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260						265						270					
Tyr	Gln	Phe	Lys	Thr	Pro	Glu	Ser	Ser	Pro	Pro	Gly	Thr	Pro	Ile	Gly		
		275					280					285					
Arg	Ile	Lys	Ala	Ser	Asp	Ala	Asp	Val	Gly	Glu	Asn	Ala	Glu	Ile	Glu		
		290				295					300						
Tyr	Ser	Ile	Thr	Asp	Gly	Glu	Gly	Leu	Asp	Met	Phe	Asp	Val	Ile	Thr		
305					310					315					320		
Asp	Gln	Glu	Thr	Gln	Glu	Gly	Ile	Ile	Thr	Val	Lys	Lys	Leu	Leu	Asp		
				325					330					335			
Phe	Glu	Lys	Lys	Lys	Val	Tyr	Thr	Leu	Lys	Val	Glu	Ala	Ser	Asn	Pro		
			340					345					350				
Tyr	Val	Glu	Pro	Arg	Phe	Leu	Tyr	Leu	Gly	Pro	Phe	Lys	Asp	Ser	Ala		
		355					360					365					
Thr	Val	Arg	Ile	Val	Val	Glu	Asp	Val	Asp	Glu	Pro	Pro	Val	Phe	Ser		
		370				375					380						
Lys	Leu	Ala	Tyr	Ile	Leu	Gln	Ile	Arg	Glu	Asp	Ala	Gln	Ile	Asn	Thr		
385					390					395					400		
Thr	Ile	Gly	Ser	Val	Thr	Ala	Gln	Asp	Pro	Asp	Ala	Ala	Arg	Asn	Pro		
				405					410					415			
Val	Lys	Tyr	Ser	Val	Asp	Arg	His	Thr	Asp	Met	Asp	Arg	Ile	Phe	Asn		
			420					425					430				
Ile	Asp	Ser	Gly	Asn	Gly	Ser	Ile	Phe	Thr	Ser	Lys	Leu	Leu	Asp	Arg		
		435					440					445					
Glu	Thr	Leu	Leu	Trp	His	Asn	Ile	Thr	Val	Ile	Ala	Thr	Glu	Ile	Asn		
		450				455					460						
Asn	Pro	Lys	Gln	Ser	Ser	Arg	Val	Pro	Leu	Tyr	Ile	Lys	Val	Leu	Asp		
465					470					475				480			
Val	Asn	Asp	Asn	Ala	Pro	Glu	Phe	Ala	Glu	Phe	Tyr	Glu	Thr	Phe	Val		
				485					490					495			
Cys	Glu	Lys	Ala	Lys	Ala	Asp	Gln	Leu	Ile	Gln	Thr	Leu	His	Ala	Val		
			500				505						510				
Asp	Lys	Asp	Asp	Pro	Tyr	Ser	Gly	His	Gln	Phe	Ser	Phe	Ser	Leu	Ala		
		515					520					525					
Pro	Glu	Ala	Ala	Ser	Gly	Ser	Asn	Phe	Thr	Ile	Gln	Asp	Asn	Lys	Asp		
		530				535					540						
Asn	Thr	Ala	Gly	Ile	Leu	Thr	Arg	Lys	Asn	Gly	Tyr	Asn	Arg	His	Glu		
545					550					555				560			
Met	Ser	Thr	Tyr	Leu	Leu	Pro	Val	Val	Ile	Ser	Asp	Asn	Asp	Tyr	Pro		
				565					570					575			
Val	Gln	Ser	Ser	Thr	Gly	Thr	Val	Thr	Val	Arg	Val	Cys	Ala	Cys	Asp		
			580				585						590				
His	His	Gly	Asn	Met	Gln	Ser	Cys	His	Ala	Glu	Ala	Leu	Ile	His	Pro		
		595					600					605					
Thr	Gly	Leu	Ser	Thr	Gly	Ala	Leu	Val	Ala	Ile	Leu	Leu	Cys	Ile	Val		
		610				615					620						
Ile	Leu	Leu	Val	Thr	Val	Val	Leu	Phe	Ala	Ala	Leu	Arg	Arg	Gln	Arg		
625					630					635				640			
Lys	Lys	Glu	Pro	Leu	Ile	Ile	Ser	Lys	Glu	Asp	Ile	Arg	Asp	Asn	Ile		
				645					650					655			
Val	Ser	Tyr	Asn	Asp	Glu	Gly	Gly	Gly	Glu	Glu	Asp	Thr	Gln	Ala	Phe		
			660				665						670				

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Asp Ile Gly Thr Leu Arg Asn Pro Glu Ala Ile Glu Asp Asn Lys Leu
675                      680                      685

Arg Arg Asp Ile Val Pro Glu Ala Leu Phe Leu Pro Arg Arg Thr Pro
690                      695                      700

Thr Ala Arg Asp Asn Thr Asp Val Arg Asp Phe Ile Asn Gln Arg Leu
705                      710                      715                      720

Lys Glu Asn Asp Thr Asp Pro Thr Ala Pro Pro Tyr Asp Ser Leu Ala
725                      730                      735

Thr Tyr Ala Tyr Glu Gly Thr Gly Ser Val Ala Asp Ser Leu Ser Ser
740                      745                      750

Leu Glu Ser Val Thr Thr Asp Ala Asp Gln Asp Tyr Asp Tyr Leu Ser
755                      760                      765

Asp Trp Gly Pro Arg Phe Lys Lys Leu Ala Asp Met Tyr Gly Gly Val
770                      775                      780

Asp Ser Asp Lys Asp Ser
785                      790

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<210> SEQ ID NO 37
<211> LENGTH: 209
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(209)
<223> OTHER INFORMATION: OGTA206 = Swiss Prot Accession No. 014493,
        Claudin-4

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<400> SEQUENCE: 37

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Met Ala Ser Met Gly Leu Gln Val Met Gly Ile Ala Leu Ala Val Leu
1                      5                      10                      15

Gly Trp Leu Ala Val Met Leu Cys Cys Ala Leu Pro Met Trp Arg Val
20                      25                      30

Thr Ala Phe Ile Gly Ser Asn Ile Val Thr Ser Gln Thr Ile Trp Glu
35                      40                      45

Gly Leu Trp Met Asn Cys Val Val Gln Ser Thr Gly Gln Met Gln Cys
50                      55                      60

Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala
65                      70                      75                      80

Arg Ala Leu Val Ile Ile Ser Ile Ile Val Ala Ala Leu Gly Val Leu
85                      90                      95

Leu Ser Val Val Gly Gly Lys Cys Thr Asn Cys Leu Glu Asp Glu Ser
100                     105                     110

Ala Lys Ala Lys Thr Met Ile Val Ala Gly Val Val Phe Leu Leu Ala
115                     120                     125

Gly Leu Met Val Ile Val Pro Val Ser Trp Thr Ala His Asn Ile Ile
130                     135                     140

Gln Asp Phe Tyr Asn Pro Leu Val Ala Ser Gly Gln Lys Arg Glu Met
145                     150                     155                     160

Gly Ala Ser Leu Tyr Val Gly Trp Ala Ala Ser Gly Leu Leu Leu Leu
165                     170                     175

Gly Gly Gly Leu Leu Cys Cys Asn Cys Pro Pro Arg Thr Asp Lys Pro
180                     185                     190

Tyr Ser Ala Lys Tyr Ser Ala Ala Arg Ser Ala Ala Ala Ser Asn Tyr
195                     200                     205

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Val

<210> SEQ ID NO 38
 <211> LENGTH: 1821
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapiens
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (1)..(1821)
 <223> OTHER INFORMATION: OGTA213 = Swiss Prot Accession No. Q14767,
 Latent-transforming growth factor beta-binding protein 2

 <400> SEQUENCE: 38

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Met Arg Pro Arg Thr Lys Ala Arg Ser Pro Gly Arg Ala Leu Arg Asn
 1           5           10           15

Pro Trp Arg Gly Phe Leu Pro Leu Thr Leu Ala Leu Phe Val Gly Ala
 20           25           30

Gly His Ala Gln Arg Asp Pro Val Gly Arg Tyr Glu Pro Ala Gly Gly
 35           40           45

Asp Ala Asn Arg Leu Arg Arg Pro Gly Gly Ser Tyr Pro Ala Ala Ala
 50           55           60

Ala Ala Lys Val Tyr Ser Leu Phe Arg Glu Gln Asp Ala Pro Val Ala
 65           70           75

Gly Leu Gln Pro Val Glu Arg Ala Gln Pro Gly Trp Gly Ser Pro Arg
 85           90           95

Arg Pro Thr Glu Ala Glu Ala Arg Arg Pro Ser Arg Ala Gln Gln Ser
100          105          110

Arg Arg Val Gln Pro Pro Ala Gln Thr Arg Arg Ser Thr Pro Leu Gly
115          120          125

Gln Gln Gln Pro Ala Pro Arg Thr Arg Ala Ala Pro Ala Leu Pro Arg
130          135          140

Leu Gly Thr Pro Gln Arg Ser Gly Ala Ala Pro Pro Thr Pro Pro Arg
145          150          155          160

Gly Arg Leu Thr Gly Arg Asn Val Cys Gly Gly Gln Cys Cys Pro Gly
165          170          175

Trp Thr Thr Ala Asn Ser Thr Asn His Cys Ile Lys Pro Val Cys Glu
180          185          190

Pro Pro Cys Gln Asn Arg Gly Ser Cys Ser Arg Pro Gln Leu Cys Val
195          200          205

Cys Arg Ser Gly Phe Arg Gly Ala Arg Cys Glu Glu Val Ile Pro Asp
210          215          220

Glu Glu Phe Asp Pro Gln Asn Ser Arg Leu Ala Pro Arg Arg Trp Ala
225          230          235          240

Glu Arg Ser Pro Asn Leu Arg Arg Ser Ser Ala Ala Gly Glu Gly Thr
245          250          255

Leu Ala Arg Ala Gln Pro Pro Ala Pro Gln Ser Pro Pro Ala Pro Gln
260          265          270

Ser Pro Pro Ala Gly Thr Leu Ser Gly Leu Ser Gln Thr His Pro Ser
275          280          285

Gln Gln His Val Gly Leu Ser Arg Thr Val Arg Leu His Pro Thr Ala
290          295          300

Thr Ala Ser Ser Gln Leu Ser Ser Asn Ala Leu Pro Pro Gly Pro Gly
305          310          315          320
  
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Leu	Glu	Gln	Arg	Asp	Gly	Thr	Gln	Gln	Ala	Val	Pro	Leu	Glu	His	Pro
				325					330					335	
Ser	Ser	Pro	Trp	Gly	Leu	Asn	Leu	Thr	Glu	Lys	Ile	Lys	Lys	Ile	Lys
				340				345					350		
Ile	Val	Phe	Thr	Pro	Thr	Ile	Cys	Lys	Gln	Thr	Cys	Ala	Arg	Gly	His
				355			360					365			
Cys	Ala	Asn	Ser	Cys	Glu	Arg	Gly	Asp	Thr	Thr	Thr	Leu	Tyr	Ser	Gln
				370		375					380				
Gly	Gly	His	Gly	His	Asp	Pro	Lys	Ser	Gly	Phe	Arg	Ile	Tyr	Phe	Cys
				385		390				395					400
Gln	Ile	Pro	Cys	Leu	Asn	Gly	Gly	Arg	Cys	Ile	Gly	Arg	Asp	Glu	Cys
				405					410					415	
Trp	Cys	Pro	Ala	Asn	Ser	Thr	Gly	Lys	Phe	Cys	His	Leu	Pro	Ile	Pro
				420				425					430		
Gln	Pro	Asp	Arg	Glu	Pro	Pro	Gly	Arg	Gly	Ser	Arg	Pro	Arg	Ala	Leu
				435			440					445			
Leu	Glu	Ala	Pro	Leu	Lys	Gln	Ser	Thr	Phe	Thr	Leu	Pro	Leu	Ser	Asn
				450		455					460				
Gln	Leu	Ala	Ser	Val	Asn	Pro	Ser	Leu	Val	Lys	Val	His	Ile	His	His
				465		470				475					480
Pro	Pro	Glu	Ala	Ser	Val	Gln	Ile	His	Gln	Val	Ala	Gln	Val	Arg	Gly
				485					490					495	
Gly	Val	Glu	Glu	Ala	Leu	Val	Glu	Asn	Ser	Val	Glu	Thr	Arg	Pro	Pro
				500				505					510		
Pro	Trp	Leu	Pro	Ala	Ser	Pro	Gly	His	Ser	Leu	Trp	Asp	Ser	Asn	Asn
				515			520					525			
Ile	Pro	Ala	Arg	Ser	Gly	Glu	Pro	Pro	Arg	Pro	Leu	Pro	Pro	Ala	Ala
				530		535					540				
Pro	Arg	Pro	Arg	Gly	Leu	Leu	Gly	Arg	Cys	Tyr	Leu	Asn	Thr	Val	Asn
				545		550				555					560
Gly	Gln	Cys	Ala	Asn	Pro	Leu	Leu	Glu	Leu	Thr	Thr	Gln	Glu	Asp	Cys
				565					570					575	
Cys	Gly	Ser	Val	Gly	Ala	Phe	Trp	Gly	Val	Thr	Leu	Cys	Ala	Pro	Cys
				580				585					590		
Pro	Pro	Arg	Pro	Ala	Ser	Pro	Val	Ile	Glu	Asn	Gly	Gln	Leu	Glu	Cys
				595			600					605			
Pro	Gln	Gly	Tyr	Lys	Arg	Leu	Asn	Leu	Thr	His	Cys	Gln	Asp	Ile	Asn
				610		615					620				
Glu	Cys	Leu	Thr	Leu	Gly	Leu	Cys	Lys	Asp	Ala	Glu	Cys	Val	Asn	Thr
				625		630				635					640
Arg	Gly	Ser	Tyr	Leu	Cys	Thr	Cys	Arg	Pro	Gly	Leu	Met	Leu	Asp	Pro
				645					650					655	
Ser	Arg	Ser	Arg	Cys	Val	Ser	Asp	Lys	Ala	Ile	Ser	Met	Leu	Gln	Gly
				660				665					670		
Leu	Cys	Tyr	Arg	Ser	Leu	Gly	Pro	Gly	Thr	Cys	Thr	Leu	Pro	Leu	Ala
				675			680					685			
Gln	Arg	Ile	Thr	Lys	Gln	Ile	Cys	Cys							

[illegible]

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Leu Gly Asp Ser Cys Glu Asp Val Asp Glu Cys Glu Asp Pro Gln	1130	1135	1140
Ser Ser Cys Leu Gly Gly Glu Cys Lys Asn Thr Val Gly Ser Tyr	1145	1150	1155
Gln Cys Leu Cys Pro Gln Gly Phe Gln Leu Ala Asn Gly Thr Val	1160	1165	1170
Cys Glu Asp Val Asn Glu Cys Met Gly Glu Glu His Cys Ala Pro	1175	1180	1185
His Gly Glu Cys Leu Asn Ser His Gly Ser Phe Phe Cys Leu Cys	1190	1195	1200
Ala Pro Gly Phe Val Ser Ala Glu Gly Gly Thr Ser Cys Gln Asp	1205	1210	1215
Val Asp Glu Cys Ala Thr Thr Asp Pro Cys Val Gly Gly His Cys	1220	1225	1230
Val Asn Thr Glu Gly Ser Phe Asn Cys Leu Cys Glu Thr Gly Phe	1235	1240	1245
Gln Pro Ser Pro Glu Ser Gly Glu Cys Val Asp Ile Asp Glu Cys	1250	1255	1260
Glu Asp Tyr Gly Asp Pro Val Cys Gly Thr Trp Lys Cys Glu Asn	1265	1270	1275
Ser Pro Gly Ser Tyr Arg Cys Val Leu Gly Cys Gln Pro Gly Phe	1280	1285	1290
His Met Ala Pro Asn Gly Asp Cys Ile Asp Ile Asp Glu Cys Ala	1295	1300	1305
Asn Asp Thr Met Cys Gly Ser His Gly Phe Cys Asp Asn Thr Asp	1310	1315	1320
Gly Ser Phe Arg Cys Leu Cys Asp Gln Gly Phe Glu Ile Ser Pro	1325	1330	1335
Ser Gly Trp Asp Cys Val Asp Val Asn Glu Cys Glu Leu Met Leu	1340	1345	1350
Ala Val Cys Gly Ala Ala Leu Cys Glu Asn Val Glu Gly Ser Phe	1355	1360	1365
Leu Cys Leu Cys Ala Ser Asp Leu Glu Glu Tyr Asp Ala Gln Glu	1370	1375	1380
Gly His Cys Arg Pro Arg Gly Ala Gly Gly Gln Ser Met Ser Glu	1385	1390	1395
Ala Pro Thr Gly Asp His Ala Pro Ala Pro Thr Arg Met Asp Cys	1400	1405	1410
Tyr Ser Gly Gln Lys Gly His Ala Pro Cys Ser Ser Val Leu Gly	1415	1420	1425
Arg Asn Thr Thr Gln Ala Glu Cys Cys Cys Thr Gln Gly Ala Thr	1430	1435	1440
Trp Gly Asp Ala Cys Asp Leu Cys Pro Ser Glu Asp Ser Ala Glu	1445	1450	1455
Phe Ser Glu Ile Cys Pro Ser Gly Lys Gly Tyr Ile Pro Val Glu	1460	1465	1470
Gly Ala Trp Thr Phe Gly Gln Thr Met Tyr Thr Asp Ala Asp Glu	1475	1480	1485
Cys Val Ile Phe Gly Pro Gly Leu Cys Pro Asn Gly Arg Cys Leu	1490	1495	1500

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Asn Thr	Val Pro Gly Tyr Val	Cys Leu Cys Asn Pro	Gly Phe His
1505	1510	1515	
Tyr Asp	Ala Ser His Lys Lys	Cys Glu Asp His Asp	Glu Cys Gln
1520	1525	1530	
Asp Leu	Ala Cys Glu Asn Gly	Glu Cys Val Asn Thr	Glu Gly Ser
1535	1540	1545	
Phe His	Cys Phe Cys Ser Pro	Pro Leu Thr Leu Asp	Leu Ser Gln
1550	1555	1560	
Gln Arg	Cys Met Asn Ser Thr	Ser Ser Thr Glu Asp	Leu Pro Asp
1565	1570	1575	
His Asp	Ile His Met Asp Ile	Cys Trp Lys Lys Val	Thr Asn Asp
1580	1585	1590	
Val Cys	Ser Glu Pro Leu Arg	Gly His Arg Thr Thr	Tyr Thr Glu
1595	1600	1605	
Cys Cys	Cys Gln Asp Gly Lys	Ala Trp Ser Gln Gln	Cys Ala Leu
1610	1615	1620	
Cys Pro	Pro Arg Ser Ser Glu	Val Tyr Ala Gln Leu	Cys Asn Val
1625	1630	1635	
Ala Arg	Ile Glu Ala Glu Arg	Glu Ala Gly Val His	Phe Arg Pro
1640	1645	1650	
Gly Tyr	Glu Tyr Gly Pro Gly	Pro Asp Asp Leu His	Tyr Ser Ile
1655	1660	1665	
Tyr Gly	Pro Asp Gly Ala Pro	Phe Tyr Asn Tyr Leu	Gly Pro Glu
1670	1675	1680	
Asp Thr	Val Pro Glu Pro Ala	Phe Pro Asn Thr Ala	Gly His Ser
1685	1690	1695	
Ala Asp	Arg Thr Pro Ile Leu	Glu Ser Pro Leu Gln	Pro Ser Glu
1700	1705	1710	
Leu Gln	Pro His Tyr Val Ala	Ser His Pro Glu Pro	Pro Ala Gly
1715	1720	1725	
Phe Glu	Gly Leu Gln Ala Glu	Glu Cys Gly Ile Leu	Asn Gly Cys
1730	1735	1740	
Glu Asn	Gly Arg Cys Val Arg	Val Arg Glu Gly Tyr	Thr Cys Asp
1745	1750	1755	
Cys Phe	Glu Gly Phe Gln Leu	Asp Ala Ala His Met	Ala Cys Val
1760	1765	1770	
Asp Val	Asn Glu Cys Asp Asp	Leu Asn Gly Pro Ala	Val Leu Cys
1775	1780	1785	
Val His	Gly Tyr Cys Glu Asn	Thr Glu Gly Ser Tyr	Arg Cys His
1790	1795	1800	
Cys Ser	Pro Gly Tyr Val Ala	Glu Ala Gly Pro Pro	His Cys Thr
1805	1810	1815	
Ala Lys	Glu		
1820			

<210> SEQ ID NO 39

<211> LENGTH: 512

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<222> LOCATION: (1)..(512)

<223> OTHER INFORMATION: OGTA214 = Swiss Prot Accession No. Q9H3R2, Mucin-13

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<400> SEQUENCE: 39

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Met Lys Ala Ile Ile His Leu Thr Leu Leu Ala Leu Leu Ser Val Asn
 1           5           10           15

Thr Ala Thr Asn Gln Gly Asn Ser Ala Asp Ala Val Thr Thr Thr Glu
 20           25           30

Thr Ala Thr Ser Gly Pro Thr Val Ala Ala Ala Asp Thr Thr Glu Thr
 35           40           45

Asn Phe Pro Glu Thr Ala Ser Thr Thr Ala Asn Thr Pro Ser Phe Pro
 50           55           60

Thr Ala Thr Ser Pro Ala Pro Pro Ile Ile Ser Thr His Ser Ser Ser
 65           70           75           80

Thr Ile Pro Thr Pro Ala Pro Pro Ile Ile Ser Thr His Ser Ser Ser
 85           90           95

Thr Ile Pro Ile Pro Thr Ala Ala Asp Ser Glu Ser Thr Thr Asn Val
100          105          110

Asn Ser Leu Ala Thr Ser Asp Ile Ile Thr Ala Ser Ser Pro Asn Asp
115          120          125

Gly Leu Ile Thr Met Val Pro Ser Glu Thr Gln Ser Asn Asn Glu Met
130          135          140

Ser Pro Thr Thr Glu Asp Asn Gln Ser Ser Gly Pro Pro Thr Gly Thr
145          150          155          160

Ala Leu Leu Glu Thr Ser Thr Leu Asn Ser Thr Gly Pro Ser Asn Pro
165          170          175

Cys Gln Asp Asp Pro Cys Ala Asp Asn Ser Leu Cys Val Lys Leu His
180          185          190

Asn Thr Ser Phe Cys Leu Cys Leu Glu Gly Tyr Tyr Tyr Asn Ser Ser
195          200          205

Thr Cys Lys Lys Gly Lys Val Phe Pro Gly Lys Ile Ser Val Thr Val
210          215          220

Ser Glu Thr Phe Asp Pro Glu Glu Lys His Ser Met Ala Tyr Gln Asp
225          230          235          240

Leu His Ser Glu Ile Thr Ser Leu Phe Lys Asp Val Phe Gly Thr Ser
245          250          255

Val Tyr Gly Gln Thr Val Ile Leu Thr Val Ser Thr Ser Leu Ser Pro
260          265          270

Arg Ser Glu Met Arg Ala Asp Asp Lys Phe Val Asn Val Thr Ile Val
275          280          285

Thr Ile Leu Ala Glu Thr Thr Ser Asp Asn Glu Lys Thr Val Thr Glu
290          295          300

Lys Ile Asn Lys Ala Ile Arg Ser Ser Ser Ser Asn Phe Leu Asn Tyr
305          310          315          320

Asp Leu Thr Leu Arg Cys Asp Tyr Tyr Gly Cys Asn Gln Thr Ala Asp
325          330          335

Asp Cys Leu Asn Gly Leu Ala Cys Asp Cys Lys Ser Asp Leu Gln Arg
340          345          350

Pro Asn Pro Gln Ser Pro Phe Cys Val Ala Ser Ser Leu Lys Cys Pro
355          360          365

Asp Ala Cys Asn Ala Gln His Lys Gln Cys Leu Ile Lys Lys Ser Gly
370          375          380

Gly Ala Pro Glu Cys Ala Cys Val Pro Gly Tyr Gln Glu Asp Ala Asn

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385              390              395              400
Gly Asn Cys Gln Lys Cys Ala Phe Gly Tyr Ser Gly Leu Asp Cys Lys
              405              410              415
Asp Lys Phe Gln Leu Ile Leu Thr Ile Val Gly Thr Ile Ala Gly Ile
              420              425              430
Val Ile Leu Ser Met Ile Ile Ala Leu Ile Val Thr Ala Arg Ser Asn
              435              440              445
Asn Lys Thr Lys His Ile Glu Glu Glu Asn Leu Ile Asp Glu Asp Phe
              450              455              460
Gln Asn Leu Lys Leu Arg Ser Thr Gly Phe Thr Asn Leu Gly Ala Glu
              465              470              475              480
Gly Ser Val Phe Pro Lys Val Arg Ile Thr Ala Ser Arg Asp Ser Gln
              485              490              495
Met Gln Asn Pro Tyr Ser Arg His Ser Ser Met Pro Arg Pro Asp Tyr
              500              505              510

<210> SEQ ID NO 40
<211> LENGTH: 1212
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(1212)
<223> OTHER INFORMATION: OGTA216 = Swiss Prot Accession No. P55011,
      Solute carrier family 12 member 2

<400> SEQUENCE: 40
Met Glu Pro Arg Pro Thr Ala Pro Ser Ser Gly Ala Pro Gly Leu Ala
1              5              10              15
Gly Val Gly Glu Thr Pro Ser Ala Ala Ala Leu Ala Ala Ala Arg Val
20              25              30
Glu Leu Pro Gly Thr Ala Val Pro Ser Val Pro Glu Asp Ala Ala Pro
35              40              45
Ala Ser Arg Asp Gly Gly Gly Val Arg Asp Glu Gly Pro Ala Ala Ala
50              55              60
Gly Asp Gly Leu Gly Arg Pro Leu Gly Pro Thr Pro Ser Gln Ser Arg
65              70              75              80
Phe Gln Val Asp Leu Val Ser Glu Asn Ala Gly Arg Ala Ala Ala Ala
85              90              95
Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Gly Ala Gly Ala Gly
100             105             110
Ala Lys Gln Thr Pro Ala Asp Gly Glu Ala Ser Gly Glu Ser Glu Pro
115            120            125
Ala Lys Gly Ser Glu Glu Ala Lys Gly Arg Phe Arg Val Asn Phe Val
130            135            140
Asp Pro Ala Ala Ser Ser Ser Ala Glu Asp Ser Leu Ser Asp Ala Ala
145            150            155            160
Gly Val Gly Val Asp Gly Pro Asn Val Ser Phe Gln Asn Gly Gly Asp
165            170            175
Thr Val Leu Ser Glu Gly Ser Ser Leu His Ser Gly Gly Gly Gly Gly
180            185            190
Ser Gly His His Gln His Tyr Tyr Tyr Asp Thr His Thr Asn Thr Tyr
195            200            205
Tyr Leu Arg Thr Phe Gly His Asn Thr Met Asp Ala Val Pro Arg Ile

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210	215	220
Asp His Tyr Arg His Thr Ala Ala Gln Leu Gly Glu Lys Leu Leu Arg 225 230 235 240		
Pro Ser Leu Ala Glu Leu His Asp Glu Leu Glu Lys Glu Pro Phe Glu 245 250 255		
Asp Gly Phe Ala Asn Gly Glu Glu Ser Thr Pro Thr Arg Asp Ala Val 260 265 270		
Val Thr Tyr Thr Ala Glu Ser Lys Gly Val Val Lys Phe Gly Trp Ile 275 280 285		
Lys Gly Val Leu Val Arg Cys Met Leu Asn Ile Trp Gly Val Met Leu 290 295 300		
Phe Ile Arg Leu Ser Trp Ile Val Gly Gln Ala Gly Ile Gly Leu Ser 305 310 315 320		
Val Leu Val Ile Met Met Ala Thr Val Val Thr Thr Ile Thr Gly Leu 325 330 335		
Ser Thr Ser Ala Ile Ala Thr Asn Gly Phe Val Arg Gly Gly Gly Ala 340 345 350		
Tyr Tyr Leu Ile Ser Arg Ser Leu Gly Pro Glu Phe Gly Gly Ala Ile 355 360 365		
Gly Leu Ile Phe Ala Phe Ala Asn Ala Val Ala Val Ala Met Tyr Val 370 375 380		
Val Gly Phe Ala Glu Thr Val Val Glu Leu Leu Lys Glu His Ser Ile 385 390 395 400		
Leu Met Ile Asp Glu Ile Asn Asp Ile Arg Ile Ile Gly Ala Ile Thr 405 410 415		
Val Val Ile Leu Leu Gly Ile Ser Val Ala Gly Met Glu Trp Glu Ala 420 425 430		
Lys Ala Gln Ile Val Leu Leu Val Ile Leu Leu Leu Ala Ile Gly Asp 435 440 445		
Phe Val Ile Gly Thr Phe Ile Pro Leu Glu Ser Lys Lys Pro Lys Gly 450 455 460		
Phe Phe Gly Tyr Lys Ser Glu Ile Phe Asn Glu Asn Phe Gly Pro Asp 465 470 475 480		
Phe Arg Glu Glu Glu Thr Phe Phe Ser Val Phe Ala Ile Phe Phe Pro 485 490 495		
Ala Ala Thr Gly Ile Leu Ala Gly Ala Asn Ile Ser Gly Asp Leu Ala 500 505 510		
Asp Pro Gln Ser Ala Ile Pro Lys Gly Thr Leu Leu Ala Ile Leu Ile 515 520 525		
Thr Thr Leu Val Tyr Val Gly Ile Ala Val Ser Val Gly Ser Cys Val 530 535 540		
Val Arg Asp Ala Thr Gly Asn Val Asn Asp Thr Ile Val Thr Glu Leu 545 550 555 560		
Thr Asn Cys Thr Ser Ala Ala Cys Lys Leu Asn Phe Asp Phe Ser Ser 565 570 575		
Cys Glu Ser Ser Pro Cys Ser Tyr Gly Leu Met Asn Asn Phe Gln Val 580 585 590		
Met Ser Met Val Ser Gly Phe Thr Pro Leu Ile Ser Ala Gly Ile Phe 595 600 605		
Ser Ala Thr Leu Ser Ser Ala Leu Ala Ser Leu Val Ser Ala Pro Lys 610 615 620		

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Ile	Phe	Gln	Ala	Leu	Cys	Lys	Asp	Asn	Ile	Tyr	Pro	Ala	Phe	Gln	Met
625					630				635						640
Phe	Ala	Lys	Gly	Tyr	Gly	Lys	Asn	Asn	Glu	Pro	Leu	Arg	Gly	Tyr	Ile
			645						650					655	
Leu	Thr	Phe	Leu	Ile	Ala	Leu	Gly	Phe	Ile	Leu	Ile	Ala	Glu	Leu	Asn
			660					665					670		
Val	Ile	Ala	Pro	Ile	Ile	Ser	Asn	Phe	Phe	Leu	Ala	Ser	Tyr	Ala	Leu
			675				680					685			
Ile	Asn	Phe	Ser	Val	Phe	His	Ala	Ser	Leu	Ala	Lys	Ser	Pro	Gly	Trp
	690					695					700				
Arg	Pro	Ala	Phe	Lys	Tyr	Tyr	Asn	Met	Trp	Ile	Ser	Leu	Leu	Gly	Ala
705					710					715					720
Ile	Leu	Cys	Cys	Ile	Val	Met	Phe	Val	Ile	Asn	Trp	Trp	Ala	Ala	Leu
				725					730					735	
Leu	Thr	Tyr	Val	Ile	Val	Leu	Gly	Leu	Tyr	Ile	Tyr	Val	Thr	Tyr	Lys
			740					745					750		
Lys	Pro	Asp	Val	Asn	Trp	Gly	Ser	Ser	Thr	Gln	Ala	Leu	Thr	Tyr	Leu
		755					760					765			
Asn	Ala	Leu	Gln	His	Ser	Ile	Arg	Leu	Ser	Gly	Val	Glu	Asp	His	Val
	770					775					780				
Lys	Asn	Phe	Arg	Pro	Gln	Cys	Leu	Val	Met	Thr	Gly	Ala	Pro	Asn	Ser
785					790					795					800
Arg	Pro	Ala	Leu	Leu	His	Leu	Val	His	Asp	Phe	Thr	Lys	Asn	Val	Gly
			805						810					815	
Leu	Met	Ile	Cys	Gly	His	Val	His	Met	Gly	Pro	Arg	Arg	Gln	Ala	Met
		820						825					830		
Lys	Glu	Met	Ser	Ile	Asp	Gln	Ala	Lys	Tyr	Gln	Arg	Trp	Leu	Ile	Lys
	835					840						845			
Asn	Lys	Met	Lys	Ala	Phe	Tyr	Ala	Pro	Val	His	Ala	Asp	Asp	Leu	Arg
	850					855					860				
Glu	Gly	Ala	Gln	Tyr	Leu	Met	Gln	Ala	Ala	Gly	Leu	Gly	Arg	Met	Lys
865					870					875					880
Pro	Asn	Thr	Leu	Val	Leu	Gly	Phe	Lys	Lys	Asp	Trp	Leu	Gln	Ala	Asp
			885						890					895	
Met	Arg	Asp	Val	Asp	Met	Tyr	Ile	Asn	Leu	Phe	His	Asp	Ala	Phe	Asp
			900					905					910		
Ile	Gln	Tyr	Gly	Val	Val	Val	Ile	Arg	Leu	Lys	Glu	Gly	Leu	Asp	Ile
		915					920					925			
Ser	His	Leu	Gln	Gly	Gln	Glu	Glu	Leu	Leu	Ser	Ser	Gln	Glu	Lys	Ser
	930					935					940				
Pro	Gly	Thr	Lys	Asp	Val	Val	Val	Ser	Val	Glu	Tyr	Ser	Lys	Lys	Ser
945					950					955					960
Asp	Leu	Asp	Thr	Ser	Lys	Pro	Leu	Ser	Glu	Lys	Pro	Ile	Thr	His	Lys
				965					970					975	
Val	Glu	Glu	Glu	Asp	Gly	Lys	Thr	Ala	Thr	Gln	Pro	Leu	Leu	Lys	Lys
			980					985					990		
Glu	Ser	Lys	Gly	Pro	Ile	Val	Pro	Leu	Asn	Val	Ala	Asp	Gln	Lys	Leu
	995						1000						1005		
Leu	Glu	Ala	Ser	Thr	Gln	Phe	Gln	Lys	Lys	Gln	Gly	Lys	Asn	Thr	
	1010					1015							1020		

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Ile Asp Val Trp Trp Leu Phe Asp Asp Gly Gly Leu Thr Leu Leu
1025                      1030                      1035

Ile Pro Tyr Leu Leu Thr Thr Lys Lys Lys Trp Lys Asp Cys Lys
1040                      1045                      1050

Ile Arg Val Phe Ile Gly Gly Lys Ile Asn Arg Ile Asp His Asp
1055                      1060                      1065

Arg Arg Ala Met Ala Thr Leu Leu Ser Lys Phe Arg Ile Asp Phe
1070                      1075                      1080

Ser Asp Ile Met Val Leu Gly Asp Ile Asn Thr Lys Pro Lys Lys
1085                      1090                      1095

Glu Asn Ile Ile Ala Phe Glu Glu Ile Ile Glu Pro Tyr Arg Leu
1100                      1105                      1110

His Glu Asp Asp Lys Glu Gln Asp Ile Ala Asp Lys Met Lys Glu
1115                      1120                      1125

Asp Glu Pro Trp Arg Ile Thr Asp Asn Glu Leu Glu Leu Tyr Lys
1130                      1135                      1140

Thr Lys Thr Tyr Arg Gln Ile Arg Leu Asn Glu Leu Leu Lys Glu
1145                      1150                      1155

His Ser Ser Thr Ala Asn Ile Ile Val Met Ser Leu Pro Val Ala
1160                      1165                      1170

Arg Lys Gly Ala Val Ser Ser Ala Leu Tyr Met Ala Trp Leu Glu
1175                      1180                      1185

Ala Leu Ser Lys Asp Leu Pro Pro Ile Leu Leu Val Arg Gly Asn
1190                      1195                      1200

His Gln Ser Val Leu Thr Phe Tyr Ser
1205                      1210

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<210> SEQ ID NO 41
<211> LENGTH: 411
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(411)
<223> OTHER INFORMATION: OGTA222 = Swiss Prot Accession No. P16444,
Dipeptidase 1

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<400> SEQUENCE: 41

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Met Trp Ser Gly Trp Trp Leu Trp Pro Leu Val Ala Val Cys Thr Ala
1      5      10      15

Asp Phe Phe Arg Asp Glu Ala Glu Arg Ile Met Arg Asp Ser Pro Val
20     25     30

Ile Asp Gly His Asn Asp Leu Pro Trp Gln Leu Leu Asp Met Phe Asn
35     40     45

Asn Arg Leu Gln Asp Glu Arg Ala Asn Leu Thr Thr Leu Ala Gly Thr
50     55     60

His Thr Asn Ile Pro Lys Leu Arg Ala Gly Phe Val Gly Gly Gln Phe
65     70     75     80

Trp Ser Val Tyr Thr Pro Cys Asp Thr Gln Asn Lys Asp Ala Val Arg
85     90     95

Arg Thr Leu Glu Gln Met Asp Val Val His Arg Met Cys Arg Met Tyr
100    105    110

Pro Glu Thr Phe Leu Tyr Val Thr Ser Ser Ala Gly Ile Arg Gln Ala
115    120    125

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Phe Arg Glu Gly Lys Val Ala Ser Leu Ile Gly Val Glu Gly Gly His
 130                135                140

Ser Ile Asp Ser Ser Leu Gly Val Leu Arg Ala Leu Tyr Gln Leu Gly
145                150                155                160

Met Arg Tyr Leu Thr Leu Thr His Ser Cys Asn Thr Pro Trp Ala Asp
                165                170                175

Asn Trp Leu Val Asp Thr Gly Asp Ser Glu Pro Gln Ser Gln Gly Leu
                180                185                190

Ser Pro Phe Gly Gln Arg Val Val Lys Glu Leu Asn Arg Leu Gly Val
 195                200                205

Leu Ile Asp Leu Ala His Val Ser Val Ala Thr Met Lys Ala Thr Leu
 210                215                220

Gln Leu Ser Arg Ala Pro Val Ile Phe Ser His Ser Ser Ala Tyr Ser
225                230                235                240

Val Cys Ala Ser Arg Arg Asn Val Pro Asp Asp Val Leu Arg Leu Val
                245                250                255

Lys Gln Thr Asp Ser Leu Val Met Val Asn Phe Tyr Asn Asn Tyr Ile
 260                265                270

Ser Cys Thr Asn Lys Ala Asn Leu Ser Gln Val Ala Asp His Leu Asp
 275                280                285

His Ile Lys Glu Val Ala Gly Ala Arg Ala Val Gly Phe Gly Gly Asp
 290                295                300

Phe Asp Gly Val Pro Arg Val Pro Glu Gly Leu Glu Asp Val Ser Lys
305                310                315                320

Tyr Pro Asp Leu Ile Ala Glu Leu Leu Arg Arg Asn Trp Thr Glu Ala
 325                330                335

Glu Val Lys Gly Ala Leu Ala Asp Asn Leu Leu Arg Val Phe Glu Ala
 340                345                350

Val Glu Gln Ala Ser Asn Leu Thr Gln Ala Pro Glu Glu Glu Pro Ile
 355                360                365

Pro Leu Asp Gln Leu Gly Gly Ser Cys Arg Thr His Tyr Gly Tyr Ser
 370                375                380

Ser Gly Ala Ser Ser Leu His Arg His Trp Gly Leu Leu Leu Ala Ser
385                390                395                400

Leu Ala Pro Leu Val Leu Cys Leu Ser Leu Leu
 405                410

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<210> SEQ ID NO 42
<211> LENGTH: 739
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(739)
<223> OTHER INFORMATION: OGTA236 = Swiss Prot Accession No. P50443,
Sulfate transporter

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<400> SEQUENCE: 42

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Met Ser Ser Glu Ser Lys Glu Gln His Asn Val Ser Pro Arg Asp Ser
 1                5                10                15

Ala Glu Gly Asn Asp Ser Tyr Pro Ser Gly Ile His Leu Glu Leu Gln
 20                25                30

Arg Glu Ser Ser Thr Asp Phe Lys Gln Phe Glu Thr Asn Asp Gln Cys
 35                40                45

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Arg	Pro	Tyr	His	Arg	Ile	Leu	Ile	Glu	Arg	Gln	Glu	Lys	Ser	Asp	Thr
50					55					60					
Asn	Phe	Lys	Glu	Phe	Val	Ile	Lys	Lys	Leu	Gln	Lys	Asn	Cys	Gln	Cys
65				70						75				80	
Ser	Pro	Ala	Lys	Ala	Lys	Asn	Met	Ile	Leu	Gly	Phe	Leu	Pro	Val	Leu
			85						90					95	
Gln	Trp	Leu	Pro	Lys	Tyr	Asp	Leu	Lys	Lys	Asn	Ile	Leu	Gly	Asp	Val
		100						105					110		
Met	Ser	Gly	Leu	Ile	Val	Gly	Ile	Leu	Leu	Val	Pro	Gln	Ser	Ile	Ala
		115					120					125			
Tyr	Ser	Leu	Leu	Ala	Gly	Gln	Glu	Pro	Val	Tyr	Gly	Leu	Tyr	Thr	Ser
		130				135					140				
Phe	Phe	Ala	Ser	Ile	Ile	Tyr	Phe	Leu	Leu	Gly	Thr	Ser	Arg	His	Ile
145					150					155				160	
Ser	Val	Gly	Ile	Phe	Gly	Val	Leu	Cys	Leu	Met	Ile	Gly	Glu	Thr	Val
			165						170					175	
Asp	Arg	Glu	Leu	Gln	Lys	Ala	Gly	Tyr	Asp	Asn	Ala	His	Ser	Ala	Pro
		180						185					190		
Ser	Leu	Gly	Met	Val	Ser	Asn	Gly	Ser	Thr	Leu	Leu	Asn	His	Thr	Ser
		195					200					205			
Asp	Arg	Ile	Cys	Asp	Lys	Ser	Cys	Tyr	Ala	Ile	Met	Val	Gly	Ser	Thr
		210				215					220				
Val	Thr	Phe	Ile	Ala	Gly	Val	Tyr	Gln	Val	Ala	Met	Gly	Phe	Phe	Gln
225					230					235					240
Val	Gly	Phe	Val	Ser	Val	Tyr	Leu	Ser	Asp	Ala	Leu	Leu	Ser	Gly	Phe
			245						250					255	
Val	Thr	Gly	Ala	Ser	Phe	Thr	Ile	Leu	Thr	Ser	Gln	Ala	Lys	Tyr	Leu
			260					265					270		
Leu	Gly	Leu	Asn	Leu	Pro	Arg	Thr	Asn	Gly	Val	Gly	Ser	Leu	Ile	Thr
		275					280					285			
Thr	Trp	Ile	His	Val	Phe	Arg	Asn	Ile	His	Lys	Thr	Asn	Leu	Cys	Asp
		290				295					300				
Leu	Ile	Thr	Ser	Leu	Leu	Cys	Leu	Leu	Val	Leu	Leu	Pro	Thr	Lys	Glu
305					310					315					320
Leu	Asn	Glu	His	Phe	Lys	Ser	Lys	Leu	Lys	Ala	Pro	Ile	Pro	Ile	Glu
			325						330					335	
Leu	Val	Val	Val	Val	Ala	Ala	Thr	Leu	Ala	Ser	His	Phe	Gly	Lys	Leu
			340					345					350		
His	Glu	Asn	Tyr	Asn	Ser	Ser	Ile	Ala	Gly	His	Ile	Pro	Thr	Gly	Phe
		355					360					365			
Met	Pro	Pro	Lys	Val	Pro	Glu	Trp	Asn	Leu	Ile	Pro	Ser	Val	Ala	Val
		370				375					380				
Asp	Ala	Ile	Ala	Ile	Ser	Ile	Ile	Gly	Phe	Ala	Ile	Thr	Val	Ser	Leu
385					390					395					400
Ser	Glu	Met	Phe	Ala	Lys	Lys	His	Gly	Tyr	Thr	Val	Lys	Ala	Asn	Gln
			405						410					415	
Glu	Met	Tyr	Ala	Ile	Gly	Phe	Cys	Asn	Ile	Ile	Pro	Ser	Phe	Phe	His
			420					425					430		
Cys	Phe	Thr	Thr	Ser	Ala	Ala	Leu	Ala	Lys	Thr	Leu	Val	Lys	Glu	Ser
		435					440					445			
Thr	Gly	Cys	His	Thr	Gln	Leu	Ser	Gly	Val	Val	Thr	Ala	Leu	Val	Leu

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450	455	460
Leu Leu Val Leu Leu Val Ile Ala Pro Leu Phe Tyr Ser Leu Gln Lys		
465	470	475 480
Ser Val Leu Gly Val Ile Thr Ile Val Asn Leu Arg Gly Ala Leu Arg		
	485	490 495
Lys Phe Arg Asp Leu Pro Lys Met Trp Ser Ile Ser Arg Met Asp Thr		
	500	505 510
Val Ile Trp Phe Val Thr Met Leu Ser Ser Ala Leu Leu Ser Thr Glu		
	515	520 525
Ile Gly Leu Leu Val Gly Val Cys Phe Ser Ile Phe Cys Val Ile Leu		
	530	535 540
Arg Thr Gln Lys Pro Lys Ser Ser Leu Leu Gly Leu Val Glu Glu Ser		
	545	550 555 560
Glu Val Phe Glu Ser Val Ser Ala Tyr Lys Asn Leu Gln Thr Lys Pro		
	565	570 575
Gly Ile Lys Ile Phe Arg Phe Val Ala Pro Leu Tyr Tyr Ile Asn Lys		
	580	585 590
Glu Cys Phe Lys Ser Ala Leu Tyr Lys Gln Thr Val Asn Pro Ile Leu		
	595	600 605
Ile Lys Val Ala Trp Lys Lys Ala Ala Lys Arg Lys Ile Lys Glu Lys		
	610	615 620
Val Val Thr Leu Gly Gly Ile Gln Asp Glu Met Ser Val Gln Leu Ser		
	625	630 635 640
His Asp Pro Leu Glu Leu His Thr Ile Val Ile Asp Cys Ser Ala Ile		
	645	650 655
Gln Phe Leu Asp Thr Ala Gly Ile His Thr Leu Lys Glu Val Arg Arg		
	660	665 670
Asp Tyr Glu Ala Ile Gly Ile Gln Val Leu Leu Ala Gln Cys Asn Pro		
	675	680 685
Thr Val Arg Asp Ser Leu Thr Asn Gly Glu Tyr Cys Lys Lys Glu Glu		
	690	695 700
Glu Asn Leu Leu Phe Tyr Ser Val Tyr Glu Ala Met Ala Phe Ala Glu		
	705	710 715 720
Val Ser Lys Asn Gln Lys Gly Val Cys Val Pro Asn Gly Leu Ser Leu		
	725	730 735
Ser Ser Asp		

<210> SEQ ID NO 43
 <211> LENGTH: 802
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapiens
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (1)..(802)
 <223> OTHER INFORMATION: OGTA237 = Swiss Prot Accession No. P22455,
 Fibroblast growth factor receptor 4

 <400> SEQUENCE: 43

Met Arg Leu Leu Leu Ala Leu Leu Gly Val Leu Leu Ser Val Pro Gly		
1	5	10 15
Pro Pro Val Leu Ser Leu Glu Ala Ser Glu Glu Val Glu Leu Glu Pro		
	20	25 30
Cys Leu Ala Pro Ser Leu Glu Gln Gln Glu Gln Glu Leu Thr Val Ala		
	35	40 45

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Leu	Gly	Gln	Pro	Val	Arg	Leu	Cys	Cys	Gly	Arg	Ala	Glu	Arg	Gly	Gly	50	55	60
His	Trp	Tyr	Lys	Glu	Gly	Ser	Arg	Leu	Ala	Pro	Ala	Gly	Arg	Val	Arg	65	70	75
Gly	Trp	Arg	Gly	Arg	Leu	Glu	Ile	Ala	Ser	Phe	Leu	Pro	Glu	Asp	Ala	85	90	95
Gly	Arg	Tyr	Leu	Cys	Leu	Ala	Arg	Gly	Ser	Met	Ile	Val	Leu	Gln	Asn	100	105	110
Leu	Thr	Leu	Ile	Thr	Gly	Asp	Ser	Leu	Thr	Ser	Ser	Asn	Asp	Asp	Glu	115	120	125
Asp	Pro	Lys	Ser	His	Arg	Asp	Pro	Ser	Asn	Arg	His	Ser	Tyr	Pro	Gln	130	135	140
Gln	Ala	Pro	Tyr	Trp	Thr	His	Pro	Gln	Arg	Met	Glu	Lys	Lys	Leu	His	145	150	155
Ala	Val	Pro	Ala	Gly	Asn	Thr	Val	Lys	Phe	Arg	Cys	Pro	Ala	Ala	Gly	165	170	175
Asn	Pro	Thr	Pro	Thr	Ile	Arg	Trp	Leu	Lys	Asp	Gly	Gln	Ala	Phe	His	180	185	190
Gly	Glu	Asn	Arg	Ile	Gly	Gly	Ile	Arg	Leu	Arg	His	Gln	His	Trp	Ser	195	200	205
Leu	Val	Met	Glu	Ser	Val	Val	Pro	Ser	Asp	Arg	Gly	Thr	Tyr	Thr	Cys	210	215	220
Leu	Val	Glu	Asn	Ala	Val	Gly	Ser	Ile	Arg	Tyr	Asn	Tyr	Leu	Leu	Asp	225	230	235
Val	Leu	Glu	Arg	Ser	Pro	His	Arg	Pro	Ile	Leu	Gln	Ala	Gly	Leu	Pro	245	250	255
Ala	Asn	Thr	Thr	Ala	Val	Val	Gly	Ser	Asp	Val	Glu	Leu	Leu	Cys	Lys	260	265	270
Val	Tyr	Ser	Asp	Ala	Gln	Pro	His	Ile	Gln	Trp	Leu	Lys	His	Ile	Val	275	280	285
Ile	Asn	Gly	Ser	Ser	Phe	Gly	Ala	Asp	Gly	Phe	Pro	Tyr	Val	Gln	Val	290	295	300
Leu	Lys	Thr	Ala	Asp	Ile	Asn	Ser	Ser	Glu	Val	Glu	Val	Leu	Tyr	Leu	305	310	315
Arg	Asn	Val	Ser	Ala	Glu	Asp	Ala	Gly	Glu	Tyr	Thr	Cys	Leu	Ala	Gly	325	330	335
Asn	Ser	Ile	Gly	Leu	Ser	Tyr	Gln	Ser	Ala	Trp	Leu	Thr	Val	Leu	Pro	340	345	350
Glu	Glu	Asp	Pro	Thr	Trp	Thr	Ala	Ala	Ala	Pro	Glu	Ala	Arg	Tyr	Thr	355	360	365
Asp	Ile	Ile	Leu	Tyr	Ala	Ser	Gly	Ser	Leu	Ala	Leu	Ala	Val	Leu	Leu	370	375	380
Leu	Leu	Ala	Gly	Leu	Tyr	Arg	Gly	Gln	Ala	Leu	His	Gly	Arg	His	Pro	385	390	395
Arg	Pro	Pro	Ala	Thr	Val	Gln	Lys	Leu	Ser	Arg	Phe	Pro	Leu	Ala	Arg	405	410	415
Gln	Phe	Ser	Leu	Glu	Ser	Gly	Ser	Ser	Gly	Lys	Ser	Ser	Ser	Ser	Leu	420	425	430
Val	Arg	Gly	Val	Arg	Leu	Ser	Ser	Ser	Gly	Pro	Ala	Leu	Leu	Ala	Gly	435	440	445

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[illegible]

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<210> SEQ ID NO 44
<211> LENGTH: 1257
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(1257)
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<223> OTHER INFORMATION: OGTA247 = Swiss Prot Accession No. P32004,
Neural cell adhesion molecule L1

<400> SEQUENCE: 44

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Met Val Val Ala Leu Arg Tyr Val Trp Pro Leu Leu Leu Cys Ser Pro
1          5          10          15

Cys Leu Leu Ile Gln Ile Pro Glu Glu Tyr Glu Gly His His Val Met
20          25          30

Glu Pro Pro Val Ile Thr Glu Gln Ser Pro Arg Arg Leu Val Val Phe
35          40          45

Pro Thr Asp Asp Ile Ser Leu Lys Cys Glu Ala Ser Gly Lys Pro Glu
50          55          60

Val Gln Phe Arg Trp Thr Arg Asp Gly Val His Phe Lys Pro Lys Glu
65          70          75          80

Glu Leu Gly Val Thr Val Tyr Gln Ser Pro His Ser Gly Ser Phe Thr
85          90          95

Ile Thr Gly Asn Asn Ser Asn Phe Ala Gln Arg Phe Gln Gly Ile Tyr
100         105         110

Arg Cys Phe Ala Ser Asn Lys Leu Gly Thr Ala Met Ser His Glu Ile
115         120         125

Arg Leu Met Ala Glu Gly Ala Pro Lys Trp Pro Lys Glu Thr Val Lys
130         135         140

Pro Val Glu Val Glu Glu Gly Glu Ser Val Val Leu Pro Cys Asn Pro
145         150         155         160

Pro Pro Ser Ala Glu Pro Leu Arg Ile Tyr Trp Met Asn Ser Lys Ile
165         170         175

Leu His Ile Lys Gln Asp Glu Arg Val Thr Met Gly Gln Asn Gly Asn
180         185         190

Leu Tyr Phe Ala Asn Val Leu Thr Ser Asp Asn His Ser Asp Tyr Ile
195         200         205

Cys His Ala His Phe Pro Gly Thr Arg Thr Ile Ile Gln Lys Glu Pro
210         215         220

Ile Asp Leu Arg Val Lys Ala Thr Asn Ser Met Ile Asp Arg Lys Pro
225         230         235         240

Arg Leu Leu Phe Pro Thr Asn Ser Ser Ser His Leu Val Ala Leu Gln
245         250         255

Gly Gln Pro Leu Val Leu Glu Cys Ile Ala Glu Gly Phe Pro Thr Pro
260         265         270

Thr Ile Lys Trp Leu Arg Pro Ser Gly Pro Met Pro Ala Asp Arg Val
275         280         285

Thr Tyr Gln Asn His Asn Lys Thr Leu Gln Leu Leu Lys Val Gly Glu
290         295         300

Glu Asp Asp Gly Glu Tyr Arg Cys Leu Ala Glu Asn Ser Leu Gly Ser
305         310         315         320

Ala Arg His Ala Tyr Tyr Val Thr Val Glu Ala Ala Pro Tyr Trp Leu
325         330         335

His Lys Pro Gln Ser His Leu Tyr Gly Pro Gly Glu Thr Ala Arg Leu
340         345         350

Asp Cys Gln Val Gln Gly Arg Pro Gln Pro Glu Val Thr Trp Arg Ile
355         360         365

Asn Gly Ile Pro Val Glu Glu Leu Ala Lys Asp Gln Lys Tyr Arg Ile
370         375         380

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Gln	Arg	Gly	Ala	Leu	Ile	Leu	Ser	Asn	Val	Gln	Pro	Ser	Asp	Thr	Met
385					390					395					400
Val	Thr	Gln	Cys	Glu	Ala	Arg	Asn	Arg	His	Gly	Leu	Leu	Leu	Ala	Asn
			405						410					415	
Ala	Tyr	Ile	Tyr	Val	Val	Gln	Leu	Pro	Ala	Lys	Ile	Leu	Thr	Ala	Asp
			420					425					430		
Asn	Gln	Thr	Tyr	Met	Ala	Val	Gln	Gly	Ser	Thr	Ala	Tyr	Leu	Leu	Cys
		435					440					445			
Lys	Ala	Phe	Gly	Ala	Pro	Val	Pro	Ser	Val	Gln	Trp	Leu	Asp	Glu	Asp
	450					455					460				
Gly	Thr	Thr	Val	Leu	Gln	Asp	Glu	Arg	Phe	Phe	Pro	Tyr	Ala	Asn	Gly
465				470						475					480
Thr	Leu	Gly	Ile	Arg	Asp	Leu	Gln	Ala	Asn	Asp	Thr	Gly	Arg	Tyr	Phe
				485					490					495	
Cys	Leu	Ala	Ala	Asn	Asp	Gln	Asn	Asn	Val	Thr	Ile	Met	Ala	Asn	Leu
		500						505					510		
Lys	Val	Lys	Asp	Ala	Thr	Gln	Ile	Thr	Gln	Gly	Pro	Arg	Ser	Thr	Ile
		515					520					525			
Glu	Lys	Lys	Gly	Ser	Arg	Val	Thr	Phe	Thr	Cys	Gln	Ala	Ser	Phe	Asp
	530					535					540				
Pro	Ser	Leu	Gln	Pro	Ser	Ile	Thr	Trp	Arg	Gly	Asp	Gly	Arg	Asp	Leu
545					550					555					560
Gln	Glu	Leu	Gly	Asp	Ser	Asp	Lys	Tyr	Phe	Ile	Glu	Asp	Gly	Arg	Leu
			565						570					575	
Val	Ile	His	Ser	Leu	Asp	Tyr	Ser	Asp	Gln	Gly	Asn	Tyr	Ser	Cys	Val
			580					585					590		
Ala	Ser	Thr	Glu	Leu	Asp	Val	Val	Glu	Ser	Arg	Ala	Gln	Leu	Leu	Val
		595					600					605			
Val	Gly	Ser	Pro	Gly	Pro	Val	Pro	Arg	Leu	Val	Leu	Ser	Asp	Leu	His
	610					615					620				
Leu	Leu	Thr	Gln	Ser	Gln	Val	Arg	Val	Ser	Trp	Ser	Pro	Ala	Glu	Asp
625					630					635					640
His	Asn	Ala	Pro	Ile	Glu	Lys	Tyr	Asp	Ile	Glu	Phe	Glu	Asp	Lys	Glu
			645						650					655	
Met	Ala	Pro	Glu	Lys	Trp	Tyr	Ser	Leu	Gly	Lys	Val	Pro	Gly	Asn	Gln
		660						665					670		
Thr	Ser	Thr	Thr	Leu	Lys	Leu	Ser	Pro	Tyr	Val	His	Tyr	Thr	Phe	Arg
		675					680					685			
Val	Thr	Ala	Ile	Asn	Lys	Tyr	Gly	Pro	Gly	Glu	Pro	Ser	Pro	Val	Ser
		690				695					700				
Glu	Thr	Val	Val	Thr	Pro	Glu	Ala	Ala	Pro	Glu	Lys	Asn	Pro	Val	Asp
705					710					715					720
Val	Lys	Gly	Glu	Gly	Asn	Glu	Thr	Thr	Asn	Met	Val	Ile	Thr	Trp	Lys
			725						730					735	
Pro	Leu	Arg	Trp	Met	Asp	Trp	Asn	Ala	Pro	Gln	Val	Gln	Tyr	Arg	Val
		740						745					750		
Gln	Trp	Arg	Pro	Gln	Gly	Thr	Arg	Gly	Pro	Trp	Gln	Glu	Gln	Ile	Val
		755					760				765				
Ser	Asp	Pro	Phe	Leu	Val	Val	Ser	Asn	Thr	Ser	Thr	Phe	Val	Pro	Tyr
	770					775					780				

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Glu	Ile	Lys	Val	Gln	Ala	Val	Asn	Ser	Gln	Gly	Lys	Gly	Pro	Glu	Pro	785	790	795	800
Gln	Val	Thr	Ile	Gly	Tyr	Ser	Gly	Glu	Asp	Tyr	Pro	Gln	Ala	Ile	Pro	805	810	815	
Glu	Leu	Glu	Gly	Ile	Glu	Ile	Leu	Asn	Ser	Ser	Ala	Val	Leu	Val	Lys	820	825	830	
Trp	Arg	Pro	Val	Asp	Leu	Ala	Gln	Val	Lys	Gly	His	Leu	Arg	Gly	Tyr	835	840	845	
Asn	Val	Thr	Tyr	Trp	Arg	Glu	Gly	Ser	Gln	Arg	Lys	His	Ser	Lys	Arg	850	855	860	
His	Ile	His	Lys	Asp	His	Val	Val	Val	Pro	Ala	Asn	Thr	Thr	Ser	Val	865	870	875	880
Ile	Leu	Ser	Gly	Leu	Arg	Pro	Tyr	Ser	Ser	Tyr	His	Leu	Glu	Val	Gln	885	890	895	
Ala	Phe	Asn	Gly	Arg	Gly	Ser	Gly	Pro	Ala	Ser	Glu	Phe	Thr	Phe	Ser	900	905	910	
Thr	Pro	Glu	Gly	Val	Pro	Gly	His	Pro	Glu	Ala	Leu	His	Leu	Glu	Cys	915	920	925	
Gln	Ser	Asn	Thr	Ser	Leu	Leu	Leu	Arg	Trp	Gln	Pro	Pro	Leu	Ser	His	930	935	940	
Asn	Gly	Val	Leu	Thr	Gly	Tyr	Val	Leu	Ser	Tyr	His	Pro	Leu	Asp	Glu	945	950	955	960
Gly	Gly	Lys	Gly	Gln	Leu	Ser	Phe	Asn	Leu	Arg	Asp	Pro	Glu	Leu	Arg	965	970	975	
Thr	His	Asn	Leu	Thr	Asp	Leu	Ser	Pro	His	Leu	Arg	Tyr	Arg	Phe	Gln	980	985	990	
Leu	Gln	Ala	Thr	Thr	Lys	Glu	Gly	Pro	Gly	Glu	Ala	Ile	Val	Arg	Glu	995	1000	1005	
Gly	Gly	Thr	Met	Ala	Leu	Ser	Gly	Ile	Ser	Asp	Phe	Gly	Asn	Ile		1010	1015	1020	
Ser	Ala	Thr	Ala	Gly	Glu	Asn	Tyr	Ser	Val	Val	Ser	Trp	Val	Pro		1025	1030	1035	
Lys	Glu	Gly	Gln	Cys	Asn	Phe	Arg	Phe	His	Ile	Leu	Phe	Lys	Ala		1040	1045	1050	
Leu	Gly	Glu	Glu	Lys	Gly	Gly	Ala	Ser	Leu	Ser	Pro	Gln	Tyr	Val		1055	1060	1065	
Ser	Tyr	Asn	Gln	Ser	Ser	Tyr	Thr	Gln	Trp	Asp	Leu	Gln	Pro	Asp		1070	1075	1080	
Thr	Asp	Tyr	Glu	Ile	His	Leu	Phe	Lys	Glu	Arg	Met	Phe	Arg	His		1085	1090	1095	
Gln	Met	Ala	Val	Lys	Thr	Asn	Gly	Thr	Gly	Arg	Val	Arg	Leu	Pro		1100	1105	1110	
Pro	Ala	Gly	Phe	Ala	Thr	Glu	Gly	Trp	Phe	Ile	Gly	Phe	Val	Ser		1115	1120	1125	
Ala	Ile	Ile	Leu	Leu	Leu	Leu	Val	Leu	Leu	Ile	Leu	Cys	Phe	Ile		1130	1135	1140	
Lys	Arg	Ser	Lys	Gly	Gly	Lys	Tyr	Ser	Val	Lys	Asp	Lys	Glu	Asp		1145	1150	1155	
Thr	Gln	Val	Asp	Ser	Glu	Ala	Arg	Pro	Met	Lys	Asp	Glu	Thr	Phe		1160	1165	1170	
Gly	Glu	Tyr	Arg	Ser	Leu	Glu	Ser	Asp	Asn	Glu	Glu	Lys	Ala	Phe					

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1175	1180	1185
Gly Ser Ser Gln Pro Ser Leu Asn Gly Asp Ile Lys Pro Leu Gly		
1190	1195	1200
Ser Asp Asp Ser Leu Ala Asp Tyr Gly Gly Ser Val Asp Val Gln		
1205	1210	1215
Phe Asn Glu Asp Gly Ser Phe Ile Gly Gln Tyr Ser Gly Lys Lys		
1220	1225	1230
Glu Lys Glu Ala Ala Gly Gly Asn Asp Ser Ser Gly Ala Thr Ser		
1235	1240	1245
Pro Ile Asn Pro Ala Val Ala Leu Glu		
1250	1255	

<210> SEQ ID NO 45
 <211> LENGTH: 864
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapiens
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (1)..(864)
 <223> OTHER INFORMATION: OGTA248 = Swiss Prot Accession No. P29376,
 Leukocyte tyrosine kinase receptor

<400> SEQUENCE: 45

Met Gly Cys Trp Gly Gln Leu Leu Val Trp Phe Gly Ala Ala Gly Ala		
1	5	10 15
Ile Leu Cys Ser Ser Pro Gly Ser Gln Glu Thr Phe Leu Arg Ser Ser		
	20	25 30
Pro Leu Pro Leu Ala Ser Pro Ser Pro Gln Asp Pro Lys Val Ser Ala		
	35	40 45
Pro Pro Ser Ile Leu Glu Pro Ala Ser Pro Leu Asn Ser Pro Gly Thr		
	50	55 60
Glu Gly Ser Trp Leu Phe Ser Thr Cys Gly Ala Ser Gly Arg His Gly		
	65	70 75 80
Pro Thr Gln Thr Gln Cys Asp Gly Ala Tyr Ala Gly Thr Ser Val Val		
	85	90 95
Val Thr Val Gly Ala Ala Gly Gln Leu Arg Gly Val Gln Leu Trp Arg		
	100	105 110
Val Pro Gly Pro Gly Gln Tyr Leu Ile Ser Ala Tyr Gly Ala Ala Gly		
	115	120 125
Gly Lys Gly Ala Lys Asn His Leu Ser Arg Ala His Gly Val Phe Val		
	130	135 140
Ser Ala Ile Phe Ser Leu Gly Leu Gly Glu Ser Leu Tyr Ile Leu Val		
	145	150 155 160
Gly Gln Gln Gly Glu Asp Ala Cys Pro Gly Gly Ser Pro Glu Ser Gln		
	165	170 175
Leu Val Cys Leu Gly Glu Ser Arg Ala Val Glu Glu His Ala Ala Met		
	180	185 190
Asp Gly Ser Glu Gly Val Pro Gly Ser Arg Arg Trp Ala Gly Gly Gly		
	195	200 205
Gly Gly Gly Gly Gly Ala Thr Tyr Val Phe Arg Val Arg Ala Gly Glu		
	210	215 220
Leu Glu Pro Leu Leu Val Ala Ala Gly Gly Gly Gly Arg Ala Tyr Leu		
	225	230 235 240
Arg Pro Arg Asp Arg Gly Arg Thr Gln Ala Ser Pro Glu Lys Leu Glu		

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245						250						255					
Asn	Arg	Ser	Glu	Ala	Pro	Gly	Ser	Gly	Gly	Arg	Gly	Gly	Ala	Ala	Gly		
			260					265					270				
Gly	Gly	Gly	Gly	Trp	Thr	Ser	Arg	Ala	Pro	Ser	Pro	Gln	Ala	Gly	Arg		
		275					280					285					
Ser	Leu	Gln	Glu	Gly	Ala	Glu	Gly	Gly	Gln	Gly	Cys	Ser	Glu	Ala	Trp		
	290					295					300						
Ala	Thr	Leu	Gly	Trp	Ala	Ala	Ala	Gly	Gly	Phe	Gly	Gly	Gly	Gly	Gly		
305					310					315					320		
Ala	Cys	Thr	Ala	Gly	Gly	Gly	Gly	Gly	Gly	Tyr	Arg	Gly	Gly	Asp	Ala		
			325						330					335			
Ser	Glu	Thr	Asp	Asn	Leu	Trp	Ala	Asp	Gly	Glu	Asp	Gly	Val	Ser	Phe		
			340					345					350				
Ile	His	Pro	Ser	Ser	Glu	Leu	Phe	Leu	Gln	Pro	Leu	Ala	Val	Thr	Glu		
		355					360					365					
Asn	His	Gly	Glu	Val	Glu	Ile	Arg	Arg	His	Leu	Asn	Cys	Ser	His	Cys		
	370					375					380						
Pro	Leu	Arg	Asp	Cys	Gln	Trp	Gln	Ala	Glu	Leu	Gln	Leu	Ala	Glu	Cys		
385					390					395					400		
Leu	Cys	Pro	Glu	Gly	Met	Glu	Leu	Ala	Val	Asp	Asn	Val	Thr	Cys	Met		
			405						410					415			
Asp	Leu	His	Lys	Pro	Pro	Gly	Pro	Leu	Val	Leu	Met	Val	Ala	Val	Val		
			420					425					430				
Ala	Thr	Ser	Thr	Leu	Ser	Leu	Leu	Met	Val	Cys	Gly	Val	Leu	Ile	Leu		
		435					440					445					
Val	Lys	Gln	Lys	Lys	Trp	Gln	Gly	Leu	Gln	Glu	Met	Arg	Leu	Pro	Ser		
	450					455					460						
Pro	Glu	Leu	Glu	Leu	Ser	Lys	Leu	Arg	Thr	Ser	Ala	Ile	Arg	Thr	Ala		
465					470					475					480		
Pro	Asn	Pro	Tyr	Tyr	Cys	Gln	Val	Gly	Leu	Gly	Pro	Ala	Gln	Ser	Trp		
			485					490						495			
Pro	Leu	Pro	Pro	Gly	Val	Thr	Glu	Val	Ser	Pro	Ala	Asn	Val	Thr	Leu		
		500						505					510				
Leu	Arg	Ala	Leu	Gly	His	Gly	Ala	Phe	Gly	Glu	Val	Tyr	Glu	Gly	Leu		
		515					520					525					
Val	Ile	Gly	Leu	Pro	Gly	Asp	Ser	Ser	Pro	Leu	Gln	Val	Ala	Ile	Lys		
	530					535					540						
Thr	Leu	Pro	Glu	Leu	Cys	Ser	Pro	Gln	Asp	Glu	Leu	Asp	Phe	Leu	Met		
545					550					555					560		
Glu	Ala	Leu	Ile	Ile	Ser	Lys	Phe	Arg	His	Gln	Asn	Ile	Val	Arg	Cys		
			565					570						575			
Val	Gly	Leu	Ser	Leu	Arg	Ala	Thr	Pro	Arg	Leu	Ile	Leu	Leu	Glu	Leu		
		580						585					590				
Met	Ser	Gly	Gly	Asp	Met	Lys	Ser	Phe	Leu	Arg	His	Ser	Arg	Pro	His		
		595				600						605					
Leu	Gly	Gln	Pro	Ser	Pro	Leu	Val	Met	Arg	Asp	Leu	Leu	Gln	Leu	Ala		
	610					615					620						
Gln	Asp	Ile	Ala	Gln	Gly	Cys	His	Tyr	Leu	Glu	Glu	Asn	His	Phe	Ile		
625				630						635					640		
His	Arg	Asp	Ile	Ala	Ala	Arg	Asn	Cys	Leu	Leu	Ser	Cys	Ala	Gly	Pro		
			645						650					655			

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Ser Arg Val Ala Lys Ile Gly Asp Phe Gly Met Ala Arg Asp Ile Tyr
    660              665              670
Arg Ala Ser Tyr Tyr Arg Arg Gly Asp Arg Ala Leu Leu Pro Val Lys
    675              680              685
Trp Met Pro Pro Glu Ala Phe Leu Glu Gly Ile Phe Thr Ser Lys Thr
    690              695              700
Asp Ser Trp Ser Phe Gly Val Leu Leu Trp Glu Ile Phe Ser Leu Gly
    705              710              715              720
Tyr Met Pro Tyr Pro Gly Arg Thr Asn Gln Glu Val Leu Asp Phe Val
    725              730              735
Val Gly Gly Gly Arg Met Asp Pro Pro Arg Gly Cys Pro Gly Pro Val
    740              745              750
Tyr Arg Ile Met Thr Gln Cys Trp Gln His Glu Pro Glu Leu Arg Pro
    755              760              765
Ser Phe Ala Ser Ile Leu Glu Arg Leu Gln Tyr Cys Thr Gln Asp Pro
    770              775              780
Asp Val Leu Asn Ser Leu Leu Pro Met Glu Leu Gly Pro Thr Pro Glu
    785              790              795              800
Glu Glu Gly Thr Ser Gly Leu Gly Asn Arg Ser Leu Glu Cys Leu Arg
    805              810              815
Pro Pro Gln Pro Gln Glu Leu Ser Pro Glu Lys Leu Lys Ser Trp Gly
    820              825              830
Gly Ser Pro Leu Gly Pro Trp Leu Ser Ser Gly Leu Lys Pro Leu Lys
    835              840              845
Ser Arg Gly Leu Gln Pro Gln Asn Leu Trp Asn Pro Thr Tyr Arg Ser
    850              855              860

<210> SEQ ID NO 46
<211> LENGTH: 176
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(176)
<223> OTHER INFORMATION: OGTA249 = Swiss Prot Accession No. Q969L2,
    Protein MAL2

<400> SEQUENCE: 46
Met Ser Ala Gly Gly Ala Ser Val Pro Pro Pro Pro Asn Pro Ala Val
1      5      10      15
Ser Phe Pro Pro Pro Arg Val Thr Leu Pro Ala Gly Pro Asp Ile Leu
20     25     30
Arg Thr Tyr Ser Gly Ala Phe Val Cys Leu Glu Ile Leu Phe Gly Gly
35     40     45
Leu Val Trp Ile Leu Val Ala Ser Ser Asn Val Pro Leu Pro Leu Leu
50     55     60
Gln Gly Trp Val Met Phe Val Ser Val Thr Ala Phe Phe Phe Ser Leu
65     70     75     80
Leu Phe Leu Gly Met Phe Leu Ser Gly Met Val Ala Gln Ile Asp Ala
85     90     95
Asn Trp Asn Phe Leu Asp Phe Ala Tyr His Phe Thr Val Phe Val Phe
100    105    110
Tyr Phe Gly Ala Phe Leu Leu Glu Ala Ala Ala Thr Ser Leu His Asp
115    120    125

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Leu His Cys Asn Thr Thr Ile Thr Gly Gln Pro Leu Leu Ser Asp Asn
 130                      135                      140

Gln Tyr Asn Ile Asn Val Ala Ala Ser Ile Phe Ala Phe Met Thr Thr
145                      150                      155                      160

Ala Cys Tyr Gly Cys Ser Leu Gly Leu Ala Leu Arg Arg Trp Arg Pro
                      165                      170                      175

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<210> SEQ ID NO 47
<211> LENGTH: 725
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(725)
<223> OTHER INFORMATION: OGTA257 = Swiss Prot Accession No. Q9H1D0,
      Transient receptor potential cation channel subfamily V member 6

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<400> SEQUENCE: 47

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Met Gly Leu Ser Leu Pro Lys Glu Lys Gly Leu Ile Leu Cys Leu Trp
 1                      5                      10                      15

Ser Lys Phe Cys Arg Trp Phe Gln Arg Arg Glu Ser Trp Ala Gln Ser
                      20                      25                      30

Arg Asp Glu Gln Asn Leu Leu Gln Gln Lys Arg Ile Trp Glu Ser Pro
                      35                      40                      45

Leu Leu Leu Ala Ala Lys Asp Asn Asp Val Gln Ala Leu Asn Lys Leu
 50                      55                      60

Leu Lys Tyr Glu Asp Cys Lys Val His Gln Arg Gly Ala Met Gly Glu
65                      70                      75                      80

Thr Ala Leu His Ile Ala Ala Leu Tyr Asp Asn Leu Glu Ala Ala Met
                      85                      90                      95

Val Leu Met Glu Ala Ala Pro Glu Leu Val Phe Glu Pro Met Thr Ser
                      100                     105                     110

Glu Leu Tyr Glu Gly Gln Thr Ala Leu His Ile Ala Val Val Asn Gln
                      115                     120                     125

Asn Met Asn Leu Val Arg Ala Leu Leu Ala Arg Arg Ala Ser Val Ser
                      130                     135                     140

Ala Arg Ala Thr Gly Thr Ala Phe Arg Arg Ser Pro Cys Asn Leu Ile
145                      150                      155                      160

Tyr Phe Gly Glu His Pro Leu Ser Phe Ala Ala Cys Val Asn Ser Glu
                      165                      170                      175

Glu Ile Val Arg Leu Leu Ile Glu His Gly Ala Asp Ile Arg Ala Gln
                      180                     185                     190

Asp Ser Leu Gly Asn Thr Val Leu His Ile Leu Ile Leu Gln Pro Asn
                      195                     200                     205

Lys Thr Phe Ala Cys Gln Met Tyr Asn Leu Leu Leu Ser Tyr Asp Arg
                      210                     215                     220

His Gly Asp His Leu Gln Pro Leu Asp Leu Val Pro Asn His Gln Gly
225                      230                      235                      240

Leu Thr Pro Phe Lys Leu Ala Gly Val Glu Gly Asn Thr Val Met Phe
                      245                     250                     255

Gln His Leu Met Gln Lys Arg Lys His Thr Gln Trp Thr Tyr Gly Pro
                      260                     265                     270

Leu Thr Ser Thr Leu Tyr Asp Leu Thr Glu Ile Asp Ser Ser Gly Asp
                      275                     280                     285

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Glu	Gln	Ser	Leu	Leu	Glu	Leu	Ile	Ile	Thr	Thr	Lys	Lys	Arg	Glu	Ala	290	295	300
Arg	Gln	Ile	Leu	Asp	Gln	Thr	Pro	Val	Lys	Glu	Leu	Val	Ser	Leu	Lys	305	310	315
Trp	Lys	Arg	Tyr	Gly	Arg	Pro	Tyr	Phe	Cys	Met	Leu	Gly	Ala	Ile	Tyr	325	330	335
Leu	Leu	Tyr	Ile	Ile	Cys	Phe	Thr	Met	Cys	Cys	Ile	Tyr	Arg	Pro	Leu	340	345	350
Lys	Pro	Arg	Thr	Asn	Asn	Arg	Thr	Ser	Pro	Arg	Asp	Asn	Thr	Leu	Leu	355	360	365
Gln	Gln	Lys	Leu	Leu	Gln	Glu	Ala	Tyr	Met	Thr	Pro	Lys	Asp	Asp	Ile	370	375	380
Arg	Leu	Val	Gly	Glu	Leu	Val	Thr	Val	Ile	Gly	Ala	Ile	Ile	Ile	Leu	385	390	395
Leu	Val	Glu	Val	Pro	Asp	Ile	Phe	Arg	Met	Gly	Val	Thr	Arg	Phe	Phe	405	410	415
Gly	Gln	Thr	Ile	Leu	Gly	Gly	Pro	Phe	His	Val	Leu	Ile	Ile	Thr	Tyr	420	425	430
Ala	Phe	Met	Val	Leu	Val	Thr	Met	Val	Met	Arg	Leu	Ile	Ser	Ala	Ser	435	440	445
Gly	Glu	Val	Val	Pro	Met	Ser	Phe	Ala	Leu	Val	Leu	Gly	Trp	Cys	Asn	450	455	460
Val	Met	Tyr	Phe	Ala	Arg	Gly	Phe	Gln	Met	Leu	Gly	Pro	Phe	Thr	Ile	465	470	475
Met	Ile	Gln	Lys	Met	Ile	Phe	Gly	Asp	Leu	Met	Arg	Phe	Cys	Trp	Leu	485	490	495
Met	Ala	Val	Val	Ile	Leu	Gly	Phe	Ala	Ser	Ala	Phe	Tyr	Ile	Ile	Phe	500	505	510
Gln	Thr	Glu	Asp	Pro	Glu	Glu	Leu	Gly	His	Phe	Tyr	Asp	Tyr	Pro	Met	515	520	525
Ala	Leu	Phe	Ser	Thr	Phe	Glu	Leu	Phe	Leu	Thr	Ile	Ile	Asp	Gly	Pro	530	535	540
Ala	Asn	Tyr	Asn	Val	Asp	Leu	Pro	Phe	Met	Tyr	Ser	Ile	Thr	Tyr	Ala	545	550	555
Ala	Phe	Ala	Ile	Ile	Ala	Thr	Leu	Leu	Met	Leu	Asn	Leu	Leu	Ile	Ala	565	570	575
Met	Met	Gly	Asp	Thr	His	Trp	Arg	Val	Ala	His	Glu	Arg	Asp	Glu	Leu	580	585	590
Trp	Arg	Ala	Gln	Ile	Val	Ala	Thr	Thr	Val	Met	Leu	Glu	Arg	Lys	Leu	595	600	605
Pro	Arg	Cys	Leu	Trp	Pro	Arg	Ser	Gly	Ile	Cys	Gly	Arg	Glu	Tyr	Gly	610	615	620
Leu	Gly	Asp	Arg	Trp	Phe	Leu	Arg	Val	Glu	Asp	Arg	Gln	Asp	Leu	Asn	625	630	635
Arg	Gln	Arg	Ile	Gln	Arg	Tyr	Ala	Gln	Ala	Phe	His	Thr	Arg	Gly	Ser	645	650	655
Glu	Asp	Leu	Asp	Lys	Asp	Ser	Val	Glu	Lys	Leu	Glu	Leu	Gly	Cys	Pro	660	665	670
Phe	Ser	Pro	His	Leu	Ser	Leu	Pro	Met	Pro	Ser	Val	Ser	Arg	Ser	Thr	675	680	685

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Ser Arg Ser Ser Ala Asn Trp Glu Arg Leu Arg Gln Gly Thr Leu Arg
690 695 700

Arg Asp Leu Arg Gly Ile Ile Asn Arg Gly Leu Glu Asp Gly Glu Ser
705 710 715 720

Trp Glu Tyr Gln Ile
725

<210> SEQ ID NO 48
<211> LENGTH: 1898
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(1898)
<223> OTHER INFORMATION: OGTA271 = Swiss Prot Accession No. Q5T021,
Protein tyrosine phosphatase, receptor type, F

<400> SEQUENCE: 48

Met Ala Pro Glu Pro Ala Pro Gly Arg Thr Met Val Pro Leu Val Pro
1 5 10 15

Ala Leu Val Met Leu Gly Leu Val Ala Gly Ala His Gly Asp Ser Lys
20 25 30

Pro Val Phe Ile Lys Val Pro Glu Asp Gln Thr Gly Leu Ser Gly Gly
35 40 45

Val Ala Ser Phe Val Cys Gln Ala Thr Gly Glu Pro Lys Pro Arg Ile
50 55 60

Thr Trp Met Lys Lys Gly Lys Lys Val Ser Ser Gln Arg Phe Glu Val
65 70 75 80

Ile Glu Phe Asp Asp Gly Ala Gly Ser Val Leu Arg Ile Gln Pro Leu
85 90 95

Arg Val Gln Arg Asp Glu Ala Ile Tyr Glu Cys Thr Ala Thr Asn Ser
100 105 110

Leu Gly Glu Ile Asn Thr Ser Ala Lys Leu Ser Val Leu Glu Glu Glu
115 120 125

Gln Leu Pro Pro Gly Phe Pro Ser Ile Asp Met Gly Pro Gln Leu Lys
130 135 140

Val Val Glu Lys Ala Arg Thr Ala Thr Met Leu Cys Ala Ala Gly Gly
145 150 155 160

Asn Pro Asp Pro Glu Ile Ser Trp Phe Lys Asp Phe Leu Pro Val Asp
165 170 175

Pro Ala Thr Ser Asn Gly Arg Ile Lys Gln Leu Arg Ser Gly Ala Leu
180 185 190

Gln Ile Glu Ser Ser Glu Glu Ser Asp Gln Gly Lys Tyr Glu Cys Val
195 200 205

Ala Thr Asn Ser Ala Gly Thr Arg Tyr Ser Ala Pro Ala Asn Leu Tyr
210 215 220

Val Arg Val Arg Arg Val Ala Pro Arg Phe Ser Ile Pro Pro Ser Ser
225 230 235 240

Gln Glu Val Met Pro Gly Gly Ser Val Asn Leu Thr Cys Val Ala Val
245 250 255

Gly Ala Pro Met Pro Tyr Val Lys Trp Met Met Gly Ala Glu Glu Leu
260 265 270

Thr Lys Glu Asp Glu Met Pro Val Gly Arg Asn Val Leu Glu Leu Ser
275 280 285

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Asn	Val	Val	Arg	Ser	Ala	Asn	Tyr	Thr	Cys	Val	Ala	Ile	Ser	Ser	Leu
290						295					300				
Gly	Met	Ile	Glu	Ala	Thr	Ala	Gln	Val	Thr	Val	Lys	Ala	Leu	Pro	Lys
305					310					315				320	
Pro	Pro	Ile	Asp	Leu	Val	Val	Thr	Glu	Thr	Thr	Ala	Thr	Ser	Val	Thr
			325						330					335	
Leu	Thr	Trp	Asp	Ser	Gly	Asn	Ser	Glu	Pro	Val	Thr	Tyr	Tyr	Gly	Ile
			340					345					350		
Gln	Tyr	Arg	Ala	Ala	Gly	Thr	Glu	Gly	Pro	Phe	Gln	Glu	Val	Asp	Gly
		355					360					365			
Val	Ala	Thr	Thr	Arg	Tyr	Ser	Ile	Gly	Gly	Leu	Ser	Pro	Phe	Ser	Glu
	370					375					380				
Tyr	Ala	Phe	Arg	Val	Leu	Ala	Val	Asn	Ser	Ile	Gly	Arg	Gly	Pro	Pro
385					390					395				400	
Ser	Glu	Ala	Val	Arg	Ala	Arg	Thr	Gly	Glu	Gln	Ala	Pro	Ser	Ser	Pro
			405						410					415	
Pro	Arg	Arg	Val	Gln	Ala	Arg	Met	Leu	Ser	Ala	Ser	Thr	Met	Leu	Val
			420					425					430		
Gln	Trp	Glu	Pro	Pro	Glu	Glu	Pro	Asn	Gly	Leu	Val	Arg	Gly	Tyr	Arg
		435					440					445			
Val	Tyr	Tyr	Thr	Pro	Asp	Ser	Arg	Arg	Pro	Pro	Asn	Ala	Trp	His	Lys
	450					455					460				
His	Asn	Thr	Asp	Ala	Gly	Leu	Leu	Thr	Thr	Val	Gly	Ser	Leu	Leu	Pro
465					470					475				480	
Gly	Ile	Thr	Tyr	Ser	Leu	Arg	Val	Leu	Ala	Phe	Thr	Ala	Val	Gly	Asp
				485					490					495	
Gly	Pro	Pro	Ser	Pro	Thr	Ile	Gln	Val	Lys	Thr	Gln	Gln	Gly	Val	Pro
			500					505					510		
Ala	Gln	Pro	Ala	Asp	Phe	Gln	Ala	Glu	Val	Glu	Ser	Asp	Thr	Arg	Ile
		515					520					525			
Gln	Leu	Ser	Trp	Leu	Leu	Pro	Pro	Gln	Glu	Arg	Ile	Ile	Met	Tyr	Glu
	530					535					540				
Leu	Val	Tyr	Trp	Ala	Ala	Glu	Asp	Glu	Asp	Gln	Gln	His	Lys	Val	Thr
545					550					555				560	
Phe	Asp	Pro	Thr	Ser	Ser	Tyr	Thr	Leu	Glu	Asp	Leu	Lys	Pro	Asp	Thr
				565					570					575	
Leu	Tyr	Arg	Phe	Gln	Leu	Ala	Ala	Arg	Ser	Asp	Met	Gly	Val	Gly	Val
			580					585					590		
Phe	Thr	Pro	Thr	Ile	Glu	Ala	Arg	Thr	Ala	Gln	Ser	Thr	Pro	Ser	Ala
		595					600					605			
Pro	Pro	Gln	Lys	Val	Met	Cys	Val	Ser	Met	Gly	Ser	Thr	Thr	Val	Arg
	610					615					620				
Val	Ser	Trp	Val	Pro	Pro	Pro	Ala	Asp	Ser	Arg	Asn	Gly	Val	Ile	Thr
625					630					635				640	
Gln	Tyr	Ser	Val	Ala	Tyr	Glu	Ala	Val	Asp	Gly	Glu	Asp	Arg	Gly	Arg
				645					650					655	
His	Val	Val	Asp	Gly	Ile	Ser	Arg	Glu	His	Ser	Ser	Trp	Asp	Leu	Val
			660					665					670		
Gly	Leu	Glu	Lys	Trp	Thr	Glu	Tyr	Arg	Val	Trp	Val	Arg	Ala	His	Thr
	675						680					685			
Asp	Val	Gly	Pro	Gly	Pro	Glu	Ser	Ser	Pro	Val	Leu	Val	Arg	Thr	Asp

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690					695					700					
Glu 705	Asp	Val	Pro	Ser	Gly 710	Pro	Pro	Arg	Lys	Val 715	Glu	Val	Glu	Pro	Leu 720
Asn	Ser	Thr	Ala	Val	His	Val	Tyr	Trp	Lys 730	Leu	Pro	Val	Pro	Ser	Lys 735
Gln	His	Gly	Gln	Ile	Arg	Gly	Tyr	Gln	Val 745	Thr	Tyr	Val	Arg	Leu	Glu
Asn	Gly	Glu	Pro	Arg	Gly	Leu	Pro	Ile	Ile 760	Gln	Asp	Val	Met	Leu	Ala
Glu	Ala	Gln	Glu	Thr	Thr	Ile	Ser	Gly	Leu 775	Thr	Pro	Glu	Thr	Thr	Tyr
Ser	Val	Thr	Val	Ala	Ala	Tyr	Thr	Thr	Lys 790	Gly	Asp	Gly	Ala	Arg	Ser 800
Lys	Pro	Lys	Ile	Val	Thr	Thr	Thr	Gly	Ala 810	Val	Pro	Gly	Arg	Pro	Thr 815
Met	Met	Ile	Ser	Thr	Thr	Ala	Met	Asn	Thr 825	Ala	Leu	Leu	Gln	Trp	His 830
Pro	Pro	Lys	Glu	Leu	Pro	Gly	Glu	Leu	Leu 840	Gly	Tyr	Arg	Leu	Gln	Tyr
Cys	Arg	Ala	Asp	Glu	Ala	Arg	Pro	Asn	Thr 855	Ile	Asp	Phe	Gly	Lys	Asp 860
Asp	Gln	His	Phe	Thr	Val	Thr	Gly	Leu	His 875	Lys	Gly	Thr	Thr	Tyr	Ile 880
Phe	Arg	Leu	Ala	Ala	Lys	Asn	Arg	Ala	Gly 890	Leu	Gly	Glu	Glu	Phe	Glu 895
Lys	Glu	Ile	Arg	Thr	Pro	Glu	Asp	Leu	Pro 905	Ser	Gly	Phe	Pro	Gln	Asn 910
Leu	His	Val	Thr	Gly	Leu	Thr	Thr	Ser	Thr 920	Thr	Glu	Leu	Ala	Trp	Asp 925
Pro	Pro	Val	Leu	Ala	Glu	Arg	Asn	Gly	Arg 935	Ile	Ile	Ser	Tyr	Thr	Val 940
Val	Phe	Arg	Asp	Ile	Asn	Ser	Gln	Gln	Glu 955	Leu	Gln	Asn	Ile	Thr	Thr 960
Asp	Thr	Arg	Phe	Thr	Leu	Thr	Gly	Leu	Lys 970	Pro	Asp	Thr	Thr	Tyr	Asp 975
Ile	Lys	Val	Arg	Ala	Trp	Thr	Ser	Lys	Gly 985	Ser	Gly	Pro	Leu	Ser	Pro 990
Ser	Ile	Gln	Ser	Arg	Thr	Met	Pro	Val	Glu 1000	Gln	Val	Phe	Ala	Lys	Asn 1005
Phe	Arg	Val	Ala	Ala	Ala	Met	Lys	Thr	Ser 1015	Val	Leu	Leu	Ser	Trp	
Glu	Val	Pro	Asp	Ser	Tyr	Lys	Ser	Ala	Val 1025	Pro	Phe	Lys	Ile	Leu	
Tyr	Asn	Gly	Gln	Ser	Val	Glu	Val	Asp	Gly 1040	His	Ser	Met	Arg	Lys	
Leu	Ile	Ala	Asp	Leu	Gln	Pro	Asn	Thr	Glu 1055	Tyr	Ser	Phe	Val	Leu	
Met	Asn	Arg	Gly	Ser	Ser	Ala	Gly	Gly	Leu 1070	Gln	His	Leu	Val	Ser	
Ile	Arg	Thr	Ala	Pro	Asp	Leu	Leu	Pro	His 1085	Lys	Pro	Leu	Pro	Ala	

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Ser	Ala	Tyr	Ile	Glu	Asp	Gly	Arg	Phe	Asp	Leu	Ser	Met	Pro	His
1100						1105					1110			
Val	Gln	Asp	Pro	Ser	Leu	Val	Arg	Trp	Phe	Tyr	Ile	Val	Val	Val
1115						1120					1125			
Pro	Ile	Asp	Arg	Val	Gly	Gly	Ser	Met	Leu	Thr	Pro	Arg	Trp	Ser
1130						1135					1140			
Thr	Pro	Glu	Glu	Leu	Glu	Leu	Asp	Glu	Leu	Leu	Glu	Ala	Ile	Glu
1145						1150					1155			
Gln	Gly	Gly	Glu	Glu	Gln	Arg	Arg	Arg	Arg	Arg	Gln	Ala	Glu	Arg
1160						1165					1170			
Leu	Lys	Pro	Tyr	Val	Ala	Ala	Gln	Leu	Asp	Val	Leu	Pro	Glu	Thr
1175						1180					1185			
Phe	Thr	Leu	Gly	Asp	Lys	Lys	Asn	Tyr	Arg	Gly	Phe	Tyr	Asn	Arg
1190						1195					1200			
Pro	Leu	Ser	Pro	Asp	Leu	Ser	Tyr	Gln	Cys	Phe	Val	Leu	Ala	Ser
1205						1210					1215			
Leu	Lys	Glu	Pro	Met	Asp	Gln	Lys	Arg	Tyr	Ala	Ser	Ser	Pro	Tyr
1220						1225					1230			
Ser	Asp	Glu	Ile	Val	Val	Gln	Val	Thr	Pro	Ala	Gln	Gln	Gln	Glu
1235						1240					1245			
Glu	Pro	Glu	Met	Leu	Trp	Val	Thr	Gly	Pro	Val	Leu	Ala	Val	Ile
1250						1255					1260			
Leu	Ile	Ile	Leu	Ile	Val	Ile	Ala	Ile	Leu	Leu	Phe	Lys	Arg	Lys
1265						1270					1275			
Arg	Thr	His	Ser	Pro	Ser	Ser	Lys	Asp	Glu	Gln	Ser	Ile	Gly	Leu
1280						1285					1290			
Lys	Asp	Ser	Leu	Leu	Ala	His	Ser	Ser	Asp	Pro	Val	Glu	Met	Arg
1295						1300					1305			
Arg	Leu	Asn	Tyr	Gln	Thr	Pro	Gly	Met	Arg	Asp	His	Pro	Pro	Ile
1310						1315					1320			
Pro	Ile	Thr	Asp	Leu	Ala	Asp	Asn	Ile	Glu	Arg	Leu	Lys	Ala	Asn
1325						1330					1335			
Asp	Gly	Leu	Lys	Phe	Ser	Gln	Glu	Tyr	Glu	Ser	Ile	Asp	Pro	Gly
1340						1345					1350			
Gln	Gln	Phe	Thr	Trp	Glu	Asn	Ser	Asn	Leu	Glu	Val	Asn	Lys	Pro
1355						1360					1365			
Lys	Asn	Arg	Tyr	Ala	Asn	Val	Ile	Ala	Tyr	Asp	His	Ser	Arg	Val
1370						1375					1380			
Ile	Leu	Thr	Ser	Ile	Asp	Gly	Val	Pro	Gly	Ser	Asp	Tyr	Ile	Asn
1385						1390					1395			
Ala	Asn	Tyr	Ile	Asp	Gly	Tyr	Arg	Lys	Gln	Asn	Ala	Tyr	Ile	Ala
1400						1405					1410			
Thr	Gln	Gly	Pro	Leu	Pro	Glu	Thr	Met	Gly	Asp	Phe	Trp	Arg	Met
1415						1420					1425			
Val	Trp	Glu	Gln	Arg	Thr	Ala	Thr	Val	Val	Met	Met	Thr	Arg	Leu
1430						1435					1440			
Glu	Glu	Lys	Ser	Arg	Val	Lys	Cys	Asp	Gln	Tyr	Trp	Pro	Ala	Arg
1445						1450					1455			
Gly	Thr	Glu	Thr	Cys	Gly	Leu	Ile	Gln	Val	Thr	Leu	Leu	Asp	Thr
1460						1465					1470			

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Val	Glu	Leu	Ala	Thr	Tyr	Thr	Val	Arg	Thr	Phe	Ala	Leu	His	Lys
1475						1480					1485			
Ser	Gly	Ser	Ser	Glu	Lys	Arg	Glu	Leu	Arg	Gln	Phe	Gln	Phe	Met
1490						1495					1500			
Ala	Trp	Pro	Asp	His	Gly	Val	Pro	Glu	Tyr	Pro	Thr	Pro	Ile	Leu
1505						1510					1515			
Ala	Phe	Leu	Arg	Arg	Val	Lys	Ala	Cys	Asn	Pro	Leu	Asp	Ala	Gly
1520						1525					1530			
Pro	Met	Val	Val	His	Cys	Ser	Ala	Gly	Val	Gly	Arg	Thr	Gly	Cys
1535						1540					1545			
Phe	Ile	Val	Ile	Asp	Ala	Met	Leu	Glu	Arg	Met	Lys	His	Glu	Lys
1550						1555					1560			
Thr	Val	Asp	Ile	Tyr	Gly	His	Val	Thr	Cys	Met	Arg	Ser	Gln	Arg
1565						1570					1575			
Asn	Tyr	Met	Val	Gln	Thr	Glu	Asp	Gln	Tyr	Val	Phe	Ile	His	Glu
1580						1585					1590			
Ala	Leu	Leu	Glu	Ala	Ala	Thr	Cys	Gly	His	Thr	Glu	Val	Pro	Ala
1595						1600					1605			
Arg	Asn	Leu	Tyr	Ala	His	Ile	Gln	Lys	Leu	Gly	Gln	Val	Pro	Pro
1610						1615					1620			
Gly	Glu	Ser	Val	Thr	Ala	Met	Glu	Leu	Glu	Phe	Lys	Leu	Leu	Ala
1625						1630					1635			
Ser	Ser	Lys	Ala	His	Thr	Ser	Arg	Phe	Ile	Ser	Ala	Asn	Leu	Pro
1640						1645					1650			
Cys	Asn	Lys	Phe	Lys	Asn	Arg	Leu	Val	Asn	Ile	Met	Pro	Tyr	Glu
1655						1660					1665			
Leu	Thr	Arg	Val	Cys	Leu	Gln	Pro	Ile	Arg	Gly	Val	Glu	Gly	Ser
1670						1675					1680			
Asp	Tyr	Ile	Asn	Ala	Ser	Phe	Leu	Asp	Gly	Tyr	Arg	Gln	Gln	Lys
1685						1690					1695			
Ala	Tyr	Ile	Ala	Thr	Gln	Gly	Pro	Leu	Ala	Glu	Ser	Thr	Glu	Asp
1700						1705					1710			
Phe	Trp	Arg	Met	Leu	Trp	Glu	His	Asn	Ser	Thr	Ile	Ile	Val	Met
1715						1720					1725			
Leu	Thr	Lys	Leu	Arg	Glu	Met	Gly	Arg	Glu	Lys	Cys	His	Gln	Tyr
1730						1735					1740			
Trp	Pro	Ala	Glu	Arg	Ser	Ala	Arg	Tyr	Gln	Tyr	Phe	Val	Val	Asp
1745						1750					1755			
Pro	Met	Ala	Glu	Tyr	Asn	Met	Pro	Gln	Tyr	Ile	Leu	Arg	Glu	Phe
1760						1765					1770			
Lys	Val	Thr	Asp	Ala	Arg	Asp	Gly	Gln	Ser	Arg	Thr	Ile	Arg	Gln
1775						1780					1785			
Phe	Gln	Phe	Thr	Asp	Trp	Pro	Glu	Gln	Gly	Val	Pro	Lys	Thr	Gly
1790						1795					1800			
Glu	Gly	Phe	Ile	Asp	Phe	Ile	Gly	Gln	Val	His	Lys	Thr	Lys	Glu
1805						1810					1815			
Gln	Phe	Gly	Gln	Asp	Gly	Pro	Ile	Thr	Val	His	Cys	Ser	Ala	Gly
1820						1825					1830			
Val	Gly	Arg	Thr	Gly	Val	Phe	Ile	Thr	Leu	Ser	Ile	Val	Leu	Glu
1835						1840					1845			
Arg	Met	Arg	Tyr	Glu	Gly	Val	Val	Asp	Met	Phe	Gln	Thr	Val	Lys

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1850	1855	1860
Thr Leu Arg Thr Gln Arg Pro Ala Met Val Gln Thr Glu Asp Gln		
1865	1870	1875
Tyr Gln Leu Cys Tyr Arg Ala Ala Leu Glu Tyr Leu Gly Ser Phe		
1880	1885	1890
Asp His Tyr Ala Thr		
1895		

<210> SEQ ID NO 49
 <211> LENGTH: 22
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 49

Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Gly
1 5 10 15
Ala Gly Ala Gly Ala Lys
20

<210> SEQ ID NO 50
 <211> LENGTH: 18
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 50

Ala Ala Gly Thr Glu Gly Pro Phe Gln Glu Val Asp Gly Val Ala Thr
1 5 10 15
Thr Arg

<210> SEQ ID NO 51
 <211> LENGTH: 14
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 51

Ala Ala Leu Glu Tyr Leu Gly Ser Phe Asp His Tyr Ala Thr
1 5 10

<210> SEQ ID NO 52
 <211> LENGTH: 15
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 52

Ala Ala Asn Asp Pro Phe Thr Ile Val His Gly Asn Thr Gly Lys
1 5 10 15

<210> SEQ ID NO 53
 <211> LENGTH: 19
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 53

Ala Ala Ser Ala Gly Gln Glu Pro Leu His Asn Glu Glu Leu Ala Gly
1 5 10 15

Ala Gly Arg

<210> SEQ ID NO 54
 <211> LENGTH: 8

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<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 54

Ala Ala Thr Tyr His Val Asp Arg
1 5

<210> SEQ ID NO 55
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 55

Ala Cys Phe Ala Leu Leu Trp Gly Cys Ala Leu Ala Ala Ala Ala
1 5 10 15

Ala Gln Gly Lys
20

<210> SEQ ID NO 56
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 56

Ala Cys Asn Pro Leu Asp Ala Gly Pro Met Val Val His Cys Ser Ala
1 5 10 15

Gly Val Gly Arg
20

<210> SEQ ID NO 57
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 57

Ala Asp Ala Ala Pro Asp Glu Lys
1 5

<210> SEQ ID NO 58
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 58

Ala Asp Glu Ala Arg Pro Asn Thr Ile Asp Phe Gly Lys
1 5 10

<210> SEQ ID NO 59
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 59

Ala Asp Phe Leu Ile Phe Arg
1 5

<210> SEQ ID NO 60
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 60

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Ala Asp Phe Val Leu Ala Ala Asn Ser Tyr Asp Leu Ala Ile Lys
1 5 10 15

<210> SEQ ID NO 61
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 61

Ala Asp Gly Ile Ser Ser Thr Phe Ser Gln Arg
1 5 10

<210> SEQ ID NO 62
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 62

Ala Glu Leu Asp Asp Ser Asp Gly His Gly Asn His Arg
1 5 10

<210> SEQ ID NO 63
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 63

Ala Glu Pro Glu Ser Glu Thr Ser Ile Leu Leu Ser Trp Thr Pro Pro
1 5 10 15

Arg

<210> SEQ ID NO 64
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 64

Ala Glu Trp Leu Asn Lys
1 5

<210> SEQ ID NO 65
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 65

Ala Phe Gly Ala Pro Val Pro Ser Val Gln Trp Leu Asp Glu Asp Gly
1 5 10 15

Thr Thr Val Leu Gln Asp Glu Arg
20

<210> SEQ ID NO 66
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 66

Ala Phe Met Ile Ile Gln Glu Gln Arg
1 5

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<210> SEQ ID NO 67
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 67

Ala Phe Ser Ser Asp Leu Ile Ser Ile His Ser Leu Ala Asp Val Glu
1 5 10 15
Val Val Val Thr Lys
20

<210> SEQ ID NO 68
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 68

Ala Phe Val Asn Cys Asp Glu Asn Ser Arg
1 5 10

<210> SEQ ID NO 69
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 69

Ala Phe Tyr Ala Pro Val His Ala Asp Asp Leu Arg
1 5 10

<210> SEQ ID NO 70
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 70

Ala Gly Glu Ile Thr Ser Asp Gly Leu Ser Phe Leu Phe Leu Lys
1 5 10 15

<210> SEQ ID NO 71
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 71

Ala Gly Leu Gly Glu Glu Phe Glu Lys
1 5

<210> SEQ ID NO 72
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 72

Ala His Thr Asp Val Gly Pro Gly Pro Glu Ser Ser Pro Val Leu Val
1 5 10 15

Arg

<210> SEQ ID NO 73
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 73

Ala Ile Asn Asp Gly Phe Arg
1 5

<210> SEQ ID NO 74

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 74

Ala Ile Ser Thr Asn Ser Glu Leu Ser Thr Phe Arg
1 5 10

<210> SEQ ID NO 75

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 75

Ala Leu Ala Leu Leu Glu Asp Glu Glu Arg
1 5 10

<210> SEQ ID NO 76

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 76

Ala Leu Gly Arg Pro Gly Pro Pro Phe Asn Ile Thr Pro Arg
1 5 10

<210> SEQ ID NO 77

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 77

Ala Leu Tyr Gln Leu Gly Met Arg
1 5

<210> SEQ ID NO 78

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 78

Ala Met Ala Thr Leu Leu Ser Lys
1 5

<210> SEQ ID NO 79

<211> LENGTH: 26

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 79

Ala Asn Leu Thr Asn Phe Pro Glu Asn Gly Thr Phe Val Val Asn Ile
1 5 10 15Ala Gln Leu Ser Gln Asp Asp Ser Gly Arg
20 25

<210> SEQ ID NO 80

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<211> LENGTH: 28
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 80
Ala Pro Gln Asp Pro Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala
1 5 10 15
Pro His Tyr Leu Thr Ala Val Gly Met Gly Ala Lys
20 25

<210> SEQ ID NO 81
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 81

Ala Gln Asp Pro Gly Glu Pro Arg
1 5

<210> SEQ ID NO 82
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 82
Ala Gln Leu Leu Val Val Gly Ser Pro Gly Pro Val Pro Arg
1 5 10

<210> SEQ ID NO 83
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 83
Ala Gln Pro Pro Glu Ala Gly Pro Gln Gly Leu His Asp Leu Gly Arg
1 5 10 15

<210> SEQ ID NO 84
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 84
Ala Gln Gln Glu Phe Ala Thr Gly Val Met Ser Asn Lys
1 5 10

<210> SEQ ID NO 85
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 85
Ala Gln Tyr Glu Gly Arg
1 5

<210> SEQ ID NO 86
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 86
Ala Ser Val Asp Ser Gly Ser Ser Glu Glu Gln Gly Gly Ser Ser Arg

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1	5	10	15
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<210> SEQ ID NO 87
 <211> LENGTH: 15
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 87

Ala	Ser	Val	Ser	Phe	Leu	Asn	Phe	Asn	Leu	Ser	Asn	Cys	Glu	Arg
1			5					10					15	

<210> SEQ ID NO 88
 <211> LENGTH: 10
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 88

Ala	Thr	Asp	Phe	Asp	Val	Leu	Ser	Tyr	Lys
1			5					10	

<210> SEQ ID NO 89
 <211> LENGTH: 11
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 89

Ala	Thr	Asp	Phe	Asp	Val	Leu	Ser	Tyr	Lys	Lys
1			5					10		

<210> SEQ ID NO 90
 <211> LENGTH: 10
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 90

Ala	Thr	Gly	Phe	Pro	Glu	Pro	Asn	Pro	Arg
1			5					10	

<210> SEQ ID NO 91
 <211> LENGTH: 7
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 91

Ala	Thr	Leu	Gln	Leu	Ser	Arg
1			5			

<210> SEQ ID NO 92
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 92

Ala	Thr	Asn	Ser	Met	Ile	Asp	Arg
1			5				

<210> SEQ ID NO 93
 <211> LENGTH: 18
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 93

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Ala Thr Gln Phe Thr Gly Ala Thr Gly Ala Ile Met Thr Thr Glu Thr
1 5 10 15

Thr Lys

<210> SEQ ID NO 94
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 94

Ala Val Asp Glu Gln Gly Trp Glu Tyr Ser Ile Thr Ile Pro Pro Glu
1 5 10 15

Arg

<210> SEQ ID NO 95
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 95

Ala Val Gly Phe Gly Gly Asp Phe Asp Gly Val Pro Arg
1 5 10

<210> SEQ ID NO 96
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 96

Ala Val Ile Phe Thr Gln Val Ser Arg
1 5

<210> SEQ ID NO 97
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 97

Ala Val Ile Ser Gln Phe Gln Arg Pro Ser Thr Gln Phe Ser Leu Met
1 5 10 15

Gln Phe Ser Asn Lys
20

<210> SEQ ID NO 98
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 98

Ala Tyr Ile Ala Thr Gln Gly Pro Leu Ala Glu Ser Thr Glu Asp Phe
1 5 10 15

Trp Arg

<210> SEQ ID NO 99
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 99

Ala Tyr Ile Phe Ser Ile Asp Glu Lys

-continued

1 5

<210> SEQ ID NO 100
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 100

Cys Asp Val Pro Ser Phe Ser Val Gln Glu Glu Leu Asp Phe Thr Leu
1 5 10 15

Lys

<210> SEQ ID NO 101
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 101

Cys Glu Ala Ser Gly Lys Pro Glu Val Gln Phe Arg
1 5 10

<210> SEQ ID NO 102
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 102

Cys Glu His His Ser Leu Tyr Gly Ala Ala Arg
1 5 10

<210> SEQ ID NO 103
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 103

Cys His Ile Gln Ala Ser Gly Arg Pro Gln Cys Ser Cys Met Pro Gly
1 5 10 15

Trp Thr Gly Glu Gln Cys Gln Leu Arg
20 25

<210> SEQ ID NO 104
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 104

Cys Ile Ile Trp Asn Thr Arg
1 5

<210> SEQ ID NO 105
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 105

Cys Leu Ala Glu Asn Ser Leu Gly Ser Ala Arg
1 5 10

<210> SEQ ID NO 106
<211> LENGTH: 13

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<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 106

Cys Met Leu Asn Ile Trp Gly Val Met Leu Phe Ile Arg
1 5 10

<210> SEQ ID NO 107
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 107

Cys Gln Gly Gln Leu Glu Val Tyr Leu Lys
1 5 10

<210> SEQ ID NO 108
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 108

Cys Ser Met Leu Ile Ala Ser Asn Glu Thr Trp Lys Lys
1 5 10

<210> SEQ ID NO 109
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 109

Asp Ala Thr Gln Ile Thr Gln Gly Pro Arg
1 5 10

<210> SEQ ID NO 110
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 110

Asp Ala Val Val Thr Tyr Thr Ala Glu Ser Lys
1 5 10

<210> SEQ ID NO 111
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 111

Asp Asp Gln His Phe Thr Val Thr Gly Leu His Lys
1 5 10

<210> SEQ ID NO 112
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 112

Asp Glu Ala Ile Tyr Glu Cys Thr Ala Thr Asn Ser Leu Gly Glu Ile
1 5 10 15

Asn Thr Ser Ala Lys
20

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<210> SEQ ID NO 113
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 113

Asp Glu Glu Glu Glu Pro Pro Ser Met Thr Gln Leu Leu Arg
1 5 10

<210> SEQ ID NO 114
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 114

Asp Glu Gly Pro Ala Ala Ala Gly Asp Gly Leu Gly Arg Pro Leu Gly
1 5 10 15

Pro Thr Pro Ser Gln Ser Arg
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<210> SEQ ID NO 115
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 115

Asp Glu Gln His Gln Cys Ser Leu Gly Asn Leu Lys
1 5 10

<210> SEQ ID NO 116
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 116

Asp Phe Leu Leu Gln Ser Ser Thr Val Ala Ala Glu Ala Gln Asp Gly
1 5 10 15

Pro Gln Glu Ala
20

<210> SEQ ID NO 117
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 117

Asp Phe Leu Pro Val Asp Pro Ala Thr Ser Asn Gly Arg
1 5 10

<210> SEQ ID NO 118
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 118

Asp Phe Leu Pro Val Asp Thr Ser Asn Asn Asn Gly Arg
1 5 10

<210> SEQ ID NO 119
<211> LENGTH: 12

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<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 119

Asp Phe Tyr Asn Pro Val Val Pro Glu Ala Gln Lys
1 5 10

<210> SEQ ID NO 120
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 120

Asp Phe Tyr Asn Pro Val Val Pro Glu Ala Gln Lys Arg
1 5 10

<210> SEQ ID NO 121
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 121

Asp Gly Glu Phe Ser Val Leu Gln Leu Val Gly Met Leu Arg
1 5 10

<210> SEQ ID NO 122
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 122

Asp Gly His Gly Thr Ala Ile Ser Asn Ala Ser Asp Val Trp Lys Lys
1 5 10 15

<210> SEQ ID NO 123
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 123

Asp Gly Asn Gly Glu Val Thr Asp Lys Pro Val Lys
1 5 10

<210> SEQ ID NO 124
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 124

Asp Gly Pro Glu Phe Thr Phe Thr Thr Pro Lys
1 5 10

<210> SEQ ID NO 125
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 125

Asp Gly Ser Phe Ser Val Val Ile Thr Gly Leu Arg
1 5 10

<210> SEQ ID NO 126

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<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 126

Asp Gly Val His Phe Lys Pro Lys
1 5

<210> SEQ ID NO 127
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 127

Asp His Pro Pro Ile Pro Ile Thr Asp Leu Ala Asp Asn Ile Glu Arg
1 5 10 15

<210> SEQ ID NO 128
<211> LENGTH: 33
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 128

Asp His Val Val Val Pro Ala Asn Thr Thr Ser Val Ile Leu Ser Gly
1 5 10 15

Leu Arg Pro Tyr Ser Ser Tyr His Leu Glu Val Gln Ala Phe Asn Gly
20 25 30

Arg

<210> SEQ ID NO 129
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 129

Asp Ile Asn Ser Gln Gln Glu Leu Gln Asn Ile Thr Thr Asp Thr Arg
1 5 10 15

<210> SEQ ID NO 130
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 130

Asp Ile Gln Asn Gln Leu Lys
1 5

<210> SEQ ID NO 131
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 131

Asp Ile Gln Val Ala Ser Asn Glu Ile Leu Arg
1 5 10

<210> SEQ ID NO 132
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 132

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Asp Leu Ala Ala Met Asp Lys
1 5

<210> SEQ ID NO 133
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 133

Asp Leu Ala Val Phe Leu Tyr His Leu Arg
1 5 10

<210> SEQ ID NO 134
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 134

Asp Leu Leu Pro Glu Asp Phe Val Val Tyr Thr Tyr Asn Lys
1 5 10

<210> SEQ ID NO 135
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 135

Asp Leu Pro Leu Leu Ile Glu Asn Met Lys
1 5 10

<210> SEQ ID NO 136
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 136

Asp Leu Pro Pro Ile Leu Leu Val Arg
1 5

<210> SEQ ID NO 137
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 137

Asp Leu Gln Glu Leu Gly Asp Ser Asp Lys
1 5 10

<210> SEQ ID NO 138
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 138

Asp Leu Gln Ser Ser Val Thr Leu Asp Leu Ala Leu Asp Pro Gly Arg
1 5 10 15

<210> SEQ ID NO 139
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 139

Asp Leu Ser Gln Met Glu Ala Leu Lys
1 5

<210> SEQ ID NO 140

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 140

Asp Leu Ser Gln Met Glu Ala Leu Lys Arg
1 5 10

<210> SEQ ID NO 141

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 141

Asp Leu Val Glu Pro Trp Val Val Val Arg
1 5 10

<210> SEQ ID NO 142

<211> LENGTH: 18

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 142

Asp Met Ala Gly Ala Gln Ala Ala Ala Val Ala Leu Asn Glu Glu Phe
1 5 10 15

Leu Arg

<210> SEQ ID NO 143

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 143

Asp Met Glu Pro Leu Thr Thr Leu Glu Phe Ser Glu Lys
1 5 10

<210> SEQ ID NO 144

<211> LENGTH: 25

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 144

Asp Asn Ile Val Ser Tyr Asn Asp Glu Gly Gly Gly Glu Glu Asp Thr
1 5 10 15Gln Ala Phe Asp Ile Gly Thr Leu Arg
20 25

<210> SEQ ID NO 145

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 145

Asp Asn Ile Tyr Pro Ala Phe Gln Met Phe Ala Lys
1 5 10

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<210> SEQ ID NO 146
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 146

Asp Asn Met Leu Trp Val Glu Trp Thr Thr Pro Arg
1 5 10

<210> SEQ ID NO 147
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 147

Asp Asn Gln Trp Leu Gly Val Thr Leu Ser Arg
1 5 10

<210> SEQ ID NO 148
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 148

Asp Asn Trp Ile Ser Val Asp Ser Val Thr Ser Glu Ile Lys
1 5 10

<210> SEQ ID NO 149
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 149

Asp Pro Ser Val Thr Gln Val Thr Arg
1 5

<210> SEQ ID NO 150
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 150

Asp Gln Ala Asp Gly Ser Arg
1 5

<210> SEQ ID NO 151
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 151

Asp Gln Phe Asp Ile Cys Ala Lys
1 5

<210> SEQ ID NO 152
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 152

Asp Gln Leu Trp Arg
1 5

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<210> SEQ ID NO 153
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 153

Asp Gln Val Ala Cys Leu Thr Phe Phe Lys
1 5 10

<210> SEQ ID NO 154
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 154

Asp Gln Val Asn Thr Val Gly Ile Pro Ile
1 5 10

<210> SEQ ID NO 155
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 155

Asp Ser Phe Ser Asp Pro Tyr Ala Ile Val Ser Phe Leu His Gln Ser
1 5 10 15

Gln Lys

<210> SEQ ID NO 156
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 156

Asp Ser Leu Leu Ala His Ser Ser Asp Pro Val Glu Met Arg
1 5 10

<210> SEQ ID NO 157
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 157

Asp Ser Leu Leu Ala His Ser Ser Asp Pro Val Glu Met Arg Arg
1 5 10 15

<210> SEQ ID NO 158
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 158

Asp Ser Tyr Leu Gly Tyr Ser Thr Glu Leu Ala Leu Trp Lys
1 5 10

<210> SEQ ID NO 159
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 159

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Asp Thr Gly Glu Ile Tyr Thr Thr Ser Val Thr Leu Asp Arg
1 5 10

<210> SEQ ID NO 160
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 160

Asp Thr Gly Glu Leu Asn Val Thr Ser Ile Leu Asp Arg
1 5 10

<210> SEQ ID NO 161
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 161

Asp Val Ile Pro Met Ala Asp Ala Ala Gly Ile Ile Arg
1 5 10

<210> SEQ ID NO 162
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 162

Asp Val Ser Ala Ile Met Asn Lys
1 5

<210> SEQ ID NO 163
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 163

Asp Val Val Val Ser Val Glu Tyr Ser Lys
1 5 10

<210> SEQ ID NO 164
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 164

Asp Trp Leu Gln Ala Asp Met Arg
1 5

<210> SEQ ID NO 165
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 165

Asp Tyr Val Leu His Met Pro Thr Leu Arg
1 5 10

<210> SEQ ID NO 166
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 166

Glu Ala Asp Leu Thr Glu Glu Thr Glu Glu Asn Leu Arg
1 5 10

<210> SEQ ID NO 167

<211> LENGTH: 24

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 167

Glu Ala Ser Val His Ile Gln Leu Glu Gly Arg Pro Ser Ile Leu Glu
1 5 10 15

Met Asp Glu Thr Ser Ala Leu Lys
20

<210> SEQ ID NO 168

<211> LENGTH: 21

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 168

Glu Asp Ala Gln Ile Asn Thr Thr Ile Gly Ser Val Thr Ala Gln Asp
1 5 10 15

Pro Asp Ala Ala Arg
20

<210> SEQ ID NO 169

<211> LENGTH: 15

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 169

Glu Asp Gly Tyr Ser Asp Ala Ser Gly Phe Gly Tyr Cys Phe Arg
1 5 10 15

<210> SEQ ID NO 170

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 170

Glu Asp Thr Gln Val Asp Ser Glu Ala Arg Pro Met Lys
1 5 10

<210> SEQ ID NO 171

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 171

Glu Glu Phe Val Ala Thr Thr Glu Ser Thr Thr Glu Thr Lys
1 5 10

<210> SEQ ID NO 172

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 172

Glu Glu Gly Val Phe Thr Val Thr Pro Asp Thr Lys
1 5 10

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<210> SEQ ID NO 173
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 173

Glu Glu His Glu Val Ala Val Leu Gly Ala Pro Pro Ser Thr Ile Leu
1 5 10 15

Pro Arg

<210> SEQ ID NO 174
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 174

Glu Glu His Ser Ser Tyr Thr Leu Thr Val Glu Ala Arg
1 5 10

<210> SEQ ID NO 175
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 175

Glu Glu Ile Gly Asn Leu Lys
1 5

<210> SEQ ID NO 176
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 176

Glu Glu Ile Asn Lys Pro Pro Ile Ala Lys
1 5 10

<210> SEQ ID NO 177
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 177

Glu Glu Ile Asn Gln Gly Gly Arg
1 5

<210> SEQ ID NO 178
<211> LENGTH: 28
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 178

Glu Glu Leu Gly Val Thr Val Tyr Gln Ser Pro His Ser Gly Ser Phe
1 5 10 15

Thr Ile Thr Gly Asn Asn Ser Asn Phe Ala Gln Arg
20 25

<210> SEQ ID NO 179
<211> LENGTH: 20
<212> TYPE: PRT

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<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 179

Glu Glu Met Ile Leu Leu Ala Asn Tyr Leu Asp Ser Met Tyr Ile Met
1 5 10 15
Leu Asn Ile Arg
20

<210> SEQ ID NO 180

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 180

Glu Glu Gln Ala Gln Arg
1 5

<210> SEQ ID NO 181

<211> LENGTH: 5

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 181

Glu Glu Arg Lys Arg
1 5

<210> SEQ ID NO 182

<211> LENGTH: 16

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 182

Glu Glu Thr Pro Phe Phe Leu Leu Thr Gly Tyr Ala Leu Asp Ala Arg
1 5 10 15

<210> SEQ ID NO 183

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 183

Glu Phe Ile Tyr Leu Arg Pro Phe Ala Cys Asp Thr Lys
1 5 10

<210> SEQ ID NO 184

<211> LENGTH: 19

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 184

Glu Phe Leu Ser Glu Ala Ser Ile Met Gly Gln Phe Glu His Pro Asn
1 5 10 15

Ile Ile Arg

<210> SEQ ID NO 185

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 185

Glu Phe Asn Gln Phe Ala Glu Gly Lys

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1 5

<210> SEQ ID NO 186
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 186

Glu Gly Ala Gln Tyr Leu Met Gln Ala Ala Gly Leu Gly Arg
1 5 10

<210> SEQ ID NO 187
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 187

Glu Gly Glu Asp Leu Ser Lys Lys
1 5

<210> SEQ ID NO 188
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 188

Glu Gly Leu Ala His Leu Ile Gln Ser Cys Gly Leu Gly Gly Met Arg
1 5 10 15

<210> SEQ ID NO 189
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 189

Glu Gly Pro Gly Glu Ala Ile Val Arg
1 5

<210> SEQ ID NO 190
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 190

Glu His Ala Leu Ala Gln Ala Glu Leu Leu Lys
1 5 10

<210> SEQ ID NO 191
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 191

Glu His Glu Glu Ala Glu Ser Gly Glu Gly Thr Arg
1 5 10

<210> SEQ ID NO 192
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 192

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Glu His Glu Glu Ala Glu Ser Gly Glu Gly Thr Arg Arg Arg
1 5 10

<210> SEQ ID NO 193
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 193

Glu His Glu Glu Tyr Leu Lys
1 5

<210> SEQ ID NO 194
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 194

Glu His Gln Pro Leu Pro Ile Gln Trp Lys
1 5 10

<210> SEQ ID NO 195
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 195

Glu His Ser Ser Thr Ala Asn Ile Ile Val Met Ser Leu Pro Val Ala
1 5 10 15

Arg

<210> SEQ ID NO 196
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 196

Glu His Ser Ser Trp Asp Leu Val Gly Leu Glu Lys
1 5 10

<210> SEQ ID NO 197
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 197

Glu Ile Ile Asp Glu Asn Phe Ala Glu Leu Lys
1 5 10

<210> SEQ ID NO 198
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 198

Glu Ile Pro Ser His His Pro Thr Asp Pro Val Glu Leu Arg
1 5 10

<210> SEQ ID NO 199
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 199

Glu	Ile	Pro	Ser	His	His	Pro	Thr	Asp	Pro	Val	Glu	Leu	Arg	Arg
1				5					10					15

<210> SEQ ID NO 200

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 200

Glu	Ile	Thr	Tyr	Gln	Gly	Thr	Arg
1				5			

<210> SEQ ID NO 201

<211> LENGTH: 18

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 201

Glu	Lys	Pro	Ala	Ile	His	His	Ile	Pro	Gly	Phe	Glu	Val	Gln	Glu	Thr
1				5					10						15

Ser Arg

<210> SEQ ID NO 202

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 202

Glu	Leu	Ala	Gln	Ser	Gln	Glu	Ala	Leu	Gln	Val	Glu	Gln	Arg
1				5					10				

<210> SEQ ID NO 203

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 203

Glu	Leu	Leu	Gly	Asn	Asn	Ile	Pro
1				5			

<210> SEQ ID NO 204

<211> LENGTH: 16

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 204

Glu	Leu	Asn	Asp	Ile	Ala	Ser	Lys	Pro	Ser	Gln	Glu	His	Ile	Phe	Lys
1				5						10					15

<210> SEQ ID NO 205

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 205

Glu	Leu	Asn	Ile	Leu	His	Glu	Met	Lys
1				5				

<210> SEQ ID NO 206

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<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 206

Glu Leu Pro Gly Glu Leu Leu Gly Tyr Arg
1 5 10

<210> SEQ ID NO 207
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 207

Glu Leu Thr Leu Pro Val Asp Ser Thr Thr Leu Asp Gly Ser Lys
1 5 10 15

<210> SEQ ID NO 208
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 208

Glu Leu Thr Tyr Ser Asn Phe His Pro Leu Leu Val Ser Gly Arg
1 5 10 15

<210> SEQ ID NO 209
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 209

Glu Leu Val His Ile Lys Pro Asp Gln Ser Asn Val Arg
1 5 10

<210> SEQ ID NO 210
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 210

Glu Met Met Glu Glu Ala Asn Gly Gln Ile Ala Pro Glu Asn Gly Thr
1 5 10 15

Gln Thr Pro Ser Pro Pro Ser Glu Lys
20 25

<210> SEQ ID NO 211
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 211

Glu Met Gln Asn Leu Ser Gln His Gly Arg
1 5 10

<210> SEQ ID NO 212
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 212

Glu Met Gln Asn Leu Ser Gln His Gly Arg Lys

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1 5 10

<210> SEQ ID NO 213
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 213

Glu Met Ser Ile Asp Gln Ala Lys
1 5

<210> SEQ ID NO 214
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 214

Glu Asn Gly Gly Ala Ser His Pro Leu Leu Asp Gln Arg
1 5 10

<210> SEQ ID NO 215
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 215

Glu Asn Pro Asp Asn Leu Ser Asp Phe Arg
1 5 10

<210> SEQ ID NO 216
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 216

Glu Pro Phe Glu Asp Gly Phe Ala Asn Gly Glu Glu Ser Thr Pro Thr
1 5 10 15

Arg

<210> SEQ ID NO 217
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 217

Glu Pro Ile Asp Leu Arg
1 5

<210> SEQ ID NO 218
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 218

Glu Pro Met Asp Gln Lys Arg
1 5

<210> SEQ ID NO 219
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 219

Glu	Gln	Phe	Gly	Gln	Asp	Gly	Pro	Ile	Ser	Val	His	Cys	Ser	Ala	Gly
1				5					10					15	

Val Gly Arg

<210> SEQ ID NO 220

<211> LENGTH: 19

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 220

Glu	Gln	Phe	Gly	Gln	Asp	Gly	Pro	Ile	Thr	Val	His	Cys	Ser	Ala	Gly
1				5					10					15	

Val Gly Arg

<210> SEQ ID NO 221

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 221

Glu	Gln	Thr	Pro	Leu	Phe	Leu	Ala	Ala	Arg
1				5					10

<210> SEQ ID NO 222

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 222

Glu	Arg	Pro	Pro	Asp	His	Gln	His	Ser	Ala	Gln	Val	Lys
1				5					10			

<210> SEQ ID NO 223

<211> LENGTH: 30

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 223

Glu	Ser	Phe	Leu	Ala	Pro	Ser	Ser	Gly	Val	Gln	Pro	Thr	Leu	Ala	Met
1				5					10					15	

Pro	Asn	Ile	Ala	Val	Gly	Gln	Asn	Val	Thr	Val	Thr	Glu	Arg
			20					25					30

<210> SEQ ID NO 224

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 224

Glu	Ser	His	Val	Ala	Met	His	Arg
1				5			

<210> SEQ ID NO 225

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 225

Glu Ser His Trp Ile Gly Leu Thr Asp Ser Glu Arg

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1 5 10

<210> SEQ ID NO 226
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 226

Glu Ser Pro Ala Gln Ala Pro Ala
1 5

<210> SEQ ID NO 227
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 227

Glu Ser Ser Pro Phe Leu Ser Pro Leu Glu Ala Ser Arg
1 5 10

<210> SEQ ID NO 228
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 228

Glu Thr Cys Val Asp Leu His Leu Pro Arg
1 5 10

<210> SEQ ID NO 229
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 229

Glu Thr Asp Ser Leu Ser Ala Gly Phe Val Val Val Met Gly Val Asp
1 5 10 15

Leu Ser Arg

<210> SEQ ID NO 230
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 230

Glu Thr Ile Glu Pro Ala Val Arg
1 5

<210> SEQ ID NO 231
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 231

Glu Thr Leu Gln Ser Glu Glu Gln Gln Arg
1 5 10

<210> SEQ ID NO 232
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 232

Glu Thr Leu Gln Ser Glu Glu Gln Gln Arg Arg
1 5 10

<210> SEQ ID NO 233

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 233

Glu Val Ile Thr Ile Tyr Ser
1 5

<210> SEQ ID NO 234

<211> LENGTH: 20

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 234

Glu Val Leu Ala Thr Pro Ser Leu Ser Ala Ser Phe Asn Ala Pro Leu
1 5 10 15

Leu Asp Thr Lys
20

<210> SEQ ID NO 235

<211> LENGTH: 18

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 235

Glu Val Pro Gly Tyr Ile Val Leu Phe Tyr Asn Met Ser Leu Asp Val
1 5 10 15

Asn Arg

<210> SEQ ID NO 236

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 236

Glu Val Pro Ile Tyr Ala Asn Arg
1 5

<210> SEQ ID NO 237

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 237

Glu Val Pro Pro Ala Val Ser Asp Ile Arg
1 5 10

<210> SEQ ID NO 238

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 238

Glu Val Pro Val Ala Ile Lys
1 5

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<210> SEQ ID NO 239
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 239

Glu Val Val Leu Leu Asp Phe Ala Ala Ala Gly Gly Glu Leu Gly Trp
1 5 10 15

Leu Thr His Pro Tyr Gly Lys
20

<210> SEQ ID NO 240
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 240

Glu Trp Gly Asp Gly Ile Arg
1 5

<210> SEQ ID NO 241
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 241

Glu Tyr Ser Ile Glu Glu Ile Glu Ala Gly Arg
1 5 10

<210> SEQ ID NO 242
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 242

Phe Ala Asp Ile Val Ser Ile Leu Asp Lys
1 5 10

<210> SEQ ID NO 243
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 243

Phe Ala Pro Gly Val Thr Ile Glu Glu Asp Asn Cys Cys Gly Cys Asn
1 5 10 15

Ala Ile Ala Ile Arg
20

<210> SEQ ID NO 244
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 244

Phe Ala Val Pro Thr Tyr Ala Ala Lys
1 5

<210> SEQ ID NO 245
<211> LENGTH: 19
<212> TYPE: PRT

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<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 245

Phe Cys Gln Ala Leu Gly Ala His Leu Ser Ser Phe Ser His Val Asp
1 5 10 15

Glu Ile Lys

<210> SEQ ID NO 246

<211> LENGTH: 15

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 246

Phe Asp Leu Ser Met Pro His Val Gln Asp Pro Ser Leu Val Arg
1 5 10 15

<210> SEQ ID NO 247

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 247

Phe Glu Gln Glu Tyr Leu Asn Asp Leu Met Lys
1 5 10

<210> SEQ ID NO 248

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 248

Phe Glu Gln Glu Tyr Leu Asn Asp Leu Met Lys Lys
1 5 10

<210> SEQ ID NO 249

<211> LENGTH: 15

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 249

Phe Glu Val Ile Glu Phe Asp Asp Gly Ala Gly Ser Val Leu Arg
1 5 10 15

<210> SEQ ID NO 250

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 250

Phe Phe Ala Ser Ile Gly Glu Arg
1 5

<210> SEQ ID NO 251

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 251

Phe Phe Pro Tyr Ala Asn Gly Thr Leu Gly Ile Arg
1 5 10

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<210> SEQ ID NO 252
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 252

Phe Gly Ala Ala Leu Thr Val Leu Gly Asp Val Asn Gly Asp Lys
1 5 10 15

<210> SEQ ID NO 253
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 253

Phe His Ile Leu Phe Lys
1 5

<210> SEQ ID NO 254
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 254

Phe His Leu Glu Tyr Arg
1 5

<210> SEQ ID NO 255
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 255

Phe Ile Lys Pro Trp Glu Ser Pro Asp Glu Met Glu Leu Asp Glu Leu
1 5 10 15

Leu Lys

<210> SEQ ID NO 256
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 256

Phe Leu Cys Glu Val Lys
1 5

<210> SEQ ID NO 257
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 257

Phe Leu Asp Asp Leu Gly Leu Lys
1 5

<210> SEQ ID NO 258
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 258

Phe Leu Glu Glu Asn Ser Ser Asp Pro Thr Tyr Thr Ser Ser Leu Gly

-continued

1	5	10	15
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Gly Lys

<210> SEQ ID NO 259
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 259

Phe	Leu	Asn	Leu	Thr	Ser	Glu	Lys
1			5				

<210> SEQ ID NO 260
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 260

Phe	Leu	Pro	Gly	Gly	Thr	Leu	Cys	Arg
1			5					

<210> SEQ ID NO 261
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 261

Phe	Met	Phe	Asp	Leu	Phe	Gln	Gln	Phe	Arg
1			5					10	

<210> SEQ ID NO 262
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 262

Phe	Met	Phe	Asp	Leu	Phe	Gln	Gln	Phe	Arg	Lys
1				5					10	

<210> SEQ ID NO 263
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 263

Phe	Pro	Gln	Val	Val	Ser	Ala	Leu	Asp	Lys
1				5					10

<210> SEQ ID NO 264
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 264

Phe	Pro	Ser	Gly	Thr	Leu	Arg
1				5		

<210> SEQ ID NO 265
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 265

Phe	Pro	Val	Thr	Phe	Gly	Glu	Glu	Cys	Leu	Tyr	Met	Ser	Ala	Lys
1				5					10					15

<210> SEQ ID NO 266

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 266

Phe	Gln	Gly	Ile	Tyr	Arg
1				5	

<210> SEQ ID NO 267

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 267

Phe	Gln	Leu	Ala	Ala	Arg
1				5	

<210> SEQ ID NO 268

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 268

Phe	Gln	Leu	Ser	Asn	Ser	Gly	Pro	Asn	Ser	Thr	Ile	Lys
1			5					10				

<210> SEQ ID NO 269

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 269

Phe	Gln	Thr	His	Phe	Thr	Phe	Glu	Glu	Phe	Arg
1				5					10	

<210> SEQ ID NO 270

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 270

Phe	Gln	Thr	His	Phe	Thr	Phe	Glu	Glu	Phe	Arg	Arg
1				5					10		

<210> SEQ ID NO 271

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 271

Phe	Gln	Val	Asp	Leu	Val	Ser	Glu	Asn	Ala	Gly	Arg
1				5					10		

<210> SEQ ID NO 272

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 272

Phe Ser Asp Val Thr Gly Lys
1 5

<210> SEQ ID NO 273

<211> LENGTH: 16

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 273

Phe Ser Phe Asp Asp Phe Leu Gly Ser Leu Gln Leu Asp Leu Asn Arg
1 5 10 15

<210> SEQ ID NO 274

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 274

Phe Ser Ser Tyr Glu Lys
1 5

<210> SEQ ID NO 275

<211> LENGTH: 15

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 275

Phe Thr Leu Thr Gly Leu Lys Pro Asp Thr Thr Tyr Asp Ile Lys
1 5 10 15

<210> SEQ ID NO 276

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 276

Phe Thr Met Leu Glu Cys Leu Ser Leu Pro Arg
1 5 10

<210> SEQ ID NO 277

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 277

Phe Thr Gln Asp Thr Phe Arg
1 5

<210> SEQ ID NO 278

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 278

Phe Thr Thr Glu Ile His Pro Ser Cys Val Thr Arg
1 5 10

<210> SEQ ID NO 279

<211> LENGTH: 9

<212> TYPE: PRT

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<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 279

Phe Val Trp Asn Gly His Leu Leu Arg
1 5

<210> SEQ ID NO 280

<211> LENGTH: 19

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 280

Phe Tyr Gln Thr Ser Val Glu Ser Thr Asp Phe Ala Asn Ala Pro Glu
1 5 10 15

Glu Ser Arg

<210> SEQ ID NO 281

<211> LENGTH: 21

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 281

Phe Tyr Gln Thr Ser Val Glu Ser Thr Asp Phe Ala Asn Ala Pro Glu
1 5 10 15

Glu Ser Arg Lys Lys
20

<210> SEQ ID NO 282

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 282

Gly Ala Glu Ala Phe Glu Ile Ala Leu Pro Arg
1 5 10

<210> SEQ ID NO 283

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 283

Gly Ala Leu Ala Asp Asn Leu Leu Arg
1 5

<210> SEQ ID NO 284

<211> LENGTH: 21

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 284

Gly Ala Leu Ile Leu Ser Asn Val Gln Pro Ser Asp Thr Met Val Thr
1 5 10 15

Gln Cys Glu Ala Arg
20

<210> SEQ ID NO 285

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 285

Gly Ala Asn Thr His Leu Ser Thr Phe Ser Phe Thr Lys
1 5 10

<210> SEQ ID NO 286

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 286

Gly Ala Pro Cys Thr Thr Pro Pro Ser Ala Pro Arg
1 5 10

<210> SEQ ID NO 287

<211> LENGTH: 21

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 287

Gly Ala Val Tyr Leu Phe His Gly Val Leu Gly Pro Ser Ile Ser Pro
1 5 10 15

Ser His Ser Gln Arg
20

<210> SEQ ID NO 288

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 288

Gly Asp Ser Asn Ser Tyr Asn Val Arg Arg
1 5 10

<210> SEQ ID NO 289

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 289

Gly Glu Gly Asn Glu Thr Thr Asn Met Val Ile Thr Trp Lys Pro Leu
1 5 10 15

Arg

<210> SEQ ID NO 290

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 290

Gly Glu Gly Pro Glu Ala Gly Ala Gly Gly Ala Gly Gly Arg
1 5 10

<210> SEQ ID NO 291

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 291

Gly Glu Gly Val Ala Tyr Arg
1 5

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<210> SEQ ID NO 292
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 292

Gly Glu Pro Gly Pro Pro Gly Pro Ala Gly Glu Arg
1 5 10

<210> SEQ ID NO 293
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 293

Gly Glu Thr Tyr Thr Tyr Asp Trp Gln Leu Ile Thr His Pro Arg
1 5 10 15

<210> SEQ ID NO 294
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 294

Gly Phe Phe Gly Tyr Lys
1 5

<210> SEQ ID NO 295
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 295

Gly Phe Pro Thr Ile Asp Met Gly Pro Gln Leu Lys
1 5 10

<210> SEQ ID NO 296
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 296

Gly Gly Ala Gln Ile Thr Phe Leu Ala Thr Phe Asp Val Ser Pro Lys
1 5 10 15

<210> SEQ ID NO 297
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 297

Gly Gly Cys Ile Thr Leu Ile Ser Ser Glu Gly Tyr Val Ser Ser Lys
1 5 10 15

<210> SEQ ID NO 298
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 298

Gly Gly Gly Ala Tyr Tyr Leu Ile Ser Arg
1 5 10

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<210> SEQ ID NO 299
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 299

Gly Gly Gln Val Ser Val Cys Pro Leu Pro Arg
1 5 10

<210> SEQ ID NO 300
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 300

Gly Ile Asp Tyr Tyr Asp Arg
1 5

<210> SEQ ID NO 301
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 301

Gly Ile Thr Glu Pro Pro Phe Gly Ile Phe Val Phe Asn Lys
1 5 10

<210> SEQ ID NO 302
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 302

Gly Leu Pro Ser Leu Thr Ser Val Ser Trp Asn Ile Ser Val Pro Arg
1 5 10 15

<210> SEQ ID NO 303
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 303

Gly Asn Leu Ser Phe Gly Trp Val Arg
1 5

<210> SEQ ID NO 304
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 304

Gly Asn Asn Val Glu Lys Pro Leu Glu Leu Arg
1 5 10

<210> SEQ ID NO 305
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 305

Gly Asn Ser Ala Gly Gly Leu Gln His Arg

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1 5 10

<210> SEQ ID NO 306
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 306

Gly Pro Gly Pro Tyr Ser Pro Ser Val Gln Phe Arg
1 5 10

<210> SEQ ID NO 307
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 307

Gly Pro Ile Val Pro Leu Asn Val Ala Asp Gln Lys
1 5 10

<210> SEQ ID NO 308
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 308

Gly Pro Pro Ser Glu Ala Val Arg
1 5

<210> SEQ ID NO 309
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 309

Gly Pro Pro Ser Glu Pro Val Leu Thr Gln Thr Ser Glu Gln Ala Pro
1 5 10 15

Ser Ser Ala Pro Arg
20

<210> SEQ ID NO 310
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 310

Gly Pro Arg Pro Asn Pro Ala Ile Met Arg
1 5 10

<210> SEQ ID NO 311
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 311

Gly Gln Ile Ile Gly Asn Phe Gln Ala Phe Asp Glu Asp Thr Gly Leu
1 5 10 15

Pro Ala His Ala Arg
20

<210> SEQ ID NO 312

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<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 312

Gly Gln Leu Ser Phe Asn Leu Arg
1 5

<210> SEQ ID NO 313
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 313

Gly Gln Val Val Thr Val His Leu Gln Thr Ser Leu Glu Asn Gly Thr
1 5 10 15

Arg

<210> SEQ ID NO 314
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 314

Gly Ser Glu Lys Pro Leu Glu Gln Thr Phe Ala Thr Met Val Ser Ser
1 5 10 15

Leu Gly Ser Gly Met Met Arg
20

<210> SEQ ID NO 315
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 315

Gly Ser Gly Pro Leu Ser Pro Ser Ile Gln Ser Arg
1 5 10

<210> SEQ ID NO 316
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 316

Gly Ser Ile Pro Val Phe Trp Ser Gln Arg Pro Asn Leu Lys
1 5 10

<210> SEQ ID NO 317
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 317

Gly Ser Pro Gly Lys Pro Gly Pro Gln Gly Ser Ser Gly Asp Pro Gly
1 5 10 15

Pro Pro Gly Pro Pro Gly Lys
20

<210> SEQ ID NO 318
<211> LENGTH: 25
<212> TYPE: PRT

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<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 318

Gly	Ser	Pro	Gln	Leu	Asp	Cys	Gly	Pro	Pro	Ala	Leu	Gln	Glu	Met	Pro
1				5					10				15		

Ile	Asn	Gln	Gly	Gly	Glu	Gly	Lys	Lys
			20				25	

<210> SEQ ID NO 319

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 319

Gly	Ser	Gln	Gly	Pro	Pro	Gly	Pro	Thr	Gly	Asn	Lys
1				5				10			

<210> SEQ ID NO 320

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 320

Gly	Ser	Gln	Pro	Ser	Gly	Glu	Leu	Leu	Ala	Ser	Phe	Glu	Leu	Ile	Gln
1				5					10					15	

Arg

<210> SEQ ID NO 321

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 321

Gly	Ser	Ser	Ala	Gly	Gly	Leu	Gln	His	Leu	Val	Ser	Ile	Arg
1				5					10				

<210> SEQ ID NO 322

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 322

Gly	Ser	Ser	Ser	Ala	Ser	Ile	Val	Lys
1				5				

<210> SEQ ID NO 323

<211> LENGTH: 18

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 323

Gly	Ser	Val	Thr	Phe	His	Cys	Ala	Leu	Gly	Pro	Glu	Val	Ala	Asn	Val
1				5					10					15	

Ala Lys

<210> SEQ ID NO 324

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 324

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Gly Thr Thr Tyr Ile Phe Arg
1 5

<210> SEQ ID NO 325
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 325

Gly Val Glu Gly Ser Asp Tyr Ile Asn Ala Ser Phe Ile Asp Gly Tyr
1 5 10 15

Arg

<210> SEQ ID NO 326
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 326

Gly Val Glu Gly Ser Asp Tyr Ile Asn Ala Ser Phe Leu Asp Gly Tyr
1 5 10 15

Arg

<210> SEQ ID NO 327
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 327

Gly Val Gln Ser Leu Val Leu Gly Ala Pro Arg
1 5 10

<210> SEQ ID NO 328
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 328

Gly Trp His Phe Tyr Asp Asp Arg
1 5

<210> SEQ ID NO 329
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 329

Gly Trp Met Ile Gly Phe Glu Glu His Lys
1 5 10

<210> SEQ ID NO 330
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 330

Gly Tyr Asn Val Thr Tyr Trp Arg
1 5

<210> SEQ ID NO 331

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<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 331

Gly Tyr Gln Val Thr Tyr Val Arg
1 5

<210> SEQ ID NO 332
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 332

His Phe Asp Ser Gln Val Ile Ile Tyr Gly Lys
1 5 10

<210> SEQ ID NO 333
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 333

His Phe Val Ser Leu Cys Gln Lys
1 5

<210> SEQ ID NO 334
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 334

His Gly Leu Pro Ser Ala Asp Ala Pro Ser Leu Lys
1 5 10

<210> SEQ ID NO 335
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 335

His Gly Gln Tyr Leu Ile Gly His Gly Thr Lys
1 5 10

<210> SEQ ID NO 336
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 336

His Ile Trp Pro Asn Val Pro Asp Pro Ser Lys
1 5 10

<210> SEQ ID NO 337
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 337

His Leu Pro Glu Thr Glu Ala Gly Arg
1 5

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<210> SEQ ID NO 338
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 338

His Met Ala Thr Thr Gln Asp Glu Val His Thr Lys
1 5 10

<210> SEQ ID NO 339
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 339

His Met Trp Pro Phe Ile Cys Gln Phe Ile Glu Lys
1 5 10

<210> SEQ ID NO 340
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 340

His Asn Ser Val Val Leu Gly Trp Pro Tyr Gly Trp Arg
1 5 10

<210> SEQ ID NO 341
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 341

His Asn Thr Asp Ala Gly Leu Leu Thr Thr Val Gly Ser Leu Leu Pro
1 5 10 15
Gly Ile Thr Tyr Ser Leu Arg
20

<210> SEQ ID NO 342
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 342

His Gln Met Ala Val Lys
1 5

<210> SEQ ID NO 343
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 343

His Gln Val Val His Lys
1 5

<210> SEQ ID NO 344
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 344

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His Ser His Thr Asn Leu Ser Ile Ser Thr Gly Val Thr Lys
1 5 10

<210> SEQ ID NO 345
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 345

His Val Glu Met Tyr Gln Trp Val Glu Thr Glu Glu Ser Arg
1 5 10

<210> SEQ ID NO 346
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 346

His Val Ser Pro Val Thr Pro Pro Arg
1 5

<210> SEQ ID NO 347
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 347

His Val Val Asp Gly Ile Ser Arg
1 5

<210> SEQ ID NO 348
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 348

His Trp Val Pro Ala Glu Lys
1 5

<210> SEQ ID NO 349
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 349

Ile Ala Asp Phe Gly Leu Ala Arg
1 5

<210> SEQ ID NO 350
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 350

Ile Ala Gly Ser Gln Leu Ser Ser Arg
1 5

<210> SEQ ID NO 351
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 351

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Ile Ala Pro Cys Tyr Gln Asp Tyr Val Lys
1 5 10

<210> SEQ ID NO 352
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 352

Ile Ala Pro Pro Ala Ser Asp Phe Leu Ala His Ile Gln Lys
1 5 10

<210> SEQ ID NO 353
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 353

Ile Asp Ala Thr Val Val Arg
1 5

<210> SEQ ID NO 354
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 354

Ile Asp Phe Ser Asp Ile Met Val Leu Gly Asp Ile Asn Thr Lys Pro
1 5 10 15

Lys

<210> SEQ ID NO 355
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 355

Ile Asp Phe Ser Asp Ile Met Val Leu Gly Asp Ile Asn Thr Lys Pro
1 5 10 15

Lys Lys

<210> SEQ ID NO 356
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 356

Ile Asp His Asp Arg Arg
1 5

<210> SEQ ID NO 357
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 357

Ile Asp His Tyr Arg
1 5

<210> SEQ ID NO 358

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<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 358

Ile Asp Ser Leu Glu Asp Gln Ile Glu Glu Phe Ser Lys
1 5 10

<210> SEQ ID NO 359
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 359

Ile Asp Thr Ile Ala Pro Asp Glu Ile Thr Val Ser Ser Asp Phe Glu
1 5 10 15

Ala Arg

<210> SEQ ID NO 360
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 360

Ile Glu Glu Val Ile Gly Ala Gly Glu Phe Gly Glu Val Cys Arg
1 5 10 15

<210> SEQ ID NO 361
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 361

Ile Glu Gly Leu Gln Ile Ser Lys
1 5

<210> SEQ ID NO 362
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 362

Ile Glu Met Val Asp Tyr Lys
1 5

<210> SEQ ID NO 363
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 363

Ile Glu Thr Gln Asn Gln Leu Leu Gly Ile Ala Asp Arg
1 5 10

<210> SEQ ID NO 364
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 364

Ile Phe Thr Val Ala Gln Met Asp Asp Asn Ser Ile Gln Met Lys
1 5 10 15

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<210> SEQ ID NO 365
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 365

Ile Phe Thr Val Ala Gln Met Asp Asp Asn Ser Ile Gln Met Lys Lys
1 5 10 15

<210> SEQ ID NO 366
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 366

Ile Gly Asp Asp Asn Glu Asn Leu Thr Phe Lys
1 5 10

<210> SEQ ID NO 367
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 367

Ile Gly Glu Thr Val Val Asp Leu Glu Asn Arg
1 5 10

<210> SEQ ID NO 368
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 368

Ile His Phe Ile Glu Ala Gln Asp Leu Gln Gly Lys
1 5 10

<210> SEQ ID NO 369
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 369

Ile His Ser Asp Leu Ala Glu Glu Arg
1 5

<210> SEQ ID NO 370
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 370

Ile Ile Asp Trp Asp Arg
1 5

<210> SEQ ID NO 371
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 371

Ile Ile Glu Gly Glu Pro Asn Leu Lys

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1 5

<210> SEQ ID NO 372
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 372

Ile Ile Met Tyr Glu Leu Val Tyr Trp Ala Ala Glu Asp Glu Asp Gln
1 5 10 15

Gln His Lys

<210> SEQ ID NO 373
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 373

Ile Leu Ala Ser Val Gln His Met Lys
1 5

<210> SEQ ID NO 374
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 374

Ile Leu Asp Ala Thr Asp Gln Glu Ser Leu Glu Leu Lys Pro Thr Ser
1 5 10 15

Arg

<210> SEQ ID NO 375
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 375

Ile Leu Asp Glu Ser Glu Asp Thr Asp Leu Pro Tyr Pro Pro Pro Gln
1 5 10 15

Arg

<210> SEQ ID NO 376
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 376

Ile Leu Glu Leu Glu Glu Lys
1 5

<210> SEQ ID NO 377
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 377

Ile Leu Leu Asn Pro Gln Asp Lys
1 5

<210> SEQ ID NO 378

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<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 378

Ile Leu Tyr Asn Gly Gln Ser Val Glu Val Asp Gly His Ser Met Arg
1 5 10 15

<210> SEQ ID NO 379
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 379

Ile Leu Tyr Asn Gly Gln Ser Val Glu Val Asp Gly His Ser Met Arg
1 5 10 15

Lys

<210> SEQ ID NO 380
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 380

Ile Met Phe Val Asp Pro Ser Leu Thr Val Arg
1 5 10

<210> SEQ ID NO 381
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 381

Ile Asn Ala Thr Asp Ala Asp Glu Pro Asn Thr Leu Asn Ser Lys
1 5 10 15

<210> SEQ ID NO 382
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 382

Ile Asn Gly Ile Pro Val Glu Glu Leu Ala Lys
1 5 10

<210> SEQ ID NO 383
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 383

Ile Asn His Leu Ile Phe Arg
1 5

<210> SEQ ID NO 384
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 384

Ile Asn Ser Trp Val Glu Ser Gln Thr Asn Glu Lys
1 5 10

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<210> SEQ ID NO 385
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 385

Ile Pro Glu Asn Phe Phe Glu Glu Glu Ser Arg
1 5 10

<210> SEQ ID NO 386
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 386

Ile Pro Asn Pro His Leu Gly Pro Val Glu Glu Arg
1 5 10

<210> SEQ ID NO 387
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 387

Ile Gln Asp Leu Leu Ala Glu Gly Thr Ile Thr Gly Val Ile Asp Asp
1 5 10 15

Arg

<210> SEQ ID NO 388
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 388

Ile Gln Leu Ser Trp Leu Leu Pro Pro Gln Glu Arg
1 5 10

<210> SEQ ID NO 389
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 389

Ile Gln Met Thr Trp Thr Arg
1 5

<210> SEQ ID NO 390
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 390

Ile Gln Asn Ser Ser Cys Thr Ser Leu Glu His Cys Phe Arg Lys
1 5 10 15

<210> SEQ ID NO 391
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 391

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Ile Gln Pro Tyr Thr Glu Gln Ser Thr Lys
1 5 10

<210> SEQ ID NO 392
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 392

Ile Ser Glu Trp Pro Ile Asp Asp His Phe Thr Tyr Ser Arg
1 5 10

<210> SEQ ID NO 393
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 393

Ile Ser Ser Asn Pro Asn Pro Val Val Gln Met Ser Val Gly His Lys
1 5 10 15

<210> SEQ ID NO 394
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 394

Ile Ser Val Thr Val Ser Glu Thr Phe Asp Pro Glu Glu Lys
1 5 10

<210> SEQ ID NO 395
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 395

Ile Thr Asp Asn Glu Leu Glu Leu Tyr Lys
1 5 10

<210> SEQ ID NO 396
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 396

Ile Thr Gln Leu Gly Gln Ser Ala Glu Asp Leu Gln Gly Ser Arg
1 5 10 15

<210> SEQ ID NO 397
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 397

Ile Thr Gln Leu Gly Gln Ser Ala Glu Asp Leu Gln Gly Ser Arg Arg
1 5 10 15

<210> SEQ ID NO 398
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 398

Ile	Thr	Val	Pro	Leu	Val	Ser	Glu	Val	Gln	Ile	Ala	Gln	Leu	Arg
1				5					10					15

<210> SEQ ID NO 399

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 399

Ile	Thr	Trp	Met	Lys	Lys
1				5	

<210> SEQ ID NO 400

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 400

Ile	Val	Ala	Ile	Ser	Glu	Asp	Tyr	Pro	Arg
1				5					10

<210> SEQ ID NO 401

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 401

Ile	Val	Phe	Thr	Pro	Thr	Ile	Cys	Lys
1				5				

<210> SEQ ID NO 402

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 402

Ile	Val	Val	Glu	Asp	Val	Asp	Glu	Pro	Pro	Val	Phe	Ser	Lys
1				5									10

<210> SEQ ID NO 403

<211> LENGTH: 15

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 403

Ile	Tyr	Pro	Leu	Pro	Glu	Asp	Pro	Ala	Ile	Pro	Met	Pro	Pro	Arg
1				5					10					15

<210> SEQ ID NO 404

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 404

Ile	Tyr	Val	Val	Asp	Leu	Ser	Asn	Glu	Arg
1				5					10

<210> SEQ ID NO 405

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 405

Lys Ala Ala Glu Leu Asp Arg
1 5

<210> SEQ ID NO 406

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 406

Lys Ala Ala Glu Leu Asp Arg Arg
1 5

<210> SEQ ID NO 407

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 407

Lys Ala Glu Ser Pro Pro Arg
1 5

<210> SEQ ID NO 408

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 408

Lys Asp Trp Leu Gln Ala Asp Met Arg
1 5

<210> SEQ ID NO 409

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 409

Lys Glu Gly Asp Ser Leu Asp Tyr Lys
1 5

<210> SEQ ID NO 410

<211> LENGTH: 15

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 410

Lys Glu Asn Ile Ile Ala Phe Glu Glu Ile Ile Glu Pro Tyr Arg
1 5 10 15

<210> SEQ ID NO 411

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 411

Lys Glu Asn Ile Thr Tyr Met Lys
1 5

<210> SEQ ID NO 412

<211> LENGTH: 9

<212> TYPE: PRT

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<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 412

Lys Glu Asn Ile Thr Tyr Met Lys Arg
1 5

<210> SEQ ID NO 413

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 413

Lys Glu Ser Cys Val Ala Ile Lys
1 5

<210> SEQ ID NO 414

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 414

Lys Glu Val Pro Val Ala Ile Lys
1 5

<210> SEQ ID NO 415

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 415

Lys Phe Val Pro Gly Cys Phe Val Cys Leu Glu Ser Arg
1 5 10

<210> SEQ ID NO 416

<211> LENGTH: 21

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 416

Lys Phe Tyr Gln Thr Ser Val Glu Ser Thr Asp Phe Ala Asn Ala Pro
1 5 10 15

Glu Glu Ser Arg Lys
20

<210> SEQ ID NO 417

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 417

Lys Gly Asp Ser Asn Ser Tyr Asn Val Arg
1 5 10

<210> SEQ ID NO 418

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 418

Lys Gly Asp Ser Asn Ser Tyr Asn Val Arg Arg
1 5 10

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<210> SEQ ID NO 419
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 419

Lys Gly Phe Gly Gly Thr Ala Gly Met Ala Phe Val Gly Thr Val Cys
1 5 10 15

Ser Arg

<210> SEQ ID NO 420
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 420

Lys Ile Asn Ser Trp Val Glu Ser Gln Thr Asn Glu Lys
1 5 10

<210> SEQ ID NO 421
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 421

Lys Lys Glu Asn Ile Thr Tyr Met Lys
1 5

<210> SEQ ID NO 422
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 422

Lys Lys Gly Asp Ser Asn Ser Tyr Asn Val Arg
1 5 10

<210> SEQ ID NO 423
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 423

Lys Leu Gly Asp Gln Thr Gly Lys
1 5

<210> SEQ ID NO 424
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 424

Lys Leu Ile Ala Asp Leu Gln Pro Asn Thr Glu Tyr Ser Phe Val Leu
1 5 10 15

Met Asn Arg

<210> SEQ ID NO 425
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 425

Lys Leu Pro Gln Gly Glu Ser Arg
1 5

<210> SEQ ID NO 426

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 426

Lys Leu Pro Ser Arg Pro Pro Pro His Tyr Pro Gly Ile Lys
1 5 10

<210> SEQ ID NO 427

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 427

Lys Met Leu Gly Asn Pro Ser Arg
1 5

<210> SEQ ID NO 428

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 428

Lys Asn Gly Tyr Asn Arg
1 5

<210> SEQ ID NO 429

<211> LENGTH: 15

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 429

Lys Asn Leu Val Asp Pro Phe Val Glu Val Ser Phe Ala Gly Lys
1 5 10 15

<210> SEQ ID NO 430

<211> LENGTH: 18

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 430

Lys Asn Pro Asn Phe Asp Ile Cys Thr Leu Phe Met Glu Val Met Leu
1 5 10 15

Pro Arg

<210> SEQ ID NO 431

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 431

Lys Pro Phe Pro Glu Asp Leu Lys
1 5

<210> SEQ ID NO 432

<211> LENGTH: 19

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<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 432

Lys Pro Leu Met Val Ile His His Leu Glu Asp Cys Gln Tyr Ser Gln
1 5 10 15

Ala Leu Lys

<210> SEQ ID NO 433
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 433

Lys Gln Asn Ala Tyr Ile Ala Thr Gln Gly Pro Leu Pro Glu Thr Met
1 5 10 15

Gly Asp Phe Trp Arg
20

<210> SEQ ID NO 434
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 434

Lys Arg Ala Glu Ser Asp Ser Arg
1 5

<210> SEQ ID NO 435
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 435

Lys Ser Asp Leu Asp Thr Ser Lys Pro Leu Ser Glu Lys Pro Ile Thr
1 5 10 15

His Lys

<210> SEQ ID NO 436
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 436

Lys Thr Asp Ala Phe Arg Arg
1 5

<210> SEQ ID NO 437
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 437

Lys Thr Glu Glu Lys Lys
1 5

<210> SEQ ID NO 438
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 438

Lys	Thr	Met	Leu	His	Leu	Thr	Asp	Ile	Gln	Leu	Gln	Asp	Asn	Lys
1				5					10					15

<210> SEQ ID NO 439

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 439

Lys	Val	Glu	Cys	Glu	His	Gly	Phe	Gly	Arg
1			5					10	

<210> SEQ ID NO 440

<211> LENGTH: 16

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 440

Lys	Val	Phe	Ala	Gln	Asn	Glu	Glu	Ile	Gln	Glu	Met	Ala	Gln	Asn	Lys
1				5					10					15	

<210> SEQ ID NO 441

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 441

Lys	Val	His	Gly	Leu	Tyr	Arg
1				5		

<210> SEQ ID NO 442

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 442

Lys	Tyr	Phe	Trp	Thr	Gly	Leu	Arg
1						5	

<210> SEQ ID NO 443

<211> LENGTH: 5

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 443

Lys	Tyr	Trp	Cys	Arg
1			5	

<210> SEQ ID NO 444

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 444

Leu	Ala	Thr	Glu	Glu	Pro	Pro	Pro	Arg
1				5				

<210> SEQ ID NO 445

<211> LENGTH: 16

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

-continued

<400> SEQUENCE: 445

Leu	Asp	Cys	Gln	Val	Gln	Gly	Arg	Pro	Gln	Pro	Glu	Val	Thr	Trp	Arg
1				5					10					15	

<210> SEQ ID NO 446

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 446

Leu	Asp	Glu	Asp	Leu	His	Val	Lys
1				5			

<210> SEQ ID NO 447

<211> LENGTH: 5

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 447

Leu	Asp	His	Tyr	Arg
1				5

<210> SEQ ID NO 448

<211> LENGTH: 16

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 448

Leu	Asp	Thr	Glu	Val	Ala	Asn	Leu	Ser	Val	Ile	Met	Glu	Glu	Met	Lys
1				5					10					15	

<210> SEQ ID NO 449

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 449

Leu	Glu	Asp	Pro	His	Val	Asp	Ile	Ile	Arg
1				5					10

<210> SEQ ID NO 450

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 450

Leu	Glu	Glu	Glu	Gln	Lys
1				5	

<210> SEQ ID NO 451

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 451

Leu	Glu	Glu	Gly	Pro	Pro	His	Thr	Lys
1						5		

<210> SEQ ID NO 452

<211> LENGTH: 11

<212> TYPE: PRT

-continued

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 452

Leu Glu Glu Gly Gln Ala Thr Ser Trp Ser Arg
1 5 10

<210> SEQ ID NO 453

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 453

Leu Glu Glu Gln Asp Glu Phe Glu Lys
1 5

<210> SEQ ID NO 454

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 454

Leu Glu Gly Val Ile Ser Lys
1 5

<210> SEQ ID NO 455

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 455

Leu Glu Asn Gly Glu Pro Arg
1 5

<210> SEQ ID NO 456

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 456

Leu Glu Thr Ala Asp Leu Lys
1 5

<210> SEQ ID NO 457

<211> LENGTH: 15

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 457

Leu Glu Trp Leu Thr Leu Met Pro Asn Ala Ser Asn Leu Asp Lys
1 5 10 15

<210> SEQ ID NO 458

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 458

Leu Phe His Ala Ser Tyr Gly Ala Arg
1 5

<210> SEQ ID NO 459

<211> LENGTH: 10

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<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 459

Leu Phe His Ala Ser Tyr Gly Ala Arg Arg
1 5 10

<210> SEQ ID NO 460
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 460

Leu Phe His Leu His Ser Gln Lys
1 5

<210> SEQ ID NO 461
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 461

Leu Gly Asp Gln Thr Gly Lys Lys
1 5

<210> SEQ ID NO 462
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 462

Leu Gly Gln Val Pro Pro Gly Glu Ser Val Thr Ala Met Glu Leu Glu
1 5 10 15

Phe Lys

<210> SEQ ID NO 463
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 463

Leu Gly Thr Ala Met Ser His Glu Ile Arg
1 5 10

<210> SEQ ID NO 464
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 464

Leu Gly Val Leu His Val Gly Gln Lys
1 5

<210> SEQ ID NO 465
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 465

Leu His Glu Asp Asp Lys
1 5

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<210> SEQ ID NO 466
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 466

Leu His Ile Thr Pro Glu Lys
1 5

<210> SEQ ID NO 467
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 467

Leu Ile Ala Asp Leu Gln Pro Asn Thr Glu Tyr Ser Phe Val Leu Met
1 5 10 15

Asn Arg

<210> SEQ ID NO 468
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 468

Leu Leu Gln Glu Ala Tyr Met Thr Pro Lys
1 5 10

<210> SEQ ID NO 469
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 469

Leu Leu Ser Asp Lys Pro Gln Asp Phe Gln Ile Arg
1 5 10

<210> SEQ ID NO 470
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 470

Leu Met Glu Trp Thr Ser Leu Gln Asn Met Arg
1 5 10

<210> SEQ ID NO 471
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 471

Leu Asn Glu Leu Leu Lys
1 5

<210> SEQ ID NO 472
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 472

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Leu Asn Glu Val Ile Val Thr Arg
1 5

<210> SEQ ID NO 473
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 473

Leu Asn Gly Ser Ser Leu His Leu Glu Trp Ser Ala Pro Leu Glu Ser
1 5 10 15

Gly Gly Arg

<210> SEQ ID NO 474
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 474

Leu Asn Val Glu Glu Arg
1 5

<210> SEQ ID NO 475
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 475

Leu Asn Tyr Gln Thr Pro Gly Met Arg
1 5

<210> SEQ ID NO 476
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 476

Leu Pro Asp Phe Glu Ser Arg
1 5

<210> SEQ ID NO 477
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 477

Leu Pro Gly Gly Gln Trp Ile Tyr Met Ser Asp Asn Tyr Thr Asp Val
1 5 10 15

Asn Gly Glu Lys
20

<210> SEQ ID NO 478
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 478

Leu Pro Gly His Gln Lys Arg
1 5

<210> SEQ ID NO 479

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<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 479

Leu Pro Pro Pro Pro Asp Cys Pro Thr Ser Leu His Gln Leu Met Leu
1 5 10 15

Asp Cys Trp Gln Lys
20

<210> SEQ ID NO 480
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 480

Leu Pro Gln Gly Glu Ser Arg
1 5

<210> SEQ ID NO 481
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 481

Leu Pro Ser Thr Ser Gly Ser Glu Gly Val Pro Phe Arg
1 5 10

<210> SEQ ID NO 482
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 482

Leu Pro Thr Gly Gly Cys Tyr Gly Val Pro Pro Asp Leu Arg
1 5 10

<210> SEQ ID NO 483
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 483

Leu Pro Thr Pro Met Asp Cys Pro Ser Ala Ile Tyr Gln Leu Met Met
1 5 10 15

Gln Cys Trp Gln Gln Glu Arg
20

<210> SEQ ID NO 484
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 484

Leu Pro Val Gly Leu Tyr Phe Ile Lys
1 5

<210> SEQ ID NO 485
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 485

Leu Gln Ala Ser Gly Asp Ala Leu Val Asp Arg
1 5 10

<210> SEQ ID NO 486

<211> LENGTH: 22

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 486

Leu Ser Leu Leu Glu Glu Pro Gly Asn Gly Thr Phe Thr Val Ile Leu
1 5 10 15

Asn Gln Leu Thr Ser Arg
 20

<210> SEQ ID NO 487

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 487

Leu Ser Leu Val Leu Val Pro Ala Gln Lys
1 5 10

<210> SEQ ID NO 488

<211> LENGTH: 16

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 488

Leu Ser Asn Thr Ser Pro Glu Phe Gln Glu Met Ser Leu Leu Glu Arg
1 5 10 15

<210> SEQ ID NO 489

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 489

Leu Ser Pro Tyr Val His Tyr Thr Phe Arg
1 5 10

<210> SEQ ID NO 490

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 490

Leu Ser Gln Cys His Glu Leu Trp Glu Arg
1 5 10

<210> SEQ ID NO 491

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 491

Leu Ser Val Phe Ala Glu Thr Tyr Glu Asn Glu Thr Lys
1 5 10

<210> SEQ ID NO 492

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<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 492

Leu Ser Val Leu Glu Glu Glu Gln Leu Pro Pro Gly Phe Pro Ser Ile
1 5 10 15

Asp Met Gly Pro Gln Leu Lys
20

<210> SEQ ID NO 493
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 493

Leu Ser Trp Tyr Asp Pro Asp Phe Gln Ala Arg
1 5 10

<210> SEQ ID NO 494
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 494

Leu Thr Ala Asp Leu Ser Leu Asp Thr Leu Asp Ala Arg
1 5 10

<210> SEQ ID NO 495
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 495

Leu Thr Ala Val Glu Ser Asp Leu Lys
1 5

<210> SEQ ID NO 496
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 496

Leu Thr Asp Val Val Ile Gly Ala Pro Gly Glu Glu Glu Asn Arg
1 5 10 15

<210> SEQ ID NO 497
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 497

Leu Thr Pro Gly Leu Tyr Glu Phe Lys
1 5

<210> SEQ ID NO 498
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 498

Leu Thr Gln Ile Glu Thr Gly Glu Asn Val Thr Gly Met Glu Leu Glu

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1	5	10	15
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Phe Lys

<210> SEQ ID NO 499
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 499

Leu	Thr	Tyr	Ser	Ser	Arg
1			5		

<210> SEQ ID NO 500
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 500

Leu	Val	His	Ile	Ile	Gly	Ala	Leu	Arg
1			5					

<210> SEQ ID NO 501
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 501

Leu	Val	Leu	Leu	Asn	Met	Pro	Gly	Pro	Pro	Arg
1			5					10		

<210> SEQ ID NO 502
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 502

Leu	Val	Leu	Ser	Asp	Leu	His	Leu	Leu	Thr	Gln	Ser	Gln	Val	Arg
1			5					10					15	

<210> SEQ ID NO 503
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 503

Leu	Val	Asn	Ile	Met	Pro	Tyr	Glu	Ser	Thr	Arg
1			5						10	

<210> SEQ ID NO 504
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 504

Leu	Val	Ser	Tyr	Thr	Asn	Leu	Thr	Gln	Gly	Ala	Lys
1			5					10			

<210> SEQ ID NO 505
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 505

Leu Trp Met Asn Val Glu Lys
1 5

<210> SEQ ID NO 506

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 506

Leu Tyr Thr Tyr Glu Pro Arg
1 5

<210> SEQ ID NO 507

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 507

Met Ala Phe Asp Phe Arg
1 5

<210> SEQ ID NO 508

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 508

Met Ala Leu His Leu Pro Trp Phe His Pro Arg
1 5 10

<210> SEQ ID NO 509

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 509

Met Ala Pro Glu Pro Ala Pro Gly Arg
1 5

<210> SEQ ID NO 510

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 510

Met Asp Ile Leu Glu Glu Arg
1 5

<210> SEQ ID NO 511

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 511

Met Asp Val Gly Thr Ile Tyr Arg
1 5

<210> SEQ ID NO 512

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 512

Met Glu Leu Gln Ala Ala Arg
1 5

<210> SEQ ID NO 513

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 513

Met Glu Pro Leu Glu Lys
1 5

<210> SEQ ID NO 514

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 514

Met Glu Ser Glu Glu Leu Ala Asp Arg
1 5

<210> SEQ ID NO 515

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 515

Met Phe Glu Leu Thr Cys Thr Leu Pro Leu Glu Lys
1 5 10

<210> SEQ ID NO 516

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 516

Met Gly Gln Pro Pro Ala Glu Glu Ala Glu Gln Pro Gly Ala Leu Ala
1 5 10 15

Arg

<210> SEQ ID NO 517

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 517

Met His Thr Ala Val Lys
1 5

<210> SEQ ID NO 518

<211> LENGTH: 22

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 518

Met Leu Ser Ala Ser Thr Met Leu Val Gln Trp Glu Pro Pro Glu Glu
1 5 10 15Pro Asn Gly Leu Val Arg
20

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<210> SEQ ID NO 519
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 519

Met Leu Trp Glu His Asn Ser Thr Ile Ile Val Met Leu Thr Lys
1 5 10 15

<210> SEQ ID NO 520
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 520

Met Leu Trp Glu His Asn Ser Thr Ile Val Val Met Leu Thr Lys
1 5 10 15

<210> SEQ ID NO 521
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 521

Met Pro His Phe Thr Val Val Pro Val Asp Gly Pro Arg
1 5 10

<210> SEQ ID NO 522
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 522

Met Pro Asn Val Pro Asn Thr Gln Pro Ala Ile Met Lys Pro Thr Glu
1 5 10 15

Glu His Pro Ala Tyr Thr Gln Ile Ala Lys
20 25

<210> SEQ ID NO 523
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 523

Met Gln Gln Tyr Thr Glu His Phe Met Ala Ala Gly Tyr Thr Ala Ile
1 5 10 15

Glu Lys

<210> SEQ ID NO 524
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 524

Met Ser Ala Gly Gly Ala Ser Val Pro Pro Pro Pro Asn Pro Ala Val
1 5 10 15

Ser Phe Pro Pro Pro Arg
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<210> SEQ ID NO 525
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 525

Met	Ser	Asp	Val	Ser	Thr	Ser	Val	Gln	Ser	Lys
1				5					10	

<210> SEQ ID NO 526
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 526

Met	Thr	Thr	Ser	Gly	Ala	Leu	Phe	Pro	Ser	Leu	Val	Pro	Gly	Ser	Arg
1				5					10					15	

<210> SEQ ID NO 527
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 527

Met	Val	Glu	Glu	Val	Asp	Gly	Arg
1				5			

<210> SEQ ID NO 528
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 528

Met	Val	Phe	Phe	Val	Gln	Asn	Glu	Pro	Pro	His	Gln	Ile	Phe	Lys
1				5					10					15

<210> SEQ ID NO 529
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 529

Met	Val	Trp	Glu	Gln	Arg
1				5	

<210> SEQ ID NO 530
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 530

Met	Tyr	Pro	Glu	Thr	Phe	Leu	Tyr	Val	Thr	Ser	Ser	Ala	Gly	Ile	Arg
1				5					10					15	

<210> SEQ ID NO 531
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 531

Met	Tyr	Tyr	Thr	His	Arg
1				5	

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<210> SEQ ID NO 532
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 532

Met Tyr Tyr Thr His Arg Arg
1 5

<210> SEQ ID NO 533
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 533

Met Tyr Tyr Thr His Arg Arg Arg
1 5

<210> SEQ ID NO 534
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 534

Asn Asp Phe Gln Asn Leu Gln Gln Val Phe Leu Gln Ala Lys
1 5 10

<210> SEQ ID NO 535
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 535

Asn Phe Ala Thr Met Met Asn Phe Val Arg
1 5 10

<210> SEQ ID NO 536
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 536

Asn Gly Val Gly Gly Met Ala Lys
1 5

<210> SEQ ID NO 537
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 537

Asn Gly Val Ile Thr Gln Tyr Ser Val Ala Tyr Glu Ala Val Asp Gly
1 5 10 15

Glu Asp Arg

<210> SEQ ID NO 538
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 538

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Asn Gly Val Ser Gly Leu Val Thr Ser Arg
1 5 10

<210> SEQ ID NO 539
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 539

Asn Ile Ala Phe Tyr Pro Ser Asn His Glu Arg
1 5 10

<210> SEQ ID NO 540
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 540

Asn Ile Phe Tyr Ile Lys
1 5

<210> SEQ ID NO 541
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 541

Asn Leu Ala Leu Phe Glu Glu Glu Leu Asp Ile Arg Pro Lys
1 5 10

<210> SEQ ID NO 542
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 542

Asn Leu Ile Ala Phe Ser Glu Asp Gly Ser Asp Pro Tyr Val Arg
1 5 10 15

<210> SEQ ID NO 543
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 543

Asn Leu Ile Thr Asn Leu Gln Arg
1 5

<210> SEQ ID NO 544
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 544

Asn Leu Gln Ser Gln Ser Ser Val Asn Val Ile Val Lys
1 5 10

<210> SEQ ID NO 545
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 545

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Asn Leu Arg Pro Met Leu Ala Ala Asp Ala Gln Arg
1 5 10

<210> SEQ ID NO 546
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 546

Asn Leu Ser Pro Asp Gly Gln Tyr Val Pro Arg
1 5 10

<210> SEQ ID NO 547
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 547

Asn Leu Val Asp Pro Phe Val Glu Val Ser Phe Ala Gly Lys
1 5 10

<210> SEQ ID NO 548
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 548

Asn Met Tyr Leu Thr Gly Leu Cys Phe Leu Leu Gly Pro Thr Gln Leu
1 5 10 15

Thr Gln Arg

<210> SEQ ID NO 549
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 549

Asn Asn Glu Pro Leu Arg
1 5

<210> SEQ ID NO 550
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 550

Asn Asn Phe Ser Asp Gly Phe Arg
1 5

<210> SEQ ID NO 551
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 551

Asn Pro Asn Phe Asp Ile Cys Thr Leu Phe Met Glu Val Met Leu Pro
1 5 10 15

Arg

<210> SEQ ID NO 552

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<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 552

Asn Pro Val Leu Asp Cys Ser Ile Ala Gly Cys Leu Arg
1 5 10

<210> SEQ ID NO 553
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 553

Asn Ser Glu Gly Asp Glu Asn Tyr Met Glu Phe Leu Glu Val Leu Thr
1 5 10 15

Glu Gly Leu Glu Arg
20

<210> SEQ ID NO 554
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 554

Asn Ser Tyr Cys Lys Lys
1 5

<210> SEQ ID NO 555
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 555

Asn Val Gly Leu Met Ile Cys Gly His Val His Met Gly Pro Arg
1 5 10 15

<210> SEQ ID NO 556
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 556

Asn Val Gly Leu Met Ile Cys Gly His Val His Met Gly Pro Arg Arg
1 5 10 15

<210> SEQ ID NO 557
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 557

Asn Val His Leu Glu Phe Thr Glu Arg
1 5

<210> SEQ ID NO 558
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 558

Asn Val Leu Glu Leu Ser Asn Val Val Arg

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1 5 10

<210> SEQ ID NO 559
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 559

Asn Val Pro Asp Asp Val Leu Arg
1 5

<210> SEQ ID NO 560
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 560

Asn Val Pro Pro Gly Leu Asp Glu Tyr Asn Pro Phe Ser Asp Ser Arg
1 5 10 15

<210> SEQ ID NO 561
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 561

Asn Val Ser Gly Phe Ser Ile Ala Asn Arg
1 5 10

<210> SEQ ID NO 562
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 562

Asn Val Ser Val Gln Pro Glu Ile Ser Glu Gly Leu Ala Thr Thr Pro
1 5 10 15

Ser Thr Gln Gln Val Lys
20

<210> SEQ ID NO 563
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 563

Asn Trp Glu Glu Ala Glu Arg
1 5

<210> SEQ ID NO 564
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 564

Asn Tyr Thr Ile Phe Tyr Arg
1 5

<210> SEQ ID NO 565
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 565

Gln Cys Leu Ile Lys Lys
1 5

<210> SEQ ID NO 566

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 566

Gln Glu Glu Leu Glu Arg
1 5

<210> SEQ ID NO 567

<211> LENGTH: 18

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 567

Gln Glu Gln Asp Ile Val Phe Leu Ile Asp Gly Ser Gly Ser Ile Ser
1 5 10 15

Ser Arg

<210> SEQ ID NO 568

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 568

Gln Glu Ser Thr Ser Val Leu Leu Gln Gln Ser Glu Lys
1 5 10

<210> SEQ ID NO 569

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 569

Gln Glu Ser Thr Ser Val Leu Leu Gln Gln Ser Glu Lys Lys
1 5 10

<210> SEQ ID NO 570

<211> LENGTH: 16

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 570

Gln Phe His Gln Leu Ala Ala Gln Gly Pro Gln Glu Cys Leu Val Arg
1 5 10 15

<210> SEQ ID NO 571

<211> LENGTH: 24

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 571

Gln Phe Gln Phe Met Ala Trp Pro Asp His Gly Val Pro Glu Tyr Pro
1 5 10 15Thr Pro Ile Leu Ala Phe Leu Arg
20

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<210> SEQ ID NO 572
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 572

Gln Phe Gln Phe Thr Asp Trp Pro Glu Gln Gly Val Pro Lys
1 5 10

<210> SEQ ID NO 573
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 573

Gln Gly Ala Gln Trp Ala Ala Leu Cys Asp Ser Ser Ser Ala Arg
1 5 10 15

<210> SEQ ID NO 574
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 574

Gln Gly His Phe Tyr Gly Glu Thr Ala Ala Val Tyr Val Ala Val Glu
1 5 10 15

Glu Arg

<210> SEQ ID NO 575
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 575

Gln Gly His Phe Tyr Gly Glu Thr Ala Ala Val Tyr Val Ala Val Glu
1 5 10 15

Glu Arg Lys

<210> SEQ ID NO 576
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 576

Gln Gly Leu Thr Val Ser Phe Ile Pro Tyr Phe Lys
1 5 10

<210> SEQ ID NO 577
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 577

Gln Gly Pro Val Gly Ser Gly Arg Arg
1 5

<210> SEQ ID NO 578
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 578

Gln His Gly Gln Ile Arg
1 5

<210> SEQ ID NO 579

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 579

Gln Ile Phe Gly Phe Glu Ser Asn Lys
1 5

<210> SEQ ID NO 580

<211> LENGTH: 19

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 580

Gln Ile Gly Pro Gly Glu Ser Cys Pro Asp Gly Val Thr His Ser Ile
1 5 10 15

Ser Gly Arg

<210> SEQ ID NO 581

<211> LENGTH: 20

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 581

Gln Asn Ala Tyr Ile Ala Thr Gln Gly Pro Leu Pro Glu Thr Met Gly
1 5 10 15Asp Phe Trp Arg
20

<210> SEQ ID NO 582

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 582

Gln Asn Cys Ser Gln His Glu Ser Ser Pro Asp Ile Ser His Phe Glu
1 5 10 15

Arg

<210> SEQ ID NO 583

<211> LENGTH: 27

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 583

Gln Pro Gly Asn Met Ala Gly Asn Phe Asn Leu Ser Leu Gln Gly Cys
1 5 10 15Asp Gln Asp Ala Gln Ser Pro Gly Ile Leu Arg
20 25

<210> SEQ ID NO 584

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 584

Gln	Pro	Gly	Ser	Val	Pro	Arg
1				5		

<210> SEQ ID NO 585

<211> LENGTH: 15

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 585

Gln	Pro	His	Tyr	Ser	Ala	Phe	Gly	Ser	Val	Gly	Glu	Trp	Leu	Arg
1				5					10					15

<210> SEQ ID NO 586

<211> LENGTH: 15

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 586

Gln	Pro	Gln	Gln	Phe	Pro	Ser	Arg	Pro	Pro	Pro	Pro	Gln	Pro	Lys
1				5					10					15

<210> SEQ ID NO 587

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 587

Gln	Ser	Pro	Glu	Asp	Val	Tyr	Phe	Ser	Lys
1				5					10

<210> SEQ ID NO 588

<211> LENGTH: 16

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 588

Gln	Ser	Ser	Gly	Glu	Asn	Cys	Asp	Val	Val	Val	Asn	Thr	Leu	Gly	Lys
1				5					10					15	

<210> SEQ ID NO 589

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 589

Gln	Ser	Ser	Gly	Glu	Asn	Cys	Asp	Val	Val	Val	Asn	Thr	Leu	Gly	Lys
1				5					10					15	

Arg

<210> SEQ ID NO 590

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 590

Gln	Val	Ile	Ile	Asn	Leu	Ile	Asn	Gln	Lys
1				5				10	

<210> SEQ ID NO 591

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<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 591

Gln Val Ser Ser Val Asn Glu Glu Asp Phe Val Arg
1 5 10

<210> SEQ ID NO 592
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 592

Gln Trp Ser Asn Val Phe Asn Ile Leu Arg
1 5 10

<210> SEQ ID NO 593
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 593

Gln Tyr Ala Gly Thr Gly Ala Leu Lys
1 5

<210> SEQ ID NO 594
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 594

Gln Tyr Asn Ser Phe Asn Phe Ala Leu Leu Glu Asp Val Gln Ala Lys
1 5 10 15

<210> SEQ ID NO 595
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 595

Arg Ala Glu Ser Asp Ser Arg Lys
1 5

<210> SEQ ID NO 596
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 596

Arg Ala Met Ala Thr Leu Leu Ser Lys
1 5

<210> SEQ ID NO 597
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 597

Arg Ala Pro Ala Phe Glu Gly Arg
1 5

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<210> SEQ ID NO 598
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 598

Arg Asp Leu Gly Ser Arg
1 5

<210> SEQ ID NO 599
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 599

Arg Asp Leu Ser Gln Met Glu Ala Leu Lys
1 5 10

<210> SEQ ID NO 600
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 600

Arg Asp Gln Leu Trp Arg
1 5

<210> SEQ ID NO 601
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 601

Arg Glu Ile Thr Tyr Gln Gly Thr Arg
1 5

<210> SEQ ID NO 602
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 602

Arg Glu Gln Leu Thr Glu Thr Asp Lys
1 5

<210> SEQ ID NO 603
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 603

Arg Gly Asp Phe Phe Tyr His Ser Glu Asn Pro Lys
1 5 10

<210> SEQ ID NO 604
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 604

Arg His Gly Glu Thr Cys Tyr Lys
1 5

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<210> SEQ ID NO 605
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 605

Arg Lys Asn Gln Arg
1 5

<210> SEQ ID NO 606
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 606

Arg Leu Asn Tyr Gln Thr Pro Gly Met Arg
1 5 10

<210> SEQ ID NO 607
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 607

Arg Met Glu Pro Leu Glu Lys
1 5

<210> SEQ ID NO 608
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 608

Arg Pro Asp Thr Ser Phe Leu Trp Phe Thr Ser Pro Tyr Lys
1 5 10

<210> SEQ ID NO 609
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 609

Arg Pro Pro Asn Ala Trp His Lys
1 5

<210> SEQ ID NO 610
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 610

Arg Pro Pro Gln Thr Leu Ser Arg
1 5

<210> SEQ ID NO 611
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 611

Arg Gln Asp Leu Glu Val Glu Val Arg
1 5

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<210> SEQ ID NO 612
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 612

Arg Gln Glu Glu Leu Glu Arg
1 5

<210> SEQ ID NO 613
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 613

Arg Gln Glu Glu Leu Glu Arg Lys
1 5

<210> SEQ ID NO 614
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 614

Arg Arg Gln Ala Glu Arg
1 5

<210> SEQ ID NO 615
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 615

Arg Thr His Leu Gly Leu Ile Met Asp Gly Trp Asn Ser Met Ile Arg
1 5 10 15

<210> SEQ ID NO 616
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 616

Arg Thr His Ser Pro Ser Ser Lys
1 5

<210> SEQ ID NO 617
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 617

Arg Thr Leu Glu Gln Met Asp Val Val His Arg
1 5 10

<210> SEQ ID NO 618
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 618

Arg Thr Pro Thr Ala Arg

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1 5

<210> SEQ ID NO 619
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 619

Ser Ala Asn Tyr Thr Cys Val Ala Ile Ser Ser Leu Gly Met Ile Glu
1 5 10 15

Ala Thr Ala Gln Val Thr Val Lys
 20

<210> SEQ ID NO 620
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 620

Ser Cys Ser Leu Val Leu Glu His Gln Pro Asp Asn Ile Lys
1 5 10

<210> SEQ ID NO 621
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 621

Ser Asp Met Gly Val Gly Val Phe Thr Pro Thr Ile Glu Ala Arg
1 5 10 15

<210> SEQ ID NO 622
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 622

Ser Asp Pro Tyr Gly Ile Ile Arg
1 5

<210> SEQ ID NO 623
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 623

Ser Asp Gln Ala Leu His Ser Phe Ser Glu Ala Lys
1 5 10

<210> SEQ ID NO 624
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 624

Ser Asp Ser Ala Val Leu Leu Arg
1 5

<210> SEQ ID NO 625
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 625

Ser Asp Thr Ile Ala Asn Tyr Glu Leu Val Tyr Lys
1 5 10

<210> SEQ ID NO 626

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 626

Ser Glu Ile Phe Asn Glu Asn Phe Gly Pro Asp Phe Arg
1 5 10

<210> SEQ ID NO 627

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 627

Ser Glu Ile Ile Asn Ser Lys
1 5

<210> SEQ ID NO 628

<211> LENGTH: 18

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 628

Ser Glu Ile Gln Phe Leu Ile Ser Asp Asn Gln Gly Phe Ser Cys Pro
1 5 10 15

Glu Lys

<210> SEQ ID NO 629

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 629

Ser Glu Gln Leu Lys Pro Leu Lys
1 5

<210> SEQ ID NO 630

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 630

Ser Glu Gln Pro Thr Ala Ser Trp Arg
1 5

<210> SEQ ID NO 631

<211> LENGTH: 16

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 631

Ser Gly Ala Leu Gln Ile Glu Ser Ser Glu Glu Ser Asp Gln Gly Lys
1 5 10 15

<210> SEQ ID NO 632

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<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 632

Ser Gly Glu Gly Phe Ile Asp Phe Ile Gly Gln Val His Lys
1 5 10

<210> SEQ ID NO 633
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 633

Ser Gly Val Val Cys Gln Thr Gly Arg
1 5

<210> SEQ ID NO 634
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 634

Ser His Ala Glu Asn Pro Thr Ala Ser His Val Asp Asn Glu Tyr Ser
1 5 10 15

Gln Pro Pro Arg
20

<210> SEQ ID NO 635
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 635

Ser His Leu Gln Asn Tyr Thr Val Asn Ala Thr Lys
1 5 10

<210> SEQ ID NO 636
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 636

Ser Ile Phe Asp Pro Pro Val Phe Pro Val Cys Met Leu Gly Asn Arg
1 5 10 15

<210> SEQ ID NO 637
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 637

Ser Ile Leu Gln Glu Glu Asn Arg
1 5

<210> SEQ ID NO 638
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 638

Ser Ile Gln Ile His Gly Thr Met Arg

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1 5

<210> SEQ ID NO 639
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 639

Ser Leu Glu Met Ser His Asp Glu His Lys Lys
1 5 10

<210> SEQ ID NO 640
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 640

Ser Leu Gly Gly Glu Gly Asn Phe Asn Trp Arg
1 5 10

<210> SEQ ID NO 641
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 641

Ser Leu His Leu Thr Cys Asp Ser Ala Pro Val Gly Ser Gln Gly Thr
1 5 10 15

Trp Ser Thr Ser Cys Arg
 20

<210> SEQ ID NO 642
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 642

Ser Leu Ser Gly Val Gly Ala Gly Gly Gly Pro Thr Pro Arg
1 5 10

<210> SEQ ID NO 643
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 643

Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg
1 5 10

<210> SEQ ID NO 644
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 644

Ser Pro Asp Leu Gln Gly Ser Trp Gln Trp Ser Asp Arg
1 5 10

<210> SEQ ID NO 645
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 645

Ser Pro Gly Trp Arg Pro Ala Phe Lys
1 5

<210> SEQ ID NO 646

<211> LENGTH: 18

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 646

Ser Gln Ala Lys Pro Gly Thr Pro Gly Gly Thr Gly Gly Pro Ala Pro
1 5 10 15

Gln Tyr

<210> SEQ ID NO 647

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 647

Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly Met
1 5 10 15

Arg

<210> SEQ ID NO 648

<211> LENGTH: 19

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 648

Ser Gln His Thr Thr Glu Val Val Gly Gly Ala Pro Gln His Glu Gln
1 5 10 15

Ile Gly Lys

<210> SEQ ID NO 649

<211> LENGTH: 19

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 649

Ser Ser His Ser Gly Val Leu Glu Ile Glu Asn Ser Val Asp Asp Leu
1 5 10 15

Ser Ser Arg

<210> SEQ ID NO 650

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 650

Ser Ser Leu Pro Tyr Ile Cys Glu Met Thr Ala Phe Arg
1 5 10

<210> SEQ ID NO 651

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 651

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Ser Ser Ser Ser Asn Phe Leu Asn Tyr Asp Leu Thr Leu Arg
1 5 10

<210> SEQ ID NO 652
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 652

Ser Ser Val Ile Asn Ser Ile Arg
1 5

<210> SEQ ID NO 653
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 653

Ser Ser Val Ile Ser Ile Tyr Val Ser Glu Ser Met Asp Arg
1 5 10

<210> SEQ ID NO 654
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 654

Ser Thr Glu Glu Phe Pro Pro Leu Gln Pro Ile Leu Gln Gln Lys
1 5 10 15

<210> SEQ ID NO 655
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 655

Ser Thr Glu Thr Ala Leu Tyr Arg
1 5

<210> SEQ ID NO 656
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 656

Ser Thr Glu Thr Ala Leu Tyr Arg Lys
1 5

<210> SEQ ID NO 657
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 657

Ser Thr Gly Pro Gly Ala Ser Leu Gly Thr Gly Tyr Asp Arg
1 5 10

<210> SEQ ID NO 658
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 658

Ser	Thr	Gly	Pro	Gly	Ala	Ser	Leu	Gly	Thr	Gly	Tyr	Asp	Arg	Lys
1				5					10					15

<210> SEQ ID NO 659

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 659

Ser	Thr	Ile	Glu	Lys	Lys
1				5	

<210> SEQ ID NO 660

<211> LENGTH: 18

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 660

Ser	Thr	Thr	Ser	Leu	Ser	Val	Ser	Trp	Ser	Ile	Pro	Pro	Pro	Gln	Gln
1				5				10						15	

Ser Arg

<210> SEQ ID NO 661

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 661

Ser	Val	Asp	Asp	Thr	Ser	Gln	Ala	Ile	Gln	Arg
1				5				10		

<210> SEQ ID NO 662

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 662

Ser	Val	Gly	Pro	Leu	Thr	Arg
1				5		

<210> SEQ ID NO 663

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 663

Ser	Val	Gly	Pro	Leu	Thr	Arg	Lys
1				5			

<210> SEQ ID NO 664

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 664

Ser	Val	Leu	Gly	Val	Ile	Thr	Ile	Val	Asn	Leu	Arg
1				5				10			

<210> SEQ ID NO 665

<211> LENGTH: 6

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<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 665

Ser Val Gln Met Met Arg
1 5

<210> SEQ ID NO 666
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 666

Ser Tyr Phe Arg Lys
1 5

<210> SEQ ID NO 667
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 667

Ser Tyr Gln Leu Ala Asn Ile Ser Ser Pro Ser Leu Val Val Glu Cys
1 5 10 15

Gly Gly Gln Thr Val Gln Ser Cys Val Ile Arg
20 25

<210> SEQ ID NO 668
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 668

Ser Tyr Ser Phe Val Leu Thr Asn Arg
1 5

<210> SEQ ID NO 669
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 669

Thr Ala Leu Leu Asn Met Asp Arg
1 5

<210> SEQ ID NO 670
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 670

Thr Ala Asn Pro Gln Trp Asn Gln Asn Ile Thr Leu Pro Ala Met Phe
1 5 10 15

Pro Ser Met Cys Glu Lys
20

<210> SEQ ID NO 671
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 671

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Thr Ala Pro Asp Leu Leu Pro His Lys Pro Leu Pro Ala Ser Ala Tyr
1 5 10 15

Ile Glu Asp Gly Arg
20

<210> SEQ ID NO 672
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 672

Thr Ala Gln Ser Thr Pro Ser Ala Pro Pro Gln Lys
1 5 10

<210> SEQ ID NO 673
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 673

Thr Ala Ser Val Ser Ile Asn Gln Thr Glu Pro Pro Lys
1 5 10

<210> SEQ ID NO 674
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 674

Thr Ala Thr Met Leu Cys Ala Ala Gly Gly Asn Pro Asp Pro Glu Ile
1 5 10 15

Ser Trp Phe Lys
20

<210> SEQ ID NO 675
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 675

Thr Ala Thr Met Leu Cys Ala Ala Ser Gly Asn Pro Asp Pro Glu Ile
1 5 10 15

Thr Trp Phe Lys
20

<210> SEQ ID NO 676
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 676

Thr Ala Thr Val Val Met Met Thr Arg
1 5

<210> SEQ ID NO 677
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 677

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Thr	Ala	Val	Asp	Gly	Pro	Asp	Leu	Glu	Met	Leu	Thr	Gly	Gln	Glu	Arg
1				5					10					15	

<210> SEQ ID NO 678
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 678

Thr	Cys	Leu	Glu	Glu	Arg
1			5		

<210> SEQ ID NO 679
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 679

Thr	Cys	Ser	Ser	Asn	Leu	Thr	Leu	Thr	Ser	Gly	Ser	Lys
1			5					10				

<210> SEQ ID NO 680
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 680

Thr	Asp	Ala	Phe	Arg	Arg	Arg
1			5			

<210> SEQ ID NO 681
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 681

Thr	Asp	Ala	Leu	Leu	Gly	Glu	Phe	Arg
1			5					

<210> SEQ ID NO 682
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 682

Thr	Asp	Glu	Asp	Val	Pro	Ser	Gly	Pro	Pro	Arg
1			5					10		

<210> SEQ ID NO 683
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 683

Thr	Asp	Glu	Asp	Val	Pro	Ser	Gly	Pro	Pro	Arg	Lys
1			5					10			

<210> SEQ ID NO 684
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 684

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Thr Asp Ile Ser Met Ser Asp Phe Glu Asn Ser Arg
1 5 10

<210> SEQ ID NO 685
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 685

Thr Asp Gln Asp Glu Glu His Cys Arg
1 5

<210> SEQ ID NO 686
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 686

Thr Asp Val His Tyr Arg
1 5

<210> SEQ ID NO 687
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 687

Thr Glu Phe Gln Gln Ile Ile Asn Leu Ala Leu Gln Lys
1 5 10

<210> SEQ ID NO 688
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 688

Thr Phe Gly His Asn Thr Met Asp Ala Val Pro Arg
1 5 10

<210> SEQ ID NO 689
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 689

Thr Phe Ile Asp Thr Val Arg
1 5

<210> SEQ ID NO 690
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 690

Thr Phe Ser Asp Leu Gln Ser Leu Arg
1 5

<210> SEQ ID NO 691
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 691

Thr	Phe	Ser	Asp	Leu	Gln	Ser	Leu	Arg	Lys
1				5					10

<210> SEQ ID NO 692

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 692

Thr	Gly	Cys	Phe	Ile	Val	Ile	Asp	Ala	Met	Leu	Glu	Arg
1				5						10		

<210> SEQ ID NO 693

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 693

Thr	Gly	Glu	Gly	Phe	Ile	Asp	Phe	Ile	Gly	Gln	Val	His	Lys
1				5						10			

<210> SEQ ID NO 694

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 694

Thr	Gly	Glu	Gln	Ala	Pro	Ser	Ser	Pro	Pro	Arg
1				5						10

<210> SEQ ID NO 695

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 695

Thr	Gly	Glu	Gln	Ala	Pro	Ser	Ser	Pro	Pro	Arg	Arg
1				5						10	

<210> SEQ ID NO 696

<211> LENGTH: 15

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 696

Thr	His	Leu	Gly	Leu	Ile	Met	Asp	Gly	Trp	Asn	Ser	Met	Ile	Arg
1				5						10				15

<210> SEQ ID NO 697

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 697

Thr	His	Gln	Ala	Phe	Met	Arg
1				5		

<210> SEQ ID NO 698

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 698

Thr His Gln Ala Phe Met Arg Lys
1 5

<210> SEQ ID NO 699

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 699

Thr His Ser Ser Asn Ser Met Leu Val Phe Leu Lys
1 5 10

<210> SEQ ID NO 700

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 700

Thr Ile His Ala Glu Leu Ser Lys
1 5

<210> SEQ ID NO 701

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 701

Thr Ile Asn Phe Ala Arg
1 5

<210> SEQ ID NO 702

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 702

Thr Leu Ala Asp Phe Asp Pro Arg
1 5

<210> SEQ ID NO 703

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 703

Thr Leu Glu Gln Met Asp Val Val His Arg
1 5 10

<210> SEQ ID NO 704

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 704

Thr Leu His Thr Glu Glu Leu Thr Ser Lys
1 5 10

<210> SEQ ID NO 705

<211> LENGTH: 9

<212> TYPE: PRT

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<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 705

Thr Leu Ser Ala Gly Ala Gly Pro Arg
1 5

<210> SEQ ID NO 706

<211> LENGTH: 27

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 706

Thr Met Gly Met Val Asn Ile Phe Asn Gly Asp Ala Asp Leu Ser Gly
1 5 10 15

Met Thr Trp Ser His Gly Leu Ser Val Ser Lys
20 25

<210> SEQ ID NO 707

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 707

Thr Met Leu His Leu Thr Asp Ile Gln Leu Gln Asp Asn Lys
1 5 10

<210> SEQ ID NO 708

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 708

Thr Met Pro Val Glu Gln Val Phe Ala Lys
1 5 10

<210> SEQ ID NO 709

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 709

Thr Asn Glu Asp Val Pro Ser Gly Pro Pro Arg Lys
1 5 10

<210> SEQ ID NO 710

<211> LENGTH: 18

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 710

Thr Asn Glu Pro Val Trp Glu Glu Asn Phe Thr Phe Phe Ile His Asn
1 5 10 15

Pro Lys

<210> SEQ ID NO 711

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 711

Thr Asn His Phe Thr Ile Pro Lys

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1 5

<210> SEQ ID NO 712
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 712

Thr Asn Gln Glu Val Leu Asp Phe Val Val Gly Gly Gly Arg
1 5 10

<210> SEQ ID NO 713
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 713

Thr Asn Ser Ile Leu Phe Tyr Gly Arg
1 5

<210> SEQ ID NO 714
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 714

Thr Asn Val Ile Gln Ser Leu Leu Ala Arg
1 5 10

<210> SEQ ID NO 715
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 715

Thr Asn Trp Val Tyr Arg
1 5

<210> SEQ ID NO 716
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 716

Thr Pro Glu Ser Ser Pro Pro Gly Thr Pro Ile Gly Arg
1 5 10

<210> SEQ ID NO 717
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 717

Thr Pro Leu His Ala Ala Val Ala Ala Asp Ala Arg
1 5 10

<210> SEQ ID NO 718
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 718

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Thr Pro Leu Ser Tyr Thr His Trp Arg
1 5

<210> SEQ ID NO 719
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 719

Thr Pro Asn Trp Asp Arg
1 5

<210> SEQ ID NO 720
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 720

Thr Pro Asn Trp Arg Pro Arg
1 5

<210> SEQ ID NO 721
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 721

Thr Pro Pro Pro Gly Gly Val Lys
1 5

<210> SEQ ID NO 722
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 722

Thr Pro Val Ser Thr Ile Ile Met Pro Asn Glu Phe Gln Gln Asp Tyr
1 5 10 15

Asp Ile Arg

<210> SEQ ID NO 723
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 723

Thr Gln Asp Leu Glu Asn Phe Leu Cys Asn Asn Leu Gln Cys Gly Ser
1 5 10 15

Phe Leu Lys

<210> SEQ ID NO 724
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 724

Thr Gln Glu Glu Thr Glu Asp Pro Ser Val Ile Gly Glu Phe Lys
1 5 10 15

<210> SEQ ID NO 725
<211> LENGTH: 21

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<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 725

Thr Gln Gln Gly Val Pro Ala Gln Pro Ala Asp Phe Gln Ala Glu Val
1 5 10 15

Glu Ser Asp Thr Arg
20

<210> SEQ ID NO 726
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 726

Thr Gln Arg Pro Ala Met Val Gln Thr Glu Asp Gln Tyr Gln Leu Cys
1 5 10 15

Tyr Arg

<210> SEQ ID NO 727
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 727

Thr Ser Gly Phe Pro Ala Lys Lys
1 5

<210> SEQ ID NO 728
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 728

Thr Ser Leu Cys Val Leu Gly Pro Gly Asp Glu Ala Pro Leu Glu Arg
1 5 10 15

<210> SEQ ID NO 729
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 729

Thr Ser Leu Cys Val Leu Gly Pro Gly Asp Glu Ala Pro Leu Glu Arg
1 5 10 15

Lys

<210> SEQ ID NO 730
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 730

Thr Ser Ser Gln Pro Gly Phe Leu Glu Arg
1 5 10

<210> SEQ ID NO 731
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 731

Thr	Ser	Val	Leu	Leu	Ser	Trp	Glu	Ile	Pro	Glu	Asn	Tyr	Asn	Ser	Ala
1				5					10					15	

Met	Pro	Phe	Lys
			20

<210> SEQ ID NO 732

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 732

Thr	Ser	Val	Leu	Leu	Ser	Trp	Glu	Val	Pro	Asp	Ser	Tyr	Lys
1				5					10				

<210> SEQ ID NO 733

<211> LENGTH: 21

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 733

Thr	Ser	Val	Thr	Val	Ser	Asp	Leu	Glu	Pro	His	Met	Asn	Tyr	Thr	Phe
1				5					10					15	

Thr	Val	Glu	Ala	Arg
				20

<210> SEQ ID NO 734

<211> LENGTH: 21

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 734

Thr	Thr	Pro	Pro	Thr	Thr	Arg	Pro	Pro	Pro	Thr	Thr	Thr	Pro	Glu	Pro
1				5					10					15	

Thr	Ala	Pro	Pro	Arg
				20

<210> SEQ ID NO 735

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 735

Thr	Val	Asp	Ile	Tyr	Gly	His	Val	Thr	Cys	Met	Arg
1				5					10		

<210> SEQ ID NO 736

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 736

Thr	Val	Asp	Ile	Tyr	Gly	His	Val	Thr	Leu	Met	Arg
1				5					10		

<210> SEQ ID NO 737

<211> LENGTH: 23

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 737

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Thr Val Gln Thr Ala Ala Ala Asn Ala Ala Ser Thr Ala Ala Ser Ser
1 5 10 15

Ala Ala Gln Asn Ala Phe Lys
20

<210> SEQ ID NO 738
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 738

Thr Val Ser Glu Trp Leu Glu Ser Ile Lys
1 5 10

<210> SEQ ID NO 739
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 739

Thr Tyr Glu Val Cys Asp Val Gln Arg
1 5

<210> SEQ ID NO 740
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 740

Thr Tyr Leu Ala Val Gly Ser Met Lys
1 5

<210> SEQ ID NO 741
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 741

Thr Tyr Gln Phe Leu Gln Glu Tyr Leu Asp Ala Ile Lys
1 5 10

<210> SEQ ID NO 742
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 742

Thr Tyr Val Asp Pro His Thr Tyr Glu Asp Pro Asn Gln Ala Val Leu
1 5 10 15

Lys

<210> SEQ ID NO 743
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 743

Val Ala Lys Pro Glu Glu Met Lys
1 5

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<210> SEQ ID NO 744
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 744

Val	Ala	Asn	His	Met	Asp	Gly	Phe	Gln	Arg
1			5					10	

<210> SEQ ID NO 745
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 745

Val	Ala	Gln	Pro	Gly	Pro	Leu	Glu	Pro	Glu	Glu	Pro	Arg
1			5						10			

<210> SEQ ID NO 746
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 746

Val	Ala	Thr	Pro	Leu	Pro	Asp	Pro	Met	Ala	Ser	Arg
1			5						10		

<210> SEQ ID NO 747
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 747

Val	Asp	Phe	Leu	Gly	Glu	Ala	Gly	Ile	Met	Gly	Gln	Phe	Ser	His	His
1			5						10					15	
Asn	Ile	Ile	Arg												
			20												

<210> SEQ ID NO 748
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 748

Val	Asp	Met	Thr	Phe	Glu	Glu	Glu	Ala	Gln	Leu	Leu	Gln	Leu	Lys
1				5					10					15

<210> SEQ ID NO 749
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 749

Val	Asp	Thr	Val	Ala	Ala	Glu	His	Leu	Thr	Arg
1				5					10	

<210> SEQ ID NO 750
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 750

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Val Asp Val Gly Gln Gln Pro Leu Arg
1 5

<210> SEQ ID NO 751
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 751

Val Glu Ala Ser Asn Pro Tyr Val Glu Pro Arg
1 5 10

<210> SEQ ID NO 752
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 752

Val Glu Asp Phe Asp Ala Leu Lys
1 5

<210> SEQ ID NO 753
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 753

Val Glu Asp Leu Pro Ala Asp Asp Ile Leu Arg
1 5 10

<210> SEQ ID NO 754
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 754

Val Glu Leu Pro Gly Thr Ala Val Pro Ser Val Pro Glu Asp Ala Ala
1 5 10 15

Pro Ala Ser Arg
20

<210> SEQ ID NO 755
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 755

Val Glu Val Glu Ala Val Asn Ser Thr Ser Val Lys
1 5 10

<210> SEQ ID NO 756
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 756

Val Glu Val Glu Pro Leu Asn Ser Thr Ala Val His Val Tyr Trp Lys
1 5 10 15

<210> SEQ ID NO 757
<211> LENGTH: 16
<212> TYPE: PRT

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<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 757

Val Glu Tyr Tyr Ile Pro Gly Ser Thr Thr Asn Pro Glu Val Phe Lys
1 5 10 15

<210> SEQ ID NO 758

<211> LENGTH: 15

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 758

Val Phe Ala Gln Asn Glu Glu Ile Gln Glu Met Ala Gln Asn Lys
1 5 10 15

<210> SEQ ID NO 759

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 759

Val Phe His Ala Glu Arg
1 5

<210> SEQ ID NO 760

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 760

Val Phe His Arg Pro Trp Arg
1 5

<210> SEQ ID NO 761

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 761

Val Phe Leu Ser Ile Glu Glu Phe Arg
1 5

<210> SEQ ID NO 762

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 762

Val Gly Glu Glu Asp Asp Gly Glu Tyr Arg
1 5 10

<210> SEQ ID NO 763

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 763

Val Gly Phe Gly Glu Glu Met Val Lys
1 5

<210> SEQ ID NO 764

<211> LENGTH: 9

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<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 764

Val Gly Gly Ser Met Leu Thr Pro Arg
1 5

<210> SEQ ID NO 765
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 765

Val Gly Asn Gln Ile Phe Gln Ser Arg
1 5

<210> SEQ ID NO 766
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 766

Val His Gly Leu Tyr Arg
1 5

<210> SEQ ID NO 767
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 767

Val Ile Glu Glu Ala Val Tyr Phe His Gln His Ser Ile Leu Ala Cys
1 5 10 15

Lys

<210> SEQ ID NO 768
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 768

Val Ile Glu Leu Asn Lys
1 5

<210> SEQ ID NO 769
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 769

Val Ile Gly Ala Gly Glu Phe Gly Glu Val Tyr Lys
1 5 10

<210> SEQ ID NO 770
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 770

Val Leu Ala Phe Thr Ala Val Gly Asp Gly Pro Pro Ser Pro Thr Ile
1 5 10 15

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Gln Val Lys

<210> SEQ ID NO 771
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 771

Val Leu Ala Leu Leu Cys Ser Gly Phe Gln Pro Lys
1 5 10

<210> SEQ ID NO 772
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 772

Val Leu Ala Pro Ala Ser Thr Leu Gln Ser Ser Tyr Gln Ile Pro Thr
1 5 10 15

Glu Asn Ser Met Thr Ala Arg
20

<210> SEQ ID NO 773
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 773

Val Leu Ala Gln Gln Gly Glu Tyr Ser Glu Ala Ile Pro Ile Leu Arg
1 5 10 15

<210> SEQ ID NO 774
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 774

Val Leu Ala Val Asn Ser Ile Gly Arg
1 5

<210> SEQ ID NO 775
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 775

Val Leu Asp Ala Gly Asp Pro Thr Ser Arg
1 5 10

<210> SEQ ID NO 776
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 776

Val Leu Asp Ser Gly Phe Arg
1 5

<210> SEQ ID NO 777
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 777

Val	Leu	Glu	Asp	Asp	Pro	Glu	Ala	Thr	Tyr	Thr	Thr	Ser	Gly	Gly	Lys
1				5					10					15	

<210> SEQ ID NO 778

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 778

Val	Leu	Glu	Gly	Met	Val	Glu	Glu	Asn	Gln	Val	Asn	Val	Glu	Val	Thr
1				5					10					15	

Arg

<210> SEQ ID NO 779

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 779

Val	Leu	Glu	Ile	Pro	Tyr	Lys
1				5		

<210> SEQ ID NO 780

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 780

Val	Leu	Glu	Asn	Tyr	Asn	Lys
1				5		

<210> SEQ ID NO 781

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 781

Val	Leu	His	Phe	Asp	Gln	Val	Thr	Glu	Asn	Thr	Thr	Glu	Lys
1				5					10				

<210> SEQ ID NO 782

<211> LENGTH: 24

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 782

Val	Leu	Met	Asp	Glu	Gly	Ala	Val	Leu	Thr	Leu	Val	Ala	Asp	Leu	Ser
1				5					10					15	

Ser	Ala	Thr	Leu	Asp	Ile	Ser	Lys
			20				

<210> SEQ ID NO 783

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 783

Val	Leu	Met	Glu	Ile	Gln	Asp	Leu	Met	Phe	Glu	Glu	Met	Arg
1				5					10				

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<210> SEQ ID NO 784
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 784

Val Leu Val Ala Leu Ala Ser Glu Glu Leu Ala Lys
1 5 10

<210> SEQ ID NO 785
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 785

Val Met Cys Val Ser Met Gly Ser Thr Thr Val Arg
1 5 10

<210> SEQ ID NO 786
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 786

Val Asn Asp Ser Asn Glu Leu Gly Gly Leu Thr Thr Ser Gly Ser Ala
1 5 10 15

Glu Val His Lys
20

<210> SEQ ID NO 787
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 787

Val Pro Ala His Gln Val Leu Phe Ser Arg
1 5 10

<210> SEQ ID NO 788
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 788

Val Pro Cys His Phe Pro Cys Lys
1 5

<210> SEQ ID NO 789
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 789

Val Pro Glu Asp Gln Thr Gly Leu Ser Gly Gly Val Ala Ser Phe Val
1 5 10 15

Cys Gln Ala Thr Gly Glu Pro Lys Pro Arg
20 25

<210> SEQ ID NO 790
<211> LENGTH: 8

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<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 790

Val Pro Glu Gly Phe Thr Cys Arg
1 5

<210> SEQ ID NO 791
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 791

Val Pro Glu Gly Leu Glu Asp Val Ser Lys
1 5 10

<210> SEQ ID NO 792
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 792

Val Pro Leu Ser Gln Leu Leu Thr Ser Glu Asp Met Thr Val Ser Gln
1 5 10 15

Arg

<210> SEQ ID NO 793
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 793

Val Gln Cys Ser Glu Gln Trp Ile Pro Phe Gln Asn Lys
1 5 10

<210> SEQ ID NO 794
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 794

Val Gln Val Ile Glu Gly Arg
1 5

<210> SEQ ID NO 795
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 795

Val Gln Trp Arg Pro Gln Gly Thr Arg
1 5

<210> SEQ ID NO 796
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 796

Val Ser Asp Phe Gly Leu Ser Arg
1 5

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<210> SEQ ID NO 797
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 797

Val Ser Thr Glu Val Thr Leu Ala Val Lys
1 5 10

<210> SEQ ID NO 798
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 798

Val Ser Trp Ser Pro Ala Glu Asp His Asn Ala Pro Ile Glu Lys
1 5 10 15

<210> SEQ ID NO 799
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 799

Val Ser Trp Val Pro Pro Pro Ala Asp Ser Arg
1 5 10

<210> SEQ ID NO 800
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 800

Val Thr Ala Ala Gly Gln Thr Lys
1 5

<210> SEQ ID NO 801
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 801

Val Thr Glu Met Met Lys
1 5

<210> SEQ ID NO 802
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 802

Val Thr Glu Met Met Lys Lys
1 5

<210> SEQ ID NO 803
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 803

Val Thr Phe Asp Pro Thr Ser Ser Tyr Thr Leu Glu Asp Leu Lys Pro
1 5 10 15

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Asp Thr Leu Tyr Arg
20

<210> SEQ ID NO 804
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 804

Val Thr Phe Thr Cys Gln Ala Ser Phe Asp Pro Ser Leu Gln Pro Ser
1 5 10 15

Ile Thr Trp Arg
20

<210> SEQ ID NO 805
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 805

Val Thr Leu Pro Ala Gly Pro Asp Leu Leu Arg
1 5 10

<210> SEQ ID NO 806
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 806

Val Thr Gln Glu Ile Val Thr Glu Arg
1 5

<210> SEQ ID NO 807
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 807

Val Thr Val Ala Ile Pro Leu Lys
1 5

<210> SEQ ID NO 808
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 808

Val Thr Tyr Gln Asn His Asn Lys
1 5

<210> SEQ ID NO 809
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 809

Val Val Glu Met Gln Gly Val Arg
1 5

<210> SEQ ID NO 810
<211> LENGTH: 10

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<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 810

Val Val Phe Gln Ile Trp Asp Asn Asp Lys
1 5 10

<210> SEQ ID NO 811
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 811

Val Val Leu Leu Glu Asp Leu Ala Ser Gln Val Gly Leu Arg
1 5 10

<210> SEQ ID NO 812
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 812

Val Val Pro Ser Phe Leu Pro Val Asp Gln Gly Gly Ser Leu Val Gly
1 5 10 15

Arg

<210> SEQ ID NO 813
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 813

Val Val Gln Met Thr Asn Asp Asp Ile Lys
1 5 10

<210> SEQ ID NO 814
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 814

Val Val Gln Met Thr Asn Asp Asp Ile Lys Arg
1 5 10

<210> SEQ ID NO 815
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 815

Val Val Tyr Ser Ala Pro Arg
1 5

<210> SEQ ID NO 816
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 816

Val Tyr Ala Pro Ala Ser Thr Leu Val Asp Gln Pro Tyr Ala Asn Glu
1 5 10 15

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Gly Thr Val Val Val Thr Glu Arg
20

<210> SEQ ID NO 817
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 817

Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala Arg
1 5 10 15

<210> SEQ ID NO 818
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 818

Val Tyr Ile Asp Pro Phe Thr Tyr Glu Asp Pro Asn Glu Ala Val Arg
1 5 10 15

<210> SEQ ID NO 819
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 819

Val Tyr Thr Glu Asn Val Asp Lys
1 5

<210> SEQ ID NO 820
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 820

Val Tyr Thr Glu Asn Val Asp Lys Arg
1 5

<210> SEQ ID NO 821
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 821

Val Tyr Thr Val Asp Leu Gly Arg
1 5

<210> SEQ ID NO 822
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 822

Val Tyr Tyr Lys Lys
1 5

<210> SEQ ID NO 823
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 823

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Val Tyr Tyr Thr Pro Asp Ser Arg
1 5

<210> SEQ ID NO 824
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 824

Trp Glu Asp Glu Glu Trp Ser Thr Asp Leu Asn Arg
1 5 10

<210> SEQ ID NO 825
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 825

Trp Glu Glu His Arg
1 5

<210> SEQ ID NO 826
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 826

Trp Glu Glu Val Cys Arg
1 5

<210> SEQ ID NO 827
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 827

Trp Leu Leu Leu Ser Asp Pro Asp Asp Phe Ser Ala Gly Ala Arg
1 5 10 15

<210> SEQ ID NO 828
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 828

Trp Leu Arg Pro Ser Gly Pro Met Pro Ala Asp Arg
1 5 10

<210> SEQ ID NO 829
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 829

Trp Met Asp Trp Asn Ala Pro Gln Val Gln Tyr Arg
1 5 10

<210> SEQ ID NO 830
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 830

Trp	Met	Met	Gly	Ala	Glu	Glu	Leu	Thr	Lys
1			5						10

<210> SEQ ID NO 831

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 831

Trp	Arg	Pro	Val	Asp	Leu	Ala	Gln	Val	Lys
1			5						10

<210> SEQ ID NO 832

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 832

Trp	Ser	Asn	Val	Phe	Lys
1			5		

<210> SEQ ID NO 833

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 833

Trp	Thr	Ala	Pro	Glu	Ala	Ile	Ala	Phe	Arg
1				5					10

<210> SEQ ID NO 834

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 834

Trp	Thr	Ala	Pro	Glu	Ala	Ile	Ser	Tyr	Arg
1				5					10

<210> SEQ ID NO 835

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 835

Trp	Thr	Ala	Pro	Glu	Ala	Ile	Ser	Tyr	Arg	Lys
1				5						10

<210> SEQ ID NO 836

<211> LENGTH: 5

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 836

Trp	Thr	Glu	Tyr	Arg
1			5	

<210> SEQ ID NO 837

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 837

Trp	Thr	Pro	Pro	Gln	Asp	Ser	Gly	Gly	Arg
1				5					10

<210> SEQ ID NO 838

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 838

Trp	Val	Ser	Gln	His	Arg
1				5	

<210> SEQ ID NO 839

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 839

Tyr	Ala	Ile	Gly	Val	Gly	Leu	Ala	Phe	Gln	Asn	Arg
1				5							10

<210> SEQ ID NO 840

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 840

Tyr	Ala	Asn	Val	Ile	Ala	Tyr	Asp	His	Ser	Arg
1				5						10

<210> SEQ ID NO 841

<211> LENGTH: 15

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 841

Tyr	Ala	Val	Tyr	Thr	Val	Val	Ser	Ser	His	Glu	Gln	Phe	Thr	Lys
1				5					10					15

<210> SEQ ID NO 842

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 842

Tyr	Asp	Ile	Glu	Phe	Glu	Asp	Lys
1					5		

<210> SEQ ID NO 843

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 843

Tyr	Glu	Gly	Val	Val	Asp	Ile	Phe	Gln	Thr	Val	Lys
1				5						10	

<210> SEQ ID NO 844

<211> LENGTH: 12

<212> TYPE: PRT

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<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 844

Tyr Glu Gly Val Val Asp Met Phe Gln Thr Val Lys
1 5 10

<210> SEQ ID NO 845

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 845

Tyr Glu Val Thr Tyr Arg
1 5

<210> SEQ ID NO 846

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 846

Tyr Glu Val Thr Tyr Arg Lys
1 5

<210> SEQ ID NO 847

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 847

Tyr Glu Val Thr Tyr Arg Lys Lys
1 5

<210> SEQ ID NO 848

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 848

Tyr Phe Asp Trp Ile Leu Ile Ser Arg
1 5

<210> SEQ ID NO 849

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 849

Tyr Phe Asp Trp Ile Leu Ile Ser Arg Arg
1 5 10

<210> SEQ ID NO 850

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 850

Tyr Phe Ile Glu Asp Gly Arg
1 5

<210> SEQ ID NO 851

<211> LENGTH: 7

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<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 851

Tyr Phe Trp Thr Gly Leu Arg
1 5

<210> SEQ ID NO 852
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 852

Tyr Gly Ile Gln Glu Lys
1 5

<210> SEQ ID NO 853
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 853

Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
1 5 10 15

Tyr Lys

<210> SEQ ID NO 854
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 854

Tyr Ile Ala Phe Asp Phe His Lys
1 5

<210> SEQ ID NO 855
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 855

Tyr Ile Glu Tyr Gln Gly Ala Glu Lys
1 5

<210> SEQ ID NO 856
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 856

Tyr Lys Pro Leu Pro Gln Ile Ser Lys
1 5

<210> SEQ ID NO 857
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 857

Tyr Lys Pro Met Met Ile Ile Thr Glu Tyr Met Glu Asn Gly Ala Leu
1 5 10 15

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Asp Lys

<210> SEQ ID NO 858
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 858

Tyr Lys Pro Thr Pro Ile Pro Ile Lys
1 5

<210> SEQ ID NO 859
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 859

Tyr Leu Ala Glu Met Ser Tyr Val His Arg
1 5 10

<210> SEQ ID NO 860
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 860

Tyr Leu Ala Asn Met Asn Tyr Val His Arg
1 5 10

<210> SEQ ID NO 861
<211> LENGTH: 32
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 861

Tyr Leu Cys Gly Ala His Ser Asp Gly Gln Leu Gln Glu Gly Ser Pro
1 5 10 15

Ile Gln Ala Trp Gln Leu Phe Val Asn Glu Glu Ser Thr Ile Pro Arg
20 25 30

<210> SEQ ID NO 862
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 862

Tyr Leu Gln Val Ser Gln Gln Leu Gln Gln Thr Asn Arg
1 5 10

<210> SEQ ID NO 863
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 863

Tyr Met Thr Glu Thr Trp Asp Pro Ser His Ala Pro Asp Asn Phe Arg
1 5 10 15

<210> SEQ ID NO 864
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 864

Tyr Pro Asp Leu Ile Ala Glu Leu Leu Arg
1 5 10

<210> SEQ ID NO 865

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 865

Tyr Pro Glu Val Gly Asp Leu Arg
1 5

<210> SEQ ID NO 866

<211> LENGTH: 5

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 866

Tyr Pro Trp His Arg
1 5

<210> SEQ ID NO 867

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 867

Tyr Gln His Thr Gly Lys
1 5

<210> SEQ ID NO 868

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 868

Tyr Gln Val Asn Asn Leu Gly Gln Arg
1 5

<210> SEQ ID NO 869

<211> LENGTH: 20

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 869

Tyr Gln Tyr Phe Val Val Asp Pro Met Ala Glu Tyr Asn Met Pro Gln
1 5 10 15

Tyr Ile Leu Arg
20

<210> SEQ ID NO 870

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 870

Tyr Ser Ala Pro Ala Asn Leu Tyr Val Arg
1 5 10

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<210> SEQ ID NO 871
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 871

Tyr Ser Glu Pro Pro His Gly Leu Thr Arg
1 5 10

<210> SEQ ID NO 872
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 872

Tyr Ser Ile Gly Gly Leu Ser Pro Phe Ser Glu Tyr Ala Phe Arg
1 5 10 15

<210> SEQ ID NO 873
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 873

Tyr Ser Val Ala Gly Leu Ser Pro Tyr Ser Asp Tyr Glu Phe Arg
1 5 10 15

<210> SEQ ID NO 874
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 874

Tyr Ser Tyr Asn Thr Glu Trp Arg
1 5

<210> SEQ ID NO 875
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 875

Tyr Val Cys Lys Arg Lys
1 5

<210> SEQ ID NO 876
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 876

Tyr Val Gln Asn Gly Thr Tyr Thr Val Lys
1 5 10

<210> SEQ ID NO 877
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 877

Ala Ala Gly Ser Arg Asp Val Ser Leu Ala Lys Ala Asp Ala Ala Pro
1 5 10 15

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Asp Glu Lys

<210> SEQ ID NO 878
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 878

Ala Glu Ala Phe Gly Met Asp Pro Ala Arg Pro Asp Gln Ala Ser Thr
1 5 10 15

Val Ala Val Lys
20

<210> SEQ ID NO 879
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 879

Ala Glu Asp Ile Ile Lys
1 5

<210> SEQ ID NO 880
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 880

Ala Glu Leu Arg Gly Leu Lys
1 5

<210> SEQ ID NO 881
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 881

Ala Gly Phe Val Gly Gly Gln Phe Trp Ser Val Tyr Thr Pro Cys Asp
1 5 10 15

Thr Gln Asn Lys
20

<210> SEQ ID NO 882
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 882

Ala Asn Leu Ser Gln Val Ala Asp His Leu Asp His Ile Lys
1 5 10

<210> SEQ ID NO 883
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 883

Ala Arg Glu Val Ile Pro Arg
1 5

<210> SEQ ID NO 884

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<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 884

Ala Thr Gly Thr Ala Phe Arg Arg
1 5

<210> SEQ ID NO 885
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 885

Ala Val Leu Gly Asp Arg
1 5

<210> SEQ ID NO 886
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 886

Ala Val Thr Ser Pro Ala Val Gly Arg
1 5

<210> SEQ ID NO 887
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 887

Cys Gly Val Ser Asn Lys Asp Ile Glu Lys
1 5 10

<210> SEQ ID NO 888
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 888

Cys Leu Asn Pro Val Pro Ala Val Pro Ser Pro Ser Pro Ser Val Arg
1 5 10 15

Lys

<210> SEQ ID NO 889
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 889

Asp Cys Lys Ile Arg Val Phe Ile Gly Gly Lys
1 5 10

<210> SEQ ID NO 890
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 890

Asp Ile Ala Pro Val Leu Asp Leu Lys
1 5

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<210> SEQ ID NO 891
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 891

Asp Ile Met Lys Lys Thr Ile Asn Phe Ala Arg
1 5 10

<210> SEQ ID NO 892
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 892

Asp Pro Cys Phe His Pro Gly Tyr Lys
1 5

<210> SEQ ID NO 893
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 893

Asp Pro Glu Leu Arg
1 5

<210> SEQ ID NO 894
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 894

Asp Ser Pro Val Ile Asp Gly His Asn Asp Leu Pro Trp Gln Leu Leu
1 5 10 15

Asp Met Phe Asn Asn Arg
20

<210> SEQ ID NO 895
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 895

Asp Ser Gln Met Gln Asn Pro Tyr Ser Arg
1 5 10

<210> SEQ ID NO 896
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 896

Asp Thr Tyr Leu Lys
1 5

<210> SEQ ID NO 897
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 897

Asp Val Leu Pro Gln Lys
1 5

<210> SEQ ID NO 898

<211> LENGTH: 5

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 898

Glu Gly Ile Ala Lys
1 5

<210> SEQ ID NO 899

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 899

Glu Ile Asp Val Ser Tyr Val Lys
1 5

<210> SEQ ID NO 900

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 900

Glu Leu Asn Glu His Phe Lys Ser Lys
1 5

<210> SEQ ID NO 901

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 901

Glu Leu Arg Glu Val Arg
1 5

<210> SEQ ID NO 902

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 902

Glu Leu Val Ser Leu Lys
1 5

<210> SEQ ID NO 903

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 903

Glu Gln Asp Ile Ala Asp Lys
1 5

<210> SEQ ID NO 904

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 904

Glu Gln Leu Thr Val Ile Arg
1 5

<210> SEQ ID NO 905

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 905

Glu Arg Glu Ala Gln Leu Val Lys
1 5

<210> SEQ ID NO 906

<211> LENGTH: 5

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 906

Glu Arg Met Phe Arg
1 5

<210> SEQ ID NO 907

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 907

Glu Ser Lys Ser Ile Lys
1 5

<210> SEQ ID NO 908

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 908

Glu Val Cys Gln Leu Leu Leu Arg
1 5

<210> SEQ ID NO 909

<211> LENGTH: 5

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 909

Glu Val Ile Pro Arg
1 5

<210> SEQ ID NO 910

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 910

Phe Leu Ile Thr Arg Arg Arg
1 5

<210> SEQ ID NO 911

<211> LENGTH: 13

<212> TYPE: PRT

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<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 911

Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys
1 5 10

<210> SEQ ID NO 912

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 912

Phe Ser Asp Val Thr Gly Lys Ile Lys
1 5

<210> SEQ ID NO 913

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 913

Gly His Glu Val Ala Ala Met Leu Lys
1 5

<210> SEQ ID NO 914

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 914

Gly Asn Ser Ala Gly Gly Leu Gln His Arg Val Thr Ala Lys
1 5 10

<210> SEQ ID NO 915

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 915

Gly Pro Gly Ile Ser Lys
1 5

<210> SEQ ID NO 916

<211> LENGTH: 18

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 916

Gly Thr Leu Ser Pro Lys Asp Ala Leu Thr Asp Leu Thr Gly Asp Ala
1 5 10 15

Glu Arg

<210> SEQ ID NO 917

<211> LENGTH: 16

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 917

His Ile Glu Glu Glu Asn Leu Ile Asp Glu Asp Phe Gln Asn Leu Lys
1 5 10 15

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<210> SEQ ID NO 918
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 918

His Ser Arg Val Thr Val Ala Ile Pro Leu Lys
1 5 10

<210> SEQ ID NO 919
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 919

Ile Asp Glu Lys Arg
1 5

<210> SEQ ID NO 920
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 920

Ile Phe Gln Ala Leu Cys Lys
1 5

<210> SEQ ID NO 921
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 921

Ile Ile Pro Lys
1

<210> SEQ ID NO 922
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 922

Ile Lys Gln Leu Arg
1 5

<210> SEQ ID NO 923
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 923

Ile Leu Tyr Asp Asp Gly Lys Met Val Glu Glu Val Asp Gly Arg
1 5 10 15

<210> SEQ ID NO 924
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 924

Ile Arg Thr Ser Thr Pro Thr Gly His Gly Ala Ser Pro Ala Lys
1 5 10 15

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<210> SEQ ID NO 925
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 925

Ile Ser Tyr Arg Ile Leu Arg
1 5

<210> SEQ ID NO 926
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 926

Ile Tyr Ile Val Arg
1 5

<210> SEQ ID NO 927
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 927

Lys Cys Ala Gln Leu Thr Val Asn Leu Thr Arg
1 5 10

<210> SEQ ID NO 928
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 928

Lys Arg Ser Ala Pro Thr Ser Arg
1 5

<210> SEQ ID NO 929
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 929

Leu Ala Leu Lys
1

<210> SEQ ID NO 930
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 930

Leu Ala Ser Ser Lys Ala His Thr Ser Arg
1 5 10

<210> SEQ ID NO 931
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 931

Leu Glu Asp Pro His Val Asp Ile Ile Arg Arg
1 5 10

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<210> SEQ ID NO 932
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 932

Leu Phe Gly Glu Lys
1 5

<210> SEQ ID NO 933
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 933

Leu Lys Asn Lys Glu Glu Val Leu Lys
1 5

<210> SEQ ID NO 934
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 934

Leu Leu Asp Phe Glu Lys
1 5

<210> SEQ ID NO 935
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 935

Leu Leu His Gly Gln Asn Gly Ser Val Pro Asn Gly Gln Thr Pro Leu
1 5 10 15

Lys

<210> SEQ ID NO 936
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 936

Leu Leu Ile Glu His Gly Ala Asp Ile Arg
1 5 10

<210> SEQ ID NO 937
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 937

Leu Leu Gln Ala Ile Ala Lys
1 5

<210> SEQ ID NO 938
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 938

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Leu Leu Ser Asp Lys
1 5

<210> SEQ ID NO 939
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 939

Leu Leu Ser Asp Pro Asn Tyr Gly Val His Leu Pro Ala Val Lys
1 5 10 15

<210> SEQ ID NO 940
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 940

Leu Leu Val Pro Lys Asp Arg
1 5

<210> SEQ ID NO 941
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 941

Leu Asn Pro Lys
1

<210> SEQ ID NO 942
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 942

Leu Asn Val Glu Glu Arg Ser Val Gly Pro Leu Thr Arg
1 5 10

<210> SEQ ID NO 943
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 943

Leu Gln Cys Glu Asn Val Gln Glu Ile Pro Val Phe Gly Ile Val Pro
1 5 10 15

Ala Ile Ile Gln Thr Pro Ser Arg
20

<210> SEQ ID NO 944
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 944

Leu Arg Gln Gly Thr Leu Arg
1 5

<210> SEQ ID NO 945
<211> LENGTH: 7

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<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 945

Leu Arg Thr Ser Ala Ile Arg
1 5

<210> SEQ ID NO 946
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 946

Leu Ser Ala Arg Asn Lys
1 5

<210> SEQ ID NO 947
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 947

Leu Ser Asp Ala Gly Gln Tyr Leu Cys Gln Ala Gly Asp Asp Ser Asn
1 5 10 15

Ser Asn Lys Lys
20

<210> SEQ ID NO 948
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 948

Leu Ser Gly Val Glu Asp His Val Lys
1 5

<210> SEQ ID NO 949
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 949

Leu Thr Val Leu Arg
1 5

<210> SEQ ID NO 950
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 950

Leu Thr Trp Thr Asn Pro Ser Ile Lys
1 5

<210> SEQ ID NO 951
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 951

Leu Val Leu Gly Lys
1 5

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<210> SEQ ID NO 952
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 952

Met Arg Tyr Glu Gly Val Val Asp Ile Phe Gln Thr Val Lys
1 5 10

<210> SEQ ID NO 953
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 953

Met Thr Pro Pro Ser Arg Ala Glu Ala Gly Val Arg Arg
1 5 10

<210> SEQ ID NO 954
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 954

Met Val Gly Asp Val Thr Gly Ala Gln Ala Tyr Ala Ser Thr Ala Lys
1 5 10 15

<210> SEQ ID NO 955
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 955

Asn Ala Asp Leu Gln Val Leu Lys Pro Glu Pro Glu Leu Val Tyr Glu
1 5 10 15

Asp Leu Arg

<210> SEQ ID NO 956
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 956

Asn Asn Leu Val Glu Ile Ile Leu Asp Ile Asn Val Ser Gln Leu Thr
1 5 10 15

Glu Arg

<210> SEQ ID NO 957
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 957

Asn Pro Ile Ala Lys
1 5

<210> SEQ ID NO 958
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 958

Asn Pro Val Asp Val Lys
1 5

<210> SEQ ID NO 959

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 959

Asn Gln Thr Ala Val Arg
1 5

<210> SEQ ID NO 960

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 960

Asn Arg Ala Gly Leu Gly Glu Glu Phe Glu Lys Glu Ile Arg
1 5 10

<210> SEQ ID NO 961

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 961

Asn Arg Ser Leu Ser Arg Val Arg
1 5

<210> SEQ ID NO 962

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 962

Gln Ile Leu Asp Gln Thr Pro Val Lys
1 5

<210> SEQ ID NO 963

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 963

Gln Leu Val Glu Ala Leu Asp Lys
1 5

<210> SEQ ID NO 964

<211> LENGTH: 18

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 964

Gln Pro His Tyr Ser Ala Phe Gly Ser Val Gly Glu Trp Leu Arg Ala
1 5 10 15

Ile Lys

<210> SEQ ID NO 965

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<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 965

Arg Asp Leu Gly Ser Arg Leu Gln Ala Gln Arg
1 5 10

<210> SEQ ID NO 966
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 966

Arg Arg Asp Leu Ser Gln Met Glu Ala Leu Lys
1 5 10

<210> SEQ ID NO 967
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 967

Arg Ser Ser Ala Ala Gly Glu Gly Thr Leu Ala Arg
1 5 10

<210> SEQ ID NO 968
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 968

Ser Ala Ala Ala Ser Asn Tyr Val
1 5

<210> SEQ ID NO 969
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 969

Ser Asp Leu Gln Arg Pro Asn Pro Gln Ser Pro Phe Cys Val Ala Ser
1 5 10 15

Ser Leu Lys

<210> SEQ ID NO 970
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 970

Ser Leu Gln Glu Ala Asn Ala Glu Lys
1 5

<210> SEQ ID NO 971
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 971

Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly Met
1 5 10 15

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Arg Leu Leu Arg
20

<210> SEQ ID NO 972
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 972

Ser Gln Thr Tyr Glu Ser Asp Gly Lys
1 5

<210> SEQ ID NO 973
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 973

Ser Ser Val Lys Glu Leu Leu Lys
1 5

<210> SEQ ID NO 974
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 974

Ser Thr Gly Phe Thr Asn Leu Gly Ala Glu Gly Ser Val Phe Pro Lys
1 5 10 15

<210> SEQ ID NO 975
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 975

Ser Thr Gly Thr Ile Ser Val Ile Ser Ser Gly Leu Asp Arg Glu Lys
1 5 10 15

<210> SEQ ID NO 976
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 976

Thr Ala Ile Glu Ile Leu Ala Trp Gly Leu Arg
1 5 10

<210> SEQ ID NO 977
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 977

Thr Ala Arg Ala Thr Gly Ala Ser Arg
1 5

<210> SEQ ID NO 978
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 978

Thr Ala Thr Gln Pro Leu Leu Lys
1 5

<210> SEQ ID NO 979

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 979

Thr Ala Thr Val Val Met Met Thr Arg Leu Glu Glu Lys
1 5 10

<210> SEQ ID NO 980

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 980

Thr Glu Leu Leu Ala Ala Asp Ser Leu Ser Lys
1 5 10

<210> SEQ ID NO 981

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 981

Thr Gly Arg Pro Val Glu Pro Glu Ser Glu Phe Ile Ile Lys
1 5 10

<210> SEQ ID NO 982

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 982

Thr Leu Ala Glu Val Cys Leu Gly Gln Lys
1 5 10

<210> SEQ ID NO 983

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 983

Thr Leu Arg Leu Gly Pro Leu Ser Lys
1 5

<210> SEQ ID NO 984

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 984

Thr Asn Gly Thr Gly Arg Val Arg
1 5

<210> SEQ ID NO 985

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 985

Thr Ser Lys Thr Thr Phe Gln Leu Glu Leu Pro Val Lys
1 5 10

<210> SEQ ID NO 986

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 986

Thr Ser Asn Gly Arg Leu Pro Val Lys
1 5

<210> SEQ ID NO 987

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 987

Thr Val Thr Ile Asn Cys Pro Phe Lys
1 5

<210> SEQ ID NO 988

<211> LENGTH: 21

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 988

Val Ala Ser Leu Ile Gly Val Glu Gly Gly His Ser Ile Asp Ser Ser
1 5 10 15
Leu Gly Val Leu Arg
20

<210> SEQ ID NO 989

<211> LENGTH: 19

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 989

Val Glu Ala Ser Asn Pro Tyr Val Glu Pro Arg Phe Leu Tyr Leu Gly
1 5 10 15
Pro Phe Lys

<210> SEQ ID NO 990

<211> LENGTH: 5

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 990

Val Phe Pro Gly Lys
1 5

<210> SEQ ID NO 991

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 991

Val Lys Cys Asp Gln Tyr Trp Pro Ala Arg
1 5 10

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<210> SEQ ID NO 992
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 992

Val Lys Thr Thr Ser Leu Thr Glu Lys Lys
1 5 10

<210> SEQ ID NO 993
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 993

Val Leu Ala Ala Asn Asn Val Arg
1 5

<210> SEQ ID NO 994
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 994

Val Leu Asp Val Val Glu Arg
1 5

<210> SEQ ID NO 995
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 995

Val Leu Leu Glu Lys
1 5

<210> SEQ ID NO 996
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 996

Val Leu Thr Asp Ile Lys
1 5

<210> SEQ ID NO 997
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 997

Val Pro Ala His Gln Val Leu Phe Ser Arg Arg
1 5 10

<210> SEQ ID NO 998
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 998

Val Gln Ala Val Asn Ser Gln Gly Lys

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1 5

<210> SEQ ID NO 999
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 999

Val Thr Ala Ala Gly Gln Thr Lys Arg Thr Arg
1 5 10

<210> SEQ ID NO 1000
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 1000

Val Thr Ala Ile Asn Lys
1 5

<210> SEQ ID NO 1001
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 1001

Val Thr Leu Pro Ala Gly Pro Asp Ile Leu Arg
1 5 10

<210> SEQ ID NO 1002
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 1002

Val Val Ile Ser Ile Arg
1 5

<210> SEQ ID NO 1003
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 1003

Val Val Asn Val Ser Asp Leu Tyr Lys
1 5

<210> SEQ ID NO 1004
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 1004

Tyr Phe Thr Ala Ser Leu Pro Phe Glu Lys
1 5 10

<210> SEQ ID NO 1005
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 1005

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```
Tyr Gly Pro Gly Glu Pro Ser Pro Val Ser Glu Thr Val Val Thr Pro
1           5           10           15
```

```
Glu Ala Ala Pro Glu Lys
20
```

```
<210> SEQ ID NO 1006
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens
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```
<400> SEQUENCE: 1006
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```
Tyr Leu Asn Asn Leu Tyr Lys
1           5
```

```
<210> SEQ ID NO 1007
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens
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<400> SEQUENCE: 1007
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```
Ile Gly Thr Phe Cys Ser Asn Gly Thr Val Ser Arg Ile Lys
1           5           10
```

```
<210> SEQ ID NO 1008
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens
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<400> SEQUENCE: 1008
```

```
Gln Thr Pro Ala Asp Gly Glu Ala Ser Gly Glu Ser Glu Pro Ala Lys
1           5           10           15
```

1-89. (canceled)

90. A method comprising administering to a patient having increased levels of OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 as compared to a healthy control a composition comprising an affinity reagent capable of specific binding to OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 as defined in SEQ ID Nos: 1-48 respectively, or a fragment thereof, and a pharmaceutically acceptable diluent or carrier.

91. The method according to claim **90**, said patient has B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (par-

ticularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma, or has increased likelihood of developing B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma.

92. The method of claim **90**, wherein said affinity reagent comprises a label.

93. The method of claim **91**, wherein said affinity reagent comprises a label.

94. The method according to claim **92**, wherein said label is a detectable label or therapeutic moiety.

95. The method according to claim **93**, wherein said label is a detectable label or therapeutic moiety.

96. The method according to claim **94**, wherein said therapeutic moiety is selected from the group consisting of a cytotoxic moiety and a radioactive isotope.

97. The method according to claim **95**, wherein said therapeutic moiety is selected from the group consisting of a cytotoxic moiety and a radioactive isotope.

98. The method of claim **90**, wherein said affinity reagent is selected from the group consisting of fusion proteins and antibodies.

99. The method of claim **98**, wherein said antibody is a monoclonal antibody, a humanized antibody, a bispecific antibody, a non-fucosylated antibody, an antibody fragment, or an antibody mimetic.

100. The method of claim **90**, wherein said affinity reagent has cytotoxicity against OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 antigen expressing cells in the presence of a human complement or in the presence of human immune effector cells.

101. A method of screening for or diagnosis of, or for monitoring or assessing treatment of B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma in a human subject, comprising analyzing a sample from a patient for:

a. the presence or absence; or

b. the quantity;

of OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271, or a fragment thereof whereby an increase in the level of OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271, or a fragment thereof relative to a healthy control is indicative of the presence of or increased likelihood of devel-

oping B-cell non-Hodgkin's lymphoma, breast cancer, cervical cancer, colorectal cancer, gastric cancer, glioblastoma, hepatocellular carcinoma, lung cancer, lymphoid leukaemia (particularly acute T-cell leukaemia and chronic lymphocytic leukaemia), melanoma, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer or retinoblastoma.

102. The method of claim **73** which comprises contacting said sample with one or more anti-:

OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 affinity reagents capable of specific binding to OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 as defined in SEQ ID Nos: 1-48 respectively, or a fragment or derivative thereof.

103. The method according to claim **101** wherein said analyzing comprises imaging said sample.

104. The method according to claim **102** wherein said analyzing comprises imaging said sample.

105. The method of claim **103**, wherein said affinity reagent comprises a detectable label.

106. The method of claim **104**, wherein said affinity reagent comprises a detectable label.

107. The method of claim **101**, wherein said method comprises detecting OGTA002, OGTA009, OGTA016, OGTA028, OGTA037, OGTA041, OGTA053, OGTA054, OGTA072, OGTA074, OGTA076, OGTA085, OGTA087, OGTA088, OGTA089, OGTA091, OGTA098, OGTA101, OGTA104, OGTA106, OGTA112, OGTA113, OGTA119, OGTA124, OGTA126, OGTA156, OGTA159, OGTA168, OGTA169, OGTA174, OGTA176, OGTA177, OGTA197, OGTA202, OGTA203, OGTA206, OGTA213, OGTA214, OGTA222, OGTA236, OGTA237, OGTA247, OGTA248, OGTA249, OGTA257 or OGTA271 mRNA.

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