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(54) **SECRETED AND TRANSMEMBRANE  
POLYPEPTIDES AND NUCLEIC ACIDS  
ENCODING THE SAME**

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**Related U.S. Application Data**

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2001, now abandoned, which is a continuation of application No. 09/908,827, filed on Jul. 18, 2001, which is a continuation of application No. 09/887,879, filed on Jun. 21, 2001, which is a continuation of application No. 09/886,342, filed on Jun. 19, 2001, now abandoned, which is a continuation of application No. 09/882,636, filed on Jun. 14, 2001, now abandoned, which is a continuation of application No. 09/874,503, filed on Jun. 5, 2001, which is a continuation of application No. 09/872,035, filed on Jun. 1, 2001, now abandoned, which is a continuation of application No. 09/866,034, filed on May 25, 2001, which is a continuation of application No. 09/866,028, filed on May 25, 2001, which is a continuation of application No. 09/860,216, filed on May 18, 2001, now abandoned, which is a continuation of application No. 09/854,280, filed on May 10, 2001, which is

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435/320.1; 435/325; 536/23.2

(57) **ABSTRACT**

The present invention is directed to novel polypeptides and to nucleic acid molecules encoding those polypeptides. Also provided herein are vectors and host cells comprising those nucleic acid sequences, chimeric polypeptide molecules comprising the polypeptides of the present invention fused to heterologous polypeptide sequences, antibodies which bind to the polypeptides of the present invention and to methods for producing the polypeptides of the present invention.

MSTMFADTLIVFISVCTALLAEGITWVLVYRTDKYKRLKAEVEKQSKKLEKKKETITESAG  
RQQKKKIERQEKLKNNRDLMSVRMKSMAIGFCFTALMGMFNSIFDGRVVAKLPFTPLSY  
IQGLSHRNLLGDDTTDCSFIFLYILCTMSIRQNIQKILGLAPSRAATKQAGGFLGPPPPSGKFS

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-myristoylation sites.**

amino acids 103-109, 163-169

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 53-57

**Related U.S. Application Data**

a continuation of application No. 09/854,208, filed on May 10, 2001, which is a continuation of application No. 09/828,366, filed on Apr. 5, 2001, which is a continuation of application No. 09/816,744, filed on Mar. 22, 2001, which is a continuation of application No. 09/808,689, filed on Mar. 14, 2001, now abandoned, which is a continuation of application No. 09/802,706, filed on Mar. 9, 2001, now abandoned, which is a continuation of application No. 09/796,498, filed on Feb. 28, 2001, now abandoned, which is a continuation of application No. 09/747,259, filed on Dec. 20, 2000.

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Dec. 1, 2000	(WO)	PCT/US00/32678
Dec. 20, 2000	(WO)	PCT/US00/34956
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Jun. 1, 2001	(WO)	PCT/US01/17800
Jun. 20, 2001	(WO)	PCT/US01/19692
Jun. 29, 2001	(WO)	PCT/US01/21066
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Nov. 10, 2000	(WO)	PCT/US00/30873

**FIGURE 1**

GTTACTCGGTGGTGGCGGAGTCTACGGAAGCCGTTTTTCGCTTCACTTTTCCTGGCTGTAGAG  
CGCTTTCCCCCTGGCGGGTGAGAGTGCAGAGACGAAGGTGCGAGATGAGCACTATGTTTCGCG  
GACACTCTCCTCATCGTTTTTATCTCTGTGTGCACGGCTCTGCTCGCAGAGGGCATAACCTG  
GGTCCTGGTTTACAGGACAGACAAGTACAAGAGACTGAAGGCAGAAGTGAAAAACAGAGTA  
AAAAATTGGAAAAGAAGAAGGAAACAATAACAGAGTCAGCTGGTCGACAACAGAAAAAGAAA  
ATAGAGAGACAAGAAGAGAAACTGAAGAATAACAACAGAGATCTATCAATGGTTTCGAATGAA  
ATCCATGTTTGCTATTGGCTTTTGTTTTACTGCCCTAATGGGAATGTTCAATTCCATATTTG  
ATGGTAGAGTGGTGGCAAAGCTTCCTTTTACCCCTCTTTCTTACATCCAAGGACTGTCTCAT  
CGAAATCTGCTGGGAGATGACACCACAGACTGTTTCCTTCATTTTCCTGTATATTCTCTGTAC  
TATGTGCGATTCGACAGAACATTGAGAAGATTCTCGGCCTTGCCCCCTTCACGAGCCGCCACCA  
AGCAGGCAGGTGGATTTCTTGGCCCACCACCTCCTTCTGGGAAGTTCTCTTGAACTCAAGAA  
CTCTTTATTTTCTATCATTCCTTCTAGACACACACACATCAGACTGGCAACTGTTTTGTAGC  
AAGAGCCATAGGTAGCCTTACTACTTGGGCCTCTTTCTAGTTTTGAATTATTTCTAAGCCTT  
TTGGGTATGATTAGAGTGAAAATGGCAGCCAGCAAACCTTGATAGTGCTTTTGGTCCTAGATG  
ATTTTTATCAAATAAGTGGATTGATTAGTTAAGTTCAGGTAATGTTTATGTAATGAAAAACA  
AATAGCATCCTTCTTGTTTCATTTACATAAGTATTTTCTGTGGGACCGACTCTCAAGGCACT  
GTGTATGCCCTGCAAGTTGGCTGTCTATGAGCATTTAGAGATTTAGAAGAAAAATTTAGTTT  
GTTTAACCCCTTGTAACCTGTTTGTTTTGTTGTTGTTTTTTTTTTCAAGCCAAATACATGACATA  
AGATCAATAAAGAGGCCAAATTTTGTAGCTGTTTTATGTACAAGGAGAGATCTGTTTCATTTT  
GTTTTGCCGTATTTCTAGATATAAGTTTTAGCATGGGCCAGGAAGGACTAAAAATAAAGTTT  
TTAAGGTACAAAAA

## **FIGURE 2**

MSTMFADTLLIVFISVCTALLAEGITWVLVYRTDKYKRLKAEVEKQSKKLEKKKETITESAG  
RQQKKKIERQEEKLKNNNRDLSMVRMKSMFAIGFCFTALMGMFNSIFDGRVVAKLPFTPLSY  
IQGLSHRNLLGDDTTDCSFIFLYILCTMSIRQNIQKILGLAPSRAATKQAGGFLGPPPPSGKFS

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-myristoylation sites.**

amino acids 103-109, 163-169

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 53-57



**FIGURE 3**

AGCCGGGGGCGGGTTTGAAGACGCGTCGTTGGGTTTTTGGAGGCCGTGAAACAGCCGTTTGAG  
TTTGGCTGCGGGTGGAGAACGTTTGTCAAGGGGCCCCGGCCAAGAAGGAGGCCCGCCTGTTACG  
ATGGTGTCCATGAGTTTCAAGCGGAACCGCAGTGACCGGTTCTACAGCACCCGGTGCTGCGG  
CTGTTGCCATGTCCGCACCGGGACGATCATCCTGGGGACCTGGTACATGGTAGTAAACCTAT  
TGATGGCAATTTTGCTGACTGTGGAAGTGACTCATCCAACTCCATGCCAGCTGTCAACATT  
CAGTATGAAGTCATCGGTAATTACTATTTCGTCTGAGAGAATGGCTGATAATGCCTGTGTTCT  
TTTTGCCGTCTCTGTTCTTATGTTTATAATCAGTTCAATGCTGGTTTTATGGAGCAATTTCTT  
ATCAAGTGGGTGGCTGATTCCATTCTTCTGTTACCGACTTTTTGACTTCGTCCTCAGTTGC  
CTGGTTGCTATTAGTTCTCTCACCTATTTGCCAAGAATCAAAGAATATCTGGATCAACTACC  
TGATTTTCCCTACAAAGATGACCTCCTGGCCTTGGACTCCAGCTGCCTCCTGTTCAATTGTTT  
TTGTGTTCTTTGCCTTATTCATCATTTTTTAAGGCTTATCTAATTAAGTGTGTTTGGAACTGC  
TATAAATACATCAACAACCGAAACGTGCCGGAGATTGCTGTGTACCCTGCCTTTGAAAGCAC  
CTCCTCAGTACGTTTTGCCAACCTATGAAATGGCCGTGAAAAATGCCTGAAAAAGAACCACCA  
CCTCCTTACTTACCTGCCTGAAGAAATTCTGCCTTTGACAATAAATCCTATACCAGCTTTTTT  
GTTTGTTTATGTTACAGAATGCTGCAATTCAGGGCTCTTCAAACCTGTTTGATATAAAATAT  
GTTGTCTTTTTGTTTAAGCATTTATTTTCAAACACTAAGGAGCTTTTTTGACATCTGTAAACG  
TCTTTTTGTTTTTTTGTAAAGTCTTTTACATTTTAATAGTTTTTGAAGACAATCTAGGTAA  
GCAAGAGCAAAGTGCCATTGTTTGCCTTTAATTGGGGGGTGGGAAGGGAAAGAGGGTACTTG  
CCACATAGTTTCCTTTTTTAAGTGCCTTTCTTTATATAATCGTTTGCATTTTGTACTTGCT  
ACCCTGAGTACTTTCAGGAAGACTGACTTAAATATTTCGGGGTGAGTAAGTAGTTGGGTATAA  
GATCTGAACTTTTCATCTGCAGAGGCAAGAAAAATATTGACATTGTGACTTGACTGTGGAA  
GATGATGGTTGCATGTTTCTAGTTTGTATATGTTTCCATCTTTGTGATAAGATGATTTAATA  
AATCTCTTTAAATACTAAAAAAAAAAAAAAAAA

## **FIGURE 4**

MVSMSFKRNRSDRFYSTRCCGCCHVRTGTIILGTWYMVVNLLMAILLTVEVTHPNSMPAVNI  
QYEVIGNYYSSERMADNACVLFAVSVLMFIISSMLVYGAIYQVGWLIPFFCYRLFDFVLSC  
LVAISSLTYLPRIKYLDQLPDFPYKDDLALDSSCLLFIVLVFFALFIIIFKAYLINCWNC  
YKYINNRRNVPEIAVYPAFESTSSVRFANL

**Important features of the protein:**

**Transmembrane domain (Possible type II transmembrane protein):**

amino acids 30-49, 81-100, 111-131, 158-175

**N-glycosylation site.**

amino acids 9-13

**Tyrosine kinase phosphorylation sites.**

amino acids 8-16, 193-202

**N-myristoylation site.**

amino acids 68-74

# **FIGURE 5**

CCCGCTGGCCCGTCAGTGCTCTCCCCGTCGTTTGCCCTCTCCAGTTCCCCCAGTGCCCTGCCC  
 TACGCACCCCCGATGGCGGAGCTGCGGCCTAGCGGCGCCCCCGGCCCCACCGCGCCCCCGGCC  
 CCTGGCCCGACTGCCCCCCCCGGCCTTCGCTTCGCTCTTTCCCCCGGGACTGCACGCCATCTA  
 CGGAGAGTGCCGCCGCCTTTACCCTGACCAGCCGAACCCGCTCCAGGTTACCGCTATCGTCA  
 AGTACTGGTTGGGTGGCCAGACCCCTTGGACTATGTTAGCATGTACAGGAATGTGGGGAGC  
 CCTTCTGCTAACATCCCCGAGCACTGGCACTACATCAGCTTCGGCCTGAGTGATCTCTATGG  
 TGACAACAGAGTCCATGAGTTTACAGGAACAGATGGACCTAGTGGTTTTTGCTTTGAGTTGA  
 CCTTTCGTCTGAAGAGAGAACTGGGGAGTCTGCCCCACCAACATGGCCCGCAGAGTTAATG  
 CAGGGCTTGGCACGATACGTGTTCCAGTCAGAGAACACCTTCTGCAGTGGGGACCATGTGTCT  
 CTGGCACAGCCCTTTGGATAACAGTGAGTCAAGAATTACGCACATGCTGCTGACAGAGGACC  
 CACAGATGCAGCCCGTGCAGACACCCCTTTGGGGTAGTTACCTTCCTCCAGATCGTTGGTGTC  
 TGCAGTGAAGAGCTACACTCAGCCCAGCAGTGGAACGGGCAGGGCATCCTGGAGCTGCTGCG  
 GACAGTGCTTATTGCTGGCGGCCCTGGCTGATAACTGACATGCGGAGGGGAGAGACCATAT  
 TTGAGATCGATCCACACCTGCAAGAGAGAGTTGACAAAGGCATCGAGACAGATGGCTCCAAC  
 CTGAGTGGTGTCAGTGCCAAAGTGTGCTGGGATGACCTGAGCCGGCCCCCGAGGATGACGA  
 GGACAGCCGGAGCATCTGCATCGGCACACAGCCCCGGCGACTCTCTGGCAAAGACACAGAGC  
 AGATCCGGGAGACCCCTGAGGAGAGGACTCGAGATCAACAGCAAACCTGTCTTCCACCAATC  
 AACCTCAGCGGCAGAATGGCCTCGCCACGACCGGGCCCCGAGCCGCAAAGACAGCCTGGA  
 AAGTGACAGCTCCACGGCCATCATTCCTCATGAGCTGATTGCGACGCGGCAGCTTGAGAGCG  
 TACATCTGAAATTCAACCAGGAGTCCGGAGCCCTCATTCCTCTCTGCCTAAGGGGCAGGCTC  
 CTGCATGGACGGCACTTTACATATAAAAGTATCACAGGTGACATGGCCATCACGTTTGTCTC  
 CACGGGAGTGGAAGGCGCCTTTGCCACTGAGGAGCATCCTTACGCGGCTCATGGACCTGGT  
 TACAACCTTGAACCTATCCTCGGAGCTCTGCCCTCCCGTCTTGAACGTCTTTCTGCCCTGA  
 GGAGAGGGTAGTCAGCATCTCCAATTTTCAGCAGCTCAAGAACCTTGGCCCCCACAGGACTT  
 CGCAGATGTACATTGCCCCCTCAGTCCCCCTGAATGCCCTTCGGACCCAACCCCAATTCCCCA  
 AGCCCCTGACCCCCTAGCTGCCGGGGTTCCCACTCCAGTGCCACAACCCCCTCACCTCCCC  
 TGGCAGCCCCCTCAGCGAGCCTGAGGCCCAGCACCCGCTGGCTCCCCAGCACATGGTCCCCCTC  
 CCATGGGCTGTTGCCCAGGGAACCGGGGCGCGGTGGGAACGAGCTGCTGGCCTCGGCATGTT  
 TCAATAAAGTTGCTGTGCTGGGAG

**FIGURE 6**

MAELRPSGAPGPTAPPAPGPTAPPAPAFASLFPPGLHAIYGECCRLYPDQPNPLQVTAIVKYWL  
GGPDPLDYVSMYRNVGSPSANIPEHWHYISFGLSDLYGDNRVHEFTGTDGPSGFGFELTFRL  
KRETGESAPPTWPAELMQGLARYVFQSENTFCSGDHVSWHSPLDNSESRIQHMLLTEDPQM  
PVQTPFGVVTFLQIVGVCTEELHSAQQWNGQGILELLRTVPIAGGPWLITDMRRGETIFEID  
PHLQERVVDKGIETDGSNLSGVSAKCAWDDL SRPPEDDEDSRSICIGTQPRRLSGKDTEQIRE  
TLRRGLEINSKPVLPPINPQRQNGLAHDRAPSRKDSLES DSSTAIIPHELIRTRQLESVHLK  
FNQESGALIPLCLRGRLLHGRHFTYKSITGDMAITFVSTGVEGAFATEEHPYAAHG PWLQL

**Important features:**

**N-glycosylation site.**

amino acids 265-268

**FIGURE 7**

CGCGAATGAAGTTTGCATTTTCCTCTGTTCTTGAGCCCAGCTTCTTCTCGTCTCCCACCCCA  
GCTTCCCGGCATTGGAAGAAGGGACCGTCCTCTTCTTGTCTTGGCCACCCAAATCCTGGTA  
TCGAAAGGGTTGAACGGACCGGAAGTGTGCAGCAGCGACGGGTCCCCAGCTAATCGACGCCG  
GAAGTAGCAATTACTAGACAAGCATTCCGCCGCCGGCTTCGCTATGGCGGCAATCCCCCAG  
ATTCTTGGCAGCCACCCAACGTTTACTTGGAGACCAGCATGGGAATCATTTGTGCTGGAGCTG  
TACTGGAAGCATGCTCCAAAGACCTGTAAGAACTTTGCTGAGTTGGCTCGTCGAGGTTACTA  
CAATGGCACAAAATTCCACAGAATTATCAAAGACTTCATGATCCAAGGAGGTGACCCAACAG  
GGACAGGTGAGGTGGTGCATCTATCTATGGCAAACAATTTGAAGATGAAC TTCATCCAGAC  
TTGAAATTCACGGGGGCTGGAATTCTCGCAATGGCCAATGCGGGGCCAGATACCAATGGCAG  
CCAGTTCTTTGTGACCCTCGCCCCACCCAGTGGCTTGACGGCAAACACACCATTTTTGGCC  
GAGTGTGTCAGGGCATAGGAATGGTGAATCGCGTGGGAATGGTAGAAACAAACTCCCAGGAC  
CGCCCTGTGGACGACGTGAAGATCATTAAGGCATACCCTTCTGGGTAGACTTGCTACCCTCT  
TGAGCAGCTCTTCTGAGATGGCCCCAGTGAACCAGCTTCTAGATGACATAGAATGACATGTA  
ATGCTAAATTTTCATTTTGGCTTTGCAAGTCATGAAGCTTAGGAGGCCTGGCATCTTGGGTGA  
GTTAGAGATGGAAGTACATTTTAATAGGATGCTTCTTTTCTCTTCCCCAGTGCCTAGGTTG  
CCAGAGCATTTCACAAAATGCCCTGTTTATCAATAGGTGACTACTTACTACACATGAACCA  
TAATGCTGCTTCTTGTGCATGTCTGCTCTGATATACGTCGAACAATGTAGCAGCCACTGTCA  
TTTCTCAGTGGTTTTGCTAACCAAACTTCTTCCTAAGGAGATTTATATTCTGGCCTACACA  
GCAGTCCTTGATGGCTGACAGCCACAGAATTCCAAACCAAGTAGTGTCTGTCAGCCCTCTTA  
ACTCTGTGCACGCCCTATTTCAGTCTTTTACATTTGTTCTTCTAGGGAATGTATGCATCTCT  
ATATATATTTTCCCTCTCAAAACCAGAACATCAACAGTGCTGTTTCTGACACTTCAGACATC  
CCACGCAAAGCCACATTGAATTTTTGCCAAATGAAAAACACATCCAACAATCAAGTTTCTAA  
GAAGGTGTCAAGTGGGGAATAATAATAATGTATAATAATCAAGAAATTAGTTTATTAAAAGG  
AAGCAGAAGCATTGACCATTTTTTCCAGAGAAGAGGAGAAATCTGTAGTGAGCAAAGGACA  
GACCATGAATCCTCCTTGAGAAGTAGTACTCTCAGAAAGGAGAAGCGCCACTCAAGTTCTTT  
TAACCCAAGACTTTAGAGAAATTAGGTCCAAGATTTTATATGTTTCAAGTTGTTTATGTATAA  
AAATAACTTTCTGGATTTTGTGGGGAGGAGCAGGAGAGGAAGGAAGTTAATACCTATGTAAT  
ACATAGAAACTTCCACAATAAAATGCCATTGATGGTTAAAAA

## **FIGURE 8**

MAAIPDSWQPPNVYLETSMGIIVLELYWKHAPKTCKNFAELARRGYNGTKFHRIIKDFMI  
QGGDPTGTGRGGASIYGKQFEDELHPDLKFTGAGILAMANAGPDTNGSQFFVTLAPTQWLDG  
KHTIFGRVCQGIGMVNRVGMVETNSQDRPVDDVKIIKAYPSG

**Important features:**

**N-glycosylation sites:**

amino acids 49-52, 108-111

**N-myristoylation sites:**

amino acids 64-69, 69-74, 143-148

**Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature:**

amino acids 48-65



## **FIGURE 10**

MWHEARKHERKLRGMMVDYKKRAERRREYYEKIKKDPAQFLQVHGRACKVHLDSAVALAAES  
PVNMMPWQGDINNIDRFVDVRAHLDHIPDYTPPLTTISPEQESDERKCNERYRGLVQNDP  
AGISEEQCLYQIYIDELYGGLQRPSEDEKKKLAEEKKASIGYTYEDSTVAEVEKAAEKPEEEE  
SAAEEESNSDEDEVIPDIDVEVDVDELNQEQVADLNKQATTYGMADGDFVRMLRKDKKEAEA  
IKHAKALEEEKAMYSGRRSRRQRREFREKRLRGRKISPPSYARRDSPTYDPYKRSPSESSSE  
SRSRSRSPTPGREEKITFITSFGGSDEEAAAAAAAAAASGVTTGKPPAPPQPGGPAPGRNAS  
ARRRSSSSSSSSASRTSSSRSSSRSSSRSRGGGYRSGRHARSRSRSWSRSRSRRYSR  
SRSRGRRHSGGGSRDGHRYSRSPARRGGYGPRRRSRSRSHSGDRYRRGGRGLRHHSSSRSR  
SWSLSPSRSLTRSRSHSPSPSQSRSRSRSPSPSPSPAREKLTRPAASPAVGEKLKKTE  
PAAGKETGAAKVTQADASGEAETEDAEGAEQAVQGG

**Important features:**

**N-glycosylation site:**

amino acids 370-373

**Glycosaminoglycan attachment site:**

amino acids 443-446

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

amino acids 159-162, 282-285, 291-294, 374-377, 375-378, 430-433, 440-443, 466-469

**Casein kinase II phosphorylation site:**

amino acids 149-152, 166-169, 171-174, 187-190, 193-196, 195-198, 303-306, 307-310, 335-338, 571-574

**N-myristoylation sites:**

amino acids 118-123, 229-234, 350-355, 446-451, 586-591

**Amidation sites:**

amino acids 263-266, 280-283, 438-441



**FIGURE 11**

GGTAGGCGCGCCAGACCTGAGACGGGTTGGGACTGGGCTGCGTCACGCGCGGGCTCTAAGC  
GCCCCGGGGCCCCGCCCAGTGGCCGGCACAGCCAATCGCAGCGCGGGAAGGCGGTGGGGGCGG  
GGAAGGCCGCTTGAAACTTAAATCCCCGAGGCGGGCGAACCTGCACCAGACCGCGGACGTCT  
GTAATCTCAGAGGCTTGTTTGCTGAGGGTGCCTGCGCAGCTGCGACGGCTGCTGGTTTTGAA  
ACATGAATCTTTCGCTCGTCCTGGCTGCCTTTTGCTTGGGAATAGCCTCCGCTGTTCCAAAA  
TTTGACCAAAATTTGGATACAAAGTGGTACCAGTGGAAGGCAACACACAGAAGATTATATGG  
CGCGAATGAAGAAGGATGGAGGAGAGCAGTGTGGGAAAAGAATATGAAAATGATTGAACTGC  
ACAATGGGGAATACAGCCAAGGGAAACATGGCTTCACAATGGCCATGAATGCTTTTGGTGAC  
ATGACCAATGAAGAATTCAGGCAGATGATGGGTTGCTTTTGAAACCAGAAATTCAGGAAGGG  
GAAAGTGTTCCGTGAGCCTCTGTTTCTTGATCTTCCCAAATCTGTGGATTGGAGAAAGAAAAG  
GCTACGTGACGCCAGTGAAGAATCAGAAAACAGTGTGGTTCTTGTTGGGCTTTTAGTGCGACT  
GGTGCTCTTGAAGGACAGATGTTCCGGAAAACCTGGGAACTTGTCTCACTGAGCGAGCAGAA  
TCTGGTGGACTGTTTCGCGTCCTCAAGGCAATCAGGGCTGCAATGGTGGCTTCATGGCTAGGG  
CCTTCCAGTATGTCAAGGAGAACGGAGGCCTGGACTCTGAGGAATCCTATCCATATGTAGCA  
GTGGATGAAATCTGTAAGTACAGACCTGAGAATTCTGTTGCTAATGACACTGGCTTCACAGT  
GGTCGCACCTGGAAAGGAGAAGGCCCTGATGAAAGCAGTCGCAACTGTGGGGCCCATCTCCG  
TTGCTATGGATGCAGGCCATTTCGTCCTTCCAGTTCTACAAATCAGGCATTTATTTTGAACCA  
GACTGCAGCAGCAAAAACCTGGATCATGGTGTTCGTTGGTGGTTGGCTACGGCTTTGAAGGAGC  
AAATTCGAATAACAGCAAGTATTGGCTCGTCAAAAACAGCTGGGGTCCAGAATGGGGCTCGA  
ATGGCTATGTAAAAATAGCCAAAGACAAGAACAACCACTGTGGAATCGCCACAGCAGCCAGC  
TACCCCAATGTGTGAGCTGATGGATGGTGAGGAGGAAGGACTTAAGGACAGCATGTCTGGGG  
AAATTTTATCTTGAACTGACCAAACGCTTATTGTGTAAGATAAACCACTTGAATCATGGAG  
GATCCAAGTTGAGATTTTAAATCTGTGACATTTTACAAGGGTAAAATGTTACCACTACTTT  
AATTATTGTTATACACAGCTTTATGATATCAAAGACTCATTGCTTAATTCTAAGACTTTTGA  
ATTTTCATTTTTTAAAAAGATGTACAAAACAGTTTGAAATAAATTTTAATTCGTATATA

## **FIGURE 12**

MNLSLVLA AFCLGIASAVPKFDQNLDTKWYQWKATHRRLYGANEEGWRRRAVWEKNMKMIELH  
NGEYSQKGHGFTMAMNAFGDMTNEEFQMMGCFRNQKFRKGKVFREPLFLDLPKSVDWRKKG  
YVTPVKNQKQCGSCWAFSATGALEGQMFRKTGKLVSLSEQNLVDCSRPQGNQGCNGGFMARA  
FQYVKENGGLDSEESYPYVAVDEICKYRPENSVANDTGFTVVAPGKEKALMKAVATVGPISV  
AMDAGHSSFQFYKSGIYFEPDCSSKNLDHGVLVVGYGFEQANSNNKYWLKNSWGP EWGSN  
GYVKIAKDKNNHCGIATAASYPNV

**Important features:**

**Signal sequence**

amino acids 1-17

**N-glycosylation sites.**

amino acids 2-6, 221-225, 292-296

**N-myristoylation sites.**

amino acids 13-19, 93-99, 136-142, 145-151, 174-180, 177-183,  
180-186, 194-200, 288-294, 324-330

**Eukaryotic thiol (cysteine) proteases cysteine active site.**

amino acids 132-144

**Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 275-286

**FIGURE 13**

GGCGGCGTCATGTGATCCGCTTCCCTGCTCCTTTAAGCGTCCACAGGCGGCGGAGCGGCCAC  
AATCACAGCTCCGGGCATTGGGGGAACCCGAGCCGGCTGCGCCGGGGGAATCCGTGCGGGCG  
CCTTCCGTCCCGGTCCCATCCTCGCCGCGCTCCAGCACCTCTGAAGTTTTGCAGCGCCCAGA  
AAGGAGGCGAGGAAGGAGGGAGTGTGTGAGAGGAGGGAGCAAAAAGCTCACCCATAAACATT  
TATTTCAAGGAGAAAAGAAAAAGGGGGGCGCAAAAATGGCTGGGGCAATTATAGAAAACAT  
GAGCACCAAGAAGCTGTGCATTGTTGGTGGGATTCTGCTCGTGTTCCAAATCATCGCCTTTTC  
TGGTGGGAGGCTTGATTGCTCCAGGGCCCACAACGGCAGTGTCTTACATGTCGGTGAAATGT  
GTGGATGCCCGTAAGAACCATCACAAAGACAAAATGGTTCGTGCCTTGGGGACCCAATCATTG  
TGACAAGATCCGAGACATTGAAGAGGCAATTCCAAGGGAAATTGAAGCCAATGACATCGTGT  
TTTCTGTTTACATTCCCCCTCCCCACATGGAGATGAGTCCTTGGTTCCAATTATGCTGTTT  
ATCCTGCAGCTGGACATTGCCTTCAAGCTAAACAACCAATCAGAGAAAATGCAGAAGTCTC  
CATGGACGTTTTCCCTGGCTTACCGTGATGACGCATTTGCTGAGTGGACTGAAATGGCCCATG  
AAAGAGTACCACGGAACTCAAATGCACCTTACATCTCCAAGACTCCAGAGCATGAGGGC  
CGTTACTATGAATGTGATGTCTTCTTTTTCATGGAAATTGGGTCTGTGGCCCATAGTTTAA  
CCTTTTAAACATCCGGCTGCCTGTGAATGAGAAGAAGAAAATCAATGTGGGAATTGGGGAGA  
TAAAGGATATCCGGTTGGTGGGGATCCACCAAAAATGGAGGCTTACCAAGGTGTGGTTTGCC  
ATGAAGACCTTCTTACGCCCAGCATCTTTCATCATTATGGTGTGGTATTGGAGGAGGATCAC  
CATGATGTCCCGACCCCCAGTGCTTCTGGAAAAAGTCATCTTTGCCCTTGGGATTTCCATGA  
CCTTTATCAATATCCCAGTGGAAATGGTTTTTCCATCGGGTTTGGACTGGACCTGGATGCTGCTG  
TTTGGTGACATCCGACAGGGCATCTTCTATGCGATGCTTCTGTCTTCTGGATCATCTTCTG  
TGGCGAGCACATGATGGATCAGCACGAGCGGAACCACATCGCAGGGTATTGGAAGCAAGTCG  
GACCCATTGCCGTTGGCTCCTTCTGCCTCTTCATATTTGACATGTGTGAGAGAGGGGTACAA  
CTCACGAATCCCTTCTACAGTATCTGGACTACAGACATTGGAACAGAGCTGGCCATGGCCTT  
CATCATCGTGGCTGGAATCTGCCTCTGCCTCTACTTCTCTGTTTCTATGCTTCATGGTATTTTC  
AGGTGTTTCGGAACATCAGTGGGAAGCAGTCCAGCCTGCCAGCTATGAGCAAAGTCCGGCGG  
CTACACTATGAGGGGCTAATTTTTAGGTTCAAGTTCTCATGCTTATCACCTTGGCCTGCGC  
TGCCATGACTGTCTCTTCTTCATCGTTAGTCAGGTAACGGAAGGCCATTGGAATGGGGCG  
GCGTCACAGTCCAAGTGAACAGTGCCTTTTTTTCACAGGCATCTATGGGATGTGGAATCTGTAT  
GTCTTTGCTCTGATGTTCTTGTATGCACCATCCATAAAAACTATGGAGAAGACCAGTCCAA  
TGGCGATCTGGGTGTCCATAGTGGGGAAGAACTCCAGCTCACCACCACTATCACCCATGTGG  
ACGGACCCACTGAGATCTACAAGTTGACCCGCAAGGAGGCCAGGAGTAGGAGGCTGCAGCG  
CCCGGCTGGGACGGTCTCTCCATACCCAGCCCCCTTAAGTAGAGTGGGGAGCATGCCAGAG  
AGAGCTCAATGTACAAATGAATGCCTCATGGCTCTTAGCTGTGGTTTCTTGGACCAGCGGCA  
TGGACATTTGTGATGATAACAAAACTCTGGTATGACACATTTTCTGTGATCATTGTTAATTAG  
TGACATAGTAACATCTGTAGCAGCTGGTTAGTAAACCTCATGTGGGGGTGGGGTGGGGTGT  
ATTCCTTGGGGGATGGTTTGGGCCGAATGGGGAGTGAATATTTGACATTTTCTCTGTTTTA  
AATTCATAGGATAGATTTTAAACATCCTTTGCGGTCCAGTCCAAGGTAGGCTGGTGTATAGT  
CTTCTCACTCCTAATCCATGACCACTGTTTTTTTCTTATTTATATCACCAGGTAGCCTACTG  
AGTTAATATTTAAGTTGTCAATAGATAAGTGTCCCTGTTTTGTGGCATAATATAACTGAATT  
TCATGAGAAGATTTATCCACCAGGGGTATTTTCAGCTTTGAAACCAATCTGTGTATCTAAT  
ACTAACCAATCTGTTGGATGTGGATTTTAAAAAATGTTTGCTAAACTACCCAAGTAAGATTT  
ACTGTATTAAATGGCCTTCGGGTCTGAAAAGCTTTTTTTAACCTCTTGCTTAAATGCGTTTT  
ATTTTGATAAGATACTTCAAATAGCCTCCAAAAGTGTAGATCCAATCACTTAAATAAACCTG  
TATGTATATGCAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 14**

MAGAI IENMSTKKLCIVGGILLVFQIIAFLVGGLIAPGPPTAVSYMSVKCVDARKNHHKTKW  
FVPWGPNHCDKIRDIEEAI PREIEANDIVFSVHIPLPHMEMSPWFQFMLFILQLDIAFKLNN  
QIRENAEVSM DVSLAYRDDAFAEWTEMAHERVPRKLKCTFTSPKTPEHEGRYYECDVLPFME  
IGSVAHKFYLLNIRLPVNEKKKINVGIGEIKDIRLVGIHQNGGFTKVWFAMKTFLTPSIFII  
MVWYWRRITMMSRPPVLLEKVIFALGISMTFINIPVEWFSIGFDWTWMLLFGDIRQGIFYAM  
LLSFWIIFCGEHMMDQHERNHIAGYWKQVGPIAVGSFCLFIFDMCERGVQLTNPFYSIWTTD  
IGTELAMAFIIVAGICLCLYFLFLCFMVFQVFRNISGKQSSLPAMSKVRRLHYEGLIFRFKF  
LMLITLACAAMTVIFFIVSQVTEGHWKWGGVTVQVNSAFFFTGIYGMWNLYVFALMFLYAPSH  
KNYGEDQSNGLGVHSGEELQLTTTITHVDGPTEIYKLTRKEAQE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-42

**Transmembrane domains:**

amino acids 239-253, 269-284, 302-318, 338-352, 377-399,  
434-452, 471-488

**N-glycosylation sites.**

amino acids 8-12, 406-410

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 254-258

**N-myristoylation sites.**

amino acids 223-229, 274-280, 305-311, 358-364, 374-380,  
386-392, 509-515

**FIGURE 15**

GTGAGGGGAACAGCTGATCCGTCTGTTGGGAGGACAGATATCTCAAGGCCAGGATGGAAGAA  
TCACCACTAAGCCGGGCACCATCCCGTGGTGGAGTCAACTTTCTCAATGTAGCCCGGACCTA  
CATCCCCAACACCAAGGTGGAATGTCACTACACCCTTCCCCCAGGCACCATGCCAGTGCCA  
GTGACTGGATTGGCATCTTCAAGGTGGAGGCTGCCTGTGTTCTGGGATTACCACACATTTGTG  
TGGTCTTCCGTGCCTGAAAGTACAAGTATGAGTGGTTCCCCCATTCACACCAGTGTCCAGTTCCA  
AGCCAGCTACCTGCCCAAACCAGGAGCTCAGCTCTACCAGTTCCGATATGTGAACCGCCAGG  
GCCAGGTGTGTGGGCAGAGCCCCCTTTCCAGTTCCGAGAGCCAAGGCCCATGGATGAACTG  
GTGACCCTGGAGGAGGCTGATGGGGGCTCTGACATCCTGCTGGTTGTCCCCAAGGCAACTGT  
GTTACAGAACCAGCTCGATGAGAGCCAGCAAGAACGGAATGACCTGATGCAGCTGAAGCTAC  
AGCTGGAGGGACAGGTGACAGAGCTGAGGAGCCGAGTGCAGGAGCTCGAGAGGGCTCTGGCA  
ACTGCCAGGCAGGAGCACACGGAGCTGATGGAACAGTACAAGGGGATTTCCCGTCCCATGG  
GGAGATCACAGAAGAGAGGGACATCCTGAGCCGGCAACAGGGAGACCATGTGGCACGCATCC  
TGGAGCTAGAGGATGACATCCAGACCATCAGTGAGAAAGTGTGACGAAGGAAGTGGAGCTG  
GACAGGCTTAGAGACACAGTGAAGGCCCTGACTCGGGAACAAGAGAAGCTCCTTGGGCAACT  
GAAAGAAGTACAAGCAGACAAGGAGCAAAGTGAGGCTGAGCTCCAAGTGGCACAACAGGAGA  
ACCATCACTTAAATTTGACCTGAAGGAGCGAAGAGCTGGCAAGAGGAGCAGAGTGTCTCAG  
GCTCAGCGACTGAAAGACAAAGTGGCCAGATGAAGGACACCCTAGGCCAGGCCCAGCAGCG  
GGTGGCCGAGCTGGAGCCCTTGAAGGAGCAGCTTCGAGGGGGCCAGGAGCTTGCAGCCTCAA  
GCCAGCAGAAAGCCACCCTTCTTGGGGAGGAGTTGGCCAGTGCAGCAGCAGCCAGGGACCGC  
ACCATAGCCGAACTACACCGCAGCCGCTGGAAGTGGCTGAAGTTAACGGCAGGCTGGCTGA  
GCTCGGTTTGCACCTTGAAGGAAGAAAAATGCCAATGGAGCAAGGAGCGGGCAGGGCTGCTGC  
AGAGTGTGGAGGCAGAGAAGGACAAGATCCTGAAGCTGAGTGCAGAGATACTTCGATTGGAG  
AAGGCAGTTCAGGAGGAGAGGACCCAAAACCAAGTGTTCAGACTGAGCTGGCCCGGGAGAA  
GGATTCTAGCCTGGTACAGTTGTGAGAAAGTAAGCGGGAGCTGACAGAGCTGCGGTGAGCCC  
TGCGTGTGCTCCAGAAGGAAAAGGAGCAGTTACAGGAGGAGAAACAGGAATTGCTAGAGTAC  
ATGAGAAAGCTAGAGGCCCGCCTGGAGAAGGTGGCAGATGAGAAGTGAATGAGGATGCCAC  
CACAGAGGATGAGGAGGCCGCTGTGGGGCTGAGCTGCCCGGCAGCTCTGACAGACTCAGAGG  
ACGAGTCCCCAGAAGACATGAGGCTCCACCCCTATGGCCTTTGTGAGCGTGGAGACCCAGGC  
TCCTCTCCTGCTGGGCCCTCGAGAGGCTTCTCCCCCTGTTGTGTCATCAGCCAGCCGGCTCCCAT  
TTCTCCTCACCTCTCTGGGCCAGCTGAGGACAGTAGCTCTGACTCGGAGGCTGAAGATGAGA  
AGTCAGTCTGATGGCAGCTGTGCAGAGTGGGGGTGAGGAGGCCAACTTACTGCTTCCTGAA  
CTGGGCAGTGCCTTCTATGACATGGCCAGTGGCTTTACAGTGGGTACCCTGTGAGAAACCAG  
CACTGGGGGGCCCTGCCACCCCCACATGGAAGGAGTGTCTATCTGTAAGGAGCGCTTTCCTG  
CTGAGAGTGACAAGGATGCCCTGGAGGACCACATGGATGGACACTTCTTTTTCAGCACCCAG  
GACCCCTTACCTTTGAGTGATCTTACTCCCTCGTACATGCACAAATACACACTCATGCACA  
CACACACTCACACACATGCATACACTTAGGTTTCATGCCCATTTTCTATCACACTGGGCTCC  
ATGATATTCTGTTCCCTAAGAACTGCTTCTGTGTGCCCTGTTTTTCATCCCAAGATTTCTCAC  
TTCATCCTCTCCTACCTGGCTCTTTTGTCCAGGGAGGGGTCTGTTTCGGAAGCAGTGGCTG  
AATTTATCCCCTGAAAGTGGTTTTTGGAGGAACCGGGATGGAGGAGGCCTTCCCCTGTGGGAA  
TAGAATCGTCCACTCCTAGCCCTGGTTGCTTCTGATACACAGCCACTGCACACACACTCA  
CACTCACACTCCCTTGTCTGATGCCCCAAAGCCAATTCCTGGGGCACCCCTACCCTCTCTTAT  
TTGGAGTTTTCCGTTGGTTTACCTGAGTTTTCTCTGGGGTCTGCACAGAGGCAGCAGCATGGA  
CATCATGGCCTCTCAGGTCCCTTTTGGTTCTCAGTTTCATTGGTTCTCTTTCTGTTCCCCC  
ATTGACTTCTGTGCCCCACCCTAGCCTTTTCCATAACCTTAGGTATTCAGTTTGGAGGGGTT  
TTTTGTATTTTTGAGGATTCTGTATTCTGTATCCTCTCCTCGCATCTCCTCACATGGAAAG  
AAATAATGTATTTGTGCTTCTGTGAGGAATGGGGGGAACAAGTGGTCCCAGGTATCCCCAT  
TTCCAAGGCCCCCTCCCTCTCCAGGTCCCCCACAGCAATAAAAGCTTCCCCCTGATATCC  
ATCCCTTTGTAGTTTGAACAAATATATTTATATGATATGTAA

## **FIGURE 16**

MEESPLSRAPSRGGVNFLNVARTYIIPNTKVECHYTLPFGTMPSASDWIGIFKVEAACVRDYH  
TFVWSSVPESTTDGSPIHSTSVQFQASYLPKPGAQLYQFRYVNRQGVCGQSPPFQFREPRPM  
DELVTLEEADGGS DILLVVPKATVLQNQLDESQQERNDLMQLKLQLEGQVTELRSRVQELER  
ALATARQEHTELMEQYKGISRSHGEITEERDILSRQQGDHVARILELEDDIQTISEKVLTK  
VELDRLRDTV KALTREQEKL LGQLKEVQADKEQSEAE LQVAQQENHHLNLDLKEAKSWQEEQ  
SAQAQRLKDKVAQM KDTLGQAQQORVAELEPLKEQLRGAQELAASSQQKATLLGEELASAAAA  
RDRTIAELHRSRLEVAEVNGRLAELGLHLKEEK CQWSKERAGLLQSVEAEKDKILKLSAEIL  
RLEKAVQEERTQNQVFKTELAREKDSSLVQLSESKRELTELRSALRVLQKEKEQLQEEKQEL  
LEYMRKLEARLEKVADEKWNEDATTEDEBAAVGLSCPAALTDSEDESPEDMRLPPYGLCERG  
DPGSSPAGPREASPLVVISQPAPISPHLSGPAEDSSSDSEAEDKSVLMAAVQSGGEEANLL  
LPELGSAFYDMASGFTVGTLSETSTGGPATPTWKECPICKERFPAESDKDALEDHMDGHFFF  
STQDPFTFE

### **Important features:**

#### **Casein kinase II phosphorylation sites:**

amino acids 28-31, 43-46, 68-71, 72-75, 129-132, 156-159, 208-  
211, 239-242, 282-285, 305-308, 376-379, 383-383, 468-471, 520-  
523, 521-524, 537-540, 539-542, 543-546, 593-596, 595-598, 597-  
600, 612-615, 639-642, 652-655, 667-670, 683-686

#### **N-myristoylation sites:**

amino acids 39-44, 107-112, 204-209, 414-419, 561-566, 613-618

#### **Cell attachment sequence:**

amino acids 557-559

#### **Leucine zipper pattern sequence:**

amino acids 163-184, 475-496, 482-503

**FIGURE 17**

GCAAGTTGGGAATTTTAGACTGTCACATGGACCTCTGGGAAGACGTCTGGCGAGAGC  
TAGGCCCACTGGCCCTACAGACGGATCTTGCTGGCTCACCTGTCCCTGTGGAGGTTCCCTG  
GGAAGGCAAGATGCCCCAACACAGCACTGCTCTGTCATTGGCCAATGTTACCTACATCACCA  
TGGAATTTTTCATTGGACTCTGCGCCATAGTGGGCAACGTGCTGGTCATCTGCGTGGTCAAG  
CTGAACCCAGCCTGCAGACCACCACCTTCTATTTTCATTGTCTCTCTAGCCCTGGCTGACAT  
TGCTGTTGGGGTGCTGGTCATGCCTTTGGCCATTGTTGTCAGCCTGGGCATCACAAATCCACT  
TCTACAGCTGCCTTTTTATGACTTGCCCTACTGCTTATCTTTACCCACGCCTCCATCATGTCC  
TTGCTGGCCATCGCTGTGGACCGATACTTGCGGGTCAAGCTTACCGTCAGATTCAGAATTCC  
TGGGCTCCCTGGGTGCATTCTATCATTCCAGTTGAAAGTTTGCTTCCTTCCAGTCATGTGGC  
TCTTCATTCTACTCTCCTTGGCTCTCATTTCAGATGCCATGGTCATGGATGAAAAGGTCAAG  
AGAAGCTTTGTGCTGGACACGGCTTCTGCCATCTGCAACTACAATGCCCACTACAAGAATCA  
CCCCAAATACTGGTGCCGAGGCTATTTCCGTGACTACTGCAACATCATCGCCTTCTCCCCTA  
ACAGCACCAATCATGTGGCCCTGAGGGACACAGGGAACCAGCTCATTGTCACTATGTCTTGC  
CTGACCAAAGAGGACACGGGCTGGTACTGGTGTGGCATCCAGCGGGACTTTGCCAGGGATGA  
CATGGATTTTACAGAGCTGATTGTAAGTACGACAAAGGAACCCCTGGCCAATGACTTTTGGT  
CTGGGAAAGACCTATCAGGCAACAAAACCAGAAGCTGCAAGGCTCCCAAAGTTGTCCGCAAG  
GCTGACCGCTCCAGGACGTCCATTCTCATCATTTGCATACTGATCACGGGTTTGGGAATCAT  
CTCTGTAATCAGTCATTTGACCAAAGGAGGAGAAGTCAAAGGAATAGAAGGGTAGGCAACA  
CTTTGAAGCCCTTCTCGCGTGTCTGACTCCAAAGGAAATGGCTCCTACTGAACAGATGTGA  
CTGAAGATTTTTTTAATTTAGTTTCATAAAGTGATGCTACAACAGAATAATCACCATGACAAC  
TGGCCCAACACCTCAGAGACTGATTCTGATCTCCAGGAATTCTGAAGGACCCTCTATCCTTG  
ACAACAATCATTTGCAGCCAGGTAGCAACGGCGGTAGTCAGAGGAGCTATGATAGACCACAC  
CCAAGCAAGGCTGCCCTCAAATAACATCTCAAGATCTTAGTTCTTATGCATTCCATCAGTCA  
GAAGTGAAGAAGAGGTGGAGAATCTGGATTGGGGACCAGGAAATCACTTGTATTTTGTTAGC  
CAATAAATTCCTAGCCAGTGTTGAATGAAAAAAAAAAAAA

## **FIGURE 18**

MPNNSTALSLANVTYITMEIFIGLCAIVGNVLVICVVKLNPSLQTTTFYFIVSLALADIAVG  
VLVMPLAIVVSLGITIHFYSCLFMTCLLLIFTHASIMSLLAIAVDRLRVKLTVRFRIPGLP  
GCILSFQLKVCFLPVMWLFILLSLALISDAMVMDEKVKRSFVLDTASAICNNAHYKNHPKY  
WCRGYFRDYCNIIAFSPNSTNHVALRDTGNQLIVTMSCLTKEDTGWYWCGIQRDFARDD MDF  
TELIVTDDKGTLANDFWSGKDLGKTRSKAPKVVRKADRSRSTSILIICILITGLGIISVI  
SHLTKRRRSQRNRRVGNTLKPFSRVLTPKEMAPTEQM

**Important features of the protein:**

**Transmembrane domains:**

amino acids 16-35, 62-80, 89-101, 134-152, 292-311

**N-glycosylation sites.**

amino acids 3-7, 4-8, 12-16, 204-208, 273-277

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 316-320

**N-myristoylation sites.**

amino acids 122-128, 125-131, 258-264

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 214-225

**G-protein coupled receptors proteins.**

amino acids 29-59, 76-116



**FIGURE 19**

CTCGGGCGCGCACAGGCAGCTCGGTTTGCCCTGCGATTGAGCTGCGGGTCGCGGCCGGCGCCGGCCTCTCCAAT  
GGCAAATGTGTGTGGCTGGAGGCGAGCGCGAGGCTTTCGGCAAAGGCAGTCGAGTGTGTCAGACCGGGGGCGAG  
TCCTGTGAAAGCAGATAAAAGAAAACATTTATTAACTGTCTATTACGAGGGGAGCGCCCGCCGGGGCTGTCCG  
ACTCCCCGCGGAACATTTGGCTCCCTCCAGCTCCGAGAGAGGAGAAGAAGAAAGCGGAAAAGAGGCAGATTAC  
GTCGTTTCCAGCCAAGTGGACCTGATCGATGGCCCTCTGAATTTATCACGATATTTGATTTATTAGCGATGCC  
CCCTGGTTTGTGTGTACGCACACACACGTGCACACAAGGCTCTGGCTCGCTTCCCTCCCTCGTTTCCAGCTCC  
TGGGCGAATCCACATCTGTTTCACTCTCCGCGGAGGGCGAGCAGGAGCGAGAGTGTGTGCAATCTGCGAGTG  
AAGAGGGACGAGGGAAGAAACAAAGCCACAGACGCAACTTGAGACTCCGCATCCCAAGAAGCACAGAT  
CAGCAAAAAAAGAGATGGGCCCCCCGAGCCTCGTGCTGTGCTTGTGCTCGCAACTGTGTTCTCCCTGCTGGG  
TGGAGCTCGGCCCTTCTGTGCGACACCACCGCTGAAAGGCAGGTTTCAGAGGGACCGCAGGAACATCCGCCCA  
ACATCATCTGCTGTGCTGACGACGACAGGATGTGGAGCTGGGTTCCATGCAGGTGATGAACAGACCCGCGC  
ATCATGGAGCAGGGCGGGCGCACTTCATCAACGCCTTCTGTACCAACCCATGTGCTGCCCTTCCAGCTCCTC  
CATCTCACTGGCAAGTACGTCCACAACCAACCTACACCAACAATGAGAATGCTCTCGCCCTCTGCGG  
AGGCACAGCAGGAGCCGACCTTTGGCGGTGTACTCTAATAGCACTGGCTACCGGCACAGCTTTCTCGGGAAG  
TATCTTAATGAATACAACGGCTCTACGTGCCACCCGGCTGGAAGGAGTGGGTCGGACTCCTTAAAACTCCCG  
CTTTTATAACTACAGCTGTGTGCGAACCGGGGTGAAAGAGAAGCACGGCTCCGACTACTCCAGGATTACCTCA  
CAGACCTCATACCAATGACAGCGTGAGCTTCTTCGCGACGTCCAAGAAGATGTACCCGCACAGGCCAGTCTCT  
ATGGTCATCAGGCATGACGCCCCCACGGCCCTGAGGATTACGCCCCACAATATTACGCCTCTTCCCAACGC  
ATCTCAGCACATCAGCCGAGCTACAACCTACGCGCCCAACCCGGACAAACCTGGATCATGCGCTACACGGGGC  
CCATGAAGCCCATCCACATGGAATTCACCAACATGCTCCAGCGGAAGCGCTTGCAGACCCCTCATGTGCGTGGAC  
GACTCCATGGAGACGATTTACAACATGCTGGTTGAGACGGGCGAGCTGGACAACACGTACATCGTATACACCGC  
CGACCACGGTTACCACATCGGCCAGTTTGGCCTGGTGAAGGGAATCCATGCCATATGAGTTTGACATCAGGG  
TCCCGTTCTACGTGAGGGGCCCCAACGTGGAAGCCGGCTGTCTGAATCCCCACATCGTCTTCAACATTGACCTG  
GCCCCCACCATCTGGACATTGACGGCCTGGACATACCTGCGGATATGGACGGGAAATCCATCTCAAGCTGCT  
GGACACGGAGCGCCGGTGAATCGGTTTCACTTGAAAAAGAAGATGAGGGTCTGGCGGGACTCCTTCTTGGTGG  
AGAGAGGCAAGCTGTACACAAGAGAGACAATGACAAGGTGGACGCCCAGGAGGAGAACTTTCTGCCCAAGTAC  
CAGCGTGTGAAGGACCTGTGTACGCGTGTGAGTACCAGACGCGGTGTGAGCAGCTGGGACAGAAGTGGCAGTG  
TGTGAGGACGCCACGGGGAAGCTGAAGCTGCATAAGTGCAAGGGCCCCATGCGGCTGGGCGGCAGCAGAGCCC  
TCTCAACCTCGTGCCCAAGTACTACGGGCAGGGCAGCGAGGCCTGCACCTGTGACAGCGGGGACTACAAGCTC  
AGCCTGGCCGGACGCGCGAAAAAATCTTCAAGAAGAAGTACAAGGCCAGCTATGTCCGCGAGTCGCTCCATCCG  
CTCAGTGGCCATCGAGGTGGACGGCAGGGTGTACCAGTAGGCCTGGGTGATGCCGCCAGCCCCGAAACCTCA  
CCAGCGGCACCTGGCCAGGGGCCCCCTGAGGACCAAGATGACAAGGATGGTGGGACTTCAGTGGCACTGGAGGC  
CTTCCCGACTACTCAGCCGCCAACCCATTAAAGTGACACATCGGTGCTACATCTAGAGAACGACACAGTCCA  
GTGTGACCTGGACCTGTACAAGTCCCTGCAGGCCTGGAAGACCACAAGCTGCACATCGACCACGAGATTGAAA  
CCCTGCAGAACAAAATTAAGAACCTGAGGGAAGTCCGAGGTCACTGAAGAAAAAGCGGCCAGAAGAATGTGAC  
TGTACAAAATCAGCTACCAACCCAGCACAAAGGCCGCTCAAGCACAGAGGCTCCAGTCTGCATCCTTTTCAG  
GAAGGCCCTGCAAGAGAAGGACAAGGTGTGGCTGTGCGGGAGCAGAAGCGCAAGAAGAAATCCGCAAGCTGC  
TCAAGCGCTGCAGAACACGACACGTGCAGCATGCCAGGCCTCACGTGCTTACCCACGACAAACAGCACTGG  
CAGACGGCGCCTTTCTGGACACTGGGGCCTTTCTGTGCTGCACCAGCGCCAACAATAACAGCTACTGGTGCAT  
GAGGACCATCAATGAGACTACAATTTCTCTTCTGTGAATTTGCAACTGGCTTCTAGAGTACTTTGATCTCA  
ACACAGACCCCTACCAGCTGATGAATGCAGTGAACACACTGGACAGGGATGTCTCAACAGCTACACGTACAG  
CTCATGGAGCTGAGGAGCTGCAAGGGTTACAAGCAGTGTAAACCCCGGACTCGAAACATGGACCTGGATGGAGG  
AAGCTATGAGCAATACAGGCAGTTTCAGCGTCGAAAGTGGCCAGAAATGAAGAGACCTTCTTCCAAATCACTGG  
GACAACTGTGGGAAGGCTGGGAAGGTAAAGAAACAACAGAGGTGGACCTCCAAAAACATAGAGGCATCACCTGA  
CTGCACAGGCAATGAAAAACCATGTGGGTGATTTCCAGCAGACCTGTGCTATTGGCCAGGAGGCCTGAGAAAGC  
AAGCAGCACTCTCAGTCAACATGACAGATTCTGGAGGATAACCAGCAGGAGCAGAGATAACTTCAGGAAGTCC  
ATTTTGGCCCTGCTTTTGTCTTGGATTATACCTCACCAGCTGCACAAAATGCATTTTTTTCGTATCAAAAAGTC  
ACCACTAACCTCCCCAGAAGCTCACAAGGAAAAACGGAGAGAGCGAGCGAGAGAGATTTCCTTGGAAATTTT  
TCCCAAGGGCGAAAGTCATTGGAATTTTTAAATCATAGGGGAAAAGCAGTCTGTTCTAAATCCTCTTATTCTT  
TTGTTTGTCAAAAGAAGGAACCTAAGAAGCAGGACAGAGGCAACGTGGAGAGGCTGAAAACAGTGCAGAGACG  
TTTGACAATGAGTCAGTAGCACAAAAGAGATGACATTTACCTAGCACTATAAACCCCTGGTTGCTCTGAAGAAA  
CTGCCCTTCAATTGATATATGTGACTATTTACATGTAATCAACATGGGAACCTTTAGGGGAACCTAATAAGAAAT  
CCCAATTTTCAGGAGTGGTGGTGTCAATAAACGCTCTGTGGCCAGTGTAAAAGAAAA

**FIGURE 20**

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQDRRNIRPNIILVLTDDQDVELGSMQ  
VMNKTRRIMEQGGAHFINAFVTTMCCPSRSSILTGKYVHNHNTYTNNENCSSPSWQAQHE  
RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSD  
YSKDYLTDLITNDSVSFFRTSKKMPHRPVLMMVISHAAPHGPEDSAPQYSRLFPNASQHITP  
SYNYAPNPDKHWIMRYTGPMKPIHMEFTNMLQQRKRLQTLMSVDDSMETIYNMLVETGELDNT  
YIVYTADHGYHIGQFGLVKGKSMPIYEFDIRVPFYVRGPNVEAGCLNPHIVLNIDLAPTILDI  
AGLDIPADMKGKSIKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNDKVDAQEEN  
FLPKYQVRVKDLQRAEYQTACEQLGQKWQCVEDATGKCLKHKCKGPMRLGGSRALSNLVPKY  
YGQGESEACTCDSDYKLSLAGRRKKLFKKKYKASYVRSRSIRSV AIEVDGRVYHVGLGDAAQ  
PRNLTKRHWPGAPEDQDDKDGGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDLDLYKS  
LQAWKDHKLHIDHEIETLQNKIKNLREVRGHLKKRPEECDCHKISYHTQHKGRCLKHRGSSL  
HPFRKGLQEKDKVWLLREQKRKKLRKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLG  
PFCACTSANNNTYWC MRTINETHNLFCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL  
HVQLMELRSCKGYKQCNPRTRNMDLDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG

**Important features:**

**Signal peptide:**

amino acids 1-17

**Sulfatases signature 1.**

amino acids 86-99

**Homologous region to sulfatase:**

amino acids 87-106, 133-146, 216-229, 291-320, 365-375

**N-glycosylation sites.**

amino acids 65-69, 112-116, 132-136, 149-153, 171-175, 198-202,  
241-245, 561-565, 608-612, 717-721, 754-758, 764-768

**FIGURE 21**

GGGCGCGGAGAGCTGCTAGGGCGGTTTCTCTGCCTCGGGCCTGTTGGGCAGGGCCGGCT  
AAGGTGCGCGTGCTCGCTGGTTCTAACCCTTCTGTTGGGCGTTTCTGCTGAGAGGCGGGA  
GGCGCTGAGAGTCTGTGCGGAGGTCCGTGGACAGACTGCTTTGCTCGTTGTTGCTCTTCG  
GAGGCGGCGATCCCCGAAGGCGAGCTGAAATACGGCTGCAGGCTACAATTTGCAGCCGAC  
GATTATGGAAGACGGAAGCGGGAGAGGTGGCCACCCCTCATGGAGCGCTTGTGCTCGGAT  
GGCTTCGCATTTCCCAATACCCCATTAACCGTATCATCTGAAGAGGATCCACAGAGCT  
GTCTTACATGGTAATCTAGAGAACTGAAGTACCTTCTGCTCACGTATTATGACGCCAAT  
AAGAGAGACAGGAAGGAAAGGACCGCCCTACATTTGGCCTGTGCCACTGGCCAACCGGAA  
ATGGTACATCTCCTGGTGTCCAGAAGATGTGAGCTTAACCTCTGCGACCGTGAAGACAGG  
ACACCTCTGATCAAGGCTGTACAACTGAGGCAGGAGGCTTGTGCAACTCTTCTGCTGCAA  
AATGGCGCCAATCCAAATATTACGGATTTCTTTGGAAGGACTGCTCTGCACTACGCTGTG  
TATAATGAAGATACATCCATGATAGAAAACTTCTTTACATGGTACAAATATTGAAGAA  
TGCAGCAAGGTATAGGTCAACCAATGTTATTTTCAAACCTATCTGAAATGAATTTATTTTA  
ACATTGACACATGTAAGGGTCAATTTTTTCATATTTGGAAGCTCAAACATTCTTGAATGA  
AAATATTTTGAAATGCCTTAACTGTCTAAGATTTTACTTTAAATATTGGAACTTTTAAAG  
AAGCATTATAGGGAACAGCCTTTTTTTCATGCACTTATGGTAAATAACTATAAAAACAAAT  
GAATTACAATAAATTTATAATTTCATGACAACTGAATTTGGGAAAGGTAATAGTTAAGTGT  
TTTTCCACTAAATTACTTTTT

## **FIGURE 22**

MERLCSDGFAFPQYPIKPYHLKRIHRAVLHGNLEKLKYLLLTYYDANKRDRKERTALHLACA  
TGQPEMVHLLVSRRCENLNCREDRTPLIKAVQLRQEACATLLLQNGANPNITDFFGRTALH  
YAVYNEDTSMIEKLLSHGTNIEECSKV

**Important features of the protein:**

**N-glycosylation site.**

amino acids 113-117

**N-myristoylation site.**

amino acids 109-115

**Microbodies C-terminal targeting signal.**

amino acids 149-153

**FIGURE 23**

GAGGCAGAAAGGCAGAAAGGAGAAAATTCAGGATAACTCTCCTGAGGGGTGAGCCAAGCCCT  
GCCATGTAGTGCACGCAGGACATCAACAAACACAGATAACAGGAAATGATCCATTCCCTGTG  
GTCACCTTATTCTAAAGGCCCAACCTTCAAAGTTCAAGTAGTGATATGGATGACTCCACAGA  
AAGGGAGCAGTCACGCCTTACTTCTTGCCCTTAAGAAAAGAGAAGAAATGAAACTGAAGGAGT  
GTGTTTCCATCCTCCCACGGAAGGAAAGCCCCTCTGTCCGATCCTCCAAAGACGGAAAGCTG  
CTGGCTGCAACCTTGCTGCTGGCACTGCTGTCTTGCTGCCTCACGGTGGTGTCTTTCTACCA  
GGTGGCCGCCCTGCAAGGGGACCTGGCCAGCCTCCGGGCAGAGCTGCAGGGCCACCACGCGG  
AGAAGCTGCCAGCAGGAGCAGGAGCCCCCAAGGCCGGCTGGAGGAAGCTCCAGCTGTCACC  
GCGGGACTGAAAATCTTTGAACCACCAGCTCCAGGAGAAGGCAACTCCAGTCAGAACAGCAG  
AAATAAGCGTGCCGTTTCAGGGTCCAGAAGAAACAGTCACTCAAGACTGCTTGCAACTGATTG  
CAGACAGTGAAACACCAACTATACAAAAAGGATCTTACACATTTGTTCCATGGCTTCTCAGC  
TTTAAAAGGGGAAGTGCCCTAGAAGAAAAAGAGAATAAAATATTGGTCAAAGAACTGGTTA  
CTTTTTTATATATGGTCAGGTTTTATATACTGATAAGACCTACGCCATGGGACATCTAATTC  
AGAGGAAGAAGGTCCATGTCTTTGGGGATGAATTGAGTCTGGTGACTTTGTTTCGATGTATT  
CAAAATATGCCTGAAACACTACCCAATAATTCCTGCTATTCAGCTGGCATTGCAAACTGGA  
AGAAGGAGATGAACTCCAACCTTGCAATACCAAGAGAAAATGCACAAATATCACTGGATGGAG  
ATGTCACATTTTTTGGTGCATTGAACTGCTGTGACCTACTTACACCATGTCTGTAGCTATT  
TTCCTCCCTTTCTCTGTACCTCTAAGAAGAAAGAATCTAACTGAAAATACCAAAAAAAAAA  
AAAAA

## **FIGURE 24**

MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCCLT  
VVSFYQVAALQGDLASLRAELQGHHA EKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAPGEGN  
SSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL EEEKENKIL  
VKETGYFFIYGQVLYTDKTYAMGH LIQRKKVHVFGDELSLVTLFR CIQNMPETLPNNSCYSA  
GIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL

**Transmembrane domain:**

amino acids 47-72

**N-glycosylation site.**

amino acids 124-127, 242-245

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 33-36, 173-176

**N-myristoylation site.**

amino acids 96-101

**TNF family proteins.**

amino acids 172-206

# **FIGURE 25**

CTGCTTGGATACCTCCAGTCCCCAACTGTGTTCCAGGAGTTTTCTTGGCCGAAGCTGCCCC  
 ATGTTTGAGCCTTTTTCTTCCCAGAGAAGAAGATGGACTGAAAGCTGCCAGTTGGGGACTTTT  
 TGTGATCACGGCGTTGCAGCGTTTTAAAGGAGGTGATGGGGCTTGCCTGGCTTGTCTTCCC  
 ACCCAAGTGAAGAGTTGATGTTCACTGGTTATGCTTAGACAATGTGCAGTTTGTGTTAATTT  
 AAAATTTTGGGTGGGATAGGGGCATAGGCTTGTGAAGGGCAGTCCGGATCCGGAGGAACTCG  
 TCTTTGTCCCTGGTAGGAGAGACACCCCCAGTCTATCCTCGATGCCGTCAGCCTTGGCCATC  
 TTCACTTGCCGCCCCGAACCTCGCACCCGTTTCAGGAGCGTCATGTCTACCTGGACGAGCCCAT  
 CAAAATCGGCCGCTCAGTGGCCCCGTGTGACCAGCGCAGAATAATGCCACTTTTGATTGCA  
 AAGTGCTATCAAGGAACCACGCTCTCGTCTGGTTTGATCACAAGACGGGCAAGTTTTATCTT  
 CAAGACACTAAAAGTAGTAATGGTACTTTTTATAAATAGCCAGAGATTGAGTCGAGGCTCTGA  
 AGAAAGTCCACCATTGTGAAATTCTTCCGGTGACATTATCCAGTTTGGATAGACGTGACAG  
 AGAATACACGGAAAGTTACCCATGGGTGTATTGTTTCCACAATAAAACTTTTTCTACCAGAT  
 GGTATGGAAGCCCGGCTCCGCTCAGATGTCTCATCCATGCACCATTACCAAGTCTGTGACAA  
 AGTTGCTGCTAACACTCCAAGTATGTACTCTCAGGAACATTATCCAGCTTTCTCAGTATCTAC  
 AGGAGGCCTTACATCGGGAACAAATGTTGGAACAGAAGTTAGCCACGCTTCAGCGGCTACTA  
 GCCATCACCCAAGAGGCTTCAGATACCAGTTGGCAGGCTTTAATAGATGAAGATAGACTCTT  
 ATCACGGTTAGAAGTTATGGGAAACCAATTACAGGCATGCTCCAAAAATCAAACAGAAGATA  
 GTTTACGAAAGGAACCTTATAGCATTACAAGAGGATAAAACATAACTATGAGACAACAGCCAAA  
 GAGTCCCTGAGGCGGGTTCTTCAGGAGAAAATTGAAGTGGTTAGAAAACCTTTCAGAAGTTGA  
 GCGAAGTCTGAGTAATACTGAAGATGAATGTACCCATCTGAAAGAAATGAATGAAAGGACTC  
 AGGAAGAATTAAAGAGAATTAGCCAACAAATATAATGGAGCAGTTAATGAGATTAAAGATTTA  
 TCTGATAAATTAAAGGTAGCAGAGGGGAAAACAAGAGGAAATCCAACAGAAGGGACAGGCTGA  
 GAAAAAAGAATTACAACATAAAATAGATGAAATGGAAGAAAAAGAACAGGAGCTCCAGGCAA  
 AAATAGAAGCTTTGCAAGCTGATAATGATTTACCAATGAAAGGCTAACAGCTTTTACAAGTA  
 CGGTTAGAACATCTTCAGGAGAAAACCTTTAAAGAATGCAGCAGCTTGGCTGATCGTCGAAG  
 GGCATCTAACCAAAGCGGTAGAAGAAACAAAGCTTTCAAAGGTTTGTTTTCTGTTTTTCTA  
 TGTTTTTTGACAGTTCTTTTGGATAATGAAGGTTAGTGTATATTTTCAAGGTTATAGTATTT  
 TAACCATCAGTTTACTTCTTATAGCTCACAAAATAGCAAGCCAGTAACAGTATCAGATAATA  
 TATAAAATAATCAGACTTCTGTTTTAAGAAGGGTATCGTAACTGGAATGTGTCTTTTTAAGT  
 GGATGTATATTTATGGTTTTTTGAATGTTAGTACTTGATATAGGTTTCTTTAGGTATTAAG  
 ATTTGTTGCAATCTCTGTCAATCCCAGCATTAAATTTAGCTTTGATCTCAAATTTTAAATCAA  
 ACACAAATGTAAGTCGTTTGTGATACAACTTAAGTGAAACATGCTTGCACTTCTATTTGGGG  
 GTTACAGTACCTTTAAAATCTCTTATGATGTTTAATATTTCTTAATTTTGGCATCTCAGT  
 TTGATTTAAACAAAATTAATGACTTTTGTGAATGTAGAATCTTCTTATATTTTATGAGTAGT  
 CCAGTAATTGCCCAAAGTAGTTTATTGTGTTAATTCTGTTACAGTTGTCAGAGAAGAAAAGT  
 GAGTTTTAAAGCACCATTATTGTCAAGTCACTTTTATACATAGGGAAATTAGGCAAATAAATT  
 TGGTGGCATGTGTTTATCATAGTAGAACTTTTATTAGACTATACCAGTATAAAATTTAAAC  
 TAGATTCACAGTCTTTTTGGCCAATTAAAAACATTGAGTTACAAAAGTTTGAGATACTTAATT  
 TTAGTACATTCTATTTTATTAAAGTAACTGGATTCAATTTGACTTTTTTAACCATGTAAGAGG  
 ATGGTGTTATTTCAAATATCTCGTGGTTTCCATTCTGAATTTTGTGCACGGCAGATGCCATA  
 TTTGGGGAAAAAATGCATAGAATATGCATCATTAATATTGTTTTGGCAAACAGGCATTGAGT  
 TTCAGAACAGTGAACATTTTTTAGTACATATGGCAATTTTTTTTACCTTATTAAAGTGAGAT  
 GAGAACAGACCTTAAATAGCTTTTACCTCACCATCAAATACCTATTCAGATTAGTTGGTT  
 GAATAGCCAGCACTTTGAAGTAGAGCCTTAGG

## **FIGURE 26**

MEARLRSDVIHAPLPSPVDKVAANTPSMYSQELFQLSQYLQEALHREQMLEQKLATLQRLLA  
ITQEASDTSWQALIDEDRLLSRLEVGMGNQLQACSKNQTEDSLRKELIALQEDKHNYETTAKE  
SLRRVLQEKIEVVRKLSEVERSLSNTEDECTHLKEMNERTQEELRELANKYNGAVNEIKDLS  
DKLKVAEGKQEEIQQKGQAEKKELQHKIDEMEEKEQELQAKIEALQADNDFTNERLTALQVR  
LEHLQEKTLKECSSLADRRRASNQSGRRNKAFKRFFVFCFSMFFDSSFG

**Important features of the protein:**

**N-glycosylation sites.**

amino acids 98-102, 271-275

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 138-142, 267-271

**Amidation site.**

amino acids 273-277

**Tropomyosins proteins.**

amino acids 169-217



# **FIGURE 27**

GAACCTGGCGCCGCCGGAACCTGATCGCGGCCTAGTCCCGACGCGTGTGTGCTAGTGAGCCGG  
AGCCGGCGACGGCGGCAGTGGCGGCCCGCCTGCAGGAGCCCGACGGGGTCTCTGCCATGGG  
GGAGTGACGCGCCTGCACCCGCTGTTCCGCGGCAGCGGCGAGACATGAGGAGACCCCGCGAC  
AGGGGCAGCGCGCGCGGCTCGTGAGCCCCGGGATGGAGGAGAAATACGGCGGGGACGTGCTG  
GCCGGCCCCGGCGCGCGCGGCCCTTGGGCCGGTGGACGTACCCAGCGCTCGATTAACAAA  
ATATATTGTGTTACTATGTTTCACTAAATTTTTGAAGGCTGTGGGACTTTTCGAATCATATG  
ATCTCCTAAAAGCTGTTACATTGTTTCACTTCAATTTTTATATTAAACTTGGGACTGCATTT  
TTTATGGTTTTGTTTCAAAAGCCATTTCTTCTGGGAAAACATTATACCAAACACCACTGGAT  
CAAAATATTTAAACATGCAGTTGCTGGGTGTATTATTTCACTCTTGTGGTTTTTTGGCCTCA  
CTCTTTGTGGACCACTAAGGACTTTGCTGCTATTTGAGCACAGTGATATTGTTGTCAATTTCA  
CTACTCAGTGTTTTGTTTACCAGTTCTGGAGGAGGACCAGCAAAGACAAGGGGAGCTGCTTT  
TTTTATTATTGCTGTGATCTGTTTATTGCTTTTTGACAATGATGATCTCATGGCTAAAATGG  
CTGAACACCCTGAAGGACATCATGACAGTGCTCTAACTCATATGCTTTACACAGCCATTGCC  
TTCTTAGGTGTGGCAGATCACAAGGGTGGAGTATTATTGCTAGTACTGGCTTTGTGTTGTAA  
AGTTGGTTTTTCATACAGCTTCCAGAAAGCTCTCTGTGCGACGTTGGTGGAGCTAAACGTCTTC  
AAGCTTTATCTCATCTTGTGTTTCTGTGCTTCTCTTGTGCCCCATGGGTCAATGTTCTTTCTGTG  
ACAACTGAGAGTAAAGTGGAGTCTTGGTTTTCTCTCATTATGCCTTTTTGCAACGGTTATCTT  
TTTTGTGATGATCCTGGATTTCTACGTGGATTCCATTTGTTTCACTCAAAATGGAAGTTTCCA  
AATGTGCTCGTTATGGATCCTTTCCATTTTTATTAGTGCTCTCCTTTTTTGGAATTTTTTG  
ACACATCCAATAACAGACCAGCTTCGGGCTATGAACAAAGCAGCACACCAGGAGAGCACTGA  
ACACGTCCTGTCTGGAGGAGTGGTAGTGAGTGCTATATTCTTCATTTTGTCTGCCAATATCT  
TATCATCTCCCTCTAAGAGAGGACAAAAAGGTACCCTTATTGGATATTCTCCTGAAGGAACA  
CCTCTTTATAACTTCATGGGTGATGCTTTTTCAGCATAGCTCTCAATCGATCCCTAGGTTTAT  
TAAGGAATCACTAAAACAAATTCTTGAGGAGAGTGACTCTAGGCAGATCTTTTACTTCTTGT  
GCTTGAATCTGCTTTTTACCTTTGTGGAATTATTCTATGGCGTGCTGACCAATAGTCTGGGC  
CTGATCTCGGATGGATTCCACATGCTTTTTGACTGCTCTGCTTTAGTCACTGGGCAATTTTTGC  
TGCCCTGATGAGTAGGTGGAAAGCCACTCGGATTTTCTCCTATGGGTACGGCCGAATTAGAAA  
TTCTGTCTGGATTTATTAATGGACTTTTTCTAATAGTAATAGCGTTTTTTGTGTTTATGGAG  
TCAGTGGCTAGATTGATTGATCCTCCAGAATTAGACACTCACATGTTAACACCAGTCTCAGT  
TGGAGGGCTGATAGTAAACCTTATTGGTATCTGTGCCCTTAGCCATGCCCATAGCCATGCC  
ATGGAGCTTCTCAAGGAAGCTGTCACTCATCTGATCACAGCCATTACACCATATGCATGGA  
CACAGTGACCATGGGCATGGTCACAGCCACGGATCTGCGGGTGGAGGCATGAATGCTAACAT  
GAGGGGTGTATTTCTACATGTTTTGGCAGATACACTTGGCAGCATTGGTGTGATCGTATCCA  
CAGTTCTTATAGAGCAGTTTGGATGGTTCATCGCTGACCCACTCTGTTCTCTTTCTACTGCT  
ATATTAATATTTCTCAGTGTTGTTCCACTGATTAAAGATGCCTGCCAGGTTCTACTCCTGAG  
ATTGCCACCAGAATATGAAAAAGAACTACATATTGCTTTAGAAAAGATACAGAAAATTGAAG  
GATTAATATCATACCGAGACCCCTCATTTTTGGCGTCATTCTGCTAGTATTGTGGCAGGAACA  
ATTCATATACAGGTGACATCTGATGTGCTAGAACAAAGAATAGTACAGCAGGTTACAGGAAT  
ACTTAAAGATGCTGGAGTAAACAATTTAAACAATTCAGTGGAAAAGGAGGCATACTTTCAAC  
ATATGTCTGGCCTAAGTACTGGATTTTATGATGTTCTGGCTATGACAAAACAAATGGAATCC  
ATGAAATACTGCAAAGATGGTACTTACATCATGTGAGATAACTCAAGAATTACCCCTGGAGA  
ATAAACAATGAAGATTAAATGACTCAGTATTTGTAATATTGCCAGAAGGATAAAAATTACAC  
ATTAAGTGTACAGAAACAGAGTTCCTACTACTGGATCAAGGAATCTTTCTTGAAGGAAATT  
TAAATACAGAATGAAACATTAATGGTAAAAAAA

## **FIGURE 28**

MEEKYGGDVLAGPGGGGGLGPVDVPSARLTKYIVLLCFTKFLKAVGLFESYDLLKAVHIVQF  
IFILKLGTAFFMVLFPKPFSSGKTITKHQWIKIFKHAVAGCIISLLWFFGLTLCGPLRTL  
FEHSDIVVISLLSVLFTSSGGGPAKTRGAFFIIAIVICLLLFDDNDLMAKMAEHPEGHDSA  
LTHMLYTAIAFLGVADHKGGVLLLVLALCCKVGFHTASRKLSDVGGAKRLQALSHLVSVLL  
LCPWVIVLSVTTESKVESWFSLIMPFATVIFVVMILDFYVDSICSVKMEVSKCARYGSFPIF  
ISALLFGNFWTHPITDQLRAMNKAHQESTEHVLSGGVVVSAIFFILSANILSSPSKRGQKG  
TLIGYSPEGTPLYNFMGDAFQHSQSIPRFIKESLKQILEESDSRQIFYFLCLNLLFTFVEL  
FYGVLTNLGLISDGFHMLFDCSALVMGLFAALMSRWKATRIFSYGYGRIEILSGFINGLFL  
IVIAFFVFMESVARLIDPPELDTHMLTPVSVGGGLIVNLIGICAFSHAHSHAHGASQGSCHSS  
DHS SHHMHGSDHGHGSHSGSAGGGMNANMRGVFLHVLADTLGSIGVIVSTVLIEQFGWFI  
ADPLCSLSTAILIFLSVVPLIKDACQVLLRLPPEYEKELHIALEKIQKIEGLISYRDPHFW  
RHSASIVAGTIHIQVTSDVLEQRIVQQVTGILKDAGVNNLTIQVEKEAYFQHMSGLSTGFHD  
VLAMTKQMESMKYCKDGTIIM

**Important features of the protein:**

**Signal peptide:**

amino acids 1-46

**Transmembrane domains:**

amino acids 59-77, 101-119, 150-167, 205-223, 239-258, 267-284,  
305-324, 343-360, 421-440, 452-469, 486-505, 522-539, 592-612,  
621-641

**N-glycosylation site.**

amino acids 721-725

**Glycosaminoglycan attachment site.**

amino acids 143-147

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 225-229

**Tyrosine kinase phosphorylation sites.**

amino acids 750-758, 756-764

**N-myristoylation sites.**

amino acids 14-20, 46-52, 102-108, 112-118, 144-150, 317-323,  
347-353, 369-375, 372-378, 437-443, 462-468, 529-535, 549-555,  
553-559, 579-585, 582-588, 583-589, 584-590, 605-611, 737-743

**Multicopper oxidases protein:**

amino acids 561-569

# **FIGURE 29**

GGCACGAGGGCAGGATATTAGAAATGGCTACTCCCCAGTCAATTTTCATCTTTGCAATCTGC  
 ATTTTAATGATAACAGAATTAATTCTGGCCTCAAAAAGCTACTATGATATCTTAGGTGTGCC  
 AAAATCGGCATCAGAGCGCCAAATCAAGAAGGCCTTTCACAAGTTGGCCATGAAGTACCACC  
 CTGACAAAAATAAGAGCCCGGATGCTGAAGCAAAATTCAGAGAGATTGCAGAAGCATATGAA  
 ACACTCTCAGATGCTAATAGACGAAAAGAGTATGATACACTTGGACACAGTGCTTTTACTAG  
 TGGTAAAGGACAAAAGAGGTAGTGGAAAGTTCTTTTGAGCAGTCATTTAACTTCAATTTTGATG  
 ACTTATTTAAAGACTTTGGCTTTTTTGGTCAAAACCAAAACACTGGATCCAAGAAGCGTTTT  
 GAAATCATTTCCAGACACGCCAGGATGGTGGTTCAGTAGACAAAGGCATCATTTCCAAGA  
 ATTTTCTTTTGGAGGTGGATTATTTGATGACATGTTTGAAGATATGGAGAAAATGTTTTCTT  
 TTAGTGGTTTTGACTCTACCAATCAGCATACAGTACAGACTGAAATAGATTTTCATGGATCT  
 AGCAAGCACTGCAGGACTGTCACTCAACGAAGAGGAAATATGGTTACTACATACACTGACTG  
 TTCAGGACAGTAGTTCTTATTCTATTCTCACTAAATCCAACGGTTGACTCTTCCTCATTAT  
 CTTTGATGCTAAACAATTTTCTGTGAACATTTTGGACAAGTGCATGATTTCACTTTAAACAA  
 TTTGATATAGCTATTAAATATATTTAAGGGTTTTTTTTTTTGACAAATTCAACATTCAACGA  
 GTAGACAAAATGCTAATTATTTCCCTGATTAGGAAAGTTTCTTTAAAAAACACGTAATTTTG  
 CCTAGTGCTTTTTCTCTACCTGCCCTTGGGCTCACTAATATCACCAGTATTATTACCAAGAA  
 AATATTGAGTTTACCTGATTAAACTTTAAAGTTAATTGTAGATTTAAATTGTGTGAACCTA  
 ATGATTTTTGCAGTGAAACCTTTACTAATTCAAAGTTGCATGTTCTATGACATCTGTGACTT  
 GCGTTGCAGAGTGATACATGAAACTGTATAATTGAGTCATTCACTAAAGGAGAACAGTATCTT  
 GGTTAATTGCTACTGAAAGGTTGAGAAAGGAATGGTTTGATATTTACCACAGCGCTGTGCCT  
 TTCTACAGTAGAACTGGGGTAAAGGAAATGGTTTTATTGCCCATAGTCATTTAGGCTGGAAA  
 AAAGTTGAAAACCTTAACGAAATATTGCCAAGAGATTGTTATGTGTTTGGTTCCAGCCTAAAA  
 ATGATTTTGTAGTGTGAAATCATAGCTACTTACATAGCTTTTTTCATATTTCTTCTTAGTT  
 GTTGGCACTCTTAGGTCTTAGTATGGATTTATGTGTTTGTGTGTGTAGTTTATCCTCTCT  
 CTCATCTTTATCTAGAGATTGACTGATACCTCATTCGTTTGTAACCAGCCAGTAATTTTC  
 TGTGCAACCTTACTATGTGCAATATTTTTAAATCCTGAGAAATGTGTGCTTTTGTTCGGA  
 TAGACTTATTTCTTTAGTTCTGCACTTTTCCACATTATACTCCATATGAGTATTAATCCTAT  
 GGATACATATTTAAACAAGTGCTCAT

## **FIGURE 30**

MATPQSIFIFAICILMITELILASKSYDILGVPKSASERQIKKAFHKLAMKYHPDKNKSPD  
AEAKFREIAEAYETLS DANRRKEYDTLGHSAFTSGKGQRGSGSSFEQSFNFNFDLFDKDFGF  
FGQNQNTGSKKRFEHFQTRQDGGSSRQRHHFQEFSEFGGGLFDDMFEDMEKMFSFSGFDSTN  
QHTVQTENRFHGSSKHCRTVTQRRGNMVTYTD CSGQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-23

**Nt-dnaJ domain signature.**

amino acids 27-59, 66-90

**Glycosaminoglycan attachment site.**

amino acids 96-100

**N-myristoylation sites.**

amino acids 32-38, 99-105, 102-108, 126-132, 211-217

# **FIGURE 31**

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG  
GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAGAACA  
ATTGAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT  
GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA  
AAATGCAGACTTTTACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT  
ACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC  
TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCAGTGATCGCGCCTGGAGA  
AACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT  
GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTGAGTGTGATGTCACTGATGACATC  
ACGGCCACTGTGCCATACAACCTTCGTGTCAGGGCCACATTGGGCTCACAGACCTCAGCCTG  
GAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTACCCGACCTGGGATGGAGA  
TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC  
CTTGTTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAAATGGTGAGGAGTGG  
GGGTATTCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGA  
CATTGCTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA  
GGAGAGGCCATTCCCTGGTACTGGCCCTGTTTGCCCTTTGTTGGCTTCATGCTGATCCTTGT  
GGTCGTGCCACTGTTCTGTCTGGAATAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCCGTGG  
TGGTCCTCCCAGACACCTTGAAAATAACCAATTCACCCCAGAAGTTAATCAGCTGCAGAAGG  
GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACTCCTCAGGGCCTGGAT  
CTCATAGGTTTTGCGGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACC  
ATGAGGGGACAAGTTGTGTTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA  
GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTTGTCTAACAGAACAC  
TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGGCTGCCACTTGCTGGCTGAGCAACC  
CTGGGAAAAGTGACTTCATCCCTTCGGTCCTAAGTTTTCTCATCTGTAATGGGGGAATTACC  
TACACACCTGCTAAACACACACACACAGAGTCTCTCTCTATATATACACACGTACACATAAA  
TACACCCAGCACTTGCAAGGCTAGAGGGAAACTGGTGACACTCTACAGTCTGACTGATTAG  
TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT  
GGCTTGAGAGCCCACTTTCCAGAAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG  
TGTTGAGTTCACCTTCAAGCCCAATGCCGGTGAGAGGGGAATGGCTTAGCGAGCTCTACAGT  
AGGTGACCTGGAGGAAGGTCACAGCCCACTGAAAATGGGATGTGCATGAACACGGAGGATC  
CATGAACTACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT  
GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTCT  
TGTTGGTAAAGTACAGAATTGAGCAATAAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA  
AAAAAAAAA

**FIGURE 32**

MQTFTMVLEEBIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLWSPVIAPGE  
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITATVPYNLRVRATLGSQTS  
SILKHPFNRNSTILTRPGMEITKDGFLVIELEDLGPQFEFLVAYWRREPGAEHVKMVRSG  
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPVLALFAFVGFMILILV  
VVPLFVWKMGRLQLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

**Important features:**

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 230-255

**N-glycosylation sites.**

amino acids 40-44, 134-138

**Tissue factor proteins.**

amino acids 92-120

**Integrins alpha chain proteins.**

amino acids 232-263

# **FIGURE 33**

GAGACACGCGAGCGGGGAGACCTCCAAGGCAGCGAGGCATCGGACATGTGTCTGAGCACATCTG  
GGGCGCACATCCGTCGAGCCCCGAGGGGAGATTTGCCGGAACAATTCAAAGTGCATATTTGAT  
CTTGGGGGTGACTGTCCCTGGCCGGCTGTCTGGGTGGGAGTGCGAGTGTGCACTCGCTCGGAA  
GTGTGTGCGAGTGTGTATGTGTGTGTGCCGTGTCTGGGCTCCCCCTTCCCCCGTTTTCCCG  
TCGAGTGATGCACTTGGAAATGAGAATCAGAGGATGGAAATAGTCTGGGAGGTGCTTTTTCTT  
CTTCAAGCCAATTTTCATCGTCTGCATATCAGCTCAACAGAATTCACCAAAATCCATGAAGG  
CTGGTGGGCATACAAGGAGGTGGTCCAGGGAAGCTTTGTTCCAGTTCCTTCTTTCTGGGGAT  
TGGTGAACCTCAGCTTGGAAATCTTTGCTCTGTGGGGAAACGGCAGTCGCCAGTCAACATAGAG  
ACCAATCAGATGATCTTCGACCCCTTTCTGACACCTCTTCGCATCAACACGGGGGGCAGGAA  
GGTCAGTGGGACCATTGACAAACACTGGAAGACACGTATCCCTTCGCCTGGACAAGGAGCACT  
TGGTCAACATATCTGGAGGGCCCATGACATACAGCCACCGGCTGGAGGAGATCCGACTACAC  
TTTGGGAGTGAGGACAGCCAAGGGTCGGAGCACCTCCTCAATGGACAGGCCTTCTCTGGGGA  
GGTGCAGCTCATCCACTATAACCATGAGCTATATACGAATGTACAGAAGCTGCAAAGAGTC  
CAAATGGATTGGTGGTAGTTTCTATATTTATAAAAGTTTCTGATTTCATCAACCCATTTCTT  
AATCGAATGCTCAACAGAGATACTATCACAAGAATAACATATAAAAATGATGCATATTTACT  
ACAGGGGCTTAATATAGAGGAACATATATCCAGAGACCTCTAGTTTCATCATTACGATGGGT  
CGATGACTATCCCACCCTGCTATGAGACAGCAAGTTGGATCATAATGAACAAACCTGTCTAT  
ATAACCAGGATGCAGATGCATTCCTTGCGCTGCTCAGCCAGAACCAGCCATCTCAGATCTT  
TCTGAGCATGAGTGACAACCTTCAGGCCTGTCCAGCCACTCAACAACCGCTGCATCCGCACCA  
ATATCAACTTCAGTTTACAGGGGAAGGACTGTCCAAACAACCGAGCCAGAAGCTTCAGTAT  
AGAGTAAATGAATGGCTCCTCAAGTAGGGAACAAAGCCAAGAAGATCCACCTCAGTGAAA  
TGCTACAACCTGTGAATTGACGTAACCTAGAATGTCCCCCTTCTTGCTTCTCTCTCTCTCTT  
CCCCAAGCCTCATTTCATTCTTTGGGATTGGCCCTTTCTTCATGAAAAGTGCTGCGAAACCA  
TGGCAGAGGAATACATCTCTCACACATACTCACAAACACACACACAAGCACTTGCACATACA  
TACAAACACATGCAAACATACCTACACACACACACTCTCTTACAACCTCCATCATGGGAAGT  
CAAGTTTCAGAAACAAAAGTCTCATTACATAAGAGGTCTTAGAAGAAAATAACCAGTTAACCT  
GATTTTCAATTTTGATACCGTTTTCCTGAACATAATAATCTACCAATGAGACTTTTTCAGCCT  
TTGTACATACAAAATTTCTTCCAAAAGAGAGAGGAGAAAATACAGCTCTGATGGCATCAAACG  
GACTTTGCATCAAGTAATTTTCAGATAGTGTCTTAGGATCCTTTGAGGGTGCTGGTAGCAGGT  
GAGCAGGACAAAGTTGACCAAGGACACTTATTTCTAGATTATGATTCTTCTGTTTACTCAAC  
AATTTACAAAGAAAAAAGGACAGACATTGAAGAGCTACACATTGTATATATATCACCACAG  
ACTATAAGGAAATGGAATTATTTCCCTCTTTGTACATATCTGTAGTAGGATTTGCCAAGAT  
CAGAAATGATCCATTTGCTGTTTCTTGTTTTCCAAAGGTCATACATTGTGTTTGGTTATTGT  
TACCAGCTCAATAAATGTGTTTAAACGAGTTAATTTTCAATTTTCTGGCTTTGGTCTGTTCTCC  
TTCCTTACAGGCTAAGCCCTGGCTCCATGCAACTGCATTCTTTGATTTCACCTGTTCTCTCA  
TCTACATGTTTTGTTTCAATTTGCAGCCAGTTTTTACTGAGTTTGTGGCAATCAGGAATGCATT  
TGCTAAGCAAGTATGACTTTAATTCCTCCATGGCTCAATCATTCACATGAGGTGAGCTTC  
AGCCTGAGATAGCAGGCGACAGACTTCTTGCGTTTCAAACTGCCATGCCCCCTGTGATGC  
TCCCGTGAAGGAATGCACTTTGCCTTGTAAGTTCTTGGGAAAGGGGTATGTTTCTCTCCAG  
GTGCAGCCAGATCTCACAAGTACAAAACGAATGCCTTTCTTTTCTTGTTTATAATGGTCACT  
TCACTGTGTTTGGTTACTGTCAAGAAATCAATAAATGTGTTTAAACAAGTTA

**FIGURE 34**

MEIVWEVLFLLQANFIVCISAQQNSPKIHEGWWAYKEVVQGSFVPVPSFWGLVNSAWNLC  
SVGKRQSPVNIETSHMIFDPFLTPLRINTGGRKVSGTMYNTGRHVSLRLDKEHLVNISGGPMTY  
SHRLEEIRLHFGSEDSQGSEHLLNGQAFSGEVQLIHYNHELYTNVTEAAKSPNGLVVVSIFI  
KVSDDSSNPFLNRMLNRDTITRITYKNDAYLLQGLNIEELYPETSSFITYDGSM TIPPCYETA  
SWIIMNKPVIITRMQMHSRLRLLSQNQPSQIFLSMSDNFRPVQPLNNRCIRTNINFSLQKDC  
PNNRAQKLQYRVNEWLLK

**Important features:**

**Signal peptide:**

amino acids 1-20

**Eukaryotic-type carbonic anhydrases proteins.**

amino acids 126-162, 220-269, 43-91

**N-glycosylation sites.**

amino acids 116-119, 168-171, 302-305



# **FIGURE 35**

GTCGGAACCCCCCTCAGGCCACCCTCGGGAGTCTGGGGTCCAGAGGGGTGTCCCTGTACCCCTTGCA  
 CACAGGACCCTCACTCTGCAGGGATAAGCCAGCTGCGCCTGCAGCCTAGGGTGCCAAGGAGGCTGCT  
 GATTGTGGCCACAGCCTCATCTGAACGCCAGGAGACCAGGATACCGAGGCACCGGATCCCTCTCT  
 GTGCCCTGGGGAGCCCCAGTGCTGCCCAGTCACCCCAGGGCTGAGGTCTGCGTCCCTAGTGTTGCAA  
 GGCCTGGTAGGACCACCGGGCAGGGAATGTGAGCGCCATCCGAGCTCAGGGTGTCTGAGTCGCGGC  
 TTCGTGACTTTGGCAGGGGCTCCGGACCAGTGACCCAGTCAAACCCAGAGGGTCTTGGGCGGCAG  
 CGACGAAGGAGGTATTAGGCTCCAGGCCAGGTGGGGCCGGACGCCCCAGCCATCCACCATGGTGG  
 TGGCACACCCACCGCCACTGCCACCACCAGCCCCACTGCCACTGTACGGCCACCCTTGTGATGAC  
 CACGGCCACCATGGACCTGCGGGACTGGCTGTTCTCTGCTACGGGCTCATCGCCTTCTGACGGAG  
 GTCATCGACAGCACCTGCCCCCTCGGTGTGCCGCTGCGACAACGGCTTCATCTACTGCAACGACC  
 GGGGACTCACATCCATCCCCGAGATATCCCTGATGACGCCACCACCCTCTACCTGCAGAAACAACA  
 GATCAACAACGCCGCATCCCCCAGGACCTCAAGACCAAGGTCAACGTGCAGGTCACTTACCTATAC  
 GAGAATGACCTGGATGAGTTCCCCATCAACCTGCCCGCTCCCTCCGGGAGCTGCACCTGCAGGACA  
 ACAATGTGCGCACCATTGCCAGGGACTCGCTGGCCCCGATCCCGCTGCTGGAGAAGCTGCACCTGGA  
 TGACAACTCCGTGTCCACCGTCAGCATTGAGGAGGACGCCTTCGCCGACAGCAAACAGCTCAAGCTG  
 CTCTTCTGAGCCGAACACCTGAGCAGCATCCCCCTCGGGGCTGCCGCACACGCTGGAGGAGCTGC  
 GGCTGGATGACAACCGCATCTCCACATCCCGCTGCATGCCTTCAAGGGCCTCAACAGCCTGCGGCG  
 CCTGGTGTGGACGGTAACCTGCTGGCCAACAGCGCATCGCCGACGACACCTTCAGCCGCCCTACAG  
 AACCTCACAGAGCTCTCGCTGGTGCGCAATTGCTGGCGCGCCACCCCTCAACCTGCCCGAGCGCC  
 ACCTGCAGAACTCTACCTGCAGGACAATGCCATCAGCCACATCCCCTACAACACGCTGGCCAAGAT  
 GCGTGAGCTGGAGCGGCTGGACCTGTCCAACAACAACCTGACCACGCTGCCCGCGGCGCTGTTTCGAC  
 GACCTGGGGAACCTGGCCAGCTGCTGCTCAGGAACAACCTTGGTTTTGTGGCTGCAACCTCATGT  
 GGCTGCGGGACTGGGTGAAGGCACGGGCGGCCGTGGTCAACGTGCGGGGCTCATGTGCCAGGGCCC  
 TGAGAAGGTTCGGGGCATGGCCATCAAGGACATTACAGCGAGATGGACGAGTGTTCCTGAGACGGGG  
 CCGCAGGGCGGCGTGGCCAATGCGGCTGCCAAGACCACGGCCAGCAACCACGCTCTGCCACCACGC  
 CCCAGGGTTCCTGTTTACCCTCAAGGCCAAAAGGCCAGGGCTGCGCCTCCCCGACTCCAACATTGA  
 CTACCCCATGGCCACGGGTGATGGCGCCAAGACCTGGCCATCCACGTGAAGGCCCTGACGGCAGAC  
 TCCATCCGCATCAGTGGAAGGCCACGCTCCCCGCCTCCTCTTCCGGCTCAGTTGGCTGCGCCTGG  
 GCCACAGCCAGCCGTGGGCTCCATCAGGAGACCTTGGTGACGGGGGACAAGACAGAGTACCTGCT  
 GACAGCCCTGGAGCCCAAGTCCACCTACATCATCTGCATGGTCACCATGGAGACCAGCAATGCCCTAT  
 GTAGCTGATGAGACACCGTGTGTGCCAAGGCAGAGACAGCCGACAGCTATGGCCCTACCACCACAC  
 TCAACCAGGAGCAGAACGCTGGCCCCATGGCGAGCCTGCCCTGGCGGGCATCATCGCGGGGCGAGT  
 GGCTCTGGTCTTCTCTTCTGGTCTGGGGGCCATCTGCTGGTACGTGCACCAGGCTGGCGAGCTG  
 CTGACCCGGGAGAGGGCCTACAACCGGGGACAGGAAAAAGGATGACTATATGGAGTCAGGGACCA  
 AGAAGGATAACTCCATCCTGGAAATCCGCGGCCCTGGGCTGCAGATGCTGCCCATCAACCCGTACCG  
 CGCCAAAGAGGAGTACGTGGTCCACACTATCTTCCCTCCAACGGCAGCAGCCTCTGCAAGGCCACA  
 CACACCATTGGCTACGGCACACGCGGGGCTACCGGGACGGCGGCATCCCCGACATAGACTACTCCT  
 ACACATGATATGCCCCGCCACCCGGGCTGCCCGCCTCAGCCCCAGCTGCCCTGGCGTGGCCATGTGGC  
 TTTGCCACGCTGCTGCAATCCAAGAGAGCAAGGAAGAGAAATTCCATGGGTGACTTTCTCCGCAG  
 AAAGCAAAGTTTGGGGAGGGCTGACGATTTTGTAGAACACAACAGTGACAATTTTTTTTAAAGAAAT  
 AGAAGGCAGGAGGGGAATTTCGACATTGTTGAAGACATAATTTATACCAAGTTATGCCAGTTGGGGA  
 GGGAAAGGACTAAAAATAATATTGCAGGCAGGGCTGGGTGGGTTTTTTTTTTTCCCCCTGAACCTGG  
 AAGGATACTACCTGTACAACATCTGTGGACACCTCATGCTCTGTTCAAGGCCATCACAAAGGAACCG  
 CCAGGGAGAAGCAGCCGGCTCTCAAAGCTCCACGCAGCTCTCCGCCACTGGCCACTCGCTGGCGA  
 CCCGATGGAAGGTTTTTCAGCTCCTCAAAAGGAGAGAGGGAAGAAAAGATCTTTTGCCCTGGAGAT  
 ATGGTCCTGAAATCTCTCCCTGGCTTATTCATACCATTTCCCTTGACAGATTGAGAAACATGGC  
 ATCTTTCACTGCATTCTTTGAACAATCATGTAGTCGATTAAAAAAGGAGCCGCTAGCTTTCC  
 GGCTGAAGCCCTCTTCAGTTCCATGCACCACGCTCCGTAGAAGCCCGCGGGAAGCCGTAGCTTTCC  
 CTGCCACCTGGAGGTGCATCTGTCTGCCTGTCTATCCCTGTGCGGGTCTCTAAGTACAGATGGGT  
 AGATAGAGCCACATGCACGGTCTTACCGTTCTTCTGGGTGAGTTCTTACCATTTCCTGAACAATA  
 GAATTGTGAAAGTGTAAAAA

**FIGURE 36**

MVVAHPTATATTTPTATVTATVVMTTATMDLRDWLFLCYGLIAFLTEVIDSTTCPSVCRCNDN  
GFIYCNDRGLTSIPADIPDDATTLYLQNNQINNAGIPQDLKTKVNVQVIYLYENDLDEFPIN  
LPRSLRELHLQDNNVRTIARDSLARIPLLEKLHLDDNSVSTVSIEDAFADSKQLKLLFLSR  
NHLSSIPSGLPHTLEELRLDDNRISTIPLHAFKGLNSLRRLVLDGNLLANQRIADDTFSRLQ  
NLTELSLVRNSLAAPPLNLPSAHLQKLYLQDNAISHIPYNTLAKMRELERLDLSNNNLTTLP  
RGLFDDLGNLAQLLLRNNPWFCGCNLMWLRDWVKARAAVVNVVRGLMCQGPEKVRGMAIKDIT  
SEMDECFETGPQGGVANAAAKTTASNHASATTPQGSFLTAKKRPGLRLPDSNIDYPMATGD  
GAKTLAIHVKALTADSIRITWKATLPASSFRLSWLRLGHSPAVGSITETLVQGDKTEYLLTA  
LEPKSTYIICMVTMETSNAIVADETPVCAKAETADSYGPTTTLNQEQNAGPMASLPLAGIIG  
GAVALVFLFLVLGAICWYVHQAGELLTRERAYNRGSRKKDDYMESGTTKDNSILEIRGPGLQ  
MLPINPYRAKEEYVVHTIFPSNGSSLCKATHITIGYGTTRGYRDGGIPDIDYSYT

**Important features of the protein:**

**Transmembrane domain:**

amino acids 552-573

**N-glycosylation sites.**

amino acids 249-252, 305-308, 642-645

**Leucine zipper pattern.**

amino acids 182-203, 299-320

**Phospholipase A2 aspartic acid active site.**

amino acids 57-67

**FIGURE 37**

[illegible]

## **FIGURE 38**

MAEPGHSHHLSARVRRRTERRIPRLWRLLLLWAGTAFQVTQGTGPELHACKESEYHYEYTACD  
STGSRWRVAVPHTPGLCTSLSDPVKGTECSFSCNAGEFLDMKDQCKPCAEGRYSLGTGIRF  
DEWDELPHGFASLSANMELDDSAAEESTGNCTSSKWVPRGDYIASNTDECTATLMYAVNLKQS  
GTVNFEYYPDSSIIFFEFFVQNDQCQPNADDSRWMKTTEKGWFEHVELNRGNVLYWRTTA  
FSVWTKVPKPVLRNIAITGVAYTSECFPCPGTYADKQGSSFCCLCPANSYSNKGETSCHQ  
CDPKYSEKSSSCNVRPACTDKDYFYTHTACDANGETQLMYKWAKPKICSEDLEGAVKLPA  
SGVKTHCPCPNPGFFKTNNSTCQPCPYGSYSNGSDCTRCPAGTEPAVGFEYKWWNTLPTNME  
TTVLSGINFHEYKGMTGWEVAGDHIYTAAGASDNDFMILTLVVPGFRPPQSVMADTENKEVAR  
ITFVFETLCSVNCELYFMVGVNSTNTPTVETWKGSGKGQSYTYIIIEENTTTTSFTWAFQRTTF  
HEASRKYTNDVAKIYSINVTNVMNGVASYCRPCALEASDVGSSCTSCPAGYYIDRDSGTCHS  
CPPNTILKAHPYGVQACVPCGPGTKNNKIHSCLYNDCTFSRNTPTRTFNYNFSALANTVTL  
AGGPSFTSKGLKYFHHTLSLSCGNQGRKMSVCTDNVTDLRIPEGESGFSKSITAYVCQAVII  
PPEVTGYKAGVSSQPVSLADRLIGVTTDMTLDGITSPAELFHLES LGIPDVIFFYRSNDVTQ  
SCSSGRSTTIRVRCSPQKTVPGLLLPGTCSDGTCDCGNFHLWESAAACPLCSVADYHAIV  
SSCVAGIQXTTYVXREPCLCSGGISLPEQRVTICKTIDFWLKVGISAGTCTAILLTVLTCYF  
WKKNQKLEYKYSKLVNATLKDCLPAADSCAIMEGEDVEDDLIFTSKKSLFGKIKSFTSKR  
TPDGFDSVPLKTSSGGPMDL

### **Important features of the protein:**

#### **N-glycosylation sites:**

amino acids 153-156, 390-393, 391-394, 404-407, 544-547, 576-579, 672-675, 717-720, 947-950

#### **cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

amino acids 15-18, 563-566, 709-712

#### **Casein kinase II phosphorylation sites:**

amino acids 42-45, 59-62, 81-84, 146-149, 168-171, 282-285, 331-334, 340-343, 431-434, 449-452, 465-468, 523-526, 557-560, 761-764, 780-783, 835-838, 860-863, 893-896, 949-952

#### **Tyrosine kinase phosphorylation sites:**

amino acids 50-56, 109-116

#### **N-myristoylation sites:**

amino acids 77-82, 88-93, 152-157, 268-273, 288-293, 320-325, 400-405, 405-410, 414-419, 463-468, 599-604, 616-621, 634-639, 644-649, 839-844, 874-879, 912-917, 916-921

#### **Amidation site:**

amino acids 707-710

#### **Cell attachment sequence:**

amino acids 162-164

# **FIGURE 39**

GGGAAGGGGTTCTGGGCTGCCGCAGGCACACAGGCCAGAGCTTCGTGGATACCTGCAGGGCC  
CAAAGGTCCCTCCCTGTTTTGAAGAGTGAGTGATGGCTATGAGGTAGCGGCCAGGCTGATCA  
CCCCTGCGTTGGCTGGAGGCAGAATTCTGTAAATCCTCGCCAAGTCTTTCTCCAGGCCACTG  
GTTAGCTCATCTCAGCCTCCTCTGGGAGCATCAACACCAACATGGCACAGGGGACTGCAGTG  
GTGTGCTTTGGACCTGTGTACCCACCCAAGGCTAAAGGCAGAGCCAGGTGACTTTGCGGGGG  
TCTCTTCTCTAGGATTATCTGTACTTCCCCTCTGTCTCTTTTACTACGGGAGATCGAGCTA  
GCTATAACCCACCTTCTTTTCATGAGAACCACACTAAATTGCAAAAATTATCCCAGTGCTGGA  
GGAGGGCAGCAGGTTGAGATTATGTTGGCAGGAAGAATGTTGGCATTGATTGGCACGCAGGG  
GACGAGAGCTGCTTTGTGCTTTAAAGGAGCCAAGTTACACCCTGTTTAAACCTGCCTTCAAA  
GGGACGACTCTGTAAGATTCTCTGCTACTTATTCAAGTTGACACGATGCCCTTCACACTCCA  
CCTGAGGTCCCGCCTTCCCTCTGCCATAAGGAGTTTGATTCTACAAAAGAAACCAACATCA  
GAAATACATCCAGCATGGCTGGAGAGCTCCGACCAGCCAGCCTGGTGGTCTGCCCAGGTCC  
CTTGCTCCAGCTTTTGAAAGATTCTGCCAGGTCAACACTGGTCTCTACCCCTGCTGGGCCA  
GAGTGAGCCAGAAAAGTGGATGCTGCCCCCTCAAGGTGCTATCTCAGAGACCAGGATGGGCC  
ATCCCCAGTTCTGGAAATACGAGTTCGGTGCCTGCACCGGTAGCCTGGCTTCGCTGGAGCAG  
TACTCGGAGCAGCTGAAGGACATGGTGGCCTTCTTCCTGGGCTGCAGCTTCTCCCTGGAGGA  
GGCCTTGAGAGAAAGCGGGGCTCCCCAGAAGAGACCCAGCAGGTACAGCCAGGCGGGTGCA  
ACAAGACAACAGTGCCTTGTGTTACCCATGCTGGCTTCTGCTGCCCTCTGGTGGTCACGATG  
AGGCCCATTCCCAAGGACAAGCTGGAAGGGCTGGTGCGGGCCCTGCTGCTCCCTCGGAGGTGA  
GCAGGGGCAACCTGTTACATGGGCGACCCAGAACTGTTGGGAATCAAAGAGCTTTCCAAAC  
CTGCCTACGGGGATGCCATGGTGTGTCCCCAGGGGAGGTTCCAGTGTTCTGGCCTTCTCCG  
CTGACCAGTCTCGGAGCTGTGAGCAGCTGTGAGACCCCACTGGCTTTTGCCAGCATCCCAGG  
CTGCACAGTTATGACTGACCTGAAGGATGCAAAGGCTCCACCTGGTTGTCTACCCCAGAGA  
GAATTCAGAGGTCCATCACATTTCCCAAGATCCTCTGCACTACAGCATCGCGTCAGTCTCT  
GCTTCTCAGAAGATCAGAGAACTAGAGTCTATGATCGGCATAGACCCAGGGAAACCGGGGGAT  
TGGGCACCTGCTCTGTAAAGATGAGCTGCTGAAGGCCCTCTCTCTCGCTGTCCCATGCCCGCT  
CAGTGCTCATCACCCTGGGTTCCTCCACACATTTCAATCATGAGCCTCCAGAAGAGACAGAT  
GGCCCACCAGGAGCTGTTGCTCTGGTTGCCTTCTGTCAGGCCTTGGAAGAGGAGTCCGCAT  
AATCGTTGACCAGAGAGCCTGGAACCTGCACCAGAAGATTGTTGAAGATGCTGTTGAGCAAG  
GTGTTCTGAAGACGCAGATCCCGATATTAACCTACCAAGGTGGATCAGTGGAAGCTGCTCAG  
GCATTCCTGTGCAAAAATGGGGACCCGACACACCTAGATTTGACCACCTGGTGGCCATAGA  
GCGTGCCGGAAGAGCTGTGATGGCAATTACTACAATGCAAGGAAGATGAACATCAAGCACT  
TGTTTGACCCCATTGACGATCTTTTTCTTGCTGCGAAGAAGATTCTGGAATCTCATCAACT  
GGAGTCGGTGATGGAGGCAACGAGCTTGGGATGGGTAAAAGTCAAGGAGGCTGTGAGGAGGCA  
CATACGGCACGGGGATGTCATCGCTGCGACGTGGAGGCTGACTTTGCCGTCAATTGCTGGTG  
TTTCTAACTGGGGAGGCTATGCCCTGGCCTGCGCACTCTACATCCTGTACTCATGTGCTGTC  
CACAGTCAGTACCTGAGGAAAGCAGTCGGACCCTCCAGGGCACCTGGAGATCAGGCCTGGAC  
TCAGGCCCTCCCGTCGGTCATTAAGGAAGAAAAATGCTGGGCATCTTGGTGCAGCACAAAG  
TCCGGAGTGGCGTCTCGGGCATCGTGGGCATGGAGGTGGATGGGCTGCCCTTCCACAACACC  
CACGCCGAGATGATCCAGAAGCTGGTGGACGTACCCACGGCACAGGTGTAAACCGTCCATGTT  
CCGTGTGAGCAGAGTCCCTACCAACGGGCAGGTCTGCATCCGGGGAGAATGCAGCTGCTTCT  
GGCGACAATCCTGCTAGTAAACACTGGTCTTCGGTGAGCAACGAACACTCGCCTGGCCTGGG  
AAACTGCATGCCCACTTTCTGGGAGGGGTTAGTGCAGGTGCCGTGGACAAAGGACAACATTT  
CTCTGGGGCTTTTTAACTTTTATTCCTAAGACTCTAAAGGCGTTGATTTCAACCCCTCCTTCA  
CTCTGGCTTCTTCAGGCAACCCACGTGGTCTCCTATGAGAATCTTCTCGACAGTTACTTATG  
GGGACACTTGTGAACAATTAAGTCCAGGGCAGAGCATGAGAACAAACATTCCCAGGCCATG  
TAGGATAGGATACTCCAGACTCCAGTCATCCTCCCCATCCATGGTTTCTGTTACTCATGGT  
TTCAGTTACTCATAGCCAACTGCAGACCGAAAATACTAAATGAAAAAFTTCAGAAATAACA  
ACTCTTAAGTTTTAAAAA

**FIGURE 40**

MPFTLHLRSRLPSAIRSLILQKKPNIRNTSSMAGELRPASLVVLPRSLAPAFERFCQVNTGP  
LPLLQSQSEPEKWMLEPPQGAISETRMGHPQFWKYEFGACTGSLASLEQYSEQLKDMVAFFLGC  
SFSLEEALEKAGLPRRDPAGHSQAGAYKTTVPCVTHAGFCCPLVVTMRIIPKDKLEGLVRAC  
CSLGGEQSQPVHMGDPPELLGIKELSKPAYGDAMVCPPEVPVFWPSPLTSLGAVSSCETPLA  
FASIPGCTVMTDLKDAKAPPGCLTPERIPEVHHISQDPLHYSIASVSASQKIRELESMIGID  
PGNRGIGHLLCKDELLKASLSLSHARSVLITTFGPTHFNHEPPEETDGPPGAVALVAFLOAL  
EKEVAIIVDQRAWNLHQKIVEDAVEQGVLTQIPIPTYQGGSVAAQAFLCKNGDPQTPRFD  
HLVAIERAGRAADGNYYNARKMNIKHLVDPIDDLFLAAKKIPGISSTGVGDGGNELGMGKVK  
EAVRRHIRHGDVIACDVEADFAVIAGVSNWGGYALACALYILYSCAVHSQYLKAVGSPSRAP  
GDQAWTQALPSVIKEEKMLGILVQHKVRSVSGIVGMEVDGLPFHNTHAEMIQKLVDVTTAQV

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 358-378, 517-539

**N-glycosylation site.**

amino acids 28-32

**Tyrosine kinase phosphorylation site.**

amino acids 444-452

**N-myristoylation site.**

amino acids 98-104, 102-108, 123-129, 149-155, 181-187, 190-196,  
238-244, 308-314, 399-405, 413-419, 448-454, 477-483, 482-488,  
487-493

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 233-244, 531-542

**FIGURE 41**

CTTTCCTGTTTTATCCGCAGCCCTTTTCTTCTTTGAGTTAGTAAAGATTTATTCTGTAACCT  
GACACTCATCTGGCCCTTTGCAGTTTGCCAGCCATATTCCCATGTGATTTCCCACTGGATCC  
AGGCCCCCATCCGGCTGGCAGGAGGGGGCTCTGACGTACAGGTTGGAAATCAGAAGTCTGTG  
AGAGCGCGGGAGTG CATGGCAGCTCTGGGTCCCAGACCTGGCCCGACCCCTCTGCTTCACCT  
CCAGCTCTGCTGCTCCTCTACTCTTGGGTGAGATCCCTTTGGAGCCACAGCGAGGAACCCCT  
GTGGTCCTCAGGCAGGTGTACCTTGAGTCAGCCAGGAGCCCTCTTTTCCTGTGTCAAAGCCT  
GCCCTCGGGCTCTGCTCACCTCTGGTGACCCTCCAAGATGCCCCTGCCCTCAGTTTCCCCTC  
ATGATCTGGCCTCTGCCCCCTTCTCTAGCCACAGCCTCTAGTACACTTTAGCAATACCACCA  
GACTAGTTAGAGTTCCCCACTCACCAAGCAAGACATGCAGTTTCATGCCTCTGTGCCTTCGC  
TCATGCTGTTTTCTTCCGACTGGAATGCCTTCCCCTGCTCCTCCTGCCTTGTCTGCCTGGCAA  
GTTTCATCTCTCACGATCCCCTCAAAGGCCCCCTCCTCCAGGAAGGCAACCCCTGTGCCCTC  
CCCTCCAGGCTACCTCTGCACTTTGTCAATGCTTCTCTTGTGGCACTTATCACACTGTATTT  
TACTTGTTTACATGTTTGTCTCCCCTTCTAGACTGTGAATCCTTAAGGGCATGGACTGTATC  
TTATGCATCTCTGTATTTCTGCGCCTAGCACGGTGCCTAGCACACAGTAGGCGCTCAATAAA  
TGTTGAATGAATGAATGATTT

**FIGURE 42**

MQFHASVPSLMLFLPTGMPSAPPALSAWQVHLSRSPQRPPPPGRQPLCPSPPGYLCTLSML  
LLWHLSHCILLVYMFVSPSRL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**Microbodies C-terminal targeting signal.**

amino acids 81-83



**FIGURE 43**

GTTTCCAACAAGGATGATATGAAGACTTCCCTGAAGAAAGTTGTGAAGGGACCTCCTACGAG  
ATGATGATGCAGTGTGTGTCCCGCATGTTGGCCACCCCCTGCATGTCATCTCAATGCGCTG  
CATGGTCCAGTTTGTGGGACGGGAGGCCAAGTACAGTGGTGTGCTGAGCTCCATTGGGAAGA  
TTTTCAAAGAGGAAGGGCTGCTGGGATTCTTCGTTGGATTAATCCCTCACCTCCTGGGCGAT  
GTGGTTTTCTTGTGGGGCTGTAACTGCTGGCCCACTTCATCAATGCCTACCTGGTGGATGA  
CAGCTTCAGCCAGGCCCTGGCCATCCGGAGCTATACCAAGTTCGTGATGGGGATTGCAGTGA  
GCATGCTGACCTACCCCTTCCTGCTAGTTGGCGACCTCATGGCTGTGAACAACCTGCGGGCTG  
CAAGCTGGGCTCCCCCTTACTCCCCAGTGTTCAAATCCTGGATTCACTGCTGGAAGTACCT  
GAGTGTGCAGGGCCAGCTCTTCCGAGGCTCCAGCCTGCTTTTCCGCCGGGTGTCATCAGGAT  
CATGCTTTGCCCTGGAGTAACTGAATCATCTAAAAACACGGTCTCAACCTGGCCACTGTG  
GGTGAGGCCTGACCACCTTGGGACACCTGCAAGACGACTCCAACCCAACAACAACCAGATGT  
GCTCCAGCCCAGCCGGCTTCAGTTCCATATTTGCCATGTGTCTGTCCAGATGTGGGGTTGA  
GCGGGGGTGGGGCTGCACCCAGTGGATTGGGTACCCGGCAGACCTAGGGAAGGTGAGGCGA  
GGTGGGGAGTTGGCAGAATCCCCATACCTCGCAGATTTGCTGAGTCTGTCTTGTGCAGAGGG  
CCAGAGAATGGCTTATGGGGGCCCAGGTTGGATGGGGAAAGGCTAATGGGGTCAGACCCAC  
CCCGTCTACCCCTCCAGTCAGCCCAGCGCCCATCCTGCAGCTCAGCTGGGAGCATCATTCTC  
CTGCTTTGTACATAGGGTGTGGTCCCCTGGCACGTGGCCACCATCATGTCTAGGCCTATGCT  
AGGAGGCAAATGGCCAGGCTCTGCCTGTGTTTTTCTCAACACTACTTTTCTGATATGAGGGC  
AGCACCTGCCTCTGAATGGGAAATCATGCAACTACTCAGAATGTGTCTCCTCATCTAATGC  
TCATCTGTTTAAATGGTGATGCCTCGCGTACAGGATCTGGTTACCTGTGCAGTTGTGAATACC  
CAGAGGTTGGGCAGATCAGTGTCTCTAGTCTACCCAGTTTTTAAAGTTCATGGTAAGATTTG  
ACCTCATCTCCCGCAAATAAATGTATTGGTGATTTGGAAAAAAAAAAAAAAAAAAAA

## **FIGURE 44**

MMMQCVSRMLAHPLHVISMRCMVQFVGREAKYSGVLSSIGKIFKEEGLLGFFVGLIPHLLGD  
VVFLWGCNLLAHFINAYLVDDSFQALAIRSYTKFVMGIAVSMLTYPFLLVGDLMVNNCG  
QAGLPPYSPVFKSWIHCWKYLSVQGQLFRGSSLLFRRVSSGSCFALE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-18

**Transmembrane domains:**

amino acids 51-72, 97-114

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 160-163

**N-myristoylation sites.**

amino acids 34-39, 100-105, 123-128, 165-170

# **FIGURE 45**

GCTCACTCTTTGGGTCCACACTGCCTTTATGAGCTGTAACTCACTGGGAATGTCTGCAGC  
TTCACCTCCTGAAGCCAGCGAGACCACGAACCCACCAGGAGGAACAACTCCAGACGCGC  
AGCCTTAAGAGCTGTAACTCACCAGCGAAGGTCTGCAGCTTCACTCCTGAGCCAGCCAGAC  
CACGAACCCACCAGAAGGAAGAACTCCAAACACATCCGAACATCAGAAGGAGCAAACCTCGT  
GACACGCCACCTTTAAGAACCGTGACACTCAACGCTAGGGTCCGCGGCTTCATTCTTGAAGT  
CAGTGAGACCAAGAACCCACCAATTCCGGACACGGCAAAGTAACATCCTAGACATGGCTTTA  
GAGATCCACATGTGAGACCCCATGTGCCTCATCGAGAACTTTAATGAGCAGCTGAAGGTTAA  
TCAGGAAGCTTTGGAGATCCTGTCTGCCATTACGCAACCTGTAGTTGTGGTAGCGATTGTGG  
GCCTCTATCGCACTGGCAAATCCTACCTGATGAACAAGCTGGCTGGGAAGAACAAGGGCTTC  
TCTGTTGCATCTACGGTGCAGTCTCACACCAAGGGAATTTGGATATGGTGTGTGCCTCATCC  
CAACTGGCCAAATCACACATTAGTTCTGCTTGACACCGAGGGCTGGGAGATGTAGAGAAGG  
CTGACAACAAGAATGATATCCAGATCTTTGCACTGGCACTCTTACTGAGCAGCACCTTTGTG  
TACAATACTGTGAACAAAATTGATCAGGGTGCTATCGACCTACTGCACAATGTGACAGAACT  
GACAGATCTGCTCAAGGCAAGAACTCACCTGACCTTGACAGGGTTGAAGATCCTGCTGACT  
CTGCGAGCTTCTTCCAGACTTAGTGTGGACTCTGAGAGATTTCTGCTTAGGCCTGGAAATA  
GATGGGCAACTTGTACACCAGATGAATACCTGGAGAATTCCTAAGGCCAAAGCAAGGTAG  
TGATCAAAGAGTTCAAATTTCAATTTGCCCGTCTGTGTATACAGAAGTTCTTTCCAAAAA  
AGAAATGCTTTATCTTTGACTTACCTGCTCACCAAAAAAGCTTGCCCACTTGAAACACTG  
CCTGATGATGAGCTAGAGCCTGAATTTGTGCAACAAGTGACAGAATTCGTTCCTACATCTT  
TAGCCATTCTATGACCAAGACTCTTCCAGGTGGCATCATGGTCAATGGATCTCGTCTAAAGA  
ACCTGGTGCTGACCTATGTCAATGCCATCAGCAGTGGGGATCTGCCTTGATAGAGAATGCA  
GTCCTGGCCTTGGCTCAGAGAGAGAACTCAGCTGCAGTGCAAAAGGCCATTGCCCACTATGA  
CCAGCAAATGGGCCAGAAAGTGACGCTGCCCATGGAAACCTCCAGGAGCTGCTGGACCTGC  
ACAGGACCAGTGAGAGGGAGGCCATTGAAGTCTTCAAGGAACTCTTCAAGGATGTAGAC  
CAAAGTTTCCAGAAAGAATTGGAGACTCTACTAGATGCAAAACAGAATGACATTTGTAAACG  
GAACCTGGAAGCATCCTCGGATTATTGCTCGGCTTTACTTAAGGATATTTTGGTCCTCTAG  
AAGAAGCAGTGAAGCAGGGAATTTATTCTAAGCCAGGAGGCCATAATCTCTTCATTAGAAA  
ACAGAAGAACTGAAGGCAAAGTACTATCGGGAGCCTCGGAAAGGAATACAGGCTGAAGAAGT  
TCTGCAGAAATATTTAAAGTCCAAGGAGTCTGTGAGTCATGCAATATTACAGACTGACCAGG  
CTCTCACAGAGACGGAAAAAAGAAGAAAGAGGCACAAGTGAAAGCAGAAGCTGAAAAGGCT  
GAAGCGCAAAGTTGGCGGCGATTCAAAGGCAGAACGAGCAAATGATGCAGGAGAGGGAGAG  
ACTCCATCAGGAACAAGTGAGACAAATGGAGATAGCCAAACAAAATTTGGCTGGCAGAGCAAC  
AGAAAATGCAGGAACAACAGATGCAGGAACAGGCTGCACAGCTCAGCACAAACATTTCAAGCT  
CAAAATAGAAGCCTTCTCAGTGAGCTCCAGCACGCCCAGAGGGCTGTTAATAACGATGATCC  
ATGTGTTTTACTCTAAAGTGCTAAATATGGGAGTTTCTTTTTTTTACTCTTTGTCACTGATG  
ACACAACAGAAAAGAACTGTAGACCTTGGGACAATCAACATTTAAATAAATTTATAATTA  
TTAAA

**FIGURE 46**

MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAKGN  
KGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALALLSS  
TFVYNTVKNIDQGAIDLLHNVTETDILLKARNSPDLDRVEDPADSASFFPDLVWTLRDFCLG  
LEIDGQLVTPDEYLENSLRPKQGSQQRVQNFNLPRLCIQKFFPKKKCFIFDLPAHQKKLAQL  
ETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVNAISSGDLPCI  
ENAVLALAQRENSAAVQKAIHAHYDQQMGQKVQLPMETLQELLDLHRTSERAIEVFMKNSFK  
DVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAVKQGIYSKPGGHNLF  
IQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQALTETEKKKKEAQVKAEA  
EKAEAQRLLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEEQQKMQEQQMQEQAQLSTT  
FQAQNRSLLSSELQHAQRAVNNDPCVLL

**Important features of the protein:**

**Transmembrane domains:**

amino acids 31-49, 114-131

**N-glycosylation sites.**

amino acids 90-94, 144-148, 287-291, 563-567

**N-myristoylation sites.**

amino acids 45-51, 283-289

**Prenyl group binding site.**

amino acids 583-588

**ATP/GTP-binding site motif A (P-loop).**

amino acids 45-53

**FIGURE 47**

CACTCATTCAATCCAAAGGGTCTCTCAAGGCAATGGTAATGTGCAAGGAGGTGATACCTAAA  
TGAATGACCAAAAGAACATGCTTCTGCTTTTGTGTGTCTCCTACATTTTAGACATTTGTTTG  
TTTCTCTTGGTAGCCTTTAAATTCCTTGAAGCCCAGGACCATGTCTCACTTACCTTTGTGTT  
TCCACTAACTAGTCTACCTCCTGGAATTGGCAGATACTCAGTGAAAGCCTGTGAAATAAGTG  
ATGTCTATTTCTAGCATATTATTCTGAGATTTAATGATAGATTTAGTGATTGAATGAGATTT  
CCATTTTCAAATACAGCAAAAGCATAACTATTTTCATTCATTCATATTCATTCAACTTCATT  
CTCAAAATTAGGTCCTGAGTTAACTAATAATTACCTTTGAAATGTGTGGGTTATTTGAGGCA  
ATCAGGTGGTGACATTGAGCTCTCAGCCAGAGTTTGTCTTCTGGAATTGATTCACTTCCATTG  
CATTGATTTTTGTCTCAGAAGCCAAGGTTTCCCATGAAAAATCATTCCCACCTTGAATTGGG  
CTGTGATTCTTGTGCGTTTAAAGTAAAGGAAGCCTCTTGGTTCTAGTTCTGCAAACTTACAC  
ACTGAACTGGGACAAGTTTTTGTTTAGAGTAATGGCTGGGAAAAGAGGAACCTTTCAATTTA  
TTCAGAAGTCAAAAAAAAGGCCTCCCAGCCACCTGGAGATGTTTTGTGTCAGACACCAGCC  
TGGCTCTGTCTTTATGCCTAACAATTGAGCATCCAGTCTTCTTTGTGCTGGGACCATTGCTC  
AGCTCTGCAAGGGGAAAAGAGGGAGAAAGCCAGAGCTGCCAGGCTTCTTGCAGTGGGGCCGG  
GGGAGGGTTCTGGGAAGCAGGTGCTCTCTGGCTTCTTGGTACGTGAGGCTCTCGGAGCTGC  
CTCTCCTCTGACCCTCAGGTCTCACCAGTTTGTCTCCAGGAGTATATTGAAAACATACCCA  
GTGCTCTCTCAAGCACCCACTGCTTAGAGGGCCAGATTTCTTTTCTTCTTTCCCTTGCAG  
AGCTGGAGACTGCATCGGGCATCTGGTGTTTAACTAAACAGGAAAAGTGAATAAGGTCCA  
CAGTGCTCATTGTGTAGACTAGCTGCCCTCCGATGGGTGCTCTGATTATCAGTGGTTCCAGT  
GCAGGGCCTGTCACTAAACAGGCCTCACTTCCTCCTTGGGGGCTTTCCCATGGGAGGTGTGG  
CTTTTTACTCTACATGGAAATGACTCTCTGCAGCCACAGAACACAGTCATTTTCTGAATTAT  
CCCAGTCTCTCATGCGCCCTGGATTCTTCCAGATGCCCTTATATCTCTTGTGCAAAGTTGTCT  
AAAATTTGGTTCCAGCTTCCAAGCCTTGCCCTTTTGGCCTTCTTGGGAAGTATTTTTGTTGAT  
GAGTCGTCTGTCAATTATTCTCTAAAATGATTTGCTTTTGTCTTTTCAATTCCTATTTCCAC  
CCCACATATACACATGCTTCTTAACTTAGGGGATTACATGCCAATAAATCTATTGTTGAA  
AATGCACTAATACTATCGCAAAGACGAAAATTCACAGGCTGAACCGTTGTAAGTCCATATGC  
TCCTCAACTTACATGTGTGATGGAGTTATGCCCAAATAAGTCCATCGTCAAGTTGAAAAATC  
AAAATCAAGCCATCTTAGGTTGAGGACCATTTGTTTGTACCTCCAAAGATGTCATATCTTTA  
AACATACTCCCTAGCTTTTCTTTTACTTTTTATTTTGAAGTAATTATAGAATCACAGAAAG  
TTGCAAAAAA

**FIGURE 48**

MGALIISGSSAGPVTKQASLPPWGLSHGRCGFLLYMENTLCSHRTQSFSELSQSLMRPGFLQ  
MPYISCAKLSKIWFPAKPCLLAFLEVFLLMSRLSLFSKMICFLFLSFLFPPHIYTHAS

**Important features of the protein:**

**Signal peptide:**

amino acids 1-41

**Transmembrane domain:**

amino acids 88-107

**Casein kinase II phosphorylation site.**

amino acids 47-50

**N-myristoylation site.**

amino acids 24-29

**FIGURE 49**

GGCTTCTACAGTCCACAACACCCACCAGCCCCAGGCCAGCAGAAATGAGCCAGTGAGTGCCGGGGCTCCCAGT  
 TTGGCTGTTGCTATGACAACGTGGCCACTGCAGCCGGTCTCTTGGGGAAGGCTGTGTGGGCCAGCCAGCCAT  
 GCCTACCCCGTGCGGTGCCGTGCTGCCAGTGGCCATGGCTCTTGTGCAGACTGGGCTGCCCGCTGGTACTTCGT  
 TGCCTCTGTGGGCCAATGTAACCGCTTCTGGTATGGCGGCTGCCATGGCAATGCCAATAACTTTGCCTCGGAGC  
 AAGAGTGCATGAGCAGCTGCCAGGGATCTCTCCATGGGCCCGTCTGCCAGCCCTGGGGCTTCTGGAAGGAGC  
 ACCCACACGGATGGTGGCGGAGCAGTCTGCAGGCGAGCAGGAACCCAGCCAGCACAGGACAGGGGCCCGGT  
 GCAGAGAAAGCCCTGGCCCTTCTGGTGTCTCTGGCGGCAAGACCAACAGCCTGGGCCAGGGGAGGCCCCCACA  
 CCCAGGCCCTTGGAGAATGGCCATGGGGGAGGAGCTTGGGTCCAGGGCCCCCTGGACTGGGTGGAGATGCCGGA  
 TCACCAGCGCCACCCCTTCCACAGCTCCTCTACAGATCTCACTTCCACCTCTCCAGGATTAGCTTGGCAGGTG  
 TGGAGCCCTCGTTTGGTGGGAGGACCCCTGGGGCAGTTGGTGGCGCTCTCTGCTCAGACGACACTGCCCCGAA  
 TCCCAGGCTGCCCTGGCAGAAAGATGGCCAGCCCATCTCTCTGACAGGCACAGGCTGCAGTTCCAGCGATCCCT  
 GATCATCCACCCCTGCAGGCAGAGGACGCGGGCAGCTACAGCTGTGGCAGCACCCGCCAGGCCGCGACTCCC  
 AGAAGATCCAATCCGCATTATAGGGGGTGACATGGCCGTGTGTCTGAGGCTGAGCTGAGCCGCTTCCCTCAG  
 CCCAGGGACCCAGCTCAGGACTTGGCCCAAGCGGGGCTGCTGGGCCCTGGGGGCCATCCCTCTTACACCC  
 ACAGCCTGCAAACAGGCTGCGTTTGGACCAGAAACAGCCCCGGGTGGTGGATGCCAGTCCAGGCCAGCGGATCC  
 GGATGACCTGCCGTGCCGAAGGCTTCCCGCCCCAGCCATCGAGTGGCAGAGAGATGGGCAGCCGTCTCTCTCT  
 CCCAGACACAGCTGCAGCCTGATGGCTCCCTGGTCATTAGCCGAGTGGCTGTAGAAGATGGCGGCTTCTACAC  
 CTGTGTCGCTTCAATGGGCGAGACCCGAGACCGAGATGGGTCCAGCTCAGAGTTCTGGGGAGCTGACAACTCT  
 CAGGACTGCCCCCTACTGTGACAGTGCCAGAGGGTGATACGGCCAGGCTATTGTGTGTGGTAGCAGGAGAAAGT  
 GTGAACATCAGGTGGTCCAGGAACGGGCTACCTGTGCAGGCTGATGGCCACCGTGTCCACCAGTCCCAGATGG  
 CACGCTGCTCATTTACAACCTTGGCGGCCAGGGATGAGGGCTCTACATGTGCAGTGCCCTACCAGGGGAGCCAGG  
 CAGTCAGCCGACGACCCGAGGTGAAGTGGTCTCACCAGCACCCACCGCCAGCCGAGGACCTGGCAGGGAC  
 TGGCTCGACCAGCCAGAGCTGGCCAACTGTGATTGTATCTGCAGGCCAGCTTTGTGGCAATGAGTATTACTC  
 CAGCTTCTGCTGTGCCAGCTGTTACGTTTTCCAGCCTCAGCTCAGCCCATCTGGCAGTAGGGATGAAGGCTAG  
 TTCCAGCCCCAGTCCAAAATAGTTTCATAGGGCTAGGGAGAAAGGAGATGGACTCTTGGCTTCTCTCTCTGCG  
 TGGCAAGGGAGTTATCTTCTGGAATACATTAGCTCTTTCAAAAACCCACCCAGTGTTTAGCCTCAACGGCAGC  
 CAGTTACAGCTTCTCTCTGTAGCCTTACAGAGTGTGGTTCATCTCTGACATAACCCAGGCTGTGTTTTTCAAG  
 AAGAGCAATCTGTTTTGGATAAGAAAACCTTTACTTTACAGCTTCCCTTTATAATTTGTTACACAGGAATAGTT  
 AAATGCATTTGTTTTGTTTTGTTTTGAGACGAGTTTTCACTCTTGTGCCCAGGCTGGAGGGCAATGGCGCGAT  
 CTCAGCTCACTGCAACCTCCGTCTCCTGGGTTCTTGATTCTCCTGTGTGAGCTTCTGAGTAGCTGGGATTACA  
 GATGCTATCACCATGCTGGTAAATTTTGTATTTTGTAGTTGAGATGGGGTTTCGCCATGTTGGCCAGGCTGG  
 TCTCGAACTTCTGACCTCAGATGATCTGCCCGCTCAGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACC  
 ACGCCAGCCATCAATGCATTTTTTTTTTATTTTTTTTTTGGAGACAGAGTTTCGCACCTCTTGCCAGGCTGGAGT  
 ACAATGGTGGCATCTTGGCTCACTGCAACCTCCACCTCCTGGGTCAAGCGCTTCTCCAGCCTCAGCCTCCTGA  
 GTAGCTGGGATTACAGGTATGTGCCACCATGCCTGGCTAATTTTGTATTTTGGTGGAGACGGGGTTTCTCCAT  
 GTTGGTCAGACTGGTCTTGAACCTCCGACCTCAGGTAATCCGCCCCCTCCGCTCCCAAAATGCTGGGATTAG  
 AGGTGTGAGCCACTGTGCCAGCCCATCAATGTGTTTTAAAGCTAGCTGTGAGGTTCCACTTAATTTAAAGCT  
 GGGCAGGGAGATGTGTAATGATTTCAAAGTTAAACCTGTTTGTCTTAAAGGGCATGCCAAGTCTCTGTGTA  
 TCAGGGAAGTATTCTGTGCTAAAATCAGCGATGGTTTCATTGCTCTAGTCTCTCTCACCTTCTAGGCAGTGCA  
 CAGTCAGCTCTAAATCTGGTGAGAGGGTTAACAGCATAAACCTTGTGGCAAAATGGAATAGATGTTAAGACC  
 TCAAATAGGGATTGGGATGAAACAGCTGCAGTTAGCACTGTTATCTGAGCATGAAAGAACTGGAACGCTCCT  
 TACGTCGAGATGTTGGACCTTGAAGCCCTCCTGAGGCCAATGCAAACTCTGGCTGTGACGGTTCTCTGACAC  
 CTGTGTAAAGCTGACCAGCCTGCTCTGTACAGTGACAATGAGGAGCCCCCTCTCTTCTTAAAGTAGGAATCTGTG  
 AAGCAAAATGTTTGTGCTGCCAAAGACAAATCAGACTGTGAGTCAATTAATAACAGCATTAGCAGGATGAGGATAGC  
 AATGGGGAAGGGTTGTGGGCAATGCAGTAACAGGGAAATGGCTTCAGAAATGGTTTGGATTGGAAGACAACATT  
 CTTTCATCTCTCAGGACTTCTAATTCCTTGATGCTAAAAGAAGAGGCATGGATTCTATGAGCTTCCAGTCCCTT  
 TCCACTTTAACCTTCTACAAATCTTTCAGAGGACTGCCTAGTAGCAAGGTTATTCCTGGACACAGGAAAGACG  
 GGCATTACAGGGACCAAGCTCTGAAAGGTGACTTTTATTACCAACACACTGGCTGGAAAAGGGACAAACCACA  
 TCACGGGTGAGTGATACTTCTCAGTCTTCTACTCATTCAACAAAGGAAATGTGGGCTGGGGCAGAGGTCTTT  
 TTTCAATTAATACTGGAAAAATATTGAAGAGCATCCATGTTCACTTATGGCTGGTTTTGCTATAGAAATTGGAA  
 AATAAGGCCACTTTTTTGT

## **FIGURE 50**

MGPVVPSLGLLEGAPTRMVAAVLQASRNPASTGQGPRCRES PGLLVVSGGKTNSLGQGRPP  
TPRPLENGHGGRSLGPGPLDWVEMPDHQRHPSTAPPTDLTSHLSRISLAGVEPSLVQAALGQ  
LVRLSCSDDTAPESQAAWQKDGQPISSDRHRLQFDGSLIIHPLQAEDAGTYSCGSTRPGRDS  
QKIQLRIIGGDMAVLSEAELSRFPQPRDPAQDFGQAGAAGPLGAIPSSHPQPANRLRLDQNO  
PRVVDASPGQIRMT CRAEGFPPPAIEWQRDQGPVSSPRHQLQPDGSLVISRVAVEDGGFYT  
CVAFNGQDRDQRWVQLRVLGELTISGLPPTVTVPEDTARLLCVVAGESVNIRWSRNLGPVQ  
ADGHRVHQSPDGTLLIYNLRARDEGSYMCSAYQGSQAVSRSTEVKVVSPAPTAQPRDPGRDC  
VDQPELANCDLILQAQLCGNEYYSFCCASC SRFQPHAQPIWQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-16

**Tyrosine kinase phosphorylation site.**

amino acids 392-400

**N-myristoylation sites.**

amino acids 9-15, 50-56, 112-118, 146-152, 173-179, 195-201,  
220-226, 229-235, 280-286, 306-312, 336-342, 397-403

**Myelin P0 protein.**

amino acids 153-182



# **FIGURE 51**

CAGGCAGAAGCGAACAAAGACCCAGCAAGAGAAGGCAGAGGCTAAGACCCATCCCGTATCTG  
 CTCTCCTGAAATAATTCTGGAGTCA**ATG**CCTGAAATGCCAGAGGACATGGAGCAGGAGGAAGT  
 TAACATCCCCTAATAGGAGGGTTCTGGTTACTGGTGCCACTGGGCTTCTTGCCAGAGCTGTAC  
 ACAAAGAATTTTCAGCAGAAATAATTGGCATGCAGTTGGCTGTGGTTTCAGAAGAGCAAGACCA  
 AAATTTGAACAGGTTAATCTGTTGGATTCTAATGCAGTTCATCACATCATTTCATGATTTTCA  
 GCCCCATGTTATAGTACATTGTGCAGCAGAGAGAAGACCAGATGTTGTAGAAAATCAGCCAG  
 ATGCTGCCCTCTCAACTTAATGTGGATGCTTCTGGGAATTTAGCAAAGGAAGCAGCTGCTGTT  
 GGAGCATTTCTCATCTACATTAGCTCAGATTATGTATTTGATGGAACAAATCCACCTTACAG  
 AGAGGAAGACATACCAGCTCCCTAAATTTGTATGGCAAAACAAAATTAGATGGAGAAAAGG  
 CTGTCTGGGAGAACAATCTAGGAGCTGCTGTTTTGAGGATTCCTATTCTGTATGGGGAAGTT  
 GAAAAGCTCGAAGAAAGTGCTGTGACTGTTATGTTTGATAAAGTGCAGTTCAGCAACAAGTC  
 AGCAAACATGGATCACTGGCAGCAGAGGTTCCCCACACATGTCAAAGATGTGGCCACTGTGT  
 GCCGGCAGCTAGCAGAGAAGAGAATGCTGGATCCATCAATTAAGGGAACCTTTCTAGTGTCT  
 GGCAATGAACAGATGACTAAGTATGAAATGGCATGTGCAATTGCAGATGCCTTCAACCTCCC  
 CAGCAGTCACTTAAGACCTATTACTGACAGCCCTGTCTAGGAGCACAACGTCCGAGAAATG  
 CTCAGCTTGACTGCTCCAAATTGGAGACCTTGGGCATTGGCCAACGAACACCATTTTCAATT  
 GGAATCAAAGAATCACTTTGGCCTTTCCTCATTGACAAGAGATGGAGACAAACGGTCTTTCA  
 T**TAG**TTTTATTTGTGTTGGGTTCTTTTTTTTTTAAATGAAAAGTATAGTATGTGGCACTTTT  
 TAAAGAACAAAGGAAATAGTTTTGTATGAGTACTTTAATTGTGACTCTTAGGATCTTTCAGG  
 TAAATGATGCTCTTGCACTAGTGAAATTGTCTAAAGAACTAAAGGGCAGTCATGCCCTGTT  
 TGCAGTAATTTTTCTTTTTATCATTTTTGTTTGTCTGGCTAAACTTGGAGTTTGAGTATAGT  
 AAATTATGATCCTTAAATATTTGAGAGTCAGGATGAAGCAGATCTGCTGTAGACTTTTCAGA  
 TGAAATTGTTCAATCTCGTAACCTCCATATTTTCAGGATTTTTGAAGCTGTTGACCTTTTCA  
 TGTGATTATTTTAAATTTGTGTGAAATAGTATAAAAATCATTGGTGTTCATTATTTGCTTTG  
 CCTGAGCTCAGATCAAAATGTTTGAAGAAAGGAACCTTATTTTTTGCAAGTTACGTACAGTTT  
 TTATGCTTGAGATATTTCAACATGTTATGTATATTGGAACCTTCTACAGCTTGATGCCCTCTG  
 CTTTTATAGCAGTTTATGGGGAGCACTTGAAAGAGCGTGTGTACATGTATTTTTTTCTAGG  
 CAAACATTTGAATGCAAACGTGTATTTTTTTAATATAAATATATAACTGTCCTTTTCATCCCA  
 TGTTGCCGCTAAGTGATATTTTCATATGTGTGGTTATACTCATAATAATGGGCCCTGTAAAGTC  
 TTTTCACCATTTCATGAATAATAATAAATATGTACTGCTGGCATGTAATGCTTAGTTTTCTTG  
 TATTTACTTCTTTTTTTAAATGTAAGGACCAAACCTTCTAAACTAATTGTTCTTTTGTGCTT  
 TAATTTTTTAAAAATTACATTCTTCTGATGTAACATGTGATACATACAAAAGAATATAGTTTA  
 ATATGTATTGAAATAAAACACAATAAAATT

**FIGURE 52**

MPEMPEDMEQEEVNIPNRRVLVTGATGLLGRAVHKEFQQNNWHAVGCGFRRARPKFEQVNLL  
DSNAVHHIIHDFQPHVIVHCAAERRPDVVENQPDAAASQLNVDASGNLAKEAAAVGAFLIYIS  
SDYVFDGTNPPYREEDIAPPLNLYGKTKLDGEKAVLENNLGA AVLRIPILYGEVEKLEESAV  
TVMFDKVQFSNKSANMDHWQQRFPTHVKDVATVCRQLAEKRMLDPSIKGTFHWSGNEQMTKY  
EMACAIADAFNLPSSHLRPITDSPVLGAQRPRNAQLDCSKLET LGIGQRTPFRIKESLWP  
FLIDKRWRQTVFH

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 105-127

**N-glycosylation site.**

amino acids 197-201

**N-myristoylation site.**

amino acids 303-309

**Short-chain dehydrogenases/reductases family proteins.**

amino acids 18-30

# **FIGURE 53**

TGGGCTCCCTCCAGCACTGCTGTTGCCCTGCTGCCCTAAGATGGGTGACACTTGGGCCCAGCTTCCTTGGCCTGGG  
CCACCCACCCAGCAATGCTGCTGATCTCCCTCCTCTTGGCAGCCGGGTTGATGCACTCGGATGCCGGCACCAG  
CTGCCCCGCTCTTTGCACATGCCCTAACAGGTGGTGGATTGTAGCAGCCAGCGGCTATTCTCCGTGCCCCAG  
ACCTGCCAATGGACACCCGAAACCTCAGCCTGGCCCCACAACCGCATCACAGCAGTGCCCGCTGGCTACCTCACA  
TGCTACATGGAGCTCCAGGTGCTGGATTGTCACAACAACCTCTTAATGGAGCTGCCCCGGGGCCTCTTCTCCA  
TGCCAAGCGCTTGGCACACTTGGACCTGAGCTACAACAATTTAGCCATGTGCCAGCCGACATGTTCCAGGAGG  
CCCATGGGCTAGTCCACATCGACCTGAGCCACAACCCCTGGCTGCGGAGGGTGATCCCCAGGCCTTTAGGGC  
CTCATGCACTCCGAGACCTGGACCTCAGTTATGGGGGCTGGCCTTCTCAGCCTGGAGGCTCTTGGGGCCT  
ACCGGGGCTGGTGACCTGCGATCGGTGGCAATCCCTGGGTGTGTGGCTGCACCATGGAACCCCTGCTGAAGT  
GGCTGCCAAACCGGATCCAGCGCTGTACAGCAGATTCTCAGCTGGCTGAGTGCCGGGGCCCTCTGAAGTCGAG  
GGCGCCCCGCTCTTCTCACTCACTGAGGAGAGCTTCAAGGCCTGCCACCTGACCTGACCTGGATGATTACCT  
ATTCAATTGCGTTCTGGTGGCTTCTGGTCTCCATTGCTTCTGTGGCCACCAACTTCTCTGGGCATCACTGCCA  
ACTGCTGCCACCGCTGGAGCAAGGCCAGTGAAGAGGAAGAGATCTGACATGCCCTGCTCTATCCCTCCATGCT  
GCTGACCGCCACAGCTGCTGGCCACCAGACGCCCCCTGATTGCTCACTCTGGTTCCATGGTGACCTGGCTGC  
CTCAGTCATGGTTCAAGCAAGGTGGGGACACTCATTTTGTATGAGCATCTGCTTTGGGCCAGGCGGCACGCTAG  
GAATTGGGAACATCAGATGAACCTGACTCAGTCCCTGCCCTCAAGGCACCTTCCCTCTGGTCAAGGAGAGAGATCC  
AAAACTATTCCCTTTAAGACTATATGTCAGGACTCTGAGCAGTCATTATGGAGGCCAGAGGAGGAGCCATC  
ATCTGTATCTAGCAATCTCAGATAGAATTATAAGATTAGAGTGATTGTGAACCTGGGTCACTCAGGAAATATCTA  
CTTTGTCAGGTAGGCAAGAAAGGGTGTCTGCACATGGCAGAGGCCAGAATATGCATAGTGTCTGTGTGTGAGAA  
GAGTGAACAGTTCTTGGTCACTTACTTGTATAGAGGGGGTGTGGCACAGAAGCTCAAACTACCCCTCACCTCCT  
GACACCAAACTGTGAGTCTCTCAGCAATGCCAGCCACTGCTACAGGGAGTAAGAACACCTCTATGACAGCCCC  
TGGCCTCCTTCCACCAGCAGCTACCAGGTGAGACCACTCCCACTGACTGCCCCCATATGACCAAAATGTCAACCA  
GTTGGTGAGGTCCCAGGCAGCAGGCTGAGGATGGACACTTCAATGCCCTTGTCTCTGCTCTCACTCAAGTTT  
TGCTTCAGAAGAGAGAGGCGAGGAGGCCAGCAACTGGGGCAGCAAGAGTCTGGCACCTTGGGATCCTAATCAT  
GTGACTGTTCTTGCCACAGTGCTCATGCCACAGGGTCTCACCAGGAAAGTGCACTGTGGGCCACAGACCACAG  
CCTGGCAGCACCCAGAGCTAAAAGGGGACAAAGGCAGCACAGTTATGACCATATGAGGCTTTGCATTTCTTCT  
AAGCAACTTACCACTTAAAGCATGAGGGTGAGAGAGCTATTAAATACTAAGCCCTTGGCCTCTCACTCAAGTTT  
TGAAAAGCTCTCTGCACAAACCATTCCTTTGACACACACACACAAATCTTTTGGAGTGAACGCTGTGTCTC  
CCATTTTACGGATGAGGCACTAAGGCTCAGAGAGGTTAAAGTCACATGCCACTATGAGCAAGATAAAGTCTGT  
GCTCTTTCTACTGCCCATCCAAGTTGGGGAACATCACCATTCCCTCTAGAGTTATATAAATTCAAATTCAACT  
AGAGCTGACAAAGTCTCAGATAAGGTCCAGGCACTCCTCTGGGCACCTTTATATCTATTGACTCACTCTTTCA  
ATTCTCAGCAAGCACTGCTGGTGGTTTTTATTATCCCATTTTACAGATGAATTAATCGTAGAGAGTTGAGT  
GACTTACCAAGGTTGTCTGGATAAGCCCTAGAAGGAAGGCGGTAGGCAGCTCCATTAGGGAAGCTGCATCTA  
ATCAGTCAGTCAAAAATCAAGTAACCTTACGAGCAAGACAAATTATCATCATCGTGGTCTTCTTCTCATGTTT  
CGTCAGCAGCATCATTATCTTCCCTTATTTGTTTCAACCGGATAGTTTATGATGTTTTCATCTTCTTCTC  
TTGACTTTTTCACATCCCTGTGTCAGGAGGTAATCAAACATCAGTAATCCTGTTTTTACAGATGGGGAAAAAGTC  
TCAAGGTTGGATATGACTTGCTATGTGGCAAGGTTGGGGCTCAACCCTAACACAGTTCTCTTTCCAGTGCTTTC  
TCAAGTGCTTGGGGAAGAGAATGCCTCAGAAGGCTGGGTAGTGGGGCCCTGGAATTCAGCATCCATGAATGTGC  
TAGTGGATAAGCTAAATAGAAGGCAGCCAAACCATCTGCTGTACAGATTGAACATGCTCAGGTAGGGCAAA  
TTGCAGGCTCTGAAACAGAGACTACACAGGTAACACCTGAATAGGAGACTCCTGCTTTACAATGTGTAGATAAA  
ACATCAGCAATGGTGGCCATGGTGGCAGTCATGTGAAAAGTAAGATCTTTGGGAATCAAGAAAGGAAGCTGTGT  
TAACCACTCCTGCTCAAGCCCTGCTGCGTGTGTGCAAGAGATACTAAGAGAGCAAGAAAGCTATAGGTGAGAA  
CCTCTGCAGTTTAGGAGAAGACATCAAGGCAGCTCAACATGCTGATAAGTCTGGCCAGGAGGAGAAATTA  
ACAGGGGCTTTCCACACCTCCCTTGCCCCAAGCTCCAGCGGTATTCTATCAGCCCATCCTCCTGGAAAGCCTGA  
AAGGAATGAAGGAGGCTAATAAGTCATCTTCCAGGAAGGCATCCCTCACTCGTGCTTCCCTGAGCTAGTCAACC  
AAAAGAGCTCTTCAAACTTTGCTAGACCTGAAGTACTTGAACCTGTGTCCCCTGAATCTTTCTTACAACATCT  
GGGACAAATCCCTGGTCTGTGACATCCGAAGCAGAAGTGTGCCCTGCTCTCTCTCTCTGTGATGACCAAGGAT  
GGTGAACCTCAAGTTGTTCTCTACAAGCCAGGCCAGCAACCTAAATACTTGGAGAGGAACCTTTAGAACTATAA  
TCCTGACAAAATAGAAAAGTTTCCCATAGGGGCATACCATAATACTATAATAACCTCCCAGGAACCTATTGTTTG  
CCAAAATGTAGTTAATATATTTAAGATATATGCTTTTTTGCATAGGACTAGAACCAGAAAAGACACCAATGC  
CCCCCTGACATCAATGCTCTTCTAGTGGGACAATTTGGTCTCCATTAATGCCAAACCTTTCTGAACAGGATAC  
ATGGCTTTTAAAGGACAGATGTTTCTCCTGCTGCTAGAGTTCTCAGTTTACTAGAGCACAATGAGGAAAGTA  
TTCAACCTCCCTACTGCCAAGGAATCCCTGCTTCTCCCCACCGCCATCATCTTGTCCAAGCTATCAGAAGCA  
ACCTTCTAGAGATAATCTAACAATCCTGATTAGAATTGCTCCCATATCCCTGGTGACCACAGGCTTCATTCAAA  
TTGTCAAACTGGTTAATCATGTATGTGATGGGGTATCTCTGCATCTGTATGTCTGTCTGCGAGGTTCTTGTAT  
ATTGGCTGTCCGCTGACTTGGGACAGATCTCTCTAGAACTTGGGTTTCAAGTTCTCTGACATAGTCCACTCAGCCA  
TAGGCTGAGTGGCTAATATGCATAAATAAGCATGCCTAAATAGGCATATAGGTTGGTGCAAAAGTAATTGC  
GGTTTTTGCCATTAAAAATGATGGCAAAAATCCCAATTACTTTTGGCTCAATCTAATATTACATTGCTTGATAG  
ATTAAGATGGAATCCACCAGGTTTAGGGTAGGACTGGATGCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAA

## **FIGURE 54**

MLLISLLLAAGLMHSDAGTSCPVLCTCRNQVVDCCSQRLFSVPPDLPMDTRNLSLAHNRITA  
VPPGYLTCYMELQVLDLHNNSLMELPRGLFLHAKRLAHLDSLNNFVSHVPADMFQEAHGLVH  
IDLSHNPWLRRVHPQAFQGLMQLRDLDSLGGGLAFLSLEALEGLPGLVTLQIGGNPWVCGCT  
MEPLLKWLNRNIQRCTADSQLAECRGPPEVEGAPLFSLTEESFKACHLTLTLDYLFIAFVG  
FVVSIA SVATN FLLGITANCCHRSKASEEEEEI

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 241-260

**N-glycosylation sites.**

amino acids 52-55, 81-84, 107-110

**Tyrosine kinase phosphorylation site.**

amino acids 148-154

**N-myristoylation sites.**

amino acids 11-15, 263-268

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 175-185

**Leucine zipper pattern.**

amino acids 77-98

# **FIGURE 55**

GGCTGCGCCCAGGCCGGCGGGCCAGCAGCTGCGAACCGCCGGCGCACCACCTGTTTCCGCG  
 CCCGGGGACTTCCCCGGCGGGGCTCAGAAAGTGTGGGGTCGGTCGCTTGGCTTCCCCCTGGCGT  
 CAGCGACCCAGGGTAACCTCCTCCACTGCTGCGTGCCGTGCAGGCCCTGCCCTGTGTGAGAGCC  
 ACGTGTGCCGCGCTCTGGGCACAGCCTTGGAAAGTCAGGACCGCGACGGCAGCAGAGCAGAA  
 ACCTTACAGAAACATGAAGCCCTCAACCATCTGCTACTCAGTTATTTCGGGGCTGACGGCGGC  
 TTCTAGAACATCCAGGTGTTCTGCAGATGCGAGAACTCATCCTGTAGTCACCAGATGGAGTC  
 CCAAACAGCCAAGCAGATGTAAGGCCTGTGCTGTGGCTCTGAGGCCCTGAATACAGAAGGGT  
 CACTTTCTTAGTGGCCAAAGAGCAGTTGTTGACATTGATGTCTAATTATTGAACACGACCAG  
 TCATTTTACTGAGCTGCAGTGAGGAAACACTGACCATAGAAGATCAAGCCAAATGAGGGATT  
 GCAAATTTCTGATTCTTTTGAATTAGGATTCCAGATGGGGGCCCTCATTTCTACAGCCCCCA  
 ACATTCCCTATAGCCGTTATCACTGCCATCACCCTGCCACCAGCATCTTCTTGCAGATTCCA  
 CCCCTGCTCCCCAGAGACTTCTGCTTTGAAAGTGAGCAGAAAGGAAGCTCTCAGAAAAATC  
 TCTAGTGGTGGCTGCCGTGCTCCAGACAATCGGAATCCTGCCTTCACCACCATGGGCTGGC  
 TTTTTCTAAAGTTTTTGTGGCGGGAGTGAGTTTCTCAGGATTTCTTTATCCTCTGTGGAT  
 TTTTGCATCAGTGGGAAAACAAGAGGACAGAAGCCAAACTTTGTGATTATTTTGGCCGATGA  
 CATGGGGTGGGGTGACCTGGGAGCAAACCTGGGCAGAAACAAAGGACACTGCCAACCTTGATA  
 AGATGGCTTCGGAGGGAATGAGGTTTGTGGATTTCCATGCAGCTGCCTCCACCTGCTCACCC  
 TCCCCGGCTTCCTTGCTCACCGGCCGGCTTGGCCCTTCGCAATGGAGTCACACGCAACTTTGC  
 AGTCACTTCTGTGGGAGGCCTTCCGCTCAACGAGACCACCTTGGCAGAGGTGCTGCAGCAGG  
 CGGGTTACGTCACTGGGATAATAGGCAAATGGCATCTTGGACACCACGGCTCTTATCACCCC  
 AACTTCCGTGGTTTTGATTACTACTTTGGAATCCCATATAGCCATGATATGGGCTGTACTGA  
 TACTCCAGGCTACAACCACCCTCCTTGTCAGCGTGTCCACAGGGTGATGGACCATCAAGGA  
 ACCTTCAAAGAGACTTTACACTGACGTGGCCCTCCCTCTTTATGAAAACCTCAACATTGTG  
 GAGCAGCCGGTGAACCTTGAGCAGCCTTGCCCAGAAGTATGCTGAGAAAGCAACCCAGTTTCAT  
 CCAGCTGCAAGCACCAGCGGGAGGCCCTTCTGCTCTATGTGGCTCTGGCCACATGCACG  
 TGCCCTTACCTGTGACTCAGTACCAGCAGCGCCACGGGGCAGAAGCCTGTATGGTGCAGGG  
 CTCTGGGAGATGGACAGTCTGGTGGGCCAGATCAAGGACAAAGTTGACCACACAGTGAAGGA  
 AAACACATTCTCTGGTTTACAGGAGACAATGGCCCGTGGGCTCAGAAGTGTGAGCTAGCGG  
 GCAGTGTGGGTCCCTTCACTGGATTTTGGCAAACCTCGTCAAGGGGAAGTCCAGCCAAGCAG  
 ACGACCTGGGAAGGAGGGCACCGGGTCCCAGCACTGGCTTACTGGCCTGGCAGAGTTCCAGT  
 TAATGTCACCAGCACTGCCTTGTTAAGCGTGCTGGACATTTTTCCAACCTGTGGTAGCCCTGG  
 CCCAGGCCAGCTTACCTCAAGGACGGCGCTTTGATGGTGTGGACGTCTCCGAGGTGCTCTTT  
 GGCCGGTCAAGCCTGGGCACAGGGTGCTGTTCCACCCCAACAGCGGGGCAGCTGGAGAGTT  
 TGGAGCCCTGCAGACTGTCCGCTGGAGCGTTACAAGGCCTTCTACATTACCGGTGGAGCCA  
 GGGCGTGTGATGGGAGCATGGTGCCTGAGCTGCAGCATAAGTTTCTCTGATTTTCAACCTG  
 GAAGACGATACCGCAGAAGCTGTGCCCTAGAAAGAGGTGGTGCAGGATACCAGGCTGTGCT  
 GCCCCAGGTACAGAAAGTTCTTGCAGACGTCCCTCCAAGACATTGCCAACGACAACATCTCCA  
 GCGCAGATTACACTCAGGACCCCTCAGTAACTCCCTGCTGTAATCCCTACCAAATTGCCTGC  
 CGCTGTCAAGCCGCATAACAGACCAATTTTTATTCCACGAGGAGGAGTACCTGGAAATTAGG  
 CAAGTTTGCTTCCAAATTTTCATTTTTACCCTCTTTACAAACACACGCTTTAGTTTAGTCTTG  
 GAGTTTAGTTTTGGAGTTAGCCTTGCAATCCCTTCTGTATCCTGTCCCCCTCCACGCCGA  
 CCCGAGAGCAGCTGAGCTGCGCTGGCTCTGGGCAGGGAGTGTGCCTTAATGGGAAGCACACG  
 GGCTTTGGAGTCAGGCACAGGTGCCAGCTCCAGCTTTTGAACCTGGGCAATTGTTTAACTA  
 ACCTGCAAGTTGATTTTGAAGGTTAAATAAAGGCATACATGAAAATGCCTGGCAACTTTAAA  
 AAAAAAAAAA

## **FIGURE 56**

MGWLFLLKVLLAGVSFSGFLYPLVDFCISGKTRGQKPNFVIIILADDMGWGDLGANWAETKDTA  
NLDKMASEGMRFVDFHAAASTCSPSRASLLTGRLGLRNGVTRNFAVTSVGGLPLNETTLAEV  
LQQAGYVTGIIIGKWHLGHHGSYHPNFRGFDYYFGIPYSHDMGCTDTPGYNHPPCPACPQGDG  
PSRNLQRDCYTDVALPLYENLNIVEQPVNLSLAQKYAEKATQFIQRASTSGRPFLLYVALA  
HMHVPLPVTQLPAAPRGRSLYGAGLWEMDSLVGQIKDKVDHTVKENTFLWFTGDNGPWAQKC  
ELAGSVGPFTGFWQTRQGGSPAKQTTWEGGHRVPALAYWPGRVPVNVTSALLSVLDIFPTV  
VALAQASLPQGRRFDDGVDVSEVLFGRSQPGHRVLFHPNSGAAGEFGALQTVRLERYKAFYIT  
GGARACDGSMPPELQHKFPLIFNLEDDTAEAVPLERGGAEYQAVLPEVRKVLADVLQDIAND  
NISSADYTQDPSVTPCCNPYQIACRCQAA

**Important features of the protein:**

**Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 353-373

**N-glycosylation sites.**

amino acids 117-120, 215-218, 356-359, 397-500

**N-myristoylation sites.**

amino acids 12-17, 33-38, 52-57, 97-102, 101-106, 113-118, 158-163, 328-333, 388-393, 418-423, 435-440, 436-441

**Amidation site.**

amino acids 382-385

**Sulfatases signature 2.**

amino acids 129-138

# **FIGURE 57**

TGGACAAGACACCTCCAGGAGCCAGCTCACAGCCACCGGTACCTTCTTCCAGGACAAGCTG  
GGGGCCTCCATGGGCGCCTGAGGGCCAGGCGCCAGGGCCGTGGGCACGAGTATGGTGAGACA  
CCAGCCCCCTGCAGTACTACGAGCCACAGCTGTGCCTCTCCTGCCTCACGGGCATCTACGGCT  
GCCGTGGGAAGCGCTACCAGCGCTCCCATGATGATAACACACCGGGCACAGCGCCATTCTCTG  
CATGTGGGGGCTGTGGCAGCAGTACCATGCTCTCCTGGATCGTGGCAGGACAGTTTCGCCCCG  
TGCAGAGCGGACCTCCTCCAGGTGACCATTCTCTGTACCTTCTTCACCGTGGTGTGTTGCC  
TCTACCTGGCCCCCTCTCACCATCTCCTCTCCCTGCATCATGGAGAAGAAAGACCTCGGCCCC  
AAGCCTGCTCTCATTGGCCACCGGGGGCCCCCATGCTGGCTCCAGAGCACACGCTCATGTCT  
CTTCCGGAAGGCCCTCGAGCAGAAGCTGTACGGGCTCCAGGCTGACATTACCATCAGCCTGG  
ACGGCGTGCCCTTCTCATGCATGACACCACCTGCGGGCGACCACCAACGTGGAGGAGGAG  
TTCCCGGAGCTGGCCCGCAGGCCTGCCTCCATGCTTAACTGGACCACCTGCAGAGACTCAA  
CGCTGGCCAGTGGTTCTGAAGACTGACCCCTTCTGGACAGCCAGCTCCCTGTCAACCTCCG  
ACCACAGAGAGGCCCAGAACCAGTCCATCTGCAGCCTGGCAGAGCTCCTGGAGCTGGCCAAG  
GGCAATGCCACACTGCTGCTCAACCTGCGTGACCCGCCCCGGGAGCACCCCTACCGCAGCAG  
TTTTATCAACGTGACTCTGGAGGCCGTGCTGCACCTCCGGCTTCCCCCAGCACCAGGTCTATGT  
GGCTGCCCTAGCAGGCGAGGCCCTGGTGCAGGAAGGTGGCTCCCGGCTTCCAACAGACATCA  
GGCTCCAAGGAGGCAGTCGCCAGCCTGCGGAGAGGCCACATCCAGCGGTGAACCTGCGCTA  
CACTCAGGTGTCCCGCCAGGAGCTCAGGGACTACGCGTCTGGAACCTGAGTGTGAACCTCT  
ACACAGTCAACGCACCGTGGCTCTTCTCCCTGCTGTGGTGTGCGGGGGTCCCATCCGTACC  
TCTGACAACCTCCACACCCTGTCCCAGGTGCCTTCCCCCTCTGGATCATGCCCCGGACGA  
GTACTGTCTCATGTGGGTCACTGCCGACCTGGTCTCCTTCACCTCATCGTGGGCATCTTCG  
TGCTCCAGAAGTGGCGCCTGGGTGGCATAACGAGCTACAACCTGAGCAGATCATGCTGAGT  
GCTGCGGTGCGCCGACAGCCGGGACGTGAGCATCATGAAGGAGAAGCTTATTTCTCAGA  
GATCAGCGATGGTGTAGAGGTCTCCGATGTGCTCTCCGTATGTTGAGACAACAGTTATGACA  
CATATGCCAACAGCACCGCCACCCCTGTGGGCCCCCGAGGGGGTGGCAGCCACACCAAGACC  
CTCATAGAGCGGAGTGGGCGTTAGCTGAAGACATGTCTGTCCCACCTGTACCTGACACAGAA  
GCTGGGGAGCCTAGGAGAGCTGGTGGAAGTGTGTCTGAACCTCGGAGTGCTCTGGGAGCGGGC  
TCCACAGCCTCCTTGTGGGCTCCAGCCCCCTTGTGAGCCGAGCCTCTCTTGAGGGGGACTCC  
CTGTCTCCTGAGGCCAGCTGGGCCAGGACTCCATCCTTTCAGATGCCCTGCAGGCCTGGG  
GCTCCTTCTGGGAAGTATGGGGCCTAGGGCTTGGTCCCCCTCTTCTGAGGCCCTCTCCTGTA  
TCCCGACCTGGAAGCTTTGATGGGTGATGGGCCATGCCATAACCCCTGTGGCAATGGAGTGT  
GTGGATGCTCACCTGTGCCATCTGTCTCCTGTCTGTGTCAGGAGGCACCTGAGTTCTCTGC  
TGTTATCCTGCCCAAGGGCCTGGGCGGAGCCTCTACCTGAAGCAACTCTGCTCTTCTCTGTC  
AGTCTCAAAGCACAAAGAGGTTTACGCCAGGAGGAAGCCAGCTGCAATGTGGAGACACGTCC  
TCCTCCCCAACCCACCTCATGCCACCGCCAACCCCTGCCCCAGGAGCGGGCCTGAGCCACG  
TCCCTTAGGAGCAGCTGGAGATGGCCAAAAGAGTGAGCTCAGGACTACTGGATCCCATGCCC  
AGGTGTCCAGCAGACCTCAAGGCAGAAGGGTCACCTAACCCAGGAGTCCACAGACTGATGTG  
ACCTCAGGTTCCACATCAGTGGCCACAGGGCAGGGCCACCTGGTAGAAGTGTCTGGATA  
TGGCCAGGGTGGGTGTGTGGCTAAGTGGGCCTGAAACAGAGGGAACCTAGGGCCCTTGGCCAA  
TGTGATTAAAGCTGCCATCTTGAAA

## **FIGURE 58**

MVRHQPLQYYEPQLCLSLCTGIYGCGRWKRYQRSHDDTTPGTAPFLHVGAVAAVTMLSWIVAG  
QFARAERTSSQVTILCTFFTVVFALYLAPLTISSPCIMEKKDLGPKPALIGHRGAPMLAPEH  
TLMSFRKALEQKLYGLQADITISLDGVFPFLMHDTTLRRTTNVEEEFPELARRPASMLNWTTL  
QRLNAGQWFLKTDPFWTASSLSPSDHREAQNQSICSLAELLEELAKGNATLLLLNLRDPPREHP  
YRSSFINVTLEAVLHSGFPQHQVMWLPSRQRPLVRKVAPGFQQTSGSKEAVASLRRGHIQRL  
NLRYTQVSRQELRDYASWNLSVNLTYTNAPWLFSLWCAGVPSVTSDNSHTLSQVPSPLWIM  
PPDEYCLMWVTADLVSFITLIVGIFVLQKWRLGGIRSYNPEQIMLSAAVRRTSRDVSIMKEKL  
IFSEISDGVESDVLVSCSDNSYDTYANSTATPVGPRGGGSHTKTLIERSGR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 47-61, 77-93, 335-350, 380-399

**N-glycosylation sites.**

amino acids 182-186, 217-221, 233-237, 255-259, 329-333, 462-466

**Tyrosine kinase phosphorylation site.**

amino acids 130-139

**N-myristoylation sites.**

amino acids 21-27, 48-54, 294-300, 404-410, 442-448, 473-479



# **FIGURE 59**

CCTGAGCAAACACAGCAGCCCCGAGTGTTCCTCAAGGCCAAAATGCTGAGAACGTCCACTCCTA  
ATCTGTGTGGTGGTCTGCATTGCCGGGCCCCCTGGCTCTCTTCTGGCATTCTCTGCCCTCTGC  
CTCATATTCTTGTTAGGCCAGGTGGGCTTGCTGCAGGGACACCCCCAGTGCCTGGATTACGG  
GCCCCCTTTCCAGCCCCCTCTGCACCTTGAGTTTTGCTCTGACTATGAGTCCTTCGGCTGCT  
GTGATCAGCACAAGGACCGCCGCATCGCTGCCCGGTACTGGGACATCATGGAATATTTTGAT  
CTGAAGAGACATGAGCTGTGTGGAGATTACATTAAAGACATCCTTTGCCAGGAGTGCTCGCC  
CTACGCAGCCCACCTCTACGACGCCGAAAACACCCAGACGCCTCTCCGGAATCTCCCGGGCC  
TCTGCTCTGATTACTGCTCTGCCCTTCCATTCTAACTGTCACTCAGCCATTTCCCTGCTGACC  
AATGACCGCGGCCCTCCAGGAGTCTCATGGAAGGGACGGTACCCGCTTCTGCCACCTCCTGGA  
CCTTCCTGACAAGGACTATTGCTTCCCTAATGTCTGAGGAACGACTATCTCAACCGCCACC  
TGGGCATGGTGGCCCCAAGATCCTCAGGGCTGCCTGCAGCTCTGCCTGAGCGAGGTGGCCAAC  
GGGCTGAGGAACCCCGTCTCCATGGTCCATGCTGGGGACGGCACCCATCGCTTCTTTGTTGTC  
CGAGCAGGTAGGAGTGGTGTGGGTCTACCTCCCTGATGGGAGTCGCCTGGAGCAACCCCTTCC  
TGGACCTCAAGAACATCGTGTGACCACCCCATGGATCGGGGATGAGAGAGGCTTCTTGGGG  
TTGGCTTTTTACCCCCAAATTCGCCACAATCGCAAGTTCTATATTTATTATTCTGCTGCTGGA  
CAAGAAGAAGGTAGAAAAGATCCGAATTAGTGAGATGAAGGTTTCTCGGGCTGATCCTAACA  
AAGCTGACCTGAAATCAGAGAGGGTCACTCTTGGAGATTGAAGAACCAGCCTCAAACCATAAT  
GGCGGACAACTTCTTTTGGCCTGGATGGCTATATGTACATATTCACTGGGGACGGGGGACA  
GGCTGGAGATCCCTTTGGCCTGTTTGGAAATGCTCAGAACAAAAGTTCCCTGCTGGGAAAAG  
TTTTAAGGATCGATGTGAACAGGGCAGGCTCACATGGCAAGCGGTACCGAGTCCCTTCGGAC  
AATCCATTTGTTTCTGAGCCAGGGGCCACCCCGCCATCTATGCCTATGGGATCAGGAACAT  
GTGGCGTTGTGCTGTGGACCGAGGGGACCCCATCACGCGCCAGGGCCGAGGCCGGATATTCT  
GTGGGGACGTGGGCCAGAACAGGTTTGAAGAGGTTGACCTCATTTTGAAGGTGGAACATAT  
GGCTGGAGAGCAAAGGAAGGTTTGCATGTTATGACAAAAAACTTTGTCACAATGCCCTCTTT  
GGATGATGTTCTGCCAATCTATGCTTATGGCCATGCAGTGGGGAAGTCAGTCACTGGAGGTT  
ATGTCTATCGTGGTTGTGAATCCCCAAATCTCAATGGCCTGTATATCTTTGGAGACTTCATG  
AGTGGTCGACTTATGGCTTTGCAGGAAGATAGAAAAACAAGAAATGGAAGAAGCAGGATCT  
TTGCCCTGGGCAGCACACGTCCTGTGCCCTTCCAGGGCTGATCAGCACCCATAGCAAGTTCA  
TCATCTCCTTTGCTGAAGATGAAGCAGGGGAGCTGTATTTCTGGCGACCTCTTACCCAAGT  
GCCTATGCACCACGTGGATCTATTTACAGTTTGTGACCCCTCAAGGCGAGCACCCCCAGG  
CAAGTGCAAATACAAGCCAGTGCCCCGTGAGAACCAAGAGTAAGCGGATCCCGTTCAGACCAC  
TCGCCAAGACAGTCTTGGACTTGCTAAAGGAACAATCAGAGAAAGCTGCTAGAAAAATCTTCC  
AGTGCAACCTTAGCTTCTGGCCCAGCCCAGGGTTTGTCTGAGAAAGGCTCCTCCAAGAAGCT  
GGCTTCTCCTACAAGCAGCAAGAATACATTGCGAGGGCCTGGTACAAAGAAGAAAGCCAGAG  
TGGGGCCCCACGTCCGCCAGGGCAAGAGGAGGAAGAGCCTGAAAAGCCACAGTGGCAGGATG  
AGGCCATCAGCAGAGCAGAAGCGAGCTGGCAGAAGTCTCCCTTGACCTATTGGTCAAGGTGG  
CCGACAGGGTGACGTGAGAGAGGAGACCTCATCAAATGAAAGTCAGTCTGAATAAAG  
ACCTTAGAAGTCTGGGAAGCCAGGGTAGAGGTGGGGCAGGGCGGTTTTCTCTCCTCGGGAA  
ATCTTGCTGTCTACTGAATAAATAAATGCACCTTCTCTGTATGCAGTGCTTCTGTGGGAGAC  
CATATCCAGATTGCTGGTGCACCTGGGTTATGGTAAGCACTAGTCCATGAGCCTGCTTGA  
ATCACACTGGATGTCTCCGTTTTGTCTTGTAATGCCTACAACCTGAGGTAATAAATCAACA  
TTTGCTCA

## **FIGURE 60**

MLRTSTPNLCGGLHCRAPWLSSGILCLCLIFLLGQVGLLQGHQPCLDYGPPFQPPLHLEFCS  
DYESFGCCDQHKDRRIAARYWDIMEYFDLKRHELCDYIKDILCQECSPYAAHLYDAENTQT  
PLRNLPGLCSDYCSAFHSNCHSAISLLTNDRGLQESHGRDGTRFCHLLDLPDKDYCFPNVLR  
NDYLNRLHGMVAQDPQGCLQLCLSEVANGLRNPVSMVHAGDGTHRFFVAEQVGVVWVYLPDG  
SRLEQPFLDLKNIVLTTPWIGDERGFLGLAFHPKFRHNRKFYIYYSCLDKKKVEKIRISEMK  
VSRADPNKADLKSERVILEIEEPASNHNGGQLLFGLDGYMYIFTGDGGQAGDPFGLFGNAQN  
KSSLLGKVLRIDVNRAGSHGKRYRVPSDNPFVSEPGAHPAIYAYGIRNMWRCVDRGDPITR  
QGRGRIFCGDVGNRFEEVDLILKGGNYGWRAKEGFACYDKKLCHNASLDDVLPYIYAYGHAV  
GKSVTGGYVYRGCESPNLNGLYIFGDFMSGRLMALQEDRKNKKWKKQDLCLGSTTSCAFPGL  
ISTHSKFIISFAEDEAGELYFLATSYPSAYAPRGSIYKFVDPSTRAPPCKYKPVFVRTKS  
KRIPFRPLAKTVLDLLKEQSEKAARKSSSATLASGPAQGLSEKGSSKKLASPTSSKNTLRGP  
GTKKKARVGPVHRQGRKRRKSLKSHSGMRPSAEQKRAGRSLP

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-41

#### **Transmembrane domain:**

amino acids 17-36

#### **N-glycosylation sites.**

amino acids 372-376, 480-484

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 645-649, 699-703

#### **Tyrosine kinase phosphorylation site.**

amino acids 81-89

#### **N-myristoylation sites.**

amino acids 11-17, 37-43, 156-162, 165-171, 357-363, 365-371,  
368-374, 408-414, 459-465, 548-554, 557-563

#### **Amidation sites.**

amino acids 391-395, 696-700

#### **Cell attachment sequence.**

amino acids 428-431

#### **Leucine zipper pattern.**

amino acids 25-47

**FIGURE 61**

CTCCATTAAACCACCACCAGCTCCCCAAGCCACCCCTTCAGCCATGAAGTTCTGCTCCTGGT  
 CTTGGCAGCCCTCGGATTCTTGACCCAGGTGATCCCAGCCAGTGCAGGTGGGTCAAAATGTGT  
 GAGTAACACCCCCAGGATACTGCAGGACATGTTGCCACTGGGGGAGACAGCATTGTTTCATGTG  
 CAACGCTTCCAGAAAATGCTGCATCAGCTACTCCTTCCTGCCGAAGCCTGACCTACCACAGCT  
 CATCGGTAAACCACTGGCAATCAAGGAGAAGAAACACACAAAGGAAAGACAAGAAGCAACAAAC  
 GACCGTAACATCATAATAACCCTGCTATCGCCTCCACCAACTCAGAGAAATATCATTTCCAC  
 AGTTCCAATTCTCCTACATTGCTGAGTACTAGCCAAGGCTCCTCTTTATGGGGCAGATATCT  
 ATAGCCAACCCCAAACTTCTGTCTTCTATCATTCTGTCAATTCATCTAGTAACTAATTTGGAG  
 TTTGTATCTATCTTACGAGAACAATCATCATGCAGATTCTGTCACAGGGGATCTGTGAGTTTG  
 GGTCTCCAAATGAAAAATGTCAAGACAGAATTGGACATGCAAAGATTGACTGGGAGAACAC  
 ACCTCTGATGGACAAAGGTGAGACAGAGCAGCCACAGGCAGGGAGAGCCTTCAGACTGCAACG  
 CTGGCCTGATACGTGTCAAAGGAGAGAGGGATAGAGGAGGATTGAATAGAAGGAGACTAAGAC  
 TGCAGCTCTAAGAAAGTCTCAGCCAAACAGATGGGGAGGCCCAAAGCAAGGCTTGCCCCCTCAG  
 AGGAGCTCACGCAGGGCAGGAATAGCCAGGTTCTCATATCCCAGGGGTTTCACTTGGCTGAG  
 AACAGCCCCCTGGAGAACATGGGGTGACTGCTACCATAGGTCTGGAAGTATGAGGCTGTCCACC  
 AACTATCCCCCTGAAGCAAGTTCTCTTGAAAGGAAATCTAAACAGTGCACCCCCATGGCTGCC  
 ACGGAGTATAAGGAGGGAGAGAAAGGAGCTGAAAGTCTAGGTTTGGCCAGCTAGGTAGACTGA  
 CTTGTGAGGTATTTATTTATTTATTTGAGTAACAAAGCAGACAGAATACATAGCCACCATTGG  
 TAGTACACCCCAAAAGCAAGGATGGCATGATGCTGGTGACTCAAACGTGCCTACTCATGGTGT  
 CAAATTGGCATAATCCTCTTGGAAGCTGTGTGGAAATAAGCACAGAGAAGCAGAACTCTAAT  
 TGCTTAATCCACTAAACATTACTTCTGGGAATTGGCTCATCATAAATTATCCAAGAGAAAGCA  
 CAAAGTTATGGGCACAAAGGTTTTCCATATAATATTATTTAAAATGCTGAGAAAATGAAAAAA  
 TCTAAATGGTGAAATATATACTAATGCCATCTATAAATACAAACAAATAGAATGTTTATAGAA  
 TAATGGAACATAATAACATTATTCAAATTTGCATTTATGCTATAGTTGTCAAATTTGTCTCCT  
 TATATGATACAAAACCTCATGAAAATTATGACTTTTTTGTGGTTGGAAAGCAGAATTATGCA  
 TAAATTTCTCTTACAGTTTCGATGCCATTAGTTTTATATAACATTTATTTGACACGTAAGTGA  
 CTTCTATCTGAGAAGAACAACCAAAACACTCAGGCCTAAATAATTAAAAACGGTCTTAAAAA  
 CTAGCAAACCAGATAAGAAAAGATGTTAATGCCCATTCCTTAACCTTATGTCTTAGACCAAAAT  
 TAATTTCTAGATGGTTTTTAAATGACAGTGTAAGTAAAGTATTAAAGATTGTGTGGTCAAA  
 TATTCAATTTAAGAGCAAGGAAATTTCTTATAAATATAACAATAGAGGCAGAACTCATGTAAGA  
 ATAAATTGATTAGGTGGTATTAAATATTAAGTTCTTATGTATGTCAAAAGATATCATTTTGAA  
 ATTCATCCATCTTATTGGGTATTGCAGGAGTTTCTTCTTTTGTATAAATACTCTTCCGT  
 CATATGAATAGTATTCTTTGTATACTGGTTTGTGATGGACATTTGGGTTGTTCCAGTTTA  
 TGGCTATTACAAATAAAGCTTCTATGAACATTTATGTACA

**FIGURE 62**

MKFLLLVLAALGFLTQVIPASAGGSKCVSNTPGYCRTCCHWGETALFMCNASRKCCISYSFL  
PKPDLQPQLIGNHWQSRRRNTQRKDKKQQTTVTS

**Important features of the protein:**

**Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 1-22

**N-glycosylation site.**

amino acids 50-53

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 79-82

**N-myristoylation site.**

amino acids 23-28

# **FIGURE 63**

GCGGAGCGCCTGGGAGAGGAGAAGGAGCCGACCTGCCGAGATGGAGGCGACCGGCACCTGGG  
CGCTGCTGCTGGCGCTGGCGCTGCTCCTGCTGCTGACGCTGGCGCTGTCCGGGACCAGGGCC  
CGAGGCCACCTGCCCCCGGGCCACGCCGCTACCACTGCTGGGAAACCTCCTGCAGCTACG  
GCCCCGGGCGCTGTATTACAGGGCTCATGCGGCTAGTAAGAAGTACGGACCGGTGTTACCA  
TCTACCTGGGACCCTGGCGGCCTGTGGTGGTCTGTTGGGCAGGAGGCTGTGCGGGAGGCC  
CTGGGAGGTGAGGCTGAGGAGTTCAGCGGCCGGGGAACCGTAGCGATGCTGGAAGGGACTTT  
TGATGGCCATGGGGTTTTCTTCTCCAACGGGGAGCGGTGGAGGCAGCTGAGGAAGTTTACCA  
TGCTTGCTCTGCGGGACCTGGGCATGGGGAAGCGAGAAGGCGAGGAGCTGATCCAGGCGGAG  
GCCCCGTGTCTGGTGGAGACATTCCAGGGGACAGAAGGACGCCATTGATCCCTCCCTGCT  
GCTGGCCAGGCCACCTCCAACGTAGTCTGCTCCCTCCTCTTTGGCCTCCGCTTCTCCTATG  
AGGATAAGGAGTTCCAGGCCGTGGTCCGGGCAGCTGGTGGTACCCTGCTGGGAGTCAGCTCC  
CAGGGGGGTGAGACCTACGAGATGTTCTCCTGGTTCCCTGCGGCCCTGCCAGGCCCCCACAA  
GCAGCTCCTCCACCACGTGAGCACCTTGGCTGCCTTCACAGTCCGGCAGGTGCAGCAGCACC  
AGGGGAACCTGGATGCTTCGGGCCCCGCACGTGACCTTGTCGATGCCTTCCTGCTGAAGATG  
GCACAGGAGGAACAAACCCAGGCACAGAATTACCAACAAGAACATGCTGATGACAGTCAT  
TTATTTGCTGTTTGCTGGGACGATGACGGTCAGCACCACGGTCGGCTATACCTCCTGCTCC  
TGATGAAATACCTCATGTCCAAAGTGGGTACGTGAGGAGCTGAATCGGGAGCTGGGGGCT  
GGCCAGGCAGCAAGCCTAGGGGACCGTACCCGCCCTCCCTTACCCGACGCGGTTCTGCATGA  
GGCGCAGCGGTGCTGGCGCTGGTGCCCATGGGAATACCCCGCACCTCATGCGGACCACCC  
GCTTCCGAGGGTACACCCTGCCCCAGGGCACGGAGGTCTTCCCCCTCCTTGGCTCCATCCTG  
CATGACCCCAACATCTTCAAGCACCCAGAAGAGTTCAACCCAGACCGTTTTCTGGATGCAGA  
TGGACGGTTAGGAAGCATGAGGCGTTCCCTGCCCTTCTCCTTAGGGAAGCGTGTCTGCCTTG  
GAGAGGGCCTGGCAAAAGCGGAGCTCTCCTCTTCTTACCACCATCCTACAAGCCTTCTCC  
CTGGAGAGCCCGTGCCCCGCGGACACCCTGAGCCTCAAGCCCACCGTCAGTGGCCTTTTCAA  
CATTCCCCCAGCCTTCCAGCTGCAAGTCCGTCCCCTGACCTTCACTCCACCACGCAGACCA  
GATGAAGGAAGGCAACTTGAAGTGGTGGGTGCCAGGACGGTGCCTCCAGCCTCAACAGTG  
GGCATGGACAGGGTTAATGTCTCCAGAGTGTAACCTGCAGGCAGCCACATTTACACGCCTGC  
AGTTGTTTTCCGGAGTCTGTCCACGGCCACACGCTCACTTGACTCATGCTGCTAAGATGC  
ACAACCGCACACCCATACACAATAACAAGGGCCACAAGCAACTGCTGGGTTAGCTTTCCAC  
AGACATAAATATAGTCCATCTGCAATCACAAGCACATAGCCAGGTAACCCACCAACTCCCT  
GGATCTGCAGCCCACACGTGGGAGTCTGGCTGTCACCTTCAAGCCACAGAAACGGCCACA  
CATGTTTACAGCTCACACGCCCTCTCCATTCATCGAATTCTCAGTGTCCCTGTCCCTGGTG  
CCTGGCACAGGGAACAGCATGCCCCCTCCGGGGTCATGCCACCCAGAGACTGTGCTGTCTA  
TGGCCCCAACTCATGCTCCCTCTCTTGGCTACACCACTCTCCAGCCTGTGACCACCGATGT  
CCACACACCCCCAACCCTTGTCCACACAGCTACCCACGTACAACATCGTCTGGCTCCCCA  
GAGTATCTTCCCACTGAGACACGCCGCCCCACAGAGGCACAGTCCCCAGCCACCTCTGCAA  
CTGCAGCCCTCAGTACCCCTTTTAAAGCACCTGATTCTACCAAATGCAAACACATCTGGG  
TCTGCGATTATGCACAGAGACTTTGGACATACGAGGACCCTCAGACCGGAGGAACACCTGCC  
CAACCCCAACACGTGCTTATGTAACCACGTGGAAGCGGCCCTGCTGCCCCCTCCACACACA  
CATACACACTCACTGATCTACAGCCCCTGTTCCGGCGTCAGAGTCCCCACTAGACCCAGTGGA  
AGGGGTTAGAGACCAAGTAGGGGCCAGTTTCCAATTACCCCTGTGAGGGAGTGAGCCGGATC  
TGACGTTCTTGTGACTTAAGGGTCCGGCTTGGGAATTAAAGTTTGTCTGGCCTTTAGCC  
TAAAAAAAAAAAAAAAAA

## **FIGURE 64**

MEATGTWALLLALALLLLLTALSGTRARGHLPPGPTPLPLLGNLLQLRPGALYSGLMRLSK  
KYGPVFTIYLGWPWPVVVLVGQEAVERALGGQAEFSGRGTVAMLEGTFDGHGVFFSNGERW  
RQLRKFTMLALRDLGMGKREGGELIQAEARCLVETFGTEGRPFDPSSLLLAQATSNVVCSSL  
FGLRFSYEDKEFQAVVRAAGGTLLGVSSQGGQTYEMFSWFLRPLPGPHKQLLHHVSTLAAFT  
VRQVQQHQGNLDASGPARDLVDAFLLKMAQEEQNPGTEFTNKNMLMTVIYLLFAGTMTVSTT  
VGYTLLLLMKYPHVQKWVREELNRELGAGQAPSLGDRTRLPYTDAVLHEAQRLALVPMGIP  
RTLMTTRFRGYTLPOGTEVFPLLGSILHDPNIFKHPEEFNPDRFLDADGRFRKHEAFLPFS  
LGKRVCLGEGLAELFLFFTTILQAFSLESPPDLSLKPTVSGLENIPPAFQLQVRPTD  
LHSTTQTR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 294-313

**Glycosaminoglycan attachment site.**

amino acids 99-103

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 128-132

**N-myristoylation sites.**

amino acids 51-57, 109-115, 115-121, 188-194, 207-213, 257-263,  
284-290, 339-345, 370-376, 444-450

**Amidation sites.**

amino acids 140-144, 435-439

**Leucine zipper pattern.**

amino acids 32-54, 39-61

**Cytochrome P450 cysteine heme-iron ligand signature.**

amino acids 433-443

**FIGURE 65**

CGGACGCGTGGGGCCGTTATGCGCGGCTCTGTGGAGTGCACCTGGGGTTGGGGGCACTGTGCC  
CCCAGCCCCCTGCTCCTTTGGACTCTACTTCTGTTTGCAGCCCCATTTGGCCTGCTGGGGGA  
GAAGACCCGCCAGGTGTCTCTGGAGGTCACTCCCTAACTGGCTGGGCCCCCTGCAGAACCTGC  
TTCATATACGGGCAGTGGGCACCAATTCCACACTGCACCTATGTGTGGAGCAGCCTGGGGCCT  
CTGGCAGTGGTAATGGTGGCCACCAACACCCCCACAGCACCTGAGCATCAACTGGAGCCT  
CCTGCTATCCCCCTGAGCCCCGATGGGGGCTGATGGTGCTCCCTAAGGACAGCATTCACTTTT  
CTTCTGCCCTTGTTTTTTACCAGGCTGCTTGAGTTTGACAGCACCAACGTGTCCGATACGGCA  
GCAAAGCCTTTGGGAAGACCATATCCTCCATACTCCTTGGCCGATTTCTCTTGGAACAACAT  
CACTGATTCATTGGATCCTGCCACCCTGAGTGCCACATTTCAAGGCCACCCCATGAACGACC  
CTACCAGGACTTTTGCCAATGGCAGCCTGGCCTTCAGGGTCCAGGCCTTTTCCAGGTCCAGC  
CGACCAGCCCCAACCCCTCGCCTCCTGCACACAGCAGACACCTGTCAGCTAGAGGTGGCCCT  
GATTGGAGCCTCTCCCCGGGGAAACCGTTCCCTGTTTGGGCTGGAGGTAGCCACATTGGGGCC  
AGGGCCCTGACTGCCCCCTCAATGCAGGAGCAGCACTCCATCGACGATGAATATGCACCGGCC  
GTCTTCCAGTTGGACCAGCTACTGTGGGGCTCCCTCCCATCAGGCCTTTCACAGTGGCGACC  
AGTGGCTTACTCCCAGAAGCCGGGGGGCCGAGAATCAGCCCTGCCCTGCCAAGCTTCCCCCTC  
TTCATCCTGCCTTAGCATACTCTCTTCCCCAGTCACCCATTTGTCCGAGCCTTCTTTGGGTCC  
CAGAATAACTTCTGTGCCTTCAATCTGACGTTCCGGGGCTTCCACAGGCCCTGGCTATTGGGA  
CCAACACTACCTCAGCTGGTCGATGCTCCTGGGTGTGGGCTTCCCTCCAGTGGACGGCTTGT  
CCCCACTAGTCTTGGGCATCATGGCAGTGGCCCTGGGTGCCCCAGGGCTCATGCTGCTAGGG  
GGCGGCTTGGTTCTGCTGCTGCACCACAAGAAGTACTCAGAGTACCAGTCCATAAATTAAGG  
CCCGCTCTCTGGAGGGAAGGACATTACTGAACCTGTCTTGCTGTGCCTCGAAACTCTGGAGG  
TTGGAGCATCAAGTTCCAGCCGGCCCCCTTCACTCCCCCATCTTGCTTTTCTGTGGAACCTCA  
GAGGCCAGCTCGACTTCCCTGGAGACCCCCAGGTGGGGCTTCCCTCATACTTTGTTGGGGGA  
CTTTGGAGGCGGGCAGGGGACAGGGCTATTGATAAGGTCCCCTTGGTGTTGCCTTCTTGCA  
CTCCACACATTTCCCTTGGATGGGACTTGCAGGCCTAAATGAGAGGCATTCTGACTGGTTGG  
CTGCCCTGGAAGGCAAGAAAATAGATTTATTTTTTTTTCACAGGGAAAAAAAAAAAAA

**FIGURE 66**

MRGSVECTWGWGHCAPSPLLLWTLTLLFAAPFGLLGKTRQVSLEVI PNWLGPLQNLHRAV  
GTNSTLHYVWSSLGPLAVVMVATNTPHSTLSINWSLLLSPEPDGGLMVLPKDSIQFSSALVF  
TRLLEFDSTNVSDTAAKPLGRPYPPYSLADFSWNNITDSLDPATLSATFQGHMNDPTRTFA  
NGSLAFRVQAFSRSSRPAQPPRLLHTADTCQLEVALIGASPRGNRSLFGLEVATLGQGPDCE  
SMQEQHSIDDEYAPAVFQLDQLLWGSLSGFAQWRPVAYSQKPGGRESALPCQASPLHPALA  
YSLPQSPIVRAFFGSQNNFCFNLTFGASTGPGYWDQHYLSWSMLLGVGFPPVDGLSPLVLG  
IMAVALGAPGLMLLGGGLVLLLHHKKYSEYQSIN

**N-glycosylation sites:**

amino acids 65-69, 95-99, 134-138, 159-163, 187-191, 230-234,  
333-337

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

amino acids 397-401

**Casein kinase II phosphorylation sites:**

amino acids 151-155, 249-253, 255-259

**N-myristoylation sites:**

amino acids 3-9, 63-69, 235-241, 273-279, 292-298, 324-330

**Leucine zipper pattern.**

amino acids 371-393



**FIGURE 67**

CGGGACAGGCGGTGAGGCCACAACACATGCGTGTATCTTGCTTGGGCTATCTTCCCTGCTCTGCCACGCCGGG  
 TCTGGAGAAGGGGTTTACGCCCCAGGACATTTACTGAGAGTCGGCGAATATTGGGAGCCGCGATGTTCCCCCTT  
 CGGGCCCTGTGTTGGTCTGGGCGCTTCTAGGAGTGGCCGGATCATGCCCGAGCCGTGCGCCTGCGTGGACAA  
 GTACGCTCACCAGTTCGCGGACTGCGCTTACAAAGAGTTGCGTGAGGTGCCGAAGGACTGCCTGCCAACGTGA  
 CGACGCTTAGTCTGTCCCGGAACAAGATCACTGTGCTGCGCGCGGGGCTTCCCGACGTACACACAGGTACAG  
 TCGTGTGGCTGGCGCACAATGAGGTGCGCACCGTGGAGCCAGGCGCACTGGCCGTGCTGAGTCAGCTCAAGAA  
 CCTCGATCTGAGCCACAACCTTCATATCCAGCTTTCGTTGGAGCGACCTGCGCAACCTGAGCGCGCTGCAGCTGC  
 TCAAAATGAACCACAACCGCTGGGCTCTCTGCCCGGGAGCGACTCGGTGCGCTACCCGACCTGCGTTCCCTG  
 CGCATCAACAACAACCGGCTGCGTACGCTGGCGCTGGCACCTTCGACGCGCTTAGCGCGCTGTACACTTGCA  
 ACTCTATCAACAATCCCTTCCACTGCGGCTGCGGCTTGTGTGGCTGCAGGCTGGGCGCGAGCACCCGGGTGT  
 CCTTACCCGAGCCGACTCCATTGCTTGTGCTCGCCTCCCGCGCTGCAGGGGTGCGGCTGTACCGCTGCC  
 GCGCTGCCCTGTGCACCGCCAGCGTGCATCTGAGTGCCGAGCCACCGCTTGAAGCACCCGGCACCCACTGCG  
 CGCAGGACTGGCGTTCTGTGTACTGTCATCGCCGAGCGCCACCTACGCTCGCTGCAATGGCAACTTGCA  
 TCCCCGGTGGCACCGTCTTAGAGCCACCGGTTCTGAGCGGGAGGACGACGGGTTGGGCGCGAGGAAGGA  
 GAGGGAGAAGGAGATGGGGATTGTGCTGACGCAGACCCAAGCCAAACGCCGACTCCAGCACCCGCTTGGCCGGC  
 GCGCCAGCCACACCGCGCTTCTTGGCCCTCGCAATGGCTCCCTGTTGGTGCCCTCTCTGAGTGCCAAAGGAGG  
 CGGGCGTCTACACTTGGCGTGCACACAATGAGCTGGGCGCAACTCTACGTCAATACGCTGGCGGTGGCAGCA  
 ACCCGGCTCCAAACACGCGCTGCGCGCGGGGAGAACCCGACGCAAGGCCCGACCTCTGAGCGCAAGTC  
 CACAGCCAAGGGCGGGGCAACAGCGTCTGCTTCCAAACCCGAGGGCAAAATCAAAGGCCAAGGCTGGCCA  
 AGGTACGACTTCTCGGGGAGACCGAGACGCGAGCCGAGGAGGACACAAGTGAGGGAGAGGAGGCCGAGACCA  
 ATCCTCGCGGACCCGCGGAGGAGCAGCGCTGTGGCAACGGGGACCCCTCTCGGTACGTTTCTAACACGCGTT  
 CAACCAGAGCGCAGAGCTCAAGCCGACGCTCTCGAGCTGGGCGTCACTCGCGCTGGATGTGGCGGAGCGGAGG  
 CGCGGGTGCGCTGACTCCGCTGGCTGCGCGCTGGGGCCCTGGGCGCGCGGGCTGGCGGAGCCCCGCGACCC  
 GGGCGGCGACCCCTGCGCCTACTCTATCTGTGTCCAGCGGGGGCGCGCGCGGAGTGAGTGGTCCCGCGTAGA  
 GGAAGCGCTAACGCGCTACTGGTTCGCGCGCTGCGGCGGGTACCACTACTCCGTGTGCTGCGCTGGCGTGGCGG  
 GCGAAGCCTGCCAAGTGCAAGTGGTGTCTTCCACCAAGAGGAGCTCCATCGCTGCTGTCATAGTGAGGAGTG  
 AGCGTATCTCTCTGGTGTGGCCACAGTGCCCTTCTGGGCGCGCCTGCTGCCATCTGCTGGCTAAACACCC  
 GGGCAAGCCCTACCGTCTGATCCTGCGGCTCAGGCCCTGACCCCTATGGAGAAGCGCATCGCCGAGACTTTCG  
 ACCCGCTGCTTCTGACCTCGAGTCCGAGAAAAGCTACCCGCGAGGCGGCGAGGCGGGCGGCGAGGAGCCAGAG  
 GACGTGCAGGGGGAGGCGCTTGATGAAGACGCGGAGCAGGAGACCCAAGTGGGGACCTGCAGAGAGGAGAG  
 TCTTGGCGGCTGCTCACTGCTGGAGTCCCAGTCCAAGGCCAACCAAGAGGAGTTGAGGCGGGCTCTGAGTACA  
 GCGATCGGCTGCCCTTGGGCGCGAGGCGGTCAACATCGCCAGGAGATTAAATGGCAACTACAGGCAGACGGCA  
 GGCTGAACCTCCGCGCTCCGCGCCGCGCCATTCCCGACCTCCACCTAGGGTGCTGGGAGCAGCAGTCTAGGGC  
 TGGCAGGACTTATGTCCCCGTCGCCAACCTTCACTACTCTCTCCCTTACTACTCCCCCTTACTACTTACTACCA  
 GGGACTTCTATTAGGGAGTGGCGGATTTTACCACTCTCTGCTACCCAGGCTGCCATTCTCCCTGCGGGCTGA  
 ATCCCTTCCCCGCCAAGCAGTGTCTTATCTTACCCCATGCAAGACTCCACCCGAGAGCGGTGGGCGATATCT  
 ATGTCCCTCCATTCCCGTCCGAGTATCTGCGAAATCCACCCCGAGCCCGCCCCACCGTGGGCTCTGGAGCCA  
 GAGGAAACGAGCGAAGACTTTGAAACCTCGCGGTAACGCGGTGGTTTCGGGGCCAGCCAAGGCGAGTGGAGT  
 GCTGTGGGGTCCCACTCGACCCCTCCTCCTCCCTTCTTTCTTTCTTTCTTTTCTTTTCTTTTCTTTTCTTTT  
 TTTATTTATTTATTTTGTGACGGAGTCTTGGTCTGTGCGCAGGCTGGAGTGCAAGTGGCGGATCTCGGCTCACT  
 GCATCTTCCGCTCCCGGTTCAAGCGATTCTCCTGCGCTCAGCCTGCTAGTAGCTGGGACTACAGGCGCGCGC  
 CACCACGACAGCTAATTTCTTCTATTTTAGTAGAGACGGGTTTACCATGTTGGCCAGGATGTTCTGGATC  
 TCTTGACCTCAGGTGATCCATCTGCGCTCGGCTCTCAAGTGCTGGGATTACAGGCGTGAGGCGACCGCCCG  
 CCCCTCCTCCTTCAATCCCTACTCCAGAAAGCCGGGATTCTGTGGCAACCCCTAGTTTTAGTTCCAAAGCCT  
 CCTGCCGCGAGGAAACCAATCCTTCTGCTCCTCCACCCCCACCCCACTTCTGGCCAGTTGGAGTCCAGCCCG  
 TGCTGGGGCGCCTTTCAGTCCGCGCTCAGATTTTCTGTGTTTCTGTTGTTTCAAAGACAGCGACATTTCCGG  
 TCTGTTGCTAACACCCCTTCCAGCCTCTGGGAAATCGAGTGTGTGTGTCGGGGGGTAGGGAGGGAATGCGT  
 TTTCTGTGCTCTCTCTCTAACTTAAAGCGCCGAGGACCGCGCGCCCTTGGCGGCTGAGCCTGTGGACTTGG  
 TCGCGGGCAATTTCTGTTGTCGTTGTTGGGCTTTCGCGAGGTCTGTGCGCCCAACAGCGCGCTCCCGCGGC  
 TCCACCCGACCCAGACCTAGCTGGAAAGCGCGGAGGCGGAGGAAGCTGACTGTGGCTCCCGGGCGCGGCT  
 CTCTGGAGGCTCGCGCCTAGTTTCGCAAAAGCCTGCTGCTGACTGTGCGACTGTGCGACGGATCCGGATGG  
 AGCCGAGCCCTCCGCTCTCGCTCTCGGCTCTCGCTGCGCCCCCGCCCCACCCGCCCCCTGCTTCCGCGGGAATC  
 GTGTTTCCCGCGCTGTAGTCCCTGACAAGCGTGCCTGTAGGAGAAAAGTCTGTGTCTGTGAAGTGTGACCG  
 TGTAGTGTAGGGGGCGGGCGGGGGGGCGGATGGGCGGGAGGAGGGAAGGGGAGGGGCGCGCGCGCGACT  
 CGGGCGGGGTTCTTTTCTATTTTGAAGAAAGCCTCGGGTTGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGT  
 CAGCCCTCTCCGCGAAGCGCAGCACAGCGGGGCTGGGACGAGTAGCCCCCGGAGCCCGTGGCCTTTTCT  
 AAACCGCTCTGTATGCACTCAATAAAACAATCGATTTGAAA

## **FIGURE 68**

MFPLRALWLWVALLGVAGSCPEPCACVDKYAHQFADCAYPEGLPANVTTLSSLSANK  
ITVLRGAFADVTQVTSWLWLAHNEVRTVEPGALAVLSQLKNLDLSHNFISSFPWSDLRNLSA  
LQLLKMNHNRLGSLPRDALGALPDLRSLRINNRLRTLAPGTFDALSALSHLQLYHNPFFHCG  
CGLVWLQAWAASTRVSLPEPDSIACASPPALQGVVPVYRLPALPCAPPSVHLSAEPPEAPGT  
PLRAGLAFVLHCIADGHPTPRLQWQLQIPGGTVVLEPPVLSGEDDGVGAEEGEGEGDGDLLT  
QTQAQTPTFPAPAWPAPPATPRFLALANGSLLVPLLMAKEAGVYTCRAHNELGANSTSIKRVAV  
AATGPPKHAPGAGGEPDQAPTSEKSTAKGRGNSVLPSKPEGKIKGQGLAKVSILGETETE  
PEEDTSEGEAEEDQILADPAEEQRCGNGDPSRYVSNHAFNQSAELKPHVFELGVIALDVAER  
EARVQLTPLAARWGPGGGAGGAPRPGRRPLRLLYLCPAGGGAQVQWSRVEEGVNAYWFRGL  
RPGTNYSVCLALAGEACHVQVVFSTKKELPSLLVIVAVSVFLLVLATVPLLGAACCHLLAKH  
PGKPYRLILRPQAPDPMEKRIAADFPRASYLESEKSYAGGEAGGEEPEDVQGEGLDEDAE  
QGDPGDLQREESLAACSLVESQSKANQEEFEAGSEYSDRLPLGAEAVNIAQEINGNYRQTAG

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-19

#### **Transmembrane domain:**

amino acids 587-610

#### **N-glycosylation sites.**

amino acids 52-55, 121-124, 337-340, 364-367, 474-477, 563-566

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 397-400

#### **Casein kinase II phosphorylation sites.**

amino acids 19-23, 202-205, 289-292, 246-249, 411-414, 431-434,  
433-436, 440-443, 544-547, 583-586, 650-653, 700-703

#### **N-myristoylation sites.**

amino acids 15-20, 48-53, 165-170, 296-301, 351-356, 362-367,  
390-395, 419-424, 514-519, 536-541, 557-562, 561-566, 610-615,  
661-666, 716-721

#### **Amidation site.**

amino acids 522-525

#### **Prokaryotic membrane lipoprotein lipid attachment sites.**

amino acids 10-20, 603-613

# FIGURE 69

GGCGGCGGGAGCAGCGAAGGGGGCGGCAGGGATCCTCCAGGCTGCCGGCTGGGAAGGCGTGG  
GCGACCCGGTGTGTGGCGCGCCAGAGCCCCGCGTTTCAGCCCTAGGGAAGGAAGCCAGTTG  
AGGGAAGTTCTCCATGAATGTACGTCACAATGATGATGACCGACCAAATCCCTCTGGAAGTGG  
CCACCATTGCTGAACGGAGAGGTAGCCATGATGCCCCACTTGGTGAATGGAGATGCAGCTCA  
GCATGTTATTCTCGTTCAAGTTAATCCAGGTGAGACTTTCACAATAAGAGCAGAGGATGGAA  
CACTTCAGTGCATTCAAGGACCTGCTGAAGTTCCTCATGATGTCACCCAATGGATCCATTCCCT  
CCCATTTCATGTGCCTCCAGGTTATATCTCACAGGTGATTGAAGATAGTACTGGAGTCCGCCC  
GGTGGTGGTCACACCCAGTCTCCTGAGTGTTATCCCCCAAGCTACCCCTCAGCCATGTCTC  
CAACCCATCATCTCCCTCCCTATCTGACTCACCATCCACATTTTATTCATAACTCACACACG  
GCTTACTACCCACCTGTTACCGGACCTGGAGATATGCCGCCCTCAGTTTTTTCCCCAGCATCA  
TCTTCCCCACACAATATATGGTGAGCAAGAAATTATACCATTTTATGGAATGTCAAGCTACA  
TCACCCGAGAAGACCAAGTACAGCAAGCCTCCGCACAAAAAACTGAAAGACCGCCAGATCGAT  
CGCCGAACCGCCTCAACAGCCCTCCTTCTTCTATCTACAAAAGCAGCTGCACAACAGATATA  
CAATGGCTATGGGAAGGGCCATAGTGGTGGAGTGGCGGAGGCGGCAGCGGTAGTGGTCCCG  
GAATTAAGAAAACAGAGCGACGAGCAAGAAGCAGCCCCAAAGTGAATGATTGAGACTTGCAA  
GAATATGAGTTGGAAGTAAAGAGGGTGCAAGACATTCTTTCGGGAATAGAGAAACCACAGGT  
TTCTAATATTGAGCAAGAGCAGTTGTGTGTCTGCTGGGCTCCCCCTGTTGGACTTTCTGTG  
GACCCACAGTGGTCTTTCTTCCCTACAGTTACGAGGTGGCCTTATCAGACAAAGGACGA  
GATGGAAAATACAAGATAATTTACAGTGGAGAAGAATTAGAATGTAACCTGAAAGATCTTAG  
ACCAGCAACAGATTATCATGTGAGGGTGTATGCCATGTACAATTCCTGTAAGGGATCCTGCT  
CCGAGCCTGTTAGCTTCACCACCCACAGCTGTGCACCCGAGTGTCTTTCCCCCCTAAGCTG  
GCACATAGGAGCAAAAGTTCACTAACCTTGCAAGTGGGAAGGCACCAATTGACAACGGTTCAA  
AATCACCACCTACCTTTTAGAGTGGGATGAGGGAAAAAGAAATAGTGGTTTCAGACAGTGCT  
TCTTCGGGAGCCAGAAGCACTGCAAGTTGACAAAGCTTTGTCCGGCAATGGGGTACACATTC  
AGGCTGGCCGCTCGAAACGACATTGGCACCAGTGGTTATAGCCAAGAGGTGGTGTGCTACAC  
ATTAGGAAATATCCCTCAGATGCCTTCTGCACCAAGGCTGGTTTCGAGCTGGCATCACATGGG  
TCACGTTGCAGTGGAGTAAGCCAGAAGGCTGTTTACCCGAGGAAGTGATCACCTACACCTTG  
GAAATTCAGGAGGATGAAAATGATAACCTTTTCCACCCAAAATACACTGGAGAGGATTTAAC  
CTGTACTGTGAAAAATCTCAAAAGAAGCACACAGTATAAATTCAGGCTGACTGCTTCTAATA  
CGGAAGGAAAAAGCTGTCCAAGCGAAGTTCTTGTGTTGTACGACGAGTCTGACAGGCCTGGA  
CCTCCTACCAGACCGCTTGTCAAAGGCCAGTTACATCTCATGGCTTTAGTGTCAAATGGGA  
TCCCCCTAAGGACAATGGTGGTTCAGAAATCCTCAAGTACTTGCTAGAGATTACTGATGGAA  
ATTCTGAAGGTGAAGTTTTTGGCAATTGTTTATTTCAAATCCAATAGCAAGCTCTGTTTTCT  
AATATAGTAAATGTCTTTATAGTAATAGTGAGTAATCATTAATTTCTAAAGATAGAATTATTA  
TTACAATAAACAACTTTTAGTCACATATTGGCAGTTTTTCTATTTCAAACACAGCACCAGAG  
ATCAGAGTCTACTTGAACTTACATTTGTGTTATTTAACAATTTTCTGTATCTTTTTCTATT  
GGTGTGTTTTGTTTTGTTTATCTTTGTTTTGTTTCTTTGGTTTTGTTTTGTTTTGTTTTGTT  
TTTTGAGATACGATCTCTGTACACAGGCTGGAGGGCAGTGGCACAGACATGGCCCATGCA  
GTCTCAGACTCCTGGGCTTAAGTGACTCTTCTGCCACAGAAGATGAGGAAGAATACATTTTT  
CATAGTGATGGGGTCTCACTATGTTATCTAGGCTGGTCTCAAACCTCCTGGCCTCAAGCAACC  
CTCCACCTTGGCCTCCCAAAGTGCTGGGACTATAGACATGAATCACCACACTCAGCTTCCAT  
GTCTTTTTATGAACTAGGGTTCCTAATTAATCAGATAAATTTGGTATTTTCTATCTCCTAACT  
TGCCATATGTTTTCTGGAAATTTCTATAAGCAGCCGAGAGTGGTGGCTCACGCTGTAGTCCC  
AGCACTTTGGGAGGCTGAGGTGGGTGGTCAAGAGATCAAGACCATCCTGGCCAACATGGTGA  
AACCCCGTCTCTACTAAAATAACAAAATTAGCTGGGTGTGGTGGCAGGCACCTGTAGTCCC  
AGCTACTTGGGAGGCTGAGGCAGAAGAATTGCTTGAACCCAGCAGGCGGAGGTTGCAGTGAG  
CTGAGATTGCACCACTGCCTCCAGCCTGGTGACAGAGTGAGACTCTGTCTCAAAAAAAAAAAAA

## **FIGURE 70**

MMMTDQIPLELPPLLNGEVAMMPHLVNGDAAQHVLVQVNPGETFTIRAEDGTLQCIQGPAE  
VPMMSPNGSIPPIHVPPGYISQVIEDSTGVRRVVVTPQSPECYPPSYPSAMSPTHHLPPYLT  
HHPHFIHNSHTAYYPPVTGPGDMPPQFFPQHHLPHHTIYGEQEIIIPFYGMSSYITREDQYSKP  
PHKKLKDRQIDRQNRNLNSPPSSIIYKSSCTTVYNGYGKGHSGSGSGSGSGSGPGIKKTERRAR  
SSPKSNSDSDLQEYELEVKRVQDILSGIEKPQVSNIQARAVVLSWAPPVGLSCGPHSGLSFPY  
SYEVALSDKGRDGKYKIIYSGEELECNLKDRLRPATDYHVRVYAMYNVKGSCSEPVSFTHS  
CAPECPPFPKLAHRSKSSLTQWKAPIDNGSKITNYLLEWDEGKRNSGFRQCFFGSQKHCKL  
TKLCPAMGYTFRLAARNDIGTSGYSQEVVVCYTLGNIPQMPSAPRLVRAGITWVTLQWSKPEG  
CSPEEVITYTLEIQEDENDNLFHPKYTGEDLTCTVKNLKRSTQYKFRLTASNTEGKSCPSEV  
LVCTTSPDRPGPPTRPLVKGPVTSHGFSVKWDPPKDNNGGSEILKYLLEITDGNSEGEVFGNC  
FIQIQ

### **Important features of the protein:**

#### **N-glycosylation sites.**

amino acids 69-73, 254-258, 401-405

#### **Glycosaminoglycan attachment sites.**

amino acids 229-233, 234-238, 236-240

#### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 416-420, 535-539

#### **Tyrosine kinase phosphorylation site.**

amino acids 319-326

#### **N-myristoylation sites.**

amino acids 52-58, 227-233, 228-234, 230-236, 231-237, 232-238,  
235-241, 239-245, 402-408, 610-616

#### **Amidation site.**

amino acids 414-418

#### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 290-301

#### **ATP/GTP-binding site motif A (P-loop).**

amino acids 546-554

#### **CUB domain proteins profile.**

amino acids 294-301

**FIGURE 71**

AAGTCATTCACTGGATGTGATCTTGGCTCACAGGGGACGATGTCAAGCTCTTCCTGGCTCCTTCTCAGCCTTGT  
TGCTGTAACCTGCTGCTCAGTCCACCATTGAGGAACAGGCCAAGACATTTTTGGACAAGTTTAACCACGAAGCCG  
AAGACCTGTTCTATCAAAGTTCACCTTGCTTCTTGGAAATTATAACACCAATATTACTGAAGAGAATGTCCAAAAC  
ATGAATAATGCTGGGGACAAATGGTCTGCCTTTTAAAGGAACAGTCCACACTTGCCCAAATGTATCCACTACA  
AGAAATTCAGAACTCTCAGCTCAAGCTTCAGCTGCAGGCTCTTCAGCAAAATGGGTCTTCAGTGTCTCAGAAAG  
ACAAGAGCAAACGGTTGAACACAATTCATAATACAAATGAGCACCACTACAGTACTGGAAAAGTTTGTAAACCA  
GATAATCCACAAGAATGCTTATTACTTGAACCAGGTTTGAATGAAATAATGGCAAACAGTTTAGACTACAATGA  
GAGGCTCTGGGCTTGGGAAAGCTGGAGATCTGAGGTGGCAAGCAGCTGAGGCCATTATATGAAGAGTATGTGG  
TCTTGA AAAATGAGATGGCAAGAGCAAATCATTATGAGGACTATGGGATTATTGGAGAGGAGACTATGAAGTA  
AATGGGGTAGATGGCTATGACTACAGCCGCGGCAGTTGATTGAAGATGTGGAAACATACCTTTGAAGAGATTAA  
ACCATTATATGAACATCTTCATGCCTATGTGAGGGCAAAGTTGATGAATGCCTATCCTTCTATATCAGTCCAA  
TTGGATGCCTCCCTGCTCATTGCTTGGTGATATGTGGGGTAGATTTTGGACAAATCTGTACTCTTTGACAGTT  
CCCTTTGGACAGAAACCAACATAGATGTTACTGATGCAATGGTGGACCAGGCCCTGGGATGCACAGAGAATATT  
CAAGGAGGCCGAGAAGTTCTTGTATCTGTTGGTCTTCTTAATATGACTCAAGGATTCTGGGAAAATTCATGTC  
TAACGAGACCCAGAAATGTTTCAAGAACAGCTCTGCCATCCACAGCTTGGGACCTGGGGAAGGGCGACTTCAGG  
ATCCTTATGTGCACAAAGGTGACAAATGGACGACTTCCTGACAGCTCATCATGAGATGGGGCATATCCAGTATGA  
TATGGCATATGCTGCACAACCTTTCTGCTAAGAAATGGAGCTAATGAAGGATTCCATGAAGCTGTTGGGAAAA  
TCATGTCACCTTCTGCAGCCACACCTAAGCATTTAAATCCATTGGTCTTCTGTCAACCCCTTTGAAGAGATTAA  
AATGAAACAGAAATAAATCTCTGCTCAAACAAGCACTCAGATTGTTGGGACTCTGCCATTTACTTACATGTT  
AGAGAAGTGGAGGTGGATGGTCTTTAAAGGGGAAATTCCAAAGACAGTGGATGAAAAAGTGGTGGGAGATGA  
AGCGAGAGATAGTTGGGGTGGTGGAACTGTGCCCATGATGAAACATACTGTGACCCCGCATCTCTGTTCCAT  
GTTTCTGATGATTACTCATTTCATTCGATATTACACAAGGACCCCTTACCAATTCAGTTTCAAGAAGCACTTTG  
TCAAGCAGCTAAACATGAAGGCCCTCTGCACAAATGTGACATCTCAAACTCTACAGAAGCTGGACAGAACTGT  
TGTAAGAAATACCTCAAAATGTTGAACCTCTCCTAGTATTCACTATTACTCATTTCATGCCCTAGGTTTGTATT  
TGATTCTTTGTTCTAAAAAGAAAAATTTATGGCCTCAAAATGTCCCTCATTTACAAACCAACATTTAATTTGT  
GGTCAGACAGGAACCTAGACCATAACAATTTGGGTGGGCCACCTCTTTCTCCCTATCACTAACACAGCCCTC  
AATGCTGGTAATTTGGAAGGAAAGAGCGGTTTAGGGTGGAAATATATCTGTTAATATGCATTTCTTTCTTATCTG  
CCAGAAGCAAATTTAGCCAAGTCAAAGAGAAGAAACCATAGATCATAGATGTAATATATGTACATCTGGAACC  
CCTCAAAGGCCCTGAACCCCTTTTTTTGTGTAGCAATATGCTGAGGCTTGGAAAATCAGAACCCTGGACCCT  
AGCATTGGAAAATGTTGTAGGAGCAAGAAATGAATGTAAGGCCACTGCTCAACTACTTTGAGCCCTTATTTAC  
CTGGCTGAAAGACCAAGAAACAAGAAATCTTTTGTGGATGGAGTACCGACTGGAGTCCATATGCAGACCCAAAGC  
ATCAAAGTGAGGATAAGCCTAAATCAGCTCTTGGAGATAAAGCATATGAATGGAACGACAATGAAATGTACCT  
GTTCCGATCATCTGTTGCATATGCTATGAGGCAGTACTTTTAAAGTAAAAAATCAGATGATTCTTTTGGGG  
AGGAGGATGTGCGAGTGGCTAAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTCACTGCACCTAAAAATGTG  
TCTGATATCATTCTAGAACTGAAGTTGAAAAGGCCATCAGGATGTCCCGGAGCCGATCAATGATGCTTTCCG  
TCTGAATGACAACAGCCTAGAGTTTCTGGGGATACAGCCAACTTGGACCTCCTAACAGCCCCCTGTTTCCA  
TATGGCTGATTGTTTTGGAGTTGTGATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATC  
AGAGATCGGAAGAAGAAAAATAAGCAAGAAGTGGAGAAAAATCCTTATGCCTCCATCGATATTAGCAAAGGAGA  
AAATAATCCAGGATTCAAAAACCTGATGATGTTTCAAGCCTCCTTTTAGAAAAATCTATGTTTTCTCTTGAG  
GTGATTTTGTGTATGTAAATGTTAATTTTATGGTATAGAAAAATATAAGATGATAAAGATATCATTAAATGTCA  
AAACTATGACTCTGTTTCAGAAAAAAATTTGTCAAAGACAACATGGCCAAGGAGAGAGCATCTTCATTGACATT  
GCTTTTCAGTATTATTTCTGTCTCTGGATTGACTTCTGTTCTGTTTCTTAATAAGGATTTGTATTAGAGTAT  
ATTAGGGAAAGTGTGATTTTGGTCTCACAGGCTGTTCAAGGATAATCTAAATGTAATGTCTGTTGAATTTCTG  
AAGTTGAAAAACAAGGATATATCATTGGAGCAAGTGTGGATCTTGTATGGAATATGGATGGATCACTTGTAAAG  
ACAGTGCCTGGGAACCTGGTGTAGCTGCAAGGATTGAGAATGGCATGCATTAGCTCACTTTCAATTAATCCATTG  
TCAAGGATGACATGCTTTCTTACAGTAACCTCAGTTCAGTACTATGGTGATTGCGCTACAGTGATTTGGAA  
TCGATCATGCTTTCTTCAAGGTGACAGGTCTAAAGAGAGAAGAAATCCAGGGAACAGGTAGAGGACATTGCTTTT  
TCACTTCCAAGGTGCTTGTATCAACATCTCCCTGACAACACAAAACCTAGAGCCAGGGGCCCTCCGTGAACCTCCCA  
GAGCATGCTTGTATAGAACTCATTCTACTGTTCTTAACCTGTGGAGTGAATGGAAATCCAACTGTATGTTCA  
CCCTCTGAAGTGGTACCCAGTCTCTTAAATCTTTGTATTGGCTCACAGTGTGAGCAGTGTGAGCACAAA  
GCAGACACTCAATAAATGCTAGATTTACAAA

## **FIGURE 72**

MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNM  
NNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMS  
TIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVL  
KNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKL  
MNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPGQKPNIDVTDAMVDQAWDAQRI FKE  
AEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTA  
HHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNET  
EINFLKQALTIVGTLPTTYMLEKWRWMVFKGEIPKDQWMKKWEMKREIVGVVEPVPHDET  
YCDPASLFHVSDDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-17

#### **N-glycosylation sites.**

amino acids 53-57, 90-94, 103-107, 322-326, 432-438, 546-550

#### **N-myristoylation sites.**

amino acids 260-266, 286-292, 395-401

#### **Cell attachment sequence.**

amino acids 204-207

#### **Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 371-381

# **FIGURE 73**

CCCACGCGTCCGAGCGGGGTGGACAAAGTGGCGTGTGTGCTGCGACCCCGAGGGAAGATGAACG  
GGACGCGGAACTGGTGTACCCTGGTGGACGTGCACCCAGAGGACCAGGCGGCGGGCGGCAGGA  
AGACCTATGCCATGGTGTCCAGCCACTCAGCTGGTCATTCTCTGGCTTCAGAACTGGTGGAGT  
CCCATGATGGACATGAGGAGATCATTAAGGTGTACTTGAAGGGGAGGTCTGGAGACAAGATGA  
TTCACGAGAAGAATATTAACCAGCTGAAGAGTGAGGTCCAGTACATCCAGGAGGCCAGGAAC  
GCCTACAGAAGCTCCGGGAGGATATAAGTAGCAAGCTTGACAGGAACCTAGGAGATTCTCTCC  
ATCGACAGGAGATACAGGTGGTGTAGAAAAGCCAAATGGCTTTAGTCAGAGTCCCACAGCCC  
TGTACAGCAGCCCACCTGAGGTGGACACCTGTATAAATGAGGATGTTGAGAGCTTGAGGAAGA  
CGGTGCAGGACTTGCTGGCCAAGCTTCAGGAGGCCAAGCGGCAACACCAGTCAGACTGTGTGG  
CTTTTGAGGTCACACTCAGCCGGTACCAGAGGGAAGCAGAACAAAGTAATGTGGCCCTTCAGA  
GAGAGGAGGACAGATGTCCAGAGTGAATTGGAGAATGTCCTGGGGGAATGAAGTTCCTTCCACA  
AACACAGCTCAGTTCTTAGCAACAAACTGTTTTGTTTTTCTACTTGCTCCATCTGCAGCCCTACG  
CTGCCCTGGCCCTCTGCAGACAGATAGTGGGGTTACCTGGCAAGGCCCTGGTGAGAGCCAGTGA  
ACCTAAGCTTTGACTGGGTGGCCTTGTCTTTCTGGGGAGGAGGGAATGTACATTAGGGAGTA  
GCCTTTTGCGGAAAAATTCTCTAGGGCTACAGACAGTCATGTGTGACTTCTCTCTGCTGTGAA  
AACTCCCAGAGTCTCTTTAGGGATTTTCCCTAAGGTGTACCACCAGGCACACCTCAGTCTTCT  
TGACCCAGAGCCTGAAAACTGTTTTCACTGGGTTCACCAGTCCCAGCAAAATCCTCTTTGTA  
TTTATTTTGCTAAGTTATTGGTGGTTTTGCTTACATCTCATGATTGATATAATACCAAAGTTC  
TATAGCCTTCTCTTGCACTATTGGGATTTGCTTGAAACCGGGAAAACTGTTCCCATTAGGCTT  
GTTAATGTCAGAGTGACACTATTATGAATCTTTCTCTCCCTTTCTCTGCTGTTTCTTCTCT  
CTTTCTCCTTCAAACCTTGCTCTGCAGCTAAGGAAGGTGAGTCTACTTTCCCTGAGGCTTTGGG  
GTCAGAGTATATGTTGTTTGGAGAAAGAGGGCAATCAGGACTCTTCTGGGACCCAGATGAGTT  
CTTCACTAGCCCTTCTGAACCCCTTGCTCCATAATGGTCTTTTTATCCTGGCTCTGAATGACC  
CTGCAGGTCATCATGGTTTTCTTTTTTTTATTGTTTTTTTTTTTTTCTGAGACAGAGTCTCACT  
CTGTCACCCAGGCTGGAGTGCAGTGGCGGATCTCAGCTCACTGCAACCTCTGCCTCCCGGAT  
TTAAGCGATTCTTCTGCCCTCAGCCTCCCGAGTAGCTGGGACTACAGGTGTGCCACCACGCCTG  
GCTGATTTTTGTATTTTTAGTAGAGATGGGGTTTACCATACTGGCTAGGCTGGTCTCGAATT  
CCTGACCTCAGGTGATCCACCCACCTCGGCTTCCCAAAGTGCTAGGATTATAGGCTTGAGCTA  
CTGCGCCCCGGCCATGGTGTTTTTCTTTAGGGCTCTTCTACAGCCTTGAGAAGTAGATAGGC  
ATCAGAGTATGGTACTATAGGAATCAGAAAAATTCAAACAAATGTGGATTAAAGTGTTAGGC  
TCTATGTGGCTCACGCAGCCAGAATCCTTAAGTCTGTGTGTTTCTGTGTCTCAAGACTGGGCT  
CACATTCTGGCTTTGTCCATAACAATGCTCTGGGATTTAGGGAGTTCCTCATTTGTAAAT  
GAGGGGGTTCAGAGCAGGTGATATCCATGTTTCTTCCCTTTCTGATATTGTTGTCTGTGGCATA  
TTCTTTGTATGGCGAATTAAATAAATTATATTAATGTGTCA

**FIGURE 74**

MNGTRNWCTLVDVHPEDQAAAGRKTYAMVSSHSAGHSLASELVESHGHEEIIKVYLKGRSGD  
KMIHEKNINQLKSEVQYIQEARNCLQKLREDISSKLDRLGDSLHRQEIQVVLEKPNGFSQSP  
TALYSSPPEVDTTCINEDVESLRKTVQDLLAKLQEAKRQHQSDCVAFEVTLSTRYQREAEQSNVA  
LQREEDRCPE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-39

**N-glycosylation site.**

amino acids 2-6

**Amidation site.**

amino acids 21-25



# **FIGURE 75**

GCTTGACACATGGCTCCGGAGGCTCCGGTTGCCCATCCGAGCCCTGCCAGGCTCTAACGTTCCCAACTGACAA  
 CACCAGTAACATAAATATAGGAGCAGATGGTGGGGACGGGCTGTCGACGGGCTCCTTTGCAGAGGTCTCCGGACT  
 GCAGATAAGGCTCAGGCCCTTTTGTGAGAAGCAGACCAGCCTGGGGGCTGGCGGCAGGACACCTGTGTCTGCATG  
 CTGAAGAAGATGGGTGAGGCCGTGGCCAGAGTAGCAAGGAAGGTCAACGAGACGGTGGAGAGCGGCTCTGACACT  
 CTGGACCTGGCCGAGTGCAGCTGGTCTCCTTTCCCATTTGGCATCTACAAGGTCTGCGGAATGTCTCTGGCCAG  
 ATCCACCTCATCACCTGGCTAACACGAGCTTAAGTCCCTCACCAGCAAGTTCATGACCACATTCACTCAGCTC  
 CGAGAGCTCCACCTGGAGGGGAACCTTCTACACCGCTCCCCAGCGAGGTCACTGCCCTGCAGCACCTCAAGGCC  
 ATTTACCTGTCCCGAACCAAGTTCAGGACTTCCCTGAGCAGCTTACCGCCCTGCCGGCGCTGGAGACCATCAAC  
 CTGGAGGAGAACGAGATCGTAGATGTGCCGTGGAGAAGCTGGCCGCCATGCCAGCCTTGGCGAGCATCAACCTC  
 CGCTTCAACCCACTCAACGCCGAGGTGCGCGTGTGCGCCCGCGCTCATCAAGTTTGACATGCTCATGTCTCCG  
 GAAGGCGCAAGAGCCCCCTACCTTAGGCCACCCCTCTCATGCCACCCAGCAAGGGACAGAGGCCACAGGCCCTG  
 GAACCCCTGGAAGGGAGGGAGGCCCATGGGAGGCCAAGCCTGGGGGCTGGGGGCGGCTGGGGCGAGCAGCACGTGG  
 TGGGTGGGGTGCAGCTGGTCTGGATAGATAGCTTACAGCAGTAGTGGGCTCTGGAATGCCCAAGGGAAGAGGCAA  
 GGTGGGGCTGCAGCTGGACTCGGCCACTCACAGCTGCTGTGCAAACCTCAGGCAGATCTCCTGCCCTCTCTGAGC  
 CTTGTCACTTGAAAAAACAGGACCCTTTCCCTCCTTTGGGCTCCCTGGAGGTTTTTAAGCAGTACGTGCCTCCA  
 AGTTACCTCCAGATCAGCAGGCACAGGTGGGCATTGCCAGGTATTTTCTGAGCCCTGCGGGTTTGAGGCCCTTGT  
 TTTTAGTGCTGAGAGCCAGTTGTCTGCCCTGAGAAGAGAAGACAACCTCCATCTAATTATTGCTTCTTGAGAACTG  
 ACCTGGATGCGGCCCTCTGCAGGGCCAGTCTTCAGTCTGTGGTCCCTGGACTGGTGGGAACCTGAAGTGGAG  
 TCCTGGGAGAGCTGTGGTGGGAATATGGGCTGGCACTGCTGCAGGGCAAGAACATTCACTAGGAGCCCGAGGAC  
 CANGCTGGGAATGGGAGCAAGTCAAGTCACTGCTGTTCATTCCCAAGTAAACAAATTGGCGGGGTGGGAA  
 GTCCTGAGTGCTCCGTCCCTCTAGCATCACTCCTGAGCTGCGGGAGAGGTGGCCAGAGAACAGCAGAGTCACT  
 ACACCTGCAGCTCTTGTCTAAAGTGATTAGATGGCCACCCTCACCAGTCTCCAGTCCAGCAGCAGCCTGGCTGCC  
 TTGTCTAGGCCCTCTGGGGGAGAGGGCGATGTGGACCACGGGATTTGTAGCCAGCCAGCTCCAGGCCAACGCC  
 CAAAGCCCTGATGACCTGGTCTTCTGAGGCCCTCAACCTGGCATCTTAGGGTATGGTCAGGCCAACAGGGTGACC  
 AGCTGTCTGGTTTTCCAGGACATGGAACCTTTCAATGCTAAAACTGGGACATTACCCAGCAAGTGGGGATGGTTG  
 GTCCCTTACCAGGAGAGGGCCTGGGGCTCTTGCTTCCCGAGAAGCCTGTGGCTTGAAGAACCTTGACTGCTTGG  
 TCCTCAGGTATCTACCTCCACCTTTCTCCTCATCTGTGGAGCAAGCCAACTCAGTGCCCCAGACCCACCTGATC  
 TGCATCTTGTGTTGCTCCAGAGACACCTGAGGCCCCAGAGCTTGAGGCAAAGCCAGGCCCTCCAAATCCTGTGTG  
 CCGTGGACGAGTGGCCACTTTACTACTCCTAAGGCTAAGATGTTGAGAGCTCAGACCACTGCTCAGAGCAGTAAT  
 CCTGCTCAGAATGTCCAGTTCCCTCGTCCCTGCCAGGTCTCTGTCTCTTGGGAAGGAACTGATAGGTCCG  
 GCCATTGTTGGGCCATCACTGAGCGCTCAGTATCTCAAGAGACTCTGTTTATTCTGCTCGTATCCCAAGGCCCTGG  
 TTGGTCAAACCTCTGGGCAAAGGGTTTTCAGGATGAGGAGGTCAAGACAGGATGTCCAGAGCTACCGAGTTTCACT  
 GTGGGTGTTGGGGGCAAGTGGGGCTGAAGTCTGTGCAGGCTGCGCTGGCCCCACCTGCCTTGTGCCCTGGAGT  
 GGGGTTTCTCCTTGTGTAAGAAGAGGCATCCTTCTGTATGTGCACAAACACAATGTATGACCAGAGCCTTGCAA  
 CTCAAAGTGTGGTCTGTGGACCAGCAGCGGCAGTGACACCTGGGAGCTTGTAGGAATGCAGAGTCTAGGCCCTCA  
 CCTATACCTCCGACTCAGACCTGCATTTTAGCAAGACCCCAAGCTGATTCTATAAGCACTTTAGAGTTTGA  
 GAAGCAAGGACCTAGGCTGGGGATGTCTCCGAGCAGAGGGTGAAGTTTCTCTCAGTTCTCTCCCTGCCACTTCC  
 AGGATCTGAGCCTGTGTTTCAAGCTCTCCCTAACCCACCTGGGAGACACTTGGCCTGTTAGATTGTTCCAGAG  
 TCTGCATGGCACTCTGAAGAAGGGAGTGTGACCTGCAGTCAACAGGAGATGAGGGTTAGGTGTGCCAGCCCTC  
 CAGACCCGGCCTTTCTGGTTAAACCCCTGCATGCCAAGCTGCCTGCTGCCCCAGGTCTCAGCTCAGGCCTTTGAA  
 GGGGAGCTTCTGGAAGTTGTTTTCTCCTCTGCTTGGAGAGTTTGGCCTTGTCTGTCTTGGAAAGTGTGGGCAGC  
 CAGAGATGCCCCCAATCAGAGCTCACAGTGAAGTGAAGCCCTAAGCTTCACTGCAATAAAGAATGCATTGGTT  
 TCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 76**

MLKKMGEAVARVARKVNETVESGSDTLDLAECKLVSFPIGIYKVLNRNVSGQIHLITLANNELK  
SLTSKFMTTFSQLRELHLEGNFLHRLPSEVSALQHLKAIDLSRNQFQDFPEQLTALPALETIN  
LEENEIVDVPVEKLAAMPALRSINLRFNPLNAEVRVIAPPLIKFDMLMSPEGARAPLP

**Important features of the protein:**

**N-glycosylation sites.**

amino acids 17-21, 47-51

# **FIGURE 77**

CACCAACAAGCAATCGTTTCATGAGAAAGCCGTGCACCCGCTGCAGTTGGGCCATGTGGTCCGCATCGTATTCCAC  
TAGGTCCCCATTGTACACCAAGTACTGTCCCGGCGTCTCCAGCAGATGCCTGCAGCCTTCCACCTTCTCAAGCAG  
GGTGGTGTGAGTGCCTGCTTTCCTTCTCGCCTGGACCGGAGCCGTGCGGGAGGCACCCCCGGGGGTGGAGAA  
AAAGCCGGCTGGCCCTCGGAGGTGGTCTCGGCCCCCGCCCCACCGACTCCCTCCTCCCTCCAGAGGCGGGC  
GGCTCCGGCGGCAGCAGCGGCAGGCAGCAACGTAAGCGGGATGCTCTCCAGGCTGCTTTTCTGCTCGGTGAGCAA  
ATGGCTGAGCTGGTACATCTCGCTCTCCAGGTAGGAGATCTCGCGGGCGTCTCTATGAAGTCCGGTAGTTCTG  
GTAGACGTTGCGCTTCAGGTTCTGCGCCGTCTCCTCCGCGAGCCTGGATGCGGTGCCGGTCTCTGGAGGTC  
CCGGTCCCCATCCGACTGCTGCGAGAGCTGCTTCAGCTACAGCCGCGCTCAAAACCCCTGACTCCAGCTGCCG  
ACGCAGGCGGCTCGCCCCACTGTCCGACATCGCCATCGCCATTTCTCTCGGGTCTCACGCACTCACTGTCACTA  
TCGGCGCCGCGAGCCGCGCGGCTGTCTAGACCCACCAAGGCCAACCGAGCTCCTGGGCTGAGGAAGCAGGAATG  
GGAACGAGACGAGTACGCTGCGCCGGGTCTGAGCGTCAGACACTGCGCCTGCGCAAGTGGGCGGAGCGCAGACA  
TTGCGCCTTCGCGAGCAATGCTCGCGGATTGACGGGCGCATGCGCAAGATGAGCTATTGCGGAAGTGGGGAGGGA  
GGCCGAGAGAAATTTCCGTACTGCGCATGAACCGAGCGTGACGTTGAGGTTTGAATAACCGGCAAGAGTAAAG  
GCTGAACTAGCTTCTGAAAGCTTCGTAGGGCCCGAGCCCTGTGAGCCAGGTTCTGCGCCCACTAGGAGGTGT  
CATGCTGACTGCTTTTTTAAAGCCCTAGAATCCTTGGCTTCGGGTTTGGGTAAGCTCCGTTCTCGTTCTCAA  
GGCGCTTCCGCGAATCTCGCGGATTGACGGGCGCATGCTCGAGAGCCGCGCATCTCCTAGAGACTAGCTCCTGGT  
CTCGGCTAGGCGGCTTGGGGTCGCGCGTAACCTGGGGAGCCAGCCTGACGCCGGCGGACCCCGCTGTGATCCTG  
GCAACGATGGATGATGACTTGATGTTGGCACTGCGGCTTCAGGAGGAGTGGAACCTGACAGGAGCGGAGCGCGAT  
CATGCCCAGGAGTCCCTGTGCTAGTGGACGCGTCTGGGAGTTGGTGGACCCACACCGGACTTGCAGGCACTG  
TTGCTTCAGTTAACCAATCTTCTTGGGGCCAGCTGCGAGGCGCTCGAGGTGAAGTGGAGCGTGCGAATGACC  
CTGTGTGCTGGGATATGCAGCTATGAAGGGAAGGGTGAATGTGTTCCATCCGCTCTCAGCGAACCCCTTTTGAAG  
TTGAGGCCAAGAAAGGATCTTGTAGAGACCTCCTGCATGAAATGATACATGCCTATTTATTTGTCACTAATAAC  
GACAAAGACCGAGAAGGGCATGGTCCAGAATTTGTAAACATATGCATCGCATCAACAGCCTGACTGGAGCCAAT  
ATAACGGTATACCATCTTTTCAAGATGAGGTGGATGAGTATCGGCGACACTGGTGGCGTGCAATGGCCGTCG  
CAGCACAGGCCACCGTATTACGGCTATGTCAAACGAGCTACTAACAGGGAACCCCTCTGCTCATGACTATTGGTGG  
GCTGAGCACCAGAAAACCTGTGAGGCCTTACATAAAAAATCAAGGAACAGAGAATTACTCAAAAAAAGGCAAA  
GGAAAGGCAAACTAGGAAAGGAACAGTATTGGCCGCGAGAGAATAAAGGTACCTTCGTGTATATTCTTCTGATT  
TTTATGTGATGATGATGATGATAAGACAATACTGCTTCAGAGAACTGGTATTAAGATAAACTTAAGGATC  
GTTTCTGGTGTAGAGTCTTCAAGTGTAGACTTAAAGAAAAATCCCACTGTCCATGAAATGATGGTAGGAAAC  
AGACTTTGCTCTGTACAGAAGTAAGTAAAGTAGGAATAGTTTCCATGGATATTTTATTTTATTAACTTTTTT  
CAGTTTCTTTTATTCAAAGAAACAAATTCATCTCTGATAATATTGAGGTAAAGTTCTTTCCCTATCTTGA  
CTCACTGAGTTATTAGGAAACAGAGGCAAAAGATTGTCAAATAAAAAACAATAATCAAGTAACAATGCCCGG  
AATATACGTCCTAATACACCCCTTCTATCAGCTGGATTCTATCCAAGTGACTCTATTGATGTATGTATGTTCA  
TTCAAAGATGGGAAAGGATATGACATATATTTGCCAGTACTTCATCTTCAAGATTTACCCCTTTCTGTGAAG  
TTCAGAGTTACTGAAGATGCTTCTTCCCTTGGGAAGTTGTTGACCCAAGAACATAGGTTATATTTCCCAAATCTT  
TAATTATTGAGTGAAGAGCTATAGATGAATTGATATGGAAGACCGTATCTTCATTTTCGTGAGTAGAAGGAAA  
GATAAGAAATGAGGCAAGCAGATTTTCCCTCCTGGAATTACACATAAAGGACACTAAGCAATTTTCAAGGTAAATGT  
TGCCCTTGTGTTGGTCTTTGGCATGATAAGATTCTTATTTAAATATGAGAGAATTTTTTTTTATCCTTTATATT  
CTCTCAATATCAGAACTCCTGAATCTGAAGATTGCCCTCTCCCATTAATAGGATTGTATGGATGTAAGATGGA  
ATAAAATACTAGTTCTTCAATTTGAGAAAACGTACATTAGTTTAAATGTTTGTACTGTATTTCTTTTGAGTTGA  
GGCACTTACATAACAATCTTCTTGTCTTTTGGCAGATAAACCCAAACAGAGGTGAGGCCAGCTAGTAATCCCT  
TTTAGTGGGAAAGGATATGTTCTAGGAGAAACAAGCAATTTACCTTCACCTGGGAACTGATCACTTCACATGCC  
ATTAATAAAACCAAGATCTTTTAAATCAAAACCATTCAGCAATGCTGTAAGACCTAATTTCAAAATCAAGGTG  
AAATTTGAACAGAATGGTTCAAGTAAAAATCTCATCTGGTCTCCCTGCTGTTAGTAACAGTCACCAAAATGTT  
CTAAGCAACTACTTTCTAGAGTATCATTTGCCAACCAAAAGGCTTTTCAGAGGTGTGAATGGATCTCCAAGGATA  
AGTGTAAACAGTTGGCAACATCCCTAAAACTCAGTCTCTTCTAGTTCTCAGAGAAGGGTTTCATCTCTAAGATA  
TCCCTAAGAAATTTCTTCAAAAGTAACGGAATCAGCATCTGTGATGCCATCCAGGATGTGAGTGGGTCTGAAGAT  
ACATTCCTCAATAAACGACCTAGGCTAGAAGATAAAAAAAA

## **FIGURE 78**

MDDDLMLALRLQEEWNLQEAERDHAQESLSLVDASWELVDPTPDLQALFVQFNDQFFWGQLEA  
VEVKWSVRMTLCAGICSYEGKGMCSIRLSEPLLKLRPRKDLVETLLHEMIHAYLFVTNNDDKD  
REGHGPEFCKHMRINSLTGANITVYHTFHDEVDEYRRHWWRCNGPCQHRPPYYGYVKRATNR  
EPSAHDYWWAEHQKTCGGTYIKIKEPENYSKKGKGKAKLGKEPVLAAENKGTFFVYILLIFM

**Important features of the protein:**

**Signal peptide:**

amino acids 1-41

**N-glycosylation sites.**

amino acids 148-151, 217-220

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 184-187

**Casein kinase II phosphorylation sites.**

amino acids 30-33, 121-124, 154-157, 187-190, 192-195

**Tyrosine kinase phosphorylation site.**

amino acids 211-218

**N-myristoylation sites.**

amino acids 59-64, 85-90, 146-151

**Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 108-117

# **FIGURE 79**

CGGACGCGTGGGTGGCAACCAGGAGAAGCCAAACTTGGTCCCCCGGCTCGCGGAGTGCCTGCG  
AGCGGTGCTCATGGCGCTCTATGAGGTCTTCTCTCACCCGGTCGAGCGCAGTTACCGCGCGGG  
GCTCTGCTCCAAAGCCGCGCTGTTCTGCTGCTGGCCGCTGCGCTCACGTACATCCCGCCGCT  
GCTGGTGGCCTTCCGGAGCCACGGGTTTTGGCTGAAGCGGAGCAGCTACGAGGAGCAGCCGAC  
CGTGCGCTTCCAACACCAGGTGCTGCTCGTGGCCCTGCTCGGACCCGAAAGCGACGGGTTCTT  
CGCTGGAGCACGTTCCCCGCCTTCAACCGGCTGCAAGGGGATCGCTGCGCGTCCCGCTCGT  
TTCGACTAGAGAAGAAGACAGGAACCAGGATGGGAAGACGGACATGTTACATTTTAAGCTGGA  
GCTTCCCCTGCAGTCCACGGAGCAGCTTCTCGGTGTGCAGCTCATCTGACTTTCTCCTATCG  
ATTACACAGGATGGCGACCCTCGTGATGCAGAGCATGGCGTTTCTCCAGTCTCCTTTCTCTGT  
CCCCGGATCCCAGTTATACGTGAACGGAGACCTGAGGCTGCAGCAGAAGCAGCCGCTGAGCTG  
TGGTGGCCTAGATGCCCCGATACAACATATCCGTGATCAACGGGACCAGCCCCTTTGCCTATGA  
CTACGACCTCACCCATATTGTTGCTGCCTACCAGGAGAGGAACGTTACCACCGTCTGAATGA  
TCCCAACCCCATCTGGCTGGTGGGCGAGGCGCAGATGCTCCATTTGTGATTAATGCTATCAT  
CCGATACCCCTGTGGAAGTCATTTCTTATCAGCCAGGATTCTGGGAGATGGTAAAGTTCGCCTG  
GGTACAGTATGTGAGCATCCTGCTTATCTTCTCTGGGTGTTTGAAGAATCAAGATCTTCGT  
GTTTCAGAATCAGGTGGTGACCACCATTCCTGTGACAGTGACGCCCCGGGGAGACTTGTGTAA  
GGAGCACTTATCTTAGAAAGGCCATTTCTGAAGACTCAGCAGGACCGTGGCTGCCTCATTGTC  
ATCTTCTGGGAACATCTTAGGACCTTTTGAAGAGCCAGCGGACACCTGCGGGCTTGTGTGC  
TTTTCCCTCAGAGACAACGGTTCTTTCCGGTTTTGCTCTACACAGTTCGGTATCTTCAGAGCT  
CCTGCAGAATTGTGAGGACTAGTTTGTGGAAGGTCTGAGAGTTCCTGGAGGCTATAATTAG  
CTTTTGGGTTTTCTTCTTTGCCTTAGCGTTGAATTTGAGGAGAAAATTGCAGTCAGTTCAG  
ACATCTTGAAAAGAGTCCCATCTCTGGTCAAGCAGAGACTTTCTCTGTTGAACTGAGGAAC  
ACACTGTGCATTTCTTCTTCTGTTGTGAGCCACTCTTACTCTTTTCAGGGCTCTCTTGTGAC  
AAACATGCCAATCACTAGCACTTTGCACCCCTGGGCTTCTCCATTTCCCATTCACAGCTTTGA  
TTTCCAGAGCTGAGGCCTTTAACTGGAGACCTGGAGGGGCGAGGGCCCAAGGGCAAGGGCCGCA  
TTAGCACAGGCAATCAGGGAGGGCCGCTGAAGGACACTTGGACCGTCCACCTGCCCCAGCCCA  
ACAGTCAGTCATCTGTCATCAGCTCAGCTGAGCAGCCCTGGATCTTTGCCGTACTGTGACTGG  
GCTCTTTGCCCTATTTTTCCCTCTGTCTGTGCCCCCTGGATGGCAGGCTGAAGTCAGAGGGGCT  
GTTTCATTTCTCAGCCCCCTCAGCAGCACTGGGGGAAGAAAGCATTTGTCAACAGGTTCTTTTC  
TGGCCCTCACCCAACAGCCTGGGCACTTGGCCCTCCTCCTCCTTGACAGCCCTCCCCCTTCTT  
GCAAAGGACAGGGGCGACAGGGGTTGGTGTGGGATTGGCTCCCGCTGCCTGACAACCACAAG  
TTTATTTGGAAGGCTAGCGGAAGCCCAGCGGCTGGCGTTTCCCTTGACTAAGGAACAGGGTG  
CCCATCAGAGTGGGGCGGCGAGCTTTGGGAAGGACACAAGAAGCAGTAAGAGTGTAAGAGGA  
TGCTGGCCTGGGCAGGCCAGTCCAGCCTGGCCACTAGCAGAATACCAAGCAGTCCAGTGGATT  
ACCCTCGTGGCTAAGCAAGTGTCTGCAGGAGCAGAGATGGCTGGAAGGGGCTCTGCACACGG  
AAGATGGCTTGTTCAGCCCATTCACCTCCTGAGGATGTGGGCAGTCTCCTCCAAGAACACATG  
GAGCTGCTTCTTGATCCCAAGCAGGTCAATTGCCACTGGAAGGACATGGCCCCGGTGATCCATG  
CTTCATGCCACCCAGAAACACACCCCTCAGTGTGTGCCTCAGTTTACTTTGGAGATCAGTTG  
TCGTTTTTAGTGCTCCTTTAGGCTTACTAAAACAGTTTTTGGAAACAAAGCTATTTTGAAGTAT  
TCAAGCAGAGGAATTCCCTAACACTGACCCCTTGTCTTTTTTTAATATTCAGGCTGTTTTAT  
ATGCCTAAATTTTTTCTTAAGATCTAAACGAAAAATAGTTTCTTGTTTAAATTCACATAAGG  
CAATGAGATATGGAAGATGACAAGATACGTATAAACATTGGTTTTGCATCTTATTAAATTATT  
CTAATGCAAACTTGTATAAAGAACCCATGATGTTTTGTAACTTTCTAATTAAAAATGTTCAA  
ATGAG

**FIGURE 80**

MALYEVFSHPVERSYRAGLCSKAALFLLLAALTYIPPLLVAFRSHGFWLKRSSYEEQPTVRF  
QHQVLLVALLGPESDGFLAWSTFPAPFNRLQGDRLRVPLVSTREEDRNQDGKTDMLHFKLELPL  
QSTEHLVGLVQLILTFSYRLHRMATLVMQSM AFLQSSFPVPGSQLYVNGDLRLQKQPLSCGGL  
DARYNISVINGTSPFAYDYDLTHIVAAYQERNVTTVLNDPNPIWLVGRAADAPFVINAIIRYP  
VEVISYQPGFWEMVKFAWVQYVSILLIFLWVFERIKIFVFQVVTIPVTVTIPRGDLCKEHL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-34

**Transmembrane domain:**

amino acids 268-284

**N-glycosylation sites.**

amino acids 194-198, 199-203, 221-225

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 51-55

**Tyrosine kinase phosphorylation site.**

amino acids 250-259

**N-myristoylation site.**

amino acids 187-193

**Cell attachment sequence.**

amino acids 307-310

**FIGURE 81**

GCCGGGAGCTTCCCTGATGGTGCCGCCGCTCCGAGCCGGGGAGGAGCTGCCAGGGGCCAGCTGGGCAGGAGCCT  
GGGTCCGCTGCTGCTGCTCCTGGCGTTGGGACACACGTGGACCTACAGAGAGGAGCCGGAGGACGGCGACAGAGA  
AATCTGCTCAGAGAGCAAAATCGCGACGACTAAATACCCGTGCTGAAGTCTTCAGGCGAGCTCACCACATGCTA  
CAGGAAAAAGTGCTGCAAAGGATATAAATTTGTTCTTGGACAATGCATCCAGAAGATTACGACGTTTGTGCCGA  
GGCTCCCTGTGAACAGCAGTGCCAGGACAACCTTTGGCCGAGTGCTGTGTACTTGTATCCGGGATACCGGATATGA  
CCGGGAGAGACACCCGAAGCGGGAGAAGCCATACTGTCTGGATATTGATGAGTGTGCCAGCAGCAATGGGACGCT  
GTGTGCCACATCTGCATCAATACCTTTGGGCGCTACCGCTGCGAGTGCCGGGAGGCTACATCCGGGAAGATGA  
TGGGAAGACATGTACCAGGGGAGACAAATATCCCAATGACACTGGCCATGAGAAGTCTGAGAACATGGTGAAAGC  
CGGAACCTTGCTGTGCCACATGCAAGGAGTTCTACCAGATGAAGCAGACCGTGCTGCAGCTGAAGCAAAAGATTGC  
TCTGCTCCCTCAACAATGCAGCTGACCTGGGCAAGTATATCACTGGTGACAAGGTGCTGGCCTCAACACCTACCT  
TCCAGGACCTCCTGGCCTGCCTGGGGGCCAGGGCCCTCCCGGCTCACCAGGACCAAAGGGAGGCCAGGCTTCCC  
CGGTATGCCAGGCCCTCCTGGGCGAGCCCGGCCACGGGGCTCAATGGGACCCATGGGACCATCTCCTGATCTGTC  
CCACATTAAGCAAGGCCGAGGGGCCCTGTGGGTCCACCAGGGGCACCAGGAAGAGATGGTTCTAAGGGGGAGAG  
AGGAGCGCTGGGCCCAGAGGGTCTCCAGGACCCCTGGTTCTTTGACTTCTGCTACTTATGCTGGCTGACAT  
CCGCAATGACATCACTGAGCTGCAGGAAAAGGTGTTGGGCGACCGGACTCACTCTTCAGCAGAGGAGTTCCCTTT  
ACCTCAGGAATTTCCAGCTACCCAGAAGCCATGGACCTGGGCTCTGGAGATGACCATCCAAGAAGAACTGAGAC  
AAGAGACTTGAGAGCCCCAGAGACTTCTACCATAGCACATCCCAACCCGTCACGCCAAAGGAAGAGAAAGAT  
CAACTCAGCTGCAGTATAAACCATCTAAAGAGAAGAAAGACCCTGGAGACCTAGAAAACATACATTTTCTCTTC  
TCTTCTCCTGACGCTCTCTCCACTCCTCTTCTTCCAATACGATGCTATTTTTCAGAGTCCCTCCTAGGCCCTGCAG  
ACATGAGGGAGTGAATGATTGATTTACCTGCTTCTCACTAAGAGTCCATTGGGGTGGTTTGCATTGTAACTTTTC  
TTTTACATCCTATTTTCCAGGAACCTTTGGATTAAAGTACTCTCACAGTGTCTTAAATCATAAATCTTGAAGTT  
AAATTTGGCAGAGTATCAAAAGGGGAAAATGACAAAGTGAGCTCTAAGAAAATGTGAGGCTACTTCTAAGATGT  
GTGTTCAACAATAGACCATAACTCCTCTAGTATCAAAATTGGGGCTCTTCAGTTAAAAGGGGTGGGGAGGACAAA  
CGTGTCGATGTGCTTTGGTGGAGAATTTTTCTTGTGCTTCTAGTAGACTTTAAATATGTATCCCTTTGTCAA  
ACCTTGTTTTCCAAATTCAATTAAAGAGAGGAGAGAATTGAATGGCGTTTAGAGAAGATAGAAAAGAATCACAGT  
CATATATTTACTGTTATATAGATTGCCACATTTCTAAAATTCAAATACGGTGCTTAAGGTTTCATGCCATGCTTAT  
CTGTAAGTATCCTATTTAGGGAAGAAGATTAACTCTCTTTTCAAAAAACAAAGTGAAATGCCTGGATTACAT  
TAAAACAATGGGCTCTCGTTTCTATAATATTTTAAAGCTGTTTAATCAACAGTGGAGTCTGCTCTATAAATATA  
GATTATTTGTTCAATAAATGGCTGAGCTTAGAGAGAGGTGCAGAATTCCTGGTCTGAGCAGGTGCCCAGAAGG  
TACCATTAGGTGCCATGATCCAGGCTGAACCAATATACAGTGGGGCTGAAGTCTGCAAGGAGGTGCTGGCTTGG  
GCTGACCTCACTAATGCCATCAGCAGCGGTAGGTAAATTTTTCTCCTTGGGTATTACAAGTTTTTGTCTGGAGC  
CAACCAAGCTTGCCACCAACATATTGAGAGTAATACACTATTGAAAGTTATCTTGGATGGGAGAAAAAAAATA  
GTGGTTTTCTTGTGTTGCAAAACTTCTTCCCTATTCTCATTTTTTCTTAATTTCTTTAATTTAGTCCAAGTTC  
CAGTTCTTTAGGCCCTCTCTTTGATTATTTTTCCCTGCACTGTGAGAAGCAGTTCAGAAAAAGGTCTATATCTC  
CACCTCCTAGTGAGTTAGAGTGTCTTCTCAGAGCACCTCTGGGTGGCAAAGGGAAGCATGTTCTGCCAAGGTTT  
GCTGTGGATTGAGAAGCACCAGGAGCAAGAGACCAGAAGGATGATCTGCTCCTTTGTAACGTTGTTGAGGGCCCT  
CTTGTTCCTCAATGAGCAGCTTATAGGTTACTCACAGTCCACTTTCTCACTGGACACACAAGTGGCTTTTATCT  
ACCTTTGCGGGAGATTTTCACTCTCCTGCAATGATCGTTCTCACACTCATATTAGCTCATGTTGGAATTTCCCA  
TCCTGCCATGTCTTTCCCATTTCTTTTTGGCTTTTTTGGCTCCACCTTTTAGCCACATCATTTAACTCCACTA  
CTGTGAAAGCTTGCTTAAAGAAAATCCCTCTTGGCCGGGTGTGGTAGCCACGCCTCTAATCCCAGCACTTTGGG  
AGGCTGAGGCGGGGAGATCACAAGGTCAGGAGATCGAGACCAGCCTGACCAACATGGTGAAACCCGTCTCTACT  
AAAAATACAAAAATTAGCTGGGCGTGTGGCACACACCTGTAATCCAGCTACTCAGGAGGCTGAGGCAGGAGAA  
TTACTTTAACTGCGGGGGAGCCTAGATTGCGCTACTGCCTCCAGCCTAGGCAACAGAGGGAGACTCTGTCTC  
ATTA AAAA

## **FIGURE 82**

MVPPPPSRGGAARGQLGRSLGPILLLLLALGHTWTYREEPEDGDREICSESKIATTKYPCLKSS  
GELTTCYRKCKCKGYKFVLGQCIPEDYDVCAEAPCEQQCTDNFGRVLCTCYPGYRYDRERHRK  
REKPYCLDIDECASSNGTLCAHICINTLGSYRCECREGYIREDDGKTCTRGDKYPNDTGHEKS  
ENMVKAGTCCATCKEFYQMKQTVLQLKQKIALLPNNAADLGKYITGDKVLASNTYLPGPPGLP  
GGQGPPGSPGPKGSPGFPMPGPPGQPGPRGSMGPMGPPSPDLSHIKQRRGPVGPAPGRDG  
SKGERGAPGPRGSPGPPGSPGDFLLMLADIRNDITELQEKVFGHRTTHSSAEFFPLPQEFPSYP  
EAMDLGSGDDHPRRTETRDLRAPRDFYP

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-34

#### **N-glycosylation sites.**

amino acids 142-148, 182-188

#### **Tyrosine kinase phosphorylation site.**

amino acids 125-132

#### **N-myristoylation sites.**

amino acids 10-16, 143-149, 155-161, 196-202, 250-256

#### **Amidation site.**

amino acids 299-303

#### **Aspartic acid and asparagine hydroxylation site.**

amino acids 150-162

#### **Cell attachment sequence.**

amino acids 176-179

#### **Clq domain proteins.**

amino acids 247-280

#### **Calcium-binding EGF-like domain proteins pattern proteins.**

amino acids 144-165



**FIGURE 83**

ATCTGAGTGAGCTAACTGACACAATGAACTGTCAGGCATGTTTCTGCTCCTCTCTCTGGCTC  
TTTTCTGCTTTTTTAACAGGTGTCTTCAGTCAGGGAGGACAGGTTGACTGTGGTGAGTTCCAGG  
ACCCCAAGGTCTACTGCACTCGGGAATCTAACCACACTGTGGCTCTGATGGCCAGACATATG  
GCAATAAATGTGCCTTCTGTAAGGCCATAGTGAAAAGTGGTGGAAAGATTAGCCTAAAGCATC  
CTGGAAAATGCTTGAGTAAAGCCAATGTTTCTTGGTGACTTGCCAGCTTTTGCAGCCTTCTTT  
TCTCACTTCTGCTTATACTTTTGCTGGTGGATTCCTTTAATTCATAAAGACATACCTACTCTG  
CCTGGGTCTTGAGGAGTTCAATGTATGTCTATTTCTCTTGATTCACCTGTCAATAAAGTACATTC  
TGCAAAAGCAAAA

**FIGURE 84**

MKLSGMFLLLSLALFCFLTGVFSQGGQVDCGEFQDPKVYCTRESNP HCGSDGQTYGNKCAFCK  
AIVKSGGKISLKHPGKC

**Important features of the protein:**

**Signal peptide:**

amino acids 1-23

**N-myristoylation sites.**

amino acids 26-32, 52-58, 56-62, 69-75

**Kazal serine protease inhibitors family signature.**

amino acids 40-63

# **FIGURE 85**

GGAGCAGACACACAGACCCGGGCCGGAGGCCCTCTTCTAGCCCTGCGGGAACCGGACAGTTCC  
 CCCAACTGGGGACTCTGGAACCACAGCTCCTAAATCATCAAATTTCTCAAGCTTTTTTTTTTCCC  
 TCTCTTCGTCCCAGCCATCCCAGTCTTCTTCTTTTTTTTTTTTTTTTTTTTTTTTTTCCC  
 TCGTCCCTGTCTATTATGAAAGTGGTCACGCCATTCAATATTAAGACTTGGAGGGAATTGGGGA  
 AAGAAAAGAAAGAATCTAAAAGAAAGAGAAGCGACCGGTGCTTTTAAGGGTGTCTAATTTTCAA  
 AAGAGACGTCTGGGAGTATTTTGCTCTGGGCGTTTGGAGCAACTTCGCGGACAGCGGAGCTCG  
 CCCAGCATGGATGTTCCAGGTTTACAGGCGCTTTCTTCTGAGAACGACCCCTGGCCCTGAACG  
 TCAGAGCCGGGGACGAAGGCCCCCGGAGGCTGCTGCGAGCTCCGCGCTTCCCTTCGCGCCCTT  
 CCGCGCCGCTCGCGCCGGCGCCGGCTCCACCCCGCGCGCCGCTCCACCAGTCCCGATGCG  
 AGGCGCCCGCGCCGGGGCCACTCGGGCTGCGGCTGATGATGCCCGGGCGCCGGGGGGCGCTGC  
 GCGAGCCTGGCGGCTGCGGATCCTGCCTGGGGGTGGCGCTGGCCCTGCTGTTGCTGCTACTGC  
 CCGCCTGCTGCCCCGTGCGGGCGCAGAACGACACGGAGCCCATCGTGCTGGAGGGCAAGTGCC  
 TGGTGGTGTGCGACTCCAGCCCCGTGCGCGGACGGCGCCGTCACTCCTCCCTAGGCATCTCCG  
 TGCGCTCCGGCAGCGCCAAGGTGGCTTCTCCGCCACGCGGAGCACCACGAGCCGTCCG  
 AGATGAGCAACCGCACCATGACCATCTATTTTCGACCAGGTATTAGTAAATATTGGCAACCCT  
 TTGATCTTGCTTCCAGTATATTTGTAGCACCGAGAAAAGGGATTTATAGCTTCAGCTTCCACG  
 TGGTCAAAGTGTATAACAGACAAACCATCCAGGTCAAGTTTAATGCAGAATGGCTACCCAGTGA  
 TCTCGGCCCTTTGCAGGAGACCAGGATGTCACCAGAGAAGCTGCTAGCAATGGCGTGTGCTGC  
 TCATGGAAGGGAAGACAAAGTGCATCTCAAACCTTGAGAGAGGCAACCTCATGGGGGGCTGGA  
 AATACTCCACATTCTCGGGCTTCTTGGTGTTCCTCTATAACACAGAGCCCCCTAGATGGTG  
 GGGGAATGGCAAACCTGGACCCAGGACTCCGCCCTTTAAACACCCCTGAACCTTACTGGAATTGG  
 ACACCTTGTTCACACCTCCGTGAGACTGTTGCAGTAGAAGAATGATTTCCCTTTGAAACCTCC  
 AGTACTTTTGTTTTGTGTTTGTGGAATACTGACAAATTCCTCGGGAACCTGGCCTCTAATTAGT  
 TTTAGATGACAAGGTCTTAAGGAGAAATGAAATTTATCGATTTGAGCAATTTGTACCTGTGATT  
 GTAAAGTCAATATCGGATTTTATTGTTGGGACCATGGACCTCTTTTGTGTTGTATGTTGTATTG  
 TCGTCCCAACGGAAGGAGAGCTCCTGACTCCAGGATGGGCTGCAGGTTGCAGTCAGGGCTGA  
 AGTAGGAGCCCGACAAAGAACCACTGCTGGACAGTCCCTGACATGTGTTCTGTGTGTGTCTG  
 TATAGCCTTAAGAAAAAGAAATGGCTTCACTTTTCATTCTGTATTCTTCCCCCACCATGTGGCT  
 GGGAGGACTTGGGAGGGGGATGGGGACATTGGGAACCTGTCAAGAAGTGCTTTATCCAGAGAA  
 GCAAATTTTGCACGATTTGGACTGCAATTTTGTGTTTGTATTGTTTGTGTTTTTCTTGAAAAG  
 CTTTACTTTTCTTTCACACTCAGCTCTCCCTCCTCAACCCCACTTTTATTTTTCTTGCTGGG  
 GTTGAGGAGAGAAAATATAGAATTCTTGATAAGACCAAACAAAACAAACATTAAAATACCT  
 GTATGTTTGTGTTTGTAGACGAGACCAACTAAACAAAAAGTATCTGTTTATCAAAGTAAAAGTA  
 ACACAAATGGACAATTTCTGCTTATTCTCTCAAAGAGATTCTAAGATGCACCTTTAGAACTATTA  
 ATAGCAACCTGCATTTTGTGTTTAAATTTATACTTCAGAAATCCTTTAAGAACCTGGTGTTCCTGA  
 GTGGTCTGAATCATATAAGTTGGTAATGGAAGCTGTAATGACCAAGTCCCTTAAACATACTA  
 TGTCTTTGCCACGTGTGCTGTGACTTCTCTGTGGGTGATTTAATTTATTTGGATCCACCTCTG  
 AGTGAGCGCACAGTGATCAGGTGCTTCAAAGCCAACAGACCAGCTCCTCTTCTCCGGATCCT  
 CTTTGTGATCTGCCCAGGAAAGGGATGCATTGACACTCTCCTGCATGCACCTGGCGAGAAGCCA  
 CCTGAAAGTCACTGTGGTTAAAGATATTGGTGGAGGTACCCAGGAGCACTGTTACAAATCCT  
 TCTTGTGTTTGGCATCTCGTACAACATTATTAAGACACAGCTGAGAGTTGATGGGTGTGTAATG  
 CATATGCCAAGGAAATGTCACTAATCCCAAAGCAATCAAAAAGGAGACCTCAAACCAGATGTT  
 AATTTGTCTTTGTGTAACAATGTAACCAAAATATTGATGATAAAAGTCATAATTTAAGATT  
 AGAATAAAATGGGTTTGATGTCTGGCAAAAAAAAAAAAAAAAAA

**FIGURE 86**

MQAPGRGPLGLRLMMPGRRGALREPGGCGSCLGVALALLLLLLLPACCPVRAQNDTEPIVLEGK  
CLVVCDSPPSADGAVTSSLGISVRSKSAKVAFSATRSTNHEPSEMSNRTMTIYFDQVLVNIGN  
HFDLASSIFVAPRKGIYSFSFHVVKVYNRQTIQVSLMQNGYPVISAFAGDQDVTREAASNGVL  
LLMEREDKVHLKLERGNLMGGWKYSTFSGFLVFPL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-48

**N-glycosylation sites.**

amino acids 53-57, 110-114

**N-myristoylation sites.**

amino acids 26-32, 27-33, 29-35, 33-39, 76-82, 205-211

**Amidation site.**

amino acids 16-20

**Clq domain signature.**

amino acids 117-148

**Clq domain proteins.**

amino acids 115-149

# **FIGURE 87**

AGGGCCCCGCGGTGGAGAGAGCGACGCCCGAGGGGATGGCGGCAGCGTCCCGGAGCGCCTCTG  
GCTGGGCGCTACTGCTGCTGGTGGCACTTTGGCAGCAGCGCGCGGCCGGCTCCGGCGTCTTCC  
AGCTGCAGCTGCAGGAGTTCATCAACGAGCGCGGCGTACTGGCCAGTGGGCGGCCTTGCGAGC  
CCGGCTGCCGACTTTCTTCCGCGTCTGCCCTAAGCACTTCCAGGCGGTCTGCTCGCCCGGAC  
CCTGCACCTTCGGGACCGTCTCCACGCCGGTATTGGGCACCAACTCCTTCGCTGTCCGGGACG  
ACAGTAGCGGCGGGGGCGCAACCCTCTCCAAGTCCCTTCAATTTACCTGGCCGGGTACCT  
TCTCGCTCATCATCGAAGCTTGGCAGCGGCCAGGAGACGACCTGCGGCCAGAGGCCTTGCCAC  
CAGATGCACTCATCAGCAAGATCGCCATCCAGGGCTCCCTAGCTGTGGGTGAGAACTGGTTAT  
TGGATGAGCAAACCAGCACCCCTCACAAGGTGCGCTACTCTTACCGGGTCACTGTCAGTGACA  
ACTACTATGGAGACAAGTGTCTCCCGCTGTGCAAGAAGCGCAATGACCACCTTCGGCCACTATG  
TGTGCCAGCCAGATGGCAACTTGTCTTGCCTGCCCTGCCCGTTGGACTGGGGAATATTGCCAACAGC  
CTATCTGTCTTTTCGGGCTGTCTGAACAGAATGGCTACTGCAGCAAGCCAGCAGAGTGCCTCT  
GCCGCCAGGCTGGCAGGGCGGCTGTGTAACGAATGCATCCCCACAATGGCTGTGCGCCACG  
GCACCTGCAGCACTCCCTGGCAATGTACTTGTGATGAGGGCTGGGGAGGCCTGTTTTGTGACC  
AAGATCTCAACTACTGCACCCACCACTCCCATGCAAGAATGGGGCAACGTGCTCCAACAGTG  
GGCAGCGAAGCTACACCTGCACCTGTGCGCCAGGCTACACTGGTGTGGACTGTGAGCTGGAGC  
TCAGCGAGTGTGACAGCAACCCCTGTGCAATGGAGGCAGCTGTAAGGACCAGGAGGATGGCT  
ACCACTGCCTGTGTCTTCCGGGCTACTATGGCCTGCACTGTGAACACAGCACCTTGAGCTGCG  
CCGACTCCCCCTGCTTCAATGGGGGCTCCTGCCGGGAGCGCAACCAGGGGGCCAACCTATGCTT  
GTGAATGTCCCCCAACTTCACCGGCTCCAAGTGGCAGAGAAAGTGGACAGGTGCACAGCA  
ACCCCTGTGCCAACGGGGGACAGTGCCTGAACCGAGGTCCAAGCCGCATGTGCCGCTGCCGTC  
CTGGATTACGGGCACCTACTGTGAAGTCCACGTCAGCGACTGTGCCCCGTAACCCCTTGCGCCC  
ACGGTGGCACTTGCCATGACCTGGAGAATGGGCTCATGTGCACCTGCCCTGCCGGCTTCTCTG  
GCCGACGCTGTGAGGTGCGGACATCCATCGATGCCTGTGCCTCGAGTCCCTGCTTCAACAGGG  
CCACCTGCTACACCGACCTCTCCACAGACACCTTTGTGTGCAACTGCCCTTATGGCTTTGTGG  
GCAGCCGCTGCGAGTTCCCCGTGGGCTTGCCGCCAGCTTCCCCTGGGTGGCCGTCTCGCTGG  
GTGTGGGCTGGCAGTGTCTGCTGGTACTGCTGGGCATGGTGGCAGTGGCTGTGCGGCAGCTGC  
GGCTTCGACGGCCGGACGACGGCAGCAGGGAAGCCATGAACAAGTGTGCGGACTTCCAGAAGG  
ACAACCTGATTCTGCGCGCCAGCTTAAAAACACAAACCAGAAGAAGGAGCTGGAAGTGGACT  
GTGGCCTGGACAAGTCCAAGTGTGGCAACAGCAAAACCACACATTGGACTATAATCTGGCCC  
CAGGGCCCCCTGGGGCGGGGACCATGCCAGGAAAGTTTCCCCACAGTGACAAGAGCTTAGGAG  
AGAAGGCGCCACTGCGGTTACACAGTGAAAAGCCAGAGTGTGCGGATATCAGCGATATGCTCCC  
CCAGGGACTCCATGTACCAGTCTGTGTGTTTGATATCAGAGGAGAGGAATGAATGTGTCAATTG  
CCACGGAGGTATAAGGCAGGAGCCTACCTGGACATCCCTGCTCAGCCCCGCGGCTGGACCTTC  
CTTCTGCATTGTTTACA

## **FIGURE 88**

MAAASRSASGWALLLLVALWQQRAGSGVFQLQLQEFINERGVLASGRPCEPGCRTFFRVCLK  
HFQAVVSPGPCTFGTVSTPVLGTNSFAVRDDSSGGGRNPLQLPFNFTWPGTFSLI IEAWHAPG  
DDLRLPEALPPDALISKIAIQGSLAVGQNWLLDEQTSTLTRLRYSYRVICSDNYYGDNCSRLCK  
KRNDHFGHYVCQPDGNLSCLPGWTGEYCQQPICLSGCHEQNGYCSKPAECLCRPGWQGRLCNE  
CIPHNGCRHGTCSTPWQCTCDEGWGGLFCDQDLNLYCTHHSPCKNGATCSNSGQRSYTCRCRPG  
YTGVDCELELSECDNPNCRNGGSKDQEDGYHCLCPPGYGLHCEHSTLSCADSPCFNGGSCR  
ERNQGANAYACEPPNFTGSNCEKKVDRCTSNPCANGGQCLNRGPPSRMCRCPGFTGTYCELHV  
SDCARNPCAHHGTCHDLENGLMCTCPAGFSGRRCEVRTSIDACASSPCFNRTATCYTDLSTDTF  
VCNCPYGFVGSRCFEPVGLPPSFPWVAVSLGVGLAVLLVLLGMVAVAVRQLRLRRPDDGSREA  
MNNLSDFQKDNLI PAAQLKNTNQKKELEVDCGLDKSNCGKQQNHTLDYNLAPGPLGRGTMPGK  
FPHSDKSLGEKAPLRLHSEKPECRISAICSPRDSMYQSVCLISEERNECVIATEV

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-26

#### **Transmembrane domain:**

amino acids 530-552

#### **N-glycosylation sites.**

amino acids 108-112, 183-187, 205-209, 393-397, 570-574, 610-614

#### **Glycosaminoglycan attachment site.**

amino acids 96-100

#### **Tyrosine kinase phosphorylation site.**

amino acids 340-347

#### **N-myristoylation sites.**

amino acids 42-48, 204-210, 258-264, 277-283, 297-303, 383-389,  
415-421, 461-467, 522-528, 535-541, 563-569, 599-605, 625-631

#### **Amidation site.**

amino acids 471-475

#### **Aspartic acid and asparagine hydroxylation site.**

amino acids 339-351

#### **EGF-like domain cysteine pattern signature.**

amino acids 173-185, 206-218, 239-251, 270-282, 310-322, 348-360,  
388-400, 426-438, 464-476, 506-518

#### **Calcium-binding EGF-like:**

amino acids 224-245, 255-276, 295-316, 333-354, 373-394, 411-432,  
449-470

**FIGURE 89**

GTCTCCGCGTCACAGGAACTTCAGCACCCACAGGGCGGACAGCGCTCCCCTCTACCTGGAGAC  
 TTGACTCCCGCGCGCCCCAACCCCTGCTTATCCCTTGACCGTCGAGTGTGAGAGATCCTGCAGC  
 CGCCCAGTCCCGGCCCTCTCCCGCCCCACACCCACCCCTCCTGGCTCTTCTGTTTTTACTCC  
 TCCTTTTTCATTACATAACAAAAGCTACAGCTCCAGGAGCCCAGCGCCGGGCTGTGACCCAAGCC  
 GAGCGTGGAAGAATGGGGTTCTCGGGACCGGCACTTGGAATTCTGGTGTAGTGCTCCCGATT  
 CAAGCTTTCCCCAAACCTGGAGGAAGCCAAGACAAATCTCTACATAATAGAGAATTAAGTGCA  
 GAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAAGAAGACAAGATTAAAAAACATATCCT  
 CCAGAAAACAAGCCAGGTCAGAGCAACTATTCTTTTGTGATAACTTGAACCTGCTAAAGGCA  
 ATAACAGAAAAGGAAAAAATTGAGAAAGAAAGACAATCTATAAGAAGCTCCCCACTTGATAAT  
 AAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAACTGATCGATGATTATGACTCT  
 ACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCATCAACTAGACGGG  
 ACTCCTTTAACCCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTTATGAAGAAAATGAC  
 AGAGCCGTGTTTGACAAGATTGTTTCTAACTACTTAATCTCGGCCTTATCACAGAAAGCCAA  
 GCACATACACTGGAAGATGAAGTAGCAGAGGTTTTACAAAAATTAATCTCAAAGGAAGCCAA  
 AATTATGAGGAGGATCCCAATAAGCCCACAAGCTGGACTGAGAATCAGGCTGGAAAAATACCA  
 GAGAAAGTGACTCCAATGGCAGCAATTCAAGATGGTCTTGCTAAGGGAGAAAACGATGAAACA  
 GTATCTAACACATTAACTTGACAAATGGCTTGAAAGGAGAACTAAAACCTACAGTGAAGAC  
 AACTTTGAGGAACTCCAATATTTCCCAAATTTCTATGCGCTACTGAAAAGTATTGATTGAGAA  
 AAAGAAGCAAAAGAGAAAGAAACACTGATTACTATCATGAAAACACTGATTGACTTTGTGAAG  
 ATGATGGTGAAATATGGAACAATATCTCCAGAAGAAGGTGTTTCTACCTTGAAAACCTGGAT  
 GAAATGATTGCTCTTCAGACCAAAAACAAGCTAGAAAAAAATGCTACTGACAATATAAGCAAG  
 CTTTTCCCAGCACCATCAGAGAAGAGTCATGAAGAAACAGACAGTACCAAGGAAGAAGCAGCT  
 AAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCCACAAAAGATGATAACTCCAACCCAGGA  
 GGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTATTTGGAAGCCATCAGAAAAAATATT  
 GAATGGTTGAAGAAACATGACAAAAGGGAAATAAAGAAGATTATGACCTTTCAAAGATGAGA  
 GACTTCATCAATAAACAGCTGATGCTTATGTGGAGAAAGGCATCCTTGACAAGGAAGAAGCC  
 GAGGCCATCAAGCGCATTTATAGCAGCCTGTAAAAAATGGCAAAAGATCCAGGAGTCTTTCAAC  
 TGTTTCAGAAAACATAATATAGCTTAAACACTTCTAATTCTGTGATTAAATTTTTTGACCC  
 AAGGGTTATTAGAAAGTGCTGAATTTACAGTAGTTAACCTTTTACAAGTGGTTAAAAACATAGC  
 TTTCTTCCCGTAAAAACTATCTGAAAGTAAAGTTGTATGTAAGCTGAAAAAAAAAAAAAAAAA  
 AAA

## **FIGURE 90**

MGFLGTGTWILVVLVLP IQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPENK  
PGQSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTKSG  
LDHKFQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTL  
EDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTMAAIQDGLAKGENDETVSNT  
LTLTNGLERRTKTYSEDNFEELQYFPNFIYALLKSIDSEKEAKEKETLITIMKTLDLDFVKMMVK  
YGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEEAAKMEK  
EYGS�KDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYDLSKMRDFIN  
KQADAYVEKGILDKEEAEAIKRIYSSL

**Important features:**

**N-glycosylation sites:**

amino acids 68-71, 346-349, 350-353

**Casein kinase II phosphorylation site:**

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-  
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-  
341, 369-372, 382-385, 386-389, 387-390

**N-myristoylation sites:**

amino acids 143-148, 239-244



**FIGURE 91**

TGCATCAGTGCCCAAGCCCAGGAGTTGACATTTCTCTGCCCAGCCATGGGCCTCACCCCT  
GCTCTTGCTGCTGCTCCTGGGACTAGAAGGTCAGGGCATAGTTGGCAGCCTCCCTGAGGTGCT  
GCAGGCACCCGTGGGAAGCTCCATTCTGGTGACGTGCCACTACAGGCTCCAGGATGTCAAAGC  
TCAGAAGGTGTGGTGCCGGTTCTTGCCGGAGGGGTGCCAGCCCCTGGTGTCTCAGCTGTGGA  
TCGCAGAGCTCCAGCGGGCAGGCGTACGTTTCTCACAGACCTGGGTGGGGGCCTGCTGCAGGT  
GGAAATGGTTACCCCTGCAGGAAGAGGATGCTGGCGAGTATGGCTGCATGGTGGATGGGGCCAG  
GGGGCCCCAGATTTTGACAGAGTCTCTCTGAACATACTGCCCCCAGAGGAAGAAGAAGAGAC  
CCATAAGATTGGCAGTCTGGCTGAGAACGCATTCTCAGACCCTGCAGGCAGTGCCAACCCCTT  
GGAACCCAGCCAGGATGAGAAGAGCATCCCCCTTGATCTGGGGTGCTGTGCTCCTGGTAGGTCT  
GCTGGTGGCAGCGGTGGTGCTGTTTGCTGTGATGGCCAAGAGGAAACAAGAATCCCTCCTCAG  
TGGTCCACCACGTCAGTGACTCTGGACCGGCTGCTGAATTGCCTTTGGATGTACCACACATTA  
GGCTTGACTCACCACTTCATTTGACAATACCACCTACACCAGCCTACCTCTTGATTCCCCAT  
CAGGAAAACCTTCACTCCCAGCTCCATCCTCATTGCCCCCTCTACCTCCTAAGGTCCTGGTCT  
GCTCCAAGCCTGTGACATATGCCACAGTAATCTTCCCGGGAGGGAACAAGGGTGGAGGGACCT  
CGTGTGGGCCAGCCCAGAATCCACCTAACAATCAGACTCCATCCAGCTAAGCTGCTCATCACA  
CTTTAACTCATGAGGACCATCCCTAGGGGTTCTGTGCATCCATCCAGCCAGCTCATGCCCTA  
GGATCCTTAGGATATCTGAGCAACCAGGGACTTTAAGATCTAATCCAATGTCCTAACTTTACT  
AGGGAAAGTGACGCTCAGACATGACTGAGATGTCTTGGGGAAGACCTCCCTGCACCCAACTCC  
CCCACTGGTTCTTCTACCATTACACACTGGGCTAAATAAACCTAATAATGATGTGCAAAAAA  
AA

## **FIGURE 92**

MGLTLLLLLLLLGLEGQGIVGSLPEVLQAPVGSSILVQCHYRLQDVKAQKVWCRFLPEGCQPLV  
SSAVDRRAPAGRRFTFLDLDGGGLLQVEMVTLQEEEDAGEYGCMVDGARGPQILHRVSLNILPPE  
EEEETHKIGSLAENAFSDPAGSANPLEPSQDEKSIPLIWGAVLLVGLLVAAVVLFAVMAKRKQ  
ESLLSGPPRQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 161-181

**N-myristoylation sites.**

amino acids 17-23, 172-178

**Amidation site.**

amino acids 73-79

# **FIGURE 93**

GGCGGCGTTGCCGGGCTCTCCGGAAGGAGACGTGGCGGCGGTTGGGCCGGTGATACCCGGGCG  
 CTTTATAGTCCCGCCGCTCCTCCTCCACCTCCTCCTCCTCCTCCTCCTCCTCCTGGGGCAGAG  
 GAGGTTGTGGCGGTGGCTGGAGAAAGCGGCGGCGGAGGATGAGGAAGGAGGCGGCGGCGTAC  
 GGAGTCTGGTCCCGGGCGGGCCGGTGTTACTGGTCCTCTGCGGCCTCCTGGAGGCGTCCGGCG  
 GCGGCCGAGCCCTTCTCAACTCAGCGATGACATCCCTTTCCGAGTCAACTGGCCCCGCCACCG  
 AGTTCTCTCTGCCCCAACCTGGAGTTTTATATAAGAAGATAATTATGTCATCATGACAACTG  
 CACATAAAGAAAAATATAAATGCATACTTCCCCTTGTGACAAGTGGGGATGAGGAAGAAGAAA  
 AGGATTATAAAGGCCCTAATCCAAGAGAGCTTTTGGAGCCACTATTTAAACAAAGCAGTTGTT  
 CCTACAGAATTGAGTCTTATTGGACTTACGAAGTATGTCATGGAAAACACATTCGGCAGTACC  
 ATGAAGAGAAAGAACTGGTCAGAAAATAAATATTACGAGTACTACCTTGGGAATATGTTGG  
 CCAAGAACCTTCTATTTGAAAAAGAACGAGAAGCAGAAGAAAAGGAAAAATCAAATGAGATT  
 CCACTAAAAATATCGAAGGTCAGATGACACCATACTATCCTGTGGGAATGGGAAATGGTACAC  
 CTTGTAGTTTGAAACAGAACCGGCCAGATCAAGTACTGTGATGTACATATGTCATCCTGAAT  
 CTAAGCATGAAATTCTTTCAGTAGCTGAAGTTACAACCTGTGAATATGAAGTTGTCAATTTGA  
 CACCACTCTTGTGCAGTCATCCTAAATATAGGTTTACAGCATCTCCTGTGAATGACATATTTT  
 GTCAATCACTGCCAGGATCTCCATTTAAGCCCCCTCACCTGAGGCAGCTGGAGCAGCAGGAAG  
 AAATACTAAGGGTGCCTTTTAGGAGAAATAAAGAGGGTGTGCGTTGGTGGAAATATGAATTCT  
 GCTATGGCAAACATGTACATCAATACCATGAGGACAAGGATAGTGGGAAAACCTCTGTGGTTG  
 TCGGGACATGGAACCAAGAAGAGCATATTGAATGGGCTAAGAAGAATACTGCTAGAGCTTATC  
 ATCTTCAAGACGATGGTACCCAGACAGTCAGGATGGTGTACATTTTTATGGAAATGGAGATA  
 TTTGTGATATAACTGACAAACCAAGACAGGTGACTGTAAACTAAAGTGCAAAGAATCAGATT  
 CACCTCATGCTGTTACTGTATATATGCTAGAGCCTCACTCCTGTCAATATATTCTTGGGGTTG  
 AATCTCCAGTGATCTGTAAATCTTAGATACAGCAGATGAAAATGGACTTCTTTCTCTCCCA  
 ACTAAAGGATATTAAAGTTAGGGGAAAGAAAAGATCATTGAAAGTCATGATAATTTCTGTCCC  
 ACTGTGTCTCATTATAGAGTTCTCAGCCATTGGACCTCTTCTAAAGGATGGTATAAAATGACT  
 CTCAACCACTTTGTGAATACATATGTGTATATAAGAGGTTATTGATAAACTTCTGAGGCAGAC  
 ATTTGTCTCGCTTTTTTTTCAATTTTTGTTGTGTCTTATAAACTGACTGTTTTTCTTTGCTTGA  
 TACTGTGATTCCAAAATAAATCTCATCCAAGCAAGTTAGAGTCCAGCCTAATCAAATGTCATA  
 ATTGTTGTACCTATTGAAAGTTTTTAAATAATAGATTTATTATGTAAATTATAGTATATGTAA  
 GTAGCTAATGAAGTAAAGATCATGAAGAAAGAAATTGATAGGTGTAAATGAGAGACCATGTAA  
 AATATGTAAATCTAGTACCTGAAATCCTTCAACAGATTTTTATATAGCAACTGCTCTCTGC  
 AAGTAGTTAAACTAGAACTGGGCACATGGTAGAGGCTCATATGGGAGTTGTCTCACCCTTG  
 TTAATCTCAAGAACTCTTATTTATAATAGGTTGCTTCTCTCTCAGAACTTTTTATCTATTACT  
 TTTTTCTTCTTATGAGTATGTTTACTCTCAGAGTATCTATCTGATGTAGACAGTTGGTGATGC  
 TTCTGAGACTCAGAATGGTTTACTCTAACAAACACTGTGCTGTCTATCCCTTGTACTTGCCT  
 ACTGTAATATGGATTTCACTTCTGAACAGTTTACAGCACAATATTTATTTTAAAGTGAATAAA  
 ATGTCCACAAGCAAAAA

## **FIGURE 94**

MEEGGGGVRS LVPGGPVLLVLCGLLEASGGGRALPQLSDDIPFRVNWPGTEFSLPTTGVLKE  
DNYVIMTTAHKEKYKCILPLVTSGDEEEKDYKGPNPRELLEPLFKQSSCSYRIESYWTYEV  
HGKHIRQYHEEKETGQKINIHEY YLGNMLAKNLLFEKEREAEKEKSNEIPTKNIEGQMT  
PYYPVGMGNGTPCSLQNRPRSSTVMYICHPEKHEILSVAEVTTC EYEVVILTPLLCSHPKYRFR  
ASPVNDIFCQSLPGSPFKPLTLRQLEQQEEILRVPFRRNKEGVGWWKYEF CYGKHVHQYHEDK  
DSGKTSVVVG TWNQEEHIEWAKKNTARAYHLQDDGTQTVRMVSHFYGN GDI CDITDKPRQVTV  
KLKCKESDSPHAVTVYMLPHSCQYILGVESPVICKILDTADENGLLSLPN

**Important features of the protein:**

**Signal peptide:**

amino acids 1-30

**Glycosaminoglycan attachment site.**

amino acids 28-32

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 337-341

**N-myristoylation sites.**

amino acids 6-12, 23-29, 29-35, 49-55, 141-147, 152-158, 192-198,  
196-202

**Gram-positive cocci surface proteins 'anchoring' hexapeptide.**

amino acids 54-60

# **FIGURE 95**

TTCCGTTTCTGGGAGGAGTGAGGGGCAACGGGTCCGAGAAAAAGGAAAAAGAAGGGCTCAGC  
 GCCTCCCCGCCGGGCGGTGGACAGAGGGGCACAGTTTCGGCAGGCGGGTGAGGTGCTGAGGG  
 CCCGCCGGAGATGTTTTCTTGTCGAGCAGGTGCAACCCAGGTTACAGTTTCTCTGAGTCA  
 TCTCATCAATGCCTTCCATACACCAAAAAACACTTCTGTTTCTCTCAGTGGAGTGTGAGTTTCT  
 TCAAAACCAGCATCGAGATGTAGTTTCTTGAGCATGAGGCTCCAGCAGTGAGCCTTCACTTAA  
 CTTAAGGGACCTTGGATTATCTGAACTAAAAATTTGGACAGATTGATCAGCTGGTAGAAAAATCT  
 ACTTCTGGATTTTGTAAAGGCAAAAAACATTTCTTCCCATTGGCATAACATCCCATGTCTCTGC  
 ACAATCCTTCTTTGAAAAATAATATGGTAACTTAGATATATTTAGTACATTACGTTTCTTCTTG  
 CTTGTATCGACATCATTCAAGAGCTCTTCAAAGCATTTGTTTCAGATCTTCAGTACTGGCCAGT  
 TTTTCATACAGTCTCGGGGTTTTTAAACTTTGAAATCAAGGACACGACGTCTCCAGTCTACCTC  
 CGAGAGATTAGCTGAAACACAGAATATAGCGCCATCATTCGTGAAGGGGTTTTCTTTTGGCGGA  
 CAGAGGATCAGATGTTGAGAGTTTGGACAACTCATGAAAACCAAAAATATACCTGAAGCTCA  
 CCAAGATGCATTTAAACTGGTTTTTGGCGAAGGTTTTCTGAAAGCTCAAGCACTCACACAAAA  
 AACCAATGATTCCCTAAGGCGAACCCGTCTGATTCTCTTCGTTCTGCTGCTATTCCGCATTTA  
 TGGACTTCTAAAAAACCCATTTTTATCTGTCCGCTTCCGGACAACAACAGGGCTTGATTCTGC  
 AGTAGATCCTGTCCAGATGAAAAATGTCACCTTTGAACATGTTAAAGGGGTGGAGGAAGCTAA  
 ACAAGAATTACAGGAAGTTGTTGAATTTCTGAAAAATCCACAAAAATTTACTATTCTTGGAGG  
 TAAACTTCCAAAAGGAATTTCTTTTAGTTGGACCCCCAGGGACTGGAAAGACACTTCTTGCCCG  
 AGCTGTGGCGGGAGAACTGATGTTTCTTTTATTATGCTTCTGGATCCGAATTTGATGAGAT  
 GTTTGTGGGTGTGGGAGCCAGCCGTATCAGAAATCTTTTTAGGGAAGCAAAGGCGAATGCTCC  
 TTGTGTTATATTTATGATGAATTAGATTCTGTTGGTGGGAAGAGAATTGAATCTCCAATGCA  
 TCCATATTCAAGGCAGACCATAAATCAACTTCTTGCTGAAATGGATGGTTTTTAAACCCAATGA  
 AGGAGTTATCATAATAGGAGCCACAACTTCCAGAGGCATTAGATAATGCCTTAATACGTCC  
 TGGTCTGTTTTTGACATGCAAGTTACAGTTCCAAGGCCAGATGTAAAAGGTGGAACAGAAATTTT  
 GAAATGGTATCTCAATAAAATAAAGTTTGATCAATCCGTTGATCCAGAAATTATAGCTCGAGG  
 TACTGTTGGCTTTTTCCGGAGCAGAGTTGGAGAATCTTGTGAACCAGGCTGCATTAAAAGCAGC  
 TGTTGATGGAAGAAGAAATGGTTACCATGAAGGAGCTGGAGTTTTTCAAAGACAAAATTTCTAAT  
 GGGGCTGAAAGAAGAAGTGTGGAATTTGATAACAAAAACAAAACCATCACAGCATATCATGA  
 ATCTGGTCATGCCATTATTGCATATTACACAAAAGATGCAATGCCTATCAACAAAGCTACAAT  
 CATGCCACGGGGGCCAACACTTGGACATGTGTCCCTGTTACCTGAGAATGACAGATGGAATGA  
 AACTAGAGCCCAGCTGCTTGCACAAATGGATGTTAGTATGGGAGGAAGAGTGGCAGAGGAGCT  
 TATATTTGGAACCGACCATATTACAACAGGTGCTTCCAGTGATTTTGATAATGCCACTAAAAAT  
 AGCAAAGCGGATGGTTACCAAATTTGGAATGAGTGAAAAGCTTGGAGTTATGACCTACAGTGA  
 TACAGGGAACTAAGTCCAGAAACCCAATCTGCCATCGAACAAGAAATAAGAATCCTTCTAAG  
 GGACTCATATGAACGAGCAAAACATATCTTGAAAACCTCATGCAAAGGAGCATAAGAATCTCGC  
 AGAAGCTTTATTGACCTATGAGACTTTGGATGCCAAAGAGATTCAAATTTGTTCTTGAGGGGAA  
 AAAGTTGGAAGTGAGATGATAACTCTCTTGATATGGATGCTTGTGCTGTTTTATTGCAAGAATA  
 TAAGTAGCATTGCAGTAGTCTACTTTTACAACGCTTTCCCTCATTCTTGATGTGGTGTAAAT  
 GAAGGGTGTGAAATGCTTTGTCAATCATTTGTACATTTATCCAGTTTGGGTATTCTCATTA  
 TGACACCTATTGCAAATTAGCATCCCATGGCAAATATATTTTGAAAAATAAAGAACTATCAG  
 GATTGAAAACAAAAA

## **FIGURE 96**

MFSLSSSTVQPVTVPLSHLINAFHTPKNTSVSLSGVSVSONQHRDVVPEHEAPSSEPSLNLRD  
LGLSELKIGQIDQLVENLLPGFCKGKNISSHWHTSHVSAQSFFENKYGNLDIFSTLRSSCLYR  
HHSRALQSICSDLQYWPVFIQSRGFKTLKSRTTLLQSTSERLAETQNIAPSFVKGFLLRDRGS  
DVESLDKLMKTKNIPEAHQDAFKTGFAEGFLKAQALTQKTNDLSLRTRLILFVLLLFGIYGLL  
KNPFLSVRFRTTGLDSAVIDPVQMKNVTFEHVKGVEEAKQELQEVVEFLKNPQKFTILGGKLP  
KGILLVGPPGTGKTLLARAVAGEADVPPFYASGSEFDEMFGVGASRIRNLFREAKANAPCVI  
FIDELDSVGGKRIESPMHPYSRQTINQLLAEMDGFKNPNEGVIIGATNFPEALDNALIRPGRF  
DMQVTVPRPDVKGRTEILKWYLNKIKFDQSVDPETIARGTVGFSGAELENLVNQAALKAADV  
KEMVTMKELEFSKDKILMGPERRSVEIDNKNKTITAYHESGHAI IAYYTKDAMPINKATIMPR  
GPTLGHVSLLPENDRWNETRAQLLAQMDVSMGGRVAEELIFGTDHITGASSDFDNATKIAKR  
MVTKFGMSEKLGVMYSDTGKLSPETQSAIEQEIRILLRDSYERAKHILKTHAKEHKNLAEL  
LTYETLDAKEIQIVLEGKKLEVR

**Important features of the protein:**

**Transmembrane domain:**

amino acids 238-259

**N-glycosylation sites.**

amino acids 28-32, 90-94, 230-234, 278-282, 535-539, 584-588,  
623-627

**N-myristoylation sites.**

amino acids 35-41, 266-272, 286-292, 325-331, 357-363, 599-605

**Amidation site.**

amino acids 387-393, 709-713

**ATP/GTP-binding site motif A (P-loop).**

amino acids 322-330

**AAA-protein family proteins**

amino acids 315-336, 343-386, 405-451

**FIGURE 97**

GATGGCGCAGCCACAGCTTCTGTGAGATTCTGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGGG  
GACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCAAA  
ACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTT  
CCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACG  
ACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCACGGGAG  
GCTTGGCAGTTTTTTCTTACTCCTGTGGTCTCCAGATTTCAGGCCTAAGATGAAAGCCTCTAGT  
CTTGCCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAG  
ACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCT  
GAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACT  
GAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTC  
TATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGC  
AGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACA  
TGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG  
GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATGGAG  
GAGACAGAAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTGAGGTCAGAGCTCCAGTCT  
TCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACTGTACTAGTCTTGTGCT  
GGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGATGATTGTCTTTATGCATCCCC  
AATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAATATCTTTCTGCTATTGGATATATT  
TATTAGTTAATATATTTATTTATTTTGTCTATTTAATGTATTTATTTTACTTGGACATG  
AACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAGAGCAGGTGATGTATTTTAT  
ACAGTAAAAAAAAAAACCTTGTAATTTCTAGAAGAGTGGCTAGGGGGGTATTCAATTTGTAT  
TCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGATATTTGAAATTGAACCAATGAC  
TACTTAGGATGGGTTGTGGAATAAGTTTTGATGTGGAATTGCACATCTACCTTACAATTACTG  
ACCATCCCAGTAGACTCCCAGTCCATAATTGTGTATCTTCCAGCCAGGAATCCTACACGG  
CCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATACCAAAAAAAAAAAAAAAAAAAAA

**FIGURE 98**

MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSEIRGSVQAKDGNIDIR  
ILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSSLANSFLTICKDLRLC  
HAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE

**Signal sequence:**

amino acids 1-24

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 107-110, 140-143

**N-myristoylation site.**

amino acids 51-56

**Interleukin 10:**

amino acids 9-176



**FIGURE 99**

[illegible]

**FIGURE 100**

MRLLPWFLLLLFGPWLLRKAVSAQIPESGRPQYLGLRPAAAGAGAPGQQLPEPRSSDGLGVGR  
AWSAWPTNHTGALARAGAAGALPAQRTKRKPSIKAARAKKIFGWGDFYFRVHTLKFSLLVTG  
KIVDHVNGTFSVYFRHNSSSLGNLSVSIVPPSKRVEFGGVWLPGPVPHPLQSTLALEGVLPGL  
GPPLGMAAAAAGPGLGGSLLGGALAGPLGGALGVPGAKESRAFNCHVEYEKTNRARKHRPCLYD  
PSQVCFTEHTQSQAAWLCAKPFKVICIFVSFLSFDYKLVQKVC PDYNFQSEHPYFG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 273-288

**N-glycosylation sites.**

amino acids 72-76, 133-137, 143-147, 149-153

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 93-97

**N-myristoylation sites.**

amino acids 35-41, 58-64, 60-66, 81-87, 84-90, 184-190, 194-200,  
203-209, 205-211, 206-212, 209-215, 217-223, 221-227, 224-230

**Cytochrome b/b6 Qo site signature.**

amino acids 5-11

**FIGURE 101**

AATGCCCCATGCGCACCCACAGCTCGCGCTCCTGCAAGTGTTCTTTCTGGTGTTCCCCGATG  
GCGTCCGGCCTCAGCCCTCTTCTCCCCATCAGGGGCAGTGCCACGTCTTTGGAGCTGCAGC  
GAGGGACGGATGGCGGAACCCCTCCAGTCCCCCTCAGAGGCGACTGCAACTCGCCCGGCCGTGC  
CTGGACTCCCTACAGTGGTCCCTACTCTCGTGACTCCCTCGGCCCCTGGGAATAGGACTGTGG  
ACCTCTTCCCAGTCTTACCGATCTGTGTCTGTGACTTGACTCCTGGAGCCTGCGATATAAATT  
GCTGCTGCGACAGGGACTGCTATCTTCTCCATCCGAGGACAGTTTTCTCCTTCTGCCTTCCAG  
GCAGCGTAAGGTCTTCAAGCTGGGTTTGTGTAGACAACTCTGTTATCTTCAGGAGTAATTCCC  
CGTTTCTTCAAGAGTTTTCATGGATTCTAATGGAATCAGGCAGTTTTGTGTCCATGTGAACA  
ACTCAAACCTAAACTATTTCCAGAAGCTTCAAAAGGTCAATGCAACCAACTTCCAGGCCCTGG  
CTGCAGAGTTTGGAGGCGAATCATTCACTTCAACATTCCAAACCTCAATCACCACCATCTTTTT  
ACAGGGCTGGGGACCCCATTTCTTACTTACTTCCCCAAGTGGTCTGTAATAAGCTTGCTGAGAC  
AACCTGCAGGAGTTGGAGCTGGGGGACTCTGTGCTGAAAGCAATCCTGCAGGTTTCTAGAGA  
GTAAAAGTACAACCTTGCACTCGTTTTTTCAAGAACCTGGCTAGTAGCTGTACCTTGGATTTCAG  
CCCTCAATGCTGCCCTCTTACTATAACTTCACAGTCTTAAAGGTTCCAAGAAGCATGACTGATC  
CACAGAAATATGGAGTTCCAGGTTCTGTAATACTTACCTCACAGGCTAATGCTCCTCTGTGG  
CTGGAAACACTTGTGAGAATGTAGTTTCTCAGGTCACCTATGAGATAGAGACCAATGGGACTT  
TTGGAATCCAGAAAGTTTCTGTGAGTTTGGGACAAACCAACCTGACTGTTGAGCCAGGCGCTT  
CCTTACAGCAACACTTCATCCTTCGCTTCAGGGCTTTTCAACAGAGCACAGCTGCTTCTCTCA  
CCAGTCCTAGAAGTGGAATCCTGGCTATATAGTTGGGAAGCCACTCTTGGCTCTGACTGATG  
ATATAAGTTACTCAATGACCCTCTTACAGAGCCAGGGTAATGGAAGTTGCTCTGTTAAAAGAC  
ATGAAGTGCAGTTTGGAGTGAATGCAATATCTGGATGCAAGCTCAGGTTGAAGAAGGCAGACT  
GCAGCCACTTGCAGCAGGAGATTTATCAGACTCTTCATGGAAGGCCAGACCAGAGTATGTTG  
CCATCTTTGGTAATGCTGACCCAGCCAGAAAGGAGGGTGGACCAGGATCCTCAACAGGCACT  
GCAGCATTTCAGCTATAAACTGTACTTCTGCTGTCTCATACCAGTTTTCCCTGGAGATCCAGG  
TATTGTGGGCATATGTAGGTCTCCTGTCCAACCCGCAAGCTCATGTATCAGGAGTTGATTC  
TATACCAGTGCCAGTCTATACAGGATTCTCAGCAAGTTACAGAAGTATCTTTGACAACCTTTG  
TGAACCTTTGTGGACATTACCCAGAAGCCACAGCCTCCAAGGGGCCAACCCAAAATGGACTGGA  
AATGGCCATTCGACTTCTTTCCCTTCAAAGTGGCATTCAGCAGAGGAGTATTCTCTCAAAAAT  
GCTCAGTCTCTCCCATCCTTATCCTGTGCCTCTTACTACTTGAGTTCTCAACCTAGAGACTA  
TGTGAAGAAAAGAAAATAATCAGATTTTCAAGTTTCCCTATGAGAACTCTGAGGCAGCCACTT  
ATCTTGGCTAAATAGAACCTCACCTGCTCATGACCAGAGAGCATTTAGGATAATAGATGACCT  
AACTGAAGGAATCCTTGTATATGAAAGGAGTTATTTTAGAAAAGCAATAAAAATATTTTATTC  
ATCNTAAAAAAAAA

## **FIGURE 102**

MRTFQQLALLQVFFLVFPDGVPRQPSSSPSGAVPTSLELQRGTDGGTLQSPSEATATRPVAVPGL  
PTVVPTLVTPSAPGNRTVDLFPVLPICVCDLTPGACDINCCCDRDCYLLHPRTVFSFCLPGSV  
RSSSWVCVDNSVIFRSNSPFPSPRVFMDSNQIRQFCVHVNNNSLNLYFQKLQKVNATNFQALAAE  
FGGESFTSTFQTQSPPSFYRAGDPILTYFPKWSVISLLRQPAGVGAGGLCAESNPAGFLESKS  
TTCTRFFKNLASSCTLDSALNAASYNFTVLKVPRSMTPQNMEFQVPVILTSQANAPLLAGN  
TCQNVVSQVTYEIEETNGTFGIQKVSLSLQTNLTVEPGASLQQHFILRFRAFQQSTAASLTSP  
RSGNPGYIVGKPLLALTDDISYSMTLLQSQNGSCSVKRHEVQFGVNAISGCKLRLKKADCSH  
LQQEIIYQTLHGRPRPEYVAIFGNADPAQKGGWTRILNRHCSISAINCTSCCLIPVSLEIQVLW  
AYVGLLSNPQAHVSGVRFLYQCQSIQDSQQVTEVSLTTLVNFVDITQKPQPPRGQPKMDWKWP  
FDFFPFKVAFSRGVFSQKCSVSPILILCLLLLGVNLNLETM

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domains:**

amino acids 484-505, 581-600

**N-glycosylation sites.**

amino acids 78-82, 165-169, 179-185, 279-285, 331-337, 347-351,  
410-414, 487-491

**N-myristoylation sites.**

amino acids 30-36, 41-47, 124-130, 232-238, 236-242, 409-415

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 420-431

# **FIGURE 103**

CCTAATTCTCAAGGTGATGCTATTTAGGAAGTCATAACTCATGTGAGTGAGCCATGTGGGAT  
 TAAGAAGTGATAGGAGAGCTTGCTGTCTGTCTCTGCTCTCCACTGTGTGAGGATACAACAGGA  
 AGACAGCCATCTGGTGAGGAAGAGAGGGCCCTCGCCAGATACCGGACCTGCTGACACCTTGAT  
 CTTGGACTTCCCATCTTCCAGGAAGGCCTGACCTCAGTTGTTCCAGGGTAAAGAATTTGGGCA  
 GTGCCCACACCCACGCTGTTGGATAACATTTCTTCCACCATAACCAGTGAGGGTGAATGTGTACA  
 CGCCCAGCTTCTGCTGTTACTCTCCACAGTATGCGAAGAATATCCCTGACTTCTAGCCCTG  
 TGCGCCTTCTTTTGTCTGCTGTTGCTACTAATAGCCTTGGAGATCATGGTTGGTGGTCACT  
 CTCTTTGCTTCAACTTCACTATAAAATCATTGTCCAGACCTGGACAGCCCTGGTGTGAAGCGC  
 AGGTCTTCTTGAATAAAAATCTTTTCTTCCAGTACAACAGTGACAACAACATGGTCAAACCTC  
 TGGGCCTCCTGGGGAAGAAGGTATATGCCACCAGCACTTGGGGAGAATTGACCCAAACGCTGG  
 GAGAAGTGGGGCGAGACCTCAGGATGCTCCTTTGTGACATCAAACCCAGATAAAGACCAGTG  
 ATCCTTCCACTCTGCAAGTCGAGATGTTTTGTCAACGTGAAGCAGAACGGTGCACTGGTGCAT  
 CCTGGCAGTTCGCCACCAATGGAGAGAAATCCCTCCTCTTTGACGCAATGAACATGACCTGGA  
 CAGTAATTAATCATGAAGCCAGTAAGATCAAGGAGACATGGAAGAAAAGACAGAGGGCTGGAAA  
 AGTATTTTCAAGGAGCTCTCAAAGGGGAGACTGCGATCACTGGCTCAGGGAATTTCTTAGGGCACT  
 GGGAGGCAATGCCAGAACCGACAGGCAGAAGATCCACCTTAGAGGTGATAACCACGGCGGCGCAG  
 AGTTGTTACCTGTGGTCCTCGATCGCTGACAGCCTTGGCTCCCACTGCTGTGTGTTCCTGA  
 GTCAAGTGGAGGCGGAGCCTGCAATGAGCGGAGATCGCGCCTCTGCATTCCAGTCTTGGCAAC  
 AGAGCAAGACTCCGTCTCAAAAAAAAAAATTTTTTTTTCAGTACATATTTTTTAAAGATAGG  
 GCTGGGCACAGCAGCTCACATCTATAATCCCAACACTTTGGGAGGCCTAGGCAGGAGGATCAC  
 TTGAGCCCAGGAATCTGAAGCTGCAGTGAGCCTTTGCTCGTGAGATTGTGGACCTATGATCCT  
 ACCACCAGCCCACCTGGTTCTAACACCCCTCCTCTATGTGTGAGAGGGAGAGAAGAAAAGTG  
 AGGGAGAAAAGAGAGATAAGCAAAGAACAGAGAGGAAAAATGAAAATAAGAGGAAATTTGGGG  
 GAATTAAACAGAGGGGAGGGCATGGATCCCCGGGAGTTAGAAGAGTAGCAGCTTGTGGATTAC  
 TACGCAGTGGAGGAAGAAGAGTTGTTGGAAATTATTTGAGAGGTAGTATAATCATTTGTGAGG  
 CAGTTTTCTGCATTACCATTTCTCACAGACTAAGTTACTCATAAGCAAACGTGCAATTCACA  
 TTACACTGAAATTCTTCCCTAATACATCATTTGCATTGGAATAAAGTACGGTTTTCAAACAAC  
 CTGATATAGCAGAACTGACTGTATAAATTATGTGAGCACAGTGCAAGTAATTTCTTTGTTTGT  
 TGTGTTTTTTTTTGGAGACAGAGTCTCACTCTATCTCCAGGCTGGAGTGTAGTGGTGCATCC  
 CGGCTCACTGCAACCTCGATCTCCAGGCTCAAGCGATTCCCCTGCCTCAGCCTCTGAGTAG  
 CTGGGATTACAGGCATGAGCCACCACGCCCCGGCTAATTTTTGTATTTTTAGTAGAGACGGGGT  
 TTCACCCTGTTGGCCAGGCTGGTCTCGAACTACGGACCTCAGGTGATCTGCCCCCTCAGCCT  
 CTCAAAGTGCTGGGATTATAGCATGAGCCACTGAGCCAGACACAAGTAGTTCTTTCTGATAA  
 ACACTTTAACTGAATGCA

## **FIGURE 104**

MRRISLTSSPVRLLLFLLLLLLIALEIMVGGHSLCFNFTIKSLSRPGQPWCEAQVFLNKNLFLQ  
YNSDNNMVKPLGLLGKKVYATSTWGELTQTLGEVGRDLRMLLCDIKPQIKTSDPSTLQVEMFC  
QREAERCTGASWQFATNGEKSLLFDAMNMTWTVINHEASKIKETWKKDRGLEKYFRKLSKGDC  
DHWLREFLGHWEAMPEPTGRRST

**Important features of the protein:**

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 11-30 (possible type II protein)

**N-glycosylation site.**

amino acids 36-39, 154-157

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 2-5, 182-185, 209-212

**Casein kinase II phosphorylation site.**

amino acids 86-89, 93-96, 142-145, 185-188

**N-myristoylation site.**

amino acids 46-51

**Amidation site.**

amino acids 77-80, 207-210

**FIGURE 105**

TTTTCCGAGTGACCTTCTTGATGCTGGCTGTTTTCTCTCACCGTTCCCCTGCTTGGAGCCATGA  
TGCTGCTGGAATCTCCTATAGATCCACAGCCTCTCAGCTTCAAAGAACCCCCGCTCTTGCTTG  
GTGTTCTGCATCCAAATACGAAGCTGCGACAGGCAGAAAGGCTGTTTGAAAATCAACTTGTTG  
GACCGGAGTCCATAGCACATATTGGGGATGTGATGTTTACTGGGACAGCAGATGGCCGGGTCG  
TAAAACTTGAAAATGGTGAAATAGAGACCATTGCCCCGTTTGGTTTCGGGCCCTTGCAAAACCC  
GAGATGATGAGCCTGTGTGTGGGAGACCCCTGGGTATCCGTGCAGGGCCCAATGGGACTCTCT  
TTGTGGCCGATGCATACAAGGGACTATTTGAAGTAAATCCCTGGAAACGTGAAGTGAAACTGC  
TGCTGTCTCCGAGACACCCATTGAGGGGAAGAACATGTCTTTGTGAATGATCTTACAGTCA  
CTCAGGATGGGAGGAAGATTTATTTTACCGATTCTAGCAGCAAATGGCAAAGACGAGACTACC  
TGCTTCTGGTGTGAGGGGCACAGATGACGGGCGCCTGCTGGAGTATGATACTGTGACCAGGG  
AAGTAAAGTTTTATTGGACCAGCTGCGGTTCCCGAATGGAGTCCAGCTGTCTCTGCAGAAG  
ACTTTGTCCTGGTGGCAGAAACAACCATGGCCAGGATACGAAGAGTCTACGTTTCTGGCCTGA  
TGAAGGGCGGGGCTGATCTGTTTGTGGAGAACATGCCTGGATTTCCAGACAACATCCGGCCCA  
GCAGCTCTGGGGGGTACTGGGTGGGCATGTCGACCATCCGCCCTAACCTGGGTTTTCCATGC  
TGGATTTCTTATCTGAGAGACCCCTGGATTAAAAGGATGATTTTTAAGCTCTTTAGTCAAGAGA  
CGGTGATGAAGTTTGTGCCGCGGTACAGCCTCGTCCTAGAACTCAGCGACAGCGGTGCCTTCC  
GGAGAAGCCTGCATGATCCCGATGGGCTGGTGGCCACCTACATCAGCGAGGTGCACGAACACG  
ATGGGCACCTGTACCTGGGCTCTTTTCAAGTCCCCCTTCCTCTGCAGACTCAGCCTCCAGGCTG  
TTTTAGCCCTCCCAGATAGCTGCCCCTGCCACGCAGGCCAGGAGTCTTCACACTCAGGCACCAG  
GCCTGGTCCAGGAGGAGCTGTGGACACAGTCGTGGTTCAAGTGTCCACATGCACCTGTTAGTC  
CCTGAGAGGTGGTGGGAATGGCTGCTTCATTCCCTCGAGGATGCCCGGGCCCCACCTGGGCTTG  
TCTTTCTGTTTAGAGGGAAGTGTAACATATCTGCCATGAGGAACATAAATTCATGTAAAGCCA  
TTTTCTCTTAAACAAAAACAAAACCTTTCTAAGTACAATCATTCTCTAGGATTTGGGAAGCTCCT  
TGCACTTGGAACAGGGCTCAGGTGGGTGGAGCAGTAAGGCACTACCCAGAGAGCTTGCTGCTG  
CGGCCCTGTCCTGCGGCCTCAAAGTTCTTCTTTACTATATATAACGTGCGGTACATACCTTTCT  
TCGTTGTGGTGGGGATGGAAGAGCAGAGGGAGCATGGCCCAGGGGTGTTGAGGCCAGCGGTGA  
GAGCCGTGTTAGCCAAGACATGGAACGTGTTCTCAAGGTTATGTGGGGCGTGGGCTCTCCA  
TAGTGTGTATGAAAAGCTTGTTGACTCTAGCGGCTCAGAGAGGACTTTGCTGGGTTTCTTTCT  
GTGAATATCTCCGTGCTGACCATGCTGGAATTGGATGATTCTGCAATTCGGGACCTACTGCAG  
GGGTCCGTTTAGTAAACGTCTTGTCTGTGATCTTTGTTCTTGACCTCTAGACCCCAAGATGTGA  
ACAGTGACGTGTTAATGTCATCTTTGCTCATGTGTTATAAGCCCCAAGTTGCTGTATATTTT  
CACAAGTATGTCTACACACTGG

## **FIGURE 106**

MLAVSLTVPLL GAMMLLES PIDPQPLSFKEPPLLLGV LHPNTKLRQAERLFENQLVGPESIAH  
IGDVMFTGTADGRVVKLENGEIETIARFGSGPCKTRDDEPVCGRPLGIRAGPNGTLFVADAYK  
GLFEVNPWKREVKLLLSSETPIEGKNMSFVNDLTVTQDGRKIYFTDSSSKWQRRDYLLLVMEG  
TDDGRLLEYDVTREVKVLLDQLRFPNGVQLSPAEDFVLVAETTMARIRRVYVSGLMKGGADL  
FVENMPGFDPNIRPSSSGGYWGMSTIRPNPGFSMLDFLSERPWIKRMIFKLFSQETVMKFVP  
RYSLVLELSDSGAFRRSLHDPDGLVATYI SEVHEHDGHLYLGSFRSPFLCRLSLQAV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-13

**Transmembrane domain:**

amino acids 1-21 (possible type II)

**N-glycosylation sites.**

amino acids 116-119, 152-155

**Casein kinase II phosphorylation sites.**

amino acids 19-22, 27-30, 98-101, 146-149, 221-224, 286-289, 332-335

**N-myristoylation sites.**

amino acids 71-76, 92-97, 189-194, 244-249, 338-343

**Amidation site.**

amino acids 164-167



# **FIGURE 107**

AACGAAGCGTGCGCGCTTTGGTAACCGGCTAGAAATCCCGCACGCGCGCTGCCTCCTCTCCC  
CAGGCCTGAGCTGCCCCCTCCCACTGCCTTTCTTCTTCCCGCAGTCAGAAGCTTCGCGAGGG  
CCCAGAGAGGCGGTGGGGTGGGCGACCTACGCCAGCTCCGGGCGGGAGAAAGCCCACCTCT  
CCCGCGCCCCAGGAAACCGCGCGCTTCGGCGCTGCGCAGAGCCATGGAATTCTCCTGGCTGG  
AGACGCGCTGGGCGCGGCCCTTTTACCTGGCGTTCTGTCTTCTGCCTGGCCCTGGGGCTGCTGC  
AGGCCATTAAGCTGTACCTGCGGAGGCAGCGCTGCTGCGGGACCTGCGCCCCCTTCCCAGCGC  
CCCCACCCACTGGTTCTTGGGCAACCAGAAAGTTTATTTCAGGATGATAACATGGAGAAGCTTG  
AGGAAATTATTGAAAAATACCCCTCGTGCCTTCCCTTTCTGGATTGGGCCCTTTCAGGCATTTT  
TCTGTATCTATGACCCAGACTATGCAAAGACACTTCTGAGCAGAACAGATCCCAAGTCCCAGT  
ACCTGCAGAAATTTCTCACCTCCACTTCTTGAAAAGGACTAGCGCTCTAGACGGACCCAAAGT  
GGTTCAGCATCGTCGCCTACTAACTCCTGGATTCCATTTTAAACATCCTGAAAGCATACATTG  
AGGTGATGGCTCATTCTGTGAAAATGATGCTGGATAAGTGGGAGAAGATTTGCAGCACTCAGG  
ACACAAGCGTGGAGGTCTATGAGCACATCAACTCGATGTCTCTGGATATAATCATGAAATGCG  
CTTTCAGCAAGGAGACCAACTGCCAGACAAACAGCACCCATGATCCTTATGCAAAAGCCATAT  
TTGAACTCAGCAAAATCATATTTACCGCTTGTACAGTTTGTGTATCACAGTGACATAATTT  
TCAAACCTCAGCCCTCAGGGCTACCGCTTCCAGAAAGTTAAGCCGAGTGTTGAATCAGTACACAG  
ATACAATAATCCAGGAAAGAAAGAAATCCCTCCAGGCTGGGGTAAAGCAGGATAAACTCCGA  
AGAGGAAGTACCAGGATTTTCTGGATATTGTCTTTCTGCCAAGGATGAAAGTGGTAGCAGCT  
TCTCAGATATTGATGTACACTCTGAAGTGAGCACATTCCTGTTGGCAGGACATGACACCTTGG  
CAGCAAGCATCTCCTGGATCCTTTACTGCCCTGGCTCTGAACCTGAGCATCAAGAGAGATGCC  
GGGAGGAGGTGAGGGGCATCCTGGGGGATGGGTCTTCTATCACTTGGGACCAGCTGGGTGAGA  
TGTCGTACACCACAATGTGCATCAAGGAGACGTGCCGATTGATTCTTCAGTCCCGTCCATTT  
CCAGAGATCTCAGCAAGCCACTTACCTTCCCAGATGGATGCACATTGCCTGCAGGGATCACCG  
TGGTCTTAGTATTTGGGGTCTTCACCACAACCTGCTGTCTGGAAAAACCCAAAGGTCTTTG  
ACCCCTTGAGGTTCTCTCAGGAGAATTCTGATCAGAGACACCCCTATGCCTACTTACCATTCT  
CAGCTGGATCAAGGAAC TGCAATTGGGCAGGAGTTTGCCATGATTGAGTTAAAGGTAACCATTG  
CCTTGATTCTGCTCCACTTCAGAGTGACTCCAGACCCACCAGGCCTCTTACTTTCCCCAACCC  
ATTTTATCCTCAAGCCCAAGAATGGGATGTATTTGCACCTGAAGAACTCTCTGAATGTTAGA  
TCTCAGGGTACAATGATTAAACGTACTTTGTTTTTTCGAAGTTAAATTTACAGCTAATGATCCA  
AGCAGATAGAAAGGGATCAATGTATGGTGGGAGGATTGGAGGTTGGTGGGATAGGGGTCTCTG  
TGAAGAGATCCAAAATCATTTCTAGGTACACAGTGTGTGAGCTAGATCTGTTTCTATATAACT  
TTGGGAGATTTTCAGATCTTTTCTGTAAACTTTCACTACTATTAAATGCTGTATACACCAATA  
GACTTTTCATATATTTTCTGTTGTTTTTAAAAATAGTTTTTCAGAATTATGCAAGTAATAAGTGCA  
TGTATGCTCACTGTCAAAAATTTCCCAACACTAGAAAAATCATGTAGAATAAAAAATTTTAAATCT  
CACTTCACCTTAGCCGACATTCCATGCCCTGACCAATCCTACTGCTTTTCTAAAAACAGAATA  
ATTTGGTGTGCATTCTTTCAGACTTTTTCTATACATTTTATATGTAGAAATGTAGCAATGTA  
TTTGTATAGATGTGATCATTCCTATATTGTTATTGATTTTTTTTCACTTAATAAAAAATTCACCT  
TATTCCTTAAAA

## **FIGURE 108**

MEFSWLETRWARPFYLA FVFCLALG LLQA IKLYLRRQRLLRDLRPFPPAPPTHWFLGHQKFIQD  
DNMEKLEEIIEKYPRAPFWIGPFQAFFCIYDPDYAKTLLSRTDPKSQYLQKFS PPLL GKGLA  
ALDGPKWFQHRLLTPGFHFNILKAYIEVMAHSVKMMLDKWEKICSTQDTSVEVYEHINSMSL  
DIIMKCAFSKETNCQTNSTHDPYAKAIFELSKIIFHRLYSLLYHSDIIFKLSPQGYRFQKLSR  
VLNQYTD TIIQERKKS LQAGVKQDNTPKRKYQDFLDIVLSAKDESGSSFS DIDVHSEVSTFLL  
AGHDTLAASISWILYCLALNPEHQERCREEVRGILGDGSSITWDQLGEMSYTTMCIKETCR LI  
PAVPSISRDL SKPLTFPDGCTLPAGITVVL SIWGLHHNPAVWKNPKVFDPLRFSQENS DQRHP  
YAYLPFSAGSRNCIGQEFAMIELKVTIALILLHFRVTPDPTRPLTFPNHFILKPKNGMYLHLK  
KLSEC

**Important features of the protein:**

**Signal peptide:**

amino acids 1-29

**Transmembrane domains:**

amino acids 310-330, 397-413, 459-473

**N-glycosylation site.**

amino acids 206-210

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 265-269, 504-520

**N-myristoylation sites.**

amino acids 25-31, 298-304, 353-359, 450-456, 456-462

**Cytochrome P450 cysteine heme-iron ligand signature.**

amino acids 447-457

**Cytochrome P450 cysteine heme-iron ligand proteins.**

amino acids 444-475

**FIGURE 109**

GGCGTTCCGGGCCTCAACTTTGGCGTCGTGAGATTCTTGTGAGGCGTCTGCCTGGAAGCCGGC  
AGCAATTTTGCTTCTTTAAAGAGAAAAAGAAGGCTAGGGACTCAGATTCCTGGATTCTGAGAT  
CCAGACCAGCTCCTCCCAGACCTCTCCAGAAGAAGCCATGGGAACCCCTCGTATCCAGCATTT  
GCTGATCCTCCTGGTCCTAGGAGCCTCCCTCCTGACCTCGGGCCTAGAGCTGTATTGTCAAAA  
GGGTCTGTCCATGACTGTGGAAGCAGATCCAGCCAATATGTTTAACTGGACCACAGAGGAAGT  
GGAGACTTGTGACAAAGGGGCACCTTTGCCAGGAAACCATACTAATAATTAAAGCAGGGACTGA  
GACAGCCATTTTGGCCACGAAGGGCTGCATCCCGGAAGGGGAGGAGGCCATAACAATTGTCCA  
GCACTCTTCACCTCCCGCCTGATCGTGACCTCCTACAGTAACTACTGTGAGGATTCTTCTG  
TAATGACAAAGACAGCCTGTCTCAGTTTGGGAGTTCAGTGAGACCACAGCTTCCACTGTGTC  
AACAACCCTCCATTGTCCAACCTGTGTGGCTTTGGGGACCTGTTTCAGTGCTCCTTCTCTTCC  
CTGTCCCAATGGTACAACCTCGATGCTATCAAGGAAAACCTTGAGATCACTGGAGGTGGCATTGA  
GTCGTCTGTGGAGGTCAAAGGCTGTACAGCCATGATTGGCTGCAGGCTGATGTCTGGAATCTT  
AGCAGTAGGACCCATGTTTGTGAGGGAAGCGTGCCACATCAGCTGCTCAACCTCGAAA  
GACTGAAAATGGGGCCACCTGTCTTCCCATTCCTGTTTGGGGGTACAGCTACTGCTGCCATT  
GCTGCTGCCATCATTTATTCACTTTTCCTAAGAAGGCACCTTCTGGGCCTGGGTCTGAGGACAT  
CTTTTTTGACTGGGAGCCTTCTTACTGTTGAGGTTCAACAAGCTGAGGAGTAGATGGGAATTT  
GAGGGAGAATACAGAGATACTATGAACGTATTTGACATTTTTAATAACAATTTCTGCTATAATT  
TTTGTATGCAGTAGGCGTTACTAATAAACATTTCTGCTGTGA

**FIGURE 110**

MGTPRIQHLLILLVLGASLLTSGLELYCQKGLSMTVEADPANMFNWTTEEVECTCDKGALCQET  
ILIIKAGTETAILATKGCIP EGEEAITIVQHSSPPGLIVTSYSNYCEDSF CNDKDSLSQFWEF  
SETTASTVSTTLHCPTCVALGTCFSAPSLPCPNGTTTCYQGKLEITGGGIESSVEVKGCTAMI  
GCRLMSGILAVGPMFVREACPHQLLTQPRKTENGATCLPIPVWGLQLLLPLLLPSFIHFS

**Important features of the protein:**

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 184-201

**N-glycosylation sites.**

amino acids 45-49, 159-163

**N-myristoylation sites.**

amino acids 31-37, 70-76, 99-105, 147-153, 160-166, 174-180,  
175-181

# **FIGURE 111**

CGAGAAGAGGACAGAGGAGACTGAGCAAAGGGGGGTGGGCTCCAGGCGACCCCTAGCCCAATTCTGCCCCCTCCAT  
 CCCAAGGGGCGAGAGAAATTGTCTTTCTTTGCTGACTCCTACGAGGAAAAAAAAAAAAAAAAAAAAACCATTTAA  
 AGGGAAAGATAAACGGAGACGGAGGAAAGGTGGCAGCCAGATTACTTAGAGAGGCACAGAGGAGAGAGATCGGGG  
 TGAGTCGCCCATGGGGACTCCCAGGGCCCAGCACCCGCCCTCCCCAGCTGCTGTTCTTAATTCTGCTGAGCTGT  
 CCCTGGATCCAGGGTCTGCCCCCTGAAGGAGGAGGAGATATTGCCAGAGCCTGGAAGTGAGACCCCCACGGTGGCC  
 TCTGAGGCCCTGGCTGAACTGCTTCATGGGGCCCTGCTGAGGAGGGGCCAGAGATGGGCTACCTGCCAGGATCT  
 GATCCGGACCCCGCTAGCCACCCCTCCGGCCGGCCAGACTCTCGCAGTGCCCTCCCTGCCACGGGCCACTGAG  
 CCGGGGACAGGGCCTCTGACAACAGCCGTACCCCTAACGGGGTCAGGGGGGCGAGGCCCACTGCCCCAGAACTG  
 CTGACCCCGCCCCAGGAACACAGCCCCACCCCAACCCAGCCCTGCCCTCCCCAGGGCCTCCCCCTGGGCCCTGAG  
 GGAGGAGAGGAGGAGACGACGACCACCATCATCACCACGAACTGTTACCACTACGGTGACCAGCCCCAGTTCTG  
 TGTAAATAACAACATCTCCGAGGGCGAAGGGTATGTGGAGTCTCCAGATCTGGGGAGCCCCGTACGCCGACCCCTG  
 GGGCTCCTGGACTGCATTACAGCATCCATGTCTACCTGGCTACGGCATTGAGATCCAGGTGCAGACGCTGAAC  
 CTGTACAGGAAGAGGAGCTCCTGGTGCTGGCTGGTGGGGGATCCCCAGGCCCTGGCCCCCGGACTCCTGGCCAAC  
 TCATCCATGCTTGGAGAAGGACAAGTCTTCCGAGGCCAACCAACCGGCTGCTTCTGCATCTCCAGAGCCAGCG  
 GTCCCAAGGGCGGCTGGCTTCCAGGATCCACTATCAGGCCCTACCTCCTGAGCTGTGGCTTCCCTCCCCGGCCGCC  
 CATGGGGACGTGAGTGTGACGGACCTGCACCCCTGGGGGCACTGCCACCTTTCACTGTGATTCTGGGCTACCACTG  
 CAGGAGAGGAGACCCTCATCTGCCCTCAATGGCACCCGGCCATCCTGGAACGGTGAAACCCCCAGCTGCATGGCA  
 TCCTGTGGTGGCACCATCCACAATGCCACCCCTGGGCGCATCGTGTCCCCAGAGCCTGGGGGAGCCGTAGGGCCC  
 AACCTCACCTGCGGTTGGGTCATTGAAGCAGCTGAGGGGCGCCGGCTGCACCTGCACCTTTGAAAGGGTCTCGCTG  
 GATGAGGACAATGACCGGTGATGGTGGCTCAGGGGGCAGCCCCCTATCCCCCGTGATCTATGATTCTGGACATG  
 GACGATGTCCCCGAGCGGGGTCTCATCAGTGACGCCAGTCCCTCTACGTGGAGCTGCTGTGAGAGACACCTGCC  
 AATCCCTGCTGTTAAGCCTTCGATTGAAGCCTTTGAGGAGGATCGCTGCTTCGCCCCCTTCTTGGCACATGGA  
 AATGTCACTACCAAGGACCTGAGTATCGCCAGGGGCACTGGCAACCTTCTCGTGCCCTCCAGGATATGCCCTG  
 GAGCCCCCTGGGCCCCCAATGCCATCGAATGTGTGGATCCACAGAACCCCACTGGAACGACACAGAGCCGGCC  
 TGCAAAGCCATGTGTGAGGGGAGCTGTGGAACAGCTGGCGTGGTCTCTCTCCCGACTGGCCCCAGAGCTAT  
 AGCCCGGGCCAAAGACTGCGTGTGGGGCGTGACGTCCAGGAAGAGAAGCGCATCTTGCTCCAAGTTGAGATATTG  
 AATGTGCGGGAAGGGGACATGCTGACGCTGTTTCGACGGGACGGTCCCAGCGCCCGAGTCTTGGCCCCAGCTGCGG  
 GGACCTCAGCCGCGCCCGCCGCTTCTCTCTTGGGCCGACCTCACACTGCAGTTTCAGGCACCGCCCGGGCCC  
 CCAATCCAGGCCTGGGCCAGGGCTTCGTATTGCATTCAAAGAGGTCCCGAGGAACGACACGTGCCCCGAGCTG  
 CCACCTCCGGAGTGGGGCTGGAGAAGGCATCCACGGGGACCTGATCCGGGGCACGGTGTCTACCTACCACTGC  
 GAGCTTGGCTACGAGCTGCTAGGCTCCGACATTCCTCACTTGGCAGTGGAACCTGTCTTGGAGCGCGCGCGCCCC  
 GCCTGCCAAAAGATCATGACTTGTGTGACCCCTGGCGAGATTGCCAACGGGCACCGCACCGCCTCGGACGCGGGC  
 TTCCCGTTGGCTCCACGTCCAGTACCGCTGCCCTGCCAGGGTACAGCCTCGAGGGGGCAGCCATGCTCACCTGC  
 TACAGCCGGGACACAGGCACACCAAGTGGAGCGATAGGGTCCCCAAATGCGCCTTGAAGTACGAGCCGTGCCCTG  
 AACCGGGGGTTCCCGAAGTGGCTACAGACGCTGTACAAGCACCACTACAGCGGGCGAGTCTCTGCGCTTC  
 TTCTGTATGAGGGCTTTGAGCTTATCGGCGAGGTACCATCACCTGTGTGCCCGGCCACCCCTCCAGTGGACC  
 AGCCAGCCCCCACTCTGCAAAGTGACCCAGACCACAGATCCATCAGGCAGCTGGAAGGGGGGAACCTGGCCCTG  
 GCCATCCTGCTGCCCTTAGGCTTGGTCATTGTCTCGGCAGTGGCGTTTACATCTACTACCAAGCTTCAGGGA  
 AAGTCCCTTTTTCGGCTTCTCGGGCTCCCACTCTACAGCCCCATCACCCTGGAGTCCGGACTTCAGCAACCCGCTG  
 TATGAAGCTTGGGATACGCGGAGTATGAAGTTTCCATCTGTAACCCCAAGACTACAGCTGCAGGACCCAGGACGC  
 CCTCCCCCTCCTCATTCTGGGCGAGGGAAATACGGGACCCGGTCTCTGCCCTCCTGGCTGCCCTCCTCCCTGGCTG  
 TGTAATAGTCTCCCTATCCACAGGGGGCTTTGATGGCCCTGGAGATCCTACAGTAAATAAACAGCATCCTG  
 CCGCCCAAAAA

## **FIGURE 112**

MGTPRAQHPPPPQLLFLILLSCPWIQGLPLKEEEILPEPGSETPTVASEALAEELLHGALLRRG  
PEMGYLPGSDPDPTLATPPAGQTLAVPSLPRATEPGTGPLTTAVTPNGVRGAGPTAPELLTPP  
PGTTAPPPPPSPASPGPPLGPEGGEEETTTTIITTTTVTTTTSVPLCNNNISEGEGYVESPD  
GSPVSRITLGLLDCTYSIHVYPGYGIEIQVQTLNLSQEEELLVLAGGGSPGLAPRLLANSSMLG  
EGQVLRSPNRLLLHFQSPRVPRGGGFRIHYQAYLLSCGFPPRPAHGDVSVTDLHPGGTATFH  
CDSGYQLQGEETLICLNGRTPSWNGETPSCMASCGGTIHNATLGRIVSPEPGGAVGPNLTCRW  
VIEAAEGRRLLHFFERVSLDEDNDRMLMVRSGGSPLSPVIYDSMDDDVPERGLISDAQSLYVEL  
LSETPANPLLLSLRFEAFEDRCFAPFLAHGNVTTTDPEYRPGALATFSCCLPGYALEPPGPPN  
AIECVDPTPEPHWNDETPACKAMCGGELSEPAGVVLSPDWPQSYSPGQDCVWGVHVQEEKRILL  
QVEILNVREGDMLTLFDGDGPSARVLAQLRGPQPRRRLSSGPDLTQLQFQAPPGPPNPGLGQG  
FVLHFKEVPRNDTCPELPPPEWGWRTASHGDLIRGTVLTYQCEPGYELLGSDILTCQWDLWS  
AAPPACQKIMTCADPGEIANGHRTASDAGFPVGS HVQYRCLPGYSLEGAAMLT CYSRDTGTPK  
WSDRVPKCALKYEPCLNPGVPENGYQTLYKH HYQAGESLRFFCYEGFELIGEVTITCVPGHPS  
QWTSQPPLCKVTQTDDPSRQLEGGNLALAILLPLGLVIVLGS GVYIYYTKLQGKSLFGFSGSH  
SYSPITVESDFSNPLYEAGDTREYEVSI

**Important features of the protein:**

**Signal peptide:**

amino acids 1-27

**Transmembrane domain:**

amino acids 842-864

**N-glycosylation sites.**

amino acids 176-180, 222-226, 247-251, 332-336, 355-359, 373-377,  
473-477, 517-521, 641-645

**Tyrosine kinase phosphorylation site.**

amino acids 61-69

**N-myristoylation sites.**

amino acids 2-8, 84-90, 111-117, 114-120, 190-196, 198-204,  
235-241, 309-315, 333-339, 351-357, 472-478, 484-490, 528-534,  
626-632, 665-671, 775-781, 842-848

**Amidation site.**

amino acids 384-388

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 12-23

**CUB domain proteins profile.**

amino acids 202-218, 376-392, 553-569

**FIGURE 113**

GCCGCGGGCGGAGCTGCCTGCCGGTCCCGCGCCGCGCTCCGCACTCCTCGGCCCTCGGGCGGTGATGGGACGG  
GGCGCCGCGGAGCAGGAGGCGCGCCCGTCCGGGTGCTCGGGCCGCGCGGAGCCCACTGTGGGGCTCGGGCATG  
GCGGGCCGCGAGACCTGAGCTCTCCTCAGGGGAGCGGGGAGGCAGCTGCTGGCCGCGATGGGGACGGAGTGGGG  
CCGTGCGCCGCGCGCCGAGCCGTGAGCGCCGAGCCACCGCCGCGCTACCTCAGCCCTTCGCGAAGCGCCGGGCA  
GCTCGGGAACATGGCCCTGGAGCGGCTCTGCTCGGTCTCAAAGTGTGTAAATAACAGTACTGGTAGTGGAAGG  
GATTGCCGTGGCCCAAAAAACCAAGATGGACAAAATATTGGAATCAAGCATATTCCTGCAACCCAGTGTGGCAT  
TTGGGTTCGAACCAGCAATGGAGGTCAATTTGCTTCGCCAAATTATCCTGACTCATATCCACCAACAAGGAGTG  
TATCTACATTTTGAAGCTGCTCCACGTCAAAGAATAGAGTTGACCTTTGATGAACATTATATATAGAACCATC  
ATTTGAGTGTGCTTTGATCACTTGAAGTTGAGATGGGCCATTTGGTTTCTCTCTCTTATAGATCGTTACTG  
TGGCGTGAAAAGCCCTCCATTAAATAGATCAACAGGGAGATTGATGTGGATTAAGTTTGTCTGATGAAGAGCT  
TGAAGGACTGGGATTTTCGAGCAAAATATTCATTTATTCAGATCCAGACTTTACTTACCTAGGAGGTATTTTAA  
TCCCATTCCAGATTGTGCTGAGCTCTCGGGAGCTGATGGAATAGTGCCTCTAGTCAGGTAGAACAAGAGGA  
GAAAACAAAACAGGCCAAGCCGTTGATTGCATCTGGACCATTAAGCCACTCCAAAAGCTAAGATTTATTTGAG  
GTTCCCTAGATTATCAAATGGAGCACTCAAATGAATGCAAGAGAACTTCGTTGCAGTCTATGATGGAAGCAGTTC  
TATTGAAAACCTGAAGGCCAAGTTTTCAGCACTGTGGCCAAATGATGTAATGCTTAAACAGGAAATGGAGTGAT  
TCGAATGTGGGCGAGATGAAGGTAGTCCGCTTAGCAGGTTTTCGAATGCTCTTTACTTCTTTGTGGAGCCTCCCTG  
CACAAGCAGCACTTTCTTTTCCCATAGCAACATGTGCATCAATAATTCTTAGTCTGTAATGGTGTCCAAAATTG  
TGCATACCCCTTGGGATGAAAATCATTTGTAAGAAAAAGAAAAAGCAGGAGTATTTGAACAAATCACTAAGACTCA  
TGAACAATTAATGGCATTACTTCAGGGATTGTCTGGTCCTTCTCATTATTTCTATTCTATGACAACTGAAACA  
GCCTCGAAAAAAGGTCATGGCTTGCAAAACCGCTTTTAAATAAACCGGGTTCCAAGAAGTGTGTGATCCTCTCA  
TTATGAAGTGTTTTCACTAAGGGACAAAGAGATTTCTGCAGACCTGGCAGACTGTGCGAAGAATTGGACAACCTA  
CCAGAAGATGCGGCGCTCCTCCACCGCCTCCCGCTGCATCCAGACCACCACTGTGGGTGCGAGGCCCTCCAGCGT  
CAAACAAAGCAGGACCAACCTCAGTTCATGGAACCTTCTTCCGAAATGACTTTGCACAACCAAGCCAATGAA  
AACATTTAATAGCACCTTCAAGAAAAGTAGTTACACTTTCAAACAGGCACATGAGTGCCCTGAGCAGGCCCTGGA  
AGACCGAGTAATGGAGGAGATTCCCTGTGAAATTTATGTGAGGGGCGAGAAGATTCTGCACAAGCATCCATATC  
CATTGACTTCTAAATCTTCTGCTAATGGTGATGTGAATCTTAGGGTGTGTACGTACGCAGCCTCCAGGGCACCAT  
ACTGTTTCCAGCAGCCAACCCCTTTCTCCCATCACAACCTACGAAGACCTTGATTACCGTTAACCTATTGTATGG  
TGATGTTTTTATTCTCTCAGGCAGTCTATATATGTAAACCAATCAAGGAACTTACTCTATTTCAGTGGAAACAAT  
AATCATCTCTATTGCTTGGTGTCAATTTATAGGAAGCACTGCCAGTTAAAGAGCATTAGAAGAGGTGGTTGGATGG  
AGCCAGGCTCAGGCTGCCTCTCGTTTTAGCAACAAGAAGACTGCTCTTGACTGATAACAGCTCTGTCAATATTT  
TGATGCCACAATAAAGTTGATTTTTTTTACATTCCTTTTATTTTCTTTCTCTAAATTTAATTTGTTTTATAA  
GCCTATCGTTTTTACCATTTTCAATTTTCTTACATAAGTACAAGTGGTTAATGTACCACATACTTCAGTATAGGCATT  
TGTTCTTGAGTGTGTCAAAATACAGCTAGTTACTGTGCCAATTAAGACCCAGTTGTATTTACCCCATCTGTTTCT  
TCTTGGCTAATCTCTGTACTTCTGCCTTTTAAATTAAGTGGCCCTTATTCCTTATTTCTGTGAGAAATAATAGAT  
GATATGATTTATTACCTTTCAATTATATTTTCTCAGTTATACCTAGAAAATTCATAATCCTGGGATATATGTAC  
CATTGTGACCTATGACTAAAAATTTGAAAAAGATAAAAAATTTCTAGCAAGCCTTTGAAGTTTACCAAGTATAGTC  
ACATTTCAGTGACAGCCATTCAATCCAGTAAAGATCATTTCATTCACTTTGGGAGAGGCCATAATTACATTTA  
TTTGCAATGTTTCTCTCGCTAGATTGTTACATAGCTCCCATTTCTGTTGGTTTTGCTTACAGCATATGTTAACCA  
AGGTTAGATGCCAGTTAAATTCCTTAGAAATTTGATGAGCCTTGAGATTGCTTCTAACTGGGACATGACATTT  
TTCTAGCTCTTATCAAGAATAACAACCTCCACTTTTTTTTAAACTGCACCTTTGACTTTTTTTTATGGTATAAAAA  
CAATAATTTATAAACATAAAAGCTCATTGTGTTTTTTAGACTTTTGATATTATTGATACTGTACAACTTTATT  
AAATCAAGATGAAAGCCTACAGGACAGATTCCTTTCAGTGTTCACATCAGTGGCTTTGTATGCAAAATATGCTGT  
GTTGGACCTGGACGCTATAACTTATTGTAAAGACCTTGGAAATGTGGACATAAGCTCTTCTTTCTTTTGTGTAC  
TGATTTAGTTTGTGATAAATTTTCACTGTGTGATATTTATGCTCTAAATCACTACACAAATCCCATATTAATA  
TATACATTTGACCTGAAAAAAA

**FIGURE 114**

MALERLCSVLKVLLITVLVVEGIAVAQKTQDGQNIGIKHIPATQCGIWVRTSNGGHFASPNYP  
DSYPPNKECIYILEAAPRQRIELTFDEHYIIEPSFECRFDHLEVRDGPFGFSPLIDRYCGVKS  
PPLIRSTGRFMWIKFSSDEELEGLGFRAKYSFIPDPDFTYLGGILNPIPDCQFELSGADGIVR  
SSQVEQEEKTKPGQAVDCIWIKATPKAKIYLRFLDYQMEHSNECKRNFVAVDGSSSIENLK  
AKFCSTVANDVMLKTGIGVIRMWADEGSRLSRFRMLFTSFVEPPCTSSTFFCHSNMCINNSLV  
CNGVQNCAYPWDENHCKEKKKAGVFEQITKTHGTIIGITSGIVLVLLIISILVQVKQPRKKVM  
ACKTAFNKTGFQEVFDPPHYELFSLRDKEISADLADLSEELDNYQKMRRSSTASRCIHDHHC  
SQASSVKQSRTNLSSMELPFRNDFAQPQPMKTFNSTFKKSSYTFKQGHECPEQALEDRVMEEI  
PCEIYVRGREDSAQASISIDF

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 348-369

**N-glycosylation sites.**

amino acids 311-315, 385-389, 453-457, 475-479

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 426-430, 479-483

**N-myristoylation sites.**

amino acids 22-28, 32-38, 54-60, 186-192, 279-285, 318-324,  
348-354, 352-358, 441-447



# **FIGURE 115**

GGTCTCTGTCCTTGGCTGTGGCTCCTGCGCTCTGGCTGAGCC**ATG**TTCTTCTCTCTCGCCCTC  
 CTCCTGAGCTTGGAAAGACTGCAAGCCACGAAGGTTCTGAAGGAATATTTCTGCATGTCACA  
 GTTCCACGGAAGATTAAGTCAAATGACAGTGAAGTTTCAGAGAGGAAGATGATTTACATCATT  
 ACAATTGATGGACAACCTTACACTCTACATCTCGGAAAACAATCATTCTTACCCCAGAACTTT  
 TTGGTTTATACATATAATGAACTGGATCTTTGCATTCTGTGTCTCCATATTTTATGATGCAT  
 TGCCATTACCAAGGATATGCTGCCGAATTTCCAAATTCATTTGTGACACTCAGTATATGTTCT  
 GGTCTCAGGGGATTTCTCCAGTTTGAAAAATATCAGTTATGGAATTGAACCAGTAGAATCTTCA  
 GCAAGATTTGAGCATATAATTTATCAAATGAAAAATAATGATCCAAATGTATCCATTTTAGCA  
 GTAAATTACAGTCATATTTGGCAGAAAGACCAGCCCTACAAAGTTCTTTAAACTCACAGATA  
 AAAAATCTTTCAAACTATTACCCCAATATCTGGAAATATACATTATAGTGGAAAAAGCTTTG  
 ATGTTTACCCAGTTCAAATTGACTGTTATACTGTCTTCTTGGAAATTGTGGTCAAATGAAAA  
 CAGATTTCCACCATGGGGATGCTGATGATATATTACAAAGATTTTTGGCATGGAAACGGGAC  
 TATCTCATCTTACGGCCCCATGACATAGCATACTTACTTGTTTACAGGAAACATCCTAAATAT  
 GTGGGAGCAACATTTCTTGGCACCCTATGCAATAAAAGCTATGATGCAGGTATTGCTATGTAT  
 CCAGATGCAATAGGTTTGGAGGGATTTTCGGTTATTATAGCTCAACTGCTTGGCCTTAATGTA  
 GGATTAACATATGATGACATCACTCAGTGTCTGTCTGAGAGCTACATGCATCATGAATCAT  
 GAAGCAGTGAGTGCCAGTGGTAGAAAGATTTTAGCAACTGCAGCATGCACGACTATAGATAT  
 TTTGTTTCAAAATTTGAGACTAAATGCCTTCAGAAGCTTTCAAATTTGCAACCATTACATCAA  
 AATCAACCAGTGTGTGTAATGGGATTTTGGAAATCCAATGAAGAATGTGACTGTGGTAATAAAA  
 AATGAATGTCAATTTAAGAAAGTGCTGTGATTATAACACATGTAAACTGAAGGGCTCAGTAAAA  
 TGTGGTTCTGGACCATGTTGTACATCAAAGTGTGAGTTGTCAATAGCAGGCACTCCATGTAGA  
 AAGAGTATTGATCCAGAGTGTGATTTTACAGAGTACTGCAATGGAACCTCTAGTAATTGTGTT  
 CCTGACACTTATGCACTGAATGGCCGTTTGTGCAAGTTGGGAAGTGCCTATTGCTATAACGGA  
 CAATGTCAAACACTACTGATAACCAAGTGTGCCAAGATATTTGGAAAAGGTGCTCAAGGTGCTCCA  
 TTTGCCTGTTTAAAGAAGTTAATTCTCTGCATGAAAGATCTGAAAAGTGTGGTTTTAAAAAT  
 TCACAACCATTACCTTGTGAACGGAAGGATGTTCTCTGTGGAAAATTAGCTTGTGTTCAGCCA  
 CATAAAAATGCTAATAAAAAGTGACGCTCAATCTACAGTTTATTTCATATATTCAAGACCATGTA  
 TGTGTATCTATAGCCACTGGTTCCTCCATGAGATCAGATGGAACAGACAATGCCTATGTGGCT  
 GATGGCACCATGTGTGGTCCAGAAATGTACTGTGTAAATAAAACCTGCAGAAAAGTTCATTTA  
 ATGGGATATAACTGTAATGCCACCACAAAATGCAAAGGGAAAGGGATATGTAATAATTTTGGT  
 AATTGTCAATGCTTCCCTGGACATAGACCTCCAGATTGTAAATTCCAGTTTGGTTCCCCAGGG  
 GGTAATGATGATGGAATTTTTCAGAAATCTGGTGACTTTTATACTGAAAAAGGCTACAAT  
 ACACACTGGAACAACTGGTTTATTCTGAGTTTCTGCATTTTCTGCCGTTTTTCATAGTTTTC  
 ACCACTGTGATCTTTAAAAGAAATGAAATAAGTAAATCATGTAAACAGAGAGAATGCAGAGTAT  
 AATCGTAATTCATCCGTTGTATCAGAAAGCGATGACGTGGGACATT**TA**ATATTGCACAGAACTT  
 CCATAGCAAATAACCTAAAGGAACGAATGTGCTTTATTTATAACCTTACGTTATCCCCAATGC  
 ATTGTAAATGTCAAACCTTTTGGAAAATAAAGCCTGCGTGCCCTCCC

**FIGURE 116**

MFLLLALLTELGRQLQAHEGSEGIFLHVTVPRIKISNDSEVSEKMIYIITIDGQPYTLHLGKQ  
SFLPQNFLVYTYNETGSLHSVSPYFMMHCHYQGYAAEFNSFVTLISCSGLRGFLQFENISYG  
IEPVESARFEHIIYQMKNDPNVSILAVNYSHIWQKDQPYKVPLNSQIKNLSKLLPQYLEIY  
IIVEKALMFTQFKLTIVILSSLELWSNENQISTSGDADDILQRFLAWKRDYLILRPHDIAYLLV  
YRKHPKYVGATFPPTVCNKSYDAGIAMYPDAIGLEGFSVIIAQLLGLNVGLTYDDITQCFCLR  
ATCIMNHEAVSASGRKIFSNCSMHDYRYFVSKFETKCLQKLSNLQPLHQNPVCNGILESNE  
ECDGKNECQFKKCCDYNTCKLKGSVKCGSGPCCTSKCELSIAGTPCRKSIDPECDFTEYCN  
GTSSNCVPTDYALNGRLCKLGTAYCYNGQCQTDTNQCAKIFGKGAQGAPFACFEVNSLHERS  
ENCGFKNSQPLPCERKDVLCGKLACVQPHKNANKSDAQSTVYSYIQDHVCVSIATGSSMRSDG  
TDNAYVADGTMCGPEMYCVNKTCKVHLMGYNCNATTKCKGKGICNNFGNCQCFPGHRPPDCK  
FQFGSPGGSIDGNGFQKSGDFYTEKGYNTHWNNWFILSFCIFLPPFIVFTTVIFKRNEISKSC  
NRENAEYNRNSSVVSESDDVGH

**Important features of the protein:**

**Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 665-684

**N-glycosylation sites.**

amino acids 36-39, 76-79, 122-125, 149-152, 156-159, 177-180,  
270-273, 335-338, 441-444, 537-540, 587-590, 601-604, 703-706

**Casein kinase II phosphorylation sites.**

amino acids 74-77, 208-211, 221-224, 304-307, 337-340, 346-349,  
376-380, 415-418, 499-502, 639-642, 708-711

**Tyrosine kinase phosphorylation site.**

amino acids 243-249

**N-myristoylation sites.**

amino acids 53-58, 79-84, 266-271, 298-303, 372-377, 403-408,  
408-413, 442-447, 462-467, 469-474, 488-493, 567-572, 610-615,  
616-621, 634-639

**Amidation site.**

amino acids 328-331

**FIGURE 117**

CCCACGCGTCCGCGGACGCGTGGGGCTCAGTGGGCGTCGCGCGAAGGCTAAGGGAGTGTGGCG  
GGCGGCTCCGGGAGCCAACATGCCTCGGTATGCGCAGCTGGTCATGGGCCCCGCGGGCAGCGG  
GAAGAGCACCTACTGTGCCACCATGGTCCAGCAGTGTGAAGCCCTCAACCGGTCTGTCCAAGT  
TGTAACCTGGATCCAGCAGCAGAACACTTCAACTACTCCGTGATGGCTGACATCCGGGAACT  
GATCGAGGTGGATGATGTAATGGAGGATGATTCTCTGCGATTCCGTCCCAACGGAGGATTGGT  
ATTTTGCATGGAGTACTTTTGCCAATAATTTTGACTGGCTGGAGAACTGTCTTGCCATGTAGA  
GGACGACTATATCCTTTTGTATTGTCCAGGTCAGATTGAGTTGTACACTCACCTGCCTGTGAT  
GAAACATCTGGTCCAGCAGCTCGAGCAGTGGGAGTTCCGAGTCTGTGGAGTTTTTCTTGTTGA  
TTCTCAGTTCATGGTGGAGTCATTCAAGTTTATTTCTGGCATCTTGGCAGCCCTGAGTGCCAT  
GATCTCTCTAGAAATCCGCAAGTCAACATCATGACAAAAATGGATCTGCTGAGTAAAAAAGC  
AAAAAGGAAATGAGAAATTTTGTAGATCCAGACATGTATTCTTTATTAGAAGATTCTACAAG  
TGACTTAAGAAGCAAAAAATCAAGAACTGACTAAAGCTATATGTGGACTGATTGATGACTA  
CAGCATGGTTCGATTTTTACCTTACGATCAGTCAGATGAAGAAAGCATGAACATTGTATTGCA  
GCATATTGATTTTGCCATTCAATATGGAGAAGACCTAGAATTTAAAGAACCAAAGGAACGTGA  
AGATGAGTCTTCCTCTATGTTTGACGAATATTTTCAAGAATGCCAGGATGAATGGAAGAGTTTA  
CTAAAAGTAACCATCTAAAGAGCTTGTGGCCAAACCAGCAGAACATTCTTCTCTTCAAAGGAT  
GCAATAGTAGAAAGCTACTTATTTTAATGAAAAAAGTAAAACTTCGTTCTTTATCAGCCTCA  
TGCCTGAATCAAATTTTTAATTATTCTGAACTGCTGCTGTTTAAAGTGGAATCTTTTAGTAT  
TATAACAGCATCACTTTAGATTTTGTAAAGTCAAAATTGAAATGAATGCACATAGATTTATATA  
TAAATTAGCACCTGAGCTAAGGTTAAGGCCGGTCTAAACTTATTTTCACTTTTTGTATTATTT  
TTGAGATGCAGGAATTACTGTAACAAAATATGTATGTCCGAAGGGAAAAAGCTGCAAGGATAT  
ATATAAGACCACCTGCTTATCTGTATCTTCCATTTTCTATATTGAAAATGTATATTATTTAT  
ATAACTTAAAAAGTAAAAATAACTATGTTTTGAGAT

**FIGURE 118**

MPRYAQLVMGPAGSGKSTYCATMVQHCEALNRSVQVVNLDPAAEHFNYSVMADIRELIEVDDV  
MEDDSLRFPGNGGLVFCMEYFANNFDWLENC LGHVEDDYILFDCPGQIELYTHLPVMKHLVQQ  
LEQWEFRVCGVFLVDSQFMVESFKFISGILAALSAMISLEIPQVNIMTKMDLLSKKAKKEIEK  
FLDPDMYSLLEDSTSDLRSKKFKKLTKAICGLIDDYSMVRFLPYDQSDEESMNIVLQHIDFAI  
QYGEDLEFKEPKEREDESSMFDEYFQECQDE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 151-170

**N-glycosylation sites.**

amino acids 31-35, 47-51

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 212-216

**Tyrosine kinase phosphorylation site.**

amino acids 189-197

**N-myristoylation sites.**

amino acids 13-19, 76-82, 154-160

**ATP/GTP-binding site motif A (P-loop).**

amino acids 10-18

# **FIGURE 119**

GGGCGCTGGGAGACACCGGACGCCCCGCTCGGCTGCGCTGCGGCTCAGGCCCCCGCTCGGGCCC  
 GACCCGCTCGGTACCGCCGGCTCGGGCGCGACCTGCCGGCTGCGGCCCCAGGGCCATGCGG  
 AGGCCCCAGGAGGGCCGGCGGCCACGCGCATCCCGTAGCCAGGTGGCCAGGTCTGCACCG  
 CGGCGGCTCGGCGCCATGGAGCCCCCGTATTGCTGACGGCGCACTACGATGAGTTCCAAGA  
 GGTCAAGTACGTGAGCCGCTGCGGCGCGGGGGCGCGCGGGGGCCTCCCTGCCCCCGGGCTT  
 CCCGTTGGGCGCTGCGCGCAGCGTCACCGGGGCCGGTCCGGGCTGCCGCGCTGGAACCGGCG  
 CGAGGTGTGCTGCTGTCGGGGCTGGTGTTCGCCGCCGGCCTCTGCGCCATTCTGGCGGCTAT  
 GCTGGCCCTCAAGTACCTGGGCCCCGGTTCGCGGCCGGCGGGCGGCGCCTGTCCCGAGGGCTGCCC  
 TGAGCGCAAGGCCTTCGCGCGCGCCGCTCGCTTCCTGGCCGCCAACCTGGACGCCAGCATCGA  
 CCCATGCCAGGACTTCTACTCGTTTCGCTGCGGCGGTTGGCTGCGGCGCCACGCCATCCCCGA  
 CGACAAGCTCACCTATGGCACCATCGCGGCCATCGGCGAGCAAAACGAGGAGCGCCTACGGCG  
 CCTGCTGGCGCGGCCCCGGGGTGGGCTGGCGGCGCGGCCAGCGCAAGGTGCGCGCCTTCTT  
 CCGCTCGTGCTCGACATGCGCGAGATCGAGCGACTGGGCCCCGCGACCCATGCTAGAGGTGAT  
 CGAGGACTCGGGGGCTGGGACCTGGGCGGCGCGGAGGAGCGTCCGGGGTTCGCGGCGCGATG  
 GGACCTCAACCGCTGCTGTACAAGGCGCAGGGCGTGTACAGCGCCGCGCGCTCTTCTCGCT  
 CACGGTCAGCCTGGACGACAGGAACCTCGCGCTACGTGATCCGCATTGACCAGGATGGGCT  
 CACCCTGCCAGAGAGGACCCTGTACCTCGCTCAGGATGAGGACAGTGAGAAGATCCTGGCAGC  
 ATACAGGGTGTTCATGGAGCGAGTGCTCAGCCTCCTGGGTGCAGACGCTGTGGAACAGAAGGC  
 CCAAGAGATCCTGCAAGTGGAGCAGCAGCTGGCCAACATCACTGTGTGAGAGTATGACGACCT  
 ACGGCGAGATGTGAGCTCCATGTACAACAAGGTGACGCTGGGGCAGCTGCAGAAGATCACCCC  
 CCACTTGCGGTGGAAGTGGCTGCTAGACCAGATCTTCAGGAGGACTTCTCAGAGGAAGAGGA  
 GGTGGTGCTGCTGGCGACAGACTACATGCAGCAGGTGTGCGAGCTCATCCGCTCCACACCCCA  
 CCGGCTCCTGCACAACTACCTGGTGTGGCGCGTGGTGGTGGTCTGAGTGAACACCTGTCCCC  
 GCCATTCCGTGAGGCACTGCACGAGCTGGCACAGGAGATGGAGGGCAGCGACAAGCCACAGGA  
 GCTGGCCCCGGTCTGCTTGGGCCAGGCCAATCGCCACTTTGGCATGGCGCTTGGCGCCCTCTT  
 TGTACATGAGCACTTCTCAGCCGCCAGCAAAGCCAAGGTGCAGCAGCTAGTGAAGACATCAA  
 GTACATCCTGGGCCAGCGCCTGGAGGAGCTGGACTGGATGGACGCCGAGACCAGGGCTGCTGC  
 TCGGGCCAAGCTCCAGTACATGATGGTGTGATGGTTCGGCTACCCGGAATTCTGCTGAAACCCGA  
 TGCTGTGGACAAGGAGTATGAGTTTGAGGTCCATGAGAAGACCTACTTCAAGAACATCTTGAA  
 CAGCATCCCCCTCAGCATCCAGCTCTCAGTTAAGAAGATTGGCAGGAGGTGGACAAGTCCAC  
 GTGGCTGCTCCCCCACAGGCGCTCAATGCCTACTATCTACCCAACAAGAACCAGATGGTGT  
 CCCCAGGGGCATCCTGCAGCCACCCCTGTACGACCCCTGACTTCCACAGTCTCTCAACTACGG  
 GGCATCGGCACCATCATTTGGACATGAGCTGACCCACGGCTACGACGACTGGGGGGGCCAGTA  
 TGACCGCTCAGGGAACCTGCTGCACTGGTGGACGGAGGCCTCTACAGCCGCTTCTGCGAAA  
 GGCTGAGTGATCGTCCGTCTCTATGACAACTTCACTGTCTACAACCAGCGGTGAACGGGAA  
 ACACACGCTTGGGGGAGAACATCGCAGATATGGGCGTCTCAAGCTGGCCTACCACGCCTATCA  
 GAAGTGGGTGCGGGAGCACGGCCAGAGCACCCACTTCCCCGGCTCAAGTACACACATGACCA  
 GCTCTTCTTCATTGCCCTTGGCCAGAACTGGTGCATCAAGCGGCGGTTCGAGTCCATCTACCT  
 GCAGGTGCTGACTGACAAGCATGCCCTGAGCACTACAGGGTGTGGGCAGTGTGTCCAGTT  
 TGAGGAGTTTGGCCGGGCTTTCACTGTCCCAAGGACTCACCCATGAACCTGCCCACAAGTG  
 TTCCGTGTGGTGAACCTGGCTGCCCCGCTGCACGCCCCCACTGCCCCCGCACGAATCACCTCC  
 TGCTGGCTACCGGGGCAGGCATGCACCCGGTGCCAGCCCCGCTCTGGGCACCACTGCTTCC  
 AGCCCCCTCAGGACCCGGTCCCCCTGCTGCCCTCACTTCAGGAGGGGCCTGGAGCAGGGTGA  
 GGCTGGACTTTGGGGGGCTGTGAGGGAAATATACTGGGGTCCCCAGATTCTGCTCTAAGGGG  
 CCAGACCCTCTGCCAGGCTGGATTGTACGGGGCCCCACCTTCGCTGTGTTCTTGCTGCAAAGTC  
 TGGTCAATAAATCACTGCACTGTTAAAAA

## **FIGURE 120**

MEPPYSLTAHYDEFQEVKYVSRGAGGARGASLPPGFPLGAARSVTGARSGLPRWNRREVCLL  
SGLVFAAGLCAILAAMLALKYLGPPVAAGGGACPEGCPERKAFARAARFLAANLDASIDPCQDF  
YSFACGGWLRRAIPDDKLTYGTIAAIGEONEERLRLLARPGGGPGGAAQRKVRAFFRSCLD  
MREIERLGPRPMLEVIEDCGGWDLGGAERPGVAARWDLNRLLYKAQGVYSAAALFSLTVSLD  
DRNSSRYVIRIDQDGLTLPERTLYLAQDEDSEKILAAAYRVFMERVLSSLGADAVEQKAQEILQ  
VEQQLANITVSEYDDLRRDVSSMYNKVTLGQLQKITPHLRWKWLLDQIFQEDFSEEEVLLA  
TDYMQQVSQILIRSTPHRVLHNYLVWRVVVLSEHLSPPFREALHELAQEMEGSDKPKQELARVC  
LGQANRHFGMALGALFVHEHFSAAASKAKVQQLVEDIKYILGQRLEELDWMDAETRAAARAKLQ  
YMMVMVGYPDFLLKPDVADKEYEFVHEKTYFKNILNSIPFSIQLSVKKIRQEVDKSTWLLPP  
QALNAYYLPNKNQMVFPAGILQPTLYDPDFPQSLNYGGIGTIIGHELTHGYDDWGGQYDRSGN  
LLHWWTEASYSRFLRKAECIVRLYDNFTVYNQRVNGKHTLGENIADMGVLKLAYHAYQKWVRE  
HGPEHPLPRLKYTHDQLFFIAFAQNWCIKRRSQSIYLVLTDKHAPEHYRVLGSVSQFEFGR  
AFHCPKDSMPMNAHKCSVW

### **Important features of the protein:**

#### **Transmembrane domain:**

amino acids 64-88

#### **N-glycosylation sites.**

amino acids 255-259, 322-326, 656-660

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 722-726

#### **N-myristoylation site.**

amino acids 24-30, 26-32, 27-33, 40-46, 47-53, 65-71, 148-154,  
169-175, 170-176, 237-243, 450-456, 604-610, 607-613

#### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 85-96

#### **Prenyl group binding site.**

amino acids 772-777

#### **Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 609-619

#### **Neutral zinc metallopeptidases, zinc-binding region proteins.**

amino acids 609-619

**FIGURE 121**

CGGACTGCCCCGACCGCGCGATGGAGTCGACCGGCAGCGTCGGGGAGGCCCCGGGCGGACCCC  
GGGTGCTGGTGGTGGGCGGCGGCATCGCGGGGCTGGGCGCGGCGCAGAGGCTCTGCGGCCACT  
CCGCCTTCCCGCACCTGCGGGTCCTGGAGGCCACGGCCCCGCGCCGGGGGCCGCATCCGCTCGG  
AGCGCTGCTTCGGTGGCGTGGTGGAGGTGGGCGCGCACTGGATCCATGGGCCCTCCCGGGGTA  
ACCCCGTCTTCCAGCTGGCTGCTGAGTACGGGCTGCTGGGGGAGAAGGAGCTGTCCCAGGAGA  
ACCAGCTGGTGGAGACCGGGGGTCACGTGGGCTGCCCTCCGTGAGCTACGCCAGCTCCGGGG  
CCAGCGTGAGCCTCCAGCTGGTGGCGGAGATGGCGACTCTGTTCTACGGCCTGATAGACCAGA  
CCCGGGAGTTCTTGACGCTGCAGAGACCCCGGTGCCAGCGTCGGGGAGTACCTCAAGAAGG  
AGATTGGCCAGCACGTGGCCGGCTGGACAGAGGATGAGGAGACCAGGAAGCTGAAGCTGGCCG  
TCCTGAACCTCCTTCTTCAACCTGGAATGCTGTGTGAGCGGCACCCACAGCATGGACCTGGTGG  
CCCTGGCACCCCTTTGGGGAGTATACCGTGCTGCCGGGGCTGGACTGCACCTTTTCTAAGGGCT  
ATCAAGGACTCACAACTGCATGATGGCCGCCCTGCCGGAGGACACTGTAGTTTTTGAGAAGC  
CTGTGAAGACCATCCACTGGAACGGGTCTTCCAGGAGGCAGCCTTTCCCGGGGAGACCTTTC  
CAGTGTGGTAGAGTGTGAGGATGGAGACCGGTTCCCGGCGCACCATGTCATCGTCACCGTGC  
CCTTAGGTTTTCTTAGGGAACATTTGGACACCTTCTTTGACCCTCCCCTGCCGGCTGAGAAGG  
CAGAAGCAATCAGGAAGATAGGCTTTGGGACCAACAACAAAATCTTCTCGAGTTTGAGGAGC  
CCTTCTGGGAGCCAGACTGCCAGCTGATCCAGCTGGTGTGGGAGGACACGTCGCCCCCTGGAGG  
ATGCTGCCCCCTGAGCTACAGGACGCCTGGTTCCGGAAGCTCATTGGCTTTGTGGTCCTGCCTG  
CCTTTGCGTCTGTCCACGTTCTCTGTGGGTTTATTGCCGACTTGAGTCTGAGTTCATGGAGA  
CTCTGTGGATGAAGAAGTACTTCTGTGTCTCACCCAAGTGCTCCGGAGAGTGACAGGAAACC  
CACGGCTCCCCGCGCCCAAGAGCGTCCTGCGGTCTCGCTGGCACAGCGCCCCGTACACTAGGG  
GGTCCTACAGCTACGTGGCCGTGGGCAGTACTGGGGGCGACCTGGACCTGCTGGCTCAGCCCC  
TCCCTGCAGACGGCGCCGGCGCCAGCTCCAGATCCTGTTTGCGGGGAAGCCACACATCGCA  
CGTTTTACTCCACGACGCACGGGGCTCTGCTGTGCGGATGGAGGGAGGCCGACCGCCTCCTCA  
GTCTGTGGGCCCCGAGGTGCAGCAGCCCAGGCCGAGGCTCTAGCTGGGCCAGCCTACTCTG  
TTCCACCCGTGTGCGGGGTAGGCTGGGACCGTCATTTCTTCTGACAGATTTAGTCTGGCTTG  
AAATTTGGGGATGTTAATGAGGGTCCTCTGGTTTTTGGTAACCAGGGCCACCTTCTCAGTTCT  
TGTGTCTGTTATTGGAGTCTGGCCAGGGTTGACTTGAGCTGAGACACCAGATGCTCACGGAGA  
TGCTGGACACATAAAGCAAGTTACAGCCACAAAAAAAAAAAA

## **FIGURE 122**

MESTGSGVEAPGGPRVLVVGGGIAGLGAAQRLCGHSAPHLRVLEATARAGGRIRSERCFGGV  
VEVGAHWIHGPSRGNPVFQLAAEYGLLGEKELSQENQLVETGGHVGLPSVSYASSGASVSLQL  
VAEMATLFYGLIDQTREFLHAAETPVPSVGEYLKKEIGQHVAGWTEDEETRKLKLAVLNSFFN  
LECCVSGTHSMDLVALAPFGEYTVLPGLDCTFSKGYQGLTNCMMAALPEDTVVFEPVKTIHW  
NGSFQEAAFPGETFPVSVECEDGDRFPAHHVIVTVPLGFLREHLDTFDPPPLPAEKAEAIRKI  
GFGTNNKIFLEFEEFPWEPCQLIQLVWEDTSPLEDAAPELQDAWFRKLIGFVVLPAFASVHV  
LCGFIAGLESEFMETLSDEEVLLCLTQVLRRTGNPRLPAPKSVLRSRWHSAPYTRGSYSYVA  
VGSTGGDLDLLAQPLPADGAGAQLQILFAGEATHRTFYSTTHGALLSGWREADRLLSLWAPQV  
QQPRPRL

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 364-385

**N-glycosylation site.**

amino acids 253-257

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 408-412

**N-myristoylation sites.**

amino acids 20-26, 21-27, 25-31, 105-111, 119-125, 164-170,  
216-222, 227-233, 443-449, 484-490

**Aminooxidase Flavin containing amine oxidase:**

amino acids 23-497



# **FIGURE 123**

CGGACGCGTGGGGGAAGATGGATAAATAATTCTGTACACGTGCCCTGGCCTCTGGAGCTCAGCTGCCAGTCCAC  
 GTCTAGGGAATCTTAGCATCTGGGACCAAGACACTTTACAGCAATCATCACCTTTTGAGAGGAGGTGAGCTCAC  
 CAGGACTCATCTGCCATTTTACAGACCTTTTGTGCTACCTGCCAGGTGGCCCCACTGCTGACGAGAGATGGTGGA  
 TCTCTCAGTCTCCCCGACTCCTTGAAGCCAGTATCGCTGACCAGCAGTCTTGTCTTCTCATGCACCTCCTCCT  
 CCTTCAGCCTGGGGAGCCGAGCTCAGAGGTCAAGGTGCTAGGCCCTGAGTATCCCATCTGGCCCTCGTCGGGGA  
 GGAGGTGGAGTTCCCGTGCCACCTATGGCCACAGCTGGATGCCAGCAAATGGAGATCCGCTGGTTCCGGAGTCA  
 GACCTTCAATGTGGTACACCTGTACCAGGAGCAGCAGGAGCTCCCTGGCAGGCAGATGCCGGCGTTCGGGAACAG  
 GACCAAGTTGGTCAAGGACGACATCGCTATGGCAGCGTGGTCTGCAGCTTACAGCATCATCCCCCTGTGACAA  
 GGGCACATATGGCTGCCGCTTCCACTCCGACAACTTCTTGCGGAAGCTCTCTGGGAACGGAGGTAGCAGGGCT  
 GGGCTCAGACCCCTCACCTCTCCCTTGAGGGCTTCAAGGAAGGAGGCATTAGCTGAGGCTCAGATCCAGTGGCTG  
 GTACCCCAAGCCTAAGTTTCACTGGAGAGACCACAGGGGACAGTGCCTGCCCTCCAGAGTTTGAAGCCATCGTCTG  
 GGATGCCAGGACCTGTTCAGTCTGGAACATCTGTGGTTGTCCGAGCGGGAGCCCTCAGCAATGTGTCCGTCTC  
 CATCCAGAATCTCCTCTTGAGCCAGAAGAAAGAGTTGGTGGTCCAGATAGCAGACGTGTTCTGTACCCGGAGCCTC  
 TGCGTGAAGAGCGCGTTCTGTGCGACCCCTGCCGCTGTGTTGGTCTCGCGCGCTGGCGCTGGGCGTCTCTCCG  
 GAAGCAGCGGAGAGCCGAGAAAGCTGAGGAAGCAGGCGGAGAGAGACAAGAGAACTCACTGCAGAGCTGGA  
 AAAGCTTCAAGCAGAGCTTGAAGAGCGGGCTGAAGGCCAGGCTGAGTGGAGAGCAGCCCAAAATATGAGT  
 GGATGTGACGCTGGAGCCCGGCTCGGCGCACCCAGCCTGGAGGTGTGGAGGATGGCAAGAGCGTGTCTTCCCG  
 CGGGGCGCGCCAGGCCCCGGCGCTGGCCACCCGACGCGTCTCGGAGCAGACGTGCGCGCTGAGCCTGGAGCG  
 GTTCTCGCGCGCCGCACTACTTGGGAGGTGACGTGGGCGCGCGCAGCCGCTGGTTCCTGGGCGCTGCTTGGC  
 CGCGGTGCGCGCGCGGGGCTGCGCGCTGAGCCCTGCGGCGGCTACTGGGTGCTGGGCTGTGGAACGGCTG  
 CGAGTACTTCTGCTCTGCGCCCGCACCGCGTTCGCGCTCACCTGCGCGTGGCCCGCGCGCTGGGCGTCTTCTC  
 GGACTACGAGGCCGAGAGCTGTCTTCTTCAACGTGTCCGACGGCTCCACATCTTCACTTCCAGACACCTT  
 CTCGGGCGCGCTCTGTGCTACTTCAAGCCAGGCGCCAGCAGCGCGGCGAACATCCGGATCCCCCTGACCATCTG  
 CCCGCTGCCGTTAGAGGACGGGCGTCCCCGAAGAGAACGACAGTGACACCTGGTCTACAGCCCTATGAGCCCGC  
 GGACCCCGCCCTGGACTGGTGGTGAAGCGCCCTCGTGGCGCGGGAAGTGGCCCGGGGGGCCCCCTGGATCCCAG  
 GCCAGCGCTTTGTCTCTCTGCTCTGAGGGAGCAGGTGCACAGCCAAATGTGAGCGAGGGGGAACAAGA  
 GAGGGACCTTTGCTACGTAGATGTGTATGTGTAGTGCAGTTTCTTCAAGGAAAGGAGACAAGTCCAAAGCTCG  
 TTTGTGATTGTGGGACTGAGCGAAGGAGTACAAATATATCCACGTGCTCAGAGCTGGGGTGTCTACGGTGGC  
 GGTGGGCAAGAAGCCAGCATGGAAGAAAGAAGGAGAAAACTTTGGTGAAGTGCCTTAGAGGGATCAGTTAATTG  
 TATAGTTTATATTTTTTGTATATGTTTGTAGCTCTAAAAAGGTGAGATGCAATAACACTTCGTAAAGCAACGA  
 GTTACCTAAGTAAGGCTCAGATCCTAGTTTAAAAACCATTTCCATTAAATGAAGTTGGAGGAACAGCTGCT  
 TCTGAGCCGGGGCAAAATTTCAAGGTGAGCCTGGAGCATTGTGTGTGGTGAAGTAAATAAAGGCTCAAAACGT  
 GACGGCAACCCGGCAAAAGGTTAGGAGCCAGGCGGAAGGGGCTCACTGACCAATTGTGGGACAATTTGAACAT  
 CAGGATGAATAATGACAGGAGAGATTATAACACACTGAATAAAAAACATAATCCATGAGTTTATGCTGATACTCAA  
 ATTTCTTTTAAAAAGGAGAAACAGGAAGGTTTCTTTTGGAGGTGAAATCTAATTATTGGTGAGAGTCTTTGGAGA  
 ACAGGCTGTTTCCAGTCTCAAAGCAGTAACCTTATACACTACTTATAAGTTTGAAGGGGAAAGGTTACCTTTAC  
 AATGGAGACATCTACCAGATCATCCAAGTGATTAAATTTAACATCATCAATGATGGGACCAAGGACATTTAGT  
 TTGACAACTGGGGAAAGAAGTGTCTTACCCCCCTACCCCAAGACATTCTCTGTGCGCCAGGCTGGAGTGCA  
 GCCTCAACCTCTGGGGCCCAAGTGATCCTCCACCTCAGCACACACACCATGCCCAATTTTAAAGTGGTTATAG  
 AGACGGGGGTCTCACTTTGTTACCCAGGCTGGTCTCAACTCCTGCGCTCAAGCAATCCTCCACCTGGGCTCC  
 CAAAATGCTGGGTGTACAGGCATGAGCCGCTGTGCTGGCTTCATTTTCAAGTGAAGACATTTGTACTGTGGCTA  
 TGTAGGAGAACATTCTTGTCTTAGCAACATACTGAAGTTTGTAGATATTAATTACACAGTGTCTGCCACTGA  
 ATTTCCAGTGACTAAGTGGAAAAATATAAAACATATGAATATAAAGAAAGAGACAAGTCAATGTAGTAAA  
 ATGACAACACTTGGTGACTCTAGGTGACTGGTGCAGAGATGTTTATGTACTATCAATGTGGCTTTGTGTGGGT  
 TTGAAATTTTGCAAACTAAGAGTTGGGTGGCGGGGAGAAAGGATACACCAAAAACTAAGTGATTATCTTTGGATG  
 GGAAATGTTTGGTAATTGCATTCTTAAATGCTCTTTGTATTTTTAAATGTTCAATAATGTATATGTATCAG  
 TTCTGTAATAAAGGGGAAACACTTTTCA

## **FIGURE 124**

MVDLSVSPDSLKPVSILTSSLVFLMHLLLLQPGEPSSEVKVLGPYPILALVGEEVEFPCHLWP  
QLDAQQMEIRWFRSQTFFNVVHLYQEQQELPGRQMPAFRNRTKLVKDDIAYGSVVLQLHSIIPS  
DKGTYGCRFHSDNFSGEALWELEVAGLGSDPHLSLEGFKEGGIQLRLRSSGWYPKPKVQWRDH  
QGQCLPPEFEAIVWDAQDLFSLETSSVVVRAGALSNVSVSIQNLLLSQKKELVVQIADVFPVGA  
SAWKSAFVATLPLLLVLAAALGVLRKQRRSREKLRKQAEKRQEKLTAELEKLQTELDWRRAE  
GQAEWRAAQKYAVDVTLDPASAHPSLEVSEDKSVSSRGAPPGPAPGHPQRFSEQTCALSLE  
FSAGRHYWEVHVGRRSRWFLGACLAAPVPRAGPARLSPAAGYWVLGLWNGCEYFVLAPHRVALT  
LRVPPRRLGVFLDYEAGELSFNVSDGSHIFTFHDTFSGALCAYFRPRAHDGGEHPDPLTICP  
LPVRGTGVPEENDSDTWLQPYEPADPALDWW

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-34

#### **Transmembrane domain:**

amino acids 247-272

#### **N-glycosylation sites.**

amino acids 102-106, 139-143, 224-228, 464-468, 516-520

#### **Tyrosine kinase phosphorylation site.**

amino acids 105-114

#### **N-myristoylation sites.**

amino acids 129-135, 220-226, 399-405, 423-429, 480-486

#### **Amidation site.**

amino acids 390-394

**FIGURE 125**

TATAGTCCCAGCTACTCATGGGGCTGATGCAGGTTGAGGCAGGAGTTTCATGAGCCCAGGAGGTTGGAGCTGTAA  
 TGAGCTAGGATTCTGCCTCTGCACTCCTAGCTGGATGACAGAGCAGACCCCTGTCTCAAAAAAGAAAAA  
 AAAAAGAAATGCATGAACCAGACATGACAGTTCTGGCCTCAAAGATCTTCCAAAGGAAATGATTTTTTTTAAAC  
 ACCAATGCTGCAGGAAAAAGCAACATATTTAAGTTATCCAATAACACCTATCCAATAATGTATAATCATTATCAT  
 GACATGGTAGAGTTGTTTTATATTTCTTTCTTTTAGGTGAAACACCATTCAAAGTCGTATCAAATCTCTTTCA  
 CCTAAAGAGTTGGTCCGGATACATGTCCCTAAACCTTTGGACAGGAATGATGGAACATTTTTTGATGAGATATAGG  
 ATGTATGAAACTGTGATGAAGGCCTGAAGATAGAGGTCCTTTATGGTGTATGAACATGTGGCTCAGTCTCCCTAT  
 ATTTTGAAAGGACAGTGTACCATGAGTACTGTGAGTGTCCGGAAGATCCTCAGGCCTGGCAGAAGACTCTTTCT  
 TGTCCAACCAAGGAACACAGATTGCAAAAGATTTTGCTTCCCTTTCCAGCATCAATCTCCAGCAAATGCTAAAA  
 GAAGTCCCCAAAGGTTTGGGGATGAGAGAGGTGCCATTGTTTCATTACAGGATTCTCAATAACCATGTTTACCGG  
 AGATCTTTAGGGAAATACACAGACTTCAAGATGTTCTCTGATGAGATTTTGTATCATTGACAAGAAAGGTCCTT  
 CTCCAGATTAGAAATTTATGTTAATCTTGAGATTGGCCCTTGAGCATCGAAAGTCAATGGAACCCCTAGC  
 CCCATACCTATCATTTATGGTGTGGCTCTCTGATTCAAGAGATGTTGTCTTCCAACGTATGACATCACCCAC  
 CCTAGCTTGAAGCCATGCGGGTGTACAAATGATCTCTCTCTATTACAGGAAATACAGGGCCTTCTCTGGATC  
 AATAAAACAGAGAGAGCTTTCTTCAAGGTAGAGACAGCCGAGAGGAGAGGCTCCAGTTGGTACAGCTGTCCAAA  
 GAAATCCTCAGCTACTAGATGCAGGAATTACAGGATATTTCTTTTCCAAGAGAAAGAAAAGGAGCTTGGAAAA  
 GCCAAGTTGATGGGTTTCTTGTATTCTTTAAGTACAAGTATCAAGTAAATGTGATGGGACCGTGGCTGCTTAC  
 AGATATCCATATCTCATGTGGGCGACAGTCTGGTTTTAAAGCAGGACTCGCCATATTATGAACATTTCTACATG  
 GCACTAGAACCTTGAAGCATTATGTTCCAATTAAGAAATCTGAGTGATTTATTAGAGAAAGTTAAATGGGCT  
 AAGGAAATGATGAAGAAGCCAAGAGATTGCAAAAGAGGACAGTTGATGGCTAGGGACCTACTACAGCCACAC  
 AGGCTTTACTGCTACTATTACCAAGTACTGCAGAAATATGCCGAGCGCCAGTCCAGCAAACCCGAAGTACGTGAT  
 GGAATGGAACCTTGTCTCAGCCAGAAGATAGCACAGCCATCTGCCAGTGCCACAGGAAAAAGCCTTCAAGAGAA  
 GAACTTTGAGTCAGCCCAGAATCACACTCCTGTGTATCCCGCTACACTTTAAGGAAAGATTGAATCTAAGCTGT  
 GAAGGACAGTATAGAAGACTGCACCAAGTGGACTAGTTCTCCCGTGGCTTTATATATGTAGATGGATATAGCAG  
 TACTGGTTGAGTATCCCTCATCTGAAATGCTTAGGACCAGGAGTGTTCAGGCTTCAGATTTTTTAAGATTTGGG  
 AATATTGCTATACATAAGGATCTTTGGGATGAGATCCAAGTCTAAACACAAAATTCATTATATTATTTAT  
 ATATACCTTGTTCACATACCCTGAAGGTAATTTATATAATATTTTAAATAATTTGTGCTAGAAACAAAGTTTGT  
 ATACATTGAACGTGTCAGAAAGCAAGGTGTCACTATCTTAGCGACCCAAGTGGTGGTGTGAGCACTAAAAAGTT  
 TTGGATTTTGGGGTATTCAGATTTTAGATTTTGTATGAGGAATGTTCAACCTGTATTGAACAAGCATTACCA  
 AATATCATTGAATATTAATATCTTTGCGTAAAAACTGCTATTATCAGCATCATAGTTTCTCTAAAAAGGAAACT  
 TGGGATCATAGCCGATAGAGAGACTTGCTAAAAATATAAATCAGCCTCTGCAAACTGTTTACATATTTATTTGGT  
 TTACATATTTTATTTGGTTTATTTCTATCCCTGTTCACTTTTCTCTTCCACTTCCAATTATGAAGAGAAAAAT  
 TTGTTCAAGGTTGTCCCCCGCCCCCGCTCACTGCATAATTTCTCCTTACAAAGCTGCTTTTGGCTTTTATTAA  
 TAACAGCTTCTTTTAGAAGGTCTGATAAGGATATTTAAGGAAGAAGAGAATGACTGTTTATTAAGGTGGCAT  
 GGAGACTGTGGAGGGAATATTTTAAAGCACTACTCATATCCTTTAAACTAAATTTTGCCAAAGCCCGAGACAA  
 CATTAAAGGAGAAATGTACCTTAAGTTAGTAATTCAAATCTATCTGAGTTGTATACCATCAAAGACAATACAG  
 TTATTAACATAGATGAAGTATGCTATAGGCATCATTCATTATCTATATGAATAGGTGAAAGATAAAGTGTAG  
 TCAGGTGAAAGGCATTATCATTTTTAAGCTGAAAAGGGATCCTTGAAAACACTGAAAACCTCTACAAACATCT  
 TCAGGAAGCCTGCTATCTTGGGATTCATAATAATAGGCCAAGAACAAGGCAAGCATCCATTCTCACTCCACC  
 ACTTTTCTATTTCACTGGGTGTCTATGCTACGATGAAGACTTTGGAATTTCTTTTCTTTTAGGACAGGGTCA  
 GGATTTAGGACTCATAGCCTGAAAGCTCATTAATCTCCTTTGTAACCATCAGTCCAAGGTTCACTTCACTAAG  
 TGATGTTCTAAAAACAAGAGCTATCCTCATTCAAATTTAAAAATATGTACTCTGGCCGGTTGCACTGGCTCAGC  
 CCTGTAATCCCAGCACTTTGGCAGGCGAGATGGGCGGATCTTTTGAGGTGAGGAGTTGAGAGTTACACCCTGGCCA  
 ACATGGTGAAACCCCGTCTCTACTAAAAATACAAAATTAGCCAGGCATGGTGGCATTTCCTGTAATCCCAGCT  
 ACTCGGGAGGCTGAGGCAGGAGAAATCACTTGAACCTGGGAGGCAGAGGTTGCACTGAGGTGAGATTACACCACTG  
 CACTCCAGCCTGGGTGACAGAGTGAGACTCCATCTCAAAAACCTGAAAATAAAAAATAAAAATATGTATTCTCTAA  
 CTGAAATATTTACTTTAATCTGGAACAATGTAACATATTTTAAAGTGGTTACATCTATTCTTGTGGAAGAACA  
 TAAACAGAATTTTTGACTAAGCATAACCAATTTTCAAGACAGTCTAATCAATGCCAAGTATCCAAGGCAAACTC  
 TAATACCCATCCATTGTGCAAAACCAAGCAGCAAGTATTAATAAGAGCAAGCTGTCTGAGCCCATACCTA  
 ATGAATTTGTGCTTAAATATTGTACATTGTGTTGAGGCTTGTCAAACTGGGATTATGGCAAGAAAGGTTGCC  
 TAACTCATACCTTTCTGCTCAAATTCAGGTGCTAAAGGCTAATGGCATTTTAAACATCTTACATTTTAAAAA  
 TTTATATTGCTCTGCCAAACAGGCCTAATAGTTAAAGCAAGTTGAGACAAACAGGCAGATTCACTGTGTGGA  
 ACAGGAAGGATGTCTTTAAAAAAGGTGGAATCCCTCAAAAATTTCTATAGGAGACAGCAGCCTTAATCTACA  
 TAATTTCTTATCTCGCAATTCAGCCGAGCCTTTAAAGAGTTAGTGTAAATGGCTTTCTGGTTTGAACAAAA  
 ATGCTCTATGTGGTTGAAAGTTTGGGAGGAGATTCCAATATCTGAGGAGAAAGTGGAGTGAAGGGAATCTT  
 ACTTTTTGCTTTATACCTTTCTATAATATTAGATTTTTTTTTTACTGTAAGTATGGATCAAATGCAAAATAAG  
 AAAATGCCAACCTTAGAAAAGACAATAATGCACAAAGATATAAACAGGAACAGCAATATTTATATTTTTTC  
 CATTTTGCTCTTTTAAATCTATGTTTGAACCTTATATCTTGGGACTTATGTATATATATACCTTTTAAATAAA  
 ATAAATTTTCTAAATAAAAGTTG

## **FIGURE 126**

MVELFIFLFLLLGETPFKVVVKSLSPKELVRIHVPKPLDRNDGTFLMRYRMYETVDEGLKIEVL  
YGDEHVAQSPYILKGPVYHEYCECPEDPQAWQKTLSCPTKEPQIAKDFASFPSINLQQMLKEV  
PKRFGDERGAIVHYTILNNHVYRRSLGKYTDFKMFSDIILLSLTRKVLLPDLEFYVNLGDWPL  
EHRKVNGTPSPIPIISWCGSLDSRDVVLPTYDITHSMLEAMRGVTNDLLSIQNGTGPSWINKT  
ERAFFRGRDSREERLQLVQLSKENPQLLDAGITGYFFFQEKELGKAKLMGFFDFFKYKYQV  
NVDGTVAAAYRYPYLMGLGDSLVLKQDSPYEHFYMALEPWKHYVPIKRNLSDLLEKVKWAKEND  
EEAKKIAKEGQLMARDLLQPHRLYCYYYQVLQKYAERQSSKPEVRDGMELVPQPEDSTAICQC  
HRKKPSREEL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-16

**N-glycosylation sites.**

amino acids 250-254, 363-367

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 444-448

**N-myristoylation site.**

amino acids 208-214, 319-325, 388-394

**Endoplasmic reticulum targeting sequence.**

amino acids 448-453

**Mitochondrial energy transfer proteins signature.**

amino acids 25-34

**FIGURE 127**

AGCCGTCGGAGGGAGCCGGAGCGCTTCTCCCGAGTTGGTGATAGATTGGTGGTCATCCAACAT  
GCAGAAATGAATGAGCAGTGAAAAGCAGCAGAGCCGATGGGTTCATGAGGATGTAAGTGCGTTT  
GAAGGCTTCCACACCCTCTACTCCAGGAATCATGAATAAACTGGAGGATAAGCAGGACCAGAT  
GATACCATGAAGAGAAGTTTACAGGCCCTCTATTGCCAACTGTTAAGTTTCTGCTGATCTTG  
GCACTGACCGAAGCGCTGGCATTGTCATCCAGGAACCATCTCCAGGGAATCTCTTCAGGT  
CTCCCTTCAGGCACTCCCCCGGAACCATGGTGACAGCACCCACAGCTCTACCAGACATACT  
TCTGTGGTGATGCTGACCCCCAATCCCGATGGACCCCCCTCACAGGCTGCAGCTCCCATGGCA  
ACACTGACACCCCGTGACAGGGGGCACCTCCTACGCACACCATCTCCACCATCGCTGCCACA  
GTAACCGCCCCCTATTCTGAAAGCTCCCTGTCCACAGGGCCCGCTCCAGCAGCCATGGCAACC  
ACATCCTCCAAGCCAGAGGGCCGCCCCGAGGGCAGGCTGCCCCCACCATCCTGCTGACAAAG  
CCACCGGGGGCCACCAGCGCCCCACCACAGCGCCCCCGCACTACCACACGCAGGCCCCCCC  
AGGCCCCCAGGCTCTTCCCGAAAAGGGGCTGGTAATTTCATCACGCCCTGTCCCGCCTGCACCT  
GGTGGCCACTCCAGGAGTAAAGAAGGACAGCGAGGACGAAATCCAAGCTCCACACCTCTGGGG  
CAGAAGCGGGCCCTGGGGAAAATCTTTTCAGATCTACAAGGGCAACTTCACAGGGTCTGTGGAA  
CCAGAGCCCTCTACCTTCACCCCCAGGACCCCACTCTGGGGCTACTCCTCTTACCACAGCCC  
CAGACAGTGGCTGCGACCACAGTGCCCAGCAATACCTCATGGGCACCCACCACCACCTCCCTG  
GGGCTGCAAAGGACAAGCCAGGCCTTCGACAGCAGCCCAGGGGGGTGGTTCTACCTTCACC  
AGCCAAGGAGGGACACCAGATGCCACAGCAGCCTCAGGTGCCCTGTTCAGTCCACAAGCTGCC  
CCAGTGCCTTCTCAGCGCCCCCACCACGGTGACCCACAGGATGGCCCCAGCCATAGTGACTCT  
TGGCTTACTGTTACCCCTGGCACCAGCAGACCTCTGTCTACCAGCTCTGGGGTCTTCACGGCT  
GCCACGGGGCCACCCAGCTGCCTTCGATACCAGTGTCTCAGCCCCCTTCCAGGGGATTCCCT  
CAGGGAGCATCCACAACCCACAAGCTCCAACCCATCCCTCCAGGGTCTCAGAAAGCACTATT  
TCTGGAGCCAAGGAGGAGACTGTGGCCACCTCACCATGACCGACCGGTGCCAGTCTCTC  
TCCACAGTGGTATCCACAGCCACAGGCAATTTCCCTCAACCGCTGGTCCCCGCCGGGACCTGG  
AAGCCTGGGACAGCAGGGAACATCTCCCATGTGGCCGAGGGGGACAAACCGCAGCACAGAGCC  
ACCATCTGCCTGAGCAAGATGGATATCGCCTGGGTGATCCTGGCCATCAGCGTGCCCATCTCC  
TCCTGCTCTGTCTGTGCTGACGGTGTGCTGCATGAAGAGGAAGAAGAAGACCGCCAACCCGGAG  
AACAACTGAGCTACTGGAACAACACCATCACCATGGACTACTTCAACAGGCATGCTGTGGAG  
CTGCCCAGGGAGATCCAGTCCCTTGAAACCTCTGAGGACCAGCTCTCAGAGCCCCGCTCCCCA  
GCCAATGGCGACTATAGAGACACTGGGATGGTCCTTGTTAACCCCTTCTGTCAAGAAACACTG  
TTTGTGGGAAACGATCAAGTATCTGAGATCTAACTACAGCAGGCATCACTTTGCCATTCCGTA  
TTTTTCGTCTCTAAATTATAAATATACAAATATATATATTATAAATATAACCTTGTGTAACCC  
TGACTTAATGAGAAACATTTTCAGCTTTTTTTTCTATGAATTGTCAACATCTTTTTTACAAGT  
GTGGTTTAAAAAAAAAAAAAACTTTACAGAATGATCTGTGGCTTTATAAAATAAAGGTATTTCT  
AAGCAAAAAAAAAAAAAAAAAA

## **FIGURE 128**

MKRSLQALYCQLLSFLLILALTEALAFAIQEPPRESLQVLPSGTPPGTMVTAPHSSTRHTSV  
VMLTPNPDGPPSQAAAPMATLTPRAEGHPPTHITISTIAATVTAPYSESSLSTGPAPAAMATTS  
SKPEGRPRGQAAPTILLTKPPGATSRPTTAPPRTTTRRPPRPPGSSSRKGAGNSSRPVPPAPGG  
HSRSKEGQRGRNPSSSTPLGQKRPLGKIFQIYKGNFTGSVEPEPSTLTPRTPLWGYSSSPQPQT  
VAATTVPNSNTSWAPTTTTSLGPAKDKPGLRRAAQGGGSTFTSQGGTPDATAASGAPVSPQAAPV  
PSQRPHHGDPQDGPSHSDSWLTVTPGTSRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGIPQG  
ASTTPQAPTHPSRVSESTISGAKEETVATLTMTDREVPSPLSTVVSTATGNFLNRLVPAGTWKP  
GTAGNISHVAEGDKPQHRATICLSKMDIAWVILAISVPISSCSVLLTVCCMKRKKKTANPENN  
LSYWNNTITMDYFNRHAVELPREIQSLETSEDQLSEPRSPANGDYRDTGMVLVNPFCQETLFV  
GNDQVSEI

**Important features of the protein:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 469-487

**N-glycosylation sites.**

amino acids 178-182, 223-227, 261-265, 446-450, 504-508, 509-513

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 495-499

**N-myristoylation sites.**

amino acids 44-50, 48-54, 175-181, 222-228, 279-285, 286-292,  
288-294, 296-302, 351-357, 374-380, 427-433, 442-448

**TonB-dependent receptor proteins signature 1.**

amino acids 1-44

# **FIGURE 129**

AGGCGAGGCGCGGCGCCGCTGCACACACGCACACGGAGCTATGGGGTGCCATGTTGCCACCAG  
 CTGCCACGTGGCCTGGCTTTTGGTGCTGATCTCTGGATGCTGGGGCCAGGTGAACCGGCTGCC  
 CTTCTTCACCAACCACCTTCTTTGATACATACCTGCTGATCAGCGAGGACACGCCTGTGGGTTC  
 TTCTGTGACCCAGTTGCTGGCCCAAGACATGGACAATGACCCCCCTGGTGTGTTGGCGTGTCTGG  
 GGAGGAGGCCTCTCGCTTCTTTGCAGTGGAGCCTGACACTGGCGTGGTGTGGCTCCGGCAGCC  
 ACTGGACAGAGAGACCAAGTCAGAGTTCACCGTGGAGTTCTCTGTCTCAGCGACACCAGGGGGT  
 GATCACACGGAAGGTGAACATCCAGGTCGGGGATGTGAATGACAACGCGCCACATTTACAA  
 TCAGCCCTACAGCGTCCGCATCCCTGAGAATACACCAGTGGGGACGCCCATCTTCATCGTGAA  
 TGCCACAGACCCGACTTGGGGGCAGGGGGCAGCGTCCTCTACTCCTTCCAGCCCCCTCCCA  
 ATTCTTCGCCATTGACAGCGCCCGCGGTATCGTCACAGTGATCCGGGAGCTGGACTACGAGAC  
 CACACAGGCCTACCAGCTCACGGTCAACGCCACAGATCAAGACAAGACCAGGCCTCTGTCCAC  
 CCTGGCCAACTTGGCCATCATCATCACAGATGTCCAGGACATGGACCCCATCTTCATCAACCT  
 GCCTTACAGCACCAACATCTACGAGCATTTCTCTCCGGGCACGACGGTGCGCATCATCACCGC  
 CATAGACCAGGATAAAGGACGTCCCCGGGGCATTGGCTACACCATCGTTTCAGGGAATACCAA  
 CAGCATCTTTGCCCTGGACTACATCAGCGGAGTGTGACCTTGAATGGCCCTGCTGGACCGGGA  
 GAACCCCTGTACAGCCATGGCTTCATCCTGACTGTGAAGGGCAGGAGCTGAACGATGACCG  
 CACCCCATCTGACGCTACAGTCAACACGACCTTCAATATCCTGGTTATTGACATCAATGACAA  
 TGCCCCGAGTTCAACAGCTCCGAGTACAGCGTGGCCATCACTGAGCTGGCACAGGTTCGGCTT  
 TGCCCTTCCACTCTTCATCCAGGTGGTGGACAAGGATGAGAATTTGGGCCTGAACAGCATGTT  
 TGAGGTGTACTTGGTGGGGAACAACCTCCACCACTTCATCATCTCCCCGACCTCCGTCCAGGG  
 GAAGGCGGACATTCTGATTCGGGTGGCCATCCCACTGGACTACGAGACCGTGGACCGCTACGA  
 CTTTGATCTCTTTGCCAATGAGAGTGTGCCTGACCATGTGGGCTATGCCAAGGTGAAGATCAC  
 TCTCATCAATGAAAATGACAACCGGCCCATCTTCAGCCAGCCACTGTACAACATCAGCCTGTA  
 CGAGAACGTACCGTGGGGACCTCTGTGCTGACAGTCCTGGTGAGTCCCCGCTTCACTGCAGG  
 GCCACTGAGCTCTCCAGGGCCGACTGTGGTGAGGCACCCAGAGGGATTTTGTCCAAGGGACCT  
 CAGCAATCAGGGAAGGAGGCACCCCCAAATCCCTGAGCTGTGTTTGTGGTGTATTTAAAATAAA  
 GTTTTTGGACTCTTCAGGAAGGGGCTCCCTTGACCTAGGTTGCAATATGAAAAGGAGCCAAC  
 CTGAGGGGTGACGAGACTGAGCTGAGGACACTGGTTTTCTGCCTTTCCCTGAGAGAGACTCAG  
 TGAGGGTGGGCTGGGAGCCCTGGAAGCCCCCTCAAATGGGTGGGAAGGTGCCAGCCATCCTTG  
 AGAAGGGCAACCCCTCTCCATGTGAGCACAGGCACCAGAGAGGGGCAGGCGCCTGGAGGGTACC  
 GGGGCACCCCCAGCTGCCCATGGCTGGACTTGCCCTTTGACAAGGGGCCCTCCAGTGTCATT  
 TGTATCTGTCTAGTACTCTTGGTTGCAAGGGACAGAAACCCTTAAGTAGTTCAAGCAAAAAAGG  
 ATTGGCTCATGTAACTCAAAAGTATAAGTGATTTTCAAGGCCGGGCTCGGTGGCTCACGCCTGTC  
 ATCCAACACCTTGAGAAAGCCGAGGTGGGCGGATCACTTGAGGTGGGAGTTTGAGACCAGCC  
 TGGCCAACATGGCAAAACCCCGTCTCTACTAAAAATACAAAAATTAGCCGGGTGTGGTGGCAC  
 ACGCCTGTAGTCCCAGCTACTAGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGCGG  
 AGGTTGCAGTGAGCCGAGATTGTGTCACTGCCCTCCAGCCTGGGCGACAGAGCCAGATTCTGT  
 CTC

## **FIGURE 130**

MGCHVATSCHVAWLLVLISGCWGQVNRLPFFTNNHFFDTYLLISEDTPVGSSVTQLLAQDMDND  
PLVFGVSGEEASRFFFAVEPDTGVVWLRQPLDRETKSEFTVEFSVSDHQGVITRKVNIQVGDVN  
DNAPTFHNQPYSVRIPENTPVGTPIFIVNATDPDLGAGGSVLYSFQPPSQFFAIDSARGIVTV  
IRELDYETTQAYQLTVNATDQDKTRPLSTLANLAIITDVQMDPIFINLPYSTNIYEHSPPG  
TTVRIITAIDQDKGRPRGIGYTIVSGNTNSIFALDYISGVLTLNGLLDRENPLYSHGFILTVK  
GTELNDDRTPSDATVTTTTFNILVIDINDNAPEFNSSEYSVAITELAQVGFALPLFIQVVDKDE  
NLGLNSMFEVYLVGNNSHHFIISPTSVQGKADIRIRVAIPLDYETVDRYDFDLFANESVPDHV  
GYAKVKITLINENDNRPIFSQPLYNISLYENVTVGTSVLTVLVSPRFTAGPLSSPGPTVVRHP  
EGFCPRDLSNQGRRHPQIPELCLLVY

**Important features of the protein:**

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 355-374

**N-glycosylation sites.**

amino acids 155-159, 206-210, 349-353, 393-397, 434-438, 466-470,  
472-476

**N-myristoylation sites.**

amino acids 2-8, 49-55, 162-168, 270-276, 278-284, 316-322

**Amidation site.**

amino acids 515-519

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 11-22

**Leucine zipper pattern.**

amino acids 298-320

**PTS HPR component serine phosphorylation site signature.**

amino acids 377-393

**Cadherins extracellular repeated domain signature.**

amino acids 120-131, 336-347

**Cadherins extracellular**

amino acids 120-144, 336-360



**FIGURE 131**

GTGGGCCGCCCCCTGCTGCTGCCGTCCATGCTGATGTTTGCGGTGATCGTGGCCTCCAGCGGGC  
TGCTGCTCATGATCGAGCGGGGCATCCTGGCCGAGATGAAGCCCCCTGCCCTGCACCCGCCCG  
GCCGCGAGGGCACAGCCTGGCGCGGAAAGCCCCCAAGCCTGGGGGCCTGTCCCTCAGGGCTG  
GGGACGCGGACTTGCAAGTGCGGCAGGACGTCCGGAACAGGACCCTGCGGGCGGTGTGCGGAC  
AGCCAGGCATGCCCCGGGACCCCTGGGACTTGCCGGTGGGGCAGCGGCGCACCCCTGCTGCGCC  
ACATCCTCGTAAAGTGACCGTTACCGCTTCCTCTACTGCTACGTCCCCAAGGTGGCCTGCTCTA  
ACTGGAAGCGGGTGATGAAGGTGCTGGCAGGCGTCCTGGACAGCGTGACGTCCGCCCTCAAGA  
TGGACCACCGCAGTGACCTGGTGTTCCTGGCCGACCTGCGGCCTGAGGAGATTGCTACCGCC  
TGCAGCACTACTTTAAGTTTCCTGTTTGTGCGGGAGCCCTTGGAACGCCTCCTCTGCTGCTACC  
GCAACAAGTTTGCGGAGATCCGAGAGTACCAGCAACGCTATGGGGCTGAGATAGTGAGGCGGT  
ACAGGGCTGGAGCGGGGCCAGCCCTGCAGGCGACGATGTCACATTCCTCGAGTTTCCTGAGAT  
ACCTGGTGGATGAGGACCCTGAGCGCATGAATGAGCATTGGATGCCCCGTGTACCACCTGTGCC  
AGCCTTGTCCTGCACTATGACTTTGTGGGCTCCTATGAGAGGCTGGAGGCTGATGCAAATC  
AGGTGCTGGAGTGGGTACGGGCACCACCTCACGTCCGATTTCCAGCTCGCCAGGCCTGGTACC  
GGCCAGCCAGCCCCGAAAGCCTGCATTACCACTTGTGCACTGCCCCCGGGCCCTGCTGCAGG  
ATGTGCTGCCTAAGTATATCCTGGACTTCTCCCTCTTTGCCTACCCACTGCCTAATGTCACCA  
AGGAGGCGTGTGAGCAGTGAACCATGGGTGTGGGGCCAGCAGCTGGTGGGGACTGGTTTCAACG  
CCAGCTTTCTGTGCTTCTGCCTGTCAATTCGGAGAACTCTGGCTCTGGGGCTTGGGGCTTCTC  
AGGATCCTGGATGGCAGAGACTGCCCTCAGAAGTTCTTGTCCAGGGTGGGCACCCACAGTGA  
CTCAGAGGACAGGGCTAGGCAGGAGACCTGCTGCTCCTCATTGGGGGGATCTCTTGGGGGGCA  
GACACCAGTTTGCCAATGAAGCAACACATCTGATCTAAAGACTGGCTCCAGACCCCGGGCTGC  
CAGGATTATGCAGTCCACTTGGTCTACCTTAATTTAACCTGTGGCCAAACTCAGAGATGGTAC  
CAGCCAGGGGCAAGCATGACCAGAGCCAGGGACCCTGTGGCTCTGATCCCCCATTTATCCACC  
CCATGTGCCTCAGGACTAGAGTGAGCAATCATACCTTATAAATGACTTTTGTGCCTTTCTGCT  
CCAGTCTCAAAATTTCTACACCTGCCAGTTCTTTACATTTTTTCCAAGGAAAGGAAAACGGAA  
GCAGGGTTCTTGCTGGTAGCTCCAGGACCCAGCTCTGCAGGCACCCAAAGACCCTCTGTGCC  
CAGCCTCTTCCTTGAGTTCTCGGAACCTCCTCCCTAATTCTCCCTTCCTTCCCCACAAGGCCT  
TTGAGGTTGTGACTGTGGCTGGTATATCTGGCTGCCATTTTTCTGATGCATTTATTTAAATTT  
TGTACTTTTTGATAGAACCCTTGTAAGGGCTTTGTTTTCTAATAGCTGACTTTTTTAATAAAG  
CAGTTTTATATAT

**FIGURE 132**

MLMFAVIVASSGLLLMIERGILAEMKPLPLHPPGREGTAWRGKAPKPGGLSLRAGDADLQVRQ  
DVRNRTLRAVCGQPGMPRPDLPVVGQRRTLLRHILVSDRYRFLYCYVPKVACSNWKRVMKVL  
AGVLDSVDVRLKMDHRSDLVFLADLRPEEIRYRLQHYFKFLFVREPLERLLSAYRNKFGEIRE  
YQORYGAEIVRRYRAGAGPSPAGDDVTFPEFLRYLVDEDPERMNEHWMPVYHLCQPCAVHYDF  
VGSYERLEADANQVLEWVRAPPHVRFPARQAWYRPASPESLHYHLCAPRALLQDVLPKYILD  
FSLFAYPLPNVTKEACQQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-23

**N-glycosylation sites.**

amino acids 67-71, 325-329

**Tyrosine kinase phosphorylation sites.**

amino acids 152-159, 183-183

**N-myristoylation sites.**

amino acids 89-95, 128-134

**FIGURE 133**

CGGCAGTTCTGGCCCCCTGCAGCTGGAGGTACCCTGAGTTCTGAGGGTCGTAGTGCTGTTTCTG  
GTATTCTCATCGCGGTACCTCTACCGGTGTGGACAAGTAAAGTTTGAATCAGCTTCTCCATG  
GCCTGGGCACCAGTTCCCGGCTGAGCCATTTTCCTTTTGGCTAAAAGTCCCCGCCAGAGGCC  
AATTCGTGCGGCGGCGGTGGAGATCGCAGGTCGCTCAGGCTTGCAGATGGGTCAAGGGTTGT  
GGAGAGTGGTCAGAAACCAGCAGCTGCAACAAGAAGGCTACAGTGAGCAAGGCTACCTCACCA  
GAGAGCAGAGCAGGAGAATGGATGCGAGCAACATTTCTAACACCAATCATCGTAAACAAGTCC  
AAGGAGGCATTGACATATATCATCTTTTGAAGGCAAGGAAATCGAAAGAACAGGAAGGATTCA  
TTAATTTGGAAATGTTGCCTCCTGAGCTAAGCTTTACCATCTTGTCCTACCTGAATGCAACTG  
ACCTTTGCTTGGCTTCATGTGTTTGGCAGGACCTTGCGAATGATGAACTTCTCTGGCAAGGGT  
TGTGCAAATCCACTTGGGGTCACTGTTCCATATACAATAAGAACCCACCTTTAGGATTTTCTT  
TTAGAAAATGTATATGCAGCTGGATGAAGGCAGCCTCACCTTTAATGCCAACCCAGATGAGG  
GAGTGAATACTTTTATGTCCAAGGGTATCCTGGATGATTCGCCAAAGGAAATAGCAAAGTTTA  
TCTTCTGTACAAGAACACTAAATTGGAAAAAACTGAGAATCTATCTTGATGAAAGGAGAGATG  
TCTTGGATGACCTTGTAACATTGCATAATTTTAGAAATCAGTTCTTGCCAAATGCACTGAGAG  
AATTTTTTCGTATATCCATGCCCTGAAGAGCGTGGAGAGTATCTTGAAACTCTTATAACAA  
AGTTCTCACATAGATTCTGTGCTTGCAACCCTGATTTAATGCGAGAACTTGGCCTTAGTCCTG  
ATGCTGTCTATGTACTGTGCTACTCTTTGATTCTACTTTCCATTGACCTCACTAGCCCTCATG  
TGAAGAATAAAATGTCAAAAAGGGAATTTATTCGAAATACCCGTCGCGCTGCTCAAAATATTA  
GTGAAGATTTTGTAGGGCATCTTTATGACAATATCTACCTTATTGGCCATGTGGCTGCATAAA  
AAGCACAATTGCTAGGACTTCAGTTTTTACTTCAGACTAAAGCTACCCAAGGACTTAGCAGAT  
ATGGGGGTTACATCAGTGCTGGTCATTGTAGCCTGAGTATACAATCAAGCTTCAGTGTGCAAC  
CTTTTTTCTTTTGCCATTTTCTATTTTAGTAATTTCTTGGGGAACATAAATAATTTTGCAGA  
ATTTTTCTTAATTTTGTATACGTTTTGCACAAAGCAGAGCCACTGTCTAACACAGCTGTT  
AACGAATGATAAACTGACATTATACTCTAAAAGATGGTGTATTTGTGCATTAGATTTGCCTGA  
AAAACCTTTATCCATTTCCATTCTTTATACAAATACCATGTAATGTGTACATATTTAACTAAAG  
AGATTTATAGTCATAATTATTTTATTGTAAAGATTTTAACTAAAGTTTTCTTTCTCTC

**FIGURE 134**

MGQGLWRVVRNQQLQQEGYSEQGYLTREQSRRMDASNISNTNHRKQVQGGIDIYHLLKARKSK  
EQEGFINLEMLPPELSFTILSYLNATDLCLASCWQDLANDELLWQGLCKSTWGHCSIYNKNP  
PLGFSFRKLYMQLDGSLTFNANPDEGVNYFMSKGILDDSPKEIAKFIFCTRTLNWKKLRIYL  
DERRDVLDLVTLHNFRNQFLPNALREFFRHIHAPEERGEYLETLITKFSHRFCACNPDLMRE  
LGLSPDAVYVLCYSLILLSIDLTSPHVKNKMSKREFIRNTRRAAQNISDFVGHLYDNIYLI  
GVAA

**Important features of the protein:**

**Transmembrane domain:**

amino acids 253-272

**N-glycosylation sites.**

amino acids 37-41, 87-91, 298-302

**N-myristoylation site.**

amino acids 110-116

**FIGURE 135**

GGCACGAGGGAGCCTCCGTTAGGGGGTGGGAAAGGACTTTGCCATAGGTCGCTGAGGCCACCA  
TCTGCTCTCTTACTGGCCAAGGGCGTAAAAAGATAGTCTTCCCATTAGCTAGAGAGCAAACCC  
CAGAAAGCCTATTGGCTGCGCCGTCCGCGGGCCTTGGTCCGCTTTGAAGGCGGGCTGCGGCTG  
CGAGAGGAGGGCGGGCGGGAGGCTAGCTGTTGTCTGCTGGTTGCTCGGAGGCACGTGTGCAGTCC  
CGGAAGCGGCGAGGGGAAACTGCTCCGCGCGCGCCGCGGGAGGAGGAACCGCCCCGGTCCCTTA  
GGGTCCGGGCCCCGGCCGGGGCCATGGATTCAATGCCTGAGCCCCGCTCCCGCTGTCTTCTGCTT  
CTTCCCTTGCTGCTGCTGCTGCTGCTGCTGCTGCCGGCCCCGGAGCTGGGCCCCGAGCCAGGCC  
GGAGCTGAGGAGAACGACTGGGTTTCGCCTGCCAGCAAATGCGAAGTGTGTAAATATGTTGCT  
GTGGAGCTGAAGTCAGCCTTTGAGGAAACCGGCAAGACCAAGGAGGTGATTGGCACGGGCTAT  
GGCATCCTGGACCAGAAGGCCTCTGGAGTCAAATACACCAAGTCGGACTTGCGGTAAATCGAA  
GTCACTGAGACCATTTGCAAGAGGCTCCTGGATTATAGCCTGCACAAGGAGAGGACCGGCAGC  
AATCGATTTGCCAAGGGCATGTCAGAGACCTTTGAGACATTACACAACCTGGTACACAAAGGG  
GTCAAGGTGGTGATGGACATCCCCATGAGCTGTGGAACGAGACTTCTGCAGAGGTGGCTGAC  
CTCAAGAAGCAGTGTGATGTGCTGGTGAAGAGTTTGAGGAGGTGATCGAGGACTGGTACAGG  
AACCACCAGGAGGAAGACCTGACTGAATTCCTCTGCGCCAACCACGTGCTGAAGGGAAAAGAC  
ACCAGTTGCCTGGCAGAGCAGTGGTCCGGCAAGAAGGGAGACACAGCTGCCCTGGGAGGGAAG  
AAGTCCAAGAAGAAGAGCAGCAGGGCCAAGGCAGCAGGCGGCAGGAGTAGCAGCAGCAAACAA  
AGGAAGGAGCTGGGTGGCCTTGAGGGAGACCCCAGCCCCGAGGAGGATGAGGGCATCCAGAAG  
GCATCCCCCTCTCACACACAGCCCCCTGATGAGCTCTTGAGCCCCACCCAGCATCCTCTGTCTTG  
AGACCCCTGATTTTGAAGCTGAGGAGTCAGGGGCATGGCTCTGGCAGGCCGGGATGGCCCCGC  
AGCCTTCAGCCCCCTCCTTGCCCTGGCTGTGCCCTCTTCTGCCAAGGAAAGACACAAGCCCCAG  
GAAGAACTCAGAGCCGTATGGGTAGCCCACGCCGTCTTTCCCCTCCCCAAGTGTTTCTCTC  
CTGACCCAGGGTTTCAGGCAGGCCTTGTGGTTTCAGGACTGCAAGGACTCCAGTGTGAACTCAG  
GAGGGGCAGGTGTCAGAACTGGGCACCAGGACTGGAGCCCCCTCCGGAGACCAAACCTACCAT  
CCCTCAGTCTCTCCCAACAGGGTACTAGGACTGCAGCCCCCTGTAGCTCCTCTCTGCTTACCC  
CTCCTGTGGACACCTTGCACTCTGCCTGGCCCTTCCCAGAGCCCAAAGAGTAAAAATGTTCTG  
GTTCTGATTTCTGAAAAAAAAAAAAAAAAAAAAATTCCT

## **FIGURE 136**

MDSMPEPASRCLLLLPLLLLLLLLLLPAPELGPSQAGAEENDWVRLPSKCEVCKYVAVELKSAF  
EETGKTKEVIGTGYGILDQKASGVKYTKSDLRLIEVTETICKRLLDYSLHKERTGSNRFAKGM  
SETFETLHNLVHKGVKVMDIPYELWNETSAEVADLKKQCDVLVEEFEEVIEDWYRNHQEEDL  
TEFLCANHVLKGKDTSCLAEQWSGKKGDTAALGGKKSKKKSSRAKAAGGRSSSSKQRKELGGL  
EGDPSPEEDEGIQKASPLTHSPDEL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**N-glycosylation site.**

amino acids 153-157

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 227-231, 228-232

**Tyrosine kinase phosphorylation site.**

amino acids 142-150

**N-myristoylation sites.**

amino acids 36-42, 74-80, 86-92, 125-131, 222-228, 237-243,  
250-256, 263-269

**Amidation sites.**

amino acids 212-216, 222-226

**ATP/GTP-binding site motif A (P-loop).**

amino acids 62-70

# **FIGURE 137**

CACGCCTCCCGCTGCCAGCCCCGGCACCGGGATCTTAATCAGTCACTATGAAAACCTCATTAGCT  
 CCACAGCAATGAGTCCTCCACTGCTGAAGCTTGGCGCTGTGCTTAGTACCATGGCAATGATCT  
 CAAACTGGATGTCCCAAACCTCTCCCATCCTTGGTGGGACTGAACACCACGAGGCTGTGCACTC  
 CGGATACCTTAACCTCAGATTAGTCCTAAAGAAGGGTGGCAGGTGTACAGCTCAGCTCAGGATC  
 CTGATGGGCGGTGCATTTGCACAGTTGTTGCTCCAGAACAAAACCTGTGTTCCCGGGATGCCA  
 AAAGCAGGCAACTTCGCCAACTACTGGAAGAGTTTTCAGAACATGTCCCAGTCTATTGAAGTCT  
 TAAACTTGAGAACTCAGAGAGATTTCCAATATGTTTTAAAAATGGAAACCCAAATGAAAGGGC  
 TGAAGGCAAAATTTCCGCGAGATTGAAGATGATCGAAAGACACTTATGACCAAGCATTTTTCAGG  
 AGTTGAAAGAGAAAAATGGACGAGCTCCTGCCTTTGATCCCCGTGCTGGAACAGTACAAAACAG  
 ATGCTAAGTTAATCACCCAGTTCAAGGAGGAAATAAGGAATCTGTCTGCTGTCTCACTGGTA  
 TTCAGGAGGAAATTTGGTGCCTATGACTACGAGGAACTACACCAAAGAGTGTGAGCTTGGAAA  
 CAAGACTTCGTGACTGCATGAAAAAGCTAACATGTGGCAAACCTGATGAAAAATCACAGGCCCAG  
 TTACAGTCAAGACATCTGGAACCCGATTTGGTGCTTGGATGACAGACCCCTTAGCATCTGAGA  
 AAAACAACAGAGTCTGGTACATGGACAGTTATACTAACAATAAAATTTGTTCTGTAATACAAAT  
 CAATTGCAGACTTTGTGCTGAGTGGGGCTGAATCAAGGACATACAACCTTCTTTCAAGTGGGCAG  
 GAACTAACCATGTTGTCTACAATGGCTCACTCTATTTTAAACAAGTATCAGAGTAATATCATCA  
 TCAAATACAGCTTTGATATGGGGAGAGTGCTTGGCCAAACGAAGCCTGGAGTATGCTGGTTTTTC  
 ATAATGTTTACCCCTACACATGGGGTGGATTCTCTGACATCGACCTAATGGCTGATGAAATCG  
 GGCTGTGGGCTGTGTATGCAACTAACCAGAATGCAGGCAATATTGTGATCAGCCAACCTTAACC  
 AAGATACCTTGGAGGTGATGAAGAGCTGGAGCACTGGCTACCCCAAGAGAAGTGCAGGGGAAT  
 CTTTCATGATCTGTGGGACACTGTATGTCACCAACTCCCCTTAACCTGGAGCCAAGGTGTATT  
 ATTCCTATTCCACCAAAACCTCCACATATGAGTACACAGACATTCCCTTCCATAACCAATACT  
 TTCACATATCCATGCTTGACTACAATGCAAGAGATCGAGCTCTCTATGCCTGGAACAATGGCC  
 ACCAGGTGCTGTTCAATGTCACCCTTTCCATATCATCAAGACAGAGGATGACACATAGGCAA  
 ATGTGACATGTTTTCATTTGATTTAAACAGTGTGATTTGTGATAAACTCTATAAGACCCCTTCC  
 GTTTTTTTCTTCACTATTATTTTTTCATCATTTCTCCAAAGCAAAGCATTTTTATTGTAAAGTT  
 GGTGTTTTCAAAAACATAGCTGAGCTTGTCTAACTTACCATGTTGGAAACACATCTTAACCTTCT  
 AAATTTACAAGGCCTATCATGTCTTGTGTCATGAAAAGCACTAAAAAAAAAAAAAGAGTTTAAGT  
 GGCTAAAGTCATAGTTTTGCAAGAGATTAATGATCTGCCTTATATTAGAGTCAGAGACTAATG  
 GTGGCTTAAATGCACGAATGTCTTTTTTTTTTAAACTGTCAATTTTTTACTGTCTTTTGCTCCA  
 TCTCAGGAAATATTTTTGGTAGGAATTAGGAGAACAAAAAGCACTTTTATCCCATTTATTTCTT  
 TAAAAAATGTAAGGATTTCAATTTATATTGAAAAATAATATTAATCATTTTGTGCTGTTAACACAA  
 TTCTCTGATGCGGTGCTGTACAGTCATTTTTAAATCTCTTGCTAACATTTTATTGGCAGTATG  
 TATTTCTACCATTGTAACCACCATTTGTGCTATTGTATCTCTTCACTTCTGTGAAAAGTAATATT  
 TTTTATAAANACACTGNAATTTTAAAAAAAAAAAAAAAAAACAAAAAAAAAAAAAAAAAAAAA

**FIGURE 138**

MSPPLLKLGAVLSTMAMISNWMSQTLPSLVGLNTTRLSTPDTLTQISPKEGWQVYSSAQDPDG  
RCICTVVAPEQNLCSDAKSRQLRQLLEKVQNMSQSIEVLNLRRTQRDFQYVLKMETQMKGLKA  
KFRQIEDDRKTLMTKHFQELKEKMDELLPLIPVLEQYKTDACLITQFKEEIRNLSAVLTGIQE  
EIGAYDYEELHQRVLSLETRLRDCMKKLTGKLMKITGPVTVKTSGTFRGAWMTDPLASEKNN  
RVWYMDSYTNNKIVREYKSIADFVSGAESRTYNLPFKWAGTNHVVYNGSLYFNKYQSNIIIKY  
SFDMGRVLAQRSLEYAGFHNVPYTWGGFSDIDLMADEIGLWAVYATNQNAGNIVISQLNQDT  
LEVMSKSWSTGYPKRSAGESFMICGTLYVTNSHLTGAKVYYSYSTKTSTYEYTDIPFHNQYFHI  
SMLDYNARDRALYAWNNGHQVLFNVTLFHIIKTEDDT

**Important features of the protein:**

**Signal peptide:**

amino acids 1-16

**N-glycosylation sites.**

amino acids 33-37, 95-99, 179-183, 299-303, 465-469

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 215-219

**Tyrosine kinase phosphorylation site.**

amino acids 106-114

**N-myristoylation sites.**

amino acids 9-15, 31-37, 235-241, 239-245



# **FIGURE 139**

GAAGCAGTGCAGAGAGGAGAGCGGAGCGGAGCTGCCGCTGAGCAAAGGCCTTCACCATGGCCG  
 AGTCCCCCGGCTGCTGCTCCGTCTGGGCCCCGCTGCCTCCACTGCCTGTATAGCTGCCACTGGA  
 GGAAATGCCCCAGAGAGAGGATGCAAACCAGCAAGTGCAGCTGTATCTGGTTTGGCCTGCTCT  
 TCCTCACCTTCCTCCTTTCCCTGAGCTGGCTGTACATCGGGCTCGTCCTTCTCAATGACCTGC  
 ACAACTTCAATGAATTCCTCTTCCGCCGCTGGGGACACTGGATGGACTGGTCCCTGGCATTCC  
 TGCTGGTCATCTCTCTACTGGTCACATATGCATCCTTGCTATTGGTCCTGGCCCTGCTCCTGC  
 GGCTTTGTAGACAGCCCCCTGCATCTGCACAGCCTCCACAAGGTGCTGCTGCTCCTCATTATGC  
 TGCTTGTGGCGGCTGGCCTTGTGGGACTGGACATCCAATGGCAGCAGGAGTGGCATAGCTTGC  
 GTGTGCTACTGCAGGCCACAGCCCCATTCTTCATATTGGAGCAGCCGCTGGAATTGCCCTCC  
 TGGCCTGGCCTGTGGCTGATACCTTCTACCGTATCCACCGAAGAGGTCCCAAGATTCTGCTAC  
 TGCTCCTATTTTTTGGAGTTGTCTGGTCATCTACTTGGCCCCCTATGCATCTCCTCACCCCT  
 GCATCATGGAACCCAGAGACTTACCACCCAAGCCTGGGCTGGTGGGACACCGAGGGGGCCCCCA  
 TGCTGGCTCCCAGAACACCCCTGATGTCTTGCAGGAAGACAGCTGAATGCGGAGCTACTGTGT  
 TTGAGACTGATGTGATGGTCAGCTCCGATGGGGTCCCCTTCCTCATGCATGATGAGCACCTCA  
 GCAGGACCACGAATGTAGCCTCTGTATTCCCAACCCGAATCACAGCCCACAGCAGTGACTTCT  
 CCTGGACTGAACTGAAGAGACTCAATGCTGGATCCTGGTTTCTAGAGAGGCGACCCCTTCTGGG  
 GGGCCAAACCGCTGGCAGGCCCTGATCAGAAAGAGGCTGAGAGTCAGACGGTACCAGCATTAG  
 AAGAGCTATTGGAGGAAGCTGCAGCCCTCAACCTTTCCATCATGTTGCACTTGCGCCGACCCC  
 CACAGAACCACACATACTATGACACTTTTGTGATCCAGACATTGGAGACTGTGCTGAATGCAA  
 GGGTGCCCCAAGCCATGGTCTTTTGGCTACCAGATGAAGATCGGGCTAATGTCCAACGACGGG  
 CACCTGGAATGCGCCAGATATATGGACGTGAGGGAGGCAACAGAACGGAGAGGCCCCAGTTTC  
 TTAACCTCCCCTATCAAGATCTGCCACTATTGGATATCAAGGCATTGCATAAGGATAATGTCT  
 CGGTGAACCTATTTGTAGTGAACAAGCCCTGGCTCTTCTCTCTGCTTTGGTGTGCAGGGGTGG  
 ATTCGGTCACCACCAACGACTGCCAGCTGCTGCAGCAGATGCGTTACCCTATCTGGCTTATTA  
 CCCCTCAAACCTACCTAATCATATGGGTCATTACCAATTGTGTTTCCACCATGCTGCTTTTGT  
 GGACCTTCCTCCTCCAAAGGAGATTTGTTAAGAAGAGAGGGAAAACCTGGCTTAGAAAACAGCAG  
 TGCTGCTGACAAGGATCAACAATTTTCATGATGGAGTGAATGCCCTGCCCTGCTTCCCCACCCA  
 AGCCAGTCTACATTGCCCAAACAGCAAGGGTTGGAGAGTGGCTTAAGTGAATGCTTCAGGGG  
 TGGTGGGTTGCAAGTGGGGGGAGCTTTGCCAACAGGAGGTTTTGAACCATGAGGGCCCTCTGC  
 CCAGGTGATGGGCATTCCCTAAGCTGCTATGGAATCTGCTCCCTTTGGGGTTTTGACCTGAGA  
 TGTTTGGGAAGAGAGTGAGTAATGAGAAGTTTCTCCTCAAATGAACTAGAACAGAGGAAGTA  
 AAAGGGAGATTGCTCGGA

**FIGURE 140**

MAESPGCCSVWARCLHCLYSCHWRKCPRERMQTSKDCIWFGLLFLTFLLSLSWLYIGLVLLN  
DLHNFNEFLFRRWGHWMDWSLAFLLVISLLVTYASLLLVLALLLRQPLHLHSLHKVLLLL  
IMLLVAAGLVGLDIQWQQEWHSRLRVSLQATAPFLHIGAAAGIALAWPVADTFYRIHRRGPKI  
LLLLLFFGVVLVIYLAPLCISSPCIMEPRDLPPKPGLVGHRGAPMLAPENTLMSLRKTAECGA  
TVFETDVMVSSDGVFPFLMHDEHLSRTTNVASVFPTRITAHSSDFSWEKRLNAGSWFLERRP  
FWGAKPLAGPDQKEAESQTVPALEELLEEEAALNLSIMFDLRRPPQNHTYYDTFVIQTLETVL  
NARVPQAMVFWLPDEDRANVQRRAPGMRQIYGRQGGNRTERPQFLNLPYQDLPLLDIKALHKD  
NVSVNLFVVNKPWLFSLLWCAGVDSVTTNDCQLLQQMRYPIWLITPQTYLIWVITNCVSTML  
LLWTFLLQRRFVKKRGKTGLETAVLLTRINNFMM

**Important features of the protein:**

**Transmembrane domains:**

amino acids 38-60, 83-107, 122-138, 156-173, 189-210, 484-506

**N-glycosylation sites.**

amino acids 349-353, 362-366, 415-419, 442-446

**N-myristoylation sites.**

amino acids 163-169, 413-419, 523-529

**Leucine zipper pattern.**

amino acids 93-115, 109-131

**Glutamine amidotransferases class-II active site.**

amino acids 1-13

**FIGURE 141**

CCGCGCCGCCCGGGCTGGAGCCGAGCGCAGCAGCCACCGCGCGCCGCCGAGAGTTTGGGTTGAACCGGAGC  
TGCCGGGAGGAAACTTTTTCTTTTTCCCCCTCCCTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAACTGTCGC  
CCGCGCCCAAGGCTCGTGGCTCGGGCTCGGCGCGGCCCGCAGAAGGGCGGGGGCTCGCCCCGCGAGGGGAGG  
CGCGCCCGGGGGCCCCGAGAGGGCGGTGAGGACCGCGGGCTGCTGGTGCAGCGCGCGCGCGCGCTGTGCCCG  
CGCAGGGGAGGGCGCCCGCCCGCTCCCGGCCCGGCTGCGAGGAGGAGGCGCGCGCGCGCAGGAGGATGTA  
GGTGGCGGGGGACAGGGGGTTTGGCCGGCTGCGGGCACCCTCGTGGTCTCGCTGCTGGGGCTGCTGCTGCTGCG  
CGCTCCCGCACCCGGCGCTGCGTCTGCTGCCCTGACGAGTCCAAGTGCAGGAGCCAGGAACCTGCCCGG  
GAGCATCGTGACGGCGCTGCGGGTGTCTGTACACGTGCGCCAGCCAGAGGAAACAGAGACTGCGCGGCACCTT  
CGGGATTACGGAACCTGCGACCGGGGGCTGCGTTGTGTATCCGCCCCCGCTCAATGGCGACTCCCTCACCG  
GTACGAAGCGGGCGTTTGCGAAGATGAGAACTGGAATGATGACCAACTGCTTGGTTTTAAACCATGCAATGAAAA  
CCTTATTGCTGGCTGCAATATAACTAATGGGAAATGTAAGTAAACCAACTCGAACCTGCAGCAATCCCTTTGA  
GTTTCAGTCCAGTCAAGATATGTCCCTTTCAGTCTTTAAAGAAATTAAGAAACAGACAGTATGCTCAAGCCCG  
CTGTGAAGTCCAGTTCTCTCCAGTTGTCTGCTGAAGATTCTGTTCTGATCGAGGGTTATGCTCCTCCTGGGGAGTG  
CTGTCCCTTACCAGCCGCTGCGTGTGCAACCCCGCAGGCTGTCTGCGCAAAGTCTGCCAGCCGGGAAACCTGAA  
CATACTAGTGTCAAAAGCCCTCAGGGAAGCCGGGAGAGTGTCTGTACCTTATGATGTCAAACGATTTTCCGGCGT  
GGACTGCAAGGACTGTGAATGCCCTCTGTTACAGACACGCGCTGTCCCCGAGCAGCTATGAAACTCAAGTCAG  
ACTAACTGCAGATGTTTGTGTACTTTTGCCAAACAGATGCGAGTGTCTCTCTGGCTTATGTGGTTTCCCGTGTG  
TGAGGTGGGATCCACTCCCGCATAGTCTCTCGTGGCGATGGGACACCTGGAAGTGTCTGTGATGTCTTTGAATG  
TGTTAATGATACAAAGCCAGCCTCGTATTAAACATGTGGAATATTATGATGGAGACATGTTTCGAATGGACAA  
CTGTGCGTTCTGTGATGCCAAGGGGGCTTGCCATCTGTCTACTGCCAGTGTGGTGAGATAAACTGCGAGAG  
GTACTACGTGCCGAAGGAGAGTGTGCCAGTGTGTGAAGATCCAGTGTATCCTTTTAAATAACCCCGTGGCTG  
CTATGCCAATGGCCTGATCCTTGCCACGGAGACCGGTGGCGGGAAGACGACTGCACATTCTGCCAGTGCCTCAA  
CGGTGATGCCCACTGCTGTTGCGACCGCTGTCGGCAGACAGCTGCACAAACCTGTGAAAGTGCCCTGGGGAGTGTG  
CCCTGTGTGCGGAAGAACCAACCATCATCAGATTGATCCACTGTGATGTGGGAGTTATCAACTGCACCTGAG  
AGGGAAGGACTGCATTAATGGTTTTCAAACCGCATCAAAATGGTTGTGCGACCTGTGAGTGCATAAAACCGGAGA  
ACTATGTTCAGAACGTAAACAGGCTGCACCTTGAAGTGTCCCTTCGGTTTCTTACTGATGCCAAACTGTGA  
GATCTGTGAGTGCCGCCCCAAGGCCAAGAGTGCGAGACCAATACTGTGACAAGATTGTCCACTTGGATTGCT  
GAAGTAATAAGCAGGCTGTGACATCTGTGCTGTAGAAATGCACAGCTCTCATGCAGTAAAGTGTCCCTT  
GGGTTTTCCAGCAGGACAGTGCACGGCTGTCTTATGTGCAAGTGCAGAGGCGCTCTGCTTCAGCTGGGCCACCAT  
CCTGTGCGGCACTTGTCTACCGTGGATGGTTCATCATATAAAATGAGGAGAGCTGGCAGCATGGGTGCCGGGA  
ATGCTACTGTCTCAATGGACGGGAATGTGTGCCCTGATCACTGCCCGGTGCCGCTGTGGCAACCCCAACCAT  
TGCCCTTGGACAGTGTGCCATCTGATGTCGATGATCTTGTGGTGCAGAACCGCAGAGCTCAGTACTCCCTCCAT  
TTGCCACGCCCTCGGAGGAGAATACTTTGTGGAAGGAGAAACGTGGAACATTGACTCCTGTACTCAGTGCACCTG  
CCACCGCGGACGGGTGCTGTGTGAGACAGAGGTGTGCCACCGCTGCTCTGCCAGAACCCCTCACGCACCCAGGA  
TTCTGCTGCCACAGGTGACAGATCAACCTTTTCGGCTTCTTGTGCCGCAATAACAGCGTACCTAATTACTG  
CAAAATGATGAAGGGGATATATTCTCGCAGCTGAGTCTGGAAGCGTGACGTTTGTACAGCTGCATCTGCAT  
TGATAGCGTAATTAGCTGTTTCTCTGAGTCTGCCCTTCTGTATCTGTGAAAGACCTGTCTTTGAGAAAAGGCCA  
GTGTTGTGCTTACTGTCATAGAAGACACAATTCCAAAGAAGGTGGTGTGCCAATCTCAGTGGGAAGGCCTATGCCGA  
CGAGGAGCGGTTGGGACCTTGACAGCTGCACCCACTGCTACTGCTGCAGGGCCAGACCTCTGCTCGACCGTCA  
TGCCCCCTCTGCCCTGTGTTGAGCCACTCAACGTGGAAGGAATGCTGCCCCATGTGTCAGAAATGTATGT  
CCCAGAACCAACCAATATACCAATTGAGAAGACAAACCATCGAGGAGAGGTTGACCTGGAGGTTTCCCTGTGTGCC  
CACGCTAGTGAATAATGATATCGTCCATCTCCCTAGAGATATGGGTCACTTCAGGTAGATTACAGAGATAACAG  
GTGCAACCCAAAGTGAAGATTCTTCACTGGACCTCATTTGCTGCTTGTGTTTCCCATAAATTATGCTCTCTAT  
TATAATGACATTCTAATTACATCAATCAGAAGAAACAGTGGATACCACTGCTTGTGGTATCGAACACCAACTAA  
GCCTTCTTCTTCAATAATCAGCTAGTATCTGTGGACTGCAGAAAGGAACAGAGTCCAGGTGGACAGTTCCTCA  
GAGAATGCTAAGAATTGCAGAACAGATGCAAGATTTCAGTGCTTCTACAGCATGCAGAAACAGAACCATCTACA  
GGCAGACAATTTCTACCAACAGTGTGAGAGAAAGGCCAATAGGATGAGTTCGAAAGACGGAAGACGCAATAAT  
CTGCTTCAAAGATGAACATAGAAATTTGTGCACTTGTCTAGTGATTTGATTTGATTTGATGATGATGATGATGATG  
TAAGACCTTAACGTGGAGTGGCTCTGTCTACAGCAATGTGCAAGAACAGCAATCCCACTTTTCTCAAAAAA

## **FIGURE 142**

MYLVAGDRGLAGCGHLLVSLGLLLLLLARSGTRALVCLPCDESKCEEPRNCPGSIVQGVCGCC  
YTCASQRNESCGGTFGIYGTCDRGLRCVIRPPLNGDSLTEYEAGVCEDENWTDQLLGFKPCN  
ENLIAGCNIINGKCECNTIRTCSNPFEFSPQDMCLSAKRIEEKPDCKARCEVQFSPRCPE  
DSVLIIEGYAPPGECCPLPSRCVCNPAGCLRKVCQPGNLNILVSKASGKPGECCLYECKPVFG  
VDCRTVECPPVQQTACPPDSYETQVRLTADGCCTLPTRCECLSGLCGFPVCEVGSTPRIVSRG  
DGTPGKCCDVFEVCVNDTKPACVFNNVEYYDGMFRMDNCRFCRCQGGVAICFTAQCGEINCER  
YYVPEGECCPVCEDPVYPFNNPAGCYANGLILAHGDRWREDDCTFCQCVNGERHCVATVCGQT  
CTNPFVKVPGECCPVCEEPTIITVDPPACGELSNCITLTGKDCINGFKRDHNGCRCTQCINTEEL  
CSERKQGCITLNCPPFGFLTDAQNCEICECRPRPKKCRPIICDKYCPLGLLKNKHGCDICRCKKC  
PELSCSKICPLGFQQDSHGCLICKCREASASAGPPILSGTCLTVDGHHHKNEESWHDGCRECY  
CLNGREMCALITCPVPACGNPTIHPGQCCPSCADDFVQKPELSTPSICHAPGGGEYFVEGETW  
NIDSTQCTCHSGRVLCETEVCPPLLCQNPSTQDSCCPQCTDQPFPRPSLSRNNSVPNYCKND  
EGDIFLAAESWKPDVCTSCICIDSVISCFSESCPSVSCERPVLRLKGQCCPYCIEDTIPKKVVC  
HFSGKAYADEERWDLDSCTHCYCLQGQTLCTVSCPPLEPCVEPINVEGSCCPMCPEMYVPEPT  
NPIEKTNRHGEVDLEVPLWPTPSENDIVHLPRDMGHLQVDYRDNRHLHPSDDSLDSIASVVV  
PIIICLSIIIAFLFINQKKQWIPLLCWYRTPTKPSSLNNQLVSVDCCKGTRVQVDSSQRMRLRI  
AEPDARFSGFYSMQKQNLQADNIFYQTV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-34

**Transmembrane domain:**

amino acids 940-962

**N-glycosylation sites.**

amino acids 71-75, 113-117, 330-334, 474-478, 746-750

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 992-996

**N-myristoylation site.**

amino acids 9-15, 58-64, 61-67, 75-81, 79-85, 362-368, 402-408, 407-413,  
439-445, 492-498, 511-517, 551-557, 558-564, 586-592, 606-612, 625-631,  
845-851

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 52-63, 844-855

**Cell attachment sequence.**

amino acids 314-317

**Leucine zipper pattern.**

amino acids 3-25

**Eukaryotic thiol (cysteine) proteases cysteine active site.**

amino acids 57-69

**VWFC domain proteins.**

amino acids 448-456, 382-390

**C-terminal cystine knot proteins**

amino acids 60-86

**FIGURE 143**

[illegible]

## **FIGURE 144**

MVARVGLLLRALQLLLWGHLLDAQPAERGGQELRKEAEAFLEKYGYLNEQVPKAPTSTRFSDAI  
RAFQWVSQLPVSGVLDRA TL RQMTRPRCGVTD TNSYAAWAERISDLFARHRTKMRRKKRFAKQ  
GNKWKQHL SYRLVNWPEHLPEPAVRGAVRAAFQLWSNVSALEFWEAPATGPADIRLTFFQGD  
HNDGLGNAFDGPGGALAHAF LPRRGEAHFDQDERWSLSRRRGRNLFVVL AHEIGHTLGLTHSP  
APRALMAPYYKRLGRDALLSWDDVLAVQSLYGKPLGGSVAVQLPGKLFTDFETWDSYSPQGRR  
PETQGPKYCHSSFDAITVDRQQQLYIFKGS HFWEVAADGNVSEPRPLQERWVGLPPNIEAAAV  
SLNDGDFYFFKGGRCWRFRGPKPVWGLPQLCRAGGLPRHPDAALFFPPLRRLILFKGARYYVL  
ARGGLQVEPYYP RSLQDWGGIPEEVSGALPRPDGSIIFRDDR YWRLDQAKLQATTSGRWATE  
LPWMGCWHANSGSALF

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**N-glycosylation sites.**

amino acids 164-168, 355-359

**N-myristoylation sites.**

amino acids 92-98, 153-159, 193-199, 202-208, 288-294, 368-374,  
509-515

**Amidation site.**

amino acids 312-316

**Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 237-247

**Matrixins cysteine switch**

amino acids 231-262, 271-284

**Hemopexin domain protein**

amino acids 66-108, 231-262

# **FIGURE 145**

GCCGGCTAGGGCGCCGGAGCCGACGACGCCGCGGGGCTCCGAGAGGCGCGCACTGGGGCTGGGACTGCGCGGCG  
 CCGCGCTGCGAGCGCCACTGAGCGGTGCGGCAACTTCGGAGGCACAGCGCCGGAGCCAGGCGAGCGCTCAGAGA  
 CCGGAGCCAGAGGGGCGCGCCGGAGCCTCGTTTCGAGAGCCGCGCCAGGCACCCACCGCGCTCCGAGTGCCAGG  
 CGGCCCTCCGCGCAGCGTGGCTTCCGCTGCCCCACGGAAGGCACGGGCTGGCGCTGCCGGGCGCCGGGGAGGAC  
 GCGAGGAGGAGGCGCGCGCGGAGACGCGCGCGGAGACTGGGGCCAGGGAGACAGCCCTGGGGGAGAGGC  
 GCCGAACCCAGGCCGCGGGAGCAATGGGGGCCCGAGCGGAGCTCGGGGCGCGCTGCTGCTGGCACTGCTGCTCTG  
 CTGGGACCCGAGGCTGAGCCAAGCAGGCACTGATTCTGGCAGCGAGGTGCTCCCTGACTCCTTCCCGTCAGCGCC  
 AGCAGAGCCGCTGCCCTACTTCTGTCAGGAGCCACAGGACGCCCTACATTGTGAAGAACAGCCCTGTGGAGCTCCG  
 CTGCCGCGCCTTCCCCGCCACACAGATCTACTTCAAGTGCAACGGCGAGTGGGTGAGCCAGAACCACACGTCAC  
 ACAGGAAGGCCTGGATGAGGCCACCGGCTGCGGGTGCAGAGGTGAGATCGAGGTGTGCGCGCAGCAGGTGGA  
 GGAGCTCTTTGGGCTGGAGGATTACTGGTGCCAGTGCCTGGGCTGGAGCTCCGAGGCACCACCAAGAGTCGCCG  
 AGCCTACGTCCGCATCGCCTACCTGCGCAAGAACTTCGATCAGGAGCCTCTGGGCAAGGAGGTGCCCTGGACCA  
 TGAGGTTCTCTGCACTGCCGCCCGCGGAGGGGGTGCTGTGGCCGAGGTGGAATGGCTCAAGAATGAGGATGT  
 CATCGACCCACCCAGGACACCAACTTCTGCTCACCATCGACCAACAACCTCATCATCCGCCAGGCCCCGCTGTG  
 GGACACTGCCAACTATACCTGCGTGGCCAAAGAACATCGTGGCCAAACGCGGAGCACCATGCCACCGTCTCATGT  
 CTACCTGAATGGCGGGTGGTCCAGCTGAGCGAGAGTGGTCAACCTGCTCCAAACCGTGTGGCCGAGGCTGGCAAA  
 GCGCACCCGGAGCTGCACCAACCCCGCTCCACTCAACGGAGGGGGCTTCTGCGAGGGCCAGGCATTCCAGAAGAC  
 CGCTGACACCATCTGCCAGTGCATGGGGCGTGGACGGAGTGGAGCAAGTGGTGCAGCTGCAGCACTGAGTG  
 TGCCCACTGGCGTAGCCGCGAGTGATGGCGCCCCACCCGAAACGGAGGCCGTGACTGCAGCGGGACGCTGCT  
 CGACTCTAAGAACTGCACAGATGGGCTGTGCATGCAAAATAAGAAACTCTAAGCGACCCCAACAGCCACCTGCT  
 GGAGGCCCTCAGGGGATGCGGCGCTGTATGCGGGGCTCGTGGTGCCATCTTCGTGGTCCGTGGCAATCCTCATGGC  
 GGTGGGGTGGTGGTGTACCGCCGCAACTGCCGTGACTTCGACACAGACATCACTGACTCATCTGCTGCCCTGAC  
 TGGTGGTTTCCACCCCGTCAACTTTAAGACGGCAAGGCCAGCAACCCGACGCTCCTACACCCCTCTGTGCTCC  
 TGACCTGACAGCCAGCGCCGCATCTACCGCGACCCGTGTATGCCCTGCAGGACTCCACCGACAAAATCCCAT  
 GACCAACTCTCCTCTGCTGGACCCCTTACCGAGCCTTAAGGTCAAGGTCTACAGCTCCAGCACCAAGGGCTCTGG  
 GCCAGGCCCTGGCAGATGGGGCTGACCTGCTGGGGTCTTGCCGCTGGCACATACCTAGCGATTTCGCCCGGGA  
 CACCCACTTCTGCACTGCGCAGCGCCAGCCTCGGTTCCAGCAGCTCTTGGGCTGCCCGGAGACCCAGGGAG  
 CAGCGTCAGCGGCACCTTTGGCTGCCCTGGGTGGGAGGCTCAGCATCCCCGCGCAGGGGTGAGTGTGCTGGTGCC  
 CAATGGAGCCATTCCCGAGGGCAAGTTCTACGAGATGTATCTACTCATCAACAAGGCAGAAAGCACTCCCTCATGGC  
 TTCAGAAGGGACCCAGACAGTATTGAGCCCTCGGTGACCTGTGGACCCACAGGCCTCCTGCTGTGCCGCCCGCT  
 CATCCTCACCATGCCCCACTGTGCCGAAGTCAGTGCCCGTGAATGCTTTCAGTCAAGACCCAGGCCACCA  
 GGGCCACTGGGAGGAGTGGTGACCTGGATGAGGAGACCTGAACACACCCTGCTACTGCCAGCTGGAGCCAG  
 GGCTGTGCATCTGCTGGACCAAGCTGGGCACCTACGTGTTACGGGCGAGTCTATTCCCGCTCAGCAGTCAA  
 GCGGCTCCAGCTGGCGCTCTTCGCCCCCGCCTCTGCACCTCCTGGAGTACAGCCTCCGGGTCTACTGCTGGA  
 GGACACGCTGTAGCACTGAAGGAGGTGCTGGAGCTGGAGCGGACTCTGGGCGGATACTTGGTGGAGGAGCCGAA  
 ACCGCTAATGTTCAAGGACAGTTACCACAACCTGCGCCTCTCCCTCCATGACCTCCCCATGCCCATTTGGAGGAG  
 CAAGCTGTGCCCCAAATACCAGGAGATCCCTTCTATCACTTTGGAGTGGCAGCCAGAAGGCCCTCCACTGCAC  
 TTTCACCTTGAGAGGCGACAGCTTGGCCTCCACAGAGCTCACCTGCAAGATCTGCGTGGCGCAAGTGAAGGGGA  
 GGGCCAGATATTCCAGCTGCATACCACTCTGGCAGAGACACCTGCTGGCTCCCTGGACACTCTCTGCTCTGCCCC  
 TGGCAGCACTGTACCAACCCAGCTGGGACCTTATGCCTTCAAGATCCACTGTCCATCCGCCAGAAGATATGCAA  
 CAGCCTAGATGCCCCCAACTCACGGGGCAATGACTGGCGGATGTTAGCACAGAAGCTCTCTATGGACCCGTTACCT  
 GAATTACTTTGCCACCAAGCGAGCCCCACGGGTGTGATCTGGACCTCTGGGAAGCTCTGCAGCAGGACGATGG  
 GGACCTCAACAGCCTGGCGAGTGCCTTGGAGGAGATGGCAAGAGTGAGATGCTGGTGGCTGTGGCCACCGACGG  
 GGACTGCTGAGCCTCTGGGACAGCGGGCTGGCAGGGACTGGCAGGAGGAGGTGAGGGAGGCTGGGGCAGCC  
 TCCTGATGGGGATGTTTGGCCTCTGCTTCTCCAGTTACAGCCAGAGTTGCCCTCTCTCTCTCTTCCCCAA  
 CCCCCAGACCATGACCAGCCTTAGAAAATCCATGTACTCTGTTGTTAGAGGGCCCAGAGTTCTTCTCCACCCCC  
 GCTCTCTCTCTTGGCTGAGATCTCTGTGCAGGAACCAAGATGGGGCTGAAGCCTCTGGAGGCAGTTGGTTGG  
 GGGCGGGCAGGCAGGAGGCCCTCCCTCCACCCCCCACCCTCAGCCCGCAACTTCTGGGTTCCGTGGGTTTTAG  
 TTCCGTTCTTCGTTTTCTTCTCCGTTATTGATTTCTCTCTTCTCCCTAAGCCCCCTCTGCTTCCACGCCCTTT  
 TCCTCTTTGAAGAGTCAAGTACAATTACAGACAAATGCTTTCTCTCTGTCCAAAAGCAAAAGGCAAGGAAAGAA  
 AGAAAGCTTCAGACCGCTAGTAAGGCTCAAAGAAGAAGAAAAACACCAAAACCAAGGGAAAAAGAAAAACCCAG  
 TTCTTAGGAAACGCAACGATTATTATCCAGATTATTTGATAAGTCCTTTTAAAA

## **FIGURE 146**

MGARSGARGALLLALLLCWDPRLSQAGTDSGSEVLPDSPFAPSAPAEPLPYFLQEPQDAYIVKNK  
PVELRCRAFPATQIYFKNGEWVSQNDHVTQEGLEATGLRVREVQIEVSRQQVEELFGLEDY  
WCQCVAWSSAGTTKSRRAYVRIAYLRKNFDQEPLGKEVPLDHEVLLQCRPPEGVPVAEVEWLK  
NEDVIDPTQDTNFLTIDHNLIIIRQARLSDTANYTCVAKNIVAKRRSTTATVIVYVNGGWSSW  
AEWSPCSNRCGRGWQKRTRCTNPAPLNGGAFCEGQAFQKTACTTICPVDGAWTEWSKWSACS  
TECAHWSRECMAPPPQNGGRDCSGTLLDSKNCTDGLCMQNKKTLSDPNSHLLEASGDAALYA  
GLVVAIFVVVAILMAVGVVVYRRNCRDFDITDSSAALTGGFHPVNFKTARPSNPQLLHPSV  
PPDLTASAGIYRGPVYALQDSTDKI PMTNSPLLDPLPSLKVKVYSSSTTGS GPGLADGADLLG  
VLPPGTYP SDFARDTHFLHLRSASLGSQQLLGLPRDPGSSVSGTFGCLGGRLSIPGTGVSLLV  
PNGAIPQKG FYEMYLLINKAESTLPLSEGTQTVLSPSVTCGPTGLLLCRPVILTMPHCAEVSA  
RDWIFQLKTQAHQGHWEVVTLDEETLNTPCYCQLEPRACHILLDQLGTYVFTGESYSRSAVK  
RLQLAVFAPALCTSLEYSLRVYCLEDT PVALKEVLELERTLGGYLVEEPKPLMFKDSYHNLRL  
SLHDLPHAHWSKLLAKYQEIPFYHIWSGSQKALHCTFTLERHSLASTELTCKICVRQVEGEG  
QIFQLHTTLAETPAGSLDTLCSAPGSTVTTQLGPYAFKIPLSIRQKICNSLDAPNSRGNDRM  
LAQKLSMDRYLNYFATKASPTGVILDLWEALQQDDGLNSLASALEEMGKSEMLVAVATDGC

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 374-395

**N-glycosylation sites.**

amino acids 222-225, 347-350

**Glycosaminoglycan attachment site.**

amino acids 492-495

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 233-236, 234-237

**Casein kinase II phosphorylation sites.**

amino acids 30-33, 87-90, 251-254, 341-344, 359-362, 629-632, 651-654, 706-709, 757-760, 827-830, 925-928, 941-944

**Tyrosine kinase phosphorylation sites.**

amino acids 216-223, 773-780

**N-myristoylation sites.**

amino acids 2-7, 6-11, 27-32, 96-101, 137-142, 179-184, 247-252, 281-286, 334-339, 379-384, 491-496, 495-500, 509-514, 542-547, 547-552, 550-555, 553-558, 560-565, 611-616, 785-790, 834-839, 844-849

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 541-551

**ATP/GTP-binding site motif A (P-loop).**

amino acids 926-933

**Growth factor and cytokines receptors family signature 2.**

amino acids 306-312



# **FIGURE 147**

GAGAGGGACAGAGGCTGGAGAAGGATGTATGGCCTGCCCTGGGCTTGTCTGTTCCCTCCTGAGCCTGAGCCCCCTT  
ACCTTCCTGACCCCATGAAGCACACACTGGCTCTGCTGGCTCCCTGCTGGGCTGGGCTGGGCTGGCCCTGA  
GTCAGCTGGCTGCAGGGGCCACAGACTGCAAGTTCTTTGGCCCGGCAGAGCACCTGACATTACCCCAGCAGCCA  
GGGCCCCGGTGGCTGGCCCCCTCGAGTTCTGTGCGCCAGGACTCCTGGACTCCCTCTATGGCACCGTGCGCCGCTTCC  
TCTCGTGGTGCAGCTCAATCCTTTCCCTTCAGAGTTGGTAAAGGCCCTACTGAATGAGCTGGCCTCCGTGAAGG  
TGAATGAGGTGGTGGGTAGCAGGCGGGCTACGTGGTATGCGCTGTGATCGCGGGCCTCTACCTGCTGCTGGTGC  
CCACTGCCGGGCTTTGCTTCTGCTGCTGCCGCTGCCACCGCGCTGCGGGGACGAGTGAAGACAGAGCACAAAG  
CGCTGGCCTGTGAGCGCGCGGCCCTCATGGTCTTCTGCTGCTGACCACTCTTGTCTGCTGATTGGTGTGGTCT  
GTGCCTTTGTACCAACCAGCGCACGCATGAACAGATGGGCCCCAGCATCGAGGCCATGCTGAGACCCTGCTCA  
GCCTCTGGGGCCTGGTCTCTGATGTCCCCAAGAGCTGCAGGCCGTGGCACAGCAATTCTCCTGCCCCAGGAGC  
AAGTCTCAGAGGAGCTGGATGGTGTGGTGTGAGCATTGGGAGCGCGATCCACTCAGCTCAGGAGCTCCGTGT  
ACCCCTTGTCTGGCGCGCTGGGCGAGTTTGGGCCAGGTCTGCAGGTCTCCGTGCACCACTGCAAACTTGAATG  
CTACAGTGGTAGAGCTGCAGGCCGGGCAGCAGGACCTGGAGCCAGCCATCCGGGAACACCGGGACCGCTCCTTG  
AGCTGTGACAGGAGGCCAGGTGCCAGGGAGATTGTGACAGGGGCCCTGAGCTGGGCCCCGACCTGGAGCTGGGTG  
CTGACTTCAGCCAGGTGCCCTCTGTGGACCATGTCTGCACAGCTAAAAGGTGTCCCCGAGGCCAACTTCTCCA  
GCATGTTCCAGGAGGAGAACAGCACCTTCAACGCCCTTCCAGCCCTGGCTGCCATGCAGACATCCAGCGTGGTGC  
AAGAGCTGAAGAAGGCAGTGGCCCCAGCAGCCGAAGGGGTGAGGACACTGGCTGAAGGGTTCCCGGGCTTGGAGG  
CAGCTTCCCGCTGGGCCCCAGGCACTGCAGGAGGTGGAGGAGAGCAGCCGCCCTACCTGCAGGAGGTGCAGAGAT  
ACGAGACCTACAGGTGGATCGTGGGCTGCGTGTGCTCCGTGGTCTATTCTGGTGTCTGCAACTGCTGG  
GCCTCAATCTGGGCATCTGGGCCCTGTCTGCCAGGGACGACCCAGCCACCCAGAAGCCAGGGCGAGGCTGGAG  
CCCCCTTCTCATGGCAGGTGTGGGCTCAGCTTCTCTTTGTGTCACCCCTCATCTCTGGTGTTCGCCACCT  
TCCTGGTGGGTGGCAACGTGCAGACGCTGGTGTGCCGGAGCTGGGAGAACGGCGAGCTCTTTGAGTTTGCAGACA  
CCCCAGGGAACCTGCCCGCTCCATGAACCTGTGCGCACTTCTTGGCCTGAGGAAGAACATCAGCATCCACCAAG  
CCTATCAGCAGTGCAGGAAGGGGAGGGCAGCGCTCTGGACAGTCTGCAGCTCAACGACTCCTACGACCTGGAGGAGC  
ACCTGGATATCAACCAGTATACCAACAAGTACGGCAGGAGTGCAGAGCCTGAAAGTAGACACACAGAGCCTGG  
ACCTGCTGAGCTCAGCCGCCCGCGGGACCTGGAGGCCCTGCAGAGCAGTGGGCTTTCAGCGCATCCACTACCCCG  
ACTTCTCTGTTTCCAGATCCAGAGGCCCGTGGTGAAGACCAAGCATGGAGCAGCTGGGCCAGGAGCTGCAGGACTGG  
CCAGGCCCAAGACAATTCTGTGCTGGGGCAGCGGCTGCAGGAGGAGGCCCAAGGACTCAGAACTTCAACCAGG  
AGAAGTGTCTCCCCAGCAGAGCCTTGTGGCAAAGCTCAACCTCAGCGTCAGGGCCCTGGAGTCTCTGCCCCGA  
ATCTCCAGCTGGAGACCTCAGATGTCTTAGCCAATGTACCTACCTGAAAGGAGAGCTGCCTGCCTGGGCAGCCA  
GGATCTCTGAGGAATGTGAGTGAAGTGTTCCTGGCCCGGAGATGGGCTACTTCTCCAGTACGTGGCTGGGTGA  
GAGAGGAGGTGACTCAGCGCATTGCCACCTGCCAGCCCTCTCCGGAGCCCTGGACAACAGCCGTGTGATCCTGT  
GTGACATGATGGCTGACCCCTGGAATGCCTTCTGGTTCTGCCTGGCATGGTGCACCTTCTTCTGATCCCCAGCA  
TCATCTTTGCCGTCAGAACCTCCAAATACTTCCGTCTATCCGGAACGCCTCAGCTCCACCAGCTCTGAGGAGA  
CTCAGCTCTTCCACATCCCCCGGTTACCTCCCTGAAGCTGTAGGGCCTTGTGGGGTGAGGTGACCTTGAGGCTG  
CCTGTCTCTCCCTTTGATTTAGCCTGGGCCACAGGACTTTCGGTAGCTCTTGCCCCAGAGCCAGGCTGGCATCCA  
GGCCTGGACTGTCCCCAGTTCGGGCTTACCTGGCCCCACCTTGCTGCTCTTTCACCCCTTTCTGCTCACGAC  
CCCCATCATTACGCTCAGAATCACATGGGACTTCTGTGCAGCTGCAGAGCCAGCAAGTCCCTACAGGTGTACC  
CGTTACCCCCATGCTGGTGGCATCCTCACAGGAAGAGCCTGTTCTCCACCTGCTGGAGCCTGGACCCCTGGGGTGG  
GACAGAGGCCCTCGTCCAACCCCACTCCCTTCCCGTGTGTCTTCCCCCTGCCAAGCCTCCCCCTGCCAAGCCTCC  
CCCTGCCCTCTCTGAGCCCTCGCCCCCACACCGTCTCATCTGGCTCCCCCTGGCCCCCACTTCCCTCTT  
ATGCCCTTCTGGCCCTTTGCTTCTCTCCCTTAGTCCCTCTTACCATATCTCCACTGTACCTTGTGGCCCCA  
GAGACCACCTTGCCCAACCAAACTCAGGTAAACGCCACTAATCAGGCAGGGGCCACCATGGCCTAGGTCTGGG  
CTGGCTGCAGGCCCTGCCTCATGGCTCTGAGCCCTCCACTGCCCCAGGGCCTTGGGCCCTCTGCAGATCTCATC  
CAGGATTTATTGTGTCCAGTGGGGTGAAGGAGGCTGTCTGAAGGCCGAGCCTCCCTGCCTGCACCCAAGTTAG  
AAATGGGGGTACCAGCACTTAGCTTCTCTGAGTGTCTGGCTCCCAAGGAAGGGACCTGGGACCTGGGCCACAGT  
GGGGCTTGGCCCTTACCTCTTCAAGGAAGCATCTTCCACAGCCCCCACCCTTCTTAGGAGTGATCTGGT  
GGCCAGAACAGGATTTTGCACGGCCCCCTTTATCTCTGCGCATGTGGCTAGGGTTCATCCCAGCCCATCCCTGTG  
TCAGCCCTGAGTGTGACACTGCGTTCCAGAAATGAGGAAGAGGAGAGAGAAGAGATGGACAGACCTCAGATCC  
ATTAAAGTGTCTCACTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 148**

MKHTLALLAPLLGLGLGLALSQLAAGATDCKFLGPAEHLTFTPAARARWLAPRVRAPGLL  
DSLYGTVRRFLSVVQLNPFPSSELVKALLNELASVKVNEVVRYEAGYVVC AVIAGLYLLL  
PTAGLCFCCCRCHRRCGGRVKTEHKALACERAALMVFLLLTLLLLIGVVCAFTVNQRT  
EQMGPSIEAMPETLLSLWGLVSDVPQELQAVAAQFSLPQEQVSEELDGVGVSIGSAIHTQ  
LRSSVYPLLAAGVSLGQVLQVSVHHLQTLNATVVELQAGQDLEPAIREHRDRLELLQE  
ARCQGDCAALSWARTLELGADFSQVPSVDHVLHQLKGVPEANFSSMVQEENSTFNALPA  
LAAMQTSSVVQELKKAVAQQPEGVRTLAEFGFPLEAASRWAQALQEEVESSRPYLQEVQR  
YETRWIVGCVLCSVVLFFVLCNLLGLNLGIWGLSARDDPSHPEAKGEAGARTLMAGVGL  
SFLFAAPLILLVFATFLVGGNVQTLVCRSWENGELFEFADTPGNLPPSMNLSQLLGLRKN  
ISIHQAYQQCKEGAALWTVLQLNDSYDLEEHLDINQYTNKLRQELQSLKVDTSQSLDLLSS  
AARRDLEALQSSGLQRIHYPDFLVQIQRPVVKTSMEQLAQELQGLAQADNSVLGQRLQE  
EAQGLRNHQQEKVVPQQSLVAKNLNSVRALESSAPNLQLETSDVLANVTYLLKGELPAWAA  
RILRNVSCEFLAREMGYFSQYVAWVREEVTQRIATCQPLSGALDNSRVILCDMMADPWNA  
FWFCLAWCTFFLIPSIIFAVKTSKYFRPIRKRLSSTSSEETQLFHIPRVTSCLKL

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 105-125, 153-173, 428-449, 476-500, 778-797

**N-glycosylation sites:**

amino acids 270-273, 343-347, 352-356, 530-534, 540-546, 563-567,  
684-688, 707-711, 725-729

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 811-815

**Tyrosine kinase phosphorylation site.**

amino acids 95-103

**N-myristoylation sites.**

amino acids 13-19, 15-21, 17-23, 26-32, 58-64, 124-130, 168-174,  
228-234, 230-236, 320-326, 338-344, 393-399, 429-435, 446-452,  
477-483, 500-506, 536-542, 644-650, 761-767

**Phospholipase A2 histidine active site.**

amino acids 129-137

**4Fe-4S ferredoxins, iron-sulfur binding region signature.**

amino acids 126-138

**Mitochondrial energy transfer proteins signature.**

amino acids 80-89

**FIGURE 149**

CACAGCTCCCTTCCCAGGACGTGAAAATCTGCCTTCTCACCATGAGGCTTCTAGTCCTTTCCA  
GCCTGCTCTGTATCCTGCTTCTCTGCTTCTCCATCTTCTCCACAGAAGGGAAGAGGCGTCCTG  
CCAAGGCCTGGTCAGGCAGGAGAACCAGGCTCTGCTGCCACCGAGTCCCTAGCCCCAACTCAA  
CAAACCTGAAAGGACATCATGTGAGGCTCTGTAAACCATGCAAGCTTGAGCCAGAGCCCCGCC  
TTTGGGTGGTGCCTGGGGCACTCCCACAGGTGTAGCACTCCCAAAGCAAGACTCCAGACAGCG  
GAGAACCTCATGCCTGGCACCTGAGGTACCCAGCAGCCTCCTGTCTCCCCTTTCAGCCTTCAC  
AGCAGTGAGCTGCAATGTTGGAGGGCTTCATCTCGGGCTGCAAGGACCCTGGGAAAGTTCCAG  
AACTCCACGTCCTTGTCTCAATTGTGCCATCAACTTTCAGAGCTATCATGAGCCAACCTCACC  
CCACAGGGCCTCAGTCGCCACCATGTGGGCCTCTCCAGTGCAAACCACCGAGCATTCCACCAT  
GACCGGTCACAGCTACAAATCCAGAGACCATCAATCCTGCTAGAGTGCAGGGTGGCAAGCACC  
CAAGGGTGGCTGACCAAGACTGCAGAGTCTCCTCCATCTTCAGGTCCATTGAGCCTCCTGGCA  
TTTAACTACCAGCATCCAGTGGTCCCCAAGGAATCCCTTCCTAGCCTCCTGACATGAGTCTGC  
TGGAAGAGCATCCAAACAAACAAGTAATAAAATAAAATAAACTCA

**FIGURE 150**

MRLLVLSLLCILLLCFSIFSTEGKRRPAKAWSGRRRLCCHRVSPNSTNLKGHHVRLCKPC  
KLEPEPRLWVVP GALPQV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation site.**

amino acids 48-52

**Amidation sites.**

amino acids 23-27, 33-37

# **FIGURE 151**

CACCGGAGGGCACGCAGCTGACGGAGCTGCGCTGCGTTGCGCTCGTTTGCCTCGCGCCCTCCA  
 CTGGAGCTGTTTCGCGCCTCCCGGCTCCCACCGCAGCCCACCCGGCAGAGGAGTCGCTACCAGC  
 GCCCAGTGCGCTCTGTCACTCCGCAAACCTCTTGCCGCCCGCCCCGGGCTGGGCACCAAATAC  
 CAGGCTACCATGGTCTACAAGACTCTCTTTCGCTCTTTGCATCTTAAGTGCAGGATGGAGGGTA  
 CAGAGTCTGCCTACATCAGCTCCTTTGTCTGTTTCTCTTCCGACAAACATTGTACCACCGACC  
 ACCATCTGGACTAGCTCTCCACAAACACTGATGCAGACACTGCCTCCCCATCCAACGGCACT  
 CACAACAACTCGGTGCTCCAGTTACAGCATCAGCCCCAACATCTCTGCTTCCTAAGAACATT  
 TCCATAGAGTCCAGAGAAGAGGAGATCACCAGCCCAGGTTCGAATTGGGAAGGCACAAACACA  
 GACCCCTCACCTTCTGGGTTCTCGTCAACAAGCGGTGGAGTCCACTTAACAACACGTTGGAG  
 GAACACAGCTCGGGCACTCCTGAAGCAGGCGTGGCAGCTACACTGTCGCAGTCCGCTGCTGAG  
 CCTCCCACTCATCTCCCTCAAGCTCCAGCCTCATCACCCTCATCCCTATCAACCTCACCA  
 CCTGAGGTCTTTTCTGCCTCCGTTACTACCAACCATAGCTCCACTGTGACCAGCACCCAACCC  
 ACTGGAGCTCCAAGTGCACCAGAGTCCCCGACAGAGGAGTCCAGCTCTGACCACACCCCACT  
 TCACATGCCACAGCTGAGCCAGTCCCCAGGAGAAAACACCCCAACAAGTGTGTGAGGCAAA  
 GTGATGTGTGAGCTCATAGACATGGAGACCACCACCCTTTCCAGGGTGATCATGCAGGAA  
 GTAGAACATGCATTAAAGTTGAGGCAGCATCGCCGCCATTACCGTGACAGTCATTGCCGTGGTG  
 CTGCTGGTGTGTTGGAGTTGCAGCCTACCTAAAAATCAGGCATTCCCTCTATGGAAGACTTTTG  
 GACGACCATGACTACGGGTCTGGGGAACTACAACAACCCCTCTGTACGATGACTCCTTACAA  
 TGGAATATGGCCTGGGATGAGGATTAAGTGTCTTTATTTATAAGTGCTTATCCAGTAGAATT  
 AATAAGTACCTGATGCGCATTGAACGACAATCTTAAGCCCTGTTTTGTTGGTATGGTTGTTTT  
 TGTTTTCTCCCTCTCCTCTGGCTGCTACAACTTCCCCTTTCTGGTACAAGAAGAACCATCT  
 TTAAAGGTGAGTGGAGGCTGATTTGCAGCTGAAGTGGGCCAGCCTTGACCAGCCAGGCCAGA  
 CCACCATGGTGAAGGCTTCTTTCCCACTGCAGGACCCACTTTGAGAAGGATCGAGGAGGAGG  
 ATTTGGGTTGTTTTGTTAGGGGTTACTTTGAGGGGAACATTTCAATTTGTGTTATTTCTTAAAC  
 TTCTATTTAGGAAATTACATTAAGTATTAATGAGGGGAAAGGAAATGAGCTCTACGAGGATTT  
 CACCTTGCATGGGAGAGAGCAGGGTTTTCTCAGATTCCTTTTAACTCTATTTATCTGGTTG  
 TTTCTGACAGGATGCTGCCTGCTTGGCTCTACGAGCTGGAAAGCAGCTTCTTAGCTGCCTAAT  
 TAATGAAAGATGAAATAGGAAGTGCCCTGGAGGGGGCCAGCAGGTCACGGGGCAGAATCTCT  
 CAGGTTGCTGTGGGATCTCAGTGTGCCCTACCTGTTCTCCCCCTCCAGGCCACCTGTCTCTGT  
 AAAGGATGTCTGCTCTGTTCAAAAGGCAGCTGGGATCCCAGCCCACAAGTGATCAGCAGAGTT  
 GCATTTCCAAAGAAAAAGGCTATGAGATGAGCTGAGTTATAGAGAGAAAGGGAGAGGCATGTA  
 CGGTGTGGGGAAAGTGAAGAGAAGCTGGCGGGGGAGAAGGAGGCTAACCTGCACTGAGTACTT  
 CATTAGGACAAGTGAGAATCAGCTATTGATAATGGCCAGAGATATCCACAGCTTGGAGGAGCC  
 CAGAGACTGTTTGCTTTATACCCACACAGCAACTGGTCCACTGCTTTACTGTCTGTTGGATAA  
 TGGCTGTAAATGTTTAAAAAC

**FIGURE 152**

MVYKTLFALCILTAGWRVQSLPTSAPLSVSLPTNIVPPTTIWTSSPQNTDADTASPSNGTHNN  
SVLPVTASAPTSLLPKNISIESREEEITSPGSNWEGTNTDPSPSGFSSTSGGVHLTTTLEEHS  
SGTPEAGVAATLSQSAAEPPTLISPQAPASSPSSLSTSPPEVFSASVTTNHSSVTSTQPTGA  
PTAPESPTEESSSDHTPTSHATAEPVPQKTPPTTVSGKVMCELIDMETTTTFPRVIMQEVEH  
ALSSGSIAAITVTVIAVLLVFGVAAYLKIRHSSYGRLDDHDYGSWGNYNPLYDDS

**Important features of the protein:**

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 258-278

**N-glycosylation sites.**

amino acids 58-61, 62-65, 80-83, 176-179

**Casein kinase II phosphorylation sites.**

amino acids 49-52, 85-88, 95-98, 100-103, 120-123, 121-124, 141-144, 164-167, 191-194, 195-198, 200-203

**Tyrosine kinase phosphorylation site.**

amino acids 289-296

**N-myristoylation sites.**

amino acids 59-64, 115-120, 128-133, 133-138, 257-262, 297-302

**FIGURE 153**

[illegible]

**FIGURE 154**

MLVHCVGLLLTGALLGLTLGAGALLASEPIYQPPSAWVPAGGLVGLALLGALLTLRWPRPFTV  
LGTTLGSAVLVACVDYFLEGLALGSWLGQRLQTLPALPSLC

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 38-55, 60-78

**N-myristoylation sites.**

amino acids 7-13, 12-18, 16-22, 22-28, 41-47, 50-56, 84-90, 88-94

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 67-78



**FIGURE 155**

TGCAATTAAAGGAGTCGGGTCTCTAACTGTTGATCTGTTTTTTTCCCTTCTGAGCAATGGAGC  
TTACCATCTTTATCCTGAGACTGGCCATTTACATCCTGACATTTCCCTTGTACCTGCTGAACT  
TTCTGGGCTTGTGGAGCTGGATATGCAAAAATGGTTCCTTACTTCTTGGTGAGGTTCACTG  
TGATATACAACGAACAGATGGCAAGCAAGAAGCGGGAGCTCTTCAGTAACCTGCAGGAGTTTG  
CGGGCCCCCTCCGGGAAACTCTCCCTGCTGGAAGTGGGCTGTGGCACGGGGGCCAACTTCAAGT  
TCTACCCACCTGGGTGCAGGGTGACCTGTATTGACCCCAACCCCAACTTTGAGAAGTTTTTGA  
TCAAGAGCATTGCAGAGAACCGACACCTGCAGTTTGAGCGCTTTGTGGTAGCTGCCGGGGAGA  
ACATGCACCAGGTGGCTGATGGCTCTGTGGATGTGGTGGTCTGCACCCTGGTGTGTGCTCTG  
TGAAGAACCAGGAGCGGATTCTCCGCGAGGTGTGCAGAGTGCTGAGACCGGGAGGGGCTTTCT  
ATTTTCATGGAGCATGTGGCAGCTGAGTGTTTCGACTTGGAATTACTTCTGGCAACAAGTCCTGG  
ATCCTGCCTGGCACCTTCTGTTTTGATGGGTGCAACCTGACCAGAGAGAGCTGGAAGGCCCTGG  
AGCGGGCCAGCTTCTCTAAGCTGAAGCTGCAGCACATCCAGGCCCCACTGTCCTGGGAGTTGG  
TGCGCCCTCATATCTATGGATATGCTGTGAAATAGTGTGAGCTGGCAGTTAAGAGCTGAATGG  
CTCAAAGAATTTAAAGCTTCAGTTTTACATTTAAATGCTAAGTGGGAGAAGAGAAACCTTTT  
TTTTGGGGGGCGGTTTTTTTTGGTTTTGTTGTTGGTTTTTTTTTTTTTTTTTGGCAGGAGAATCTC  
TTGAACCCAGAAGGCGAAGGTTGCAGTGAACCGAGATCATGCCATTGTACTCTAGCCTGGGTG  
ACAAGAGCAAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAGTAGAGACAGGGAGAC  
GGGGTCTCACTGTGTTGCCTAGGCCGGTCTTGAACCTCTGGGCTCAAGTGATTCTCCACCTT  
GACCTCCTAAATTGTTGGGATTACAGGTGTGAGACAGTGCACCTGGCCGAAATAGCTCAAGTT  
TCTGAAAAACAAATCTGAATCTATTTGTTATTCTTAGCGTCACTGGTCTGGCTTTCAGAATTA  
ACATACAAGGTTGCCACACCTAGTTCTGCCAGCTTTATGTCTTTTATTCCAGTATTCCACCA  
AAGTTTGTTTTCTTGCAATTCAGTTCTCAAGTCTTAAGATAAAGATTGTACTTGACAGTTTAG  
TATATCCATAAACTATTTGAGGTGGTTAAGGTTCTTGGGTTCATTTTCTTAATACTTTGCT  
GAATATTGTAGATTGTAGGCAATGAAAAAGTCTACTAAATTAGGAAAACCTTGAATAATTAGG  
TATCCTAGGTAAGAGCCCCCTAAACATCAAGCAATCTGTGAGTCTGTAAAGAAATAAATATTTT  
TTGGATTATTCTTATCTAATTCACCCCTGTTGGAAGATGATTTCTTTGTTCTTTGCAACTAT  
GGAAGCTGTGAAAATCATCACAAGTGCCTCTGAAAGCGAGTGTTAGGTGGTTAGAGGGTTTA  
ATATTTTCTGCAATGGTTTGTAGGAATTTTAATAAATGTAGTATATTTTCTGAGATGATTTTG  
TAAAAGTACTATTTTAAATATCAAATCAACCAATAAATTCACATTTGTGTTAGGAACAAAA

**FIGURE 156**

MELTIFILRLAIYILTFPLYLLNFLGLWSWICKKWFPYFLVRFTVIYNEQMASKKRELFSLNQ  
EFAGPSGKLSLLEVCGGTGANFKFYPPGCRVTCIDPNPNFEKFLIKSIAENRHLQFERFVVAA  
GENMHQVADGSVDVVCTLVLCVKNQERILREVCVRVLRPGGAFYFMEHVAAECSTWNYFWQQ  
VLDPAWHLLFDGCNLTRESWKALERASFSLKLQHIQAPLSWELVRPHIYGYAVK

**Signal peptide:**

amino acids 1-29

**N-glycosylation site.**

amino acids 203-207

**N-myristoylation sites.**

amino acids 78-84, 80-86, 91-97, 201-207

**FIGURE 157**

CCGCTGAGATGTACGAACTTCCGGTTCTCCGGGCAGCTGCCACTGCTGTAGCTTCTGCCACCT  
GCCACGACCGGGCCTCTCCCTGGCGTTTGGTCACCTCTGCTTCATTCTCCACCGCGCCTATGG  
TCCCTCTTGGAGCCAGCGTGGCGGGCCTGGCGGGCTCCCGGGTGGTGAGAGAGCGGTCCGGGAA  
CGATGAAGGCCTCGCAGTGCTGCTGCTGTCTCAGCCACCTCTTGGCTTCCGTCTCTCCTGCTG  
TGTTGCTGCCTGAACTAAGCGGGCCCCTGGCAGTCCTGCTGCAGGCAGCCGAGGCCGCGCCAG  
GTCTTGGGCCTCCTGACCCCTAGACCACGGACATTACCGCCGCTGCCACCGGGCCCTACCCCTG  
CCCAGCAGCCGGGCCGTGGTCTGGCTGAAGCTGCGGGGCCGCGGGGCTCCGAGGGAGGCAATG  
GCAGCAACCCTGTGGCCGGCTTGAGACGGACGATCACGGAGGGAAGGCCGGGGAAGGCTCGG  
TGGGTGGCGGCCTTGCTGTGAGCCCCAACCTGGCGACAAGCCCATGACCCAGCGGGCCCTGA  
CCGTGTTGATGGTGGTGAGCGGCGCGGTGCTGGTGTACTTCGTGGTCAGGACGGTCAGGATGA  
GAAGAAGAAACCGAAAGACTAGGAGATATGGAGTTTTTGGACACTAACATAGAAAAATATGGAAT  
TGACACCTTTAGAACAGGATGATGAGGATGATGACAACACGTTGTTTGATGCCAATCATCCTC  
GAAGATTAAGAATGTGCCTTTTGATGAAAGAACTTTATCTTTCTACAATGAAGAGTGGAATTC  
TATGTTTTAAGGAATAAGAAGCCACTATATCAATGTTGGGGGGGTATTTAAGTTACATATATTT  
TAACAACCTTTAATTTGCTGTTGCAATAAATACCGTATCCTTTTATTATATCTTTATATGTAT  
AGAAGTACTCTATTAATGGGCTCAGAGATGTTGGGGATAAAGTATACTGTAATAATTTATCTG  
TTTGAAAATTACTATAAAACGGTGTCTTCTGGTCGGTTTTTGTTTCCTGCTTACCATATGATT  
GTAAATTGTTTTATGTATTAATCAGTTAATGCTAATTATTTTTGCTGATGTCATATGTAAAG  
AGCTATAAATTCCAACAACCAACTGGTGTGTAAAAATAATTTAAAAATTTCTTTACTGAAAGG  
TATTTCCATTTTTGTGGGGAAAAGAAGCCAAATTTATTACTTTGTGTTGGGGTTTTTAAAAAT  
ATTAAGAAATGTCTAAGTTATTGTTTGCAAAACAATAAATATGATTTTAAATTCTCTTAAAAA  
AAAAA

**FIGURE 158**

MKASQCCCLSHLLASVLLLLLLPELSGPLAVLLQAAEAAPGLGPPDPRPRTLPPPLPPGPTPA  
QQPGRGLAEAAGPRGSEGGNGSNPVAGLETDDHGKAGEGSVGGGLAVSPNPGDKPMTQRALT  
VLMVVSGAVLVYFVVVRTVRMRRNRKTRRYGVLDTNIE NMELTPLEQDDEDDNTLFDANHPRR

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 124-140

**N-glycosylation site.**

amino acids 83-87

**N-myristoylation sites.**

amino acids 69-75, 78-84, 81-87, 97-103, 103-109, 106-112,  
157-160

# **FIGURE 159**

GCTGCAGGCGGGCAGGGCTACACCATGGGCGGGCTGCTGCGGGCCGCCCGGCTGCCGCGGCTG  
CTTTGCGCCGCTGCTGCTTCTGCTGGTTGGGGGAGCGTTCCTGGGTGCCCTGTGTGGCTGGGTCT  
GATGAGCCTGGCCCAGAGGGCCTCACCTCCACCTCCCTGCTAGACCTCCTGCTGCCCACTGGC  
TTGGAGCCACTGGACTCAGAGGAGCCTAGTGAGACCATGGGCCTGGGAGCTGGGCTGGGAGCC  
TCTGGCTCAGGCTTCCCCAGCGAAGAGAATGAAGAGTCTCGGATTCTGCAGCCACCACAGTAC  
TTCTGGGAAGAGGAGGAAGAGCTGAATGACTCAAGTCTGGACCTGGGACCCACTGCAGATTAT  
GTTTTTCTGACTTAAGTGAAGGAGGTTCCATTGAAGACACTAGCCAGGCTCAAGAGCTG  
CCAAACCTCCCCCTCTCCCTTGCCCAAGATGAATCTGGTTGAGCCTCCCTGGCATATGCCTCCC  
AGAGAGGAGGAAGAAGAGGAAGAGGAAGAGGAGGAGAGGGAGAAGGAAGAGGTAGAGAAACAA  
GAGGAGGAGGAAGAGGAGGAGCTGCTCCCTGTGAATGGATCCCAAGAAGAAGCCAAGCCTCAG  
GTCCGTGACTTTTCTCTCACCAGCAGCAGCCCCAGGGGCCACCAAAGCAGGCATGAA  
GACTCCGGGGACCAGGCCTCATCAGGTGTGGAGGTGGAGAGCAGCATGGGGCCCGCTTGCTG  
CTGCCTTCAGTCACCCCAACTACAGTGACTCCGGGGGACCAGGACTCCACCAGCCAAGAGGCA  
GAGGCCACAGTGCTGCCAGCTGCAGGGCTTGGGGTAGAGTTCGAGGCTCCTCAGGAAGCAAGC  
GAGGAAGCCACTGCAGGAGCAGCTGGTTTGTCTGGCCAGCACGAGGAGGTGCCGGCCTTGCT  
TCATTCCCTCAAACCACAGTCCCAGTGGGGCCGAGCACCCAGATGAAGATCCCCTTGCTCT  
AGAACCTCAGCCTCTTCCCCACTGGCCCCCTGGAGACATGGAAGTACACCTTCCTCTGCTACC  
TTGGGACAAGAAGATCTCAACCAGCAGCTCCTAGAAGGGCAGGCAGCTGAAGCTCAATCCAGG  
ATACCCTGGGATTCTACGCAGGTGATCTGCAAGGACTGGAGCAATCTGGCTGGGAAAACTAC  
ATCATTCTGAACATGACAGAGAACATAGACTGTGAGGTGTTCCGGCAGCACCGGGGGCCACAG  
CTCCTGGCCCTGGTGGGAAGAGGTGCTGCCCCGCCATGGCAGTGGCCACCATGGGGCCTGGCAC  
ATCTCTCTGAGCAAGCCCAGCGAGAAGGAGCAGCACCTTCTCATGACACTGGTGGGCGAGCAG  
GGGTGGTGGCCACTCAAGATGTCCTTTCCATGCTGGGTGACATCCGCAGGAGCCTGGAGGAG  
ATTGGCATCCAGAACTATTCCACAACCAGCAGCTGCCAGGCGCGGGCCAGCCAGGTGCGCAGC  
GACTACGGCACGCTCTTCGTGGTGCTGGTGGTCATTGGGGCCATCTGCATCATCATCATTGCG  
CTTGGCCTGCTCTACAACCTGCTGGCAGCGCGGCTGCCCAAGCTCAAGCACGTGTGCGACGGC  
GAGGAGCTGCGCTTCGTGGAGAACGGCTGCCACGACAACCCACGCTGGACGTGGCCAGCGAC  
AGCCAGTCGGAGATGCAGGAGAAGCACCCAGCCTGAACGGCGGCGGGGCCCTCAACGGCCCCG  
GGGAGCTGGGGGGCGCTCATGGGGGGCAAGCGGGACCCCGAGGACTCGGACGTGTTGAGGAG  
GACACGCACCTGTGAGCGCAGCCGAGGCGCAGGCCGAGTGGGCCGCCAGGACCAAGCGAGGTG  
GACCCCGAAACGGACGGCCCCGAGCCCCGACCAGCCCCGCGCCTACCCGGGGCCGCCCCGCGG  
CCTGGCCCTCGGCGCGGGCTCCTTCCCCTTCCCCGACTTCACACGGCGGCTTCGGACCAAC  
TCCCTCACTCCCGCCCCAGGGGCGAGCCTCAAAGCCCGCCTTGGCCCCGCTTCCC GCCCCTG  
AACCCCGGCCCCCGGGCGGGCGGGCGGCTTCTGCGCCCCGGGACTCAATTAAACCCGCC  
GGAGACCACGCCGGGCCAGCAAAA

**FIGURE 160**

MGRLLRARLPPLLSPLLLLLLVGGAFGLGACVAGSDEPGPEGLTSTSLDLLLPTGLEPLDSEE  
PSETMGLGAGLGASGSGFPSEENEESRILQPPQYFWEEEEELNDSSLDLGPTADYVFPDLTEK  
AGSIEDTSQAQELPNLPSPLPKMNLVEPPWHMPPREEEEEEEEEEREKEEFVEKQEEEEEEEL  
LPVNGSQEEAKPQVRDFSLTSSSQTPGATKSRHEDSGDQASSGVEVESSMGPSSLLPSVTPPT  
VTPGDQDSTSQAEEATVLPAAGLGVEFEAPQEASEEATAGAAGLSGQHEEVPALPSFPQTTP  
SGAEHPDEDPLGSRTSASSPLAPGDMELTPSSATLGQEDLNQQLLEGQAAEAQSRIPWDSTQV  
ICKDWSNLAGKNYIILNMTENIDCEVFRQHRGPQLLALVEEVLPRHGSGHHGAWHISLSKPSE  
KEQHLLMTLVGEQGQVVPQTQDVL SMLGDIRRSLEEIGIQNYSTTSSCQARASQVRSDYGTLFVV  
LVVIGAICIIIIALGLLYNCWQRRLPKLKHVSHGEELRFVENGCHDNPTLDVASDSQSEMQEK  
HPSLNGGGALNGPGSWGALMGGKRDPESDVFEEDTHL

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 499-521

**N-glycosylation sites.**

amino acids 106-110, 193-197, 395-399, 480-484

**Glycosaminoglycan attachment site.**

amino acids 77-81

**N-myristoylation sites.**

amino acids 24-30, 28-34, 41-47, 69-75, 71-77, 73-79, 75-81,  
216-222, 327-333, 455-461, 519-525, 574-580, 581-587, 584-590

**Amidation site.**

amino acids 588-592

**FIGURE 161**

CCAGGGCGGAGCGCAGCTGCGCCGGGCTTGGGCGCCTGGGGCCGCCGCTCCCCACCGTCGTTT  
TCCCCACCGAGGCCGAGGCGTCCCGGAGTCATGGCCGGCCTGAACTGCGGGGTCTCTATCGCA  
CTGCTAGGGGTTCTGCTGCTGGGTGCGGCGCGCCTGCCGCGCGGGGCAGAAGCTTTTGAGATT  
GCTCTGCCACGAGAAAGCAACATTACAGTTCTCATAAAGCTGGGGACCCCGACTCTGCTGGCA  
AAACCCTGTTACATCGTCATTTCTAAAAGACATATAACCATGTTGTCCATCAAGTCTGGAGAA  
AGAATAGTCTTTACCTTTAGCTGCCAGAGTCCTGAGAATCACTTTGTTCATAGAGATCCAGAAA  
AATATTGACTGTATGTCAGGCCCATGTCTTTTGGGGAGGTTTCAGCTTCAGCCCTCGACATCG  
TTGTTGCCTACCCTCAACAGAACTTTTCATCTGGGATGTCAAAGCTCATAAGAGCATCGGTTTA  
GAGCTGCAGTTTTTCCATCCCTCGCCTGAGGCAGATCGGTCCGGGTGAGAGCTGCCCAGACGGA  
GTCACTCACTCCATCAGCGGCCGAATCGATGCCACCGTGGTCAGGATCGGAACCTTCTGCAGC  
AATGGCACTGTGTCCCGGATCAAGATGCAAGAAGGAGTGAAAATGGCCTTACACCTCCCATGG  
TTCCACCCCAGAAATGTCTCCGGCTTCAGCATTGCAAACCGCTCATCTATAAAACGTCTGTGC  
ATCATCGAGTCTGTGTTTGAGGGTGAAGGCTCAGCAACCCTGATGTCTGCCAACTACCCAGAA  
GGCTTCCCTGAGGATGAGCTCATGACGTGGCAGTTTGTTCGTTCCCTGCACACCTGCGGGCCAGC  
GTCTCCTTCCTCAACTTCAACCTCTCCAAGTGTGAGAGGAAGGAGGAGCGGGTTGAATACTAC  
ATCCCGGGCTCCACCACCAACCCCGAGGTGTTCAAGCTGGAGGACAAGCAGCCTGGGAACATG  
GCGGGGAACTTCAACCTCTCTCTGCAAGGCTGTGACCAAGATGCCCAAAGTCCAGGGATCCTC  
CGGCTGCAGTTCCAAGTTTTGGTCCAACATCCACAAAATGAAAGCAGTGAGTGAGCCCCACTT  
TCCTTTTTCTTCCTCCTCCAGCACCTTCGTTGTTTCCTGGGTAGTCTGCCTGGGTGAGGCTCC  
CTTCCTGTTTCTCATCTGTGGCTTCTGAAACACTTAGACTCTGGACCCAGCAAGAGTTTCAGG  
AAGTGGGTTGCTAGGCAGTTAGACAGGCTTGTGTTGGTGAACACCCGGTATGTAGTTCCATTTC  
GCACAATAAAAAGAAATCTTGCAATCAAGATGCTAAATTGTTTTTAACGAAAA

**FIGURE 162**

MAGLNCGVSIALLGVLLLGAAARLPRGAEEAFEIALPRESNITVLIKLGTPDLLAKPCYIVISKR  
HITMLSIKSGERIVFTFSCQSPENHFVIEIQKNIDCMGSPCPFGGEVQLQPSTSLPTLNRTFI  
WDVKAHKSIGLELQFSIPRLRQIGPGESCPDGVTHSISGRIDATVVRIGTFCSNGTVSRIKMQ  
EGVKMALHLPWFHPRNVSGFSIANRSSIKRLCIIESVFEGEGSATLMSANYPEGFPEDELMTW  
QFVVPAPHLRASVSFLNFNLSNCERKEERVEYYIPGSTTNPEVFKLEDKQPGNMAGNFNLSLQG  
CDQDAQSPGILRLQFQVLVQHPQNESSE

**Signal peptide:**

amino acids 1-29

**N-glycosylation sites.**

amino acids 39-43, 122-126, 180-184, 205-209, 213-217, 270-274,  
310-314, 339-343

**Tyrosine kinase phosphorylation site.**

amino acids 276-284

**N-myristoylation sites.**

amino acids 3-9, 7-13, 158-164, 175-181, 191-197, 303-309



# **FIGURE 163**

CAACCACACACCTGGGGAATTGCTGGCCTGACTTCTGACCCCTGACTCCTCATACCCCTTCCTC  
CAGAGCATGACATTTGACCACCAACTGAAACCTGACCTCTGACCCCAGACCACTGGCCCTTCC  
CCCGCCCTGTGGTGACTTCATAAAGGTTACTAGCTTCTCCCCTGGCCTTGAGACCCACACGAT  
GGCCCTGCTGGCTCTGGCCAGTGCCGTCCCCCTGCCCCTGCTGGCCCTGGCTGTCTTCAGGGT  
GCCCCCTGGGCCTGTCTCCTCTGCTTTCACAACCTACTCTGAGCGCCTCCGCATCTGCCAGAT  
GTTTGTGGGATGCGGAGCCCCAAGCTTGAAGAGTGTGAGGAGGCCCTTCACGGCCGCCCTTCCA  
GGGCCTCTCTGACACCGAAATCAGTGAGGAGACCATCCACACTTCATCAGTGTCTTGGGGAAG  
GTGCAGAGGGAGGGCAGGAGAGGCCAGAGGGTTCAGGCTGAGGGACAGACAGAGAGAAACAGT  
CAGAGGAGAAAGGCTCAAAGACCATGAGAACAACAGAGACTTAGGGACAGAGAGACACAGACA  
GGGGAAGACAGCAGGGCAAAGACTCAGAGAGGGGAGGATGGAGAGTTCAGAGAGGGGAAGATGG  
AGACTCAGAGAGAGGGGAGGATGGAGACTCAGAGAGAGAGGAAGATGGAGACTCAGAGGGAAA  
GATGGAGACTCAGGAGTATGGAGAGTTCAGAGAGGGGAGGATGGACACTCAGGGGAGGATGGAG  
AGTCAGGAGGATGGAGACTCATAGAAAGGGGAGGATGGAGAGTTCAGGAGAGGTTGGAGACTGG  
AGAGGGGAATAGAGACCCAGAAAGGGGAGGATGGAGACTCAGAGGGTGGAAGATGGAGACTCAA  
AGAGGATGGAAACCCAGAGAGAGGAGGACAGAGATGAGGACAGAGACTAGGGGAAGCAGGATAG  
CGACTGGTTCGGGGCAGAGACTCAGGGAGGATAGAGACTCACAGAGAGGTGAGGATAGAGACT  
TGGGAGGGACTCAGGAAGCATAGCGACTGTGGGGCAAAGAGTTCAGAGAGGGGAGGATACAGAC  
TTGGGAGGGCAGAGACTCAGAAAAGAAATGTTTCGCATTAGGGACATGGTGTTCGGGGGAGCTG  
CCTCCCCCAGCCCCCTGCTCCCTCCCTCACCGCCAGACTATGATGAGAGAAGCCACCTGCATGA  
CACCTTCACCCAGATGACCCATGCCCTGCAGGAGCTGGCTGCTGCCAGGGATCCTTTGAGGT  
TGCCCTTCCCTGATGCTGCAGAGAAAATGAAGAAGGTTCATTACACAGCTTAAAGAAGCCCAGGC  
TTGCATCCCTCCCTGCGGTCTCCAGGAGTTCGCCCCGGCGTTTCCTCTGCAGCGGGTGCTACTC  
TAGGGTCTGCGACCTCCCGCTGGACTGCCCAGTTTCAGGATGTGACAGTGACTCGGGGCGACCA  
GGCTATGTTTTCTTGCATCGTAACTTCCAGCTGCCAAAGGAGGAGATCACCTATTCCTGGAA  
GTTTCGAGGAGGAGGTCTCCGGACTCAGGACTTGTCTTATTTCCGAGATATGCCGCGGGCCGA  
AGGATACCTGGCGCGGATCCGGCCGGCTCAGCTCACGCACCGCGGGACGTTCTCCTGCGTGAT  
CAAGCAAGACCAGCGCCCCCTGGCCCGGCTCTACTTCTTTCTTAACGTCTCTCGGGGCCCTCGC  
ATCAGCGAGTGCGACAGTGTGGCGTGGTGAGTTCTGGGGACTCCGGAGCCCCAGCATCTAGC  
TCCCCGCTGTCTCAGATCCCACCGAGAAGTCTGGGTTCCAGCAACCTCCAACCCAGGAGGAT  
GTTCTTTTCGATGGTACTGCAGTGGAACCTAACAAAGGTATCTTTCCTCCTTCCCTATCCTATT  
TCCATCCTGAAAATAAAGAATATATTTCAACTCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAA

## **FIGURE 164**

MALLALASAVPSALLALAVFRVPAWACLLCFTTYSERLRICQMFVGMRSKLEECCEEAFTAAF  
QGLSDTEISEETIHTSSVSWGRCRGRAGEAQRVRLRDRQRETVRGERLKDHENNRDLGTERHR  
QGKTAGQRLREGRMESQRGEDGDSERGEDGDSEREEDGDSEGKMETQEYGESERGGWTLRGGW  
RVRRMETHRKGRMESQERLETGEGIETQKGEDGDSEGGRWRLKEDGNPERGGQR

**Signal peptide:**

amino acids 1-26

**N-myristoylation site.**

amino acids 65-71

**FIGURE 165**

[illegible]

**FIGURE 166**

MELSDVTLIEGVGNEVMVAGVVVLILALVLAWLSTYVADSGSNQLLGAIVSAGDTSVLHLGH  
VDHLVAGQGNPEPTELPHPSEGNDKAEFEAGEGRGDSTGEAGAGGGVEPSLEHLLDIQGLPKR  
QAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLNDTEELAVARPEDTVGALKSKYFPGQES  
QMKLIYQGRLLQDPARTLRSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVMVGS  
LMVPVFVLLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLVFGMYGR

**Signal peptide:**

amino acids 1-36

**Transmembrane domains:**

amino acids 246-267, 275-301

**N-glycosylation sites.**

amino acids 162-166, 211-215

**N-myristoylation sites.**

amino acids 48-54, 105-111, 109-115, 129-135, 177-183, 247-253

**Cell attachment sequence.**

amino acids 97-100

# **FIGURE 167**

GGCGGCTGTGTGTCGCCGGAGCCGAAGCGCGCAGGCCCGTCCCGGTGGCCGGGAGCGGGCGGGTGGGGGCGCCA  
TGTGGTTCATGTACCTGCTGAGCTGGCTGTGCTCTTCATCCAGGTGGCCCTTCATCACGCTGGCTGTCGCGGCTG  
 GACTCTATTACCTGGCAGAACTGATAGAAGAATACACAGTGGCCACCAGCAGGATCATAAAATACATGATCTGGT  
 TCTCCACCGCTGTACTGATTGGCCTCTACGTCTTTGAGCGCTTCCCCACCAGCATGATTGGAGTGGGCCTATTCA  
 CCAACCTCGTCTACTTTGGCCCTCCTCCAGACCTTCCCCTTCATCATGCTGACCTCGCCTAACTTCATCCTGTGCT  
 GTGGACTAGTGGTGGTGAATCATTACCTAGCATTTCAGTTTTTTGCGAGAAGAATATTATCCCTTCTCAGAGGTCC  
 TGGCCTATTTCACTTTCTGCTGTGGATAATTCCGTTTGGCTTTTTTGTGTCACTTTCCGGCCGGGAGAACGTCC  
 TGCCCTCTACCATGCAGCCAGGAGATGATGTCGTCTCCAATTATTTACCAAAGGCAAGCGGGGCAACCGCTTAG  
 GGATCCTGGTTGTCTTCTCCTTCATCAAAGAGGCCATTCTACCCAGTTCGTGAGAAGATATACTGACCCCCATGCA  
 GGCAGGATGTGGGGGGCAAGATCAGGAGAGTCAAGCCCCCTGGGCCTTATGCCAGGTGGGGACCAGAAGTCGGGA  
 AGGCACCTACCACCTGCCCTGGCTTTCTTCCCCTCAACTCTGGAGCCCCATCCCCACCTCCTTGGGGGGCTCAG  
 CTTGGCTCAGATCTGATGCTTCAAGAGGCTGTAACCTCAGAGGGCACCAAGGAGGGTGGCAGAGCCTGCTTAGCC  
 AGGAGGCCGAGGTCCCTCAGTCTCCCTGTCCCTTCCAAGGTGGGTGAGGAGTCTGGCCCCGTGGGGCAGG  
 CAGGGCAGGGTCTGTGAAGCTTAAGAGCAGATGGTGACAAGTTCTCTGGGCAGGTGGCCATGGGGAGGGGCCATG  
 GCTTGGCATGTCCAACAGAAATAGTTTTTGTCTGTGAACGGTGATTCTGTCCAAGTGCAGATTTCCGTTTGAAT  
 AAAGCTTCGCTTCTAGGTGGCACTGTTTGCCTTAATACCTGACAGTTCATCTTCCCTTTCTCCTGCTAACCTTC  
 TGCTCCGACTGGACTCACTTTTCTGCTCCAGGGACTCCTTTCTGGGTTTGGGTCTTGGCCTTCCCAAGGGACT  
 GTTCTTGTGGCCCTTAATGGGAAGGGGGCAGGGGTGAGGAGCTGAGCCTGCTCAAGGAGTGGGAAGTGGGGCTAT  
 AGGCAGCCTCTCTGATGCACTCTCTTCCATCTCTTCCCCAAGGCTCCGTGACTGTCAAACCTGGGAGTAGGAGAG  
 GGGACAATTTAGGACTGGGCTAGATTTTCAAGAAGCATCTACAATATCCTATTTATAAATCTTCCCTCTGGGAAA  
 AGGAGTGGTTTCTGGCTGAATACTATCTTAGGCTCAAGGAGAAAACAAAATAAAATTAAGCTTCCAGGCAGCCTGT  
 TTTTAAAGAAATGGGACTAATGGGAGAAGCTGTTTGTCACTCTAAGAGCATCCAAGCCCTGGCCCGTCTGTGCAC  
 TCTTGGCTCCTGGGGAGATATATCTGCCTTCTAAGAAGGCAGGCCAGGTCTTGGGCACAGACCTGCATTTGTTGA  
 CCTTGCACCTCCAATATAGTGCCTTGCAAGTGCTCAACAGTACATATTGGAATGAAGTCCCTATGAGAGCCATT  
 CTGGCCATGTTCTATACCTCAAAGTGAGGCTGGCAGGTACAGAGATGAACGTACACATGTGATACATTTAAGCC  
 ACTGGAAAAACCCCTGTGCTTGAATAATTTCTCTATATCATGCCCTGGAGTTCATCATAGCCCTTCATTTCTT  
 TGGCTTTAGCATTTACCTTCTCTTAAGAATACCAGCTTTCCCTTTCTCCTGAGAGGAAGAGCACATGTTGGTCTC  
 CTCTTAGTGTGAACGAGATTGCCAGGCCCTTTTCTCCTATGCACACCAGGATAGACAAGGCAGGGGATACTGGCA  
 GCCTGCATCATCCTCCCATTTGGGCTGACAGCTGGCCCTACTTTCTCCTCTGCTGCTTGGTCCCTCACCTTGAT  
 GATGTGGCTTCGCCCCCTCCACTCTACTGCCAGTGTCTCCCAGGGGTGCTAAATCCAGCAGACCCCTTTCTCTG  
 TCTTACTAGATCTGGGCAGCATTTGACATGGCTGATCACCCCTTGCTTCTTGGATGGCACTTCCCTGGCACCTCT  
 GTGGCTAGTTGTCTTACCTCCCTGGCTGTCTCTTTCAGGCTTCCGTGCAGGCTTCTCCACTTGCCCATGCACAGT  
 AGGGTCTTTCAGGGTTCTGCTGTGGGCTCCCTAGGGAAGCCCATCCATCTGGATGGTTTTCAAGGATGGTGAGGAA  
 TTTAGAGTTGACCTCCAGCCCCAACATCCTTCTGATCACCTGAACCACAGTTTTGCTGCCCTCTAGGTGCACAG  
 ACAATTCAGGTCCATGGCCCCAGATGGTACTTGCTGTCTTCTGCAAACCTGCCCTTCTGGGTACTTCCCTTGACC  
 CCGAGATCACTCAGGAGCCAGACAGGAACTTATTCTATTCTGTTTTCTCTTCTGCCCCACACATCCAATCTC  
 TCAAAACGGTCAGGTCTACCTTAACATCTCTTGATTGAGCCACTCCCACTGTCTCATGCTTTACCTGGATTAT  
 CGTGACAGCCTCCTACTGCTTCTCTATCATGTGGCCAGAGCTATCTTCTAAATGCAATTGCATAGTTGATCAAG  
 TCACTCTCTGGCCATAAACCTTCTTGGCTCCCTGCTGCCCTCAGGATAAAGTCTGGACCCCTCAGCATGGCTTG  
 TGAGACTCATGGTGTCTTGTCCCTGCTCACCTCTCTGGTCTCATCACTTGCCTTCTTGCAATTCTGGGTCCCAGC  
 CTCTGTATCCAGAGATGCAGTGGCTCTCCATTGCCACTCTGATTCTCTTCTTTTGGTTCACAGAGAAAGGGT  
 ACTTTCTCTGTCAAATCTCAACTTAGACTTGACTTCTCCAGGAGCTTTGGCTATACTCTCTCTCCCGACCCC  
 CACCCTGGCATACTACACAGATCACTCTGGGCTCACTTGCCTGCCTAATGGTCACTCTCCCGAGTAGACTGTAAGC  
 TCCTTGAGGGCAAGGATTGTGTGAATTTTTGTATTAAACAGTGCCTGGCTTGGTGCCTGGCACCTAGAAAGCAC  
 TCAATAAATGTTTTGTTAATGAA

## **FIGURE 168**

MWFMYLLSWLSLFIQVAFITLAVAAGLYYLAELIEEYTVATSRIIKYMIWFSTAVLIGLYVFE  
RFPTSMIGVGLFTNLVYFGLLQTFPFIMLTSPNFILSCGLVVVNHYLAFQFFAEYYPFSEVL  
AYFTFCLWIIIPFAFFVSLSAGENVLPSTMQPGDDVVSNYFTKGKRGKRLGILVVFSFIKEAIL  
PSRQKIY

**Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 126-146

**Casein kinase II phosphorylation site.**

amino acids 145-148

**N-myristoylation sites.**

amino acids 73-78, 82-87

**Amidation sites.**

amino acids 168-171, 171-174

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 91-101

**FIGURE 169**

CAAAGCCCTACCCCTCACCATTACCCAGGTCCTGTGGGAAGAGCAGCGTGGAGGTGGGCTGAGG  
TTAGAAGGTGCAGAGCGTGGGAAGAAGATTGTGAGCTGAGTATTGGACATCTGTTCTTGAATAG  
TCCCTGGGCCTGCCATAGGAAAGGAAGTTCTCCAGGGTTACAGTTCTTATCCGCGTGAATACA  
**CATGGCTCTGT**TACGAAAAATTAATCAGGTGCTGCTGTTCTTCTGATCGTGACCCCTCTGTGT  
GATTCTGTATAAGAAAGTTTATAAGGGGACTGTGCCCAAGAATGACGCAGATGATGAATCCGA  
GACTCCTGAAGAACTGGAAGAAGAGATTCTGTGGTGATTTGTGCTGCAGCAGGGAGGATGGG  
TGCCACTATGGCTGCCATCAATAGCATCTACAGCAACACTGACGCCAACATCTTGTTCTATGT  
AGTGGGACTCCGGAATACTCTGACTCGAATACGAAAATGGATTGAACATTCCAACTGAGAGA  
AATAAACTTTAAATCGTGGAATTCAACCCGATGGTCCTCAAAGGGAAGATCAGACCAGACTC  
ATCGAGGCCTGAATTGCTCCAGCCTCTGAACTTTGTTTCGATTTTATCTCCCTCTACTTATCCA  
CCAACACGAGAAAGTCATCTATTTGGACGATGATGTAATTGTACAAGGTGATATCCAAGAACT  
GTATGACACCACCTTGGCCCTGGGCCACGCGGCGGCTTTCTCAGATGACTGCGATTTGCCCTC  
TGCTCAGGACATAAACAGACTCGTGGGACTTCAGAACACATATATGGGCTATCTGGACTACCG  
GAAGAAGGCCATCAAGGACCTTGGCATCAGCCCCAGCACCTGCTCTTTCAATCCTGGTGTGAT  
TGTTGCCAACATGACAGAATGGAAGCACCAGCGCATCACCAAGCAATTGGAGAAATGGATGCA  
AAAGAATGTGGAGGAAAACTCTATAGCAGCTCCCTGGGAGGAGGGGTGGCCACCTCCCCAAT  
GCTGATTGTGTTTCATGGGAAATATTCACAATTAACCCCTGTGGCACATAAGGCACCTGGG  
CTGGAATCCAGATGCCAGATATTCGGAGCATTTTCTGCAGGAAGCTAAATTACTCCACTGGAA  
TGGAAGACATAAACCTTGGGACTTCCCTAGTGTTCAACGACTTATGGGAAAGCTGGTTTGT  
TCCTGACCCTGCAGGGATATTTAAACTCAATCACCATAGCT**TGA**TATAACTCTACCCTTAAAT  
ATTCCTGTATAGAAATGTGGAATTGTCCCTTTGTAGCCAACTATAACATTGTTCTTTATGAA  
TATTACCTTTGATACATATGATCCACAATATAAAAAACCAAAACTACTGTGTGCAAATTATAC  
CTTGGACCATATAGGCATTGATTAACTTCTTTAAGTACATGTGATAACTATGGAAATCAAGAT  
TATGTGACTGAAAAACATAAAGGAAGAGACCCATCTAGATAACAGCAATCAACCTGCTTAATT  
CTGAATGACAATTATATCCACAAATTTTAAACTTCTACATGTATTTTTCACATGAAGATCT  
CCTTAACAGGTTGCCAACCTTTTCTTTTATAAACTATTACATTTAAATATGGACGTCTGAA  
AAATAAAATATTCATCATTTTTTAAAA

**FIGURE 170**

MALLRKINQVLLFLLIVTLCVILYKKVHKGTVPKNDADDESETPEELEEIEIPVVICAAAGRMG  
ATMAAINSIYSNTDANILFYVVGRLRNTLTRIRKWIEHSLREINFKIVEFNPMVLKGKIRPDS  
SRPELLQPLNFVRFYLPLLIHQHEKVIYLDLDDVIVQGDIQELYDTTLALGHAAAFSDDCDLPS  
AQDINRLVGLQNTYMGYLDYRKKAIKDLGISPSTCSFNPGVIVANMTEWKHQIRITKQLEKWMQ  
KNVEENLYSSSLGGGVATSPMLIVFHGKYSTINPLWHIRHLGWNPDARYSEHFLQEAKLLHWN  
GRHKPWDFPSVHNDLWESWFVPDPAGIFKLNHHS

**Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 234-238

**Tyrosine kinase phosphorylation site.**

amino acids 253-261

**N-myristoylation sites.**

amino acids 63-69, 86-92, 198-204, 218-224, 229-235, 265-271,  
266-272



**FIGURE 171**

GCCAGAGGCTGCAGCTGGAGCCCAGAGCCCAAGATGGAGCCCCAGCTGGGGCCTGAGGCTGCC  
GCCCTCCGCCCTGGCTGGCTGGCCCTGCTGCTGTGGGTCTCAGCCCTGAGCTGTTCTTTCTCC  
TTGCCAGCTTCTTCCCTTTCTTCTCTGGTGCCCCAAGTCAGAACCAGCTACAATTTTGAAGG  
ACTTTCCTCGGTCTTGATAAATGCAATGCCTGCATCGGGACATCTATTTGCAAGAAGTTCTTT  
AAAGAAGAAATAAGATCTGACAACTGGCTGGCTTCCCACCTTGGAAGTGCCTCCCGATTCTTG  
CTTTCTTATCCTGCAAATTACTCAGATGATTCCAAAATCTGGCGCCCTGTGGAGATCTTTAGA  
CTGGTCAGCAAATATCAAAACGAGATCTCAGACAGGAGAATCTGTGCCTCTGCATCAGCCCCA  
AAGACCTGCAGCATTGAGCGTGTCTGCGGAAAACAGAGAGGTTCCAGAAATGGCTGCAGGCC  
AAGCGCCTCACGCCGGACCTGGTGCAGGACTGTCACCAGGGCCAGAGAGAACTAAAGTTCCTG  
TGTATGCTGAGATTAACACCAGTGAAAAAGCCTGGCATGGAGCCCAGCACTGAGAACTTCCAGA  
AAGTGTTAGCCTTCTCCCAACTGTGTTATACCAACCACATTTTCAAATAGTAATCATTAAGA  
GGCTTCTGCATCAA

**FIGURE 172**

MEPQLGPEAAALRPGWLALLLWVSALSCSFSLPASSLSSLVPQVRTSYNFGRTFLGLDKCNAC  
IGTSICKKFFKEEIRSDNWLASHLGLPPDSLLSYPANYSDDSKIWRPVEIFRLVSKYQNEISD  
RRICASASAPKTCSEIRVLRLKTERFQKWLQAKRLTPDLVQDCHQGQRELKFLCMLR

**Signal peptide:**

amino acids 1-28

**N-glycosylation site.**

amino acids 100-103

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 158-161

**N-myristoylation sites.**

amino acids 56-61, 65-70

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 18-28

**Prenyl group binding site (CAAX box).**

amino acids 179-182

**Leucine zipper pattern.**

amino acids 5-26

**FIGURE 173**

GCTGGACTGCTCGCTGGCCGGCAGCGCACCGTTTTGAAGGTCCTAGCCACCTGGGCTGGCTC  
ACGCGCACGACTAGCCGCTCCCATACAGCACGCCCGGACTCTGTCTGCTCGCTTAAGGCCACTCC  
TATTCTACGGCTGACCCCTGGTGGTCACGTGGATCTGTTGCGCCACGCAAGTCTGGGTCCTTCG  
GCGATTGACCGGGGTCCTTGCTGTTGCGGAGCCTCTCCTAAGCTGCCTGTTGCGCGGAGAGTT  
TGGAGGGGCGGGTTTGGGGTCGGTGTCTGATTGGGGCTCGCACCGCAGCACGCTGGAGTCCCG  
CTTAGGTACCAGTTAGCGTCAGGGGAGCTGGGTCAGGCGGTCGCCGGGACACCCCGTGTGTGG  
CAGGCGGCGAAGCGCTCTGGAGAATCCCGACAGCCCTGCTCCCTGCAGCCAGGTGTAGTTTC  
GGGAGCCACTGGGGCCAAAGTGAGAGTCCAGCGGCTTCCAGCGCTTGGGGCCACGGCGGCGGC  
CCTGGGAGCAGAGGTGGAGCGACCCATTACGCTAAAGATGAAAGGCTGGGGTTGGCTGGCCC  
TGCTTCTGGGGGCCCTGCTGGGAACCGCCTGGGCTCGGAGGAGCCAGGATCTCCACTGTGGAG  
CATGCAGGGCTCTGGTGGATGAACTAGAATGGGAAATTGCCCAGGTGGACCCCAAGAAGACCA  
TTCAGATGGGATCTTTCCGGATCAATCCAGATGGCAGCCAGTCAGTGGTGGAGGTGCCTTATG  
CCCGCTCAGAGGCCACCTCACAGAGCTGCTGGAGGAGATATGTGACCGGATGAAGGAGTATG  
GGGAACAGATTGATCCTTCCACCCATCGCAAGAACTACGTACGTGTAGTGGGCCGGAATGGAG  
AATCCAGTGAACCTGGACCTACAAGGCATCCGAATCGACTCAGATATTAGCGGCACCCCTCAAGT  
TTGCGTGTGAGAGCATTGTGGAGGAATACGAGGATGAACTCATTGAATTCTTTTCCCGAGAGG  
CTGACAATGTTAAAGACAACTTTGCAGTAAGCGAACAGATCTTTGTGACCATGCCCTGCACA  
TATCGCATGATGAGCTATGAACCACTGGAGCAGCCCACACTGGCTTGATGGATCACCCCCAGG  
AGGGGAAAATGGTGGCAATGCCTTTTATATATTATGTTTTTACTGAAATTAAGTAAAAAATA  
TGAAACCAAAAGT

**FIGURE 174**

MKGWGWLALLLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTIQMGSFRINPDGS  
QSVVEVPYARSEAHLTELEEICDRMKEYGEQIDPSTHRKNYVRVVGRNGESSELDLQGIRID  
SDISGTLKFACESIVEEYEDELIEFFSREADNVKDKLCSKRTDLCDHALHISHDEL

**Signal peptide:**

amino acids 1-20

**N-myristoylation sites.**

amino acids 12-18, 16-22, 29-35

**Endoplasmic reticulum targeting sequence.**

amino acids 179-184

# **FIGURE 175**

CGCAGCGCGGCAGTCCTGATGGGCCCCGGCATGGGTTACCGCTGCTGCCCCCTGCTGTCTCGCTCCTG  
 GTCGGCGCGTGGCTCAAGCTAGGAAATGGACAGGCTACTAGCATGGTCCAACCTGCAGGGTGGG  
 AGATTCTGATGGGAACAAATTTCTCCAGACAGCAGAGATGGTGAAGGGCCTGTGCGGGAGGCG  
 ACAGTGAAACCCCTTTGCCATCGACATATTTCTCTGTACCAACAAAGATTTTCAGGGATTTTGTCT  
 AGGGAGAAAAAGTATCGGACAGAAGCTGAGATGTTTGGATGGAGCTTTGTCTTTGAGGACTTT  
 GTCTCTGATGAGCTGAGAAACAAAGCCACCCAGCCAATGAAGTCTGTACTCTGGTGGCTTCCA  
 GTGGAAAAGGCATTTTGGAGGCAGCCTGCAGGTCTGGCTCTGGCATCCGAGAGAGACTGGAG  
 CACCCAGTGTTACACGTGAGCTGGAATGACGCCCGTGCCTACTGTGCTTGGCGGGGAAAACGA  
 CTGCCCACGGAGGAAGAGTGGGAGTTTGCCGCCCCGAGGGGGCTTGAAGGGTCAAGTTTACCCA  
 TGGGGGAACTGGTTCAGCCAAACCGCACCAACCTGTGGCAGGGAAAGTTCCCCAAGGGAGAC  
 AAAGCTGAGGATGGCTTCCATGGAGTCTCCCCAGTGAATGCTTTCCCCGCCCAGAACAACCTAC  
 GGGCTCTATGACCTCTGGGGAACGTGTGGGAGTGGACAGCATCACCGTACCAGGCTGCTGAG  
 CAGGACATGCGCGTCTCCGGGGGGCATCCTGGATCGACACAGCTGATGGCTCTGCCAATCAC  
 CGGGCCCCGGTCAACCACAGGATGGGCAACACTCCAGATTAGCCTCAGACAACCTCGGTTTC  
 CGCTGTGCTGCAGACGCAGGCCGGCCGCGCAGGGGAGCTGTAAGCAGCCGGGTGGTGACAAGGA  
 GAAAAGCCTTCTAGGGTCACTGTCAATCCCTGGCCATGTTGCAAACAGCGCAATTCCAAGCTC  
 GAGAGCTTCAGCCTCAGGAAAGAACTTCCCCCTTCCCTGTCTCCCATCCCTCTGTGGCAGGCGC  
 CTCTCACCAGGGCAGGAGAGGACTCAGCCTCCTGTGTTTTGGAGAAGGGGCCCAATGTGTGTT  
 GACGATGGCTGGGGGCCAGGTGTTTTCTGTTAGAGGCCAAGTATTATTGACACAGGATTGCAAA  
 CACACAAACAGTTGGAACAGAGCACTCTGAAAGGCCATTTTTTTAAGCATTTTAAAATCTATTCT  
 TCTCCCCCTTTCTCCCTGGATGATTTCAGGAAGCTGACATTGTTTTCTCAAGGCAGAATTTTCC  
 TGGTTCTGTTTTCTCAGCCAGTTGCTGTGGAAGGAGAATGCTTTCTTTGTGGCCTCATCTGTG  
 GTTTCGTGTCCCTCTGAAGGAACTAGTTTCCACTGTGTAAACAGGCAGACATGTAACCTATTTA  
 AAGCACAGTTCAGTCTTAAAGGGTCTGGGAGAACCAGATGATGTACTAGGTGAAGCATTGCA  
 TTGTGGGAATCACAAAGCAAATAGTACTCCAGAAAGACAAATATCAGAAGCTTCCTATTCTTT  
 TTTTTTTTTTTTTTTTTTTTTTTTGGAGACAGGGTCTTTCTCTGTTGCCAGGCTAGAGTGCACTG  
 GTGATCACGGCTCACTCTAGCCTTGAATTCCTGGGCCCCAAGCAATTCTCCACCTCAGCCTCC  
 TGAGTAGCTGGGACTACAAGTGTGCACCACCATGCCTGGCTAATTTTTTTGAATTTTTGTAGTG  
 ATGGGATCTCGCTCTGTTGCCCAGGGTGGTCTCGAACTCCTGGCCTCAAGCGATCCTCCACC  
 TCGACCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACCTCGCCTGGGCCCCCTTCTCCATA  
 TGCCTCCAAAAACATGTCCCTGGAGAGTAGCCTGCTCCACACTGTCACTGGATGTATGGGG  
 CCAATAAAATCTCCTGCAATTGTGTATCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAA

**FIGURE 176**

MARHGLPLLPLLSLLVGAWLKLGNQGATSMVQLQGGRFLMGNTNSPDSRDGEGPVREATVKPFA  
IDIFPVTNKDFRDFVREKKYRTEAEMFGWSFVFEDFVSEDLRNKATQPMKSVLWWLPVEKAFW  
RQPAGPGSGIRERLEHPVLHVSWNDARAYCAWRGKRLPTEEEWEFAARGGLKGQVYPWGNWFQ  
PNRTNLWQGKFPKGDKAEDGFHGVSPVNAFPAQNNGLYDLLGNVWEWTASPYQAAEQDMRVL  
RGASWIDTADGSANHRARVTTTRMGNTPDASDNLGFRCAADAGRPPGEL

**Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 191-195

**N-myristoylation sites.**

amino acids 23-29, 25-31, 175-181

**Amidation site.**

amino acids 159-163

**FIGURE 177**

GCCTTCTCGCGCCTGACCATGCACCCCTGCATCTTCCTGCTGGGCCACAGGCGAGCGCTTTAT  
TTCTGGAGCTGAGGGCTAAACCTTTTTTGACTTTTCTTCTCCTCAACATCTGAATCATGCCAT  
GTGCCCAGAGGAGCTGGCTTGCAAACCTTTCCGTGGTGGCTCAGCTCCTTAACTTTGGGGCGC  
TTTGCTATGGGAGACAGCCTCAGCCAGGCCCGGTTTCGCTTCCCGGACAGGAGGCAAGAGCATT  
TTATCAAGGGCCTGCCAGAATACCACGTGGTGGGTCCAGTCCGAGTAGATGCCAGTGGGCATT  
TTTTGTTCATATGGCTTGCACTATCCCATCACGAGCAGCAGGAGGAAGAGAGATTTGGATGGCT  
CAGAGGACTGGGTGTACTACAGAATTTCTCACGAGGAGAAGGACCTGTTTTTTAACTTGACGG  
TCAATCAAGGATTTCTTTCCAATAGCTACATCATGGAGAAGAGATATGGGAACCTCTCCCATG  
TTAAGATGATGGCTTCCTCTGCCCCCTCTGCCATCTCAGTGGCACGGTTCTACAGCAGGGCA  
CCAGAGTTGGGACGGCAGCCCTCAGTGCCTGCCATGGACTGACTGGATTTTTTCCAACCTACCAC  
ATGGAGACTTTTTTCATTGAACCCGTGAAGAAGCATCCACTGGTTGAGGGAGGGTACCACCCGC  
ACATCGTTTACAGGAGGCAGAAAGTTCCAGAAACCAAGGAGCCAACCTGTGGATTAAAGGGTA  
TTGTGACTCACATGTCCTCCTGGGTTGAAGAATCTGTTTTGTTCTTTTGGTAGTTTTTATTAAA  
ACATGACCTATTCTTACTCAAGTCTCTTATCTCCTCTGTATTCTTTTTTTTTTAATATCTTCA  
TGACATTCAAATCTCTTCTGTATTCTCTTGCCAGAAAGTGATACATTCTTTTTTGCTTGTATAAA  
CCCTTTCACCTTGTC

**FIGURE 178**

MPCAQRSWLANLSVVAQLLNFGALCYGRQPQPGPVRFPDRRQEHFIKGLPEYHVVGPPVRVDAS  
GHFLSYGLHYIPITSSRRKRDLGSEDWVYYRISHEEKDLFFNLTVNQGFLSNSYIMEKRYGNL  
SHVKMMASSAPLCHLSGTVLQQGTRVGTAALSACHGLTGFFQLPHGDFFIEPVKKHPLVEGGY  
HPHIVYRRQKVPETKEPTCGLKGIVTHMSSWVEESVLFFW

**Signal peptide:**

amino acids 1-27

**N-glycosylation sites.**

amino acids 11-15, 105-109, 125-129

**N-myristoylation site.**

amino acids 149-155



# **FIGURE 179**

CAGATTTAAAAAGAAAACCTTTACTGAATCAGCTGAGTGTTAATAATACGAATTTCCCTTTCT  
 TGCCAATTCTGATCTGAACAGAAAATCCAAGAACAGGGATATGTTGTGGATTACAGTTTCTCT  
 GCCTTGCCCTACGACTGTTTCTGGTTGTTACCTGTTATCTTTATTATTACTCCACAAAGAAAT  
 ACTTGATGTTTCGTCTGTTTGTGAGCTCTGCACTGGGAGACAAATTAAGTCCGTAAGTACTAGG  
 CCTTTCGAGTATTCCTAAGAATTTTCTGAAAGTACAGTTTTTCTGTATCTGACTGGGAATAA  
 TATATCTTATATAAATGAAAGTGAATTAACAGGACTTCATTCTCTGTAGCATTTGATTTGGA  
 TAATTCTAACATTCGTATGTATATCCAAAAGCCTTTGTTCAATTGAGGCATCTATATTTCT  
 ATTTCTAAATAATAATTTTCATCAAACGCTTAGATCCTGGAATATTTAAGGGACTTTTAAATCT  
 TCGTAATTTATATTTACAGTATAATCAGGTATCTTTTGTCCGAGAGGAGTATTTAATGATCT  
 AGTTTCAGTTTCAGTACTTAAATCTACAAAGGAATCGCCTCACTGTCTTGGGAGTGGTACCTT  
 TGTGTTGATGGTTGCTCTTCGGATACTTGATTTATCAAACAATAACATTTTGAGGATATCAGA  
 ATCAGGCTTTCAACATCTTGAAAACCTTGCTTGTGTTGATTTAGGAAGTAATAATTTAACAAA  
 AGTACCATCAAATGCCTTTGAAGTACTTAAAGTCTTAGAAGACTTTCTTTGTCTCATAATCC  
 TATTGAAGCAATACAGCCCTTTGCATTTAAAGGACTTGCCAATCTGGAATACCTCCTCCTGAA  
 AAATTCAAGAATTAGGAATGTTACTAGGGATGGGTTTAGTGGAATTAATAATCTTAAACATTT  
 GATCTTAAGTCATAATGATTTAGAGAATTTAAATCTGACACATTCAGTTTGTAAAGAATTT  
 AATTTACCTTAAGTTAGATAGAAACAGAATAATTAGCATTGATAATGATACATTTGAAAATAT  
 GGGAGCATCTTTGAAGATCCTTAATCTGTCAATTAATAATCTTACAGCCTTGCAATCCAGGGT  
 CCTTAAGCCGTTGTCTTCATTGATTCACTTCAGGCAAATCTAATCCTTGGGAATGTAACCTG  
 CAACTTTTGGGCCTTCGAGACTGGCTAGCATCTTCAGCCATTACTCTAAACATCTATTGTCA  
 GAATCCCCCATCCATGCGTGGCAGAGCATTACGTTATATTAACATTACAAATTTGTGTTACATC  
 TTCAATAAATGTATCCAGAGCTTGGGCTGTTGTAAATCTCCTCATATTCATCACAAGACTAC  
 TGCGCTAATGATGGCCTGGCATAAAGTAACCACAAATGGCAGTCCTCTGGAAAATACTGAGAC  
 TGAGAACATTACTTTCTGGGAACGAATTCCTACTTCACCTGCTGGTAGATTTTTTCAAGAGAA  
 TGCCTTTGGTAATCCATTAGAGACTACAGCAGTGTTACCTGTGCAAAATACAACTTACTACTTC  
 TGTACCTTGAACCTTGAAAAAACAGTGCTCTACCGAATGATGCTGCTTCAATGTCAGGGAA  
 AACATCTCTAATTTGTACACAAGAAGTTGAGAAGTTGAATGAGGCTTTTGACATTTTGTCTAGC  
 TTTTTTCATCTTAGCTTGTGTTTTAATCATTTTTTTGATCTACAAAGTTGTTCAAGTTTAAACA  
 AAAACTAAAGGCATCAGAAAACCAAGGGAAATAGACTTGAATACTACAGCTTTTATCAGTC  
 AGCAAGGTATAATGTAAGTGCCTCAATTTGTAACACTTCCCCAAATTCCTAGAAAGTCTGG  
 CTTGGAGCAGATTCGACTTCATAAACAAATTTGTTCTGAAAATGAGGCACAGGTCATTCTTTT  
 TGAACATTCTGCTTTATTAAGTCAACTAAATATTGTCTATAAGAACTTCAGTGCCATGGACAT  
 GATTTAAAGTGAACCTCCTTATATAATTATATACTTTAGTTGGAAATATAATGAATTATATG  
 AGGTTAGCATTATTAAATATGTTTTTTNTTAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 180**

MCGLQFSLPCLRLFLVVTCYLLLLLHKEILGCSSVCQLCTGRQINCRNLGLSSIPKNFPESTV  
FLYL TGNNISYINESELTGLHSLVALYLDNSNILYVYPKAFVQLRHLYFLFLNNNFIKRLDPG  
IFKGLLNLRNLYLQYNQVSFVPRGVFNDLVSVQYLNLRNRLTVLGSGTFVGMVALRILDLSN  
NNILRISESGFQHLENLACLYLGSNMLTKVPSNAFEVLKSLRRLSLSHNPIEAIQPPFAFKGLA  
NLEYLLLKNSRIRNVTRDGFSGINNLKHLILSHNDLENLNSDTFSLLKNLIYKLDRNRIISI  
DNDTFENMGASLKILNLSFNNLTALHPRVLKPLSSLIHLQANSNPWECNCKLLGLRDWLASSA  
ITLNIYCQNPPSMRGRALRYINITNCVTSSINVSRAWAVVKSPIHHKTTALMMAWHKVTTNG  
SPLENTETENITFWERIPTSPAGRFFQENAFGNPLETTAVLPVQIQLTTSVTNLNLEKNSALPN  
DAASMSGKTSLIC TQEVEKLNEAFDILLAFFILACVLIIFLIYKVVFQKQKLKASENSRENRL  
EYYSFYQSARYNVTASICNTSPNSLES PGLEQIRLHKQIVPENE AQVILFEHSAL

**Signal peptide:**

amino acids 1-41

**Transmembrane domain:**

amino acids 530-547

**N-glycosylation sites.**

amino acids 71-75, 76-80, 215-219, 266-270, 317-321, 331-335,  
336-340, 400-404, 410-414, 451-455, 579-583

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 231-235

**N-myristoylation sites.**

amino acids 3-9, 69-75, 126-132, 174-180

**ATP/GTP-binding site motif A (P-loop).**

amino acids 506-514



**FIGURE 182**

MMPSRTNLATGIPSSKVKYSRLSSTDDGYIDLQFKKTPPKIPYKAIALATVLFLLIGAFLLIIIG  
SLLLSGYISKGGADRAVPVLLIIGILVFLPGFYHLRIAYYASKGYRGYSYDDIPDFDD

**Transmembrane domains:**

amino acids 45-66, 79-95

**N-myristoylation sites.**

amino acids 11-17, 75-81

# **FIGURE 183**

CTAAAAAATACAAAAATTAGCTGGGCGTGGTGTCTATGTACCTGTAATCCCAGCTACTCAAGAGGCTGAGGCAGGA  
GAATCGCTTGAAACCCAGGAGGCAGAGGTTGCAGTGAGCCAAGATTAAAGTCACTGCCTCCAGCCTGGGTGACAGA  
GCAAGACTCTGTATCAAAATAAATAAATAAAGTACAACCTCTGGATGGGCATGGTGGCTTATGTCTGTAATCCCAG  
CACTTTGGGAACCTTGAGGCGGGTAGATTGCTTGAGTCCGGGAGTTTGAGACCAGTCTGGGTAATATGGTAACCCCT  
GTCTACCAAAAAATACAGGTATTAGCCAGTCTCATAACTCGGTCTCAAAATAAATAAATACATACATACATAGATG  
AAAATTTAAAAATAAAGTCCAACCTCAGCGGTTTTTCAGCATATTTACAGAGTTGTACAATTTTCACCACTATCTA  
ATTTCAGAACATTTTCATCACCCCCAAAAGAACCTAACCCATTGACTATCTCTCCATTTCCTCCCTCTCCCTAG  
CCTCTGGCAACCACTAATCTCTTTTGTCTCTATAGATTTGCCTATTTTGACAGTTCATATACAAGGAATCAT  
ACCACATGTAGCCTTTTGTGTCCGCTTCTTTGATTAAATAGAAATGTTTTCAAGGCTCATCTATGCTGTAGCCTGT  
ATCAGCACTTCATTCTTTCTATGGCTGAATAATAGTCCACTGTAGGGATGTGCCATGTTTTTCCACTAGCTGAT  
GGACATTTGGGTTGTTTTCCACCTTCTGGCTATTATAAATATTGCTGCTATAAATATTCACTTACAAGTTTTTGTG  
TGGACATATGTTTTTATTTCTTCTGCTATATCCTTCGGAGTGGAACCTGCTGGATCAGGTGGTAACCTAGGTCTA  
ACCTGGCAGTTAAACAGAATCCTATGCATGCTGTAGTCCATGAGTTGAAATAAACACTTGACCCATAGTAAGTGC  
CAGATCATCTTCATTTACAGCAACCACTAATTTACAGATGAGGAAATGAAGGCTCCAGAGGTGAAGTGGCTT  
TTCCCATTTGAGCAGTTCCAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT  
GGCATTGAGGCTGCTCTCTGGGCTACGGGCTGGCATTTAGAATAGAGCTAAGGTCTGCTGCCAAGGCAGGTGC  
CCCAGTCTGCCTCTCTGTCTCTTATTCACCTTTCTCTGCAGCCCTCCAGGGGACCCCTCTCTCAGCCACCCCTC  
TCTCTGGTGATGTCACAGTGTCTGCCGGAAGATCAAAGATACGGTGCAGAACTGGCTTCGGACCATAAAGGACATT  
CACAGCAGTGTATCCCGAGTGGGCAAGCCATTGACAGGAACCTTCGACTCTGAGATCTGTGGTGTGTGTGTCAGAT  
GCGGTGTGGGACGCGCGGGAACAGCAGCAGCAGATCCTGCAGATGGCCATCGTGGAACACCTGTATCAGCAGGGC  
ATGCTCAGCGTGGCCGAGGAGCTGTGCCAGGAATCAACGCTGAATGTGGACTTGGATTTCAGCAGCCTTTCTTA  
GAGTTGAATCGAATCCTGGAAGCCCTGCACGAACAAGACCTGGGTCTGCGTTGGAATGGGCCGTCTCCACAGG  
CAGCGCTGTGGAACCTCAACAGCTCCTGGAGTTCAAGCTGCACCGACTGCACCTTCATCCGCTCTTGGCAGGA  
GGCCCCGGAAGCAGCTGGAGGCCCTCAGCTATGCTCGGCACTTCAGCCCTTTGCTCGGCTGCACAGCGGGAG  
ATCCAGGTGATGATGGGCAGCCTGGTGTACCTGCGGCTGGGCTTGGAGAAGTCAACCTACTGCCACCTGCTGGAC  
AGCAGCCACTGGGCAGAGATCTGTGAGACCTTTACCCGGGACGCTGTTCCCTGCTGGGCTTTCTGTGGAGTCC  
CCCCCTTAGCGTCAGCTTTGCCCTCTGGCTGTGTGGCGCTGCCCTGTGTTGATGAACATCAAGGCTGTGATTGAGCAG  
CGGCAGTGCCTGGGCTCTGGAATCACAAAGGACGAGTTACCGATTGAGATTGAAGTGGATGAAGTGTGCTGGTAC  
GCTCATCTGTGGCCATGTTATCTCCCGAGATGCACTCAATAAGCTCATTAAATGAGGAAACACTCCGTGTTGCT  
TGCCCCATCCTCCGCCAGCAGCGTCAGATTCCAACCTCCCATCAAGCTGAAGTGTCCCTACTGTCCCATGGAG  
CAGAACC CGCAGATGGGAAACGCATCATATTCTGATTCTACCTGGAAGGAATTTTGTGAAAGGGGTTTTTCAC  
CTGTGAGCCTTGGTCTGTCTCGGTAGGGTGGTCAACTTCAGTGGACTGTGGTTGGTTTCAGAGCGCTGGCTGAG  
GAGTTCCACTGAGGGGAGCACTGGAGCAGCCCTTTGGCAGAGGCTGAGGAGGGAGATGGACCAGCCACGCTGG  
CACCTGGCTCATGGCATAAGGAAAGGGAGATGCTGGCCTCTGTGCTCCTGCTCTTTTCTGTTTCTGTTTGC  
GTTTGACTTAGTAGCAACCGACAGAGTGGCAAGGGATTTGGTCTTCAGCAGTAGACATCCTTCCACCCCTGCCCT  
CAGCCAAGTCTCTGTGCTGCCAATGCTATGTCCACCCTTGCCCTCGGCCAAGAGTGTCCAGCGGTGGCC  
CACCTCTTCTCTCCACTACAGCCTCAACAGTATGTACCATCTCCCACTGTAAATAGTCCAGTTAGAACGGAATG  
CGGTGTTTTATACTTTGAACAAATGTATTTACTGCCTTCTCAAAA

**FIGURE 184**

QCCRKIKDTVQKLASDHKDIHSSVSRVGKAIDRNFDS EICGVVSDAVWDAREQQQQILQMAIV  
EHLYQQGMLSVAEELCQESTLNVDLDFKQPFLELNRIEALHEQDLGPALEWAVSHRQRLLEL  
NSSLEFKLHRLHFIRLLAGGPAKQLEALSYARHFQPFARLHQREIQVMMGSLVYLRLGLEKSP  
YCHLLDSSHWAEICETFTRDACSLGLSVESPLSVSFASGCVALPVLMMNIKAVIEQRQCTGVW  
N HKDELPIEIELGMKCWYHSVFACPI LRQQTSDSNPPIKLI CGHVISR DALNKLINGGKLKCP  
YCPMEQNPADGKRIIF

**Transmembrane domain:**

amino acids 222-241

**N-glycosylation site.**

amino acids 129-133

**Tyrosine kinase phosphorylation site.**

amino acids 151-159, 184-193

**Amidation site.**

amino acids 327-331

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 222-233

**FIGURE 185**

GAGCGACGCTGTCTCTAGTCGCTGATCCCAAATGCACCGGCTCATCTTTGTCTACACTCTAAT  
CTGCGCAAACCTTTTGCAGCTGTCTGGGACACTTCTGCAACCCCGCAGAGCGCATCCATCAAAGC  
TTTGGCGCAACGCCAACCTCAGGCGAGATGACTTGTACCGAAGAGATGAGACCATCCAGGTGAA  
AGGAAACGGCTACGTGCAGAGTCCTAGATTCCCGAACAGCTACCCAGGAACCTGCTCCTGAC  
ATGGCGGCTTCACTCTCAGGAGAATACACGGATACAGCTAGTGTTTGACAATCAGTTTGGATT  
AGAGGAAGCAGAAAATGATATCTGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAAC  
CAGTACCATTATTAGAGGACGATGGTGTGGACACAAGGAAGTTCTCCAAGGATAAAATCAAG  
AACGAACCAAATTAAAATCACATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAA  
GATTTATTATTCTTTGCTGGAAGATTTCCAACCCGCAGCAGCTTCAGAGACCAACTGGGAATC  
TGTCAACAAGCTCTATTTTCAGGGGTATCCTATAACTCTCCATCAGTAACGGATCCCCTCTGAT  
TGCGGATGCTCTGGACAAAAAATTGCAGAATTTGATACAGTGGAAGATCTGCTCAAGTACTT  
CAATCCAGAGTCATGGCAAGAAGATCTTGAGAATATGTATCTGGACACCCCTCGGTATCGAGG  
CAGGTCATACCATGACCGGAAGTCAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCG  
TTACAGTTGCACTCCCAGGAATTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGGCCAATGT  
GGTCTTCTTTCCACGTTGCCTCCTCGTGCAGCGCTGTGGAGGAAATTGTGGCTGTGGAAGTGT  
CAACTGGAGGTCCTGCACATGCAATTCAGGGAAAACCGTGAAAAAGTATCATGAGGTATTACA  
GTTTGAGCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCATGGCTCTAGTTGACATCCA  
GTTGGATCACCATGAACGATGCGATTGTATCTGCAGCTCAAGACCACCTCGATTAAGAGAATGT  
GCACATCCTTACATTAAGCCTGAGAGAA

**FIGURE 186**

MHRLIFVYTLICANFCSCRDTSATPQASIKALRNANLRRDDLYRRDETIQVKNGYVQSPRF  
PNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLLEEAENDICRYDFVEVEDISETSTIIRGRWCG  
HKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSLLEDFQPAAASETNWESVTSSISGVSY  
NSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESWQEDLENMYLDTPRYRGRSYHDRKSKV  
DLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFPRCLLVQRCGGNCGCGTVNWRSTCNSG  
KTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCICSSRPPR

**Signal peptide:**

amino acids 1-18

**N-glycosylation site.**

amino acids 270-274

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 262-266

**Tyrosine kinase phosphorylation site.**

amino acids 256-265

**N-myristoylation sites.**

amino acids 94-100, 186-192, 297-303, 298-304

**TonB-dependent receptor proteins signature 1.**

amino acids 1-56



# **FIGURE 187**

CATGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCCTG  
TGTCTCTGGTGGTTTTGCCTAAACCTGCAAAACATCACCTTCTTATCCATCAACATGAAGAATGT  
CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTT  
CATATATGGGCAAAAGAAATGGCTGAATAAATCAGAATGCAGAAATATCAATAGAACCTACTG  
TGATCTTTCTGCTGAAACTTCTGACTACGAACACCAGTATTATGCCAAAAGTTAAGGCCATTTG  
GGGAACAAAAGTGTTCCAAATGGGCTGAAAGTGACGGTCTATCCTTTTTTTAGAAACACAAAT  
TGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTCTTGACAGCTCC  
AGAGAAGTGAAGAGAAATCCAGAAGACCTTCTGTGTTCCATGCAACAAATATACTCCAATCT  
GAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCAGTGTTGTGACCAA  
CCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTCCTT  
CGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTTGCCAGGACTTTGAAAAG  
TCAATCATCAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTTGCCCATATCTATTACCGT  
GTTTCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACA  
CCCAGCAAATTTGATTTTGATTTATGGAAATGAATTTGACAAAAGATTCTTTGTGCTGCTGA  
AAAAATCGTGATTAACTTTATCACCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGA  
TATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAA  
CCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGA  
AATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCTCTCAGCCAGCAAGAGTCCCTCAG  
CAGAACAAATACCCCCGGATAAAACAGTCATTGAATATGAATATGATGTCAGAACCACTGACAT  
TTGTGCGGGGCCTGAAGAGCAGGAGCTCAGTTTGCAGGAGGAGGTGTCCACACAAGGAACATT  
ATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCGCAAACGTTACAGTACTCATACACCCC  
TCAGCTCCAAGACTTAGACCCCCCTGGCGCAGGAGCACACAGACTCGGAGGAGGGGCGGAGGA  
AGAGCCATCGACGACCTTGGTCGACTGGGATCCCCAAACTGGCAGGCTGTGTATTCTTTCGCT  
GTCCAGCTTCGACCAGGATTCTAGAGGGCTGCGAGCCTTCTGAGGGGGATGGGCTCGGAGAGGA  
GGGTCTTCTATCTAGACTCTATGAGGAGCCGGCTCCAGACAGGCCACCAGGAGAAAATGAAAC  
CTATCTCATGCAATTCTATGGAGGAATGGGGTTTATATGTGCAGATGGAAAACTGATGCCAACA  
CTTCCTTTTGCCTTTTGTTCCTGTGCAAACAAGTGAGTCACCCCTTTGATCCCAGCCATAAA  
GTACCTGGGATGAAAGAAGTTTTTTCCAGTTTGTGTCAGTGTCTGTGAGAA

**FIGURE 188**

MPLPPLLLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPEGLQGKVTYTVQYF  
IYGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQI  
GPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTN  
HTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQCARTLKDQSSEFKAKIIFWYVLPISITV  
FLFSVMGYSIYRYIHVGKEKHPANLILYGNFEDKRFFVPAEKIVINFITLNISSDDSKISHQD  
MSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFCDSEENTEGTSLTQQESLS  
RTIPDPKTVIEYEYDVRTTDCAGPEEQELSLQEEVSTQGTLLSQAALAVLGPQTLQYSYTP  
QLQDLPLAQEHTDSEEGPEEEEPSTTLVDWDPQTGRLCIPSLSSFDQDSEGCEPSEGDGLGEE  
GLLSRLYEPPAPDRPPGENETYLMQFMEEWGLYVQMEN

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 240-260

**N-glycosylation sites.**

amino acids 31-34, 72-75, 80-83, 171-174, 180-183, 189-192,  
304-307, 523-526

**Tyrosine kinase phosphorylation site.**

amino acids 385-392, 518-526

**N-myristoylation sites.**

amino acids 53-58, 106-111, 368-373, 492-497

**Tissue factor**

amino acids 1-278

# **FIGURE 189**

**ATGTGCTGCTGGCCGCTGCTCCTGCTGTGGGGGCTGCTCCCCGGGACGGCGGCGGGGGGCTCG**  
 GGCCGAACCTATCCGCACCGGACCCCTCCTGGACTCGGAGGGCAAGTACTGGCTGGGCTGGAGC  
 CAGCGGGGCAGCCAGATCGCCCTCCGCCTCCAGGTGCGCACTGCAGGCTACGTGGGCTTCGGC  
 TTCTCGCCCCACGGGGCCATGGCGTCCGCGACATCGTCGTGGGCGGGGTGGCCCCACGGGCGG  
 CCTACCTCCAGGATTATTTTACAAATGCAAATAGAGAGTTGAAAAAAGATGCTCAGCAAGAT  
 TACCATCTAGAATATGCCATGGAAAATAGCACACACACAATAATTGAATTTACCAGAGAGCTG  
 CATACTGTGACATAAATGACAAGAGTATAACGGATAGCACTGTGAGAGTGATCTGGGCCTAC  
 CACCATGAAGATGCAGGAGAAGCTGGTCCCAAGTACCATGACTCCAATAGGGGCACCAAGAGT  
 TTGCGGTTATTGAATCCTGAGAAAACCTAGTGTGCTATCTACAGCCTTACCATACTTTGATCTG  
 GTAAATCAGGACGTCCCCATCCCAAACAAAGATACAACATATTGGTGCCAAATGTTTAAAGATT  
 CCTGTGTTCCAAGAAAAGCATCATGTAATAAAGGTTGAGCCAGTGATACAGAGAGGCCATGAG  
 AGTCTGGTGCACCACATCCTGCTCTATCAGTGCAGCAACAACCTTTAACGACAGCGTTCTGGAG  
 TCCGGCCACGAGTGCTATCACCCCAACATGCCCGATGCATTCTCACCTGTGAAACTGTGATT  
 TTTGCTGGGCTATTGGTGGAGAGGGCTTTTCTTATCCACCTCATGTTGGATTATCCCTTGGC  
 ACTCCATTAGATCCGCATTATGTGCTCCTAGAAGTCCATTATGATAATCCCACTTATGAGGAA  
 GGCTTAATAGATAATTCTGGACTGAGGTTATTTTACACAATGGATATAAGGAAATATGATGCT  
 GGGGTGATTGAGGCTGGCCTCTGGGTGAGCCTCTTCCATACCATCCCTCCAGGGATGCCTGAG  
 TTCCAGTCTGAGGGTCACTGCACTTTGGAGTGCCTGGAAGAGGCTCTGGAAGCCGAAAAGCCA  
 AGTGGAATTCATGTGTTTGCTGTTCTTCTCCATGCTCACCTGGCTGGCAGAGGCATCAGGCTG  
 CGTCATTTTCGAAAAGGGAAGGAAATGAAATTACTTGCCTATGATGATGATTTTGACTTCAAT  
 TTCCAGGAGTTTCAGTATCTAAAGGAAGAACAACAATCTTACCAGGAGATAACCTAATTACT  
 GAGTGTGCTACAACACGAAAGATAGAGCTGAGATGACTTGGGGAGGACTAAGCACCAGGAGT  
 GAAATGTGTCTCTCATACCTTCTTTATTACCCAAGAATTAATCTTACTCGATGTGCAAGTATT  
 CCAGACATTATGGAACAACCTTCAGTTTATTGGGGTTAAGGAGATCTACAGACCAGTCACGACC  
 TGGCCTTTTCAATTATCAAAAAGTCCCAAGCAATATAAAAACCTTTCTTTTCATGGATGCTATGAAT  
 AAGTTTAAATGGACTAAAAAGGAAGGTCTCTCCTTCAACAAGCTGGTCTCAGCCTGCCAGTG  
 AATGTGAGATGTTCCAAGACAGACAATGCTGAGTGGTGGATTCAAGGAATGACAGCATTACCT  
 CCAGATATAGAAAAGACCCTATAAAGCAGAACCTTTGGTGTGTGGCACGTCTTCTTCTCTTCC  
 CTGCACAGAGATTTCTCCATCAACTTGCTTGTGTTGCTTCTGCTACTCAGCTGCACGCTGAGC  
 ACCAAGAGCTTGTGATCAAAATTTCTGTTGGACTTGACAATGTTTTCTATGATCTGAACCTGTC  
 ATTTGAAGTACAGGTTAAAGACTGTGTCCACTTTGGGCATGAAGAGTGTGGAGACTTTTCTTC  
 CCCATTTTCCCTCCCTCCTTTTTCTTTCCATGTTACATGAGAGACATCAATCAGGTTCTCTT  
 CTCTTTCTTAGAAATACCTGATGTTATATATACATGGTCAATAAAATAAACTGGCCTGACTT  
 AAGATAACCATTTTAAAAAATTGGGCTGTCTGTGGGAATAAAAGAATTCCTTTCTTCTCTAAA  
 AAAAAAAA

**FIGURE 190**

MCCWPLLLLWGLLPGTAAGGSGRTYPHRTLDDSEGKYWLGWSQGRGSQIAFRLQVRTAGYVGFG  
FSPTGAMASADIVVGGVAHGRPYLQDYFTNANRELKKDAQQDYHLEYAMENSTHTTIEFTREL  
HTCDINDKSITDSTVRVIWAYHHEDAGEAGPKYHDSNRGTKSLRLLNPEKTSVLSTALPYFDL  
VNQDVPIPNKDTTYWCQMFKIPVFQEKHHVIKVEPVIQRGHESLVHHILLYQCSNNFNDVLE  
SGHECYHPNMPDAFLTCTVIFAWAIGGEGFSYPPHVGLSLGTPLDPHYVLLEVHYDNPTYEE  
GLIDNSGLRLFYTMDIRKYDAGVIEAGLWVSLFHTIPPGMPEFQSEGHCTLECLEEAEAEKP  
SGIHVFAVLLHAHLAAGRGI RL RHFRKGKEMKLLAYDDDFDNFQEFQYLKEEQTILPGDNLIT  
ECRYNTKDRAEMTWGGLSTRSEMCLSYLLYYPRINLTRCASIPDIMEQLQFIGVKEIYRPVTT  
WPFIIKSPKQYKNLSFMDAMNKFKWTKEGLSFNKLVLSPVNVRCSTDNAEWSIQGMTALP  
PDIERPYKAEPLVCGTSSSSSLHRDFSINLLVCLLLLSCTLSTKSL

**Signal peptide:**

amino acids 1-18

**Transmembrane domains:**

amino acids 56-73, 378-393, 583-602

**N-glycosylation sites.**

amino acids 114-118, 247-251, 476-480, 517-521

**N-myristoylation sites.**

amino acids 11-17, 15-21, 20-26, 45-51, 68-74, 79-85, 290-296,  
316-322, 337-343, 342-348, 456-462, 534-540, 582-588

**Copper type II, ascorbate-dependent monooxygenases proteins.**

amino acids 271-321, 422-474

**FIGURE 191**

GCTTCAGCTGAAGAAAAGAGAGGAATGAAGCGCCTTCTGCTTCTGTTTTGTTCCTTTATAACAT  
TTTTCTTCTGCATTTCCCTTAGTCCGGATGACGGAAAATGAAGAAAATATGCAACTGGCTCAGG  
CATATCTCAACCAGTTCTACTCTCTTGAAATAGAAGGGAATCATCTTGTTCAAAGCAAGAATA  
GGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCATTTTTTTGGATTGACAGTGAAGTGGAA  
AACTGGACTCAAACACCCTTGAGATCATGAAGACACCCAGGTGTGGGGTGCCTGATGTGGGCC  
AGTATGGCTACACCCTCCCTGGGTGGAGAAAATACAACCTCACCTACAGAATAATAAACTATA  
CTCCGGATATGGCAGGAGCTGCTGTGGATGAGGCTATCCAAGAAGGTTTAGAAGTGTGGAGCA  
AAGTCACTCCACTAAAATTCACCAAGATTTCAAAGGGGATTGCAGACATCATGATTGCCTTTA  
GGACTCGAGTCCATGGTCGGTGTCTCGCTATTTTTGATGGTCCCTTGGGAGTGCCTTGGCCATG  
CCTTTCCTCCTGGTCCGGGTCTGGGTGGTGACACTCATTTTTGATGAGGATGAAAAGTGGACCA  
AGGATGGAGCAGGATTCAACTTGTCTTGTGGCTGCTCATGAATTTGGTCATGCACTGGGGC  
TCTCTCACTCCAATGATCAAACAGCCTTGATGTTCCCAAATTATGTCTCCCTGGATCCCAGAA  
AATACCCACTTTCTCAGGATGATATCAATGGAATCCAGTCCATCTATGGAGGTCTGCCTAAGG  
TACCTGCTAAGCCAAAGGAACCCACTATACCCCATGCCTGTGACCCTGACTTGACTTTTGACG  
CTATCACAACTTTCCGCAGAGAAGTAATGTTCTTTAAAGGCAGGCACCTATGGAGGATCTATT  
ATGATATCACGGATGTTGAGTTTGAATTAATTGCTTCATTCTGGCCATCTCTGCCAGCTGATC  
TGCAAGCTGCATACGAGAACCCAGAGATAAGATTCTGGTTTTTAAAGATGAAAAGTCTTGGA  
TGATCAGAGGATATGCTGTCTTGCCAGATTATCCCAAATCCATCCATACATTAGGTTTTCCAG  
GACGTGTGAAGAAAATAGATGCAGCCGTCTGTGATAAGACCACAAGAAAACCTACTTCTTTG  
TGGGCATTTGGTGTGGAGGTTTGATGAAATGACCCAAACCATGGACAAAGGATTCCCGCAGA  
GAGTGGTAAACACTTTCCTGGAATCAGTATCCGTGTTGATGCTGCTTTCCAGTACAAAGGAT  
TCTTCTTTTTCAGCCGTGGATCAAAGCAATTTGAATACAACATTAAGACAAAGAATATTACCC  
GAATCATGAGAACTAATACTTGGTTTCAATGCAAAGAACCAAAGAACTCCTCATTGTTTGG  
ATATCAACAAGGAAAAAGCACATTCAAGGAGGCATAAAGATATTGTATCATAAGAGTTTAAGCT  
TGTTTATTTTTGGTATTGTTTCATTTGCTGAAAAACACTTCTATTTATCAATAAATTCATAGAC  
CTAAAAATAACCTCAACAGGTCTTTTAATATAAATTCTGCTTCAAAATAGAATAAAACCATTC  
TTTAACAAC

**FIGURE 192**

MKRLLLFLFFITFSSAFFLVRMTENEENMQLAQAYLNQFYSLEIEGNHLVQSKNRSLLDDKI  
REMQAFFGLTVTGKLDSENTLEIMKTPRCGVPDVGQYGYTLPGWRKYNLTYRIINYTPDMARAA  
VDEAIQEGLEVWSKVTPLKFTKISKGIADIMIAFRTRVHGRCPRYFDGPLGVLGHAFPPGPGL  
GGDTHFDEDENWTKDGAGFNLFVAAHEFGHALGLSHSNDQTALMFPNYVSLDPRKYPLSQDD  
INGIQSIYGGLPKVPKPKPEPTIPHACDPDLTFDAITTFRREVMFFKGRHLWRIYYDITDVEF  
ELIASFWPSLPADLQAAYENPRDKILVFKDENFWMIRGYAVLPDYPKSIHTLGFPGRVKKIDA  
AVCDKTTTRKTYFFVGIWCWRFDGMTQMDKGFPQRVVXHFPGISIRVDAAFQYKGFFFFSRGS  
KQFEYNIKTKNITRIMRTNTWFOCKEKNSSFGFDINKEKAHSGGIKILYHKSLSLFIFGIVH  
LLKNTSIYQ

**Signal peptide:**

amino acids 1-17

**N-glycosylation sites.**

amino acids 55-59, 110-114, 200-204, 452-456, 470-474, 508-512

**N-myristoylation site.**

amino acids 71-77, 205-211, 223-229

**Hemopexin domain signature.**

amino acids 171-202, 207-238, 318-334

**Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 213-223

**Matrixins cysteine switch.**

amino acids 89-97, 207-238

**FIGURE 193**

CACAATCAGGTCCCATTCTATAGATGGGGAAACTGAGGCTTGAGGTCACATAGGCGTCGTTCA  
AGGCTGGTATACCTGCACCCCTCTCCCATGTGAACAACATGGTTCTGGGTAATGGGGGCTGTCA  
TCCAGTCTCCTCCCTGCCCCTGCTGGTGCACCTTCCTGCCTCTGCTGGTGCACCTTCTGCCCCCT  
ACTGGTATATTTGCTGCCTCTGCTGGGGCGCTTCCTGCCTCGGCTGGTGTATCTCCTGCCCCCT  
GCTGGTGCACCTTCTGCCCCCGCTGATGCACCTTCCTGCCTCTGCTGGTGCACCTTCCTGGCTCT  
GCTGGCACACTTCCTGCCTCTGCTGGTGCACCTTCCTGGCTCTGCTGGCGCACTTTCCTGCCCC  
TGCTGGTGTATTTCTGCCCCCTGCTGGTGTACTTCCTTCCCCTGCTGGTGCACCTTCCTGCCTC  
TGCTGGCGCACTTCTTGCTCTCCAGGCCCTACCTTAGCCTCTCCCTCTTATATATGGAAGTCT  
TCCCAGTTCACTGACACTGGTAACAGGGACTCTGCTCTTGGTGTGCTGTCTGCCCTGGGGAT  
GGGCATCTGTGTCTTCCTTTACTACTGCTGGCTCAGGACCCAGAGCTTTGAAGCATGTCCAGA  
TGCAGGTCCGGGCACCAGAGTCTAAGGAGCCCCCTACACCCACCAGGATTTTCCAATAAAGAGA  
TGTTCACCA

**FIGURE 194**

MVLGNGGCHPVSSLP LLVHFLP LLVHFLP LLVYLLP LLGRFLP RL VYLLP LLVHFLP PLMHFL  
P LLVHFLA LLAHFLP LLVHFLA LLAHFPAPAGVFPAPAGVLPSPAGALPASAGALLASPGPT

**Signal peptide:**

amino acids 1-39

**N-myristoylation sites.**

amino acids 4-10, 109-115, 116-122

**Leucine zipper pattern.**

amino acids 14-36, 16-38, 17-39, 21-43, 24-46, 28-50, 31-53,  
35-57, 38-60, 42-64, 45-67, 49-71, 52-74, 56-78, 59-81, 63-85,  
65-87, 66-88



**FIGURE 195**

[illegible]

**FIGURE 196**

MRRLTRRLVLPVFGVLWITVLLFFWVTKRKLEVP TGPEVQTPKPSDADWDDLWDQFDERRYLN  
AKKWRVGDDPYKLYAFNQRESERISSNRAIPDTRHLRCTLVYCTDLPPTSIIITFHNEARST  
LLRTIRSVLNRTPTHLIREIILVDDFSNDPDDCKQLIKLPKVKCLRNNERQGLVRSRIRGADI  
AQGTTLTFLDSHCEVNRDWLQPLLHRVKEDYTRVVCVIDIINLDTFTYIESASELRGGFDWS  
LHFQWEQLSPEQKARRLDPTEPIRTPIIAGGLFVIDKAWFDYLGKYDMDMDIWGGENFEISFR  
VWMCSSLEIVPCSRVGHVFRKKHPYVFPDGNANTYIKNTKRTAEVWMDEYKQYYAARPFAL  
ERPFGNVESRLDLRKNLRCQSFKWYLENIYPELSIPKESSIQKGNIRQRQKCLESQRQNNQET  
PNLKLSPCAKVKGEDAKSQVWAFYYTQQILQEELCLSVITLFPGAPVVLVLCKNGDDRQQWTK  
TGSHEHIAHSLCLD TDMFGDGTENGKEIVVNPCSSLMSQHWDMVSS

**Transmembrane domain:**

amino acids 475-493

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 2-6

**Tyrosine kinase phosphorylation sites.**

amino acids 68-75, 401-409

**N-myristoylation sites.**

amino acids 178-184, 186-192, 192-198, 346-352, 383-389, 526-532

**FIGURE 197**

CGAGCTCACCCCTTCGCAGCCGCGATGCGGGGAAGACGACGCCGCGCTTCGGGCTGGCAGCAGGGGGCTCTCCGACC  
CGTGGGCAGACTCAGTGGGAGTGCAGACCCGCGACCCAGGAGCGCCACATCGCCGATACACAAGCGGCTTGTGCTGG  
CCTTCGCTGTGTCCCTCGCTGGCATTCTCGCGGTTCGCAATGCTCGTGTGCTGCTCAGCCTCGCCTTCGACGAGT  
GCGGGCGAGTGCAGCCGCGCAGCGCGCAGCTGGCCCTCAGCCTTTCCGAGCGCGCGCGCAACGGGAGCCTCC  
CTGGATCGCGCCCGCGCAACACCACGCGAGGCGGGGACTCCTGGCAGCCCGAGGCGGGTGGGGTGGCCAGTCCGG  
GGACCACGTTCGGCCAGCCGCGCTCGGAGGAGGAGCGGGAGCCGTGGGAGCCGTGACAGCGAGCTTCGCGCTGTTCGG  
GCCACCTGAAGCCGCTGCACTACAATCTGATGCTCACCCGCTTCATGGAGAACTTCACTTCTCCGGGGAGGTCA  
ACGTGGAGATCGCGTGGCGGAACGCCACCCGCTACGTAGTGTGCACGTTCCCGAGTGGCGGTGGAGAAAGTGC  
AGCTGGCCGAGGACCGGCGGCTTGGGGCTTCTCCCTAGTACCGGTTTTTTCCTCTACCCGCAAAACCCAGGTCTTAG  
TGGTGGTGTCTGAATAGGACACTGGACGCGCAGAGGAATTACAATCTGAAGATTATCTACAACGCGCTCATCGAGT  
ATGAGCTTCTGGGCTTCTTCCGCGAGCTTCTATGTGCTCCAGCGGGAGAGGAATCTTGGTGTACTACGATTTT  
CGCTTACATAGCCAGAAAGGCATTTCTTCTGTTTGTAGTAGCCAACTCTACAGGCTACTTTCAAATCAGCATCT  
AGCATCAAGCAACCTATTATTTATTTATCTAATATGCCATGGAAACTTCCGTGTTTGAAGGAAGATGGATGGGTTA  
CGGATCACTTTTTCAGACCCCTCTCATGTCCACATATTATTTAGCCTGGGCAATTTGCAACTTCACATACAGAG  
AAACTACACCAAGAGTGGGGTTGTAGTACGATTATATGCAAGACCTGATGCTATCAGAAGAGGATCCGGGGACT  
ATGCTCTCCATATAACAAGAGATTAAATGAATTTTATGAAGACTACTTTAAAGTGCCCTATTCTTGCCAAAAC  
TAGATCTTTAGCTGTGCTTAAGCATCCGTATGCTGCTATGGAGAATCGGGGACATAGTATTTTTGTGGAACAAA  
GAATACCTGTGATCCCGAGTGTTCATCTATTTCTATTTGCTGGATGTCACCATGGTCAATTGTTTCATGAGATAT  
GTCACCAAGTGGTTTGGTGACCTTGTGACGCTGTGTGGTGGGAAGACGTGTGGCTGAAGGAAGGGTTTTCTCACT  
ACTTTGAATTTGTTGGTACAGACTACCTCTATCCTGGCTGGCAACTGAAAAGCAGAGGTTTCTGACCGATGTTT  
TGCATGAAGTGAATGCTGCTGGACGGTTTGGCGAGTCCCATCCGATATCAGAGGAAGTCTCGAGGCAAGATA  
TTGACAGGGGTGTTTGACTGGATCGCATATAAAAAGGGTGTGCTTTAATAAGAATGCTGGCTAATTTTATGGGCC  
ATTGAGTTTTCCAGAGGGGTTTGCAGATTATTTAAACATTATAAGTATGTTAATGACGCGAGAAATGATCTCT  
GGAATACATTATCGGAGGCTTTAAAAAGAAATGGGAATATGTAAATATACAAGAAAGTAAAGGATCGTGGACAC  
TCCAGATGGGTTATCTCTGTTATCACCATTCTGGGAACAACAACAGCAGAAAAATAGAATAATAATTAACCAACAGC  
ATTTTATCTATGATATCAGTGCTAAAACTAAAGCACTTAAACTTCAGAATAACAGTTACCTGTGGCAGATTCCAT  
TAACTATTGTGTAGGAATAGAAGCCATGTGTTCAGAGCAATATTTGGGTGTCTAACAAATCAGAGCACC  
ACAGAAATAACTTATTTGGACAAAGGAAGCTGGCTGCTGGGAACATCAATCAAATGGCTATTTTAGAGTCAACT  
ATGACCTAAGGAAGTGGAGATTATTAATTGATCAATTAATCCGGAATCATGAGGTTCTTTCTGTGAGTACCGAG  
CGGGCTTGATCGATGATGCTTCAGCTAGCCAGGCTGGCTATTTGGCTCAGAATATTCTCTGGAGATTATCA  
GATACCTGTCTGAGGAGAAGGATTTTCTCCTTGGCATGCTGCCAGCGAGCTCTTTATCCTTAGATAAATTAC  
TGGACCGGCTAGGAAAACTACAACTTTCAATGAATATTTTAAAGCAAGTTGCAACAACATATCAAGCTTG  
GGTGGCCGAAAAATATTTAATGGATCTCTTGTTCAGCATCTTACCAACATGAAACATCATGAGAAAGTTA  
TAATGCTGGCCTGCAGTTTTTGGCAACAAGCACTGTCAACCAAGGCATCAACACTTATTTTCAGATTGGATTCCA  
GCAACAGGAACAGAATACCACTAAATGTTAGAGACATCGTATCTGTACAGGAGTGTCACTATCTGGATGAGGAT  
TCTGGGAATTCATATGGATGAAATCCATTCCACCACAGCAGTTCGTGAGAGAAAAATATTATTGGAAGCCTTAA  
CTTGCAGTGATGACAGGAATTTTATAACAGGCTTCTAAATCTGTCACTGAATCTCAGGTGGTGTGATCAAG  
ATGCAATTTGATGTCAATAATCATGTAGCTCGAAATCCACATGGTTCGAGACCTTGCCTGGAAGTTTTTCAGGGAT  
AATGGAAGATATTTAAATACCAAGTATGGAGAAGCATTGTTTATGTATTCCAAATCATCAGTGTGTACAGAAAT  
TTCTTAATCTGAAGGTGAAGCTCAAAGAGCTCAAGAACCTTATGAAAAAATCATGATGGGGTAGCTGTCTCTT  
TCTCACGAGCTGTGGAAACTGTCCAGGCCAATGTGCGCTGGAAATGCTTTACCAAGCAGCTTTTCCAATGGT  
TAGGAAAAAGCTCTAAGACATTAATATGTATCTTATAAACAACAACTTCAACTCAGAAGTTTATGAGAAGACAC  
GCTTTTTTGTGGAATGAGGAAATGTACTACCTAGAAAATGGCCAGATTTTCAGTGTTAACGTGTGGGAGGAATTT  
TTTTTTTTTAGTTTTTATTTTTTGGTTTTTGGGGGATATTTTATTTGTTTTTCACTTCTGTTCTGTTCTCTAC  
TGGGTGTTTCTCTCTAAGAAACTCTTGCAAGTGAACATGACCATGATGCTTCAGCTGACATTCTTGCTGTGA  
CAGGACCAATATCATAGTATGATGATGTTGATGTACAGTCAATTTGGAAAAACATATCAGAAATATCTGTGCAT  
GGATATATTGTCTGCTGTGTTCCAGCATGCTTATTTCAAACGTCCAGTGTGTGTGTGAATATGTGTTACACC  
TAGGATGGGCATTTGATCAAAAGCAAAAGATATATATGACAAATCAGTATGTCGAATGAAAGAAAACTAAAAACA  
GAAATGATATTTCTCAATTTTGGGCAATGTGAGAGGTAATAGCCCTTGACATGATGAACATCACTTATTTCACT  
ACCTGGATTGTCTGGCAATGATTACTGTGTTGCTAACTATTTCTTTGAGTTAAAGCTGTGTATATCACTTTTAA  
AGGCATATAGATAGTGTATGCATATGTATGTACATAGGGAAGCCCCATATGTATATAGTATGTTGTACACTGC  
ACATGTACAAAGAATGTCTTCAGATCAAAGAAAATTTATCTCTTTTATAAACTTAAGGACAGTTGCAAAAGGCT  
TCAAGGAATTTTATCTCAACATTATTTCTTCTATGTCTTAATAAATTTCTCACTGTTATGAATTTTTCATCTAC  
TTCTTGAACAGTGGTCTATTCTGCTACATGAAGTGAATCAACAACAAATTTTGTATAAACTCCCAAAAAAAA  
AAAAA

**FIGURE 198**

MGEDDAALRAGSRGLSDPWADSVGVRPRTTERHIAVHKRLVLAFVSLVALLAVTMLAVLLSL  
RFDECGASATPGADGGPSGFFPERGGNGSLPGSARRNHHAGGDSWQPEAGGVASPGTTSAQPPS  
EEEREPEWEPWTQLRLSGHLKPLHYNLMLTAFMENFTFSGEVNVEIACRNATRYVVLHASRVAV  
EKVQLAEDRAFGAVPVAGFFLYPQTQVLVVVLNRTLDAQRNYNLKIINYNALIENELLGFFRSS  
YVLHGERRFLGVTQFSPTHARKAFPCFDEPIYKATFKISIKHQATYLSLSNMPVETSVFEEDG  
WVTDHFSQTPLMSTYYLAWAICNFTYRETTTKSGVVVRLYARPD AIRRGSGDYALHITKRLIE  
FYEDYFKVPYSLPKDLLAVPKHPYAAMENWGLSIFVEQRILLDPSVSSISYLLDVTMIVVHE  
ICHQWFGDLVTPVWVEDVWLKEGFAHYFEFVGTDYLYPGWNMEKQRFLLTDVLHEVMILLDGLAS  
SHPVSQEVQLQATDIDRVFDWIAYKKGAALIRMLANFMGHSVFQRLQDYLTIHKYGNAARNDL  
WNTLSEALKRNGKYVNIQEVMDQWTLQMGYPVITILGNTTAENRIIITQQHFIYDISAKTKAL  
KLQNNSYLWQIPLTIVVGNRSHVSSEAI IWVSNKSEHHRITYLDKGSWLLGNINQTYFRVNY  
DLRNWRLLDQLIRNHEVLSVSNRAGLIDDAFSLARAGYLPQNIPLEIIRYLSSEKDFLPWHA  
ASRALYPLDKLLDRMENYNIFNEYILKQVATTYIKLGWPKNNFNGSLVQASYQHEELRREVIM  
LACSFNGKHCHQQASTLISDWISSNRNRNRIPLNVRDIVYCTGVSLLEDVWEFIWMKFHSTTAV  
SEKKILLEALTCSDDRNLLNRLNLSLNSEVVLDDQDAIDVIIHVARNPHGRDLAWKFFRDKWK  
ILNTRYGEALFMYSKLISGVTEFLNTEGELKELKNFMKNYDGVAAASFRAVETVEANVRWKM  
LYQDELFWLGLKALRH

**Transmembrane domain:**

amino acids 44-63

**N-glycosylation sites.**

amino acids 89-93, 160-164, 175-179, 222-226, 338-342, 605-609,  
634-638, 649-653, 663-667, 684-688, 800-804, 906-910

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 362-366

**Tyrosine kinase phosphorylation site.**

amino acids 520-528

**N-myristoylation sites.**

amino acids 78-84, 87-93, 90-96, 118-124, 501-507, 604-610,  
825-831, 987-993

**Neutral zinc metalloproteinases, zinc-binding region signature.**

amino acids 437-447

# **FIGURE 199**

GCGCCCGGCGCAGCTCGGCCAGAGCGACCGCGGGGCTGAGCGCGCTCCGCCAGGGGGCTCCGGAAGCTGCCCC  
 GGCCCGCGGCTCCTCCCTCGCTCCCGCTTCCCTTTCTCGCTCACC CGCGCCCTCCTTCCCCAGCTCCCTCGCC  
 GTCCGCCCGCCCCACAGCCAGCGGCTCCGCGCCCCCTGCAGCCACGATGCCCCGCGGCGGCGGCGGCGGCGGCGG  
 ACTCCGCGGGATCTCGCTGTTCTCGCTCTGCTCCTGGGGAGCCCCGCGGCAGCGCTGGAGCGAGATGCTCTTCC  
 CGAGGGAGATGCTAGCCCTTTGGGTCTTACCTCCTGCCCTCAGGAGCCCCGGAGAGAGGAGCTCCTGGCAAAGA  
 GCACCTTGAAGAGAGAGTGGTAACAGCGCCCCCAGTTTCTCACAGTCGGCGGAAGTGCTGGGCGAGCTGGTGCT  
 GGATGGGACCGCACCTCTGCACATCACGACATCCCGGCCCTGTCAACGCTGCTTCCAGAGGAGGCCCGCCCCAA  
 GCACGCTTGGCCCCCAGAAGAACTGCCCTTGCCTCAAGCAGGTGAAGTCTGCCAGGAAGCAGCTGAGGCCAA  
 GGCCACCTCCGAGCCACTGTCCAAAGGGCAGGGTCCAGCCAGCGTCCAGGGCCTAGATCTCCTCTCCTCCTC  
 CACGAGAAGCCTGGCCCCACCGGGGACCCGGACCCCATCGTGGCCTCCGAGGAGGCATCAGAAGTGCCCTTTG  
 GCTGGATCGAAAGGAGAGTGCGGTCCCTACAACACCCGACCCCTGCAATCTCCCCCTTCACTTCGAGCCCTA  
 TGTGGCCACACACTCCCCAGAGGCCAGAACCCGGGGAGCCTGGGCGCTGACATGGCCAGGAGGCCCGCCAGGA  
 GGACACAGCCCCATGGCCCTGATGGACAAAGGTGAGAATGAGCTGACTGGGTGAGCCTCAGAGGAGAGCCAGGA  
 GACCACTACCTCCACCATTATCACACCACGGTCATCACCCAGGCAAGCACCAGCTCTCTGAGTGTGAGCTT  
 CTCCAATCCTGAGGGGTACATTGACTCCAGCGACTACCACTGCTGCCCCCTCAACAACCTTTGAGAGTGACATA  
 CAACGTGACAGTCTACACTGGCTATGGGTGGAGCTCCAGGTGAAGAGTGTGAACCTGTCCGATGGGGAAGTGTCT  
 CTCCATCCGCGGGGTGGACGGCCCTACCTGACCGTCTGGCCAAACAGACACTCCTGGTGGAGGGGAGGTAAT  
 CCGAAGCCCCACCAACACCATCTCCGTCTACTTCCGGACCTTCCAGGACGACGGCCTTGGGACCTTCCAGCTTCA  
 CTACAGGCCCTTATGCTGAGCTGCAACTTTCCCGCGCGCTGACTCTGGGGATGTACGGGTGATGGACCTGCA  
 CTCAGGTGGGGTGGCCACTTTCAGTCCACCTGGGCTATGAGCTCCAGGGCGCTAAGATGCTGACATGCAATCAA  
 TGCTTCAAGCCGCACTGGAGCAGCCAGGAGCCCATCTGCTCAGCTCCTTGTGGAGGGGAGTGCACAATGCCAC  
 CATCGGCCGCTCCTCTCCCCAAGTTACCTGAAAACACAAATGGGAGCCAATTCTGCATCTGGACGATTGAAGC  
 TCCAGAGGGCCAGAAGCTGCACCTGCACCTTTGAGAGGCTGTTGCTGCATGACAAGGACAGGATGACGGTTACAG  
 CGGGCAGACCAACAGTCACTCTTCTACGACTCCCTTCAAACCGAGAGTGTCCCTTTTGGGGCTGCTGAG  
 CGAAGGCAACACCATCCGCATCGAGTTCAGTCCGACACAGGCCCGGGCGGCCTCCACCTTCAACATCCGATTGA  
 AGCGTTTGAGAAAGGCCACTGCTATGAGCCCTACATCCAGAAATGGGAACCTTCACTACATCCGACCCGACCTATAA  
 CATTTGGGACTATAGTGGAGTTCACCTGCGACCCCGGCCACTCCCTGGAGCAGGGCCCCGGCCATCATCGAATGCAT  
 CAATGTGCGGGACCCATACTGGAATGACACAGAGCCCTGTGTCAGAGCCATGTGTGGTGGGGAGCTCTCTGCTGT  
 GGTGGGGTGGTATTGTCCCCAACTGGCCCCGAGCCCTACGTGGAAGGTGAAGATTGTATCTGGAAGATCCACGT  
 GGGAGAAGAGAAACGGATCTTCTTAGATATCCAGTTCTTGAATCTGAGCAACAGTGACATCTTGACCATCTACGA  
 TGGCGACGAGGTTCATGCCCCACATCTTGGGGCAGTACCTTGGGAACAGTGGCCCCCAGAACTGTACTCCTCCAC  
 GCCAGACTTAACCATCCAGTTCCATTCCGACCCCTGCTGGCCTCATCTTTGGAAAGGGCCAGGGATTATCATGAA  
 CTACATAGAGGTATCAAGGAATGACTCCTGCTCGGATTTACCCGAGATCCAGAATGGCTGGAAAACCACTTCTCA  
 CACGGAGTTGGTGCAGGGGAGCCAGAATCACCTACAGTGTGACCCCGGCTATGACATCGTGGGGAGTGACACCTT  
 CACCTGCCAGTGGGACCTCAGCTGGAGCAGCGACCCCCATTGTGTGAGAAAATTATGTAAGTGCACCGACCCCGG  
 AGAGGTGGATCACTCGACCCGCTTAATTTGGGATCCTGTGCTGCTGGTGGGGACCAACATCAATACCTGCAA  
 CCCCCTTTTGTGCTTGAAGGGAGTCTCTTCTGACCTGCTACAGCCGTGAAACAGGGACTCCCATCTGGACGTC  
 TCGCTGCCCACTGCGTTTTCGGAGGAGTCCCTGGCATGTGACAACCCAGGGCTGCCTGAAAATGGATACCAAAAT  
 CCTGTACAAGCGACTCTACCTGCCAGGAGAGTCCCTCACCTTCATGTGCTACGAAGGCTTTGAGCTCATGGGTGA  
 AGTGACCATCCGCTGCATCCTGGGACAGCCATCCCACTGGAACGGGCCCCCTGCCCGTGTGTAAAGTTAATCAAGA  
 CAGTTTTGAACATGCTTTAGAAGCAGAAGCGGCAGCAGAGCGTCTGGAAGGGGGGAACATGGCCCTGGCTAT  
 CTTTCATCCCGGCTCATCATCTCCTTACTGCTGGGAGGAGCCTACATTTACATCACAAGATGTGCTACTATTC  
 CAACCTCCGCTGCTCTGATGTACTCCACCCCTACAGCCAGATCACCGTGAACCCGAGTTTGACAACCCCAT  
 TTACGAGACAGGGGAAACAGAGAGTATGAGGTTTCTATCTAAAGAGAGCTACACTTGAGAAGGGGACTTGTGAA  
 CTCAACCACAATCTCCTCGAGACATTATCCAGAGACCATGTGGCACTTGATTGAACCCAGAAATGTGCACTGT  
 CTTTTGTTGACTCTTTATCAAAGTTTACTGTTTTCTCCCTGTATTTATTATTTAAAGTGAAAAAAA  
 AAAAAAAAAA

**FIGURE 200**

MPAARPPAAGLRGISLFLALLLGSPAAALERDALPEGDASPLGPYLLPSGAPERGSPGKEHPE  
ERVVTAPPSSSQSAEVLGELVLDGTAPSAHHDIPALSPLLPEEARPKHALPPKKKLPSLKQVN  
SARKQLRPKATSAATVQRAGSQPASQGLDLLSSSTEKPGPPGDPDPDIVASEEASEVPLWLDRK  
ESAVPTTPAPLQISPFTSQPYVAHTLPQRPEPGEPGPDMAQEAPQEDTSPMALMDKGENELTG  
SASEESQETTTSTIITTTVITTEQAPALCSVSFSNPEGYIDSSDYPLLPLNNFLECTYNVTVY  
TGYGVELQVKS VNLS DGELLSIRGVDGPTLTVLANQTLLVEGQVIRSPTNTISVYFRTFQDDG  
LGT FQLHYQAFMLSCNFPRRPDSGDVTVM DLHSGGVAHFHCHLGYELQGAKMLTCINASKPHW  
SSQEPIC SAPCGGAVHNATIGRVLSPSY PENTNGSQFCIWTIEAPEGQKLHLHFERLLLHDKD  
RMTVHSGQTNKSALLYDSLQTESVPFEGLLSEGNTIRIEFTSDQARAASTFNIRFEAFEKGHC  
YEPYIQNGNFTTSDPTYNIGTIVEFTCDPGHSLEQGP AIECINVRDPYWN DTEPLCRAMCGG  
ELSAVAGVVLSPNWPEPYVEGEDCIWKI HVGEEKRIFLDIQFLNLSNSDILT IYDGDEVM PHI  
LGQYLGNSGPQKLYSSTPDLTIQFHSDPAGLIFGKGQGFIMNYIEVSRNDSCSDLPEIQNGWK  
TTSHTELVRGARITYQCDPGYDIVGSDTLTLCQWDL SWSSDPFFCEKIMYCTDPGEVDHSTRLI  
SDPVLLVGTTIQYTCNPGFVLEGSSLLTCYSRETGTPIWTSRLPHCVSEESLACDNPGLPENG  
YQILYKRLYLPGESLTFM CYEGFELMG EVTIRCILGQPSHWNGPLPVCKVNQDSFEHALEAEA  
AAETSLEGGNMALAIFIPVLIISLLLG GAYIYITRCRYYSNLRLPLMYSHPY SQITVETEFDN  
PIYETGETREYEVS I

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 893-915

**N-glycosylation sites.**

amino acids 311-315, 328-332, 350-354, 435-439, 458-462, 474-478,  
514-518, 576-580, 618-622, 674-678, 742-746

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 188-192

**N-myristoylation sites.**

amino acids 23-29, 87-93, 146-152, 454-460, 475-481, 575-581,  
629-635, 695-701, 723-729, 766-772, 877-883, 953-959

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 383-394

# **FIGURE 201**

**GATGGCTACGGCAGGGGGTGGCTCTGGGGCTGACCCGGGAAGTCGGGGTCTCCTTCGCCTTCT**  
**GTCTTTCTGCGTCTACTAGCAGTTTGTGCAGGGGAACTCAGTGGAGAGGAAGATATATAT**  
**CCCCTTAAATAAAACAGCTCCCTGTGTTTCGCCTGCTCAACGCCACTCATCAGATTGGCTGCCA**  
**GTCTTCAATTAGTGGAGACACAGGGGTATCCACGTAGTAGAGAAAGAGGAGGACCTACAGTG**  
**GGTATTGACTGATGGCCCCAACCCCCCTTACATGGTTCTGCTGGAGAGCAAGCATTTTACCAG**  
**GGATTTAATGGAGAAGCTGAAAGGGAGAACCAGCCGAATTGCTGGTCTTGCAGTGTCTTGAC**  
**CAAGCCCAGTCTGCCTCAGGCTTCTCTCCTAGTGTACAGTGCCCAAATGATGGGTGGTGT**  
**TTACTCCAATTCTATGGGCCAGAGTTTGCTCACTGCAGAGAAATACAGTGGAATTCGCTGGG**  
**CAATGGTTTGGCTTATGAAGACTTTAGTTTCCCCATCTTTCTTTGAAGATGAAAATGAAAC**  
**CAAAGTCATCAAGCAGTGCTATCAAGATCACAACCTGAGTCAGAATGGCTCAGCACCAACCTT**  
**CCCCTATGTGCCATGCAGCTCTTTTACACATGCATGCTGTGCATCAGCACTGCCACCTGCAT**  
**GCGGCGCAGCTCCATCCAAAGCACCTTCAGCATCAACCCAGAAATCGTCTGTGACCCCTGTCT**  
**TGATTACAATGTGTGGAGCATGCTAAAGCCTATAAATACAACCTGGGACATTAAAGCCTGACGA**  
**CAGGGTTGTGGTTGCTGCCACCCGGCTGGATAGTCGTTCTTTTCTGGAATGTGGCCCCAGG**  
**GGCTGAAAGCGCAGTGGCTTCTTTGTCAACCCAGCTGGCTGCTGCTGAAGCTTTCGAAAAGGC**  
**ACCTGATGTGACCACCTGCCCGCAATGTCATGTTTGTCTTCTTTCAAGGGGAACTTTTGA**  
**CTACATTGGCAGCTCGAGGATGGTCTACGATATGGAGAAGGGCAAGTTTCCCGTGCAGTTAGA**  
**GAATGTTGACTCATTTGTGGAGCTGGGACAGGTGGCCTTAAGAACTTCATTAGAGCTTTGGAT**  
**GCACACAGATCTGTTTCTCAGAAAAATGAGTCTGTACGGAACCAGGTGGAGGATCTCCTGGC**  
**CACATTGGAGAAGAGTGGTGTCTGGTGTCCCTGCTGTCTCCTCAGGAGGCCAAATCAGTCCCA**  
**GCCTCTCCCAACCATCTTCCCTGCAGCGATTTCTTCGAGCTCGAAACATCTCTGGCGTTGTTCT**  
**GGCTGACCACTCTGGTGCCTTCCATAACAAATATTACCAGAGTATTTACGACACTGCTGAGAA**  
**CATTAATGTGAGCTATCCCGAATGGCTGAGCCCTGAAGAGGACCTGAACCTTGTAAACAGACAC**  
**TGCCAAGGCCCTGGCAGATGTGGCCACGGTGCTGGGACGTGCTCTGTATGAGCTTGCAGGAGG**  
**AACCAACTTCAGCGACACAGTTTCAGGCTGATCCCCAAACGGTTACCCGCTGCTCTATGGGTT**  
**CCTGATTAAAGCCAACAACCTCATGGTTCCAGTCTATCCTCAGGCAGGACCTAAGTCTACTT**  
**GGGTGACGGGCTCTTCAACATTACATCGCTGTCTCCAGCCCCACCAACCACTTATGTTGT**  
**ACAGTATGCCCTTGGCAAATTTGACTGGCACAGTGGTCAACCTCACCCGAGAGCAGTGCCAGGA**  
**TCCAAGTAAAGTCCCAAGTGAACAAAGGATCTGTATGAGTACTCATGGGTCCAGGGCCCTTT**  
**GCATTCTAATGAGACGGACCGACTCCCCCGGTGTGTGCGTTCTACTGCACGATTAGCCAGGGC**  
**CTTGCTCCTGCCTTTGAACTGAGTCAGTGGAGCTCTACTGAATACTCTACATGGACTGAGAG**  
**CCGCTGGAAAGATATCCGTGCCCGGATATTTCTCATCGCCAGCAAAGAGCTTGAGTTGATCAC**  
**CCTGACAGTGGGCTTCGGCATCCTCATCTTCTCCCTCATCGTCACCTACTGCATCAATGCCAA**  
**AGCTGATGTCTTTTCATTGCTCCCCGGGAGCCAGGAGCTGTGTCTACTGAGGAGGACCCCA**  
**GCTTTTCTTGCCAGNTCAGCAGTTCACTTCTTAGAGCATCTGTCCCACTGGGACACAACCACT**  
**AATTTGTCACTGGAACCTCCCTGGGCCTGTCTCAGATTGGGATTAAACATAAAAGAGTGGAAC**  
**ATCCAAAAGAGACAGGGAGAAATAAATAAATTGCCTCCCTTCTCCGCTCCCTTTCCCATCA**  
**CCCCTTCCCCATTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT**  
**TCTTGCTCCTGTTTAACTCCCTAGTTACCCACCCTAATTTGCCCTTCAGGACCCTTCTACTTT**  
**TTCTTCTCTGCCCTGTACCTCTCTCTGCTCCTCACCCCCACCCCTGTACCCAGCCACCTTCT**  
**GACTGGGAAGGACATAAAAGGTTTAAATGTCAGGGTCAAACCTACATTGAGCCCCTGAGGACAGG**  
**GGCATCTCTGGGCTGAGCCTACTGTCTCCTTCCCACTGTCTTTCTCCAGGCCCTCAGATGGC**  
**ACATTAGGGTGGGCGTGTGCGGGTGGGTATCCACCTCCAGCCCACAGTGCTCAGTTGTACT**  
**TTTTATTAAAGCTGTAATATCTATTTTTGTTTTTGTCTTTTCTTTTCTTTTCTTTTGTAAATAT**  
**ATATATAATGAGTTTCATTAAATAGATTATCCC**

## **FIGURE 202**

MATAGGGSGADPGSRGLLRLLSFCVLLAGLCRGNSVERKIYIPLNKTAPCVRLLNATHQIGCQ  
SSISGDTGVIHVVEKEEDLQWVLTGDPNPPYMVLLSKHFTRDLMEKLGKRTSRIAGLAVSLT  
KPSPASGFSPSVQCPNDGFGVYSNSYGPEFAHCREIQWNSLGNGLAYEDFSFPIFLEENET  
KVIKQCYQDHNLSQNGSAPTFLCAMQLFSHMHAVISTATCMRRSSIQSTFSINPEIVCDPLS  
DYNVWSMLKPINTTGTCLKPDDRVVVAATRLDSRSFFWNVAPGAESAVASFVTQLAAAEALQKA  
PDVTTLPARNVMFVFFQGETFDYIGSSRMVYDMEKGKFPVQLENVDSFVELGQVALRTSLELWM  
HTDPVSQKNESVRNQVEDLLATLEKSGAGVPAVILRRPNQSQPLPPSSLQRFLRARNISGVVL  
ADHSGAFHNKYYQSIYDTAENINVSYPEWLSPEEDLNFVTD TAKALADVATVLGRALYELAGG  
TNFSDTVQADPQTVTRLLYGFLIKANNSWFQSILRQDLRSYLGDGPLQHYIAVSSPTNTTYVV  
QYALANLTGTVVNL TREQCQDPSKVPSENKDLYEYSWVQGPHLSNETDRLPRCVRSTARLARA  
LSPAFELSQWSSTEYSTWTESRWKDIRARIFLIASKELELITLTVGFGILIFSLIVTYCINAK  
ADVLFIAPREPGAVSY

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 671-692

**N-glycosylation sites.**

amino acids 45-49, 55-59, 187-191, 200-204, 204-208, 264-268,  
387-391, 417-421, 435-439, 464-468, 506-510, 530-534, 562-566,  
573-577, 580-584, 612-616

**Glycosaminoglycan attachment site.**

amino acids 404-408

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 232-236

**N-myristoylation site.**

amino acids 5-11, 6-12, 9-15, 29-35, 61-67, 120-126, 146-152,  
168-174, 205-211, 294-300, 438-444, 446-452, 504-510, 576-582



**FIGURE 203**

GCTAGACCGAGCCCTGGGAGGCTACGGGCTCCCCCGGAAACCCTGCCAGGGGAGCCGGGTTTT  
GAGCTCAGGCGCCTCTAGCGGCGGCCCCAGAAATCTGACTCGCGAGGCCAGAGTTGCAGGGA  
CTGAATAGCAAACCTGAGGCTGAGTAGGGAACAGACCATGAGGTCAGTGCAGATCTTCCTCTCC  
CAATGCCGTTTGTCTCTTCTACTAGTTCCGACAATGCTCCTTAAGTCTCTTGGCGAAGATGTA  
ATTTTTCACCCCTGAAGGGGAGTTTGACTCGTATGAAGTCAACATTCTGAGAAGCTGAGCTTC  
CGGGGAGAGGTGCAGGGTGTGGTCAGTCCCGTGTCTACCTACTGCAGTTAAAAAGCAAGAAG  
CACGTCCCTCCATTTGTGGCCCAAGAGACTTCTGTTGCCCCGACATCTGCGCGTTTTCTCCTTC  
ACAGAACATGGGGAACCTGCTGGAGGATCATCCTTACATAACCAAGGACTGCAACTACATGGGC  
TCCGTGAAGAGTCTCTGGACTCTAAAGCTACTATAAGCACATGCATGGGGGGTCTCCGAGGT  
GTATTTAATATTGATGCCAAACATTACCAAAATTGAGCCCCCTCAAGGCCTCTCCAGTTTTTGAA  
CATGTCGTCTATCTCCTGAAGAAAGAGCAGTTTTGGGAATCAGTTTTGTGGCTTAAGTGATGAT  
GAAATAGAATGGCAGATGGCCCCCTTATGAGAATAAGGCGAGGCTAAGGGACTTTCTGGATCC  
TATAAACACCCAAAGTACTTGAATTGATCCTACTCTTTGATCAAAGTAGGTATAGGTTTTGTG  
AACACAATCTTTCTCAAGTCATACATGATGCCATTCTTTTGACTGGGATTATGGACACCTAC  
TTTCAAGATGTTTCGTATGAGGATACACTTAAAGGCTCTTGAAGTATGGACAGATTTTAACAAA  
ATACGCGTTGGATATCCAGAGTTAGCTGAAGTTTTAGGCAGATTTGTAATATATAAAAAAGT  
GTATTAAATGCTCGCCTGTCTCAGATTTGGGCACATTTATATCTTCAAAGAAAATATAATGAT  
GCTCTTGCATGGTCGTTTTGGAAGGTGTGTTCTCTAGAATATGCTGGATCAGTGAGTACTTTA  
CTAGATACAAATATCCTTGCCCCCTGCTACCTGGTCTGCTCATGAGCTGGGTCTGCTGTAGGA  
ATGTCACATGATGAACAATACTGCCAATGTAGGGGTAGGCTTAATTGCATCATGGGCTCAGGA  
CGCACTGGGTTTAGCAATTGCAGTTATATCTCTTTTTTTAAACATATCTCTTCGGGAGCAACA  
TGTCTAAATAATATCCAGGACTAGGTTATGTGCTTAAGAGATGTGGAAACAAAATTGTGGAG  
GACAATGAGGAATGTGACTGTGGTTCCACAGAGGAGTGTGAGAAAGATCGGTGTTGCCAATCA  
AATTGTAAGTTGCAACCAGGTGCCAAGTGTAGCATTGGACTTTGCTGTCTGATGATTGTGCGTTT  
CGTCCATCTGGATACGTGTGTAGGCAGGAAGGAAATGAATGTGACCTTGCAGAGTACTGCGAC  
GGGAATTCAAGTTCCTGCCCAAATGACGTTTTATAAGCAGGATGGAACCCCTTGCAAGTATGAA  
GGCCGTTGTTTTGAGGAAGGGGTGCAGATCCAGATATATGCAGTGCCAAAGCATTTTTGGACCT  
GATGCCATGGAGGCTCCTAGTGAGTGCTATGATGCAGTTAACTTAATAGGTGATCAATTTGGT  
AACTGTGAGATTACAGGAATTCGAAATTTTAAAAAGTGTGAAAGTGCAAAATCAATATGTGGC  
AGGCTACAGTGATAAATGTTGAAACCATCCCTGATTTGCCAGAGCATACGACTATAATTTCT  
ACTCATTTACAGGCAGAAAATCTCATGTGCTGGGGCACAGGCTATCATCTATCCATGAAACCC  
ATGGGAATACCTGACCTAGGTATGATAAATGATGGCACCTCCTGTGGAGAAGGCCGGGTATGT  
TTTAAAAAAATTTGCGTCAATAGCTCAGTCTGTCAGTTTGACTGTTTGCCTGAGAAATGCAAT  
ACCCGGGGTGTGTTGCAACAACAGAAAAAACTGCCACTGCATGTATGGGTGGGCACCTCCATTTC  
TGTGAGGAAGTGGGGTATGGAGGAAGCATTGACAGTGGGCCTCCAGGACTGCTCAGAGGGGCG  
ATTCCTTCGTCAATTTGGGTTGTGTCCATCATAATGTTTCGCCTTATTTTATTAATCCTTTCA  
GTGGTTTTTGTGTTTTTCCGGCAAGTGATAGGAAACCCTTAAACCCCAAACAGGAAAAAATG  
CCACTATCCAAAGCAAAAACCTGAACAGGAAGAATCTAAACAAAAAACTGTACAGGAAGAATCT  
AAAACAAAAAACTGGACAGGAAGAATCTGAAGCAAAAACCTGGACAGGAAGAATCTAAAGCAAAA  
ACTGGACAGGAAGAATCTAAAGCAAAACATTGAAAGTAAACGACCCAAAGCAAAGAGTGTCAAG  
AAACAAAAAAAGTAAACCGGGCAATCCATACTCATTTCAGTAACACAGGCTCATTTATTTAACCA  
GCTAATCATTTATCCAAAGGCTTTCCATTCTTCTCCCAATATTTTTTTTACTTTAATTTTTCCC  
ACAAGTTTTGATCAGCAATAAACAGCATTCTTGTTTTGGAACAAAA

## **FIGURE 204**

MRSVQIFLSQCRLLLLLLVPTMLLKSLGEDVIFHPEGEFDSYEVTIPEKLSFRGEVQGVVSPVS  
YLLQLKGKKHVLHLWPKRLLLLPRHLRVFSFTEHGELLEHPYIPKDCNYMGSVKESLDSKATI  
STCMGGLRGVFNIDAKHYQIEPLKASPSFEHVYLLKKEQFGNQVCGLSDDEIEWQMAPYENK  
ARLRDFPGSYKHPKYLELILLFDQSRVRFVNNNLSQVIHDAILLTGIMDTYFQDVRMRIHLKA  
LEVWTD FNKIRVGYPELAEVLGRFVIYKKSVLNARLSSDWAHLYLQRKYNDALAWSFGKVCSL  
EYAGSVSTLLDTNILAPATWSAHELGHAVGMSHDEQYCQCRGLNCIMGSGRTGFSNCSYISF  
FKHISSGATCLNNIPGLGYVLKRCGNKIVEDNEECDCGSTEECQKDRCCQSNCKLQPGANCSI  
GLCCHDCRFRPSGYVCRQEGNECDLAEYCDGNSSSCPNDVYKQDGTGPCKYEGRCFRKGCRSRY  
MQCQSIFGPDAMEAPSECYDAVNLI GDQFGNCEITGIRNFKKCESANSICGRLQCINVTIPD  
LPEHTTIIISTHLQAENLMCWGTGYHLSMKPMGIPDLGMINDGTSCGEGRVCFKKNCVNSSVLQ  
FDCLPEKCNTRGVCNNRKNCHCMYGWAPPFCEEVGYGGSIDSGPPGLLRGAIPSSIWVVSIIIM  
FRLILLILSVFVFFRQVIGNHLKPKQEKMPLSKAKTEQEESKTKTVQEESKTKTGQEESEAK  
TGQEESKAKTGQEESKANIESKRPKAKSVKKQKK

**Signal peptide:**

amino acids 1-27

**Transmembrane domain:**

amino acids 684-705

**N-glycosylation sites.**

amino acids 222-226, 372-376, 438-442, 473-477, 625-629

**N-myristoylation sites.**

amino acids 131-137, 168-174, 235-241, 319-325, 364-370, 436-442,  
472-478, 609-615, 642-648, 668-674, 676-680, 680-686, 749-755,  
758-764, 767-773

**Amidation site.**

amino acids 69-73

**Disintegrins proteins**

amino acids 429-479

**EGF-like domain proteins**

amino acids 650-662

**Neutral zinc metallopeptidases, zinc-binding region proteins**

amino acids 335-345

# FIGURE 205

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGGGAAGGTTGAATGGGGTAGAAGGCCTG  
 TTGTGGAGGGAAACCACCCATCCTCCTGCCTCCCACCACCACCATCATCCTGGCTGGACGGAG  
 AGGGTGACGGGGGCTGGGAAGGGGCAGCTCATGTTTCAGGTTTCCAGGAGGGGCTACCTGTTGA  
 CTGTCTTTGCAGGAAGAAGAAAAACCTGAGTGACCAGATGTCCAGCTCCAGGTGCCCTTGCC  
 AGATGGCCAGAACCACACCTCTTGAAGAGTGACAGTGCTGTGGAGCATGGTTTCTGCACACCT  
 GGAATGACTGGAACCCCAAAGACTCAAGAAGGAGCTAAAGATCTTGAAGTAGACATGAATAAA  
 ACAGAAGGCTGTGGACCACCTGTGAGATGGAGAAGTCCTTCTGAGGCTATCCAAACACGGAC  
 CAGGCCATGAGACCCCGATGACCATCCCTGAATTTTTTTCGAGAGTCAGTCAACCGATTTGGAA  
 CTTATCCAGCCCTCCCATCCAAGAATGGCAAAAAGTGGGAAATTTCTGAATTTCAACCAGTACT  
 ATGAGGCTTGTGCGAAGGCTGCAAAAATCCTTGATCAAGCTGGGTTTGGAGCGTTTCCACGGAG  
 TTGGTATCCTGGGGTTTAACTCTGCAGAGTGGTTTATCACTGCTGTTGGTGCCATCCTAGCCG  
 GGGTCTTTGTGTTGGTATTTATGCCACCAACTCTGCCGAGGCTTGTCAATATGTCATCACTC  
 ATGCCAAAGTGAACATCTTGCTGGTTGAGAATGATCAACAGTTACAGAAAATCCTTTCGATTTC  
 CACAGAGCAGCCTAGAGCCCCATAAAGCGATCATCCAGTACAGACTGCCAATGAAGAAGAACA  
 ACAACTTGTACTCTTGGGATGATTTTCATGGAACCTTGGCAGAAGTATCCCTGACACCCCACTGG  
 AGCAGGTCATCGAGAGCCAGAAGGCGAATCAATGCCGAGTGCTCATCTACACTTCAGGGACCA  
 CAGGCATACCCAAGGGAGTGATGCTCAGTCATGACAACATCACGTGGATTGCAGGAGCAGTGA  
 CAAAGGACTTTAAACTGACAGACAAGCATGAGACGGTGGTTAGCTACCTCCCACTCAGCCATA  
 TTGCAGCATTGATGATGACATCTGGGTACCCATAAAGATTGGGGCGCTCACATACTTTGCTC  
 AAGCAGATGCTCTCAAGGGCACCTTGGTAAGTACTCTAAAGGAGGTAAACCTACTGTCTTCA  
 TTGGAGTGCCTCAAATTTGGGAGAAGATACATGAGATGGTGAAGAAAAATAGTGCCAAGTCCA  
 TGGGCTTGAAGAAGAAGGCATTTCGTGTGGGCAAGAAACATTGGCTTCAAGGTCAACTCAAAAA  
 AGATGTTGGGGAAATATAATACTCCCGTGAGCTACCGCATGGCTAAGACTCTCGTGTTTCAGCA  
 AAGTCAAGACATCCCTTGGCTTGGATCACTGTCACTCTTTTATCAGTGGGACTGCGCCCCCTCA  
 ACCAAGAGACTGCCGAGTCTTTCTAAGCTTGGACATACCTATAGGCGAGTTGTATGGGTTGA  
 GTGAGAGCTCGGGACCCACACGATATCCAACCAGAATAACTACAGGCTTCTAAGCTGTGGCA  
 AGATCTTGACTGGGTGTAAGAATATGCTGTTCCAGCAGAACCAAGGATGGCATTGGGGAGATCT  
 GCCTCTGGGGTAGGCACATCTTCATGGGCTATCTGGAAAGTGAGACTGAACTACAGAGGCCA  
 TCGATGATGAAGGCTGGCTACACTCTGGGGATCTGGGCCAGCTGGACGGTCTGGGTTTCTCTCT  
 ATGTCACCGGCCACATCAAAGAAATCCTTATCACTGCTGGTGGTGAAAATGTGCCCCCCATTCT  
 CTGTTGAGACCTTGGTTAAGAAGAAGATCCCATCATCAGTAACGCCATGTTAGTAGGAGATA  
 AACTGAAGTTTCTGAGCATGTTGCTGACGCTGAAGTGTGAGATGAATCAGATGAGCGGAGAAC  
 CTCTGGACAAGCTGAACTTCGAGGCCATCAACTTCTGTGCGGGTCTGGGCAGCCAGGCATCCA  
 CCGTGACTGAGATTGTGAAGCAGCAAGACCCCCTGGTCTACAAGGCCATCCAGCAAGGCATCA  
 ATGCTGTGAACCAGGAAGCCATGAACAATGCACAGAGGATTGAAAAGTGGGTCACTTGGAGA  
 AGGACTTTTCCATCTATGGTGGAGAGCTAGGTCCAATGATGAACTTAAGAGACATTTTGTAG  
 CCCAGAAATACAAAAACAAATTGATCACATGTACCCTGACTGCTTTGATGGAGCTGCTCTC  
 AGCTGTTCTGATGCCCTCAGCAGGAAGACCTCATTGCAATAAGTGAAATGCTGCTCTAGGTAG  
 AAGCTCTCCCTGCTGTTTTTAAGAAGCCACATTCCTCATTGGTCAGTTTCTTGATTGTTTCGTC  
 TGTTGGAGAGGTGCTCCCTAGAAGAACCTGCCATACGTTTCAAAGCAATAAAATCACTGTATA  
 TCTTTCTAAGGACCTTCAAGTCATGACTCCAGGGAAGCCTATTGGGAAGTCTACTAAAACTG  
 CCTGATTTACAAGAAAGACCTGAACTTGTGGGCTCCCATTTGATTTTTTCTCCTCAGGGGAC  
 TCAGACATTAGAAAGAAAAAGCCTCACAGATTTGAAGAACTGGACCCCCAAATCACTCACCT  
 GCCTGGAAGCAACTGGGAAACCTTCCAATAAGTCCTGATAATAAGCACTTTCAGGGTCCCAA  
 AAAAAAAAAA

## **FIGURE 206**

MTIPEFFRESVNRFGTYPALPSKNGKKWEILNFNQYYEACRKAASLIKGLERFHGVGILGF  
NSAEWFITAVGAILAGGLCVGIYATNSAEACQYVITHAKVNILLVENDQQLOKILSIPQSSLE  
PLKAI IQYRLPMKKNNNLYSWDDFMELGRSIPDTQLEQVIESQKANQCAVLIYTSGETTGIPKG  
/MLSHDNITWIAGAVTKDFKLTDKHETVVSYP LSHIAAQMMDIWVPIKIGALTYFAQADALK  
JTLVSTLKEVKPTVFIGVPQIWEKIHVMVKNSAKSMGLKKKAFVWARNIGFKVNSKKMLGKY  
JTPVSYRMAKTLVFSKVKTSGLGDHCHSFISGTAPLNQETAEFFLSLDIPIGELYGLSESSGP  
HTISNQNNYRLSLSCGKILTGCKNMLFQQNKDGIGEICLWGRHIFMGYLESETETTEAIDDEGW  
LHSGDLGQLDGLGFLYVTGHIKEILITAGGENVPPIPVETLVKKKIPIISNAMLVGDKLKFLS  
MLLTLKCEMNQMSGEPLDKLNFEAINFCRGLGSQASTVTEIVKQDPLVYKAIQQGINAVNQE  
AMNNAQRIEKWVILEKDFSIYGGELGPMMLKLRHFVAQKYKKQIDHMYH

**Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 65-86

**N-glycosylation site.**

amino acids 196-200

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 282-286

**Tyrosine kinase phosphorylation sites.**

amino acids 547-555, 608-616

**N-myristoylation sites.**

amino acids 15-21, 74-80, 80-86, 84-90, 185-191, 189-195,  
253-259, 337-343, 371-377, 448-454, 536-542

**Amidation site.**

amino acids 24-28

**Putative AMP-binding domain signature.**

amino acids 177-189

**Putative AMP-binding domain proteins.**

amino acids 173-190

**FIGURE 207**

[illegible]

## **FIGURE 208**

MAYRVLGRAGPPQPRRARLLFAFTLSLSCTYLCYSFLCCDDLGSRLLGAPRCLRGPSAGG  
QKLLQKSRPCDPSGPTPSEPSAPSAPAAAVPAPRLSGSNHSGSPKLGTKRLPQALIVGVKKGG  
TRAVLEFIRVHPDVRA LGTEPHFFDRNYGRGLDWYRSLMPRTLESQITLEKTPSYFVTQEAPR  
RIFNMSRDTKLI VVRNPVTRAI SDYTQTL SKKPD IPTFEGLSFRNRTLGLVDVSWNAIRIGM  
YVLHLESWLQYFPLAQIHFVSGERLITDPAGEMGRVQDFLGIKRFITDKHFYFNKTKGFPCLK  
KTESSLLPRCLGKSKGRTHVQIDPEVIDQLREFYRPNYKIFYETVGQDFRWE

**Signal peptide:**

amino acids 1-33

**N-glycosylation sites.**

amino acids 102-106, 193-197, 235-239, 306-310

**Tyrosine kinase phosphorylation site.**

amino acids 296-305

**N-myristoylation sites.**

amino acids 51-57, 100-106, 121-127, 125-131

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 20-31

# FIGURE 209

CTTTCCTTATCTGTGTGTACTCTTATCTCACTGTTCTATTTTTTCTCCTCATTTATATTAAC  
CTTTCCTTACCTTTTTTTTCTGAACTTCTAGGCCTTCTCTTTCCAGAACTGGTGGAAGACAAATG  
AAACGGCCAAGATGGTAAGAAACAAGCCGCATTTCTCCTTGGGGAGACTGATAATTTAAAAGG  
TTTGTGTGTGTGAGAAACATTCCAGCTTCATACCAACCCTTTCTTCCACCTCTGCCCCACTG  
GAGACCACTTACATCCCGAAGCGGACGCGGCAGCTGAAGTCAGGAAACCATGCATCACATTAG  
CAGGAGCCAACCTGCAGACTTTAAACTCCGTTCAACATGTGGATGCGGCAGAGAAATGACCTGT  
CCAGACAAGCCGGGGCAGCTCATAACTGGTTTCATCTGCTCCCTGTGCGTCCCGCGGGTGCGT  
AAGCTCTGGAGCAGCCGGCGTCCAAGGACCCGGAGAAACCTTCTGCTGGGCACTGCGTGTGCC  
ATCTACTTGGGCTTCTTGGTGAGCCAGGTGGGGAGGGCCTCTCTCCAGCATGGACAGGCGGCT  
GAGAAGGGGCCACATCGCAGCCGCGACACCGCCGAGCCATCCTTCCCTGAGATACCCCTGGAT  
GGTACCCTGGCCCTCCAGAGTCCAGGGCAATGGGTCCACTCTGCAGCCCAATGTGGTGTAC  
ATTACCCTACGCTCCAAGCGCAGCAAGCCGGCAATATCCGTGGCACCGTGAAGCCCAAGCGC  
AGGAAAAGCATGCAGTGGCATCGGCTGCCCGAGGGCAGGAGGCTTTGGTCCGACCATCCCTT  
CAGCCGCAGGAAGCGGCAAGGGAAGCTGATGCTGTAGCACCTGGGTACGCTCAGGGAGCAAAC  
CTGGTTAAGATTGGAGAGCGACCTTGGAGGTTGGTGCGGGGTCCGGGAGTGCGAGCCGGGGGC  
CCAGACTTCTTGCAGCCAGCTCCAGGGAGAGCAACATTAGGATCTACAGCGAGAGCGCCCCC  
TCTGGCTGAGCAAAGATGACATCCGAAGAATGCGACTCTTGGCGGACAGCGCAGTGGCAGGG  
CTCCGGCCTGTGTCTCTTAGGAGCGGAGCCCGTTTGTGCTGGTGTGAGGGGGGGCGCACCTGGC  
GCTGTGCTCCGCTGTGGCCCTAGCCCTGTGGGCTTCTCAAGCAGCCCTTGGACATGAGTGAG  
GTGTTGCTTCCACCTAGACAGGATCCTGGGGCTCAACAGGACCCTGCCGTCTGTGAGCAGG  
AAAGCAGAGTTCATCCAAGATGGCCGCCCATGCCCATCATCTTTGGGATGCATCTTTATCT  
TCAGCAAGTAATGACACCCATTCTTCTGTTAAGCTCACCTGGGGAACCTTATCAGCAGTTGCTG  
AAACAGAAATGCTGGCAGAATGGCCGAGTACCCCAAGCCTGAATCAGGTTGTACTGAAATACAT  
CATCATGAGTGGTCCAAGATGGCACTCTTTGATTTTTTTGTTACAGATTTATAATCGCTTAGAT  
ACAAATGTCTGTGGATTACAGACCTCGCAAGGAAGATGCCTGTGTACAGAATGGATTGAGGCCA  
AAATGTGATGACCAAGGTTCTGCGGCTCTAGCACACATTATCCAGCGAAAGCATGACCCCAAGG  
CATTTGGTTTTTATAGACAACAAGGGTTTCTTTGACAGGAGTGAAGATAACTTAAACTTCAA  
TTGTTAGAAGGCATCAAAGAGTTTCCAGCTTCTGCAGTTTCTGTTTTGAAGAGCCAGCACTTA  
CGGCAGAACTTCTTCAGTCTCTGTTTCTTGATAAAGTGATTGGGAAAGTCAAGGAGGTAGA  
CAAGGAATTGAAAAGCTTATCGATGTAATAGAACACAGAGCCAAAATTCCTATCACCTATATC  
AATGCACACGGGGTCAAAGTATTACCTATGAATGAATGACAAAAGAATCTTCTGGCTAGGGTG  
TTAGATATATTTATGCATTTTGGTTTTGTTTTTAAATCAAGCACATCAACCTCAAGCCCGTT  
TAGCAATGAGGCAGTGTAGATGAATACGTAAATAAATGACTTTAAACCAAGTAGCTATAAAGG  
GACTTAGCACTGTATGCATACTTAAAAAGGTTTTGAAAAACAACTACTTGAGAAATATTTGT  
TTATATTTTTCTCTAACATCATGCTATGTGTGAGTCTGAACATCTGACAACAGAAATTTGAGT  
TATTATTCTAGCTAAGTTTTGAAAAACATTTGTGCTGCTGTTAATAGAAAACTGCAAAACCAGA  
GATACTGACTCCATTAATAAACCATATTTTGTGCGGTTTTGACTGTTCTGACCAAATACTAAT  
GGGAACAATTCTTGACGTTTTTCTGTTGCTGATTGTTAACATAGAGCAGTCTCTACACTACCC  
TGAGGCAACTCTACATTGGAACACTGAGGCTTACAGCCTGCAAGAGCATCAGAGCTGACCATA  
CATTTAAACAGAAATGCTGGTTTTATTTGCAAAATCACCAGTATATTTTCTATTGTGTCTATAA  
AAAATCAGTCATTTAAGTACAAGAATCATATTTCCATTCTTTTTAGAAATTTATTTTGTG  
TCCCTATGGAATCATTACATCTGACAATTTATATGTTAAAGAGTTTTACTCTCTATTTTT  
GGTCCAATTTGTATCTAGTGGCTGAGAAATTAATAATTCTAAAGTATGAAGTTACCTATCTG  
AAAATGTACTTACAGAGTATCATTTTTAAATGGATGTCTCTTTAAAAATTTTGTACTTTTAC  
CAACAATGTAATATAATTTATGTATATTTTATTAATAATAGTGAATTCCTTAAATTTGTTCT  
ATGTACTTATATTTAATTTGATTTAATGGTTACTGCCAGATATTGAGAAATGGTTCAAATAT  
TGAGTGTGTTTCAATAA

**FIGURE 210**

MTCPDKPGQLINWFICSLCVPRVRKLWSSRRPRTRNLLLGTACAIYLGFLVSQVGRASLQHG  
QAAEKGPHRSDTAEPSFPEIPLDGTLAPPESQNGSTLQPNVVYITLRSKRSPANIRGTVK  
PKRRKKHAVASAAPGQEALVGPSLQPQEAAREADAVAPGYAQGANLVKIGERPWRLLVRGPGVR  
AGGPDFLQPSSRESNIRIYSESAPSWLSKDDIRRMRLLDASAVAGLRPVSSRSGARLLVLEGG  
APGAVLRCGPSPCGLLKQPLDMSEVFAPHLDRILGLNRTLPSVSRKAEFIQDGRPCPIILWDA  
SLSSASNDTHSSVKLTWGTYYQLLKQKCWQNGRVKPKPESGCTEIHHEWSKMALFDFLLQIYN  
RLDTNCCGFRPRKEDACVQNGLRPKCDDQGSAAALAHIIQRKHDPRHLVFIDNKGFFDRSEDNL  
NFKLLEGIKEFPASAVSVLKSQHLLRQKLLQSLFLDKVYWESQGGRQGIEKLIDVIEHRAKILI  
TYINAHGVKVLPMNE

**Transmembrane domain:**

amino acids 40-56

**N-glycosylation sites.**

amino acids 98-102, 289-293, 322-326

**N-myristoylation sites.**

amino acids 8-14, 41-47, 97-103, 187-193, 251-257, 252-258,  
287-293, 484-490



**FIGURE 211**

[illegible]

## **FIGURE 212**

MRRCSGSGPPPSLLLLLLWLLAVPGANAAPRSALYSPSDPLTLLQADTVRGAVLGSRSAWAV  
EFFASWCGHCIAFAPTWKALAEDVKAWRPALYLAALDCAEETNSAVCRDFNIPGFPTVRFFKA  
FTKNGSGAVFPVAGADVQTLRERLIDALESHHDTWPPACPPLEPAKLEEIDGFFARNNEEYLA  
LIFEKGGSYLGREVALDLSQHKGVAVRRVLNTEANVVRKFGVTDFPSCYLLFRNGSVSRVPVL  
MESRSFYTAYLQRLSGLTREAAQTTVAPT'TANKIAPT'VWKLADRSKIYMADLESALHYILRIE  
VGRFPVLEGQRLVALKKFVAVLAKYFPGRPLVQNFLHSVNEWLKRQKRNKIPYSFFKTALDDR  
KEGAVLAKKVNWIGCQGSEPHFRGFP'CSLWVLFHFLT'VQAARQNV'DHSQEAAKAKEVLP'PAIRG  
YVHYFFGCRDCASHFEQMAAASMRV'GSPNAAVLWLWSSHN'RVNARLAGAPSED'PQFPKVQWP  
PRELCSACHNERLDVPVWDVEATLNFLKAHFSPSNIILDFPAAGSAARRDVQNVAAPELAMG  
ALELESRNSTLDPGKPEMMKSP'TNTT'PHVPAEGPEASRPPKLHPGLRAAPGQEPPEHMAELQR  
NEQEQLGQWHL'SKRD'TGAALLAESRAEKNRLWGPLEVRRVGRSSKQLVDIPEGQLEARAGRG  
RGQWLQVLGGGFSYLDISLCVGLYSLSFMGLLAMYT'YFQAKIRALKGHAGHPAA

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 705-728

**N-glycosylation sites.**

amino acids 130-134, 243-247, 575-579

**Glycosaminoglycan attachment site.**

amino acids 6-10

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 644-648

**N-myristoylation sites.**

amino acids 52-58, 56-62, 196-202, 381-387, 392-398, 448-454,  
468-474, 684-690, 702-708

**Cytochrome c family heme-binding site signature.**

amino acids 509-515

**Thioredoxin family proteins**

amino acids 62-78

# **FIGURE 213**

GCACGAGGCCGACTTCCAGACCATCTACAACCTGCACGGCCTGGAACAGCTTCGGCTCCGACAC  
 TGAGATCATCCGGCTCAAGGAGCAAGGTTTCGGAAATGAAGTCGGGAGCCGGGCTGGAAGCAGA  
 GTCTGTGCCGATGGCCGTCATCATTTGGGGTGGCCGTAGGAGCTGGTGTGGCCTTCCTCGTCCT  
 TATGGCAACCATCGTGGCGTTCTGCTGTGCCCGTTCCAGAGAAATCTCAAAGGTGTTGTGTC  
 AGCCAAAAATGATATCCGAGTGGAATTTGTCCACAAGGAACCAGCCTCTGGTCGGGAGGGTGA  
 GGAGCACTCCACCATCAAGCAGCTGATGATGGACCGGGGTGAATTCAGCAAGACTCAGTCCT  
 GAAACAGCTGGAGGTCCTCAAAGAAGAGGAGAAAGAGTTTCAGAACCTGAAGGACCCACCAA  
 TGGCTACTACAGCGTCAACACCTTCAAAGAGCACCCTCAACCCCGACCATCTCCCTCTCCAG  
 CTGCCAGCCCCGACCTGCGTCTGCGGGTAAGCAGCGTGTGCCACAGGCATGTCTTACCAA  
 CATCTACAGCACCTTGAGCGGCCAGGGCCGCCTCTACGACTACGGGCAGCGGTTTGTGCTGGG  
 CATGGGCAGCTCGTCCATCGAGCTTTGTGAGCGGGAGTTCCAGAGAGGCTCCCTCAGCGACAG  
 CAGCTCCTTCTGGACACGCAGTGTGACAGCAGCGTCAGCAGCAGCGGCAAGCAGGATGGCTA  
 TGTGCAGTTCGACAAGGCCAGCAAGGCTTCTGCTTCCTCCTCCCACTCCCAGTCCTCGTC  
 CCAGAACTCTGACCCCGAGTCGACCCCTGCAGCGGCGGATGCAGACTCACGTCTTAAGGATCACA  
 CACCGCGGGTGGGGACGGGCCAGGGAAGAGGTCAGGGCACGTTCTGGTTGTCCAGGGACGAGG  
 GGTACTTTGCAGAGGACACCAGAATTGGCCACTTCCAGGACAGCCTCCCAGCGCCTCTGCCAC  
 TGCCTTCCTTTCGAAGCTCTGATCAAGCACAAATCTGGGTCCCAGGTGCTGTGTGCCAGAGGT  
 GGGCGGGTGGGGAGACAGACAGAGGCTGCGGCTGAGTGCCTGTGCTTAGTGCTGGACACCCG  
 TGTCCCCGGCCCTTTCTGGAGGCCCTCTACCACCTGCTCTGCCACAGGCACAAGTGGCAG  
 CTATAACTCTGCTTTCATGAACTGCGGTCCACTCTCTGGTCTCTCTGTGGGCTCTACCCCTC  
 ACTGACCACAAGCTCTACCTACCCCTGTGCCTGTGCTCCCATACAGCCCTGGGGAGAAGGGGA  
 TGACGTCTTCCAGCACTGAGCTGCCCCAGAAACCCCGGCTCCCCACTGCTGCTCATAGCCCA  
 TACCCTGGAGGCTGACAAGCCAGAAATGGCCTTGGCTAAAGGAGCCTCTCTCTACCAGGCTG  
 GCCGGGAGCCACCCCAATTTGTTTGGTGTTTTGTGTCCATACTCTTGAGTTCTGTCTTG  
 GACTTGATGCCGCTGAACTCTGCGGTGGGACCGGTCCCGTCAGAGCCTGGTGTACTGGGGGA  
 GGGAGGGAGGAGGGAGCCTGTGCTGACGGAGCACCTCGCCGGGTGTGCCCCCTCCTGGGCTGTG  
 TGACCCAGCCTCCCCACCCACCTCCTGCTTTGTGTACTCCTCCCCCTCCCCCTCAGCACAATC  
 GGAGTTCATATAAGAAGTGCGGGAGCTTCTCTGGTCAGGGTTCTCTGAACACTTATGGAGAGA  
 GTGCTTCCTGGGAAGTGTGGCGTTTGAAGGGGCTGGAGGGCAGGTCTTTAAGATGGCGAGACT  
 GCCCTTCTCAGCTGATAAACACAAGAACGGCGATCCTGTCTTCAGTAAGGCTCCACGAGAAGA  
 GAGGAAGTATATCTACACCTCAACCTCCTAGTCACCACCTGAAATAAATGTTAGGGAAAAAAA

**FIGURE 214**

MAVIIGVAVGAGVAFVLMTIVAFCCARSQRNLKGVVSAKNDIRVEIVHKEPASGREGEEHS  
TIKQLMMDRGEFQQDSVLKQLEVLKEEEKEFQNLKDPTNGYYSVNTFKEHHSTPTISLSSCQP  
DLRPAGKQRVPTGMSFTNIYSTLSGQGRLYDYGQRFVLGMGSSSIELCEREFQRGSLSDSSSF  
LDTQCDSSVSSSGKQDGYVQFDKASKASASSSHHSQSSSQNSDPSRPLQRRMQTHV

**Signal peptide:**

amino acids 1-28

**Glycosaminoglycan attachment site.**

amino acids 150-154

**N-myristoylation sites.**

amino acids 6-12, 10-16, 36-42, 139-145, 165-171

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 114-125

**FIGURE 215**

CAGCCTTCCTCCCCAGCCTGAGTGACTACTCTATTTCCTTGGTCCCTGCTATTGTGCGGGACG  
ATTGCATGGGGTACGCCAGGAAAGTAGGCTGGGTGACCGCAGGCCTGGTGATTGGGGCTGGCG  
CCTGCTATTGCATTTATAGACTGACTAGGGGAAGAAAACAGAACAAAGGAAAAAATGGCTGAGG  
GTGGATCTGGGGATGTGGATGATGCTGGGGACTGTTCTGGGGCCAGGTATAATGACTGGTCTG  
ATGATGATGATGACAGCAATGAGAGCAAGAGTATAGTATGGTACCCACCTTGGGCTCGGATTG  
GGACTGAAGCTGGAACCAGAGCTAGGGCCAGGGCAAGGGCCAGGGCTACCCGGGCACGTCTGGG  
CTGTCCAGAAACGGGCTTCCCCCAATTGAGATGATACCGTTTTGTCCCCTCAAGAGCTACAAA  
AGGTTCTTTGCTTGGTTGAGATGTCTGAAAAGCCTTATATTCTTGAAGCAGCTTTAATTGCTC  
TGGGTAACAATGCTGCTTATGCATTTAACAGAGATATTATTCTGTGATCTGGGTGGTCTCCCAA  
TTGTGCGCAAAGATTCTCAATACTCGGGATCCCATAGTTAAGGAAAAGGCTTTAATTGTCTGA  
ATAACTTGAGTGTGAATGCTGAAAATCAGCGCAGGCTTAAAGTATACATGAATCAAGTGTGTG  
ATGACACAATCACTTCTCGCTTGAACTCATCTGTGCAGCTTGCTGGACTGAGATTGCTTACAA  
ATATGACTGTTACTAATGAGTATCAGCACATGCTTGCTAATTCCATTTCTGACTTTTTTCGTT  
TATTTTCAGCGGGAAATGAAGAAACAAACTTCAGGTTCTGAAACTCCTTTTGAATTTGGCTG  
AAAATCCAGCCATGACTAGGGAACTGCTCAGGGCCCAAGTACCATCTTCACTGGGCTCCCTCT  
TTAATAAGAAGGAGAAACAAAGAAGTTATTCTTAAACTTCTGGTCATATTTGAGAACATAAATG  
ATAATTTCAAATGGGAAGAAAATGAACCTACTCAGAATCAATTGGTGAAGGTTCACTTTTTT  
TCTTTTTTAAAGAATTTCAAGTGTGTGCTGATAAGGTTCTGGGAATAGAAAGTCACCATGATT  
TTTTGGTGAAAGTAAAGTTGGAAAATTCATGGCCAAACTTGCTGAACATATGTTCCCAAAGA  
GCCAGGAATAAACACCTTGATTTTGTAAATTTAGAAGCAACACACATTGTAACTATTCATTTTT  
TCCACCTTGTTTATATGGTAAAGGAATCCTTTGAGCTGCCAGTTTTGAATAATGAATATCATA  
TTGTATCATCAATGCTGATATTTAACTGAGTTGGTCTTTAGGTTTAAGATGGATAAATGAATA  
TCACTACTTGTTCTGAAAACATGTTTGTGCTTTTTATCTCGCTGCCTAGATTGAAATATTTT  
GCTATTTCTTCTGCATAAGTGACAGTGAACCAATTCATCATGAGTAAGCTCCCTTCTGTCATT  
TTCATTGATTTAATTTGTGTATCATCAATAAAATTGTATGTTAATGCTGGAAAGA

**FIGURE 216**

MGYARKVGWVTAGLVIGAGACYCIYRLTRGRKQNKKEKMAEGGSGDVDDAGDCSGARYNDWSDD  
DDDSNESKSIWVYPPWARIGTEAGTRARARARARATRRARRAVQKRASPNSDDTVLSPQELQKV  
LCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRD LGGLPIVAKILNTRDPIVKEKALIVLNN  
LSVNAENQRRLKVYMNQVCDTITSR LNSSVQLAGLRLLTNMTVTNEYQHMLANSISDFFRLF  
SAGNEETKLQVLKLLLNLAENPAMTRELLRAQVPSSLGSLFNKKENKEVILKLLVIFENINDN  
FKWEENEPTQNQFGEGSLFFFLKEFQVCADKVLGIESHHDFLVKVKVGKFMAKLAEHMFPKSQE

**Signal peptide:**

amino acids 1-20

**N-glycosylation sites.**

amino acids 68-72, 189-193, 217-221, 230-234

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-111

**N-myristoylation sites.**

amino acids 13-19, 17-23, 19-25, 54-60, 83-89, 147-153, 255-261,  
290-296

**Amidation site.**

amino acids 29-33

**FIGURE 217**

GAGACACAAAGGCAGGCGGGATGCGGGAGCAGGCAAAGGGAAGCGAAAGCCGCGCGCCCGGC  
CGGTGACTGGGTGAAGGCGCCGCGCAGCTTTCCCGACGCCGGCTGTACCCGGACCTCCTGGTC  
GAGCCTGGCGCGCCCGCAGCCATGGCCATCGCTCAACTGGCCACGGAGTACGTGTTCTCGGATT  
TCTTGCTGAAGGAGCCCACGGAGCCCAAGTTCAAGGGGCTGCGACTGGAGCTGGCTGTGGACA  
AGATGGTCACGTGCATTGCGGTGGGGCTGCCCCCTGCTGCTCATCTCGCTGGCCCTTCGCGCAGG  
AGATCTCGATTGGTACACAGATAAGCTGTTTTCTCTCCAAGTTCTTTCTCCTGGCGTCAGGCTG  
CCTTTGTGGATTTCATATTGCTGGGCGGCTGTTTCAGCAGAAGAACTCACTGCAGAGCGAGTCTG  
GAAACCTCCCACTGTGGCTGCATAAGTTTTTCCCTACATCCTGCTGCTCTTTGCGATCCTCC  
TGTACCTGCCCCCGCTGTTCTGGCGTTTTCGCAGCTGCTCCTCATATTTGCTCAGACTTGAAGT  
TTATCATGGAAGAACTTGACAAAGTTTACAACCGTGCAATTAAGGCTGCAAAGAGTGCGCGTG  
ACCTTGACATGAGAGATGGAGCCTGCTCAGTTCCAGGTGTTACCGAGAACTTAGGGCAAAGTT  
TGTGGGAGGTATCTGAAAGCCACTTCAAGTACCCAATTGTGGAGCAGTACTTGAAGACAAAGA  
AAAATTCTAATAATTTAATCATCAAGTACATTAGCTGCCGCCTGCTGACACTCATCATTATAC  
TGTTAGCGTGTATCTACCTGGGCTATTACTTCAGCCTCTCCTCACTCTCAGACGAGTTTGTGT  
GCAGCATCAAATCAGGGATCCTGAGAAACGACAGCACCGTGCCCGATCAGTTTCAGTGCAAAC  
TCATTGCCGTGGGCATCTTCCAGTTGCTCAGTGTCAATTAACCTTGTGGTTTATGTCCTGCTGG  
CTCCCGTGGTTGTCTACACGCTGTTTGTTCATTCCGACAGAAGACAGATGTTCTCAAAGTGT  
ACGAAATCCTCCCCACTTTTGATGTTCTGCATTTCAAATCTGAAGGTACAACGATTTGAGCC  
TCTACAATCTCTTCTTGAGGAAAATATAAGTGAGGTCAAGTCATACAAGTGTCTTAAGGTAC  
TGGAGAATATTAAGAGCAGTGGTCAGGGGATCGACCCAATGCTACTCCTGACAAACCTTGGCA  
TGATCAAGATGGATGTTGTTGATGGCAAACTCCCATGCTCTGCAGAGATGAGAGAGGAGCAGG  
GGAACCAGACGGCAGAGCTCCAAGGTATGAACATAGACAGTGAACTAAAGCAAATAATGGAG  
AGAAGAATGCCCGACAGAGACTTCTGGATTCTTCTTGCTTGATGATTTTTTTTCCTTGAGCTGT  
AAATCTGTGACTTCTGCGACATGGGATTTAATTTGGCTAAAGCACCCCTGTTGGTTTCACAGC  
TGGTTTGCAATAAATGGTTCTTGGTGGA

**FIGURE 218**

MAIAQLATEYVFSDFLKPEPTEPKFKGLRLELAVDKMVTCTIAVGLPLLLISLAFQAQEISIGTQ  
ISCFSPSSFSWRQAAFVDSYCWAAVQQKNSLQSESGNLPLWLHKFFPYILLFFAILLYLPPLF  
WRFAAAPHCSDLKFIMEELDKVYNRAIKAAKSARDLDMRDGACSVPGVTENLGQSLWEVSES  
HFKYPIVEQYLKTKKNSNNLI IKYISCRLLTLIIILLACTIYLGYYFSLSSLSDEFVCSIKSGI  
LRNDSTVPDQFQCKLIAVGIFQLLSVINLVVYVLLAPVVVYTLFVFPFRQKTDVLKVYEILPTF  
DVLHFKSEGYNDLSLYNLFLEENISEVKSYKCLKVLENIKSSGQGIDPMLLLTNLGMKMDVV  
DGKTPMSAEMREEQGNQTAELQGMNIDSETKANNGEKNARQRLLDSSC

**Transmembrane domains:**

amino acids 37-55, 108-126, 216-232, 273-290

**N-glycosylation sites.**

amino acids 255-259, 338-342, 394-398

**Glycosaminoglycan attachment site.**

amino acids 357-361

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 203-207

**N-myristoylation sites.**

amino acids 61-67, 174-180, 251-257, 393-399

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 218-229



**FIGURE 219**

CTGTGAGTGACACACGCTGAGTGGGGTGAAGGGAAATGCTGGTGAATTTCAATTTGAGGTGTG  
GGTTGCTGTTAGTCACTCTGTCTCTTGCCATTGCCAAGCACAAAGCAATCTTCCTTCACCAAAA  
GTTGTTACCCAAGGGGAACATTGTCCCAAGCTGTTGACGCTCTCTATATCAAAGCAGCATGGC  
TCAAAGCAACGATTCCAGAAGACCGCATAAAAAATATACGATTATTAAGAAAGAAAACAAAA  
AGCAGTTTATGAAAACTGTCAATTTCAAGAACAGCTTCTGTCCTTCTTCATGGAAGACGTTT  
TTGGTCAACTGCAATTGCAAGGCTGCAAGAAAATACGCTTTGTGGAGGACTTTCATAGCCTTA  
GGCAGAAATTGAGCCACTGTATTTCTGTGCTTCATCAGCTAGAGAGATGAAATCCATTACCA  
GGATGAAAAGAATATTTTATAGGATTGGAAACAAAGGAATCTACAAAGCCATCAGTGAACTGG  
ATATTCTTCTTTCTGGATTAAAAAATTATTGGAAAGCAGTCAGTAAACCAAAGCCAAGTACA  
TTGATTTTACAGTTATTTTGAAATACAATAAGAACTGCTAGAAATATGTTTATAACAGTCTAT  
TTCTTTTAAAACTTTTTAACATAATACTGACGGCATGTTAGGTGATTGAGAATAGACAAGAA  
GGATTTAGTAAATTAACGTTTTGGATATAAGTTGTCACTAATTTGCACATTTTCTGTGTTTTT  
AAATAATGTTTCCATTCTGAACATGTTTTGTCAATCACAAGTACATTGTGTCAACTTAATTTA  
AAGTATGTAACCTGAATTAACTCGTGTAATATTTGTGTGTGGAGTGGGATGTGGGGGGTGGAG  
GGGGAATGACAGATTTCTGGAATGCAATGTAATGTTACTGAGACTTAAATAGATGTTATGTAT  
ATGATTGTCTGTTAAGTGTGTTGAAAATTGTTAATTATGCCAGTGTGAACTTAGTACTTAAC  
ACATTTTGATTTTAATTAAATAAATTGGGTTTCCTTCTCAAAAAAAAAAAAAAAAAAAAAA  
AAAAA

**FIGURE 220**

MLVNFILRCGLLLVTLSLAIAKHKQSSFTKSCYPRGTL SQAVDALYIKA AAWLKATIPEDRIKN  
IRLLKKKTKKQFMKNCQFQEQLLSFFMEDVFGQLQLQGCKKIRFVEDFHSLRQKLSHCISCAS  
SAREMKSITRMKRIFYRIGNKGIYKAISELDILLSWIKKLLESSQ

**Signal sequence:**

amino acids 1-21

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 68-71

**N-myristoylation site.**

amino acids 148-153

**Interleukin-10 proteins.**

amino acids 58-94, 74-102, 128-170

**FIGURE 221**

GACCACGGCCCTGCGCCCCAGCCAGGCCTGAGGACATGAGGCGGCCGGCGGGTGCCGCTCC  
TGCTGCTGCTGTGTTTTGGGTCTCAGAGGGCCAAGGCAGCAACAGCCTGTGGTCGCCCCAGGA  
TGCTGAACCGAATGGTGGGCGGGCAGGACACGCAGGAGGGCGAGTGGCCCTGGCAAGTCAGCA  
TCCAGCGCAACCGAAGCCACTTCTGCGGGGGCAGCCTCATCGCGGAGCAGTGGGTCTTGACGG  
CTGCGCACTGCTTCCGCAACACCTCTGAGACGTCCCTGTACCAGGTCCTGCTGGGGGCAAGGC  
AGCTAGTGAGCCGGGACCACACGCTATGTATGCCCCGGGTGAGGCAGGTGGAGAGCAACCCCC  
TGTACCAGGGCACGGCCTCCAGCGCTGACGTGGCCCTGGTGGAGCTGGAGGCACCAGTGCCCT  
TCACCAATTACATCCTCCCCGTGTGCCTGCCTGACCCCTCGGTGATCTTTGAGACGGGCATGA  
ACTGCTGGGTCACTGGCTGGGGCAGCCCCAGTGAGGAAGACCTCCTGCCCGAACC GCGGATCC  
TGCAGAACTCGCTGTGCCCATCATCGACACACCCAAGTGCAACCTGCTCTACAGCAAAGACA  
CCGAGTTTGGCTACCAACCCAAAACCATCAAGAATGACATGCTGTGCGCCGGCTTCGAGGAGG  
GCAAGAAGGATGCCTGCAAGGGCGACTCGGGCGGCCCCCTGGTGTGCCTCGTGGGTGAGTCGT  
GGCTGCAGGCGGGGGTGATCAGCTGGGGTGAGGGCTGTGCCCCGCCAGAACCGCCAGGTGTCT  
ACATCCGTGTACCGCCCCACCACAACCTGGATCCATCGGATCATCCCCAACTGCAGTTCCAGC  
CAGCGAGGTTGGGCGGCCAGAAGTGAGACCCCCGGGGCCAGGAGCCCCCTTGAGCAGAGCTCTG  
CACCCAGCCTGCCCCGCCACACCATCCTGCTGGTCCTCCAGCGCTGCTGTTGCACCTGTGAG  
CCCCACCAGACTCATTTGTAAATAGCGCTCCTTCCTCCCCTCTCAAATACCCTTATTTTATTT  
ATGTTTCTCCCAATAAAAAACCAGCCTGTGTGCCAGCTGAAAAAAAAAAAAAAAAAAAA

## **FIGURE 222**

MRRPAAVPLLLLLLFCFGSQRAKAATACGRPRMLNRMVGGQDTQEGEWPWQVSIQRNGSHFCGGS  
LIAEQWVLTAAHCFRNTSETSLYQVLLGARQLVQPGPHAMYARVRQVESNPLYQGTASSADVA  
LVELEAPVPFTNYILPVCLPDPSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKLAVPIIDTP  
KCNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSGGPLVCLVGQSWLQAGVISWGEG  
CARQNRPGVYIRVTAHHNWIHRIIPKLQFQPARLGGQK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**N-glycosylation sites.**

amino acids 55-58, 79-82

**Casein kinase II phosphorylation sites.**

amino acids 121-124, 165-168, 167-170, 248-251

**Tyrosine kinase phosphorylation sites.**

amino acids 78-86, 197-203

**N-myristoylation sites.**

amino acids 16-21, 37-42, 56-61, 62-67, 118-123

**Amidation site.**

amino acids 219-222

**Serine proteases, trypsin family, histidine active site.**

amino acids 71-76

**FIGURE 223**

CAAGATGTGGACAGCTCTTGTGCTCATTTGGATTTTCTCCTTGTCCTTATCTGAAAGCCATGC  
GGCATCCAACGATCCACGCAACTTTGTCCCTAACAAAATGTGGAAGGGATTAGTCAAGAGGAA  
TGCATCTGTGGAAACAGTTGATAATAAAACGTCTGAGGATGTAACCATGGCAGCAGCTTCTCC  
TGTCACATTGACCAAAGGGACTTCGGCAGCCACCTCAACTCTATGGAAGTCACAACAGAGGA  
CACAAGCAGGACAGATGTGAGTGAACCAGCAACTTCAGGAGTTGCAGCTGATGGTGTGACCTC  
CATTGCTCCACGGCTGTGGCCTCCAGTACGACTGCGGCCTCCATTACGACTGCGGCCTCCAG  
TATGACTGTGGCCTCCAGTGTCTCCACGACTGCAGCCTCCAGTACAACCTGTGGCCTCCATTGC  
TCCCACGACTGCAGCCTCCAGTATGACTGCGGCCTCCAGCACTCCCATGACACTTGCCTCCC  
CGCGCCACGTCCACTTCCACAGGGCGGACCCCGTCCACTACCGCCACTGGGCATCCATCTCT  
CAGCACAGCCCTCGCACAAAGTGCCAAAGAGCAGCGGTTGCCAAGAACAGCAACCCTGGCCAC  
ATTGGCCACACGTGCTCAGACTGTAGCGACCACAGCAAACACAAGCAGCCCCATGAGCACTCG  
TCCAAGTCCTTCCAAGCACATGCCCAGTGACACCGCGGCAAGCCCTGTACCCCCCTATGCGTCC  
CCAAGCACAAGGTCCCATTAGCCAGGTGTCAGTGGACCAGCCTGTGGTTAACACAACAAATAA  
ATCCACACCCATGCCCTCAAACACAACCCAGAGCCCGCCCCACCCCCACAGTGGTGACCAC  
CACCAAGGCACAAGCCAGGGAGCCAACTGCCAGCCAGTGCCAGTACCTCACACCAGCCCAAT  
CCCTGAGATGGAGGCCATGTCCCCACGACACAGCCAAGCCCCATGCCATATACCCAGAGGGC  
CGCTGGGCCAGGCACATCCCAGGCACCGGAGCAGGTAGAGACTGAAGCCACACCAGGTACTGA  
TTCCACTGGGCCAACACCCAGGAGCTCAGGGGGCACTAAGATGCCAGCCACGGACTCGTGCCA  
GCCCAGCACCCAAGGCCAGTACATGGTGGTCACCACTGAGCCCCCTCACCCAGGCCGTGGTAGA  
CAAACTCTCCTTCTGGTGGTGCTGTTACTCGGGGTGACCCTTTTCATCACAGTCTTGGTTTT  
GTTTGCCCTGCAGGCCTATGAGAGCTACAAGAAGAAGGACTACACCAGGTGGACTACTTAAT  
CAACGGGATGTATGCGGACTCAGAAATGTGAGGGGGGCGGGGGCCTGGCGGGAGGCCTGGCCC  
CTTCCTCGTCCTTTTCTTTTGCCTTTGAGACCAAACCAAGTGCTTCCAAATTCTTTTGGTGCA  
ATTGAGGAGATATGCCAGATGCTTAAACACATTTAATTGCTGTCAGATTAATTCCATGATCAC  
TAAAGAGTTGCTGCTTTTTTTCATATTTATTTTTGTAAATGATTCTGTGCCAGGAGCAGCTGG  
GGGTTCCACCTCAGGGTGGGGCGGGCAGGACCCCGTCTCCCCAGGTGTGCGAGCCTGACCTGA  
ATTAAAGTACTGACTGCTCGCCA

**FIGURE 224**

MWTALVLIWIFSLSLSESHAASNDPRNFVPNKMWKGLVKRNASVETVDNKTSSEDTMAAASPV  
TLTKGTSAAHLNSMEVTTEDTSRTDVSEPATSGVAADGVTSIAPTAVASSTTAASITTAASSM  
TVASSAPTTAASSTTVASIAPTTAASSMTAASSTPMTLALPAPTSTSTGRTPSTTATGHPSLS  
TALAQVPKSSALPRTATLATLATRAQTVATTANTSSPMSTRPSPSKHMPSDTAASPVPMPRPQ  
AQGPISQVSVDQPVVNTTNKSTPMPSNTTPEPAPTPTVVTTTKAQAREPTASPVFPVPHTSPI  
EMEAMSPTTQPSPMPYTQRAAGPGTSQAPEQVETEATPGTDSTGPTPRSSGGTKMPATDSCQP  
STQGQYMVVTTEPLTQAVVDKTLTLLVLLLVLTGVTLFITVLVLFALQAYESYKKKDYTQVDYLIN  
GMYADSEM

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 396-420

**N-glycosylation sites.**

amino acids 41-44, 49-52, 222-225, 268-271, 271-274

**Casein kinase II phosphorylation sites.**

amino acids 14-17, 51-54, 80-83, 85-88, 280-283, 434-437

**N-myristoylation sites.**

amino acids 68-73, 354-359

**Aldo/keto reductase family putative active site signature.**

amino acids 195-210

**FIGURE 225**

GGAAAGGCGCTCAAGGTGCGCGCGGCCCGGGGCGCGCTACTTGGGGGCGCCCTCCGCGGTGGGCAGC  
GCGCCAGGGATCGGCCTGGGCAGCCGCGGGGCGCGCAAGGCTGCGCTTTCCCTACGGCCCCC  
CTCGCTTCTCTCCGGCACGGCGGCAACGGAGATTTCTCTCGGGGAAACTACGCGGATCCTTTT  
CGGGGATCCTCGCCCCGCCCCAGTTCTCCGCCCCCTCCCCCTTTGCTGGGGCGCCTGGGCTGGC  
CCGCGCAGGGGAGGAGGCTCTGGCAGCCTGGGCAGGGAGGCGGCGGGGGGCCGCGGAGCCGCT  
GGCCATCGATTCTCCCCGCCATGTGACGCCGTCTTAGCCCTGCGACCCCCAGCGCGTCCCCG  
GCCTGCGCCTCCGCCCCGCGCGCAGCGCACGATGCTTCTGCCGGGACGCGCACGCCAACCGC  
CGACGCCCCAGCCCGTGAGCATCCCGGCCTCCGCCGGCAGGTAGAGCCGCCGGGGCAGCTCC  
TGCGCCTCTTCTACTGCACTGTCTGGTCTGCTCCAAAGAGATCTCAGCGCTCACCAGCTTCT  
CTGGTTACCTAACCAAACCTCTGCAAAACCACACCCTATGCCTGTGATGGGGACTATTTGA  
ATCTACAGTGCCCTCGGCATTCTACGATAAGTGTCCAATCGGCATTTTATGGGCAAGATTACC  
AAATGTGTAGTTCCAGAAAGCCTGCCTCCAGAGGGAAGACAGCTTAACCTGTGTGGCAGCCA  
CCACCTTCCAGAAGGTGCTGGACGAATGCCAGAACCAGCGGGCCTGCCACCTCCTGGTCAATA  
GCCGTGTTTTTGGACCTGACCTTTGTCCAGGAAGCAGTAAATACCTCCTGGTCTCCTTTAAAT  
GCCAACCTAATGAATTAATAAAACAAAACCGTGTGTGAAGACCAGGAGCTGAAACTGCACTGCC  
ATGAATCCAAGTTCTCAACATCTACTCTGCGACCTACGGCAGGAGGACCCAGGAAAGGGACA  
TCTGCTCCTCCAAGGCAGAGCGGCTCCCCCTTTTCGATTGCTTGTCTTACTCAGCTTTGCAAG  
TCCTATCCCGAAGGTGCTATGGGAAGCAGAGATGCAAAATCATCGTCAACAATCACCATTTTG  
GAAGCCCCTGTTTGGCAGGCGTGAAAAATACCTCACTGTGACCTACGCATGTGTTCCCAAGA  
ACATACTCACAGCGATTGATCCAGCCATTGCTAATCTAAAACCTTCTTTGAAGCAGAAAGATG  
GTGAATATGGTATAAACTTCGACCCAAGCGGATCGAAGGTTCTGAGGAAAGATGGAATTCTTG  
TTAGCAACTCTCTGGCAGCCTTTGCTTACATTAGAGCCACCCAGAGAGAGCTGCCCTGCTGT  
TCGTGTCCAGTGTCTGCATCGGCCTGGCCCTCACACTGTGCGCCCTGGTCATCAGAGAGTCTC  
GTGCCAAGGACTTCCGCGACTTGCGAGCTGGGGAGGGAGCAGCTGGTGCCAGGAAGTGACAAGG  
TCGAGGAGGACAGCGAGGATGAAGAAGAGGAGGAGGACCCCTCTGAGTCTGATTTCCCAGGGG  
AACTGTGCGGGTCTGTAGGACTTCATATCCTATATACAGTTCCATAGAAGCTGCAGAGCTCG  
CAGAAAGGATTGAGCGCAGGGAGCAAATCATTCAGGAAATATGGATGAACAGTGGTTTGGACA  
CCTCGCTCCCAAGAAACATGGGCCAGTTCTACTGAAACCACATGCATCTTGATGCGATCGCA  
CTTTCTGAAGAAGGAAGGATCCCAAATGCCCTCCAGTTCTGGTTACCTGTACCTTCTATGA  
AGGAGAATTCGTGATGTCATTCAACACTCGTGAGGCCAGGAAGCTATTAAAGGGATGTTTCAA  
GCTGTTTTCTAGCACATTCAAAATAAATGAGGAGGGAGGAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAA

**FIGURE 226**

MLLPGRARQPPTPQPVQHPGLRRQVEPPGQLLRIFYCTVLVCSKEISALTDGSGYLTKLLQNH  
TTYACDGDYLNQLQCPRHSTISVQSAFYGQDYQMCSSQKQPASQREDSLTCAATTFOKVLDECQ  
NQRACHLLVNSRVFGPDLCPGSSKYLIVSFKCQPNELKNKTVCEDQELKLHCHESKFLNIYSA  
TYGRRQTQERDICSskaerLPPFDCLSYSALQVLSRRCYGKQQRCKIIVNNHHFGSPCLPGVKKY  
LTVTYACVPKNILTAIDPAIANLKPSLKQKDGEYGINFDPGSKVLRKDGILVSNSLA AFAYI  
RAHPERAALLFVSSVCIGLALTLCALVIRESCAKDFRDLQLGREQLVPGSDKVEEDSEDEEEEE  
EDPSESDFPGELSGFCRTSYPIYSSIEAAELAERIERREQIIQEIWMNSGLDTS LPRNMGQFY

**Transmembrane domains:**

amino acids 32-49, 322-343

**N-glycosylation sites.**

amino acids 62-66, 165-169

**Tyrosine kinase phosphorylation site.**

amino acids 280-287

**N-myristoylation site.**

amino acids 302-308, 333-339, 428-434

**Amidation site.**

amino acids 191-195



**FIGURE 227**

GGCACGAGGTGGAAGGGCTTTTACAAACAGATTGCTGGCCCCACCCCCAGAATTTCTCATCA  
GGAGTGGGCAAGACCAATCATTTGCATTTCTGACAAGTTCCCAGGAGCTGCAGCTGCTGGCCC  
TGGAACCACACTTTGAGAACCACTGCTTTAGACCAAACACCAAAGGAAGATGCAGCCACCCTC  
CTTTACATGTCACAACGCTCAGGGTCCATGAGTACCTCAGGCTGTCCAGCTGAGCTCCACCTG  
CAGCAGCCGAGATTCCCGACTCGCTCCACCATTGGGGGCTAGGAGTGAAGCGTGTCA~~CC~~ATGG  
TCAGCTCATGGCCAGCCAGGAAAGCCTCTCTGCTGTGCGTCTGTGCAGTTCTTGTTCTTCCCT  
GGAGGACTCTTGATCGCCTGTGATCTTGGCCAGGAGACCAGGTGCCTGGGTCCCTTCCTGGA  
AGGGGACAAGTTACACACCCCAGCCCCATTTTCCCACCAACTTCTACATGCCTTGGGAGAACC  
TTCTACATGTTGGCTGCCCCCTTCCCTATTTTCAGCAGTGCCAGTCCTGCTTATAAACCTGA  
GGCCTGCTCCCCATACCTTCCCTGTGCAAGTGCCAGCCGTTATTCCAGGCAGCCCAATGTTGT  
TGAGGCCAGATGGATTCTGGAAGCAGCTGGCCCATGGATGTGAGTGCATCACAGTATTCTAGA  
AACAGAGAAGAGGCTTTAACCTAATGCGCATAGAGAAATTGTTCTCATTGTAAACATACCCCT  
GTCCTTAGCTGATCTAGGTGGAAGCCCAGCTTCATGTGCTAGGGGGCATGATAATGATAATAA  
AGGAATTGTATCTAGGACTAA

**FIGURE 228**

MVSSWPARKASLLCVCAVLVLPWRTLGSPPVILARRPGAWVPSWKGTSYTPQPHFPTNFYMPWE  
NLLHVGCPPLPLFQQCPVLLINLRPAPHTFPVQVPAVIPGSPMLLRPDGFLEAAGPWM

**Signal peptide:**

amino acids 1-27

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 8-12

# **FIGURE 229**

GGGAAGGGATGCAAGGAAGCCCTCCGGCGCTGCGCTCCGAGGCGGGAGACAGCGTCCCGCTGA  
AAATGTGTGTCTGACATGCAAGCTCAGTGGGGCAGAGACCCGTGGATTGCTGTGCCCTGCCCT  
CCGGACCTGGATCATGAAGGTGTTGGGAAGAAGCTTCTTCTGGGTGCTGTTTCCCGTCTTTCC  
CTGGGCGGTGCAGGCTGTGGAGCACGAGGAGGTGGCGCAGCGTGTGATCAAACCTGCACCGCGG  
GCGAGGGGTGGCTGCCATGCAGAGCCGGCAGTGGGTCCGGGACAGCTGCAGGAAGCTCTCAGG  
GCTTCTCCGCCAGAAGAATGCAGTTCTGAACAACTGAAAACCTGCAATTGGAGCAGTGGAGAA  
AGACGTGGGCCTGTCCGATGAAGAGAACTGTTTCAGGTGCACACGTTTGAAATTTTCCAGAA  
AGAGCTGAATGAAAGTGAAAATTCGGTTTTCCAAGCTGTCTACGGAAGTGCAGAGAGCCCTGCA  
GGGGGATTACAAAGATGTCGTGAACATGAAGGAGAGCAGCCGGCAGCGCCTGGAGGGCCCTGAG  
AGAGGCTGCAATAAAGGAAGAAACAGAATATATGGAACCTTCTGGCAGCAGAAAAACATCAAGT  
TGAAGCCCTTAAAAATATGCAACATCAAAACCAAAGTTTATCCATGCTTGACGAGATTCTTGA  
AGATGTAAGAAAGGCAGCGGATCGTCTGGAGGAAGAGATAGAGGAACATGCTTTTGACGACAA  
TAAATCAGTCAAGGGGTCAATTTTGAGGCAGTTCTGAGGGTGGAGGAAGAAGAGGCCAATTC  
TAAGCAAAATATAACAAACGAGAAGTGGAGGATGACTTGGGTCTTAGCATGCTGATTGACTC  
CCAGAACAAACAGTATATTTTGACCAAGCCCAGAGATTCAACCATCCCACGTGCAGATCACCA  
CTTTATAAAGGACATTGTTACCATAGGAATGCTGTCTTGCCTTGTGGCTGGCTATGTACAGC  
CATAGGATTGCCTACAATGTTTGGTTATATTTTGTGGTGTACTTCTGGGACCTTCAGGACT  
AAATAGTATTAAGTCTATTGTGCAAGTGGAGACATTAGGAGAATTTGGGGTGTTTTTTACTCT  
TTTTCTTGTGGCTTAGAATTTTCTCCAGAAAAGCTAAGAAAGGTGTGGAAGATTTCTTTACA  
AGGGCCGTGTTACATGACACTGTTAATGATTGCATTTGGCTTGCTGTGGGGGCATCTCTTGCG  
GATCAAAACCCACGCAGAGCGTCTTCATTTCCACGTGTCTGTCTTGTCAAGCACACCCCTCGT  
GTCCAGGTTCTCATGGGCAGTGCTCGGGGTGACAAAGAAGGCGACATTGACTACAGCACCCGT  
GCTCCTCGGCATGCTGGTGACGCAGGACGTGCAGCTCGGGCTCTTCATGGCCGTCATGCCGAC  
TCTCATACAGGCGGGCGCCAGTGCATCTTCTAGCATTGTCTGTGGAAGTTCTCCGAATCCTGGT  
TTTGATTGGTCAGATTCTTTTTCTACTAGCGGCGGTTTTTCTTTTATGTCTTGTATATAAGAA  
GTATCTCATTTGAGCCCTATTATCGGAAGCTGCACATGGAAGCAAGGGGAACAAAGAAATCCT  
GATCTTGGGAATATCTGCCTTTATCTTCTTAATGTTAACGGTCACGGAGCTGCTGGACGTCTC  
CATGGAGCTGGGCTGTTTTCTGGCTGGAGCGCTCGTCTCCTCTCAGGGCCCCGTGGTCACCGA  
GGAGATCGCCACCTCCATCGAACCCATCCGCGACTTCCTGGCCATCGTTTTCTTCGCCTCCAT  
AGGGCTCCACGTGTTCCCCACGTTTGTGGCGTACGAGCTCACGGTGCTGGTGTTCTCTCACCTT  
GTCAGTGGTGGTGATGAAGTTTCTCCTGGCGGCGCTGGTCTGTCTCTCATCTGCCCAGGAG  
CAGCCAGTACATCAAGTGGATCGTCTCTGCGGGGCTTGCCAGGTGACCGAGTTTCTTTTGT  
CCTGGGGAGCCGGGCGCGAAGAGCGGGCGTCATCTCTCGGGAGGTGTACCTCCTTATACTGAG  
TGTGACCACGCTCAGCCTCTTGCTCGCCCCGCTGCTGTGGAGAGCTGCAATCACGAGGTGTGT  
GCCCAGACCGGAGAGACGGTCCAGCCTCTGATGGCTCGGAGATGATGGACCGTGGAAGGGAAG  
CGTCTGTGGGGAGTGAGCGCTTAGATGGCCAGCAGCTGCTCCTTCTGGGAAGCTCGCACCTTG  
GCAACAGAACAGCCCTCTAGCAGAGCGTCAGTGCAGTCTGTATATCCCGGCTTTTACAGAATA  
TTCTTGTCTATTTTAGAATTTTCCGGAGTAGTTTATTTGCAGTCTGTTGATTATGTGCAGTA  
GACCCGGGACACTGCGTTTTACCGATCACCTTGAATGTGGTGCCTGGATGTGCCTTTTTTTTT  
TTTCCCTGAAATTATTATTAATTTTCTATTGTGAGTTCATCAGTTCATAGTTTTTTTAGTAAA  
GAAGCAAAATTAAAGGCTTTTAAAAATGTACAACCTCAGAATTATAATCTGTTAGTCAAATA  
TTTGTTATTAACATTTCTGTAATATGAAGTTGTAATCCTGGCCGTGAGCTTGGGAAGCTTACT  
TTTGATTCTTAAAGCCTATGTTTTCTAAAAATGAGACAAATACGGATGTCTATTGCTTTTTAT  
TGTAACTTTTAAATGAAATAATTTTATGTCAATTTCTATTAGATATATCACTTAAATATTTG  
GTTTTAAATCACAAGAATATGTATTCTTTAATAAAGATAATTTATGATCATGGTAAAAAAAAA

**FIGURE 230**

MKVLGRSFFWVLPFVLPWAVQAVEHEEVAQRVIKLRGRGVAAMQSRQWVRDSCRKLSGLLRQ  
KNAVLNKLKTAIGAVEKDVGLSDEEKLFQVHTFEIFQKELNESENSVFQAVYGLQRALQGDYK  
DVVNMKESSRQRLEALREAAIKEETEFYMELLAAEKHQVEALKNMQHQNQSLSMLEILEDVRK  
AADRLEEEIEEHAFDDNKS VKGVNFEAVLRVEEEEANSKQNITKREVEDDLGLSMLIDSQNNQ  
YILTKPRDSTIPRADHHFIKDIVTIGMLSLPCGWLCTAIGLPTMFGYIICGVLLGPSGLNSIK  
SIVQVETLGEFGVFFTLFLVGLLEFSPEKLRKVWKISLQGPCYMTLLMIAFGLLWGHLLRIKPT  
QSVFISTCLSLSSTPLVSRFLMGSARGDKEGDIDYSTVLLGMLVTQDVQLGLFMAVMPTLIQA  
GASASSIVVEVLRLVLIGQILFSLAAVFLCLVIKKYLIGPYRKLHMESKGNKEILILGI  
SAFIFLMLTVTELLEDVSMELGCFLAGALVSSQGPVVTEEIATSIEPIRDFLAIVFFASIGLHV  
FPTFVAYELTVLVFLTLVVMKFLAALVLSLILPRSSQYIKWIVSAGLAQVSEFSFVLGSR  
ARRAGVISREVYLLILSVTTLSLLLAPVLWRAAITRCVPRPERRSSL

**Signal peptide:**

amino acids 1-22

**Transmembrane domains:**

amino acids 282-304, 322-337, 354-370, 379-395, 445-474, 501-520,  
576-598, 641-660

**N-glycosylation sites.**

amino acids 104-108, 174-178, 206-210, 230-234

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 55-59, 673-677

**Tyrosine kinase phosphorylation site.**

amino acids 407-414

**N-myristoylation sites.**

amino acids 116-122, 327-333, 366-372, 401-407, 419-425, 429-435,  
442-448, 525-531, 530-536

**Cell attachment sequence.**

amino acids 404-407

**FIGURE 231**

GAGAAAAACAACAGGAAGCAGCTTACAAACTCGGTGAACAACTGAGGGAACCAAACCAGAGAC  
GCGCTGAACAGAGAGAATCAGGCTCAAAGCAAGTGGAAGTGGGCAGAGATTCCACCAGGACTG  
GTGCAAGGCGCAGAGCCAGCCAGATTTGAGAAGAAGGCAAAAAGATGCTGGGGAGCAGAGCTG  
TAATGCTGCTGTTGCTGCTGCCCTGGACAGCTCAGGGCAGAGCTGTGCCTGGGGGCAGCAGCC  
CTGCCTGGACTCAGTGCCAGCAGCTTTTACAGAAGCTCTGCACACTGGCCTGGAGTGCACATC  
CACTAGTGGGACACATGGATCTAAGAGAAGAGGGAGATGAAGAGACTACAAATGATGTTCCCC  
ATATCCAGTGTGGAGATGGCTGTGACCCCCAAGGACTCAGGGACAACAGTCAGTTCTGCTTGC  
AAAGGATCCACCAGGGTCTGATTTTTTTATGAGAAGCTGCTAGGATCGGATATTTTACAGGGG  
AGCCTTCTCTGCTCCCTGATAGCCCTGTGGGCCAGCTTCATGCCTCCCTACTGGGCCCTCAGCC  
AACTCCTGCAGCCTGAGGGTCACCACTGGGAGACTCAGCAGATTCCAAGCCTCAGTCCCAGCC  
AGCCATGGCAGCGTCTCCTTCTCCGCTTCAAAATCCTTCGCAGCCTCCAGGCCTTTGTGGCTG  
TAGCCGCCCGGGTCTTTGCCCATGGAGCAGCAACCCTGAGTCCCTTAAAGGCAGCAGCTCAAGG  
ATGGCACTCAGATCTCCATGGCCCAGCAAGGCCAAGATAAATCTACCACCCAGGCACCTGTG  
AGCCAACAGGTTAATTAGTCCATTAATTTTAGTGGGACCTGCATATGTTGAAAATTACCAATA  
CTGACTGACATGTGATGCTGACCTATGATAAGGTTGAGTATTTATTAGATGGGAAGGAAATT  
TGGGGATTATTTATCCTCCTGGGGACAGTTTGGGGAGGATTATTTATTGTATTTATATTGAAT  
TATGTACTTTTTTCAATAAAGTCTTATTTTTGTGGCTAAAAAAAAAAAAA

## **FIGURE 232**

MLGSRAVMLLLLLPWTAAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEGDEE  
TTNDVPHIQCGDGCDDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSPVGQLHA  
SLLGLSQLLQPEGHHWETQQIPSLSPSQPWQRLLLRFKILRSLQAFVAVAAARVFAHGAATLSP

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Casein kinase II phosphorylation site.**

amino acids 64-67

**N-myristoylation sites.**

amino acids 25-30, 81-86, 122-127

**FIGURE 233**

CCCACGCGTCCGGCCCTGTAAACCAAGATACTGACTGAACATGGCTGGCGGACTCAGGCTGGGGTCTGCAGTGCAG  
 CATTAAATGGGCGCTGCATGAATATGGAGTAGTTTTCTCTAGCAAAGAGTAATGTGGGCCATGGAGTCAGGCCA  
 CCTCCTCTGGGCTCTGCTGTTTCATGCAGTCTCTTGGCCCTCAACTGACTGATGGAGCCACTCGAGTCTACTACCT  
 GGGCATCCGGGATGTGCAGTGGAACTATGCTCCCAAGGGAAGAAATGTCATCACGAACCAGCCTCTGGACAGTGA  
 CATAGTGGCTTCCAGCTTCTTAAAGTCTGACAAGAACCGGATAGGGGGAACCTACAAGAAGACCATCTATAAAGA  
 ATACAAGGATGACTCATACACAGATGAAGTGGCCAGCCTGCCTGGTGGGCTTCTGGGGCCAGTGTTCAGGC  
 TGAAGTGGGGGATGTCTTCTTATTCACCTGAAGAATTTTGGCACTCGTCCCTATACCATCCACCCCTCATGGTGT  
 CTTCTACGAGAAGGACTCTGAAGGTTCCCTATACCAGATGGCTCCTCTGGGCCACTGAAAGCTGATGACTCTGT  
 TCCCCCGGGGGGAGCCATATCTACAACCTGGACCATTCAGGAAGGCCATGCACCCACCGATGCTGACCCAGCGTG  
 CCTCACCTGGATCTACCATTCTCATGTAGATGCTCCACGAGACATTGCAACTGGCCTAATTGGGCTCTCATCAC  
 CTGTAAAAGAGGAGCCCTGGATGGGAACCTCCCTCCTCAACGCCAGGATGTAGACCATGATTTCTTCTCCTCTT  
 CAGTGTGGTAGATGAGAACCTCAGCTGGCATCTCAATGAGAACATTGCCACTTACTGCTCAGATCCTGCTTCAGT  
 GGACAAAGAAGATGAGACATTTCAGGAGAGCAATAGGATGCATGCAATCAATGGCTTTGTTTTGGGAATTTACC  
 TGAGCTGAACATGTGTGCACAGAAACGTGTGGCCTGGCACTTGTTTGGCATGGGCAATGAAATTGATGTCCACAC  
 AGACTTTTTCATGGACAGATGCTGACTACCCGTGGACACCACACTGATGTGGCTATTTCCAGCCACTT  
 TGTGACTGCTGAGATGGTGGCCTGGGAACCTGGTACCTGGTTAATTAGCTGCCAAGTGAACAGTCACTTTGAGA  
 TGGCATGCAGGCACTCTACAAGGTCAAGTCTTGCTCCATGGCCCTCCTGTGGACCTGCTCACAGGCAAGTTCG  
 ACAGTACTTCAATGAGGCCCATGAGATTCAATGGGACTATGGCCGATGGGGCATGATGGGAGTACTGGGAAGAA  
 TTTGAGAGAGCCAGGCTGATCTCAGATAAGTTTTCCAGAAGAGCTCCAGCCGAATTGGGGGCACTTACTGGAA  
 AGTGCATATGAAGCCTTTCAAGATGAGACATTCAGAGAAGATGCATTTGGAGGAAGATAGGCATCTTGGAAAT  
 CCTGGGGCCAGTGTATCCGGGCTGAGGTGGGTGACACCATTCAGGTGGTCTTCTACAACCGTGCCTCCAGCCATT  
 CAGCATGCAGCCCATGGGGTCTTTTATGAGAAAGACTATGAAGGCATGTGTACATGATGGCTCATCTTACCC  
 TGGCTTGGTTTGGCAAGCCCTTTGAGAAAGTAACATACCGCTGGACAGTCCCCCTCATGCCGCTCCACTGCTCA  
 GGATCTGCTTGTCTCACTTGGATGTACTTCTCTGCTGCAGATCCCATAGAGACACAAATCTGGCCTGGTGGG  
 CCGCTCTCTGGTGTGCAGGCTGGTGCCTTGGGTGCAGATGGCAAGCAGAAAGGGTGGATAAAGAATTTCTTCT  
 TCTCTTCACTGTGGATGAGAACAGAGCTGGTACAGCAATGCCAATCAAGCAGCTGATGTGGATTTCCG  
 ACTGCTTTCAGAGGATATTGAGGGCTTCCAAGACTCCAATCGGATGCATGCCATTAATGGGTTTCTGTCTCTAA  
 CCTGCCAGGCTGGACATGTGCAAGGGTGACACAGTGGCCTGGCACCTGCTCGGCTGGGCACAGAGACTGATGT  
 GCATGGAGTCACTTCCAGGGCAACACTGTGCAGCTTCAGGGCATGAGGAAGGGTGCAGCTATGCTCTTCTCTCA  
 ATACAAGAAAGCTGTATTTCAGGGAATACACTGATGGTACATTCAGGATCCCTCGGCCAAGGATGGACAGAGA  
 ACACTTGGGAATCTTGGTCCACTTATCAAAGGTGAAGTTGGTGATATCTGACTGTGGTATTCAAGAATAATGC  
 CAGCCGCCCTACTCTGTGCATGCTCATGGAGTGTAGAACTACTACTGTCTGGCCACTGGCTGCTGAGCCTGG  
 TGAGGTGGTCACTTATCAGTGGAAACATCCCAGAGAGGTCTGGCCCTGGGCCCAATGACTCTGCTTGTGTTTCTG  
 GATCTATTATTCTGCAGTGGATCCCATCAAGGACATGTATAGTGGCTGGTGGGGCCCTTGGCTATCTGCCAAAA  
 GGGCATCTCGAGCCCATCGGAGGACGGAGTGACATGGATCGGGAATTTGCATTGTTGTTCTTGATTTTGTATGA  
 AAATAAGTCTTGTATTGAGGGAATGTGGCAACCCATGGGTCCAGGATCCAGGCAGTATTAACTACAGGA  
 TGAACTTTCTTGGAGAGCAATAAATGATGCAATCAATGGGAACTCTATGCCAACCTTAGGGGTCTTAGCAT  
 GTACCAAGGAGAACGAGTGGCTGGTACATGCTGGCCATGGGCCAAGATGTGGATCTACACACCATCCACTTTCA  
 TGCAGAGAGCTTCTCTATCGGAATGGCGAGAACTACCGGCAGATGTGGTGGATCTGTTCCAGGGACTTTTGA  
 GGTGTGGAGATGGTGGCCAGCAACCTGGGACATGGCTGATGCACTGCCATGTGACTGACCATGTCCATGCTGG  
 CATGGAGACCTCTTCACTGTTTTTCTCGAACAGAACACTTAAGCCCTCTCACCGTCATCACCAAGAGAGCTGA  
 AAAAGTGGCCCCCAGAGACATTGAAGAAGGCAATGTGAAGATGCTGGGCATGCAGATCCCCATAAAGAATGTTGA  
 GATGCTGGCCTCTGTTTTGGTTGCCATTAGTGTACCCCTTCTGCTCGTTGTTCTGGCTCTTGGTGGAGTGGTTG  
 GTACCAACATCGACAGAGAAAGCTACGACGCAATAGGAGGTCCATCTGGATGACAGCTTCAAGCTTCTGTCTTT  
 CAAACAGTAAACATCTGGAGCCTGGAGATATCCTCAGGAAGCACATCTGTAGTGCACTCCAGCAGGCCATGGACT  
 AGTCACTAACCCCACTCAAAGGGGCATGGGTGGTGGAGAAGCAGAAGGAGCAATCAAGCTTATCTGGATATTT  
 CTTTCTTTATTTATTTTACATGGAATAATATGATTTCACTTTTTCTTAGTTTCTTTGCTCTACGTGGGCACCT  
 GGCACTAAGGGAGTACCTTATTATCTACATCGCAATTTCAACAGCTACATTATATTTCTTCTGACACTTGGGA  
 AGGTATTGAAATTTCTAGAAATGTATCCTTCTCACAAAGTAGAGACCAAGAGAAAACTCATTGATTGGGTTTCT  
 ACTTCTTTCAAGGACTCAGGAATTTCACTTTGAAGTGAAGGCAAGTGAAGTGTGTTAAGATAACCCCACTTAAAC  
 TAAAGGCTAAGAAATATAGCTTGTAGGGAATGAAGGTAGGCTGAGTATTGGGAATCCAAATTGAATTTTGATT  
 CTCCTTGGCAGTGAACACTTTGAAGAAGTGGTCAATGGGTTGTTGCTGCCATGAGCATGTACAACCTCTGGAGC  
 TGAAGCTCCTCAGGAAAGCCAGTTCTCCAAGTTCTTAACCTGTGGCACTGAAAGGAATGTTGAGTTACCTCTTC  
 ATGTTTTAGACAGCAACCCATCCATTAAAGTACTTGTAGACCAAAAAAAAAAAAA

**FIGURE 234**

MWAMESGHLLWALLFMQSLWPQLTDGATRVYYLGIRDVQWNYAPKGRNVITNQPLDSDIVASS  
FLKSDKNRIGGTYKKTIYKEYKDDSYTDEVAQPAWLGFLGPVLQAEVGDVILIHLLKNFATRPY  
TIHPHGVPFYEKDSEGSLLYPDGSSGGLKADDSVPPGGSHIYNWTIPEGHAPTADAPACLTWIIYH  
SHVDAPRDIATGLIGPLITCKRGALDGNSPQQRQDVHDFFLLFSVVDENLSWHLNENIATYC  
SDPASVDKEDETFQESNRMHAINGFVFGNLPELNMCAQKRVAVHLLFGMGNEIDVHTAFFHGM  
LTTRGHHTDVANIFPATFVTAEMVPWEPGTWLISCQVNSHFRDGMQALYKVKSCSMAPPVDLL  
TGKVRQYFIEAHEIQWDYGPMDHGDSTGKNLREPGSISDKFFQKSSSRIGGTYWKVRYEAFQD  
ETFQEKMHLEEDRHLGILGPVIRAEVGDITQVVFYNRASQPFMSQPHGVFYEKDYEGTVYNDG  
SSYPGLVAKPFEKVITYRWTPPHAGPTAQDPACLTWMYFSAADPIRDTNSGLVGPLLVCRA  
LGADGKQKGVDKFEFFLLFTVLDENKSWYSNANQAAAMLDFFRLLEDIEGFQDSNRMHAINGFL  
FSNLPRLDCKGDTVAVHLLGLGTETDVHGVMFQGNVQLQGMRKGAAMLFPHTFVMAIMQPD  
NLGTFEIIYQAGSHREAGMRAIYNVSQCPCGHQATPRQRYQAARIYYIMAEVEWDYCPDRSWE  
REWHNQSEKDSYGYIFLSNKDGLLGSRYKAVFREYTDGTFRIIPRPTGPPEHLGILGPLIKG  
EVGDILTUVFKNNASRPYSVHAHGVLESTTVWPLAAEPGEVVITYQWNIPERSGPGPNDSACVS  
WIYYSADVPIKDMYSGLVGPLAICQKGILEPHGGRSDMDREFALLFLIFDENKSWYLEENVAT  
HGSQDPGSINLQDETFLSNKMHAINGKLYANLRGLTMYQGERVAWYMLAMQDQDVLHTIHFH  
AESFLYRNGENYRADVDLFPGTFEVVEMVASNPGTWLMHCHVTDHVHAGMETLFTVFSRTEH  
LSPLTVITKETEKVPPRDIEEGNVKMLGMQIPIKNVEMLASVLVAISVTLLLVVLALGGVVWY  
QHRQKRLRRNRRSILDDSFKLLSFKQ

**Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 1109-1130

**N-glycosylation sites.**

amino acids 167-171, 239-243, 591-595, 717-721, 761-765, 832-836,  
876-880, 934-938

**Glycosaminoglycan attachment site.**

amino acids 871-875

**Tyrosine kinase phosphorylation sites.**

amino acids 82-90, 137-145, 494-502, 513-521

**N-myristoylation sites.**

amino acids 212-218, 313-319, 498-504, 566-572, 672-678, 778-784,  
843-849

**Multicopper oxidases signature 1.**

amino acids 344-365, 696-717, 1043-1064

**Multicopper oxidases signature 2.**

amino acids 1048-1060



**FIGURE 235**

GGAAAGAGTGTGGTACTACAACAGGAAGTGACAGATAATGTGCTTTAACTACATTAGAAAAGCTTCTCATAG  
 CAAAAGTGTAGAGATTGAAGCAGTGATTATTTTTACATAGTTGTCATTAAATATTTGGAGCTGTCTGTGCATAGA  
 GATGGCAACATACTTAGAATACACAGCTTTCTGGGCCAGAAATTGATCTTCTGACTTTTGAGCCTTATCTGATTA  
 CTGCTTGGTTTCATCTTTATTTTGTAAACTACTCTGTAGGCTGAAAGGGAGAGACTCTCCTTGGTTTGCAGAGCC  
 TGACTAGACAGGAATTCTGGCAACTGCTCCAGCAGAACTATGGCACTGAGCTAGGTTTAAATGCTGAGGAGATGG  
 AAAACTTGTCTCACTGTCTGATTGAGGATGTGCAGCCAGAAGTCCAGGAAGAAGCAGCTTGGATGACTCTGGGGAGA  
 GAGATGAAAAATTATCCAAGTCAATCAGTTTTACCAGTGAATCAATTAGTCGGGTTTCAGAAAACAGAGTCATTCTG  
 ATGGAAATTTCATCAAAAGGAGGATTAGGCCAAAGAGGAGTCCCAAAATGAGAAAACAGACCAAAAAGAGTCTCTTAC  
 CACTTTGGAAAAGAAGTTAACTAGAGTGCCATCAAAGTCACTGGACTTGAATAAAAATGAATATCTTTCTCTGG  
 ACAAAGCAGCACTTCAGATTCTGTTGATGAAGAAAATGTTCTGAGAAAAGATCTTCATGGAAGACTTTTATATCA  
 ACCGTATTTTTTCATATCAGTGCTGACAGAATGTTTGAATTGCTCTTTACCAGTTCACGCTTTATGCAGAAATTTG  
 CCAGTTCTAGAAATATAATAGATGTAGTATCTACCCCTTGGACTGCAGAACTTGGAGGTGATCAGCTGAGAACGA  
 TGACCTACACTATAGTCCCTTAATAGTCCACTTACTGGAAAATGCACCTGCTGCCACTGAAAAGCAGACACTGTATA  
 AAGAAAGTCGGGAAGCAGGATTTTATTTGGTAGATTTCAGAAGTACTGACACATGATGTCCCTTACCATGATTACT  
 TCTATACCGTGAACAGATACCTGTATCATCCGATCTTCAAAACAGAAATGCAGGCTAAGAGTTTCCACAGATTTGA  
 AATACAGAAAACAGCCATGGGGCCTTGTCAAATCTTAAATTGAAAAGAATTCCTGGAGTTCTTTGGAGGACTATT  
 TCAAAACAGCTTGAATCAGATTTGTTAATTGAAGAATCTGTATTAATCAGGCCATTGAAGACCTGAAAACTTA  
 CTGGCCTACGAAGGAGAAGGCCAACCTTCAACCGAACAGCAGAAACAGTTCTTAACTTTCTCTCAGCATCTCT  
 CTGAGATGTGGGCTTAGGTGCCAAAGGGGATATTACAGGAAAGAAAAGGAAATGGAACCTATAACCTCACTC  
 TTATTGTGGTAATGAGTATTTTTGTGTTGTTATTTAGTTTTGTTGAATGTGACACTGTTTCTGAAGCTGTCAAAGA  
 TAGAATATGCTGCTCAGTCTTTTTACCGTCTCCGCTCCAGAAAGAGAAATCTTAAATTTAGCCTCTGATATGG  
 TGTCAAGAGCAGAACTATTCAGAAGAATAAGATCAGGCCCATCGTTTAAAGGGAGTGCTCCGAGACTCCATAG  
 TGATGCTTGACAGCTGAAGAGCTCACTCATTATGCTTCAGAAAACGTTTGATCTACTAAATAAGAATAAGACTG  
 GCATGGCTGTTGAAAGCTAGTGATCTGAAGGACTAAAACCGCAGAGATACTTGGAACTTAAAGAAAATACCTGGA  
 AGAAAACAGACGAATGAAGGATTTTGGCATAGAACATTTCTATGTTTTTCTATTATTGAGATTTCTAATATGAA  
 CATTTCTTTTCAGTAACATTTATTTGATAATTAGTTTCTGCTGGCCTTAATAATCCATCCTTTCACTTCTTATAGA  
 TATTTTAAAGCTGTGAATTTCTTCAGTGAACCATGAAATATATATAGAATGAAATTTCTCTGATACAAAAGAA  
 AATGACACACCTGAATTGAGTGGTATGGTCTCATTTCTACAGTGAAGTCTGATGCTTTGTTAGCACAGAATCCG  
 TACATGTCCAATAGGTCGCTTTTGTAACTGAGATAAGACCAAGAGGATAAACAGGACAATATAAGAAGAAACCTC  
 TATGTCATTACTGATTTTAAAGGTTCTGTTTTCAGGCATATAACATTTCCAGGTTTGTGTACTGTAAAGATTATA  
 ATGCTTTCATTTATTTAGCATGCAAAATTTAATAGTCAAACTTTTGAATCTGCATGTTGATGATGATTATCAGAA  
 AGGGTCTTCTGCCATGCTGTATCTTTATGAAAGAAATAGTTGTTTTTCTTAAAGTAACTATCAGAGGTGGGATT  
 ATCTTGCCCTCCTCACTTAGAATACCAACAGTCAAAAGGAAGAACCATCCTCTGAGTTTAAAAACAGAGGTTA  
 TGTTAAATCTGGGCATTAGTGACAGATCAATGCATACCTTGAACCTAAGATTGGCTTCAGCTTAGCAGTCTTTC  
 ATGGTGGAAGTGACACATCTGGTTGAAAATAATTTGTGTATTTTTCAGTAACCATGTATGGCTTCTTCTTATGT  
 ATGTGTGTGACTTGTTTTTAATTGGTAAGTTATAAGCCAGACATAGATTTTAGCTCTTTAATAAAAAAATTCAGGGG  
 CACGTATGTCCAGTACAAGTGTACTGACTATCAAGTTTTAACTCAGATGCAAGCTTTGGCTCTTTCATAAAAAG  
 TTTTATGCATATGTGTCTCCATACAAGTGGCTCATTAATAAAGAACTTTGTAACTGACTTAAATCAGATAT  
 TTTTCAAGAGTTAGGGAAAGTTGAAGTGTTTTACTGTTTTGTCTCTTGAGCCCTTCTCTGGGGAAAAAATACA  
 TATCCATCTATCTATCTATATATAAACTGTGTATACATCTTACTGTTTGAACAACATATTGCCTTTAATTAAATG  
 TTTTCAATTTTCTCCAGAGTCCCAAGCCACATGGCATTATTATAGTCATTTTGTAGATGCCTGTAGAGAATGAA  
 AGTATTGACTCCGTTAGAGGGAAATGGGTTTCTCTGGGTGAATTCCAACGAAGCATACCTAGGGGTAACAGTGA  
 ACCTACCTGGGTTTGTGTTTTGTTTGGTAAGGATTTATGTAGTGTCTGGCTGTAAGCAAGAATGAGTGGATTATAA  
 ACTTGAAGATTTCTCTGTAAAGTCACAAAAATGATCGACAAAACATATTTTGTGATGTTTTTAAACGTTGT  
 ATTTTATAACATACTCAAGGAAGAGTATCGAAGTAAGTTGCTTTATAAATTAAGACTAAATTCGTATGGATGCA  
 GAATTCATTAATAAAATTTGAGCCTGTACGTAAATGAATATTAATAAAATTTGAAAATTTCAAAA

**FIGURE 236**

MENLSLSIEDVQPRSPGRSSLDSDGERDEKLSKSI SFTSESISRVS ETESEFDGNSSKGGLGKE  
ESQNEKQTKKSLLPTLEKKLTRVPSKSLDLNKNEYL SLDKSSTSDSVDEENVPEKDLHGRLFI  
NRIFHISADRMFELLFTSSRFMQKFASSRNIIDVVSTPWTAE LGGDQLRTMTYTIVLNSPLTG  
KCTAATEKQTLYKESREARFYLV DSEVLTHDVPYHDYFYTVNRYCIIRSSKQKCRLRVSTD LK  
YRKQPWGLVKSLIEKNWS SLEDYFKQLES DLLIEESVLNQAIEDPGKLTGLRRRRRTFNRTA  
ETVPKLSSQHSSGDVGLGAKGDI TGGKKEMENYNVT LIVVMSIFVLLLVLNVT LFLKLSKIE  
HAAQSFYRLRLQEEKSLNLASDMVSRAETIQKNKDQAHRLKGVL RDSIVMLEQLKSSLIMLQK  
TFDLLNKNKTGMAVES

**Transmembrane domain:**

amino acids 352-371

**N-glycosylation sites.**

amino acids 3-7, 54-58, 312-316, 349-353, 367-371, 449-453

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 81-85, 307-311

**Tyrosine kinase phosphorylation sites.**

amino acids 202-211, 246-254, 341-349

**N-myristoylation site.**

amino acids 259-265

**Amidation site.**

amino acids 339-343

**FIGURE 237**

CAGGGGCTGGAGGGCAGGGGAGGGGATGATGTCATTCCCTGCTCGGCGCAATCCTGACCCTGCT  
CTGGGCGCCACGGCTCAGGCTGAGGTTCTGCTGCAGCCTGACTTCAATGCTGAAAAGTTCTC  
AGGCCTCTGGTACGTGGTCTCCATGGCATCTGACTGCAGGGTCTTCCTGGGCAAGAAGGACCA  
CCTGTCCATGTCCACCAGGGCCATCAGGCCCACAGAGGAGGGCGGCCTCCACGTCCACATGGA  
GTTCCCGGGGGCGGACGGCTGTAACCAGGTGGATGCCGAGTACCTGAAGGTGGGCTCCGAGGG  
ACACTTCAGAGTCCCGGCCTTGGGCTACCTGGACGTGCGCATCGTGGACACAGACTACAGCTC  
CTTCGCCGTCCTTTACATCTACAAGGAGCTGGAGGGGGCCCTCAGCACCATGGTGCAGCTCTA  
CAGCCGGACCCAGGATGTGAGTCCCCAGGCTCTGAAGTCCTTCCAGGACTTCTACCCGACCCT  
GGGGCTCCCCAAGGACATGATGGTCATGCTGCCCCAGTCAGATGCATGCAACCCTGAGAGCAA  
GGAGGCGCCCTGACACCTCCGGAGCCCCACCCCGCCCTTCCCAGGTGGAGCCAAAGCAGCAG  
GCGCCTTTGCCCTGGAGTCAAGACCCACAGCCCTCGGGGACCACCTGGAGTCTCTCCATCCT  
CCACCCCCCGCCTGTGGGATGCCTTGTGGGACGTCTCTTTCTATTCAATAAACAGATGCTGCA  
GCCTCA

**FIGURE 238**

MMSFLLGAILTLLWAPTAQAEVLLQPDFNAEKFSGLWYVVSMA SD CRVFLGKKDHLSMSTRAI  
RPTEEGGLHVHMEFPGADGCNQVDAEYLKVGSEGHFRVPALGYLDVRIVDTDYSSFAVLYIYK  
ELEGALSTMVQLYSRTQDVSPQALKSFQDFYPTLGLPKDMMVMLPQSDACNPESKEAP

**Signal peptide:**

amino acids 1-20

**Tyrosine kinase phosphorylation site.**

amino acids 110-117

**N-myristoylation sites.**

amino acids 7-13, 79-85, 130-136

**Amidation site.**

amino acids 50-54

**FIGURE 239**

GGCGCGCTGGTCCAGGTGAGCGGGCGCGTCCCCGCGACGGCGCTGCCTGCCCAGGCGGTTCA  
CGTAAAGACAGCGAGATCCTGAGGGCCAGCCGGGAAGGAGGCGTGGATATGGAGCTGGCTGCT  
GCCAAGTCCGGGGCCCCGCGCCGCTGCCTAGCGCGTCTCTGGGGAATCTGTGGGGACGCGCCCCG  
CGCCGCGGCTCGGGGACCCGTAGAGCCCGGCGCTGCGCGCATGGCCCTGCTCTCGCGCCCCGC  
GCTCACCTCCTGCTCCTCCTCATGGCCGCTGTTGTGAGGTGCCAGGAGCAGGCCAGACCAC  
CGACTGGAGAGCCACCCTGAAGACCATCCGGAACGGCGTTTCATAAGATAGACACGTACCTGAA  
CGCCGCCTTGGACCTCCTGGGAGGCGAGGACGGTCTCTGCCAGTATAAATGCAGTGACGGATC  
TAAGCCTTTCCACGTTATGGTTATAAACCTCCCCACCGAATGGATGTGGCTCTCCACTGTT  
TGGTGTTTCATCTTAACATTGGTATCCCTTCCCTGACAAAGTGTTGCAACCAACACGACAGGTG  
CTATGAGACCTGTGGCAAAAGCAAGAATGACTGTGATGAAGAATTCAGTATTGCCTCTCCAA  
GATCTGCCGAGATGTACAGAAAACACTAGGACTAACTCAGCATGTTTCAGGCATGTGAAACAAC  
AGTGGAGCTCTTGTTTGACAGTGTTATACATTTAGGTTGTAAACCATATCTGGACAGCCAACG  
AGCCGCATGCAGGTGTCATTATGAAGAAAAAATGATCTTTAAAGGAGATGCCGACAGCTAGT  
GACAGATGAAGATGGAAGAACATAACCTTTGACAAATAACTAATGTTTTTACAACATAAAACT  
GTCTTATTTTTGTGAAAGGATTATTTTGAGACCTTAAAATAATTTATATCTTGATGTTAAAAC  
CTCAAAGCAAAAAAAGTGAGGGAGATAGTGAGGGGAGGGCACGCTTGTCTTCTCAGGTATCTT  
CCCCAGCATTGCTCCCTTACTTAGTATGCCAAATGTCTTGACCAATATCAAAAACAAGTGCTT  
GTTTAGCGGAGAATTTTGAAAAGAGGAATATATAACTCAATTTTCACAACCACATTTACCAA  
AAAAGAGATCAAATATAAAATTCATCATAATGTCTGTTCAACATTATCTTATTTGGAAAATGG  
GGAAATTATCACTTACAAGTATTTGTTTACTATGAAATTTTAAATACACATTTATGCCTAGAA  
GGAACGGACTTTTTTTTTCTATTTTAATTACACATAATATGTAATTAAAGTACAACATAATAT  
GTTGTTTCTCTGTAGCCCGTTGAGCATATGAGTAAGTCACATTTCTATTAGGACTACTTACAA  
GGACAAGGTTTCCATTTTCCAGTTGTAAAATTGGAACCATCAGCTGATAACCTCGTAGGGAG  
CAACCCAGGATAGCTAAGTGTTATGTAATATGCCTAGAAGGTGATGTGAATGCGATTGAGAA  
GCATAGCCACTCCATTTTATGAGCTACTCACATGACAAATGTCATCTTTTGCTATAACCTTT  
GCCAAGTTAGAGAAAAGATGGATTTAATGAGATAAATGAAAAGATATTTAACCTAAAAA  
AAAAAAAAAAAAAAAAAAAA

**FIGURE 240**

MALLSRPALTL L L L L L L M A A V V R C Q E Q A Q T T D W R A T L K T I R N G V H K I D T Y L N A A L D L L G G E D G L C  
Q Y K C S D G S K P F P R Y G Y K P S P P N G C G S P L F G V H L N I G I P S L T K C C N Q H D R C Y E T C G K S K N D C D E  
E F Q Y C L S K I C R D V Q K T L G L T Q H V Q A C E T T V E L L F D S V I H L G C K P Y L D S Q R A A C R C H Y E E K T D L

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-myristoylation sites:**

amino acids 57-63, 93-99

**Phospholipase A2 histidine active site:**

amino acids 106-114

**Neuraxin and MAP1B proteins repeat proteins Block:**

amino acids 109-137

**FIGURE 241**

GATTCCGAGCGCCTCCACTGCTGGTCCGTTGGCCAGATCAACTCGCCGCGTGGGCCGGCCGTT  
CCCTGAGAGTCTGAGCGCTCGCCGCACCCCTTCCGAGCTTCTATTGGCCGTAGCAGACGTCC  
GTCTGCCGCTATCTCCGCCCCAATACGGAAGCGGCCTAGTCCTCCGGCTCCGACAGCTGGGTG  
TCCAGGCCATGGGGCAGCCCTGGGCGGCTGGGAGCACGGACGGGGCGCCCGCGCAGCTGCCTC  
TCGTGCTCACCGCGCTGTGGGCCGCGGCCGTGGGCCTGGAGCTGGCTTACGTGCTGGTGCTCG  
GTCCCGGGCCGCCCGCGCTGGGACCCCTGGCCCGGGCCTTGACAGCTGGCGCTGGCCGCCTTCC  
AGCTGCTCAACCTGCTGGGCAACGTGGGGCTCTTCCTGCGCTCGGATCCCAGCATCCGTGGCG  
TGATGCTGGCCGGCCGCGGTCTGGGCCAGGGCTGGGCTTACTGCTACCAATGCCAAAGCCAGG  
TGCCGCCACGCAGCGGACACTGCTCTGCCTGCCGCGTCTGCATCCTGCGTCGGGACCACCACT  
GCCGCCTGCTGGGCCGCTGCGTGGGCTTCGGCAACTACCGGCCCTTCTGTGCCTGCTGCTTC  
ATGCCGCCGGCGTCCTGCTCCACGTCTCTGTGCTGCTGGGCCCTGCACTGTCGGCCCTGCTGC  
GAGCCACACGCCCCCTCCACATGGCTGCCCTCCTCCTGCTTCCCTGGCTCATGTTGCTCACAG  
GCAGAGTGTCTCTGGCACAGTTTGCCTTGGCCTTCGTGACGGACACGTGCGTGGCGGGTGCGC  
TGCTGTGCGGGGCTGGGCTGCTCTTCCATGGGATGCTGCTGCTGCGGGGCCAGACCACATGGG  
AGTGGGCTCGGGGCCAGCACTCCTATGACCTGGGTCCCTGCCACAACCTGCAGGCAGCCCTGG  
GGCCCCGCTGGGCCCTCGTCTGGCTCTGGCCCTTCTGGCCTCCCCATTGCCTGGGGATGGGA  
TCACCTTCCAGACCACAGCAGATGTGGGACACACAGCCTCCTTGACTCCAGGAAGAGCCAGAGC  
TGTGCAGGGAGGAAGGGGTGAGAGGGGGGCCCCACACCTAGACTCAGTAAGGAAGTCGGGTT  
GGACCTTAACATCTGCATTGGACAACTCCACCCCTTCTTGGCCTTGCCCCTGCCCGCCTACA  
CTCCTACGTGTCCAGGGCTTGGGCCGTGACTTAGGCAGAGGAGTGCAGAGGAGGGTCTGGCAG  
GGGCTGCTCAGGCCGCCTAGCTGCCCCCTTTGCCAGGTTAATAAAGCACTGACTTGTTAA

**FIGURE 242**

MGQPWAAGSTDGAPAQPLPLVLTALWAAVGLLAYVLVLGPGPPPLGPLARALQLALAAFQLL  
NLLGNVGLFLRSDPSIRGVMLAGRGLGQGWAYCYQCQSQVPPRSGHCSACRVCILRRDHHCLL  
LGRCVGFGNYPFLCLLLHAAGVLLHVSVLLGPALSALLRAHTPLHMAALLLLPWLMLLTGRV  
SLAQFALAFVTDTCVAGALLCGAGLLFHGMILLRGQTTWEWARGQHSYDLGPCHNLQAALGPR  
WALVWLWPFLASPLPGDGITFQTTADVGHSTAS

**Important features:**

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 51-66,143-160,174-191,198-214

**N-myristoylation sites:**

amino acids 2-8,8-14,30-36,81-87,88-94,90-96,206-212

**Leucine zipper pattern:**

amino acids 143-165,150-172,157-179,164-186



# **FIGURE 243**

CTTGTCTTTGTGTCGGTTGTGATTTTCCTAATCTCTGATTTTCCTTTTCTCTCGGACGCTCTC  
CCTCTTCGGACCCATTTTCTCCCGTGCTTCATGCCCTGATAGCCTGGCCCCCTTCCCGGCTTCC  
TTCGCTACCGGGGACGCCTCTAGTTTTTCTGAATTTCTGGCTGGCTCCACCCTCCGCGTTCAT  
CTTCCTCAAGAGTTCGCCCCCTCTGGGGGCTCCTCTGTGTAATCGTCGCCTTCTCTGGGTATTT  
CTGTGAACTCCGTCTCACACCATCCCGCCATCTTCTCTGCCTTGGCCCCCTTTTCTCTGTACAG  
CCAGCTCTGTGTCCTTTTCTTCTCCCCCTCTAAATCGACTCCTCTTCTCCCTGAGAGCCCCA  
CCTTTGTGCCCCACTCCTCATTTTCTACGCCTCCCTCTCTCTGCTGGTCTCTCTCTCCCTG  
CAAGGTTCCATTCCATCAATTTGTTTGTCTTTTGTAGGGGTGGCATCCCCCTCTGACTACTGCT  
CCATCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGCTTGAGGATTTCACTTCAATCTTTTCTGGT  
TGCGTCTCCACTTGTACTCAGCTTGTAGGTCCAGGTCCAGTTGTTCTGCATCTGAGGCTGGC  
GTGTGCTGTCTTCTCTGATTGGCCTAATCTCCCTCACCCCGTGAGATCTGTTGTGAGCCTTC  
GTTTCTCTTTCCTGTGTCCAGCTTTTCTGCGGGTCTTGGCACCTTTCTTGGCCACAGATTTTCT  
TGGGTTACAGAGCATGTGTGTCTGAGGCATTGCAGGCAGAAAAGGGTGGCCGACGTGACCTCT  
AGCTGGACTGCTGGGCAGGGGAGCTGTCTAGATAAAATTGGAAAGAAACAGTGACCCAGAGA  
CAGGTGGACAAAGAATTGCGGGACTGATGGGAACTGAGCTTGGGATCCAGACTGAAACTGATT  
CCAGACTGACCTCTAGCACCCAGGACCCAGACACAGGGCCATGGGACCCAGCATTGTGAGACT  
TGTGCAGCTGTTCTGCCTTCTAGGGGCCATCCCCACTCTGCCTCGGGCTGGAGCTCTTTTGTG  
CTATGAAGCAACAGCCTCAAGATTGAGAGCTGTTGCTTTCCATAACTGGAAGTGGCTTCTGAT  
GAGGAACATGGTGTGTAAGCTGCAAGAGGGCTGCGAGGAGACGCTAGTGTTCAATTGAGACAGG  
GACTGCAAGGGGAGTTGTGGGCTTTAAAGGCTGCAGCTCGTCTTTCGTCTTACCCTGCGCAAAT  
CTCCTACCTTGTTTCCCCACCCGGAGTGTCCATTGCCTCCTACAGTCGCGTCTGCCGGTCTTA  
TCTCTGCAACAACCTCACCAATTTGGAGCCTTTTGTGAAACTCAAGGCCAGCACTCCTAAGTC  
TATCACATCTGCGTCCTGTAGCTGCCCCGACCTGTGTGGGCGAGCACATGAAGGATTGCCTCCC  
AAATTTTGTCAACCTAATTCTTGCCCCCTTGGCTGCTTCTACGTGTTACAGTTCCACCTTAAA  
ATTTGAGGCAGGGTTTCTCAATACCACCTTCTCCTCATGGGGTGTGCTCGTGAACATAACCA  
GCTTTTAGCAGATTTTCATCATATTGGGAGCATCAAAGTGAAGTGAAGTGAAGTGAAGTGAAGT  
GAAGTCTCAGATTGTTGGTGCAGCATCCTCCAGGCAAGATCCTGCTTGGGGTGTGCTCTTAGG  
CCTCCTGTTTGCCTTCAGGGACTGACCATCTAGCTGCACCCGACAAGCACCCAGACTCTTTCA  
CATAACAAATAAAATAGCAGAGTTCCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAA

**FIGURE 244**

MGPQHRLRLVQLFCLLGAIPTLPRAGALLCYEATASRFRAVAFHNWKWLLMRNMVCKLQEGCEE  
TLVFIETGTARGVVGFKGCSSSSSYPAQISYLVSPPGVSIASYSRVCRSYLCNNLTNLEPFVK  
LKASTPKSITSASCSCPTCVGEHMKDCLPNFVTTNSCPLAASTCYSSTLKFQAGFLNTTFLLM  
GCAREHNQLLADFHHIGSIKVTEVLNILEKSQIVGAASSRQDPAWGVVLGLLFAFRD

**Important features:**

**Signal peptide:**

amino acids 1-20

**N-glycosylation sites:**

amino acids 117-121,183-187

**N-myristoylation sites:**

amino acids 16-22,25-31,60-66,71-77,81-87,100-106,224-230,  
235-241,239-245

**Prokaryotic membrane lipoprotein lipid attachment site:**

amino acids 181-192

# **FIGURE 245**

GTGGAGTTGGGTGGTGTCTGGGAGCCTCTCCCTGAGGGGCACCGCGTCTTCAGGAGCTGGGCCTCCAGTGCGGCGC  
GATGTCAGGCGCGGTGACAGCTCTGTGAGTCCGAGGCCGCGGCCGTGGCGCTGGGCGGCTGCGGGGCCTGACCGG  
TCCGCTC**A**TGGTGCCGCCACGACGCCATCGCGGGGCAGGAAGGCCAGGGGTGCTGAGTTCTTCACCTCCTTTTAG  
ACTGAGATCTGCCAAGTTTTCCGGCATTGCTCTTGAGGATCTCAGAAGGGCTCTTAAGACAAGACTGCAATGGT  
GTGTGTATTTGTCATGAACCGAATGAATTCCCAGAACAGTGGTTTCACTCAGCGCAGGCGAATGGCTCTTGGGAT  
TGTTATTTCTTCTGCTTGTGATGTGATATGGGTGCTTCCCTCTGAACCTTACTTCGTATGTTTTACCCAGTACAA  
CAAACCATTTCTCAGCACCTTTGCAAAAACATCTATGTTTGTGTTTGTACCTTTTGGGCTTTATTATTTGGAAGCC  
ATGGAGACAACAGTGTACAAGAGGACTTCGCGGAAAGCATGCTGCTTTTTTTGTCAGATGCTGAAGGTTACTTTGTC  
TGCTTGCAACAACAGATACAACTATGAATAGTTCTTTGAGTGAACCTCTGTATGTGCTGTGAATTCATGATCT  
TCCAAGTGAAAAACCTGAGAGCACAAACATTGATACTGAAAAAACCCCAAAAGTCTCGTGTGAGGTTCAAGTAA  
TATCATGGAGATTTCGACAGCTTCCGTCAGTCATGCATTGGAAGCAAAGTTGTCTCGCATGTCTATCTGTGAA  
AGAACAAGAAATCCATACTGAAAACTGTGGGAAACTTACTGCAACTCAAGTAGCGAAAATTAGCTTTTTTTTTTTG  
CTTTGTGTGGTTTTTTGGCAAATTTGTCATATCAAGAAGCACTTTCAGACACACAAGTTGCTATAGTTAATATTTT  
ATCTTCAACTTCCGACTTTTTACCTTAATCCTTGCTGCAAGTATTTCCAAGTAACAGTGGAGATAGATTTACCTT  
TTCTAAACTATTAGCTGTAATTTTAAGCATTGGAGGCGTTGTACTGGTAAACCTGGCAGGGTCTGAAAAACCTGC  
TGGAAGAGACACAGTAGGTTCCATTTGGTCTCTTGTCTGGAGCCATGCTCTATGCTGTCTATATTGTTATGATTAA  
GAGAAAAGTAGATAGAGAAGACAAGTTGGATATTCGAATGTTCTTTGGTTTTGTAGGTTTGTTTAATCTGCTGCT  
CTTATGGCCAGGTTTCTTTTACTTCATTATACTGGATTGAGGACTTCGAGTTTCCCAATAAAGTAGTATTAAT  
GTGCATTATCATTAAATGGCCTTATTGGAAACAGTACTCTCAGAGTTCTGTGGTTGTGGGGCTGCTTTCTTACCTC  
ATCATTGATAGGCACACTTGCACTAAGCCTTACAATACCTCTGTCCATAATAGCTGACATGTGTATGCAAAAGGT  
GCAGTTTTCTTGGTTATTTTTTGCAGGAGCTATCCCTGTATTTTTTTTCATTTTTTATGTAACTCTCCTATGCCA  
TTATAATAATTGGGATCCTGTGATGGTGGGAATCAGAAGAATATTGCTTTTATATGCAGAAAACATCGAATTCA  
GAGAGTTCCAGAAGACAGCGAACAGTGTGAGAGTCTCATTTCTATGCACAGTGTCTCAGGAGGATGGAGCTAG  
**T****T****A****G****C**TGTCTGTGTTCTGTAGCCCAGCTTGATAATGGAACATACAGCGAAGAGACAATCTCTGGCAAGTTTTTG  
TAGAAAAAATGTTTTCAGTGCCTAGTCTGAAAAATAACAGTTTGAGTTCTTTGAAACTCTAAAATATATTTTTCTC  
ATACCTGTTTTCTTCATTTTCATAATGAAGCACTTTGCTATGTAGCTGTGTACATATCACTACAGTTATAGGAAG  
TTTCAGTCTACAGTCCATCCAAAGGACCAACCTGCCCTTACACATCTCAAGGAATTCAGCTGTTGAAATCATTGGA  
ACTAATCAAGGAATAAATCCTAATGTTCTGGGACTTTATTTTACATGTTAAATGCTGGAATATATTATGAAAAAT  
GTTTTCAAGAAATCACTTAAGTGTTCATAGACCAGTATTTCTGACAGGTAAAATGCTAAAATAAGCTACCTGTAA  
TAAGTGTGGATTATATTTTTTGGTTTTGTAGAATATTGCAAATTAACCACACAAAAATGTTTAATTTATGCAAC  
AAGCATGTTTGTGCAATTTTCATGGGACTTTAAAAAGAATAAGTATTTGAGAAAATATCTGGTTCACTTACACTA  
CATTTACTGTATTATTTCTTTATAGCATTAGGTGCCCTGTATTTTAAATCTGTGACAAACCATGGCAAATTTTAA  
AAGGGGAAGTATTATATAAAATGAAGAAATATGATTTCTAAAGGCTATATTGCTGTAAACTTAATTGATAAAG  
CTCTGTTTTAATTTAGAGTTTGAAGAAATAGTCTCCCTCAATTAAGAAATTTTCATAATGGAATGATTTAAATT  
GAAGTGACAAAGAGTATTATTAAAAATACAATGTTTATAAAAAA

**FIGURE 246**

MVPPRRHRGAGRPGVLSSSPFRLRSKAFSGIALEDLRRALKTRLQMVCVFVMNRMNSQNSGF  
TQRRRMALGIVILLLLVDVIWVASSELTSYVFTQYNKPFSTFAKTSMFVLYLLGFIIWKPWQR  
QCTRGLRGKHAAFFADAEGYFAACTTDTTMNSSLSEPLYVPVKFHDLPSEKPESTNIDTEKTP  
KKSrvRFSNIMEIRQLPSSHALEAKLSRMSYPVKEQESILKTVGKLTATQVAKISFFFCFVWF  
LANLSYQEALSDTQVAIVNILSSTSGLFTLILAAVFPNSGDRFTLSKLLAVILSIGGVVLVN  
LAGSEKPAGRDTVGSISLAGAMLYAVYIVMIKRKVDREDKLDIPMFFGFVGLFNLLLLWPGE  
FLLHYTGFEDEFEPNKVVLNCIIINGLIGTVLSEFLWLWGCFLTSSLIGTLALSITPLSIIA  
DMCMQKVQFSWLFFAGAIPVFFSFFIVTLLCHYNNWDPVMVGIRRIFAFICRKHRIQRPEDS  
EQCESLISMHSVSQEDGAS

**Important features:**

**Transmembrane domain:**

amino acids 69-87,105-118,237-256,266-285,300-316,332-346,  
364-379,399-419,453-472

**N-glycosylation sites:**

amino acids 157-161,255-259

**N-myristoylation sites:**

amino acids 14-20,329-335,404-410,407-413,418-424

**FIGURE 247**

CGTCTGTAGAGATATCATGAACTTCAACTTAGCTTTGGTACTTTCTTCCCTGAAGACAGAGGG  
CAGAACTCTGAGTTCCAGAACCATTTTCAACTGTATTGGGGACCAATCACTTGACTCTATTCT  
TGTCTCTCTGACAGATGACGCTACACTCTCCTCTGAATAATGGACACCATTTCTAAAAC TGAA  
TCCTGCTACTAAAATAATTGAGATGATATATTTTTCCAATTCTACAATCTTGCTTTGTTTTAT  
TTAGTTGTTTTCTCTCTCTCTTCCCAGTTTTCCAGAGACTGGAGCTAAACTGGGCTTTCAACA  
TCATCATGAAGTTTATCCTCCTCTGGGCCCTCTTGAATCTGACTGTTGCTTTGGCCTTTAATC  
CAGATTACACAGTCAGCTCCACTCCCCCTTACTTGGTCTATTTGAAATCTGACTACTTGCCCT  
GCGCTGGAGTCCTGATCCACCCGCTTTGGGTGATCACAGCTGCACACTGCAATTTACCAAAGC  
TTCGGGTGATATTGGGGTTACAATCCAGCAGACTCTAATGAAAAGCATCTGCAAGTGATTG  
GCTATGAGAAGATGATTCATCATCCACACTTCTCAGTCACTTCTATTGATCATGACATCATGC  
TAATCAAGCTGAAAACAGAGGCTGAACTCAATGACTATGTGAAATTAGCCAACCTGCCCTACC  
AACTATCTCTGAAAATACCATGTGCTCTGTCTCTACCTGGAGCTACAATGTGTGTGATATCT  
ACAAAGAGCCCGATTCACTGCAAACGTGAACATCTCTGTAATCTCCAAGCCTCAGTGTGCGG  
ATGCCTATAAAACCTACAACATCACGGAAAATATGCTGTGTGTGGGCATTGTGCCAGGAAGGA  
GGCAGCCCTGCAAGGAAGTTTCTGCTGCCCCGGCAATCTGCAATGGGATGCTTCAAGGAATCC  
TGTCTTTTGC GGATGGATGTGTTTTGAGAGCCGATGTTGGCATCTATGCCAAAATTTTTTACT  
ATATACCCTGGATTGAAAATGTAATCCAAAATAACTGAGCTGTGGCAGTTGTGGACCATATGA  
CACAGCTTGTCCCATCGTTACCTTTAGAATTAAATATAAATTAAC TCCTC

## **FIGURE 248**

MKFILLWALLNLTVALAFNPDYTVSSTPPYLVYLKSDYLP CAGVLIHPLWVITA AHCNLPKLR  
VILGVTIPADSNEKHLQVIGYEKMIHHPHFSVTSIDHDIMLIKLTEAELNDYVKLANLPYQT  
ISENTMCSVSTWSYNVCDIYKEPDSLQTVNISVISKPQCRDAYKTYNITENMLCVGIVPGRRQ  
PCKEVSAAAPAICNGMLQGILSFADGCVLRADVGIYAKIFYIIPWIENVIQNN

**Important features:**

**Signal peptide:**

amino acids 1-17

**N-glycosylation sites:**

amino acids 11-15,156-160,173-177

**Tyrosine kinase phosphorylation site:**

amino acids 108-117

**N-myristoylation sites:**

amino acids 182-188,203-209

**Amidation site:**

amino acids 185-189

**Serine proteases, trypsin family, histidine active site:**

amino acids 52-58

**FIGURE 249**

GCGAGGCGGCCGCTGTCTTCTGCTGCGGCTTCCGCGACCACAAGTACTGCTGCGACGACCCGC  
ACAGCTTCTTCCCCCTACGAGCACAGCTACATGTGGTGGCTCAGCATTGGCGCTCTCATAGGCC  
TGTCCGTAGCAGCAGTGGTTCTTCTCGCCTTCATTGTTACCGCCTGTGTGCTCTGCTACCTGT  
TCATCAGCTCTAAGCCCCACACAAAGTTGGACCTGGGCTTGAGCTTACAGACAGCAGGCCCTG  
AGGAGGTTTCTCCTGACTGCCAAGGTGTGAACACAGGCATGGCGGCAGAAGTGCCAAAAGTGA  
GCCCTCTCCAGCAGAGTTACTCCTGCTTGAACCCGCAGCTGGAGAGCAATGAGGGGCAGGCTG  
TGAACTCCAAACGCCTCCTCCATCATTGCTTCATGGCCACAGTGACCACCAGTGACATTCCAG  
GCAGCCCTGAGGAAGCCTCTGTACCCAACCTGACCTATGTGGACCAGTCCCATTAAACATTCA  
ATAAATGTCTCCATACCATCAA

**FIGURE 250**

MWWLSIGALIGLSVAAVVLLAFIVTACVLCYLFISSKPHTKLDLGLSLQTAGPEEVSPDCQGV  
NTGMAAEVPKVSPLQQSYSCLNPQLESNEGQAVNSKRLLHHCFMATVTTSDIPGSPEEASVPN  
PDL CGPVP

**Important features:**

**Signal peptide:**

Amino acids 1-26

**N-myristoylation sites:**

Amino acids 7-13, 11-17, 62-68, 93-99



**FIGURE 251**

GTGGTTTGGATTGAGCCGGGCCCCGGCCGGGGCGCCGAGTCGGAGGGGGTGGCAGTGAGCGGCG  
GCAGAGGCTACGGGGCTCGGTTTGGCTGACTGGGGAGTCGGCAGGCGGCAGGAACCATGCGAG  
GCCAGCGGAGCCTGCTGCTGGGCCCGGCCCGCCTCTGCCTCCGCCTCCTTCTGCTGCTGGGTT  
ACAGGCGCCGCTGTCCACCTCTACTCCGGGGTCTAGTACAGCGCTGGCGCTACGGCAAGGTCT  
GCCTGCGCTCCCTGCTCTACAACTCCTTTGGGGGCGAGTGACACCGCTGTTGATGCTGCCTTTG  
AGCCTGTCTACTGGCTGGTAGACAACGTGATCCGCTGGTTTGGAGTGGTGTTCGTGGTCCTGG  
TGATCGTGCTGACAGGCTCCATTGTAGCTATCGCCTACCTGTGTGTCTGCCTCTCATCCTCC  
GAACCTACTCAGTGCCACGACTCTGCTGGCATTCTTCTATAGCCACTGGAATCTGATCCTGA  
TTGTCTTCCACTACTACCAGGCCATCACCCTCCGCCTGGGTACCCACCCAGGGCAGGAATG  
ATATCGCCACCGTCTCCATCTGTAAGAAGTGCATTTACCCCAAGCCAGCCCGAACACACCACT  
GCAGCATCTGCAACAGGTGTGTGCTGAAGATGGATCACCCTGCCCCCTGGCTAAACAATTGTG  
TGGGCCACTATAACCATCGGTACTTCTTCTCTTTCTGCTTTTTTCATGACTCTGGGCTGTGTCT  
ACTGCAGCTATGGAAGTTGGGACCTTTTCCGGGAGGCTTATGCTGCCATTGAGACTTATCACC  
AGACCCACCCACCCACCTTCTCCTTTTCGAGAAAGGATGACTCACAAGAGTCTTGTCTACCTCT  
GGTTCCTGTGCAGTTCTGTGGCACTTGCCCTGGGTGCCCTAACTGTATGGCATGCTGTTCTCA  
TCAGTCGAGGTGAGACTAGCATCGAAAGGCACATCAACAAGAAGGAGAGACGTCGGCTACAGG  
CCAAGGGCAGAGTATTTAGGAATCCTTACAACCTACGGCTGCTTGGACAACCTGGAAGGTATTC  
TGGGTGTGGATACAGGAAGGCACTGGCTTACTCGGGTGCTCTTACCTTCTAGTCACTTGCCCC  
ATGGGAATGGAATGAGCTGGGAGCCCCCTCCCTGGGTGACTGCTCACTCAGCCTCTGTGATGG  
CAGTGAGCTGGACTGTGTGAGCCACGACTCGAGCACTCATTCTGCTCCCTATGTTATTTCA  
AGGGCCTCCAAGGGCAGCTTTTCTCAGAAATCCTTGATCAAAAAGAGCCAGTGGGCCTGCCTTA  
GGGTACCATGCAGGACAATTCAAGGACCAGCCTTTTTTACCCTGCAGAAGAAAGACACAATGT  
GGAGAAATCTTAGGACTGACATCCCTTTACTCAGGCAAACAGAAGTTCCAACCCCAGACTAGG  
GGTCAGGCAGCTAGCTACCTACCTTGCCCAGTGCTGACCCGGACCTCCTCCAGGATACAGCAC  
TGGAGTTGGCCACCACCTCTTCTACTTGCTGTCTGAAAAAACACCTGACTAGTACAGCTGAGA  
TCTTGGCTTCTCAACAGGGCAAAGATACCAGGCCTGCTGCTGAGGTCACTGCCACTTCTCACA  
TGCTGCTTAAGGGAGCACAAATAAAGGTATTCGATTTTAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAA

## **FIGURE 252**

MRGQRSLLLGPRLCLRLLLLLGYRRRCPLLRLVQRWRYGKVCLRSLLYNSFGGSDTAVDA  
AFEPVYWLVDNVIRWFGVVVVLVIVLTGSIVAIAYLCVLPILRTYSVPRLCWHFFYSHWNL  
ILIVFHYQAITTPPGYPPQGRNDIATVSICKKCIYPKPARTHHCSICNRCVLKMDHHCPWLN  
NCVGHYNHRYFFSFCCFMTLGCVCYCSYGSWDLFREAYAAIETYHQTPPTFSFRERMTHKSLV  
YLWFLCSSVALALGALTVWHAVLISRGETSIERHINKKERRRLQAKGRVFRNPYNYGCLDNWK  
VFLGVDTGRLHWLTRVLLPSSHLPHGNGMSWEPPPWVTAHSASVMAV

**Important features:**

**Transmembrane domain:**

amino acids 88-100,202-216,254-274

**N-myristoylation sites:**

amino acids 55-61,56-62,92-98,210-216,309-315,319-325,340-346

**Prokaryotic membrane lipoprotein lipid attachment site:**

amino acids 201-212

**FIGURE 253**

GATCAAGCGCCTTCCTTTCCCTTCCTCTCCCTACTTGGCCTTTGCCCTAAGCCAAGACCTGGCCATCAGCCTGGC  
TGCAGGGGCCCTGCAGAGCCAGCTGCACTTTTTTCAGGTATGGGGGAGGGCCAGGCACCAATGAAGCCAGTGTGGGT  
GCCACCTTCTGTGGATGCTACTGCTGGTGCCAGGCTGGGGGCCGCCCGGAAGGGGTCCCCAGAAGAGGCCTCC  
TTCTACTATGGAACCTTCCCTCTTGGCTTCTCCTGGGGCGTGGGCAGTTCTGCCTACCAGACGGAGGGCGCCTGG  
GACCAGGACGGGAAAGGGCCTAGCATCTGGGACGTCTTCACACACAGTGGGAAGGGGAAAGTGCTTGGGAATGAG  
ACGGCAGATGTAGCCTGTGACGGCTACTACAAGGTCCAGGAGGACATCATTCTGCTGAGGGAACTGCACGTCAAC  
CACTACCGATTCTCCCTGTCTTGGCCCCGGCTCCTGCCACAGGCATCCGAGCCGAGCAGGTGAACAAGAAGGGA  
ATCGAATTCTACAGTGATCTTATCGATGCCCCTTCTGAGCAGCAACATCACTCCCATCGTGACCTTGCACCACTGG  
GATCTGCCACAGCTGCTCCAGGTCAAATACGGTGGGTGGCAGAATGTGAGCATGGCCAACTACTTCAGAGACTAC  
GCCAACCTGTGCTTTGAGGCCTTTGGGGACCGTGTGAAGCACTGGATCACGTTCACTGATCCTCGGGCAATGGCA  
GAAAAAGGCTATGAGACGGGCCACCATGCGCCGGGCCCTGAAGCTCCGCGGCACCGGCCTGTACAAGGCAGCACAC  
CACATCATTAAGGCCACGCCAAAACCTGGCATTCTTATAACACCACGTGGCGCAGCAAGCAGCAAGGTCTGGTG  
GGAATTTCACTGAAGTGTGACTGGGGGGAACCTGTGGACATTAGTAACCCCAAGGACCTAGAGGCTGCCGAGAGA  
TACCTACAGTTCTGTCTGGGCTGGT'TTGCCAACCCCATTTATGCCGGTGACTACCCCAAGTCATGAAGGACTAC  
ATTGGAAGAAAGAGTGCAGAGCAAGGCCTGGAGATGTGAGGTTACCGGTGTTCTCACTCCAGGAGAAGAGCTAC  
ATTAAAGGCACATCCGATTTCTTGGGATTAGGTCATTTTACTACTCGGTACATCACGGAAAGGAACTACCCCTCC  
CGCCAGGGGCCCAGCTACCAGAACGATCGTGACTTGATAGAGCTGGTTGACCCAACTGGCCAGATCTGGGGTCT  
AAATGGCTATATTCTGTGCCATGGGGATTTAGGAGGCTCCTTAACCTTGTCTCAGACTCAATACGGTGATCCTCCC  
ATATATGTGATGAAAAATGGAGCATCTCAAAAATTCCACTGTACTCAATTATGTGATGAGTGGAGAATTCATAAC  
CTTAAAGGATACATAAATGAAATGCTAAAAGCTATAAAAGATGGTGCTAATATAAAGGGGTATACTTCTGCTCT  
CTGTTGGATAAGTTTGAATGGGAGAAAGGATACTCAGATAGATATGGATTCTACTATGTTGAATTTAACGACAGA  
AATAAGCCTCGCTATCCAAAGGCTTCAGTTCAATATTACAAGAAGATTATCATTGCCAATGGGTTTCCCAATCCA  
AGAGAGGTGAAAGTTGGTACCTCAAAGCTTTGGAACTTGCTCTATCAACAATCAGATGCTTGCTGCAGAGCCT  
TTGCTAAGTCACATGCAAATGGTTACGGAGATCGTGGTACCCACTGTCTGCTCCCTCTGTGCTCCTCATCACTGCT  
GTTCTACTAATGCTCCTCCTGAGGAGGCAGAGCTGAGACAGGATTATCAATTTTGAGCTTCATAAGAGAATCTT  
CAGGATCTTCTCTCCCTTTTCTGCTTTGAGGGTTTCCATACATTGCTGTTTTTCAGGTTCTACAATAATTACCTTTT  
TTTCTCTTCTCTTTTGGCTTGTGCTGGGATTTAAGAATTAGAAAATAAAAATAAGCAGAAATTA

## **FIGURE 254**

MKPVVWATLLWMLLLVPRLLGAARKGSPEEASFYYGTFFPLGFSWVGSSAYQTEGAWDQDGKGPSIWDVFTHSGKG  
KVLGNETADVACDGYIKVQEDIILLRELHVNHYRFSLSWPRLLPTGIRAEQVNKKGIEFYSDLIDALLSSNITPI  
VTLHHWDLPLQLQVKYGGWQNVSMANYFRDYANLCFEAFGDRVKHWITFSDPRAMAEGYETGHHAPGLKLRGTG  
LYKAAHHIIKAHAKTWHHSYNTTWRSKQQGLVGISLNCDWGEPVDISNPKDLEAAERYLQFCLGWGFANPIYAGDYP  
QVMKDYIGRKSAEQGLEMSRLPVFSLQEKSYIKGTSDFLGLGHFTTRYITERNYPSRQGPSYQNDRLIELVDPN  
WPDLGSKWLYSVPWGFRRLLNFAQTQYGDPPYVMENGASQKFHCTQLCDEWRIQYLKGYINEMLKAIKDGANIK  
GYTSWSLLDKFEWEKGYSDRYGFYYVEFNDNRNKPYPKASVQYYKKIIANGFPNPREVESWYLKALETCSINNQ  
MLAAEPLLSHMQMVTEIVVPTVCSLCVLITAVLLMLLLRRQS

**Important features:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 541-558

**N-glycosylation sites:**

amino acids 80-84,171-175,245-249

**Glycosaminoglycan attachment site:**

amino acids 72-76

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

amino acids 23-27,564-568

**Tyrosine kinase phosphorylation sites:**

amino acids 203-211,347-355,460-468,507-514

**N-myristoylation sites:**

amino acids 44-50,79-85,167-173,225-231,257-263,315-321

**Amidation site:**

amino acids 307-311

**Glycosyl hydrolases family 1 active site:**

amino acids 407-416

**Glycosyl hydrolases family 1 N-terminal signature:**

amino acids 41-56

**Motif name Glycosyl hydrolases family:**

amino acids 37- 67

**FIGURE 255**

CGCGAAGATGCGAAAGGTGGTTTTTGATCACCGGGGCTAGCAGTGGCATTGGCCTGGCCCTCTG  
CAAGCGGCTGCTGGCGGAAGATGATGAGCTTCATCTGTGTTTGGCGTGCAGGAACATGAGCAA  
GGCAGAAGCTGTCTGTGCTGCTCTGCTGGCCTCTCACCCCACTGCTGAGGTCACCATTGTCCA  
GGTGGATGTCAGCAACCTGCAGTCGGTCTTCCGGGCCTCCAAGGAACTTAAGCAAAGGTTTTCA  
GAGATTAGACTGTATATATCTAAATGCTGGGATCATGCCTAATCCACAACATAAATATCAAAGC  
ACTTTTCTTTGGCCTCTTTTCAAGAAAAGTGATTTCATATGTTCTCCACAGCTGAAGGCCTGCT  
GACCCAGGGTGATAAGATCACTGCTGATGGACTTCAGGAGGTGTTTGAGACCAATGTCTTTGG  
CCATTTTATCCTGATTGGGAACCTGGAGCCTCTCCTCTGTCCACAGTGACAATCCATCTCAGCT  
CATCTGGACATCATCTCGCAGTGCAAGGAAATCTAATTTTCAGCCTCGAGGACTTCAGCACAG  
CAAAGGCAAGGAACCTACAGCTCTTCCAAATATGCCACTGACCTTTTGAGTGTGGCTTTGAA  
CAGGAACCTTCAACCAGCAGGGTCTCTATTCCAATGTGGCCTGTCCAGGTACAGCATTGACCAA  
TTTGACATATGGAATTCTGCCTCCGTTTATATGGACGCTGTTGATGCCGGCAATATTGCTACT  
TCGCTTTTTTTGCAAATGCATTCACTTTGACACCATATAATGGAACAGAAGCTCTGGTATGGCT  
TTTCCACCAAAGCCTGAATCTCTCAATCCTCTGATCAAATATCTGAGTGCCACCACTGGCTT  
TGGAAGAAATTATATTATGACCCAGAAGATGGACCTAGATGAAGACACTGCTGAAAAATTTTA  
TCAAAAGTTACTGGAACCTGGAAAAGCACATTAGGGTCACTATTCAAAAAACAGATAATCAGGC  
CAGGCTCAGTGGCTCATGCCTATAATTTCCAGCACTTTGGGAGGCCAAGGCAGAAGGATCACTT  
GAGACCAGGAGTTCAAGACCAGCCTGAGAAACATAGTGAGCCCTTGTCTCTACAAAAGAAAT  
AAAAATAATAGCTGGGTGTGGTGGCATGCGCATGTAGTCCCAGCTACTCAGAAGGATGAGGTG  
GGAGGATCTCTTGAGGCTGGGAGGCAGAGGTTGCAGTGAGCTGAGATTGTGCCACTGCACTCC  
AGCCTGGGTGACAGCGAGACCCTGTCTCAAATATGTATATATTTAATATATATATAAAACCA  
GAGCTGACAATGACACTCTGGAACATTGCATACCTTCTGTACATTCTGGGGTACATGGATTTCT  
TACTGAGTTGGATAATATGCATTTGTAATAAACTATGAACTATGAA

**FIGURE 256**

MRKVVLITGASSGIGLALCKRLLAEDDELHLCLACRNMSKAEAVCAALLASHPTAEVTIVQVD  
VSNLQSVFRASKELKQRFQRLDCIYLNAGIMPNPQLNIKALFFGLFSRKVIHMFSTAEGLLTQ  
GDKITADGLQEVFETNVFGHFILIRELEPLLCHSDNPSQLIWTSSRSARKSNFSLEDFOHSGK  
KEPYSSSKYATDLLSVALNRNFNQQGLYSNVACPGTALTNLTYGILPPFIWTLMPAILLLRF  
FANAFTLTPYNGTEALVWLFHQKPESLNPLIKYLSATTGFGRNYIMTQKMDLDEDTAEKFYQK  
LLELEKHIRVTIQKTDNQARLSGSCL

**Important features:**

**Transmembrane domain:**

amino acids 234-254

**N-glycosylation sites:**

amino acids 37-41,178-182,229-233,263-267

**Glycosaminoglycan attachment site:**

amino acids 12-16

**N-myristoylation sites:**

amino acids 9-15,13-19,15-21,215-221,224-230

**FIGURE 257**

CGGACGCGTGGGGCCGTATGCGCGGCTCTGTGGAGTGCACCTGGGGTTGGGGGCACTGTGCCC  
CCAGCCCCCTGCTCCTTTGGACTCTACTTCTGTTTGCAGCCCCATTTGGCCTGCTGGGGGAGA  
AGACCCGCCAGGTGTCTCTGGAGGTCATCCCTAACTGGCTGGGCCCCCTGCAGAACCTGCTTC  
ATATACGGGCAGTGGGCACCAATTCACACTGCACTATGTGTGGAGCAGCCTGGGGCCTCTGG  
CAGTGGTAATGGTGGCCACCAACACCCCCCACAGCACCCCTGAGCATCAACTGGAGCCTCCTGC  
TATCCCCTGAGCCCGATGGGGGCTGATGGTGCTCCCTAAGGACAGCATTAGTTTTCTTCTG  
CCCTTGTTTTTACCAGGCTGCTTGAGTTTGACAGCACCAACGTGTCCGATACGGCAGCAAAGC  
CTTTGGGAAGACCATATCCTCCATACTCCTTGGCCGATTTCTCTTGGAAACAACATCACTGATT  
CATTGGATCCTGCCACCCTGAGTGCCACATTTCAAGGCCACCCCATGAACGACCCTACCAGGA  
CTTTTGCCAATGGCAGCCTGGCCTTCAGGGTCCAGGCCTTTTCCAGGTCCAGCCGACCAGCCC  
AACCCCTCGCCTCCTGCACACAGCAGACACCTGTCAGCTAGAGGTGGCCCTGATTGGAGCCT  
CTCCCCGGGGAAACCGTTCCCTGTTTGGGCTGGAGGTAGCCACATTGGGCCAGGGCCCTGACT  
GCCCCCTCAATGCAGGAGCAGCACTCCATCGACGATGAATATGCACCGGCCGTCTTCCAGTTGG  
ACCAGCTACTGTGGGGCTCCCTCCCATCAGGCTTTGCACAGTGGCGACCAGTGGCTTACTCCC  
AGAAGCCGGGGGGCCGAGAATCAGCCCTGCCCTGCCAAGCTTCCCCTCTTCATCCTGCCTTAG  
CATACTCTCTTCCCCAGTCACCCATTGTCCGAGCCTTCTTTGGGTCCCAGAATAACTTCTGTG  
CCTTCAATCTGACGTTTCGGGGCTTCCACAGGCCCTGGCTATTGGGACCAACACTACCTCAGCT  
GGTCGATGCTCCTGGGTGTGGGCTTCCCTCCAGTGGACGGCTTGTCCCCACTAGTCTGGGCA  
TCATGGCAGTGGCCCTGGGTGCCCCAGGGCTCATGCTGCTAGGGGGCGGCTTGGTTCTGCTGC  
TGCACCACAAGAAGTACTCAGAGTACCAGTCCATAAATTAAGGCCCGCTCTCTGGAGGGAAGG  
ACATTACTGAACCTGTCTTGCTGTGCCTCGAACTCTGGAGGTTGGAGCATCAAGTTCAGCC  
GGCCCCCTTCACTCCCCCATCTTGCTTTTCTGTGGAACCTCAGAGGCCAGCCTCGACTTCCTGG  
AGACCCCCAGGTGGGGCTTCCTTCATACTTTGTTGGGGGACTTTGGAGGCGGGCAGGGGACAG  
GGCTATTGATAAGGTCCCCTGGTGTTCCTTGCATCTCCACACATTTCCCTTGGATGGG  
ACTTGCAGGCCTAAATGAGAGGCATTCTGACTGGTTGGCTGCCCTGGAAGGCAAGAAAATAGA  
TTTATTTTTTTTTTACAGGGAAAAAAAAAAAAA

**FIGURE 258**

MRGSVECTWGWGHCAPSPLLLWTLLLFAAPFGLLGEKTRQVSLEVIPNWLGPLQNLHRAVG  
TNSTLHYVWSSLGPLAVVMVATNTPHSTLSINWSLLLSPEPDGGLMVLPKDSIQFSSALVFTR  
LLEFDSTNVSDTAAKPLGRPYPPYSLADFSWNNITDSLDPATLSATFQGHMNDPTRTFANGS  
LAFRVQAQFSRSSRPAQPPRLLHTADTCQLEVALIGASPRGNRSLFGLEVATLGQGPDCPSMQE  
QHSIDDEYAPAVFQLDQLLWGS LPSGFAQWRPVAYSQKPGGRESALPCQASPLHPALAYSLPQ  
SPIVRAFFGSQNNFCAFNLTFGASTGPGYWDQHYLSWSMLLGVGFPFVDGLSPLVLGIMAVAL  
GAPGLMLLGGGLVLLLHHKKYSEYQSIN

**Important features:**

**Signal peptide:**

amino acids 1-35

**Transmembrane domain:**

amino acids 365-386

**N-glycosylation sites:**

amino acids 65-69, 95-99, 134-138, 159-163, 187-191, 230-234, 333-337

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

amino acids 397-401

**N-myristoylation sites:**

amino acids 3-9, 63-69, 235-241, 273-279, 292-298, 324-330

**Leucine zipper pattern:**

amino acids 371-393



**FIGURE 259**

CAGGCGGGCCCCCGCGCGGCAGGGCCCTGGACCCGCGCGGCTCCCGGGGATGGTGAGCAAGGCGCTGCTGCGCCT  
 CGTGTCTGCCGTCAACCGCAGGAGGATGAAGCTGCTGCTGGGCATCGCCTTGCTGGCCTACGTCGCCCTCTGTTTG  
 GGGCAACTTCGTTAATATGAGGTCTATCCAGGAAATGGTGAACATAAAATTGAAAGCAAGATTGAAGAGATGGT  
 TGAACCACTAAGAGAGAAAATCAGAGATTTAGAAAAAAGCTTTACCCAGAAATACCCACCAGTAAAGTTTTATC  
 AGAAAAGGATCGGAAAAGAATTTTGATAACAGGAGGCGCAGGGTTCGTGGGCTCCCATCTAACTGACAAACTCAT  
 GATGGACGGCCACGAGGTGACCGTGGTGGACAATTTCTTCACGGGCAGGAAGAGAAACGTGGAGCACTGGATCGG  
 ACATGAGAACTTCGAGTTGATTAACCACGACGTGGTGGAGCCCTCTACATCGAGGTTGACCAGATATACCATCT  
 GGCATCTCCAGCCTCCCCCTCCAACTACATGTATAATCCTATCAAGACATTAAAGACCAATACGATTGGGACATT  
 AAACATGTGGGGCTGGGAAAACGAGTCGGTGCCCGTCTGCTCCTGGCCTCCACATCGGAGGTGTATGGAGATCC  
 TGAAGTCCACCCTCAAAGTGAGGATTACTGGGGCCACGTGAATCCAATAGGACCTCGGGCCTGCTACGATGAAGG  
 CAAACGTGTGTCAGAGACCATGTGCTATGCCATACATGAAGCAGGAAGGCGTGAAGTGCGAGTGGCCAGAATCTT  
 CAACACCTTTGGGGCCACGCATGCACATGAACGATGGGCGAGTAGTCAGCAACTTCATCTGCAGGCGCTCCAGGG  
 GGAGCCACTCACGGTATACGGATCCGGGTCTCAGACAAGGGCGTTCCAGTACGTCAGCGATCTAGTGAATGGCCT  
 CGTGGCTCTCATGAACAGCAACGTGAGCAGCCCGTCAACCTGGGGGAACCCAGAAGAACACACAATCTAGAAATT  
 TGCTCAGTTAATTAAAAACCTTGTTGGTAGCGGAAGTGAAATTCAGTTTCTCTCCGAAGCCCAGGATGACCCACA  
 GAAAAGAAAACAGACATCAAAAAGCAAAGCTGATGCTGGGGTGGGAGCCCGTGGTCCCGCTGGAGGAAGGTTT  
 AAACAAAGCAATTCACACTTCCGTAAAGAACTCGAGTACCAGGCAAATAATCAGTACATCCCCAAACCAAAGCC  
 TGCCAGAATAAAGAAAGGACGGAAGTCCGCCACAGCTGAACCTCTCACTTTTAGGACACAAGACTACCATTGTACAC  
 TTGATGGGATGTATTTTTGGCTTTTTTTTGTGTGCTTTAAAGAAAGACTTTAAACAGGTGTCATGAAGAACAAC  
 TGGAATTTCAATTCGAAGCTTGCTTTAATGAAATGGATGTGCTAAAGCTCCCTCAAAAACTGCAGATTTTG  
 CCTTGCACTTTTTGAATCTCTCTTTTATGTAATAAGCGTAGATGCATCTCTGCGTATTTTCAAGTTTTTTTAT  
 CTTGCTGTGAGAGCATATGTTGTGACTGTGCTTGACAGTTTATTTACTGGTTCTTTGTGAAGCTGAAAAGGAA  
 CATTAAAGCGGGACAAAAATGCCGATTTTATTTATAAAAGTGGGTACTTAATAAATGAGTCGTTATACTATGCAT  
 AAAGAAAAATCCTAGCAGTATTGTGAGGTGGTGGTGCAGCGGATGATTTTAGGGCAGATAAAGAATTCTGTG  
 TGAGAGCTTTATGTTTCTCTTTAATTGAGATTTTTTCAAGGTCTACTTTTGAGTTGCAAACTTGACTTTGAAA  
 TATTCCTGTTGGTCATGATCAAGGATATTTGAAATCACTACTGTGTTTGTGCGTATCTGGGGCGGGGCGAGGT  
 TGGGGGGCACAAAGTTAACATATCTTGTTAACCATGGTTAAATATGCTATTTTAATAAAATATGAAACTCA

**FIGURE 260**

MVSKALLRLVSAVNRRRMKLLLGIALLAYVASVWGNFVNMRSIQENGELKIESKIEEMVEPLR  
EKIRDLEKSFTQKYPPVKFLSEKDRKRILITGGAGFVGSHLTDKLMMDGHEVTVVDNFFTGRK  
RNVEHWIGHENFELINHDVVEPLYIEVDQIYHLASPASPPNYMYPNIKTLKTNTIGTLNMLGL  
AKRVGARLLLASTSEVYGDPEVHPQSEDIWGHVNPIGPRACYDEGKRVAETMCYAYMKQEGVE  
VRVARIFNTFGPRMHMNDGRVVSFILQALQGEPLTVYSGSQTRAFQYVSDLVNGLVALMNS  
NVSSPVNLGNPEEHTILEFAQLIKNLVGSGSEIQFLSEAQDDPQKRKPDIKKAKMLGWEPVV  
PLEEGLNKAIHYFRKELEYQANNQYIPKPKPARIKKGRTRHS

**Important features:**

**Signal peptide:**

amino acids 1-32

**N-glycosylation site:**

amino acids 316-320

**Tyrosine kinase phosphorylation site:**

amino acids 235-244

**N-myristoylation sites:**

amino acids 35-41,101-107,383-389

**Amidation sites:**

amino acids 123-127,233-237

**FIGURE 261**

GCGTGGTGCGGGGCGTGGGGAAATCGGGTTGCCCCAGCCGTTACTGGTCCGCGCAGTCAGGG  
CATCCTCCGCATCCTCCACATCCTTCCATGGCTCTGAAGAATAAAATTCAGTTGTTTATGGATC  
TTGGGTCTGTGTTTGGTAGCCACTACATCTTCCAAAATCCCATCCATCACTGACCCACACTTT  
ATAGACAACTGCATAGAAGCCCACAACGAATGGCGTGGCAAAGTCAACCCTCCCGCGGCCGAC  
ATGAAATACATGATTTGGGATAAAAGGTTTAGCAAAGATGGCTAAAGCATGGGCAAACCAGTGC  
AAATTTGAACATAATGACTGTTTGGATAAAATCATATAAATGCTATGCAGCTTTTGAATATGTT  
GGAGAAAATATCTGGTTAGGTGGAATAAAGTCATTACACCAAGACATGCCATTACGGCTTGG  
TATAATGAAACCCAATTTTATGATTTTGATAGTCTATCATGCTCCAGAGTCTGTGGCCATTAT  
ACACAGTTAGTTTGGGCCAATTCATTTTATGTGCGTTGTGCAGTTGCAATGTGTCTTAACCTT  
GGGGGAGCTTCAACTGCAATATTTGTATGCAACTACGGACCTGCAGGAAATTTTGCAAATATG  
CCTCCTTACGCAAGAGGAGAATCTTGCTCTCTCTGCTCAAAGAAGAGAAATGTGTAAAGAAC  
CTCTGCAGGACTCCACAACCTATTATACCTAACCAAAATCCATTTCTGAAGCCAACGGGGAGA  
GCACCTCAGCAGACAGCCTTTAATCCATTCAGCTTAGGTTTTCTTCTTCTGAGAATCTTTTAA  
TGTCAATTTATATACAAAAGAAATCTCAAATGTTAAAATAAAGGAATAGTTTATTGCTTAATA

**FIGURE 262**

MALKNKFSLWILGLCLVATTSSKIPSITDPHFIDNCIEAHNEWRGKVNPPAADMKYMIWDKG  
LAKMAKAWANQCKFEHNDCLDKSYKCYAAFEYVGENIWLGGIKSFTPRHAITAWYNETQFYDF  
DSLSCSRVCGHYTQLVWANSFYVGCAMCPNLGGASTAIFVCNYGPAGNFANMPYPARGESC  
SLCSKEEKCVKNLCRTPQLIIPNQNPFLLKPTGRAPQQTAFNPFSLGFLLLRIF

**Important features:**

**Signal peptide:**

amino acids 1-23

**N-glycosylation site:**

amino acids 119-123

**N-myristoylation sites:**

amino acids 103-109,150-156,160-166,161-167,175-181

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1:**

amino acids 136-156

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2:**

amino acids 166-178

**FIGURE 263**

CGCCCTCCGACCCGCCCGCGGCGCATTGTGGGATCTGTGGCTTGTGAGGTGGTGGAGGAAA  
AGGCGCTCCGTCATGGGGATCCAGACGAGCCCCGTCCTGCTGGCCTCCCTGGGGGTGGGGCTG  
GTCACTCTGCTCGGCCTGGCTGTGGGCTCCTACTTGGTTTCGGAGGTCCCGCCGGCCTCAGGTC  
ACTCTCCTGGACCCCAATGAAAAGTACCTGCTACGACTGCTAGACAAGACGACTGTGAGCCAC  
AACACCAAGAGGTTCCGCTTTGCCCTGCCCCACGCCCCACCACACTCTGGGGCTGCCCTGTGGGC  
AAACATATCTACCTCTCCACCCGAATTGATGGCAGCCTGGTCATCAGGCCATACACTCCTGTGTC  
ACCAGTGATGAGGATCAAGGCTATGTGGATCTTGTTCATCAAGGTCTACCTGAAGGGTGTGCAC  
CCCAAATTTCTGAGGGAGGGAAGATGTCTCAGTACCTGGATAGCCTGAAGGTTGGGGATGTG  
GTGGAGTTTTCGGGGGCCAAGCGGGTTGCTCACTTACACTGGAAAAGGGCATTTTAACATTAG  
CCCAACAAGAAATCTCCACCAGAACCCCGAGTGGCGAAGAACTGGGAATGATTGCCGGCGGG  
ACAGGAATCACCCCAATGCTACAGCTGATCCGGGCCATCCTGAAAGTCCCTGAAGATCCAACC  
CAGTGCTTTCTGCTTTTTTGCCAACCAGACAGAAAAGGATATCATCTTGCGGGAGGACTTAGAG  
GAACTGCAGGCCCGCTATCCCAATCGCTTTAAGCTCTGGTTCACTCTGGATCATCCCCAAAA  
GATTGGGCCTACAGCAAGGGCTTTGTGACTGCCGACATGATCCGGGAACACCTGCCCGCTCCA  
GGGGATGATGTGCTGGTACTGCTTTGTGGGCCACCCCCAATGGTGCAGCTGGCCTGCCATCCC  
AACTTGGACAACTGGGCTACTCACAAAAGATGCGATTACCTACTGAGCATCCTCCAGCTTC  
CCTGGTGCTGTTTCGCTGCAGTTGTTCCCCATCAGTACTCAAGCACTATAAGCCTTAGATTCTT  
TTCCTCAGAGTTTCAGGTTTTTTTCAGTTACATCTAGAGCTGAAATCTGGATAGTACCTGCAGG  
AACAATATTCTGTAGCCATGGAAGAGGGCAAGGCTCAGTCACTCCTTGGATGGCCTCCTAAA  
TCTCCCCGTGGCAACAGGTCCAGGAGAGGCCCATGGAGCAGTCTCTCCATGGAGTAAGAAGG  
AAGGGAGCATGTACGCTTGGTCCAAGATTGGCTAGTTCCTTGATAGCATCTTACTCTCACCTT  
CTTTGTGTCTGTGATGAAAGGAACAGTCTGTGCAATGGGTTTTACTTAAACTTCACTGTTCAA  
CCTATGAGCAAATCTGTATGTGTGAGTATAAGTTGAGCATAGCATACTTCCAGAGGTGGTNTT  
ATGGAGATGGCAAGAAAGGAGGAAATGATTTCTTCAGATNTCAAAGGAGTCTGAAATATCATA  
TTTCTGTGTGTGTCTCTCTCAGCCCCTGCCCAGGCTAGAGGGAAACAGCTACTGATAATCGAA  
AACTGCTGTTTGTGGCANGAACCCCTGGCTGTGCAAATAAATGGGGCTGAGGCCCTGTGTGA  
TATTGAAGA

**FIGURE 264**

MGIQTSPVLLASLGVLVTLLGLAVGSYLVRRSRRPQVTLLDPNEKYLLRLLDKTTVSHNTR  
FRFALPTAHHTLGLPVGKHIYLSTRIDGSLVIRPYTPVTSDEDQGYVDLVIKVYLKGVHPKFP  
EGGKMSQYLDLKVGDVVEFRGPSGLLTYTGKGHFNIQPNKKSPPEPRVAKKLGMIAGGTGIT  
PMLQLIRAILKVPEDPTQCFLLFANQTEKDIILREDLEELQARYPNRFKLWFTLDHPPKDWAY  
SKGFVTADMIREHLPAPGDDVLVLLCGPPPMVQLACHPNLDKLGYSQKMRFTY

**Important features:**

**Signal peptide:**

amino acids 1-26

**N-glycosylation site:**

amino acids 214-218

**N-myristoylation sites:**

amino acids 22-28, 76-82, 128-134, 180-186

**FIGURE 265**

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAGA  
ACGCGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTATAG  
AATAACATCCACTTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAAGTGCACCTCGGT  
TCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGGCCCCGCCTCAGG  
CTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCAATGCC  
TCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCCAGGAAC  
AGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGACCATCTAC  
AGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATGAGCAGA  
AGATACCTCTGCATGGATTTTCAGAGGCAACATTTTTGGATCACACTATTTTCGACCCGGAGAAC  
TGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACCTCTCCTCAGTATCAC  
TTCTTGGTCACTCTGGGCCGGGCGAAGAGAGCCTTCTGCCAGGCATGAACCCACCCCCGTAC  
TCCCAGTTCTGTCCCGGAGGAACGAGATCCCCCTAATTCACCTTCAACACCCCCATACCACGG  
CGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCTGAACGTGCTGAAGCCCCGG  
GCCCCGATGACCCCGCCCCGGCCTCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGC  
CCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTGAGTGAACACGCACGCTGGGGGA  
ACGGGCCCCGAAGGCTGCCGCCCTTCGCCAAGTTCATCTAGGGTCGCTGG

**FIGURE 266**

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSWGGLIHLYTATARNSYHLQIHKNGHVDG  
APHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQQTLENGYDV  
YHSPQYHFLVSLGRAKRAFLPGMNPPYPYSQFLSRRNEIPLIHFNTPIPRRHTRSAEDDSERDP  
LNVLKPRARMTTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTTHAGGTGPEGCRPFACFI

**Important features:**

**Signal peptide:**

amino acids 1-24

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 175-179

**N-myristoylation site.**

amino acids 33-39, 100-106, 225-231, 229-235

**HBGF/FGF family proteins**

amino acids 73-124



# **FIGURE 267**

GGCTGAGGGGAGGCCCGGAGCCTTTCTGGGGCCTGGGGGATCCTCTTGCACTGGTGGGTGGAGAGAAGCGCCTGC  
AGCCAACCAGGGTCAGGCTGTGCTCACAGTTTCTCTGGCGGCATGTAAAGGCTCCACAAAGGACTTGGGAGTTC  
AAATGAGGCTGCTGCGGACGGCCTGAGGATGGACCCCAAGCCCTGGACCTGCCGAGCGTGGCACTGAGGCAGCGG  
CTGACGCTACTGTGAGGGAAGAAGGTTGTGAGCAGCCCCGAGGACCCCTGGCCAGCCCTGGCCCCAGCCTCTG  
CCGAGGCCCTCTGTGGAGGCAGAGCCAGTGGAGCCAGTGGGCAGGGCTGCTTGGCAGCCACCGGCCTGCAACT  
CAGGAACCCCTCCAGAGGCCATGGACAGGCTGCCCCGCTGACGGCCAGGGTGAAGCATGTGAGGAGCCGCCCGG  
AGCCAAGCAGGAGGGAAGAGGCTTTCATAGATTCTATTACAAAGAATAACCACCATTTTGCAAGGACCATGAGG  
CCACTGTGCGTGACATGCTGGTGGCTCGGACTGCTGGCTGCCATGGGAGCTGTTGCAGGCCAGGAGGACGGTTTT  
GAGGGCACTGAGGAGGGCTCGCCAAGAGAGTTCAATTTACCTAAACAGGTACAAGCGGGCGGGCAGTCCCAGGAC  
AAGTGACCTACACCTTCATTGTGCCCCAGCAGCGGGTACGCGGTGCCATCTGCGTCAACTCCAAGGAGCCTGAG  
GTGCTTCTGGAGAACCGAGTGCATAAGCAGGAGCTAGAGCTGCTCAACAATGAGCTGCTCAAGCAGAAGCGGCAG  
ATCGAGACGCTGCAGCAGCTGGTGGAGTGGACGGCGGCATTGTGAGCGAGGTGAAGCTGCTGCGCAAGGAGAGC  
CGCAACATGAAGCTCGCGGGTACGCGAGCTCTACATGCAGCTCCTGCACGAGATCATCCGCAAGCGGGACAACGCG  
TTGGAGCTCTCCAGCTGGAGAACAGGATCCTGAACCAGACAGCCGACATGCTGCAGCTGGCCAGCAAGTACAAG  
GACCTGGAGCACAAGTACCAGCACCTGGCCACACTGGCCCAACAACCAATCAGAGATCATCGCGCAGCTTGAGGAG  
CACTGCCAGAGGGTGCCCTCGGCCAGGCCCGTCCCCAGCCACCCCCGCTGCCCCGCCCCGGTCTACCAACCA  
CCCACCTACAACCGCATCATCAACCAGATCTCTACCAACGAGATCCAGAGTGACCAGAACCTGAAGGTGCTGCCA  
CCCCCTCTGCCCACTATGCCCACTCTCACCAGCCTCCCATCTTCCACCGACAAGCCGTGGGGCCATGGAGAGAC  
TGCTTGAGGCCCTGGAGGATGGCCACGACACCAGCTCCATCTACCTGGTGAAGCCGGAGAACAACAACCGCCTC  
ATGCAGGTGTGGTGCGACCAGAGACACGACCCCGGGGCTGGACCGTCATCCAGAGACGCTGGATGGCTCTGTT  
AACTTCTTCAGGAAGTGGGAGACGTACAAGCAAGGGTTTGGGAACATTGACGGCGAATACTGGCTGGGCCTGGAG  
AACATTTACTGGCTGACGAACCAAGGCAACTACAACTCCTGGTGACCATGGAGGACTGGTCCGGCCGCAAAGTC  
TTTGCAGAATACGCCAGTTTCCGCCCTGGAACCTGAGAGCGAGTATTATAAGCTGCGGCTGGGGCGCTACCATGGC  
AATGCGGGTGACTCCTTTACATGGCACAAACGGCAAGCAGTTACACCCTGGACAGAGATCATGATGTCTACACA  
GGAACTGTGCCCACTACCAGAAGGGAGGCTGGTGGTATAACGCCTGTGCCCACTCCAACCTCAACGGGGTCTGG  
TACCGCGGGGGCCATTACCGGAGCCGCTACAGGACGGAGTCTACTGGGCTGAGTTCCGAGGAGGCTCTTACTCA  
CTCAAGAAAGTGGTGATGATGATCCGACCGAACCCCAACACCTTCCACTTAAGCCAGCTCCCCCTCCTGACCTCTC  
GTGGCCATTGCCAGGAGCCCAACCTGGTCACGCTGGCCACAGCACAAAGAACAACCTCCTACCAAGTTTATCCTGA  
GGCTGGGAGGACCGGGATGCTGGATTCTGTTTTCCGAAGTCACTGCAGCGGATGATGGAAGTGAATCGATACGGT  
GTTTTCTGTCCCTCCTACTTTCCCTTACACCAGACAGCCCTCATGTCTCCAGGACAGGACAGGACTACAGACAA  
CTCTTTCTTTAAATAAATTAAGTCTCTACAATAAAAAAA

## **FIGURE 268**

MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIVPQQ  
RVTGAICVNSKEPEVLLLENRVHKQELELLNNELLKQKRQIETLQQLVEVDGGIVSEVKLLRKE  
SRNMNSRVTLQYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYKDLEHKYQHLATL  
AHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPRVYQPPTYNRIINQISTNEIQSDQNLKVLP  
PPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTNRLMQVWCDQRHDPGG  
WTVIQRRLDGSVNFFRNWETKQGFNIDGEYWLGLENIYWLTNQGNKLLVTMEDWSGRKVF  
AEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLDRDHDVYTGNCAYQKGGWWYN  
ACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKKVMMIRPNPNTFH

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-glycosylation sites:**

amino acids 164-168, 192-196

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

amino acids 124-128

**Tyrosine kinase phosphorylation sites:**

amino acids 177-184, 385-393, 385-394, 461-468

**N-myristoylation sites:**

amino acids 12-18, 18-24, 22-28, 29-35, 114-120, 341-347, 465-471,  
473-479

**Amidation site:**

amino acids 373-377

**Fibrinogen beta and gamma chains C-terminal domain signature:**

amino acids 438-451

**Fibrinogen beta and gamma chains C-terminal domain proteins:**

amino acids 305-343, 365-402, 411-424, 428-458

**Trehalase proteins:**

amino acids 275-292

# **FIGURE 269**

GCCGAGCTGAGCGGATCCTCACATGACTGTGATCCGATTCTTTCCAGCGGCTTCTGCAACCAA  
GCGGGTCTTACCCCCGGTCCTCCGCGTCTCCAGTCTTCGCACCTGGAACCCCAACGTCCCCGA  
GAGTCCCCGAATCCCCGCTCCAGGCTACCTAAGAGGATGAGCGGTGCTCCGACGGCCGGGGC  
AGCCCTGATGCTCTGCGCCGCCACCGCCGTGCTACTGAGCGCTCAGGGCGGACCCGTGCAGTC  
CAAGTCGCCGCGCTTTGCGTCCCTGGGACGAGATGAATGTCTGGCGCACGGACTCCTGCAGCT  
CGGCCAGGGGCTGCGCGAACACGCGGAGCGCACCCGCAGTCAGCTGAGCGCGCTGGAGCGGCG  
CCTGAGCGCGTGCGGGTCCGCTGTCTAGGGAACCGAGGGGTCCACCGACCTCCCGTTAGCCCC  
TGAGAGCCGGGTGGACCTGAGGTCTTTCACAGCCTGCAGACACAACCTCAAGGCTCAGAACAG  
CAGGATCCAGCAACTCTTCCACAAGGTGGCCAGCAGCAGCGGCACCTGGAGAAGCAGCACCT  
GCGAATTACAGCATCTGCAAAGCCAGTTTGGCCTCCTGGACCACAAGCACCTAGACCATGAGGT  
GGCCAAGCCTGCCCCAAGAAAGAGGCTGCCCGAGATGGCCAGCCAGTTGACCCGGCTCACAA  
TGTCAGCCGCCTGCACCGGCTGCCAGGGATTGCCAGGAGCTGTTCCAGGTTGGGGAGAGGCA  
GAGTGGACTATTTGAAATCCAGCCTCAGGGGTCTCCGCCATTTTGGTGAAGTGAAGATGAC  
CTCAGATGGAGGCTGGACAGTAATTCAGAGGCGCCACGATGGCTCAGTGGACTTCAACCGGCC  
CTGGGAAGCCTACAAGGCGGGGTTTGGGGATCCCCACGGCGAGTTCTGGCTGGGTCTGGAGAA  
GGTGATAGCATCACGGGGGACCGCAACAGCCGCTGGCCGTGCAGCTGCGGGACTGGGATGG  
CAACGCCGAGTTGCTGCAGTTCTCCGTGCACCTGGGTGGCGAGGACACGGCCTATAGCCTGCA  
GCTCACTGCACCCGTGGCCGGCCAGCTGGGCGCCACCACCGTCCCACCCAGCGGCCTCTCCGT  
ACCCTTCTCCACTTGGGACCAGGATCACGACCTCCGCAGGGACAAGAAGTGCGCCAAGAGCCT  
CTCTGGAGGCTGGTGGTTTGGCACCTGCAGCCATTCCAACCTCAACGGCCAGTACTTCCGCTC  
CATCCACAGCAGCGGCAGAAGCTTAAGAAGGGAATCTTCTGGAAGACCTGGCGGGGCCGCTA  
CTACCCGCTGCAGGCCACCACCATGTTGATCCAGCCCATGGCAGCAGAGGCAGCCTCCTAGCG  
TCCTGGCTGGGCCTGGTCCCAGGCCCACGAAAGACGGTGACTCTTGGCTCTGCCCGAGGATGT  
GGCCGTTCCCTGCCTGGGCGAGGGCTCCAAGGAGGGGCCATCTGGAAACTTGTGGACAGAGAA  
GAAGACCACGACTGGAGAAGCCCCCTTTCTGAGTGCAGGGGGGCTGCATGCGTTGCCTCCTGA  
GATCGAGGCTGCAGGATATGCTCAGACTCTAGAGGCGTGACCAAGGGGCATGGAGCTTCACT  
CCTTGCTGGCCAGGGAGTTGGGGACTCAGAGGGACCACTTGGGGCCAGCCAGACTGGCCTCAA  
TGGCGGACTCAGTCACATTGACTGACGGGGACCAGGGCTTGTGTGGGTGAGAGCGCCCTCAT  
GGTGCTGGTGCTGTTGTGTGTAGGTCCCCTGGGGACACAAGCAGGCGCCAATGGTATCTGGGC  
GGAGCTCACAGAGTTCTTGAATAAAAGCAACCTCAGAACAC

## **FIGURE 270**

MTVIRFFPAASATKRVLPVLRVSSPRTWNPVNPESPRIPAPRLPKRMSGAPTAGAALMLCAA  
TAVLLSAQGGPVQSKSPRFASWDEMNVLAHGLLQLGQGLREHAERTRSQLSALERRLSACGSA  
CQGTEGSTDLPLAPESRVDPEVLHSLQTQLKAQNSRIQQLFHKVAQQQRHLEKQHLRIQHLQS  
QFGLLDHKHLDHEVAKPARRKRLPEMAQPVDPAHNVSRLHRLPRDCQELFQVGERQSGLFEIQ  
PQGSPPFLVNCKMTSDGGWTVIQRRHDGSVDFNRPWEAYKAGFGDPHGEFWLGLEKVHSITGD  
RNSRLAVQLRDWDGNAELLQFSVHLGGEDTAYSLQLTAPVAGQLGATTVPSPGLSVPFSTWDQ  
DHDLRRDKNCAKSLSGGWWFGTCSHSNLNGQYFRSIPQQRQKLKKGIFWKTRGRYYPLQATT  
MLIQPMAAEAAAS

**Important features:**

**Signal peptide:**

Amino acids 1-13

**Transmembrane domain:**

Amino acids 53-70

**N-glycosylation site:**

Amino acids 224-228

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 46-50;118-122

**N-myristoylation sites:**

Amino acids 50-56;129-135;341-347;357-363

**Fibrinogen beta and gamma chains C-terminal domain signature:**

Amino acids 396-409

**FIGURE 271**

CGGACGCGTGGGGGAAACCCCTTCCGAGAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGGG  
AACAAGATGGCGGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAAGCTGGGGCTCCCGCCGCTG  
CTGCTGCTGACCATGGCCTTGGCCGGAGGTTGCGGGACCGCTTCGGCTGAAGCATTTGACTCG  
GTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGACACCTAC  
CCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTCAGTTT  
GTGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAGCA  
TATTCCTCAATCTGATGAGCAATATGCTTGCCATCTTGTTGCCAGAATCAGCTGCCATTTCGCT  
GAACTGAGACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTCCTCTAACT  
CTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACCTCTTCATGG  
ACTTTTTATCTTCAAGCCGATGACGGAAAAATAGTTATATTCAGTCTAAGCCAGAAATCCAG  
TACGCACCACATTTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAAGCAAAATGTCC  
TATCTGCAAATGAGAAATTCACAAGCGCACAGGAATTTTCTTGAAGATGGAGAAAGTGATGGC  
TTTTTAAGATGCCTCTCTCTTAACTCTGGGTGGATTTTAACTACAACTCTTGTCTCTCGGTG  
ATGGTATTGCTTTGGATTGTTGTGCAACTGTTGCTACAGCTGTGGAGCAGTATGTTCCCTCT  
GAGAAGCTGAGTATCTATGGTGACTTGGAGTTTATGAATGAACAAAAGCTAAACAGATATCCA  
GCTTCTTCTCTTGTGGTTGTTAGATCTAAACTGAAGATCATGAAGAAGCAGGGCCTCTACCT  
ACAAAAGTGAATCTTGCTCATCTGAAATTTTAAGCATTTTTCTTTTAAAAGACAAGTGTAATA  
GACATCTAAATTCCTCCTCATAGAGCTTTTAAATGGTTTCATTGGATATAGGCCTTAAG  
AAATCACTATAAAATGCAAATAAAGTTACTCAAATCTGTG

## **FIGURE 272**

MAAPKGS LWVRTQLGLPPLLLLLTMALAGGSGTASAEAFDSVLGDTASCHRA CQLTYPLHTYPK  
EEELYACQ RGCRLFSICQFVDDGIDLNR TKLECESACTEAYSQSDEQYACHLGCQNQLPFAEL  
RQEQLMSLMPKMHLLFPLTLVRSFWSDMMDSAQS FITSSWTFYLQADDGKIVIFQSKPEIQYA  
PHLEQEPTNLRESSLSKMSY LQMRNSQAHRNFLEDGESDGFRLCLSLNSGWILTTTLVLSVMV  
LLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLN RYPASSLVVVRSKTEDHEEAGPLPTK  
VNLAHSEI

**Important features:**

**Signal peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 241-260

**N-glycosylation site:**

amino acids 90-94

**N-myristoylation sites:**

amino acids 28-34,29-35,31-37,86-92

**FIGURE 273**

CCCACGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCCCGCTGCTGCCCAACCTCACTCTGTG  
CTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGCGCCATGACCGA  
CCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCACGT  
GCAGGTCAACGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGGCAAGCTCAT  
AGTGGAGACGGACACGTTTGGCAGCCGGGTTCGCATCAAAGGGGCTGAGAGTGAGAAGTACAT  
CTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCCAGCGGGAAGAGCAAAGACTGCGTGTT  
CACGGAGATCGTGCTGGAGAACAACCTATACGGCCTTCCAGAACGCCCCGGCACGAGGGCTGGTT  
CATGGCCTTCACGCGGCAGGGGCGGCCCCGCCAGGCTTCCCGCAGCCGCCAGAACCAGCGCGA  
GGCCCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCCAACACGCCGAGAAGCA  
GAAGCAGTTCGAGTTTGTGGGCTCCGCCCCCACC CGCCGACCAAGCGCACACGGCGGCCCCA  
GCCCCCTCAGTAGTCTGGGAGGCAGGGGGCAGCAGCCCCCTGGGCGCCTCCCCACCCCTTTCC  
CTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCCGAGGGAGGACCC  
TGAGGGCCGCGAAGCATCCGAGCCCCCAGCTGGGAAGGGGCAGGCCGGTGCCCCAGGGGCGGC  
TGGCACAGTGCCCCCTTCCCGACGGGTGGCAGGCCCTGGAGAGGAACTGAGTGTACCCCTGA  
TCTCAGGCCACCAGCCTCTGCCGGCCTCCAGCCGGGCTCCTGAAGCCCGCTGAAAGGTCAGC  
GACTGAAGGCCTTGACAGACAACCGTCTGGAGGTGGCTGTCCTCAAAATCTGCTTCTCGGATCT  
CCCTCAGTCTGCCCCCAGCCCCCAAACCTCCTCCTGGCTAGACTGTAGGAAGGGACTTTTGT'TT  
GTTTGT'TTGT'TTCAGGAAAAAAGAAAGGGAGAGAGAGGAAAAATAGAGGGTTGTCCACTCCTCA  
CATTCCACGACCCAGGCCTGCACCCCCACCCCAACTCCCAGCCCCGGAATAAAACCATTTTCC  
TGC

**FIGURE 274**

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRIS  
ATAEDGNKFAGLIVETDTFGSRVRIKGAESEKYICMNRGKLGKPSGKSKDCVFTEIVLENN  
YTAFQONARHEGWFMFAFTRQGRPRQASRSRQNRQEAHFIKRLYQGQLPFPNHAEKQKQFEFVGS  
APTRRTKRTRRPQPLT

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 9-13, 126-130

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 60-64

**Casein kinase II phosphorylation site.**

amino acids 65-69

**Tyrosine kinase phosphorylation site.**

amino acids 39-48, 89-97

**N-myristoylation site.**

amino acids 69-75, 188-194

**Amidation site.**

amino acids 58-62

**HBGF/FGF family signature.**

amino acids 103-128



**FIGURE 275**

TATTTACCATATCAGATTCACATTCAGTCCTCAGCAAAATGAAGGGCTCCATTTTCACTCTGT  
TTTTATTCTCTGTCCTATTTGCCATCTCAGAAGTGCGGAGCAAGGAGTCTGTGAGACTCTGTG  
GGCTAGAATACATACGGACAGTCATCTATATCTGTGCTAGCTCCAGGTGGAGAAGGCATCTGG  
AGGGGATCCCTCAAGCTCAGCAAGCTGAGACAGGAACTCCTTCCAGCTCCACATAAACGTG  
AGTTTTCTGAGGAAAATCCAGCGCAAAACCTTCCGAAGGTGGATGCCTCAGGGGAAGACCGTC  
TTTGGGGTGGACAGATGCCCACTGAAGAGCTTTGGAAGTCAAAGAAGCATTCAGTGATGTCAA  
GACAAGATTTACAACTTTGTGTTGCACTGATGGCTGTTCCATGACTGATTTGAGTGCTCTTT  
GCTAAAGACAAGAGCAAATACCCAATGGGTGGCAGAGCTTTATCACATGTTTAATTACAGTGTT  
TTACTGCCTGGTAGAACACTAATATTGTGTTATTAAAAATGATGGCTTTTGGGTAGGCAAAAC  
TCTTTTCTAAAAGGTATAGCTGAGCGGTTGAAACCACAGTGATCTCTATTTTCTCCCTTTGCC  
AAGGTTAATGAACTGTTCTTTTCAAATTTCTACTAATGCTTTGAAATTTCAAATGCTGCGCAA  
ATTGCAATAAAAAATGCTATAAA

**FIGURE 276**

MKGSIFTLFLFSVLFAISEVRSKESVRLCGLEYIRTVIYICASSRWRRHLEGIPQAQQAETGN  
SFQLPHKREFSEENPAQNLPKVDASGEDRLWGGQMPTEELWKSCKHVSMSRQDLQTLCTDGC  
SMTDLSALC

**Important features:**

**Signal sequence:**

amino acids 1-18

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

amino acids 107-111

**N-myristoylation sites:**

amino acids 3-9, 52-58, 96-102, 125-131

**Insulin family signature:**

amino acids 121-136

**Insulin family proteins:**

amino acids 28-46

# **FIGURE 277**

GCAGCTGGTTACTGCATTCTCCATGTGGCAGACAGAGCAAAGCCACAACGCTTTCTCTGCTGGATTAAAGACGG  
 CCCACAGACCAGAACTTCCACTATACTACTTAAATACATAGGTGGCTTGTCAAATTCATTGATTAGTATTGT  
 AAAAGGAAAAAGAAAGTTCTTCTTACAGCTTGGATTCAACGGTCCAAAACAAAATGCAGCTGCCATTAAAGTCT  
 CAGATGAACAACTTCTACACTGATTTTTTAAATCAAGAATAAGGGCAGCAAGTTTCTGGATTCACTGAATCAAC  
 AGACACAAAAGCTGGCAATATAGCAACTATGAAGAGAAAAGCTACTAATAAAATTAAACCAACGCATAGAAGAC  
 TTTTTTTCTCTTCTAAAAACAACCTAAGTAAAGACTTAAATTTAAACACATCATTTTACAACCTCATTTCAAAAT  
 GAAGACTTTTACCTGGACCTTAGGTGTGCTATTCTCTCTACTAGTGGACACTGGACATTGCAGAGGTGGACAATT  
 CAAAATTAATAAATAAACCAGAGAAGATACCTCTCGTGCCACAGATGGTAAAGAGGAAGCAAAGAAATGTGCATA  
 CACATTCTGTGCTACCTGAACAAAGAATAACAGGGCCAATCTGTGTCAACACCAAGGGGCAAGATGCAAGTACCAT  
 TAAAGACATGATCACCAGGATGGACCTTGAAAACCTGAAGGATGTGCTCTCCAGGCAGAAGCGGGAGATAGATGT  
 TCTGCAACTGGTGGTGGATGTAGATGGAACATTGTGAATGAGGTAAAGCTGCTGAGAAAAGGAAAGCCGTAACAT  
 GAACCTCTGCTGTACTCAACTCTATATGCAATTATTACATGAGATTATCCGTAAGAGGGATAATTCACTTGAACCT  
 TTCCCAACTGGAAAACAAAATCTCAATGTCAACACAGAAATGTTGAAGATGGCAACAGATACAGGGAACTAGA  
 GGTGAATAACGCTTCTTGACTGATCTTGTCAATAACCAATCTGTGATGATCACTTTGTTGGAAGAACAGTGCTT  
 GAGGATATTTTCCCGACAAGACACCCATGTGTCTCCCACTTGTCCAGGTGGTCCACAACATATTCTTAAACAG  
 CCAACAGTATACTCTGGTCTGCTGGGAGGTAAACGAGATTCAAGGGATCCAGGTTATCCAGAGATTTAATGCC  
 ACCACCTGATCTGGCACTTCTCCCAACAAAAGCCCTTTCAAGATACACCCGTAACCTTTCATCAATGAAGGACC  
 AATCAAAGACTGTCAGCAAGCAAAGAAGCTGGGCATTGGTCACTGGGATTTATATGATTAAACCTGAAAACAG  
 CAATGGACCAATGTCAGTTATGGTGTGAAAAACAGTTTGGACCTGGGGGTTGACTGTTTATTTCAGAAAAGACAGA  
 CGGCTCTGTCACTTCTTCAGAAATTTGGGAAAATTATAAGAAAGGGTTTGGAAACATTGACGGAGAATACTGGCT  
 TGGACTGGAAAATATCTATATGCTTAGCAATCAAGATAATTACAAGTTATTGATTGAATTAGAAGACTGGAGTGA  
 TAAAAAGTCTATGCAGAATACAGCAGCTTTCGTCTGGAACCTGAAAGTGAATTCTATAGACTGCGCCTGGGAAC  
 TTACCGGGAAATGCAGGGGATTCTATGATGTGGCATAATGGTAAACAATTCAACACACTGGACAGAGATAAAGA  
 TATGTATGCAGGAACTGCGCCCACTTTCATAAAGGAGGCTGGTGTACAAATGCCTGTGCACATTCTAACCTAAA  
 TGGAGTATGGTACAGAGGAGGCCATTACAGAAGCAAGCACAAGATGGAATTTCTGGGCCGAATACAGAGGCGG  
 GTCATACTCCTTAAGAGCAGTTTCAAGTATGATCAAGCCTATTGACTGAAGAGAGACACTCGCCAATTTTAAATGA  
 CACAGAACTTTTGTACTTTTCACTCTTAAAAATGTAAATGTTACATGTATATTACTTGGCACAATTTATTCTAC  
 ACAGAAAGTTTTTAAATGAATTTTACCGTAACCTATAAAGGGAACCTATAAATGTAGTTTTCATCTGTCTCAAT  
 TACTGCAGAAAATATGTGTATCCACAACCTAGTTATTTTAAAAATTTATGTTGACTAAATACAAAGTTTGTCTT  
 TAAAAATGTAAATATTTGCCACAATGTAAAGCAAATCTTAGCTATATTTTAAATCATAAATAACATGTTCAAGATA  
 CTTAACAATTTATTTAAATCTAAGATTGCTCTAACGTCTAGTGAAAAAATATTTTAAATTTTCAAGCCAAATA  
 ATGCATTTTATTTTATAAATAACAGACAGAAAATTTAGGGAGAAAATCTAGTTTTCGCAATAGAAAATGTTCTT  
 CCATTGAATAAAAGTTATTTCAAATTTGAATTTGTGCTTTTCAACGTAATGATTAAATCTGAATTTCTTAATAATA  
 TATCCTATGCTGATTTTCCCAAAACATGACCCATAGTATTAAATACATATCATTTTAAAAATAAAAAAAACCC  
 AAAAATAATGCATGCATAATTTAAATGGTCAATTTATAAAGACAAATCTATGAATGAATTTTTCAGTGTATCTT  
 CATATGATATGCTGAACACCAAAATCTCCAGAAATGCATTTTATGTAGTTCTAAATCAGCAAAATATTGGTATT  
 ACAAAAATGCAGAAATTTTAGTGTGCTACAGATCTGAATTATAGTTCTAATTTATTACTTTTCTAATTT  
 ACTGATCTTACTACTACAAAGAAAAAAACCCAAACCATCTGCAATTCAAATCAGAAAGTTTGGACAGCTTTAC  
 AAGTATTAGTGCATGCTCAGAACAGGTGGGACTAAACAACTCAAGGAAGTGTGGCTGTTTTCCCGATACTGA  
 GAATTCACAGCTCCAGAGCAGAGCCACAGGGGCATAGCTTAGTCCAACTGCTAATTTTCAATTTTACAGTGTAT  
 GTAACGCTTAGTCTCACAGTGTCTTAACTCATCTTTGCAATCAACAACCTTACTAGTGACTTTCTGGAACAAT  
 TCCTTTTCAAGAAATACATATTCACTGCTTAGAGGTGACCTTGCCCTTAATATATTTGTGAAGTTAAAAATTTAAAGA  
 TAGCTCATGAACTTTTGTCTTAAGCAAAAAGAAAACCTCGAATTGAAATGTGTGAGGCAAACTATGCATGGGAAT  
 AGCTTAATGTGAAGATAATCATTTTGACAACCTCAAATCCATCAACATGACCAATGTTTTTCATCTGCCACATCTC  
 AAAATAAACTTCTGGTGAACAAATTAACAAAATATCCAAACCTCAAAAAAA

**FIGURE 278**

MKTFTWTLGVLFFLLVDTGHCRRGGQFKIKKINQRRYPRATDGKEEAKKCAYTFLVPEQRITGP  
ICVNTKGQDASTIKDMITRMDLENLKDVLRSQKREIDVLQLVVDVDGNIVNEVKLLRKESRNM  
NSRVTQLYMQLLHEIIRKRDNSLELSQLENKILNVTTEMLKMATRYRELEVKYASLTDLVNNQ  
SVMITLLEEQLRIFSRQDTHVSPPLVQVVPQHIPNSQQYTPGLLGNEIQRDPGYPRDLMPP  
PDLATSPTKSPFKIPPVTFINEGPFKDCQQAKEAGHSVSGIYMIKPENSNGPMQLWCENSLDP  
GGWTVIQKRTDGSVNFFRNWENYKKGFGNIDGEYWLGLENIYMLSNQDNYKLLIELEDWSDKK  
VYAEYSSFRLEPESEFYRLRLGTYQGNAGDSMMWHNGKQFTTLDRDKDMYAGNCAHFHKGWW  
YNACAHSNLNGVWYRGGHYRSKHQDGIFWAEYRGGSYSLRAVQMMIKPID

**Important features:**

**Signal sequence:**

Amino acids 1-23

**N-glycosylation sites:**

Amino acids 160-164;188-192

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 120-124

**Tyrosine kinase phosphorylation sites:**

Amino acids 173-180;387-396

**N-myristoylation sites:**

Amino acids 70-76;110-116;232-238,343-349;400-406;467-473;  
475-487

**Fibrinogen beta and gamma chains C-terminal domain signature:**

Amino acids 440-453

**FIGURE 279**

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCGCGATCCCggc  
CCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCGGACCGCCG  
CCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTGC GGAGAAGCC  
CGGGCAAACGCAGGCTAAGGAGACCAAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAGCGGA  
GGAGAAGGAGGAGGAGGCGAACCAGAGAGGGGCAGCAAAAGAAGCGGTGGTGGTGGGCGTCG  
TGGCCATGGCGGCGGCTATCGCCAGCTCGCTCATCCGTGAGAAGAGGCAAGCCCGCGAGCGCG  
AGAAATCCAACGCCTGCAAGTGTGTCAGCAGCCCCAGCAAAGGCAAGACCAGCTGCGACAAAA  
ACAAGTTAAATGTCTTTTCCCGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAGAAGAAGAC  
CAGAGCCTCAGCTTAAGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACCACTTGCAGC  
TGCAGGCGGATGGAACCATTGATGGCACCAAAGATGAGGACAGCACTTACACTCTGTTTAACC  
TCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCTGTACTTGGCAA  
TGAACAGTGAGGGATACTTGTACACCTCGGAACTTTTACACCTGAGTGCAAATTCAAAGAAT  
CAGTGTGTTGAAAATTATTATGTGACATATTCAATGATATACCGTCAGCAGCAGTCAGGCC  
GAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAACCATGTGAAGAAGA  
ACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGTACAAGGAGCCATCAC  
TGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACCAAGAGCAGAAGTGTCT  
CTGGCGTGCTGAACGGAGGCAAATCCATGAGCCACAATGAATCAACGTAGCCAGTGAGGGCAA  
AAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAATTCTTCTAGCAGTCCTTCA  
CCCAAAAGTTCAAATTTGTGAGTGACATTTACCAAACAAACAGGCAGAGTTCACTATTCTATC  
TGCCATTAGACCTTCTTATCATCCATACTAAAGC

**FIGURE 280**

MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGKTSCKDNKLNVFSRVKLFSGSKRRRRRPE  
PQLKGIVTKLYSRQGYHLQLQADGTIDGTKDEDDSTYTLFNLIPVGLRVVAIQGVQTKLYLAMN  
SEGILYTSELFTPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLNKEGEIMKGNHVKKNK  
PAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSMHNEST

**Important Features:**

**N-glycosylation site:**

Amino acids 242-246

**Glycosaminoglycan attachment sites:**

Amino acids 165-169, 218-222

**Tyrosine kinase phosphorylation site:**

Amino acids 93-100

**N-myristoylation sites:**

Amino acids 87-93, 231-237

**ATP/GTP-binding site motif A (P-loop):**

Amino acids 231-239

**HBGF/FGF family proteins:**

Amino acids 78-94, 102-153

**FIGURE 281**

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGGA  
CTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGGCA  
ACCTGGATATTCTGAGACATATTTTGGGGGGATTTCAGTGAAAAAGTGGGGGATCCCCCTCCA  
TTTAGAGTGTAGCAAAGGAAAAACACCAAGGTTGGGTTCTTCTGACATTGGCAGTGCCCC  
AGTAGGGGTGGGATGAGCGAATATTCCTCAAAGCTAAAGTCCCACACCCTGTAGATTACAAGAG  
TGGATTTGGCAGGAGTGTGCCCCAAAATACAGTGGAAAGGTGCCTGAAGATATTTAAACCACG  
TCTTGAAATTTAGTGGGTCTTGGCTTTGGGATAGGTGAAGTGAGGACAGACACTGGAGAGGA  
GGGAAAGGGGACGTTTTCAATAGGAGGCAAACTCGAGGGTGGGATCCACTGAGGAGTACATA  
GGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCCACGGGTGGTAACTGGCTGCTGTGGAGGGG  
GGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGGTCCTGTGGGTGGGGCAGCGAGTCGGGG  
CCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCCAGCGCGCTCCGGG  
CGCCTGCCGTTTGGGGGTGTCTCCTCCCGGGGCGCTATGGCGGGCGCTGGCCAGTAGCCTGAT  
CCGGCAGAAGCGGGAGGTCCGCGAGCCCGGGGCGAGCCGGCCGGTGTGCGCGCAGCGGCGCGT  
GTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCCTGCTGTCCAAGGTGCG  
ACTGTGCGGGGGGCGGCCCGCGCGGCGGACCGCGGCCCCGAGCCTCAGCTCAAAGGCATCGT  
CACCAAAGTGTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCGACGGAAGCATCCAGGG  
CACCCCAGAGGATACCAGCTCCTTCACCCACTTCAACCTGATCCCTGTGGGCCTCCGTGTGGT  
CACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGCTGAGGGACTGCTCTACAG  
TTCGCCGCATTTACAGCTGAGTGTGCTTTAAGGAGTGTGTCTTTGAGAATTACTACGTCCT  
GTACGCCTCTGCTCTTACCGCCAGCGTCGTTCTGGCCGGGCTGGTACCTCGGCCTGGACAA  
GGAGGGCCAGGTCATGAAGGGAACCGAGTTAAGAAGACCAAGGCAGCTGCCCACTTTCTGCC  
CAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCCACAGTGTCCCCGAGGCCTCCCC  
TTCCAGTCCCCCTGCCCCCTGAATGTAGTCCCTGGACTGGAGGTTCCCTGCACTCCCAGTGA  
GCCAGCCACCACACAACCTGT

**FIGURE 282**

MAALASSLIRQKREVREPGGSRPVSAQRRVCPRGTKSLCQKQLLILLSKVRLCGGRPARPDRG  
PEPQLKGIVTKLFCRQGFYLOANPDGSIQGTPEDTSSFTHFNLIPVGLRVVTIQSAKLGHYMA  
MNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNRVKK  
TKAAAHFLPKLLEVAMYQEPSLHSVPEASPSPPAP

**Important features:**

**Tyrosine kinase phosphorylation site:**

Amino acids 199-207

**N-myristoylation sites:**

Amino acids 54-60; 89-95; 131-137

**HBGF/FGF family signature:**

Amino acids 131-155



**FIGURE 283**

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTGG  
GACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGCTCTGCAACGGC  
AACCTGGTGGATATCTTCTCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGGCGC  
CAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTTGCAA  
ATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCTTCAAC  
CTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTATATAGCC  
ATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTTTAAAGAA  
TCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGGAATCTGGT  
AGAGCCTGGTTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGAGTAAAGAAA  
ACCAAACCAGCAGCTCATTTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCGAGAACCATCT  
TTGCATGATGTTGGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAAGCACAAAGTGCG  
TCTGCAATAATGAATGGAGGCAAACAGTCAACAAGAGTAAGACAACATAG

**FIGURE 284**

MAAAIASGLIRQKRQAREQHWDRPSASRRRSSPSKNRGLCNGNLVDIFSKVRIFGLKKRRLRR  
QDPQLKGIVTRLYCRQGYLQMHPDGALDGTKDDSTNSTLFNLIIPVGLRVVAIQGVKTGLYIA  
MNGEGYLYPSELFTEPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNRVKK  
TKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKSITT

**Important features:**

**N-glycosylation sites:**

Amino acids 100-104, 242-246

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 28-32, 29-33

**Tyrosine kinase phosphorylation site:**

Amino acids 199-207

**N-myristoylation sites:**

Amino acids 38-44, 89-95, 118-124, 122-128, 222-228

**HBGF/FGF family proteins:**

Amino acids 104-155, 171-198

# **FIGURE 285**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGTTTCAGGTCCAGGTTTGTCTTGA  
 TCCTTTTCAAAAAGTGGAGACACAGAAGAGGCTCTAGGAAAAAGTTTGGATGGGATTATGTGGAAGTACCT  
 GCGATTCTCTGCTGCCAGAGCAGGCTCGGCGCTTCCACCCAGTGCAGCCTTCCCCTGGCGGTGGTGAAAGAGAC  
 TCGGGAGTCGCTGCTTCCAAAGTGCCCGCGTGAGTGAGCTCTCACCCAGTCAGCCAAATGAGCCTCTTCGGGC  
 TTCTCCTGCTGACATCTGCCCTGGCCGGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTGAGTAGTAAATTCC  
 AGTTTTCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAATTATTACTGTGTCTACTAATG  
 GAAGTATTCACAGCCCAAGGTTTCTCATACTTATCCAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAG  
 AGGAAAATGTATGGATACAACCTTACGTTTGTATGAAAGATTGGGCTTGAAGACCCAGAAGATGACATATGCAAGT  
 ATGATTTTGTAGAAGTTGAGGAACCCAGTGATGGAATATATTAGGGCGCTGGTGTGGTCTGGTACTGTACCAG  
 GAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTGTATCTGATGAATATTTTCTTCTGAACCAGGCT  
 TCTGCATCCACTACAACATTGTCTATGCCACAATTCACAGAAGCTGTGAGTCCCTTCAGTGTACCCCTTCAGCTT  
 TGCCACTGGACCTGCTTAATAATGCTATAACTGCCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACCAG  
 AGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTTTTGGAA  
 GAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACCTCT  
 CAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTCTGCGCAGGTTGTCTCCTGGTTAAACGCTGTG  
 GTGGGAAGTGTGCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAGTTACTAAAAAATACC  
 ACGAGGTCCTTCAGTTGAGACCAAGACCGGTGTGAGGGGATTGCACAAATCACTCACCGACGTGGCCCTGGAGC  
 ACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGGATAGCCGCATCACCACCAGCAGCTCTGCCCA  
 GAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGTCT  
 TCAAGGACCTTTTCACTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAAAGAAATTAGGAGTTGTGCA  
 ACAGCTCTTTTGTAGAGGAGGCCCTAAAGGACAGGAGAGAAAGGCTCTCAATCGTGAAAGAAAATTAAATGTTGTAT  
 TAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTTCACTTCTTTC  
 GATACGGCTTAGGGTAATGTCTAGTACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCGGTGTGCTTGTCTTAAC  
 TCTAAAGCTCCATGTCTTGGGCTTAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTGTCTCATATTACAT  
 ATGTAAACCAGAACATTTCTATGTACTACAAACCTGGTTTTTAAAAAGGAATATGTTGCTATGAATTAACTTGT  
 GTCATGCTGATAGGACAGACTGGATTTTCATATTTCTTATTAAATTTCTGCCATTTAGAAGAAGAGAACTACA  
 TTCATGGTTTGAAGAGATAAACCTGAAAAGAGAGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTG  
 TTTCACTGTGTACATTTTTATATTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTAAATATATCT  
 ATTTTTACCAAAGGTATTTAATATTCTTTTTTATGACAACTTAGATCAACTATTTTTCAGCTTGGTAAATTTTCT  
 AAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTCA  
 TTCTCGTATGGTGTAGAGTTAGATTAACTGTGCAATTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAA  
 GACTTTTTGAAAATAATTAAATTATCATATCTTCCATTCTGTTATTGGAGATGAAAATAAAAAGCAACTTATGA  
 AAGTAGACATTGAGATCCAGCCATTACTAACCTATTCCTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACAT  
 AAAGCACCTTGAAAAGAGCTTGGCAGCTTCTGATAAAGCGTGTGTGTGTGAGTAGGAACACATCCTATTTA  
 TTGTGATGTTGTGGTTTTATTATCTTAACTCTGTTCCATACACTTGTATAAATACATGGATATTTTATGTACA  
 GAAGTATGTCTTTAACAGTTCACTTATTGTACTCTGGCAATTTAAAAAGAAAATCAGTAAATATTTTGTCTGT  
 AAAATGCTTAATATNGTGCCTAGGTTATGTGGTGACTATTTGAATCAAAAATGTATGAATCATCAAATAAAGA  
 ATGTGGCTATTTTGGGGAGAAAATTAAAAAAGGTTTAGGGATAACAGGGTAATGCGGCC

## **FIGURE 286**

MSLFGLLLLT SALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRF  
PHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWCGS  
GTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNNA  
ITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLITEEVRLYCTP  
RNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRPKT  
GVRGLHKS LTDVALEHHHEECDCVCRGSTGG

**Important features:**

**signal sequence:**

Amino acids 1-14

**N-glycosylation sites:**

Amino acids 25-29;55-59;254-258

**N-myristoylation sites:**

Amino acids 15-21;117-123;127-133;281-287;282-288;319-325

**Amidation site:**

Amino acids 229-233

**FIGURE 287**

CAGCGCTGACTGCGCCGCGGAGAAAAGCCAGTGGGAACCCAGACCCATAGGAGACCCGCGTCCC  
CGCTCGGCCTGGCCAGGCCCCGCGCT**ATG**GAGTTCCTCTGGGCCCCTCTCTTGGGTCTGTGCT  
GCAGTCTGGCCGCTGCTGATCGCCACACCGTCTTCTGGAACAGTTCAAATCCCAAGTTCCGGA  
ATGAGGACTACACCATACATGTGCAGCTGAATGACTACGTGGACATCATCTGTCCGCACTATG  
AAGATCACTCTGTGGCAGACGCTGCCATGGAGCAGTACATACTGTACCTGGTGGAGCATGAGG  
AGTACCAGCTGTGCCAGCCCCAGTCCAAGGACCAAGTCCGCTGGCAGTGCAACCGGCCAGTG  
CCAAGCATGGCCCGGAGAAGCTGTCTGAGAAGTTCCAGCGCTTCACACCTTTCACCCTGGGCA  
AGGAGTTCAAAGAAGGACACAGCTACTACTACATCTCCAAACCCATCCACCAGCATGAAGACC  
GCTGCTTGAGGTGAAGGTGACTGTGAGTGGCAAAATCACTCACAGTCTCAGGCCCATGACA  
ATCCACAGGAGAAGAGACTTGCAGCAGATGACCCAGAGGTGCGGGTTCTACATAGCATCGGTC  
ACAGTGTGCCCCACGCCTCTTCCCACTTGCCTGGACTGTGCTGCTCCTTCCACTTCTGCTGC  
TGCAAAACCCCG**TGA**AGGTGTGTGCCACACCTGGCCTTAAAGAGGGACAGGCTGAAGAGAGGGA  
CAGGCACTCCAAACCTGTCTTGGGGCCACTTTCAGAGCCCCCAGCCCTGGGAACCACTCCCAC  
CACAGGCATAAGCTATCACCTAGCAGCCTCAAAACGGGTCAATATTAAGGTTTTCAACCGGAA  
GGAGGCCAACCAGCCCGACAGTGCCATCCCCACCTTCACCTCGGAGGGATGGAGAAAGAAGTG  
GAGACAGTCCTTTCCCACCATTCCTGCCTTTAAGCCAAAGAAACAAGCTGTGCAGGCATGGTC  
CCTTAAGGCACAGTGGGAGCTGAGCTGGAAGGGGCCACGTGGATGGGCAAAGCTTGTCAAAGA  
TGCCCCCTTCAGGAGAGAGCCAGGATGCCCAGATGAACTGACTGAAGGAAAAGCAAGAAACAG  
TTTCTTGCTTGGAAGCCAGGTACAGGAGAGGCAGCATGCTTGGGCTGACCCAGCATCTCCCAG  
CAAGACCTCATCTGTGGAGCTGCCACAGAGAAGTTTGTAGCCAGGTACTGCATTCTCTCCCAT  
CCTGGGGCAGCACTCCCCAGAGCTGTGCCAGCAGGGGGGCTGTGCCAACCTGTTCTTAGAGTG  
TAGCTGTAAGGGCAGTGCCCATGTGTACATTCTGCCTAGAGTGTAGCCTAAAGGGCAGGGCCC  
ACGTGTATAGTATCTGTATATAAGTTGCTGTGTGTCTGTCTGATTTCTACAACCTGGAGTTTT  
TTTATACAATGTTCTTTGTCTCAAAATAAAGCAATGTGTTTTTTTCGG

**FIGURE 288**

MEFLWAPLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSADAAM  
EQYILYLVEHEEYQLCQPQSKDQVRWQCNRPQSAKHGPEKLSEKFQRFPTFTLGKEFKEGHSYY  
YISKPIHQHEDRCLRLKVTVSGKITHSPQAHNDNPQEKRLAADDPEVRVLHSIGHSAAPRLFPL  
AWTVLLLLPLLLLQTP

**Important features:**

**Signal sequence:**

Amino acids 1-17

**N-glycosylation site:**

Amino acids 26-30

**Tyrosine kinase phosphorylation site:**

Amino acids 118-127

**N-myristoylation site:**

Amino acids 10-16

**FIGURE 289**

CGGACGCGTGGGCGGACGCGTGGGCGGCCACGGCGCCCGGGCTGGGGCGGTCGCTTCTTC  
 CTTCTCCGTGGCTTACGAGGGTCCCCAGCCTGGGTAAAGATGGCCCCATGGCCCCGAAGGGC  
 CTAGTCCCAGCTGTGCTCTGGGCGCTCAGCCTCTTCTCAACCTCCCAGGACCTATCTGGCTC  
 CAGCCCTCTCCACCTCCCCAGTCTTCTCCCCCGCCTCAGCCCCATCCGTGTCATACCTGCCGG  
 GGA CTGGTTGACAGCTTTAACAAGGGCCTGGAGAGAACCATCCGGGACAACTTTGGAGGTGGA  
 AACACTGCCTGGGAGGAAGAGAATTTGTCCAAATACAAAGACAGTGAGACCCGCTGGTAGAG  
 GTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCTGAGTGAG  
 GAGCTGGTGGAGAGCTGGTGGTTTCACAAGCAGCAGGAGGCCCGGACCTCTTCCAGTGGCTG  
 TGCTCAGATTCCCTGAAGCTCTGCTGCCCCGAGGCACCTTCGGGCCCTCTGCTTCCCTGT  
 CCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGGGACACGAGGG  
 GGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCCAGTGTGGCCTT  
 GGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTCCGGCTTGTTTTGGCCCCCTGT  
 GCCCGATGCTCAGGACCTGAGGAATCAAACCTGTTTGCAATGCAAGAAGGGCTGGGCCCTGCAT  
 CACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAACCTGTGGAGCTGACCAA  
 TTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAGGCCCTGCTAGGCTGC  
 ATGGGGGCGAGGGCCAGGTCGCTGTAAGAAGTGTAGCCCTGGCTATCAGCAGTGGGCTCCAAG  
 TGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGAACAAGCAGTGTGAAAAAC  
 ACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAGATGGAAGGCATCTGTGTG  
 AAGGAGCAGATCCCAGAGTCAGCAGGCTTCTTCTCAGAGATGACAGAAGACGAGTTGGTGGTG  
 CTGCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCACGCTGGCTGCTAAGGGCGAC  
 TTGGTGTTACCGCCATCTTCATTGGGGCTGTGGCGCCATGACTGGCTACTGGTTGTCAGAG  
 CGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATAATCGCGGCCACCACCTGTAGGA  
 CCTCCTCCCACCCACGCTGCCCCAGAGCTTGGGCTGCCCTCCTGCTGGACACTCAGGACAGC  
 TTGGTTTATTTTTGAGAGTGGGGTAAGCACCCCTACCTGCCTTACAGAGCAGCCAGGTACCC  
 AGGCCCCGGGCGAGACAAGGCCCTGGGGTAAAAAGTAGCCCTGAAGGTGGATACCATGAGCTCT  
 TCACCTGGCGGGGACTGGCAGGCTTCACAATGTGTGAATTTCAAAGTTTTCTTAATGGTG  
 GCTGCTAGAGCTTTGGCCCCTGCTTAGGATTAGGTGGTCCTCACAGGGGTGGGGCCATCACAG  
 CTCCCTCCTGCCAGCTGCATGCTGCCAGTTCCTGTTCTGTGTTACCCACATCCCCACCCCCA  
 TTGCCACTTATTTATTCATCTCAGGAAATAAAGAAAGGTCTTGGAAGTTAAAAA  
 AAAAAAAAAA

**FIGURE 290**

MAPWPPKGLVPAVLWGLSLFLNLP GPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLERT  
IRDNFGGGNTAWEEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQQE  
APDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGGSGHCDCQAGYGG  
EACGQCGLGYFEAERNASHLVCSACFGPCARCSGPEESNCLQCKKGWALHHLKCVDIDECGTE  
GANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECETEVCP  
GENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTDELVLVQMFFGIICAL  
ATLAAGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

**Important features:**

**Signal sequence:**

Amino acids 1-29

**Transmembrane domain:**

Amino acids 342-392

**N-glycosylation sites:**

Amino acids 79-83;205-209

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 290-294

**Aspartic acid and asparagine hydroxylation site:**

Amino acids 321-333

**EGF-like domain cysteine pattern signature:**

Amino acids 181-193



# **FIGURE 291**

CAGGTCCAAC TGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGACCCAC  
 GCGTCCGAACACAGGTCTTGTGTGCTGCAGAGAAGCAGTTGTTTTGTGGAAGGAGGGAGTGC GCGGGCTGCCCC  
 GGGTCTCTCCCTGCCGCTCCTCTCAGTGGATGGTTCAGGCACCCCTGTCTGGGGCAGGGAGGGCACAGGCCTGC  
 ACATCGAAGGTGGGGTGGGACCAGGCTGCCCCCTCGCCCCAGCATCCAAGTCTCTCCCTTGGGCGCCCGTGGCCCTG  
 CAGACTCTCAGGGCTAAGGTCTCTGTGTGCTTTTTGGTTCCACCTTAGAAGAGGCTCCGCTTGACTAAGAGTAGC  
 TTGAAGGAGGCACCATG CAGGAGCTGCATCTGCTCTGGTGGGCGCTTCTCCTGGGCTGGCTCAGGCCTGCCCTG  
 AGCCCTGCGACTGTGGGGAAGATATGGCTTCAGATCGCCGACTGTGCCTACCGCGACCTAGAATCCGTGCCGC  
 CTGGCTTCCCGCCAATGTGACTACACTGAGCCTGT CAGCCAACCGGCTGCCAGGCTTGGCGGAGGGTGCCTTCA  
 GGGAGGTGCCCTGTCTGCAGTGCCTGTGGCTGGCACACAATGAGATCCGCACGGTGGCGCGGAGCCCTGGCCT  
 CTCTGAGCCATCTCAAGAGCCTGGACCTCAGCCACAATCTCATCTCTGACTTTGCCTGGAGCGACCTGCACAACC  
 TCAGTGCCCTCCAATTGTCTAAGATGGACAGCAACGAGCTGACCTTCATCCCCCGGACGCTTCCGCAGCCTCC  
 GTGCTCTGCGCTCGCTGCAACTCAACCACAACCGCTTGACACATTGGCCGAGGGCACCTTCAACCCGCTCACCG  
 CGCTGTCCACCTGCAGATCAACGAGAACCCCTTCGACTGCACCTGCGGCATCGTGTGGCTCAAGACATGGGCCC  
 TGACCACGGCCGTGTCCATCCCGGAGCAGGACAACATCGCCTGCACCTCACCCCATGTGCTCAAGGGTACACCGC  
 TGAGCCGCTTCCCGCACTGCCATGCTCGGCGCCCTCAGTGCAGCTCAGCTACCAACCCAGCCAGGATGGTGCCG  
 AGCTGCGGCTGTGTTTTGTGCTGGCACTGCCTGTGATGTGGACGGGCAGCCGGCCCCCTCAGCTTCACTGGCACA  
 TCCAGATACCCAGTGGCATTGTGAGATCACCAGCCCCAACGTGGGCACTGATGGGCGTGCCCTGCCTGGCACCC  
 CTGTGGCCAGCTCCCAGCGCGCTTCCAGGCCTTTGCCAATGGCAGCCTGCTTATCCCCGACTTTGGCAAGCTGG  
 AGGAAGGCACCTACAGCTGCCTGGCCACCAATGAGCTGGGCAGTGTCTGAGAGCTCAGTGGACGTGGCACTGGCCA  
 CGCCCGGTGAGGGTGGTGGAGACACACTGGGGCGCAGGTTCCATGGCAAAGCGGTTGAGGGAAAGGGCTGTATA  
 CGGTTGACAACGAGGTGCAGCCATCAGGGCCGGAGGACAATGTGGTCATCATCTACCTCAGCCGTGCTGGGAACC  
 CTGAGGCTGCAGTCGCAGAAGGGGTCCCTGGGCAGCTGCCCCCAGGCCTGCTCCTGCTGGGCCAAAGCCTCCTCC  
 TCTTCTTCTTCTCACCTCCTTCTAGCCCCACCCAGGGCTTCCCTAACTCCTCCCCCTTGCCCCCTACCAATGCCCC  
 TTTAAGTGCTGCAGGGGTCTGGGGTTGGCAACTCCTGAGGCCTGCATGGGTGACTTCAATTTTCTACCTCTCC  
 TTCTAATCTCTTCTAGAGCACCTGCTATCCCCAACTTCTAGACCTGCTCCAACTAGTGACTAGGATAGAATTTG  
 ATCCCTAACTCACTGTCTGCGGTGCTCATTTGCTGCTAACAGCATTGCCTGTGCTCTCCTCTCAGGGGCAGCATG  
 CTAACGGGGCGACGTCTAATCCAAC TGGGAGAAGCCTCAGTGGTGGAATTCAGGCACCTGTGACTGTCAAGCTG  
 GCAAGGGCCAGGATTGGGGGAATGGAGCTGGGGCTTAGCTGGGAGGTGGTCTGAAGCAGACAGGGAATGGGAGAG  
 GAGGATGGGAAGTAGACAGTGGCTGGTATGGCTCTGAGGCTCCCTGGGGCTGCTCAAGCTCCTCCTGCTCCTTG  
 CTGTTTTCTGATGATTTGGGGGCTTGGGAGTCCCTTTGTCTCATCTGAGACTGAAATGTGGGGATCCAGGATGG  
 CCTTCCTTCTCTTACCCTTCTCCCTCAGCCTGCAACCTCTATCCTGGAACCTGTCTCCTTCTCTCCCAACT  
 ATGCATCTGTTGTCTGCTCCTCTGCAAAGGCCAGCCAGCTTGGGAGCAGCAGAGAAATAAACAGCATTTCTGATG  
 CCAAAAAAAAAAAAAAAAAAGGGCGGCCGCACTCTAGAGTCGACCT

**FIGURE 292**

MQELHLLWALLLLGLAQACPEPCDCGEKYGFQIADCAYRDLESVPPGFANVTTLSSLNRLP  
GLPEGAFREVPLLQSLWLAHNEIRTVAAAGALASLSHLKSLDLNLSLISDFAWSDLNLSALQL  
LKMDSNELTFIPRDAFRSLRALRSLQLNHNRLHTLAEGTFTPLTALSHLQINENPFDCCTCGIV  
WLKTWALTAVSIPEQDNIACTSPHVLKGTPLSRLPPLPCSAPSVQLSYQPSQDGAELRPGFV  
LALHCDVDGQPAPQLHWHIQIPSGIVEITSPNVGTDGRALPGTFVASSQPRFQAFANGSLLIP  
DFGKLEEGTYSCLATNELGSAESSVDVALATPGEGEDTLGRRFHGKAVEGKGCTYVDNEVQP  
SGPEDNVVITYLSRAGNPEAAVAEGVPGQLPPGLLLLGQSLLLFFFLTSTF

**Important features:**

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 403-418

**N-glycosylation sites:**

Amino acids 51-55,120-124,309-313

**Tyrosine kinase phosphorylation site:**

amino acids 319-326

**N-myristoylation sites:**

amino acids 14-20,64-70,92-98,218-224,294-300,323-329,334-340,  
350-356,394-400

**Amidation site:**

amino acids 355-359

**Leucine Rich Repeat:**

amino acids 51-74,75-98, 99-122,123-146,147-170

**Leucine rich repeat C-terminal domain:**

amino acids 180-230

# **FIGURE 293**

ACTTGGAGCAAGCGGCGGCGGCGGAGACAGAGGCAGAGGCAGAAGCTGGGGCTCCGTCCTCGCCTCCCACGAGCG  
ATCCCCGAGGAGAGCCGCGGCCCTCGGCGAGGCGAAGAGGCCGACGAGGAAGACCCGGGTGGCTGCGCCCCCTGCC  
TCGCTTCCCAGGCGCGCGGCTGCAGCCTTGCCCCCTTTGGCTCGCCTTGAAAATGGAAGATGCTCGCAGGCT  
GCTTTCTGCTGATCCTCGGACAGATCGTCTCTCCCTGCCGAGGCCAGGGAGCGGTACGTTGGGAGGTCCATCT  
CTAGGGGCGACACGCTCGGACCCACCCGCGAGACGGCCCTTCTGGAGAGTTTCTGTGAGAAACAGCGGGCAGACC  
TGGTTTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTTCATCGTGGACA  
TCTTGCAATTCTTGGACATTGGTCTCTGATGTCAACCGAGTGGGCTGCTCCAATATGGCAGCAGTGTCAAGAAATG  
AGTTCTCCCTCAAGACCTTCAAGAGGAAGTCCGAGGTGGAGCGTGTGTCAAGAGGATGCGGCATCTGTCCACGG  
GCACCATGACTGGGCTGGCCATCCAGTATGCCCTGAACATCGCATTCTCAGAAGCAGAGGGGGCCCGGCCCTGA  
GGGAGAATGTGCCACGGGTCTAATGATCGTGACAGATGGGAGACCTCAGGACTCCGTGGCCGAGGTGGCTGCTA  
AGGCACGGGACACGGGCTCTAATCTTTGCCATTGGTGGCCAGGTAGACTTCAACACCTTGAAGTCCATTG  
GGAGTGAGCCCCATGGAGGACCATGTCTTCTTGTGGCCAAATTCAGCCAGATTGAGACGCTGACCTCCGTGTTCC  
AGAAGAAGTTGTGCACGCGCCACATGTGCAGCACCTGGAGCATAACTGTGCCACTTCTGCATCAACATCCCTG  
GCTCATACGTCTGCAGGTGCAACAAAGGCTACATTTCTCAACTCGGATCAGACGACTTGCAGAATCCAGGATCTGT  
GTGCCATGGAGGACCACAACTGTGAGCAGCTCTGTGTGAGTGTGGCTGTGGACTACTGTGCCTCAGAAAACCAGGATGTGAAC  
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCCTCAGAAAACCAGGATGTGAAC  
ATGAGTGTGTAATGCTGATGGCTCTACCTTTGCCAGTGCCATGAAGGATTTGCTCTTAACCCAGATGAAAAAA  
CGTGCAACAAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGCGTCAACATGGAGGAGAGCT  
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAAACCTGCAGCCGAGTGAGCATTGTGCAC  
AGCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGGAGGATTCTTCTGTCTGCCAGTGTCTCAGAAGGCTTCC  
TCATCAACGAGGACCTCAAGACCTGCTCCCGGTGGATTACTGCTGCTGAGTGACCATGGTTGTGAATACTCCT  
GTGTCAACATGGACAGATCCTTTGCCCTGTCAGTGTCTGAGGGACAGTGTCTCCGAGCGATGGGAAGACGTGTG  
CAAAATTGGACTCTTGTGCTCTGGGGGACACGGTGTGAACATTCTGTGTGAAGCAGTGAAGATTCTGTTGTGT  
GCCAGTGCTTTGAAGGTTATATACTCCGTGAAGATGGAAAAACCTGCAGAAGGAAAGATGTCTGCCAAGCTATAG  
ACCATGGCTGTGAACACATTTGTGTGAACAGTGACGACTCATACAGTGCAGAGTGTCTGGAGGGATTCCGGCTCG  
CTGAGGATGGGAAACGCTGCCGAAGGAAGGATGTCTGCAATCAACCCACCATGGCTGCGAACACATTTGTGTTA  
ATAATGGGAATTCCTACATCTGCAATGCTCAGAGGGATTGTCTTAGCTGAGGACGGAAGACGGTGCAAGAAAT  
GCACTGAAGGCCCAATTGACCTGGTCTTTGTGATCGATGGATCCAAGAGTCTTGGAGAAGAGAATTTTGAGGTCG  
TGAAGCAGTTTGTCACTGGAATTATAGATTCTTTGACAATTTCCCCAAAGCCGCTCGAGTGGGGCTGCTCCAGT  
ATTCACACAGGTCCACACAGAGTTCACTCTGAGAACTTCAACTCAGCCAAAGACATGAAAAAAGCCGTGGCCC  
ACATGAAATACATGGGAAAGGGCTCTATGACTGGGCTGGCCCTGAAACACATGTTTGAGAGAAGTTTTACCCAAG  
GAGAAGGGGCCAGGCCCTTTCCACAAGGGTGCCAGAGCAGCCATTGTGTTACCCGACGGACGGGCTCAGGATG  
ACGTCTCCGAGTGGGCCAGTAAAGCCAGGCCAATGGTATCACTATGTATGCTGTTGGGGTAGGAAAAGCCATTG  
AGGAGGAACTACAAGAGATTGCTCTGAGCCCAACAAAGCATCTCTTCTATGCCGAAGACTTCAGCACAAATGG  
ATGAGATAAGTGAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCGATGGGAAGACAGGACTCTCCAG  
CAGGGGAAC TGCCAAAAACGGTCCACAGCCACAGAACTCTGAGCCAGTCACCATAAATATCCAAGACCTACTTT  
CCTGTTCTAATTTTTCAGTGTCAACACAGATATCTGTTTGAAGAAGACAATCTTTTACGGTCTACACAAAAGCTTT  
CCCATTCAACAAAACCTTCAGGAAGCCCTTTGGAAGAAAAACAGATCAATGCAATGTGAAAACCTTATAATGT  
TCCAGAACCTTGCAACGAAGAAGTAAGAAAAATTAAACACAGCGCTTAGAAGAAATGACACAGAGAATGGAAGCCC  
TGGAAAATCGCCTGAGATACAGATGAAGATTAGAAATCGCGACACATTTGTAGTCATTGTATCACGGATTACAAT  
GAACGCAGTGCAGAGCCCCAAGCTCAGGCTATTGTTAAATCAATAATGTGTGAAGTAAAAACATCAGTACTGA  
GAAACCTGTTTGGCCACAGAACAAAGACAAGAAGTATACACTAATCTGTATAAAATTTATCTAGGAAAAAATCCT  
TCAGAATCTAAGATGAATTTACCAGGTGAGAATGAATAAGCTATGCAAGGTATTTTGTAAATATACTGTGGACAC  
AACTTGCTTCTGCCTCATCTGCCTTAGTGTGCAATCTCATTGACTATACGATAAAGTTTGCACAGTCTTACTT  
CTGTAGAACACTGGCCATAGGAAATGCTGTTTTTTGTACTGGACTTTACCTTGATATATGTATATGGATGTATG  
CATAAAATCATAGGACATATGTACTTGTGGAACAAGTTGGATTTTTTATACAATATTAATAATTCACCACTTCAG

## **FIGURE 294**

MEKMLAGCFLLILGQIVLLPAEARERSRGRSISRGRHARTHPTALLESSCENKRADLVFIID  
SSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAVKR  
MRHLSTGTMGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARDTGI  
LIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHNCAHF  
CINIPGSYVCRCKQGYILNSDQTTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYALAEDG  
KRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCRINYCALNKPGEHECVN  
MEESYYCRCHRGYTLDPNGKTCSRVDHCAQQDHGCEQLCLNTEDSFVCQCEGFLINEDLKTC  
SRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDGKTCAKLDSALGDHGCEHSCVSSD  
SFVCQCFEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLAEDGKRCRRK  
DVCKSTHHGCEHICVNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLVFVIDGSKSLGEENF  
EVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVAHMKYMGKGSMT  
GLALKHMFERSFTQEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKANGITMYAVGVGKA  
IEEELQETIASEPTNKHLYAEDFSTMDEISEKLKKGICEALEDSDGRQDSPAGELPKTVQQPT  
ESEPVTINIQDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSPLEEKHDQCKCENLIM  
FQNLANEEVRKLTQRLEMTQRMEALENRLRYR

**Important features:**

**Signal sequence:**

Amino acids 1-23

**N-glycosylation site:**

Amino acids 221-225

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 115-119;606-610;892-896

**N-myristoylation sites:**

Amino acids 133-139;258-264;299-305;340-346;453-459;494-500;  
639-645;690-694;  
752-758;792-798

**Amidation sites:**

Amino acids 314-318;560-564;601-605

**Aspartic acid and asparagine hydroxylation sites:**

Amino acids 253-265;294-306;335-347;376-388;417-429;  
458-470;540-552;581-593

**FIGURE 295**

GGCCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACCCGC  
CAATGCGCCTGCCGCGCCGGGCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCCGCCCCG  
GCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGCTGGTGGACAAGTTTAA  
CCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGCTTGGGAGGAAAA  
GACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATCCTGGAGGGGCTGTGCGA  
GAGCAGCGACTTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGAGCACCTGGAGGCCTGGTG  
GCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTTTTGTGTGAAGACACTGAAAGT  
GTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGCCAGGGCGGATCCCAGAGGCC  
CTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACAGGGCGACGGGTCTGCCGGTG  
CCACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGGACGGCTACTTCAGCTCGCTCCG  
GAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCCTGCAAGACGTGCTCGGGCCTGAC  
CAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGT  
GGACGAGTGTGCGGCCGAGCCGCTCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGG  
CTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCCAGGAAA  
CTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTG  
CTCACTAGCAGAAAAAACCTGTGTGAGGAAAAACGAAAACCTGCTACAATACTCCAGGGAGCTA  
CGTCTGTGTGTGTCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGC  
TGAAGCCACAGAAGGAGAAAGCCCCGACACAGCTGCCCTCCCGGAAGACCTGTAATGTGCCGG  
ACTTACCCTTTAAATTATTGAGAAGGATGTCCCGTGGAATAATGTGGCCCTGAGGATGCCGTCT  
CCTGCAGTGGACAGCGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTTGTCCC  
TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTTTGT  
AATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA

## **FIGURE 296**

MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAWEEK  
TLSKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLLKV  
CCSPGTYGPDCLACQGGSORPCSGNGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLR  
NETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEPPPCSAAQFCKNANG  
SYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKT CVRKNENCYNTPGSY  
VCVCPDGFEEETEDACVPPAEAEATEGESPTQLPSREDL

**Important features:**

**Signal peptide:**

Amino acids 1-24

**N-glycosylation sites:**

Amino acids 190-194;251-255

**Glycosaminoglycan attachment sites:**

Amino acids 149-153;155-159

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 26-30

**Tyrosine kinase phosphorylation site:**

Amino acids 303-310

**N-myristoylation sites:**

Amino acids 44-50;54-60;55-61;81-87;150-156;158-164;164-170;  
252-258;313-319

**Aspartic acid and asparagine hydroxylation site:**

Amino acids 308-320

**EGF-like domain cysteine pattern signature:**

Amino acids 166-178

**Leucine zipper pattern:**

Amino acids 94-116

# **FIGURE 297**

GACATCGGAGGTGGGCTAGCACTGAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAGAAAGAAGAGGAAG  
 ATGTTGGGCAACATTTATTTAACATGCTCCACAGCCCGGACCCTGGCATCATGCTGCTATTCTGCAAATACTGA  
 AGAAGCATGGGATTTAAATATTTTACTTCTAAATAAATGAATTACTCAATCTCCTATGACCATCTATACATACTC  
 CACCTTCAAAAAGTACATCAATATTATATCATTAAGGAAATAGTAACCTTCTCTTCTCCAATATGCATGACATTT  
 TTGGACAATGCAATTGTGGCACTGGCACTTATTTTCAAGTGAAGAAAACTTTGTGGTTCTATGGCATTTCATCATTT  
 GACAAATGCAAGCATCTTCTTATCAATCAGCTCCTATTGAACCTTACTAGCACTGACTGTGGAATCCTTAAGGGC  
 CCATTACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACTCCGAATTTCATGTGCTACTTGGCCTAGCTA  
 TCACTACACTAGTACAAGCTGTAGATAAAAAAGTGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTTGGT  
 TTACACCCAGATCCATTTATATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCTTTTAACTTTCCAGCCA  
 GATTGGCCAGCTAACACACAGATTCTTCTCTACAGACTAACAAATATTGCAAAAATTGAATACTCCACAGACTTTC  
 CAGTAAACCTTACTGGCCTGGATTATCTCAAAACAATTTATCTTCAAGTACCAATATTAATGTAAAAAGATGC  
 CTCAGCTCCTTTCTGTGTACCTAGAGGAAAACAAACCTTACTGAACTGCCTGAAAAATGTCTGTCCGAACCTGAGCA  
 ACTTACAAGAACTCTATATTAATCACAACCTTGCTTTCTACAATTTACCTGGAGCCTTTATTGGCCTACATAATC  
 TTCTTCGACTTCATCTCAATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTTGATGCTCTTCCAATCTAG  
 AGATTCTGATGATTGGGGAAAATCCAATTATCAGAATCAAAGACATGAACCTTAAAGCCTTATCAATCTTCGCA  
 GCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCTTGGTTGGACTGGAAAACTTAGAAAGCA  
 TCTCTTTTACGATAACAGGCTTATTAAGTACCCCATGTTGCTCTTCAAAAAGTTGTAAATCTCAATTTTGG  
 ATCTAAATAAAAACTCTATTAATAGAATACGAAGGGGTGATTTTAGCAATATGCTACACTTAAAGAGTTGGGGA  
 TAAATAATATGCTGAGCTGATTTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTTAAGAAAAATAGAAG  
 CTACTAACAAACCTAGATTGTCTTACATTACCCCAATGCATTTTTCAGACTCCCCAAGCTGGAATCACTCATGC  
 TGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCATTGAGTCTCTGCCAAACCTCAAGGAAATCAGCATA  
 ACAGTAACCCCATCAGGTGTGACTGTGTCTATCCGTTGGATGAACATGAACAAAACCAACATTGATTTCATGGAGC  
 CAGATTCACTGTTTTGCTGGGACCCACCTGAATTCGAAGTCAAGATGTTCCGCAAGTGCATTTTCAGGGACATGA  
 TGGAAATTTGTCTCCCTCTTATAGCTCCTGAGAGCTTTCCTTCTAATCTAAATGTAGAAGCTGGGAGCTATGTTT  
 CCTTTCACTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTTCTGGTCAAAAACCTTTC  
 CTAATACCCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAACACTAGATATAAATGGCGTAACTCCCAAAGAAG  
 GGGGTTTATATACTTGTATAGCAACTAACCTAGTTGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGAT  
 CTTTTCCACAAGATAACAATGGCTCTTTGAATATTAATAAGAGATATTCAGGCCAATTCAGTTTTGGTGTCTT  
 GGAAAGCAAGTTCTAAATTTCTCAAATCTAGTGTTAAATGGACAGCCTTTGTCAAGACTGAAAAATCTCATGCTG  
 CGCAAAGTGCTCGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATCCATCAACTGAGTATAAAA  
 TTTGTATTGATATTCCCACCATCTATCAGAAAAACAGAAAAAATGTGTAAATGTCAACACCAAAGGTTTGCACC  
 CTGATCAAAAAGAGTATGAAAAGAATAATACCACAACACTTATGGCCTGTCTTGGAGGCCTTCTGGGGATTATTG  
 GTGTGATATGTCTTATCAGCTGCCTCTCTCCAGAAATGAACGTGTGATGGTGGACACAGCTATGTGAGGAATTACT  
 TACAGAAACCAACCTTTGCATTAGGTGAGCTTTATCCTCCTGATAAATCTCTGGGAAGCAGGAAAAGAAAAA  
 GTACATCACTGAAAGTAAAGCAACTGTTATAGGTTTACCAACAAATATGTCTTAAAAACCACCAAGGAAACCTA  
 CTCAAAAATGAAC

**FIGURE 298**

MKDMPLRIHVLLGLAITTLVQAVDKKVDPCRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLTF  
PARLPANTQIILLQTNNAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLEEN  
KLTELPEKCLSELSNLQELYINHNLSTISPGAFIGLHNLLRLHLNSNRLQMINSKWFDALPN  
LEILMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVP  
HVALQKVVLKFLDLNKNPINRIRRGDFSNNMLHLKELGINNMPELISIDSLAVDNLPDLRKIE  
ATNNPRLSYIHPNAFFRLPKLESLMLNSNALSALYHGTIESLPNLKEISIHSPNPIRCDVCVIRW  
MNMNKTNIRFMEPDSLFCVDPPEFQGGQNVVRQVHFRDMMEICLPLIAPESFPSNLNVEAGSYVS  
FHCRAEAEPQPEIYWIPTSGQKLEPNTLTDFKYVHSEGTLDINGVTPKEGGLYTCIATNLVGA  
DLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFAVKTENSHAAQ  
SARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKEYEKNNTTTLN  
ACLGGLLGIIGVICLISCLSPENMNCDDGHSYVRNYLQKPTFALGELYPPLINLWEAGKEKSTS  
LKVKATVIGLPTNMS

**Important features:**

**Signal sequence:**

amino acids 1-22

**Transmembrane domain:**

amino acids 633-650

**N-glycosylation site.**

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,  
608-612, 624-628, 625-629

**Casein kinase II phosphorylation site.**

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

**Tyrosine kinase phosphorylation site.**

amino acids 570-579

**N-myristoylation site.**

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,  
491-497, 492-498, 634-640, 702-708

**Cell attachment sequence.**

amino acids 277-280



**FIGURE 299**

GCTGTGGGAACCTCTCCACGCGCACGAACTCAGCCAACGATTTCTGATAGATTTTTGGGAGTT  
TGACCAGAGATGCAAGGGGTGAAGGAGCGCTTCCTACCGTTAGGGAACTCTGGGGACAGAGCG  
CCCCGGCCGCTGATGGCCGAGGCAGGGTGCGACCCAGGACCCAGGACGGCGTCGGGAACCAT  
ACCATGCCCCGGATCCCCAAGACCCCTAAAGTTCGTTCGTTCGTTCATCGTCGCGGTCCCTGCTGCCA  
GTCCTAGCTTACTCTGCCACCACTGCCCCGGCAGGAGGAAGTTCCCCAGCAGACAGTGGCCCCA  
CAGCAACAGAGGCACAGCTTCAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAACAT  
ACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACCAACGCTTCCAACAATGAACCT  
TCTTGCTTCCCATGTACAGTTTGTAAATCAGATCAAAAACATAAAAAGTTCCTGCACCATGACC  
AGAGACACAGTGTGTTCAGTGTAAGAAGGCACCTTCGGAATGAAAACCTCCCCAGAGATGTGC  
CGGAAGTGTAGCAGGTGCCCTAGTGGGGAAGTCCAAGTCAGTAATTGTACGTCCTGGGATGAT  
ATCCAGTGTGTTGAAGAATTTGGTGCCAATGCCACTGTGGAAACCCAGCTGCTGAAGAGACA  
ATGAACACCAGCCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGAACACCAGCCCAGGG  
ACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCCGGGGACTCCTGCCCCAGCTGCT  
GAAGAGACAATGACCACCAGCCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACC  
AGCCCCGGGGACTCCTGCCTCTTCTCATTACCTCTCATGCACCATCGTAGGGATCATAGTTCTA  
ATTGTGCTTCTGATTGTGTTTGTTGAAAGACTTCACTGTGGAAGAAAATTCCTTCCTTACCTG  
AAAGGTTCAGGTAGGCGCTGGCTGAGGGCGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCT  
CTGCTGTGTTCCACAGACAGAAACGCCTGC

**FIGURE 300**

MARIPKTLKFVVVIVAVLLPVLAYSATTARQEEVPQQTVA PQQRHSFKGEECPAGSHRSEHT  
GACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSCTMTRDTVCQCKEGTFRNENSPEMCR  
KCSRCPSGEVQVSNCTSWDDIQCVEEFGANATVETPAAEETMNTSPGTPAPAAEETMNTSPGT  
PAPAAEETMTTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPASSHYLSCTIVGIIIVLI  
VLLIVFV

**Important features:**

**Signal peptide:**

Amino acids 1-29

**Transmembrane domain:**

Amino acids 240-259

**N-glycosylation site:**

Amino acids 77-81;140-144;156-160

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 126-130

**N-myristoylation sites:**

Amino acids 56-62;72-78;114-120;154-160;233-239

**FIGURE 301**

CACAAGCATCTTAATTTGAATCCACAAAGTTTCATGTAATGAAAAGAAATACATAATTTTAAT  
 TCAACCCGAGTGTTTTCCAAGAAGATTGTATTTGCTTAAATTGCTACAGTAATTCAGAGACA  
 GCCCTGTCTGGACACAGAGTTACTGTGGATTTTTTAAGAGACTCAGTTAAAGAATTTAGGAATT  
 TCTGATTCATTTAAAGGATTTACAAATTCATCAACCCCTGAAAACTAAAGCAAATTGAACAGG  
 AAAAAAAAAAAGAAGATGGGTTTTTTAAGTCCAATATATGTTATTTTCTTCTTTTTTGGAGTC  
 AAAGTACATTGCCAATATGAACTTATCAGTGGGATGAAGACTATGACCAAGAGCCAGATGAT  
 GATTACCAAACAGGATTTCCCATTTTCGTCAAAATGTAGACTACGGAGTTCCTTTTCATCAGTAT  
 ACTTTAGGCTGTGTGTCAGTGAATGCTTCTGTCCAATACTTTCCATCATCAATGTACTGTGAT  
 AATCGCAAACCTCAAGACTATCCCAAATATTCGGATGCACATTGAGCAACTCTACCTTCAGTTC  
 AATGAAATTGAGGCTGTGACTGCAAATTCATTCATCAATGCAACTCATCTTAAAGAAATTAAC  
 CTCAGCCACAACAAAATTAATCTCAAAAGATTGATTATGGTGTGTTTGCTAAGCTTCCAAAT  
 CTACTACAACCTTCATCTAGAGCATAATAATTTAGAAGAATTTCCATTTCTCTTCTTAAATCT  
 CTGGAAAGACTCCTTCTTGGTTACAATGAAATCTCCAAACTGCAGACAAATGCTATGGATGGG  
 CTAGTAAACTTGACCATGCTTGATCTCTGTTATAATTATCTTCATGATTCTCTGCTAAAAGAC  
 AAAATCTTTGCCAAAATGGAAAACTAATGCAGCTCAACCTCTGCAGTAACAGATTAGAATCA  
 ATGCCTCCTGGTTTGCCTTCTTCACTTATGTATCTGTCTTTAGAAAATAATTCAATTTCTTCT  
 ATACCCGAAAAATACTTCGACAAACTTCCAAACTTCATACTCTAAGAATGTCACACAACAAA  
 CTACAAGACATCCCATATAATATTTTAAATCTTCCCAACATTGTAGAACTCAGTGTGGACAC  
 AACAAATTGAAGCAAGCATTTCTATATTCGAAGAAATTTGGAACACCTATACCTACAAAATAAT  
 GAAATAGAAAAGATGAATCTTACAGTGTGATGTCCTTCTATTGACCCACTACATTACCACCAT  
 TTAACATACATTTCGTGTGGACCAAATAAACTAAAAGAACCAATAAGCTCATACATCTTCTTC  
 TGCTTCCCTCATATACACACTATTTATTATGGTGAACAACGAAGCACTAATGGTCAAAACAATA  
 CAACTAAAGACACAAGTTTTTCAGGAGATTTCCAGATGATGATGATGAAAGTGAAGATCAGGAT  
 GATCCTGACAATGCTCATGAGAGCCGAGAACAAGAAGGAGCAGAAGGGCACTTTGACCTTCAT  
 TATTATGAAATCAAGAAATAGCAAGAACTATATAGGTATACACTTACGACTTCACAAAACCTA  
 TACTTAATATAGTAAATCTAAGTAAACATGTATTACTCAAAGTAATATATTTAGAATTATGTA  
 TTAGTATAAGATCAGAATTGAATTTAAGTTGTTGGTGACATCTGCATCATTTTCATAGGATTAG  
 AACTTACTCAAAATAATGTAAATCTTTAAAAATATAAATTAGAATGACAAGTGGGAATCATAA  
 ATTAAACGTTAATGGTTTCTTATGCTCTTTTTTAAATATAGAAATATCATGTTAAAGAAAAAA  
 AAAAAA

## **FIGURE 302**

MGFLSPIYVIFFFFGVKVHCQYETYQWDEDDYDQEPDDDDYQTGFPPFRQNVGYGVPFHQYTLGCV  
SECFCTNFPSSMYCDNRKLKTIPNIPMHIQQLYLQFNEIEAVTANSFINATHLKEINLSHNK  
IKSQKIDYGVFAKLPNLLQLHLEHNNLEEFPPFLPKSLERLLLGYNEISKLQTNAMDGLVNLT  
MLDLCYNYLHDSLLKDKIFAKMEKLMQLNLCSNRLESMPPGLPSSLMYLSLENNSSISSIPEKY  
FDKLPKLHTLRMSHNKLQDIPYNIFNLPNIVELSVGHNKLKQAFYIPRNLEHLYLQNNIEKM  
NLTVMCPSIDPLHYHHLTYIRVDQNKLEPISSYIFFCFPHIHTIYYGEQRSTNGQTIQLKTQ  
VFRRFPDDDDDESEDHDDPDNAHESPEQEGAEGHFDLHYENQE

**Important features:**

**N-glycosylation sites:**

Amino acids 113-117;121-125; 187-191;242-246;316-320

**Tyrosine kinase phosphorylation sites:**

Amino acids 268-275;300-307

**N-myristoylation site:**

Amino acids 230-236

**Leucine zipper patterns:**

Amino acids 146-168;217-239

**FIGURE 303**

GCCCCGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAGC  
TGCAGCCTTTTGAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTACCA  
CGCTTGTTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCCAGCATGAATCTGGT  
AGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTTGTTCTTATGAT  
ACTGTGCTTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCCTCTGGGGGTTT  
AAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCTCCTGAAACAGT  
CTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTAAAGGACCTCCA  
TCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTGAGTTTATCGATGAGCATGCCTTCAA  
AGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAGTGTGCACAA  
AAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAACCCCTGGCACTGCGACTG  
TACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCACAACGTGATCTG  
TAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGCCAACGACGCTGA  
CCTTTGTAACCTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCATGTTTGGCTGGTT  
CACTATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAGGATGCCCCGAGACA  
CCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGAACCTGATGATATTAG  
CACTGTGGTATAGTGTCCAACTGACTGTCAATTGAGAAAGAAAGAAAGTAGTTTGCGATTGCA  
GTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAAACATTTGAACTTTGTATTTTCTAGTTT  
TTTTTGAATTATGCCACTGCTGAACTTTTTAACAAACACTACAACATAAATAATTTGAGTTTAG  
GTGATCCACCCCTTAATTGTACCCCGATGGTATATTTCTGAGTAAGCTACTATCTGAACATT  
AGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTTAATTTAAAGCAAATAAAAG  
CTTAACCTTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAAAAAAACA

**FIGURE 304**

MNLVDLWLTRSLSMCLLLQSFLMILCFHSASMC PKGCLC SSSGGLNVTCSNANLKEIPRDLP  
PETVLLYLDSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGV AETLQTLDLSDNRIQ  
SVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPFLNAA  
NDADLCNLPKKT TDYAMLVTMFGWFTMVISYV VYYVRQNQEDARRHLEYLKS LPSRQKKADEP  
DDISTVV

**Important features:**

**Signal sequence:**

Amino acids 1-33

**Transmembrane domain:**

Amino acids 204-219

**N-glycosylation sites:**

Amino acids 47-51;94-98

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 199-203

**Casein kinase II phosphorylation site.**

amino acids 162-166, 175-179

**N-myristoylation sites:**

Amino acids 37-43;45-51;110-116

# **FIGURE 305**

CGCCACCACTGCGGCCACCGCCAATGAAACGCCTCCCGCTCCTAGTGGTTTTTCCACTTGTGTAATTGTTCTCT  
 ATACTCAAAATGACCAAGACACCTTGTCTCCCAATGCAAAATGTGAAATACGCAATGGAATTGAAGCCTGCT  
 ATTGCAACATGGGATTTTCAGGAAATGGTGTCACAATTTGTGAAGATGATAATGAATGTGGAAATTTAACTCAGT  
 CCTGTGGCGGAAATGCTAATTGCACTAACACAGAAGGAAGTTATTTATGTATGTGTGTACCTGGCTTCAGATCCA  
 GCAGTAACCAAGACAGGTTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACTGCCATTTAG  
 ATAATGTCTGTATAGCTGCAAAATATTAATAAACTTTAAACAAAATCAGATCCATAAAAGAACCTGTGGCTTTC  
 TACAAGAAGTCTATAGAAATTCGTGACAGATCTTTCACCAACAGATATAATTACATATATAGAAATATTAGCTG  
 AATCATCTTCATTACTAGGTTACAAGAACAACTATCTCAGCCAAGGACACCCCTTTCTAACTCAACTCTTACTG  
 AATTTGTAATAACCCGTAATAATTTTGTTCAAAGGGATACATTTGTAGTTTGGGACAAGTTATCTGTGAATCATA  
 GGAGAACACATCTTACAAAACCTCATGCACACTGTTGAACAAAGCTACTTTAAGGATATCCAGAGCTTCCAAAAGA  
 CCACAGAGTTTGATACAAATTCACGGATATAGCTCTCAAAGTTTTCTTTTTGATTTCATATAACATGAACATA  
 TTCATCCTCATATGAATATGGATGGAGACTACATAAATATATTTCCAAAGAGAAAAGCTGCATATGATTCAAATG  
 GCAATGTTGCAGTTGCATTTTATATTATAAGAGTATTGGTCTTTGCTTTTCATCATCTGACAACCTCTTATTGA  
 AACCTCAAAATTATGATAATCTGAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTTCAGTCTCAATGAGCTCAA  
 ACCCACCACATTATATGAACCTGAAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATAGGTATAGGA  
 GTCTATGTGCATTTTGGGAATTACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAGGGCTGTGAGCTGACAT  
 ACTCAAATGAGACCCACACCTCATGCGCTGTAATCACCTGACACATTTTGCAATTTTGATGTCTCTGGTCCTT  
 CCATTGGTATTAAAGATTATAATATTCTTACAAGGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTG  
 CCATATGCATTTTTACCTTCTGGTTCTTCAGTGAAATTCAAAGCACCAGGACAACAATTCACAAAAATCTTTGCT  
 GTAGCCTATTTCTGTGTAACCTGTTTTCTTGTGGGATCAATACAAATACTAATAAGCTCTTCTGTTCAATCA  
 TTGCCGGACTGCTACACTACTTCTTTTTAGCTGCTTTTGCATGGATGTGCATTGAAGGCATACATCTCTATCTCA  
 TTGTTGTGGGTGTCTCTACAACAAGGGATTTTTGCACAAGAATTTTTATATCTTTGGCTATCTAAGCCCAGCCG  
 TGGTAGTTGGATTTTCGGCAGCACTAGGATACAGATATTATGGCACAACCAAGTATGTTGGCTTAGCACCAGAAA  
 ACACTTTTATTTGGAGTTTATAGGACCAGCATGCCTAATCATTCTTGTTAATCTCTTGGCTTTTGGAGTCATCA  
 TATACAAAGTTTTTCGTCACTGCAAGGTTGAAACCAAGGTTAGTTGCTTTGAGAACATAAGGTCTTTGTGCAA  
 GAGGAGCCCTCGCTCTCTGTCTCTCGGCACCACCTGGATCTTTGGGGTCTCCATGTTGTGCACGCATCAG  
 TGGTTACAGCTTACCTCTTCACAGTCAGCAATGCTTTCAGGGGATGTTCAATTTTTTATTCTGTGTGTTTTAT  
 CTAGAAAGATTCAAGAAGAATATTACAGATTGTTCAAAAATGTCCCTGTTGTTTTGGATGTTTAAAGGTAACAT  
 AGAGAATGGTGGATAATTACAACCTGCACAAAAATAAAAAATTCAGCTGTGGATGACCAATGTATAAAAAATGACT  
 CATCAAATTATCCAATTATTAACCTAGACAAAAAGTATTTTAAATCAGTTTTTCTGTTTATGCTATAGGAACT  
 GTAGATAATAAGGTAAATATGTATCATATAGATATACTATGTTTTCTATGTGAAATAGTTCTGTCAAAAAATA  
 GTATTGCAGATATTTGGAAAGTAATTGGTTTCTCAGGAGTGATATCACTGCACCCAAGGAAAGATTTCTTTCTA  
 ACACGAGAAGTATATGAATGCTCTGAAGGAAACCACTGGCTTGATATTTCTGTGACTCGTGTTGCCTTTGAAACT  
 AGTCCCTTACCACCTCGGTAATGAGCTCCATTACAGAAAGTGGAACATAAGAGAATGAAGGGGCAGAATATCAAA  
 CAGTGAAAAGGGAATGATAAGATGTATTTGAATGAAGTGTGTTTTCTGTAGACTAGCTGAGAAATTGTTGACAT  
 AAAATAAAGAAATTGAAGAAACACATTTTACCATTTTGTGAATTGTTCTGAACTTAAATGTCCACTAAAACAACTT  
 AGACTTCTGTTTGCTAAATCTGTTTCTTTTCTAATATTCTAAAAAAGGTTTACCTCCACAAATTGA  
 AA

## **FIGURE 306**

MKRLPLLVVFTLLNCSYTQNTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNECGNLTQSCGENANC  
TNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIEENVNANCHLDNVCIANINKTLTKIRSIKEPVALLQEVYRNS  
VTDLSPTDIITYIEILAESSSLGYKNNTISAKDTLSNSTLTETVKTVNNFVQRDTFVVWDKLSVNHRRTHLTKL  
MHTVEQATLRISQSFSQKTTEFDTNSTDIALKVFFFDSDYNMKHIHPHMNDGDYINIFPKRKAAYDSNGNVAVAF  
YYKSIGPLLSDDNFFLLKPQNYDNSEEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDRYRSLCAFWNY  
SPDTMNGSWSSEGCETYSNETHTSCRCNHLTHFAILMSSGPSIGIKDYNILTRITQLGIIISLICLAICIFTFW  
FFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSTIAGLLHYFFLAFAWMCIEGILYLIIVGVIYN  
KGFLHKNFYIFGYLSPAVVVGFSALGYRYYGTTKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVRHT  
AGLKPEVSCFENIRSCARGALALLFLLGTTWIFGVLVHVVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEY  
YRLFKNVPCCFGCLR

**Important features:**

**Signal peptide:**

Amino acids 1-19

**Transmembrane domain:**

Amino acids 431-450;494-515;573-594;619-636;646-664

**N-glycosylation sites:**

Amino acids 15-19;21-25;64-68;74-78;127-131;177-181;

188-192;249-253;381-385;395-399

**Glycosaminoglycan attachment site:**

Amino acids 49-53

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 360-364

**Tyrosine kinase phosphorylation sites:**

Amino acids 36-44;670-677

**N-myristoylation sites:**

Amino acids 38-44;50-56;52-58;80-86;382-388;388-394;

434-440;480-486;521-527

**Aspartic acid and asparagine hydroxylation site:**

Amino acids 75-87



# FIGURE 307

CCAGGCCGGGAGGCGACGCGCCAGCCGTCTAAACGGGAACAGCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGT  
ATCTGACGGCGCCAGGTTGCGTAGGTGCGGCACGAGGAGTTTTCCCGGCAGCGAGGAGGTCCTGAGCAGCATGGC  
CCGGAGGAGCGCCTTCCCTGCCGCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGA  
GGCCGGGCGCCGAGGAGGAGCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCATAGGATTTGA  
AGAAGATATCCTGATTGTTTTAGAGGGGAAAAATGGCACCTTTTACACATGATTTTCAAAAAAGCGAACAGAGAAT  
GCCAGCTATTCTGTCAATATCCATTCATGAATTTTACCTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGA  
ATTCTGTCTTGGCTCCCTGGATAAAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGT  
GCCTCACAAGGCATCAGTTGTTCAAGTTGGTTTTCCCATGTCTTGGAAAAACAGGATGGGGTGGCAGCATTTGAAGT  
GGATGTGATTGTTATGAATTTGAAGGCAACACCATTCTCCAAACACCTCAAAATGCTATCTTTTAAAAACATG  
TCAACAAGCTGAGTGCCAGGCGGGTGCCGAAATGGAGGCTTTTGTAATGAAAGACGCATCTGCGAGTGTCTGA  
TGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTTGTACCCACGATGTATGAATGGTGGACTTTTGTGTGACTCC  
TGGTTTCTGCACTCTGCCACCTGGATTCTATGGAGTGAACGTGACAAAGCAAACCTGCTCAACCACCTGCTTTAA  
TGGAGGGACCTGTTTTACCTCGAAAAATGTATTGCCCCCTCAGGACTAGAGGGAGAGCAGTGTGAAATCAGCAA  
ATGCCACACAACCTGTGAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGTTCAAAGGTTACCAGGG  
AGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGACATGGAACCTGCCATGAACCCAAACAAATGCCA  
ATGTCAAGAAGGTTGGCATGGAAGACACTGCAATAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGC  
AGGCGCCAGCTCAGGCAGCACACGCCCTTCACTTAAAAAGGCCGAGGAGCGCGGGATCCACCTGAATCCAATTA  
CATCTGGTGAACTCCGACATCTGAAACGTTTTTAAGTTACACCAAGTTCATAGCCTTTGTTAACCTTTCATGTGTT  
GAATGTTCAAATAATGTTCACTTACACTTAAGAATACTGGCCTGAATTTTATTAGCTTCATTATAAATCACTGAGC  
TGATATTTACTCTTCCTTTTAAGTTTTCTAAGTACGCTGTAGCATGATGGTATAGATTTTCTTGTTTCAGTGCT  
TTGGGACAGATTTTATATTATGTCAATTGATCAGGTTAAATTTTCACTGTGTAGTTGGCAGATATTTTCAAAT  
TACAATGCATTIATGGTGTCTGGGGCAGGGGAACATCAGAAAGGTTAAATTTGGGCAAAATGCGTAAGTCACAA  
GAATTTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTTCAATTTTATTGTCAGATATTTAGATGTTTGTAC  
ATTTTTAAAAATTGCTCTTAATTTTTAACTCTCAATACAATATATTTTGACCTTACCATTATTCCAGAGATTCA  
GTATTAAAAAATAAATACTGTGGTAGTGGCATTTAAACAATATAATATATTCTAAACACAATGAAATAG  
GGAATATAATGTATGAACTTTTTGCATTGGCTTGAAGCAATATAATATATTGTAAACAAAAACAGCTCTTACCT  
AATAAACATTTTATACTGTTTGTATGTATAAATAAAGGTGCTGCTTTAGTTTTTTGGAAAAAATAAATAA  
AAAAA

**FIGURE 308**

MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGKM  
APFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLLSLRSLDKGIMADPTVNVPLLGT  
VPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPPGGCRNG  
GFCNERRICECPDGFHGPHEKALCTPRCMNGGLCVTPGFCICPPPGFYGVNCDKANCSTTCFN  
GGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCIGKSKCKCSKGYQGDLCSPVCEPGCG  
AHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEEERDPPESNYIW

**Important features:**

**Signal sequence:**

Amino acids 1-28

**N-glycosylation sites:**

Amino acids 88-92;245-249

**Tyrosine kinase phosphorylation site:**

Amino acids 370-378

**N-myristoylation sites:**

Amino acids 184-190;185-191;189-195;315-321

**ATP/GTP-binding site motif A (P-loop):**

Amino acids 285-293

**EGF-like domain cysteine pattern signatures:**

Amino acids 198-210;230-242;262-274;294-306;326-338

# **FIGURE 309**

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTTCGCGCACAGATGCGGG  
 TTAGACTGGCGGGGGAGGAGGCGGAGGAGGGAAGGAAGCTGCATGCATGAGACCCACAGACT  
 CTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATGGAG  
 ATGGATTTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTGGCCG  
 TGATCCTGTGGTTTTAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTTCGATG  
 ACCTTCAAGTGTGTGCTGACCCCGGCATTCCCAGAAATGGCTTCAGGACCCCGAGCGGAGGGG  
 TTTTCTTTGAAGGCTCTGTAGCCCGATTTCACTGCCAAGACGGATTCAAGCTGAAGGGCGCTA  
 CAAAGAGACTGTGTTTTGAAGCATTTTAATGGAACCCTAGGCTGGATCCCAAGTGATAATTCCA  
 TCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTATAACAAGACAT  
 ATAGACATGGAGAGAAGCTAATCATCACTTGTTCATGAAGGATTCAAGATCCGGTACCCCGACC  
 TACACAATATGGTTTTATTATGTCGCGATGATGGAACGTGGAATAATCTGCCCATCTGTCAAG  
 GCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGCTCCAGACCTCCT  
 TCCCGGTGGGGACTGTGATCTCCTATCGCTGCTTTCCCGGATTTAAACTTGATGGGTCTGCGT  
 ATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCACCCCGGTGCTTGCTCTGGAAG  
 CCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTCTGCTGCCACCCGCGGCCTT  
 GTGAGCGCTACAACCACGGAAGTGTGGTGGAGTTTTACTGCGATCCTGGCTACAGCCTCACCA  
 GCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTTCTTCTTATCAAGTCTACTGCA  
 TCAAATCAGAGCAAACGTGGCCCGAGCACCCTGAGACCCCTCCTGACCACGTGGAAGATTGTGG  
 CGTTCACGGCAACAGTGTGCTGCTGGTGTGCTGCTCGTCATCCTGGCCAGGATGTTCCAGA  
 CCAAGTTCAAGGCCCCACTTTCCCCCAGGGGGCCTCCCCGAGTTCAGCAGTGACCCTGACT  
 TTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCTTATGACGAAGCTGTGAGTGGCGGCT  
 TGAGTGCTTAGGCCCCGGGTACATGGCCTCTGTGGGCCAGGGCTGCCCCTTACCCGTGGACG  
 ACCAGAGCCCCCAGCATAACCCGGCTCAGGGGACACGGACACAGGCCCAGGGGAGTCAGAAA  
 CCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAAGTCTGTATTACCTCCCAGGTGCC  
 AAGAGAGCACCCACCTGCTTCGGACAACCCCTGACATAATTGCCAGCACGGCAGAGGAGGTGG  
 CATCCACCAGCCAGGCATCCATCATGCCCACTGGGTGTTGTTCCCTAAGAAACTGATTGATTA  
 AAAAATTTCCAAAGTGTCTGAAGTGTCTCTTCAAATACATGTTGATCTGTGGAGTTGATTC  
 CTTTCCTTCTCTTGGTTTTAGACAAATGTAAACAAAGCTCTGATCCTTAAATTGCTATGCTG  
 ATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTCTGTTTCTTCTTGACACAGACTGATTAAA  
 AATTAAAAGNAAAAA

**FIGURE 310**

MYHGMNPSNGDGFLEQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGIP  
ENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRIPQ  
IEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLASSNG  
YVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLPPMVS  
HGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQTWPSTH  
ETLLTTWKIVAFTATSVLLVLLLVILARMFQTKFKAHFPPRGPPRSSSSDPDFVVVDGVPVML  
PSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGD TDTGPGESETCDSVSGSSEL  
LQSLYSPPRCQESTHPASDNPDI IASTAEVASTSPGIHHAHWVLFRLN

**Important features:**

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 325-344

**N-glycosylation site.**

amino acids 104-108, 134-138, 192-196

**Casein kinase II phosphorylation site.**

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,  
364-368, 380-384, 467-471, 468-472

**N-myristoylation site.**

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,  
478-484

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405

**FIGURE 311**

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGAG  
CGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTGCTCGGCCCTCGGACTAGGCCTGG  
AGGCCGCCGCGAGCCCGCTTTCCACCCCGACCTCTGCCCAGGCCGAGGCCCCAGCTCAGGCT  
CGTGCCCACCCACCAAGTTCCAGTGCCGCACCAGTGGCTTATGCGTGCCCTCACCTGGCGCT  
GCGACAGGGACTTGGA CTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCCATGTA  
CCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCCTGCCCTGCACCGGCGTCAGTGACT  
GCTCTGGGGGA ACTGACAAGAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCAGGCGAGC  
TCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCACCCAGACT  
GTCCCGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGGAAGGGGATGCCA  
CAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTACCTCTCTCAGGAATGCCACAACCATGG  
GGCCCCCTGTGACCCTGGAGAGTGTCCCTCTGTGCGGAATGCCACATCCTCCTCTGCCGGAG  
ACCAGTCTGGAAGCCCAACTGCCATATGGGGTTATTGCAGCTGCTGCGGTGCTCAGTGCAAGCC  
TGGTCACCGCCACCCTCCTCCTTTTGTCTGGCTCCGAGCCCAGGAGCGCCTCCGCCCCACTGG  
GGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTCAGAACAGAAGACCTCGCTGCCCTTGAG  
GACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACAGGAGGAGAGCAGTGA  
TGCGGATGGGTACCGGGCACACCAGCCCTCAGAGACCTGAGTTCTTCTGGCCACGTGGAACC  
TCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCCTGGACACTCCCTATGGA  
GATCCGGGGAGCTAGGATGGGGAACCTGCCACAGCCAGAACTGAGGGGCTGGCCCCAGGCAGC  
TCCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTGCCCCGTCTGAGGGTGGCGA  
TTAAAGTTGCTTC

**FIGURE 312**

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCRT  
SGLCVPLTWRCRDLDCSDGSDEEEECRIEPTQKGQCPPPPGLPCPCTGVSDCSGGTDKKLRN  
CSRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELGCGTNEILPEGDATTMGPPVTLES  
VTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAVLSASLVTATLLLLSW  
LRAQERLRPLGLLVAMKESLLLSEQKTSLP

**Important features:**

**Signal sequence:**

Amino acids 1-30

**Transmembrane domain:**

Amino acids 231-248

**N-glycosylation sites:**

Amino acids 126-130;195-199;213-217

**Casein kinase II phosphorylation site.**

amino acids 84-88, 140-144, 161-165, 218-222

**N-myristoylation sites:**

Amino acids 3-9;10-16;26-32;30-36;112-118;166-172;212-218;  
224-230;230-236;263-269

**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 44-55

**Leucine zipper pattern:**

Amino acids 17-39

**FIGURE 313**

CGGACGCGTGGGCGTCCGGCGGTGCGCAGAGCCAGGAGGCGCGCGGGCCAGCCTGGGCCCCAGCCCCACAC  
CTTACCAGGGGCCAGGAGCCACCATGTGGGCGATGTCCACTGGGGCTACTGCTGTTGCTGCCGCTGGCTGGCCAC  
TTGGCTCTGGGTGCCCAGCAGGGTCTGTGGGCGCCGGGAGCTAGCACCGGGTCTGCACCTGCGGGGCATCCGGGAC  
GCGGGAGGCCGTTACTGCCAGGAGCAGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCCTACCTG  
GGCGCCATCTGTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTCTGC  
CTCGGCGTGCCACCCCCCTTTTCCCCCGATCCAAGGATGTATGCATGGAGGTCGTATCTATCCAGTCTTGGGAACG  
TACTGGGACAACTGTAACCGTTGCACCTGCCAGGAGAACAGGCAGTGGCATGGTGGATCCAGACATGATCAAAGC  
CATCAACCAGGGCAACTATGGCTGGCAGGCTGGGAACCAAGCGCCTTCTGGGGCATGACCTGGATTGAGGGGCAT  
TCGCTACCGCTGGGCACCATCCGCCCATCTTCTCGGTGATGAACATGCATGAAATTTATACAGTGTGTAACCC  
AGGGGAGGTGCTTCCACAGCCTTCGAGGCGCTGAGAAAGTGGCCCAACCTGATTGATGAGCCTCTTGACCAAGG  
CAACTGTGCAGGCTCCTGGGCGCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCTCAATCCATTCTCTGGGACA  
CATGACGCTGTCTGTGCGCCCGAAGCTGTGTCTTGTGACACCCACCAGCAGCAGGGCTGCCGCGTGGGCG  
TCTCGATGGTGCTGTGGTTCCTGCGTCGCCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGA  
ACGAGACGAGGCTGGCCCTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTGCGGGCAAGCGCCAGGCCAC  
TGCCCACTGCCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCTCGGCTCCAA  
CGACAAGGAGATCATGAAGGAGCTGATGGGAAATGGCCCTGTCCAAGCCCTCATGGAGGTGCATGAGGACTTCTT  
CCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGGAGGCCAGAGAGATACCGCCGGCATGGGAC  
CCACTCAGTCAAGATCACAGGATGGGGAGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGC  
CAACTCCTGGGGCCAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGC GCGCGGTCAATGAGTGC GACATCGA  
GAGCTTCGTGCTGGGCGTCTGGGGCCGCGTGGGCATGGAGGACATGGGTCACTGAGGCTGCGGGCACCACGC  
GGGGTCCGGCCTGGGATCCAGGCTAAGGGCCGCGGGAAGAGGCCCAATGGGGCGGTGACCCAGCCTCGCCCGA  
CAGAGCCCGGGCGCAGGCGGGCGCCAGGGCGCTAATCCCGCGCGGGTTCGCTGACGCAGCGCCCCGCTGGG  
AGCCGCGGGCAGGCGGAGCTGGCGGAGCCCCAGACCTCCAGTGGGGACGGGGCAGGGCCTGGCCTGGGAAGAG  
CACAGCTGCAGATCCAGGCGCTTGGCGCCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGCCC  
CAATACCCCAACCAATCCCGTATTCTTTTTTTTTTTTTTTAGACAGGGTCTTGCTCCGTTGCCAGGTTGGAG  
TGCAGTGGCCCATCAGGGCTCACTGTAACTCCGACTCCTGGGTTCAGTGACCCCTCCACCTCAGCCTCTCAAG  
TAGCTGGGACTACAGGTGCACCACCACCTGGCTAATTTTTGTATTTTTTGTAAAGAGGGGGTCTCACTGTGT  
TGCCAGGCTGGTTTCGAACTCTGGGCTCAAGCGGTCCACCTGCCTCCGCTCCCAAAGTGTGGGATTGCAGG  
CATGAGCCACTGCACCCAGCCCTGTATTCTTATTCTTCAGATATTTATTTTTCTTTTCACTGTTTTAAATAAAA  
CCAAAGTATTGATAAAAAAAA

**FIGURE 314**

MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADDCA  
LPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPFPPIQGCMHGGRIYPVLGTYWDNCNRCT  
CQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

**Important features:**

**N-glycosylation site.**

amino acids 78-82, 161-165

**Casein kinase II phosphorylation site.**

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,  
411-415

**N-myristoylation site.**

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,  
269-275, 378-384, 442-448

**Amidation site.**

amino acids 26-30, 318-322

**Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 398-409



**FIGURE 315**

CGGACGCGTGGGCCCCCTGGTGGGCCCAGCAAGATGGATCTACTGTGGATCCTGCCCTCCCTGT  
GGCTTCTCCTGCTTGGGGGGCCTGCCTGCCTGAAGACCCAGGAACACCCAGCTGCCCAGGAC  
CCAGGGAAGTGGAGCCAGCAAGTTGTCTCCTGCCAGTTGTCCCGGAGCTCCAGGAAGTC  
CTGGGGAGAAGGGAGCCCCAGGTCTCAAGGGCCACCTGGACCACCAGGCAAGATGGGCCCCA  
AGGGTGAGCCAGGCCCCAGAACTGCCGGGAGCTGTTGAGCCAGGGCGCCACCTTGAGCGGCT  
GGTACCATCTGTGCCTACCTGAGGGCAGGGCCCTCCCAGTCTTTTGTGACATGGACACCGAGG  
GGGGCGGCTGGCTGGTGTTCAGAGGGCGCCAGGATGGTTCTGTGGATTTCTTCCGCTCTTGGT  
CCTCCTACAGAGCAGGTTTGGGAACCAAGAGTCTGAATTCTGGCTGGGAAATGAGAATTTGC  
ACCAGCTTACTCTCCAGGGTAACTGGGAGCTGCGGGTAGAGCTGGAAGACTTTAATGGTAACC  
GTACTTTGCCCCACTATGCGACCTTCCGCCTCCTCGGTGAGGTAGACCACTACCAGCTGGCAC  
TGGGCAAGTTCTCAGAGGGCACTGCAGGGGATTCCCTGAGCCTCCACAGTGGGAGGCCCTTTA  
CCACCTATGACGCTGACCACGATTCAAGCAACAGCAACTGTGCAGTGATTGTCCACGGTGCCT  
GGTGGTATGCATCCTGTTACCGATCAAATCTCAATGGTCGCTATGCAGTGTCTGAGGCTGCCG  
CCCACAAATATGGCATTGACTGGGCCTCAGGCCGTGGTGTGGGCCACCCCTACCGCAGGGTTC  
GGATGATGCTTCGATAGGGCACTCTGGCAGCCAGTGCCCTTATCTCTCCTGTACAGCTTCCGG  
ATCGTCAGCCACCTTGCCCTTGCCAACCACCTCTGCTTGCCGTCCACATTTAAAAATAAAAT  
CATTTTAGCCCTTTCA

**FIGURE 316**

MDLLWILPSLWLLLLGGPACLKTQEHPSCPGPRELEASKVVLPLSCPAPGSPGEKGAPGPQG  
PPGPPGKMGPKEPGPRNCRELLSQGATLSGWYHLCLPEGRALPVFCMDTEGGGWLVFQRRQ  
DGSVDFFRSWSSYRAGFGNQESEFWLGNENLHQLTLQGNWELRVELEDFNGNRTFAHYATFRL  
LGEVDHYQLALGKFSEGTAGDSLHSGRPFTTYDADHDSSNSNCAVIVHGAWWYASCYRSNL  
NGRYAVSEAAAHKYGIDWASGRGVGHPYRRVRMMLR

**Important features:**

**Signal peptide:**

Amino acids 1-16

**N-glycosylation site:**

Amino acids 178-182

**Glycosaminoglycan attachment site:**

Amino acids 272-276

**Tyrosine kinase phosphorylation site:**

Amino acids 188-197

**N-myristoylation sites:**

Amino acids 16-22;89-95;144-150;267-273

**Fibrinogen beta and gamma chains C-terminal domain signature:**

Amino acids 242-255

# **FIGURE 317**

CCCAAGCCAGCCGAGCCGCCAGAGCCGCGGGCCGCGGGGTGTGCGGGGCCCAACCCAGGAT  
GCTCCCCCTGCGCCTCCTGCCTACCCGGGTCTCTACTGCTCTGGGCGCTGCTACTGTTGCTCTT  
 GGGATCAGCTTCTCCTCAGGATTCTGAAGAGCCCCGACAGCTACACGGAATGCACAGATGGCTA  
 TGAGTGGGACCCAGACAGCCAGCACTGCCGGGATGTCAACGAGTGTCTGACCATCCCTGAGGC  
 CTGCAAGGGGGAAATGAAGTGCATCAACCACTACGGGGGCTACTTGTGCCTGCCCCGCTCCGC  
 TGCCGTCATCAACGACCTACATGGCGAGGGACCCCCGCCACCAGTGCCTCCCGCTCAACACCC  
 CAACCCCTGCCCCACCAGGCTATGAGCCCGACGATCAGGACAGCTGTGTGGATGTGGACGAGTG  
 TGCCCAAGGCCCTGCACGACTGTGCCCCAGCCAGGACTGCCATAACTTGCCCTGGCTCCTATCA  
 GTGCACCTGCCCTGATGGTTACCGCAAGATCGGGCCCCGAGTGTGTGGACATAGACGAGTGCCG  
 CTACCGCTACTGCCAGCACCGCTGCGTGAACCTGCCTGGCTCCTTCCGCTGCCAGTGCGAGCC  
 GGGCTTCCAGCTGGGGCCTAACAACCGCTCCTGTGTTGATGTGAACGAGTGTGACATGGGGGC  
 CCCATGCGAGCAGCGCTGCTTCAACTCCTATGGGACCTTCTGTGTGCTGCCACCAGGGCTA  
 TGAGCTGCATCGGGATGGCTTCTCCTGCAGTGATATTGATGAGTGTAGCTACTCCAGCTACCT  
 CTGTGAGTACCGCTGCGTCAACGAGCCAGGCCGTTTCTCCTGCCACTGCCACAGGGTTACCA  
 GCTGCTGGCCACACGCCTCTGCCAAGACATTGATGAGTGTGAGTCTGGTGCGCACCAGTGCTC  
 CGAGGCCCAAACCTGTGTCAACTTCCATGGGGGCTACCGCTGCGTGGACACCAACCGCTGCGT  
 GGAGCCCTACATCCAGGTCTCTGAGAACCGCTGTCTCTGCCCCGGCCTCCAACCTCTATGTCG  
 AGAGCAGCCTTCATCCATTGTGCACCGCTACATGACCATCACCTCGGAGCGGAGCGTGCCCGC  
 TGACGTGTTCCAGATCCAGGCGACCTCCGTCTACCCCGGTGCCTACAATGCCTTTTCAGATCCG  
 TGCTGGAAACTCGCAGGGGGACTTTTACATTAGGCAAATCAACAACGTGAGCGCCATGCTGGT  
 CCTCGCCCGGCCGGTGACGGGGCCCCGGGAGTACGTGCTGGACCTGGAGATGGTCACCATGAA  
 TTCCCTCATGAGCTACCGGGCCAGCTCTGTACTGAGGCTCACCGTCTTTGTAGGGGCCTACAC  
 CTCTCTGAGGAGCAGGAGGGAGCCACCCTCCCTGCAGCTACCCTAGCTGAGGAGCCTGTTGTGA  
 GGGGCAGAATGAGAAAGGCAATAAAGGGAGAAAGAAAGTCTGGTGGCTGAGGTGGGCGGGTC  
 AACTGCGAGGAAGCCTCAGGCTGGGGCAGGGTGGCACTTGGGGGGGCAGGCCAAGTTACCTA  
 AATGGGGGTCTCTATATGTTTCAAGCCCAGGGGCCCCCATTGACAGGAGCTGGGAGCTCTGCAC  
 CACGAGCTTCAGTCACCCCCGAGAGGAGAGGAGGTAACGAGGAGGGCGGACTCCAGGCCCCGGC  
 CCAGAGATTTGGACTTGGCTGGCTTGCAGGGGTCTAAGAAACTCCACTCTGGACAGCGCCAG  
 GAGGCCCTGGGTTCCATTCTAACTCTGCCTCAAACCTGTACATTTGGATAAGCCCTAGTAGTT  
 CCCTGGGCCTGTTTTTCTATAAAACGAGGCAACTGGAAAAAAAAAAAAA

**FIGURE 318**

MLPCASCLPGSLLLWALLLLLLLGSASPQDSEEPDSYTECTDGYEWDPSQHCRDVNECLTIPE  
ACKGEMKCINHYGGYLCLPRSAAVINDLHGEGPPPPVPPAQHPNPCPPGYEPDDQDSCVDVDE  
CAQALHDCRPSQDCHNLPGSYQCTCPDGYRKIGPECVDIDECRYRYCQHRCVNLPGSFRCQCE  
PGFQLGPNNRSCVDVNECDMGAPCEQRCFNSYGTFLCRCHQGYELHRDGFSCSDIDECSYSSY  
LCQYRCVNEPGRFSCHCPQGYQLLATRLCQDIDECESGAHQCEAQTVCVNFHGGYRCVDTNRC  
VEPYIQVSENRCLCPASNPLCREQPSSIVHRYMTITSERVSPADVFIQATSVYPGAYNAFQI  
RAGNSQGDIFYIRQINNVSAMLVLARPVGTGREYVLDLEMVTMNSLMSYRASSVLRLTVFVGAYTF

**Important features:**

**Signal sequence:**

Amino acids 1-25

**N-glycosylation sites:**

Amino acids 198-202;394-398

**N-myristoylation sites:**

Amino acids 76-82;145-151;182-188;222-228;290-296;305-311;  
371-377;381-387

**Aspartic acid and asparagine hydroxylation sites:**

amino acids 140-152;177-189;217-229;258-270

**FIGURE 319**

GCTGGGGACATGAGAGGCACACCGAAGACCCACCTCCTGGCCTTCTCCCTCCTCTGCCTCCTC  
TCAAAGGTGCGTACCCAGCTGTGCCCCGACACCATGTACCTGCCCCCTGGCCACCTCCCCGATGC  
CCGCTGGGAGTACCCCTGGTGTGGATGGCTGTGGCTGCTGCCGGGTATGTGCACGGCGGGTG  
GGGAGCCCTGCGACCAACTCCACGTCTGCGACGCCAGCCAGGGCCTGGTCTGCCAGCCCCGG  
GCAGGACCCGGTGGCCGGGGGGCCCTGTGCCTCTTGGCAGAGGACGACAGCAGCTGTGAGGTG  
AACGGCCGCCTGTATCGGGAAGGGGAGACCTTCCAGCCCCACTGCAGCATCCGCTGCCGCTGC  
GAGGACGGCGGCTTCACCTGCGTGCCGCTGTGCAGCGAGGATGTGCGGCTGCCCAGCTGGGAC  
TGCCCCCAGGGAGGGTTCGAGGTCTGGGCAAGTGCTGCCCTGAGTGGGTGTGCGGCCAA  
GGAGGGGGACTGGGGACCCAGCCCCCTCCAGCCCCAAGGACCCAGTTTTCTGGCCTTGTCTCT  
TCCCTGCCCCCTGGTGTCCCCTGCCAGAATGGAGCACGGCCTGGGGACCCCTGCTCGACCACC  
TGTGGGCTGGGCATGGCCACCCGGGTGTCCAACCAGAACCGCTTCTGCCGACTGGAGACCCAG  
CGCCGCCTGTGCCTGTCCAGGCCCTGCCACCCCTCCAGGGGTGCGAGTCCACAAAACAGTGCC  
TTCTAGAGCCGGGCTGGGAATGGGGACACGGTGTCCACCATCCCAGCTGGTGGCCCTGTGCC  
TGGGCCCTGGGCTGATGGAAGATGGTCCGTGCCCAGGCCCTTGGCTGCAGGCAACACTTTAGC  
TTGGGTCCACCATGCAGAACACCAATATTAACACGCTGCCTGGTCTGTCTGGATCCCAGGTA  
TGGCAGAGGTGCAAGACCTAGTCCCCCTTCTCTAACTCACTGCCTAGGAGGCTGGCCAAGGT  
GTCCAGGGTCTCTAGCCCACTCCCTGCCTACACACAGCCTATATCAAACATGCACACGGG  
CGAGCTTTCTCTCCGACTTCCCCTGGGCAAGAGATGGGACAAGCAGTCCCTTAATATTGAGGC  
TGCAGCAGGTGCTGGGCTGGACTGGCCATTTTTCTGGGGGTAGGATGAAGAGAAGGCACACAG  
AGATTCTGGATCTCCTGCTGCCTTTTCTGGAGTTTGTAAAATTGTTCTGAATACAAGCCTAT  
GCGTGA

**FIGURE 320**

MRGTPKTHLLAFSLCLLSKVRTQLCPTPCTCPWPPPRCPLGVPLVLDGCGCCRVCAARRLGEP  
CDQLHVCDASQGLVCQPGAGPGGRGALCLLAEDDSSCEVNGRLYREGETFQPHCSIRCRCEGDG  
GFTCVPLCSEDVRLPSWDCPHPRRVEVLGKCCPEWVCGQGGGLGTQPLPAQGPQFSGLVSSLP  
PGVPCPEWSTAWGPCSTTCGLGMATRVSNQNRFCRLETQRRRLCLSRPCPPSRGRSPQNSAF

**Important features:**

Signal sequence:

Amino acids 1-23

**N-myristoylation sites:**

Amino acids 3-9;49-55;81-87;85-91;126-132;164-170;166-172;  
167-173;183-189;209-215

**Insulin-like growth factor binding proteins signature:**

Amino acids 49-65

**von Willebrand C1 domain:**

Amino acids 107-124

**Thrombospondin 1 Homology Block:**

Amino acids 201-216

**IGF binding protein site:**

Amino acids 49-58

FIGURE 321

[illegible]

**FIGURE 322**

MMGLSLASAVLLASLLSLHLGTATRGSDISKTCFQYSHKPLPWTWVRSYEFTSNSCSQRAVI  
FTTKRGKKVCTHPRKKWVQKYISLLKTPKQL

**Important features:**

**Signal peptide:**

amino acids 1-23

**N-myristoylation sites.**

amino acids 3-9, 26-32

**Amidation site.**

amino acids 68-72

**Small cytokines (intecrine/chemokine).**

amino acids 23-88



# **FIGURE 323**

ACCGAGCCGAGCGGACCGAAGGCGCGCCCGAGATGAGGTGAGCAAGAGGATGCTGGCGGGGGCGTGAGGAGCA  
TGCCCAGCCCCCTCCTGGCCTGCTGGCAGCCCATCCTCCTGCTGGTGCTGGGCTCAGTGCTGTGAGGCTCGGCCA  
CGGGTGCCCCGCCCCGCTGCGAGTGCTCCGCCCAGGACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAG  
TCCCCGAGGGCATCCCCACCGAGACGCGCCTGCTGGACCTAGGCAAGAACCGCATCAAAACGCTCAACCAGGACG  
AGTTTCGCCAGCTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGCCCGGCGCCT  
TCAACAACCTCTTCAACCTCCGGACGCTGGGTCTCCGAGCAACCGCCTGAAGCTCATCCCGCTAGGCGTCTTCA  
CTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAGATCGTTATCCTACTGGACTACATGTTTCAGG  
ACCTGTACAACCTCAAGTCACTGGAGGTTGGCGACAATGACCTCGTCTACATCTCTACCGCGCCTTCAGCGGCC  
TCAACAGCCTGGAGCAGTGACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCACCTGC  
ACGGCCTCATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGCTGTACC  
GACTCAAGGTCTTGGAGATCTCCCACTGGCCCTACTTGGACACCATGACACCAACTGCCTCTACGGCCTCAACC  
TGACGTCCCTGTCCATCACACATGCAATCTGACCGCTGTGCCCTACCTGGCCGTCCGCCACCTAGTCTATCTCC  
GCTTCTCAACCTCTCTACAACCCATCAGCACCATTTAGGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGG  
AGATCCAGCTGGTGGGCGGGCAGCTGGCCGTGGTGGAGCCCTATGCCTTCCGCGGCCTCAACTACCTGCGCGTGC  
TCAATGTCTCTGGCAACAGCTGACCACACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGGAGACACTCA  
TCCTGGACTCCAACCCGCTGGCCTGCGACTGTGCGCTCCTGTGGGTGTTCCGGCGCCGCTGGCGGCTCAACTTCA  
ACGGGCAGCAGCCACGTGCGCCACGCCGAGTTTGTCCAGGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTAC  
TGCCCAACTACTTCACCTGCCGCGCGCCCGCATCCGGGACCGCAAGGCCCAGCAGGTGTTTGTGGACGAGGGCC  
ACACGGTGCAAGTTTGTGTGCCGGGCGGATGGCGACCCGCGCCCGCCCATCCTCTGGCTCTCACCCCGAAAGCACC  
TGGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCTACGCCCAGGTAC  
AGGACAACGGCACGTACCTGTGCATCGCGGCCAACGCGGGCGGCAACGACTCCATGCCCGCCACCTGCATGTGC  
GCAGCTACTCGCCGACTGGCCCCATCAGCCCAACAAGACCTTCGCTTTCATCTCCAACAGCCGGGCGAGGGAG  
AGGCCAACAGCACCCGCGCCACTGTGCCCTTCCCTTCGACATCAAGACCCTCATCATCGCCACCACCATGGGCT  
TCATCTCTTCTGGGCGTCTCCTCTTCTGCTGGTGCTGCTGTTCTCTGGAGCCGGGCAAGGGCAACACAA  
AGCACAAATCGAGATCGAGTATGTGCCCCGAAAGTCGGACGCAGGCATCAGCTCCGCCGACGCGCCCCGCAAGT  
TCAACATGAAGATGATATGAGGCCGGGGCGGGGGCAGGGACCCCCGGGCGGCGGGCAGGGGAAGGGGCTGGT  
CGCCACCTGCTCACTCTCCAGTCCTTCCACCTCCTCCCTACCTTCTACACAGTTCTCTTTCTCCCTCCCGCC  
TCCGTCCCTGCTGCCCCCGCCAGCCCTCACCACCTGCCCTCCTTCTACAGGACCTCAGAAGCCAGACCTGG  
GGACCCACCTACACAGGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCGGCAGAGTCAATAAT  
TCAATAAAAAAGTTACGAACTTCTCTGTAACCTGGGTTTCAATAATTATGGATTTTATGAAACTTGAAATAA  
TAAAAAGAGAAAAAACTAAAAA

## **FIGURE 324**

MQVSKRMLAGGVRSMPSPLLACWQPILLLLVLGSVLSGSATGCPPRCECSAQDRAVLCHRKCFVAVPEGIPTETRL  
LDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFNLRTLGLRSNRLKLIPLGVFTGLSNLTQDI  
SENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRAFSGLSLEQLTLEKCNLTSSIPTEALSHLHGLIVLRHL  
NINAIRDYSFKRLRLKVLKLEISHWPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPIS  
TIEGSMHELLRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLEESVFHSGVNLETILDSNPLACDC  
RLLWVFRRRWRLNFRNQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQVFVDEGHTVQFVCRADG  
DPPPAIILWLSPRKHLVSAKSNGRITVFPDGTLEVRVYQVQDNGTYLCIAANAGGNDSPAHHLVRSYSPDWPHQP  
NKTFAFISNQPGEGEANSTRATVPFPFDIKTLIIATTMGFISFLGVVLFCLVLLFLWSRGKGN TKHNIETIEYVPR  
KSDAGISSADAPRKFNMKMI

**Important features:**

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 556-578

**N-glycosylation site.**

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345, 492-496,  
505-509, 526-530, 542-546

**Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353, 607-611

**Tyrosine kinase phosphorylation site.**

amino acids 590-598

**N-myristoylation site.**

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143, 262-268, 320-326,  
344-350, 359-365, 493-499, 503-509, 605-611

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

**FIGURE 325**

CCCACGCGTCCGCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGAG  
 GCAGGAGAGGAGGAGGTGGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGAGG  
 AGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAAAGGAGAGAGGGAGGAGGAGGAG  
 GAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAACGGAG  
 AGGAGGTGTGGTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGAGTAGG  
 AAGATCAGGAGCTAGAGGGAGACTGGAGGGTTCCGGGAAAAGAGCAGAGGAAAGAGGAAAGAC  
 ACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTGGCTGCTT  
 TGGCATTGTTGGGGAACCTGGGACTCCCTGTGGGGAGGAGAGGAAAGCTGGAAGTCTGGAGGGAC  
 AGGGTCCCAGAAGGAGGGGACAGAGGAGCTGAGAGAGGGGGCAGGGCGTTGGGCAGGGGTCC  
 CTCGGAGGCCTCCTGGGGATGGGGCTGCAGCTCGTCTGAGCGCCCTCGAGCGCTGGTACTC  
 TGGGCTGCAGTGGGGGCAGCAGCTCACATCGGACCAGCACCTGACCCGAGGACTGGTGGAGC  
 TACAAGGATAATCTCCAGGGAACTTCGTGCCAGGGCCTCCTTTCTGGGGCCTGGTGAATGCA  
 GCGTGGAGTCTGTGTGCTGTGGGGAAGCGGCAGAGCCCCGTGGATGTGGAGCTGAAGAGGGTT  
 CTTTATGACCCCTTTCTGCCCCCATTAAGGCTCAGCACTGGAGGAGAGAAGCTCCGGGAACC  
 TTGTACAACACCGCCGACATGTCTCCTTCCTGCCTGCACCCCGACCTGTGGTCAATGTGTCT  
 GGAGGTCCCCTCCTTTACAGCCACCGACTCAGTGAAGTGCAGGCTGCTGTTTGGAGCTCGCGAC  
 GGAGCCGGCTCGGAACATCAGATCAACCACAGGGCTTCTCTGCTGAGGTGCAGCTCATTCAC  
 TTCAACCAGGAATCTACGGGAATTTAGCGCTGCCCTCCCGCGCCCCAATGGCCTGGCCATT  
 CTCAGCCTCTTTGTCAACGTTGCCAGTACCTCTAACCATTCTCAGTCGCCTCCTTAACCGC  
 GACACCATCACTCGCATCTCCTACAAGAATGATGCCTACTTTCTTCAAGACCTGAGCCTGGAG  
 CTCCTGTTCCCTGAATCCTTCGGCTTCATCACCTATCAGGGCTCTCTCAGCACCCCGCCCTGC  
 TCCGAGACTGTACCTGGATCCTCATTGACCGGGCCCTCAATATCACCTCCCTCAGATGCAC  
 TCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCTTCCAGAGCCTCAGCGGTAACAGC  
 CGGCCCCCTGCAGCCCTTGGCCACAGGGCACTGAGGGGCAACAGGGACCCCCGGCACCCCGAG  
 AGGCGCTGCCGAGGCCCCAACTACCGCTGCATGTGGATGGTGTCCCCATGGTGCCTGAGAGC  
 TCCCCCTCGAGGATTGCACCCGCCGTCTTAAGCCTCCCCACAAGGCGAGGGGAGTTACCCCT  
 AAAACAAAGCTATTAAAGGGACAGAATACTTA

**FIGURE 326**

MGAAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLCA  
VGKRQSPVDVELKRVLYDPFLPPLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPLLY  
SHRLSELRLLLFGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSLFVN  
VASTSNPFLSRLNLRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSETVTW  
ILIDRALNITSLQMHSRLRLSQNPFSQIFQSLSGNSRPLQPLAHRALRGNRDPRHPERRCRGP  
NYRLHVDGVPHGR

**Important features:**

**Signal peptide:**

Amino acids 1-23

**Transmembrane domain:**

Amino acids 177-199

**N-glycosylation sites:**

Amino acids 118-122;170-174;260-264

**Eukaryotic-type carbonic anhydrases proteins:**

Amino acids 222-271;128-165;45-93

# **FIGURE 327**

GGACTAATCTGTGGGAGCAGTTTATTCCAGTATCACCCAGGGTGCAGCCACACCAGGACTGTGTTGAAGGGTGT  
TTTTTCTTTTAAATGTAATACCTCCTCATCTTTCTTCTTACACAGTGTCTGAGAACATTTACATTATAGATAA  
GTAGTACATGGTGGATAACTTCTACTTTTAGGAGGACTACTCTCTTCTGACAGTCTTAGACTGGTCTTCTACACT  
AAGACACCATGAAGGAGTATGTGCTCCTATTATTCTGGCTTTGTGCTCTGCCAAACCCTTCTTTAGCCCTTCAC  
ACATCGCACTGAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATGATGATG  
ATGATGATGAGGACAACCTCTCTTTTCCAACAAGAGAGCCAAGAAGCCATTTTTTCCATTTGATCTGTTTCCAA  
TGTGTCCATTTGGATGTCTAGTGTATTACAGAGTTGTACATTGCTCAGATTTAGGTTTGACCTCAGTCCCAACCA  
ACATTCCATTTGATACTCGAATGCTTGATCTTCAAAACAATAAAATTAAGGAAATCAAAGAAAATGATTTTAAAG  
GACTCACTTCACTTTATGGTCTGATCCTGAACAACAACAGCTAACGAAGATTACCCAAAAGCCTTTCTAACCA  
CAAAGAAGTTGCGAAGGCTGTATCTGTCCCACAATCAACTAAGTGAATACCACTTAATCTTCCCAAATCATTAG  
CAGAACTCAGAATTATGAAAATAAAGTTAAGAAAATACAAAAGGACACATTCAAAGGAATGAATGCTTTACACG  
TTTTGGAATGAGTGCAAAACCCTCTTGATAATAATGGGATAGAGCCAGGGGCATTTGAAGGGTGACGGTGTTC  
ATATCAGAATGTCAGAAGCAAACTGACCTCAGTTCCTAAAGGCTTACCACCAACTTTATTGGAGCTTCACTTAG  
ATTATAATAAAATTTCAACAGTGGAACCTTGAGGATTTTAAACGATACAAAGAACTACAAGGCTGGGCCTAGGAA  
ACAACAAATCACAGATATCGAAAATGGGAGTCTTGCTAACATACCACGTGTGAGAGAAATACATTTGGAAAACA  
ATAAACTAAAAAAATCCCTTCAGGATTACCAGAGTTGAAATACCTCCAGATAATCTTCTTCATTCTAATTCAA  
TTGCAAGAGTGGGAGTAAATGACTTCTGTCCAACAGTGCCAAAGATGAAGAAATCTTTATACAGTGCAATAAGTT  
TATTCAACAACCCGGTGAAATACTGGGAAATGCAACCTGCAACATTTTCGTTGTGTTTGGAGCAGAATGAGTGTC  
AGCTTGGGAACCTTTGGAATGTAATAATTAGTAATTGGTAATGTCCATTTAATATAAGATTCAAAAATCCCTACAT  
TTGGAATACTTGAACCTATTATAAATGGTAGTATTATATATACAAGCAAATATCTATTCTCAAGTGGTAAGTCC  
ACTGACTTATTTTATGACAAGAAATTTCAACGGAATTTTGCCAAACTATTGATACATAAGGGGTTGAGAGAAACA  
AGCATCTATTGCAGTTTCCTTTTGGCTACAAATGATCTTACATAAATCTCATGCTTGACCATTCTTCTTCAT  
AACAAAAAGTAAGATATTCGGTATTTAACACTTTGTTATCAAGCACATTTTAAAAAGAACTGTACTGTAAATGG  
AATGCTTGACTTAGCAAAATTTGTGCTCTTTCATTTGCTGTTAGAAAAACAGAATTAACAAAGACAGTAATGTGA  
AGAGTGCACTTACACTATTCTTATTCTTTAGTAACCTGGGTAGTACTGTAATATTTTAAATCATCTTAAAGTATGA  
TTTGATATAATCTTATTGAAATACCTTATCATGTCTTAGAGCCCGTCTTATGTTTAAAACTAATTTCTTAAAA  
TAAAGCCTTCAGTAAATGTTTATTACCAACTTGATAAATGCTACTCATAAGAGCTGGTTTGGGGCTATAGCATAT  
GCTTTTTTTTTTTTAAATTATTACCTGATTTAAAAATCTCTGTAAAAACGTGTAGTGTTCATAAAATCTGTAAC  
CGCATTTTAAATGATCCGCTATTATAAGCTTTAATAGCATGA~~AA~~ATTTGTTAGGCTATATAACATTGCCACTTCAA  
CTCTAAGGAATATTTTGGAGATATCCCTTTGGAAGACCTTGCTTGAAGAGCCTGGACACTAACAAATCTACACC  
AAATTGTCTCTTCAAATACGTATGGACTGGATAACTCTGAGAAAACACATCTAGTATAACTGAATAAGCAGAGCAT  
CAAATTAACAGACAGAAACCGAAAGCTCTATATAAATGCTCAGAGTTCTTTATGTATTCTTATTGGCATTCAA  
CATATGTAAATCAGAAAACAGGGAATTTTCATTAAAAATATGGTTTGAAAT

**FIGURE 328**

MKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDEDNSLFPTREPRS  
HFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTS  
LYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDT  
FKGMNALHVLEMSANPLDNNGIEPGA FEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKI  
STVELEDFKRYKELQRLGLGNNKITDIENGLANI PRVREIHLENNKLKKIPSGLPELKYLQI  
IFLHSNSIARVGVNDFCPTVPKMKKSLSAISLFNNPVKYWEMQPATFRCVLSRMSVQLGNFGM

**Important features:**

**Signal sequence.**

amino acids 1-15

**N-glycosylation site.**

amino acids 281-285

**N-myristoylation sites.**

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

**Leucine zipper pattern.**

amino acids 154-176

**FIGURE 329**

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGCA  
TCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGTGT  
TTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCCATGATCACTGGTGTGTT  
CAGCATGCGCTTGTGGACCCCAAGTGGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACCAGCG  
GCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGCCTGCT  
GAAGTTGAAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCCGCTCCC  
GCTGGAGGAGCAGGTAGAGTGGAACCCCAAGCTATTAGAGGTCCCACCCCAAACCTCAGTTTGA  
TTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCTCAATACCA  
TGAGACCACCCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTGGGCATGCAGCAAAT  
GTTTGCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTCTTTACCAAC  
CTTCAACCCACAGGAGGTCTTTATTTCGTTCCACTAACATTTTTCGGAATCTGGAGTCCACCCG  
TTGTTTGCTGGCTGGGCTTTTCCAGTGTGAGAAAGAGGCCCATCATCATCCACACTGATGA  
AGCAGATTCAGAAGTCTTGTATCCCAACTACCAAAGCTGCTGGAGCCTGAGGCAGAGAACCAG  
AGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTTGAAAAAGGTGAAGGA  
CAGGATGGGCATTGACAGTAGTGATAAAGTGGAATTCTTCATCCTCCTGGACAACGTGGCTGC  
CGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTTGCACGGATGATCGAACA  
GAGAGCTGTGGACACATCCTTGATACATACTGCCCAAGGAAGACAGGGAAAGTCTTCAGATGGC  
AGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGCCATGGACTCTGCCACTGC  
CCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATGTGACCTTCATACCGCTCTT  
AATGACCCCTGGGGATTTTTGACCACAAATGGCCACCGTTTGCTGTTGACCTGACCATGGAAC  
TTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTATTACCACGGGAAGGAGCAGGT  
GCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGTTCTTGAATGCCATGTCAGTTTA  
TACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAAACCTCAGGTGATGGAAGTTGGAAA  
TGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGATTTTAAAAATAAAGTGCCTTTATACAATG

## **FIGURE 330**

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVFRHGARSPLKPLPLEEQVE  
WNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQLTKVGMQQMFALGERLRKNYVEDIPFL  
SPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKEGPPIIHTDEADSEVLYPNYQSCWSLRQRTGRRTASLQ  
PGISEDLLKKVKDRMGIDSSDKVDFILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMA  
VGPFLHILESNNLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEWFVQ  
LYYHGKEQVERGCPDGLCPLDMFLNAMS VYTLSPEKYHALCSQTQVMEVGNEE

**Important features:**

**Signal sequence:**

amino acids 1-23

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 218-222

**Casein kinase II phosphorylation site.**

amino acids 87-91, 104-108, 320-324

**Tyrosine kinase phosphorylation site.**

amino acids 280-288

**N-myristoylation site.**

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

**Amidation site.**

amino acids 216-220

**Leucine zipper pattern.**

amino acids 10-32

**Histidine acid phosphatases phosphohistidine signature.**

amino acids 50-65



# **FIGURE 331**

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGTGGCTACAACATTTTCCCTTTCCT  
AACAAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTCTTCTTGTCTGGAGAAGAAAGGGCTGAGGGCAG  
AGCAGGGGCACTCTCACTCAGGGTGACCAGCTCCTTGCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGAT  
GCAGCGGAGTGAGGTGATGGAAGTCTAAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGA  
CCTGGAGAGCCTGGGGGAGGGCCTGCCTAACAAAGCTTTCAAAAACAGGAGCGACTTCCACTGGGCTGGGATAAG  
ACGTGCCGGTAGGATAGGGAAGACTGGGTTTAGTCCCTAATATCAAATTGACTGGCTGGGTGAACTTCAACAGCCT  
TTTAACCTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAATAGAGATGCTTTGTAAAATAAAATTTTAA  
AAAAAGCAAGTATTTTATAGCATAAAGGCTAGAGACCAAAATAGATAACAGGATTCCCTGAACATTCTTAAGAGG  
GAGAAAGTATGTTAAAAATAGAAAAACCAAATGCAGAAGGAGGAGACTCACAGAGCTAAACAGGATGGGGACC  
CTGGGTGACGGCCAGCCTCTTTGCTCTCCCGAAATTATTTTGGTCTGACCACTCTGCCTTGTGTTTTGCAGAA  
TCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCTCCTCACCGCCGCCCCCTCTC  
AGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGGACAGCCGCTCTGTGGTCCTGCTCTCAGTGGTC  
TGGGTGCTGCTGGCCCCCAGCAGCCGGCATGCCTCAGTTCAGCACCTTCCACTCTGAGAATCGTGACTGGACC  
TTCAACCACTTGACCGTCCACCAAGGGACGGGGGCCGTCTATGTGGGGGCCATCAACCGGTCTATAAGCTGACA  
GGCAACCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCGCCCTCATC  
GTGCAGCCCTGCAGCGAAGTGCTCACCTCACCAACAATGTCAACAAGCTGCTCATCATTGACTACTCTGAGAAC  
CGCTGCTGGCCTGTGGGAGCCTCTACCAGGGGTCTGCAAGCTGCTGCGGCTGGATGACCTCTTCATCCTGGTG  
GAGCCATCCACAGAAGGAGCACTACCTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGTGATTGTGCGC  
TCTGAGGTGAGGATGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCGACCTGTCTC  
AGCCGGAAGCTGCCCCGAGACCCTGAGTCTCAGCCATGCTCGACTATGAGCTACACAGCATTTTGTCTCTCT  
CTCATCAAGATCCCTTCAGACACCCTGGCCCTGGTCTCCCACTTTGACATCTTCTACATCTACGGCTTTGCTAGT  
GGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCGAGACCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTC  
TTCTACACCTCACGCATCGTGGGCTCTGCAAGGATGACCCCAAGTTCCACTCATACGTGTCCCTGCCCTTCGGC  
TGCAACCGGGCCGGGTGGAATACCGCTCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCAG  
GCCTTCAATATCACCAGCCAGGACGATGTACTCTTTGCCATCTTCTCAAAGGGCAGAAGCAGTATCACCACCCG  
CCCGATGACTCTGCCCTGTGTGCCTTCCCTATCCGGGCCATCAACTGCAGATCAAGGAGCGCTGCAGTCTGCTC  
TACCAGGGCGAGGGCAACCTGGAGCTCAACTGGCTGCTGGGGAAGGACGTCCAGTGCACGAAGGCGCCTGTCCCC  
ATCGATGATAACTTCTGTGGACTGGACATCAACCAGCCCCCTGGGAGGCTCAACTCCAGTGGAGGGCCTGACCCTG  
TACACCACCAGCAGGGACCGCATGACCTCTGTGGCTCCTACGTTTACAACGGCTACAGCGTGGTTTTTGTGGGG  
ACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTCAGATGCTCCAATGCCATTACCTCCTCAGCAAA  
GAGTCCCTCTTGAAGGTAGCTATTGGTGGAGATTTAACTATAGGCAACTTTATTTTCTTGGGGAACAAAGGTGA  
AATGGGGAGGTAAGAAGGGTTAATTTGTGACTTAGCTTCTAGCTACTTCTCCAGCCATCAGTCATTGGGTAT  
GTAAGGAATGCAAGCGTATTTCAATATTTCCCAAACCTTAAGAAAAAATTTAAGAAGGTACATCTGCAAAAGCAAA

**FIGURE 332**

MGTLGQASLFAPPGNYFWSHDHSAFCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWPR  
ALEVDSRSVLLSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRVYK  
LTGNLTIQVAHKTGPPEEDNKSRYPPILVQPCSEVLTLTNNVNKLLIIDYSENRLACGSLYQG  
VCKLLRLDDLFIIVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDYFPTL  
SSRKLPRDPRESSAMLDYELHSDVFSSLIKIPSDTLALVSHFDIFYIYGFASSGGFVYFLTQPE  
TPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKPGDSLQ  
AFNITSQDDVLFAlFSKGQKQYHHPDDSAFCFAPIRAINLQIKERLQSCYQEGNLELNWLL  
GKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNGYSVVFVGT  
KSGKLLKVRVYEFRCNAIHLLESKESLLEGSYWWRFNRYRQLYFLGEQR

**Important features:**

**Signal sequence:**

amino acids 1-32

**Transmembrane domain:**

amino acids 71-87

**N-glycosylation site.**

amino acids 130-134, 145-149, 217-221, 381-385

**Casein kinase II phosphorylation site.**

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,  
384-388, 471-475, 481-485, 530-534

**N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

**FIGURE 333**

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCTCCAGCCTGTAACCTGTGCCTACACCACGCCAGG  
CCCCCCCAGAGCCCTCACCACGCTGGGCGCCCCAGAGCCCACACCATGCCGGGCACCTACGC  
TCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGGCCCTGAT  
GCGGGACTTCCCCTCGTGGACGGCCACAACGACCTGCCCCCTGGTCCTAAGGCAGGTTTACCA  
GAAAGGGCTACAGGATGTTAACCTGCGCAATTTCAGCTACGGCCAGACCAGCCTGGACAGGCT  
TAGAGATGGCCTCGTGGGCGCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCG  
GGATGCCCTGCGCCTCACCTGGAGCAGATTGACCTCATACGCCGCATGTGTGCCTCCTATTCT  
TGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTCAT  
CGGTGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTTCTACATGCT  
GGGAGTGCGCTACCTGACGCTCACCCACACCTGCAACACACCCTGGGCAGAGAGCTCCGCTAA  
GGGCGTCCACTCCTTCTACAACAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGTGGC  
AGAAATGAACCGCCTGGGCATGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCG  
GGCCCTGGAAGTGTACAGGCACCTGTGATCTTCTCCCACTCGGCTGCCCCGGGTGTGTGCAA  
CAGTGCTCGGAATGTTCTGATGACATCCTGCAGCTTCTGAAGAAGAACGGTGGCGTCTGAT  
GGTGTCTTTGTCCATGGGAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGA  
TCACTTCGACCACATCAAGGCTGTCAATTGGATCCAAGTTCATCGGGATTGGTGGAGATTATGA  
TGGGGCCGGCAAATTCCTCAGGGGCTGGAAGACGTGTCCACATACCCGGTCTTGATAGAGGA  
GTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCTTTCGTGGAAACCTGCTGCG  
GGTCTTCAGACAAGTGGAAGGTACAGGAAGAAAACAAATGGCAAAGCCCCCTTGGAGGACAA  
GTTCCCGGATGAGCAGCTGAGCAGTTCCTGCCACTCCGACCTCTCACGTCTGCGTCAGAGACA  
GAGTCTGACTTCAGGCCAGGAACTCACTGAGATTCCCATACACTGGACAGCCAAGTTACCAGC  
CAAGTGGTCAGTCTCAGAGTCCTCCCCCACATGGCCCCAGTCCTTGCAATTGTGGCCACCTT  
CCCAGTCCTTATTCTGTGGCTCTGATGACCCAGTTAGTCCTGCCAGATGTCACTGTAGCAAGC  
CACAGACACCCCACAAAGTTCCCTGTTGTGCAGGCACAAATATTTCTGAAATAAATGTTTT  
GGACATAG

**FIGURE 334**

MPGTYAPSTTLSSPSTQGLQEQARALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYGQ  
TSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIRRMCASYSLELVTSAKALNDTQ  
KLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGLTDF  
GEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQLLKK  
NGGVVMVSLSMGVIQCNP SANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLEDVSTY  
PVLIEELLSRGWSEEELOQVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSSCHSDLS  
RLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHMAPVLAVVATFPVLILWL

**Important features:**

**N-glycosylation sites.**

amino acids 58-62, 123-127, 182-186, 273-277

**N-myristoylation sites.**

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

**Renal dipeptidase active site.**

amino acids 134-157

**FIGURE 335**

CCCAGAAGTTCAAGGGCCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCCTCGACCTCCTCAG  
AGCAGCCGGCTGCCGCCCCGGGAAGATGGCGAGGAGGAGCCGCCACCGCCTCCTCCTGCTGCT  
GCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGGTTTTCTGCCCCAAAAGA  
CCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAAAAACCCCAAAGAA  
GACTGTTTCCTCCAGATTAGAGTGGAAGAACTGGGTCCGAGTGTCTCCTTTGTCTACTATCA  
ACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCGGATCAA  
AAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTGAGCAAGG  
CCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTTCCATCATG  
TGAAGTACCCCTCTTCTGCTCTGAGTGGAAGTGTGGTAGAGCTACGATGTCAAGACAAAGAAGG  
GAATCCAGCTCCTGAATACACATGGTTTAAAGGATGGCATCCGTTTGCTAGAAAATCCCAGACT  
TGGCTCCCAAAGCACCAACAGCTCATACACAATGAATACAAAACTGGAAGTCTGCAATTTAA  
TACTGTTTCCAACTGGACACTGGAGAATATTCCTGTGAAGCCCGCAATTCTGTTGGATATCG  
CAGGTGTCCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCATCATAGCAGCCGT  
AGTAGTTGTGGCCTTAGTGATTTCCGTTTGTGGCCTTGGTGTATGCTATGCTCAGAGGAAAGG  
CTACTTTTCAAAGAAACCTCCTTCCAGAAGAGTAATTCTTCATCTAAAGCCACGACAATGAG  
TGAAAATGTGCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGAAGGCCGCGCGGGCGGATC  
ACGAGGTGAGGAGTTCTAGACCAGTCTGGCCAATATGGTGAAACCCCATCTCTACTAAAATAC  
AAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGCTTGGGAGACAGGAGAATC  
ACTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGCCACTGCAGTCCAGCCTGGG  
TAACAGAGCAAGATTCCATCTCAAAAAATAAAATAAATAAATAAATAAATACTGGTTTTTACC  
TGTAGAATTCTTACAATAAATATAGCTTGATATTC

**FIGURE 336**

MARRSRHRLLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTIVSSRLEW  
KKLGRSVSFVYYQQTQGD FKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTV  
TLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGQSQTNSS  
YTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVVALVIS  
VCGLGVCYAQRKGYFSKETS FQKSNSSSKATTMSENVQWLTPVIPALWCAAAGGSRGQEF

**Important features:**

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 130-144, 238-258

**N-glycosylation site.**

amino acids 98-102, 187-191, 236-240, 277-281

**Casein kinase II phosphorylation site.**

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

**N-myristoylation site.**

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

**Amidation site.**

amino acids 226-230

# **FIGURE 337**

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTGCGGCAGCCTCGG  
CACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCCTGACTCCGTCCCGGCCAGGGAGGGCCA  
TGATTTCCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTTGTTCTTGGGGCTGAGTG  
CCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAGGCGG  
TGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGCGGGAGGTGTCTTCATCCC  
AGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATCAGGTGT  
TGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCCATGCCCT  
CCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCCTACAGCTGCT  
CCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCTTAGAACTCA  
ATGTACTGGTTCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCATGTGGGGGCAA  
ACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCAGTGGGATCGGC  
AGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCC  
TCACCAACCTTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCACAATGAGGTGGGCA  
CTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAG  
CTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCTCTTGTACCACCGCC  
GGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCC  
TGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCTTCTCTGTACCTCCG  
CACGAGCCCTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCAATTGACCCCCACGCCCAGTC  
TCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCCACGACAGATGGGGCCCCACCTCAACCAA  
TATCCCCCATCCCTGGTGGGGTTTTCTTCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA  
TGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATTGATGACCCCACTCATTTGGCTAAAG  
GATTTGGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCACAGAGGCCCTGAGTCATGGGAAAG  
AGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAAAACCATCTCA  
GTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGAATTGGGAGGAGC  
CTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAGCTACTACCAAGAGT  
GAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGCCCCCTTGATCTGTACCCCAACCCCTAT  
CTAACACCACCCCTTGGCTCCCACTCCAGCTCCCTGTATTGATATAACCTGTCAGGCTGGCTTG  
GTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCTTATTAAACTAACATGAAATATGTGTT  
GTTTTCATTTGCAAATTTAAATAAAGATACATAATGTTTGTATGAAAAA

**FIGURE 338**

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSSS  
QPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPYSC  
SVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPVHGAVNLTSLSCQSPRSKPAVQYQWDR  
QLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAADVAG  
AVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWKSSDTISKNGTLSSVTS  
ARALRPPHGPFRPGALTPTPSLSSQALPSPRLPTTDGAHPQIPISPIPGGVSSSGLSRMGAVPV  
MVPAQSQAGSLV

**Important features:**

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 245-267

**N-glycosylation site.**

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

**N-myristoylation site.**

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,  
262-268, 308-314, 363-369, 364-370

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175



# **FIGURE 339**

GCGAGAACCTTTGCACGCGCACAACTACGGGGACGATTTCCTGATTGATTTTGGCGCTTTCGATCCACCCTCCT  
 CCCTTCTC**ATGGG**ACTTTGGGGACAAAGCGTCCCAGCCGCTCGAGCGCTCGAGCAGGGCGCTATCCAGGAGCCA  
 GGACAGCGTCGGGAACCAGACCATGGCTCCTGGACCCCAAGATCCTTAAGTTGCTCGTCTTCATCGTCGCGGTTT  
 TGCTGCCGGTCCGGTTGACTCTGCCACCATCCCCCGGCAGGACGAAGTTCCCCAGCAGACAGTGGCCCCACAGC  
 AACAGAGCGCAGCCTCAAGGAGGAGGAGTGCCAGCAGGATCTCATAGATCAGAATATACTGGAGCCTGTAAAC  
 CGTGACAGAGGGTGTGGATTACACCATTGCTTCCAACAATTTGCCCTTCTTGCCCTGCTATGTACAGTTTGTAAAT  
 CAGGTCAAACAAATAAAAGTTCTCTGTACCACGACCAGAGACACCGTGTGTCAAGTGTGAAAAAGGAAGCTTCCAGG  
 ATAAAACTCCCTGAGATGTGCCGGACGTGTAGAACAGGGTGTCCCAGAGGGATGGTCAAGGTGAGTAATTGTA  
 CGCCCCGAGTGACATCAAGTGCAAAAATGAATCAGCTGCCAGTTCCACTGGGAAAACCCAGCAGCGGAGGAGA  
 CAGTGACCACCATCCTGGGGATGCTTGCCCTCTCCCTATCACTACCTTATCATCATAGTGGTTTTAGTCATCATTT  
 TAGCTGTGGTTGTGGTTGGCTTTTCATGTGCGAAGAAATTCATTTCTTACCTCAAAGGCATCTGCTCAGGTGGTG  
 GAGGAGGTCCCGAACGTGTGCACAGAGTCTTTTTCCGGCGGCGTTTCATGTCTTTCAGAGTTTCTGGGCGGAGG  
 ACAATGCCCGCAACGAGACCCCTGAGTAACAGATACTTGCAGCCCACCCAGGTCTCTGAGCAGGAAATCCAAGGT  
 AGGAGCTGGCAGAGCTAACAGGTGTGACTGTAGAGTCGCCAGAGGAGCCACAGCGTCTGCTGGAACAGGCAGAAG  
 CTGAAGGTGTGTGAGGAGGAGGCTGCTGGTTCCAGTGAATGACGCTGACTCCGCTCAAAGGCATCTGCTCAGGTGG  
 ATGCCCTCGGCAACACTGGAAGAAGGACATGCAAGGAAACAATTCAGGACCAACTGGTGGGCTCCGAAAAGCTCT  
 TTTATGAAGAAGATGAGGCAAGGCTCTGCTACGTCCTGCTCTG**TGA**AAGAATCTCTTCAGGAAACAGAGCTTCCCT  
 CATTTACCTTTTCTCCTACAAAGGGAAGCAGCCTGGAAGAACAGTCCAGTACTTGACCCATGCCCCAACAACT  
 CTACTATCAATATGCGGCGAGCTTACCAATGGTCTTAGAACTTTGTAAACGCACTTGGAGTAATTTTATGAAAT  
 ACTGCGTGTGATAAGCAAACGGGAGAAATTTATATCAGATTCTTGGCTGCATAGTTATACGATTGTGTATTAAGG  
 GTCGTTTTAGGCCACATGCCGTGGCTCATGCCGTGTAATCCCAGCACTTTGATAGGCTGAGGCAGGTGGATTGCTT  
 GAGCTCGGGAGTTTGAGACCAGCCTCATCAACACAGTGAACTCCATCTCAATTTAAAAAGAAAAAAGTGGTTT  
 TAGGATGTCAATCTTTGAGTTCTTCATCATGAGACAAGTCTTTTTTCTGCTCTTATATGCAAGCTCCATCT  
 CTACTGGTGTGTGATTTAATGACATCTAACTACAGATGCCGCACAGCCACAATGCTTTGCCTTATAGTTTTTTA  
 ACTTTAGAACGGGATATCTTGTATTACCTGTATTTTCAGTTTCGATATTTTGACTTAATGATGAGATTATC  
 AAGACGTAGCCCTATGCTAAGTCATGAGCATATGGACTTACGAGGGTTCGACTTAGAGTTTTCAGCTTTAAGATA  
 GGATTATTGGGGCTTACCCCCACCTTAATTAGAGAAACATTTATATTGCTTACTACTGTAGGCTGTACATCTCTT  
 TTCCGATTTTTGTATAATGATGTAAACATGGAAAACTTTAGGAAATGCACTTATAGGCTGTTTACATGGGTG  
 CCTGGATACAAATCAGCAGTCAAAAATGACTAAAAATATACTAGTGACGGAGGGAGAAATCCTCCCTCTGTGGG  
 AGGCACCTACTGCATTCCAGTTCTCCCTCTGCGCCCTGAGACTGGACCAGGGTTTGATGGCTGGCAGCTTCTCA  
 AGGGGCAGCTTGTCTTACTTGTAAATTTTAGAGGTATATAGCCATATTTATTTATAAAATAAATATTTATTTATTT  
 ATTTATAAGTAGATGTTTACATATGCCAGGATTTTGAAGAGCCTGGTATCTTTGGGGAAGCCATGTGTCTGGTTT  
 GTCGTGCTGGGACAGTCATGGGACTGCATCTTCCGACTTGTCCACAGCAGATGAGGACAGTGAGAATTAAGTTAG  
 ATCCGAGACTGCCAAGAGCTTCTCTTTCAAGCGCCATTACAGTTGAACGTTAGTGAATCTTGAGCCTCAITGGG  
 CTCAGGGCAGAGCAGGTGTTTATCTGCCCGGCATCTGCCATGGCATCAAGAGGGAAGAGTGGACGGTGTCTGGG  
 AATGGTGTGAAATGTTTGGCGACTCAGGCATGGATGGGCCCTCTCGCTTCTGGTGGTCTGTGAAGTGAAGTCCCT  
 GGGATGCCCTTTAGGGCAGAGATTCCTGAGCTGCGTTTATGGGTACAGATTCCCTGTTTGAAGAGCTTGGCCCCCT  
 CTGTAAGCATCTGACTCATCTCAGAGATATCAATTTCTAAACACTGTGACAACGGGATCTAAAATGGCTGACACA  
 TTTGTCTTGTGTACGTTCCATTATTTTATTTAAAAACCTCAGTAATCGTTTTAGCTTCTTTCCAGCAAACTCT  
 TCTCCACAGTAGCCAGTCGTGGTAGGATAAATTACGGATATAGTCATTCTAGGGGTTTCAGTCTTTTCCATCTC  
 AAGGCATTGTGTGTTTGTTCGGGACTGGTTTGGCTGGGACAAAGTTAGAACTGCCTGAAGTTCGCACATTCAG  
 ATTGTTGTGTCCATGGAGTTTAGGAGGGGATGGCTTTCCGGTCTTCGCACTTCCATCCTCTCCCACTTCCATC  
 TGGCGTCCACACCTTGTCCCTGCACTTCTGGATGACACAGGGTGTGCTGCTGCCCTCTAGTCTTTGCTTTGCTG  
 GGCCTTCTGTGACGAGACTTGGTCTCAAAGCTCAGAGAGAGCCAGTCCGGTCCAGCTCCTTTGCTCCCTTCTC  
 AGAGGCCTTCTTGAAGATGCATCTAGACTACCAGCCTTATCAGTGTTTAAGCTTATTTCTTTAAACATAAGCTTC  
 CTGACAACATGAAATGTTGGGGTTTTTTGGCGTGTGGTTGATTGTTTAGGTTTGTCTTTATACCCGGGCCAAAT  
 AGCACATAACACCTGGTTATATATGAAATACTCATATGTTTATGACCAAAATAAATATGAAACCTCATRTTAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 340**

MGLWGQSVPTASSARAGRYPGARTASGTRPWLLDPKILKFVVFIVAVLLPVRVDSATIPRQDEVPPQTVAPQQQR  
RSLKEEECPAGSHRSEYTGACNPCTEGVDYTIASNNLPSCLLCTVCKSGQTNKSSCTTTRDTCQCEKGSFQDKN  
SPEMCRTTCRTGCPRGMVKVSNCTPRSDIKCKNESAAASSTGKTPAAEETVTTLGMLASPYHYLIIIVVLVIILAV  
VVVGFSCRRKFISYLGKICSGGGGGPERVHRVLFRRRSCPSRVPGAEDNARNETLSNRYLQPTQVSEQEIQQQEL  
AELTGVTVESPEEPQRLLEQAEAGCQRRRLLPVNDADSADISTLLDASATLEEGHAKETIQDQLVGSEKLFYE  
EDEAGSATSCSL

**Important features:**

**Transmembrane domains:**

amino acids 35-52, 208-230

**N-glycosylation sites.**

amino acids 127-131, 182-186, 277-281

**Glycosaminoglycan attachment site.**

amino acids 245-249

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 260-264

**N-myristoylation sites.**

amino acids 21-27, 86-92, 102-108, 161-167, 242-248, 270-276, 297-303, 380-386

**ATP/GTP-binding site motif A (P-loop).**

amino acids 185-193

**TNFR/NGFR cysteine-rich region.**

amino acids 99-139

**FIGURE 341**

GCCTCTGAATTGTTGGGCAGTCTGGCAGTGGAGCTCTCCCCGGTCTGACAGCCACTCCAGAGG  
CCATGCTTCGTTTCTTGCCAGATTGGCTTTCAGCTTCCTGTTAATTCTGGCTTTGGGCCAGG  
CAGTCCAATTTCAAGAATATGTCTTTCTCCAATTTCTGGGCTTAGATAAGGCGCCTTCACCCC  
AGAAGTTCCAACCTGTGCCTTATATCTTGAAGAAAATTTTCCAGGATCGCGAGGCAGCAGCGA  
CCACTGGGGTCTCCCGAGACTTATGCTACGTAAAGGAGCTGGGCGTCCGCGGGAATGTACTTC  
GCTTTCCTCCAGACCAAGGTTTCTTTCTTTACCCAAAGAAAATTTCCCAAGCTTCCTCCTGCC  
TGCAGAAGCTCCTCTACTTTAACCTGTCTGCCATCAAAGAAAGGGAACAGTTGACATTGGCCC  
AGCTGGGCCTGGACTTGGGGCCCAATTCTTACTATAACCTGGGACCAGAGCTGGAAGTGGCTC  
TGTTCCCTGGTTCAGGAGCCTCATGTGTGGGGCCAGACCACCCCTAAGCCAGGTAAAATGTTTG  
TGTTGCGGTCAGTCCCATGGCCACAAGGTGCTGTTCACTTCAACCTGCTGGATGTAGCTAAGG  
ATTGGAATGACAACCCCCGGAAAAATTTCGGGTTATTCTTGAGATACTGGTCAAAGAAGATA  
GAGACTCAGGGGTGAATTTTCAGCCTGAAGACACCTGTGCCAGACTAAGATGCTCCCTTCATG  
CTTCCCTGCTGGTGGTGACTCTCAACCTGATCAGTGCCACCCTTCTCGGAAAAGGAGAGCAG  
CCATCCCCTGTCCCCAAGCTTTCCTGTAAGAACCTCTGCCACCGTCACCAGCTATTCATTAAC  
TCCGGGACCTGGGTTGGCACAAGTGGATCATTGCCCCCAAGGGGTTTCATGGCAAATTACTGCC  
ATGGAGAGTGTCCCTTCTCACTGACCATCTCTCTCAACAGCTCCAATTATGCTTTCATGCAAG  
CCCTGATGCATGCCGTTGACCCAGAGATCCCCCAGGCTGTGTGTATCCCCACCAAGCTGTCTC  
CCATTTCATGCTCTACCAGGACAATAATGACAATGTCATTCTACGACATTATGAAGACATGG  
TAGTCGATGAATGTGGGTGTGGGTAGGATGTCAGAAATGGGAATAGAAGGAGTGTTCCTTAGGG  
TAAATCTTTTAATAAAAACCTACCTATCTGGTTTATGACCACCTTAGATCGAAATGTC

**FIGURE 342**

MLRFLPDLAFFSFLILALGQAVQFQEYVFLQFLGLDKAPSPQKFQVPYILKKIFQDREAAAT  
TGVSRDLCYVKELGVRGNVLRFLPDQGFFLYPKKISQASSCLQKLLYFNLSAIKEREQLTLAQ  
LGLDLGPNSYYNLGPELELALFLVQEPHVWGQTTPKPGKMFVLRSPWPQGAHVFNLLDVAKD  
WNDNPRKNFGLFLEILVKEDRDSGVNFQPEDTCARLRCSLHASLLVVTLNPDQCHPSRKRRAA  
IPVPKLSCKNLCHRHQLFINFRDLGWHKWIIAPKGFMANYPCHGECPFSLTISLNSSNYAFMQA  
LMHAVDPEIPQAVCIPTKLSPISMPLYQDNNDNVILRHYEDMVVDECGCG

**Important features:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 112-116, 306-310

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 96-100

**N-myristoylation site.**

amino acids 77-83

**TGF-beta family proteins.**

amino acids 264-299, 327-341, 345-364

# **FIGURE 343**

CCCACGCGTCCGGCCTTCTCTCTGGACTTTGCATTTCCATTCCCTTTTCATTGACAACTGACTTTTTTTATTTCT  
TTTTTTCATCTCTGGGCCAGCTTGGGATCCTAGGCCGCCCTGGGAAGACATTTGTGTTTTACACACATAAGGAT  
CTGTGTTTGGGGTTTCTTCTCCCTCCCTGACATTGGCATTGCTTAGTGGTTGTGTGGGGAGGGAGACCACGTGG  
GCTCAGTGCTTGCTTGCACTTATCTGCCTAGGTACATCGAAGTCTTTTGACCTCCATACAGTGATTATGCCTGTC  
ATCGCTGGTGTATCCTGGCGGCCTTGCTCCTGCTGATAGTTGTGCTGCTCTGTCTTTACTTCAAAATACACAAC  
GCGCTAAAAGCTGCAAAGGAACCTGAAGCTGTGGCTGTAAAAATCACAAACCAGACAAGGTGTGGTGGGCCAAG  
AACAGCCAGGCCAAAACCATTTGCCACGGAGTCTTGTCTGCTGCCCTGCAGTGCTGTGAAGGATATAGAATGTGTGCC  
AGTTTTGATTCCCTGCCACCTTGCTGTTGCGACATAAATGAGGGCCTCTGAGTTAGGAAAGGCTCCCTTCTCAA  
GCAGAGCCCTGAAGACTTCAATGATGTCAATGAGGCCACCTGTTTGTGATGTGCAGGCACAGAAGAAAGGCACAG  
CTCCCATCAGTTTCATGGAAAATAACTCAGTGCCCTGCTGGGAACCAGCTGCTGGAGATCCCTACAGAGAGCTTC  
CACTGGGGGCAACCTTCCAGGAAGGAGTTGGGGAGAGAGAACCTCACTGTGGGAATGCTGATAAACCACTCA  
CACAGCTGCTCTATTCTCACACAAATCTACCCCTTGCGTGGCTGGAACTGACGTTTCCCTGGAGGTGTCCAGAAA  
GCTGATGTAACACAGAGCCTATAAAAGCTGTCCGTCTTAAGGCTGCCAGCGCCTTGCCAAAATGGAGCTTGT  
AGAAGGCTCATGCCATTGACCCCTCTTAATTCTCTCTGTTTGGCGGAGCTGACAATGGCGGAGGCTGAAGGCAAT  
GCAAGCTGCACAGTCAGTTAGGGGGTGCCAATATGGCAGAGACCCACAAAGCCATGATCCTGCAACTCAATGCC  
AGTGAGAACTGCACCTGGACAATAGAAAGACCAGAAAACAAAGCATCAGAATTATCTTTTCTATGTCCAGCTT  
GATCCAGATGGAAGCTGTGAAAGTGAAACATTAAAGTCTTTGACGGAACCTCCAGCAATGGGCCTCTGCTAGGG  
CAAGTCTGCAGTAAAAACGACTATGTTCTGTATTGAAATCATCATCCAGTACATTGACGTTTCAAATAGTTACT  
GACTCAGCAAGAATTCAAAGAACTGTCTTTGTCTTCTACTACTTCTTCTCTCCTAACATCTGATTCCAACTGT  
GGCGGTTACCTGGATACCTTGAAGGATCCTTCACCAGCCCCAATTACCCAAAGCCGCATCCTGAGCTGGCTTAT  
TGTGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAACTAAACTTCAAAGAGATTTTCTAGAAATAGAC  
AAACAGTGCAAAATTTGATTTTCTTGCCATCTATGATGGCCCCTCCACCAACTCTGGCCTGATTGGACAAGTCTGT  
GGCCGTGTGACTCCACCTTCGAATCGTCATCAAACTCTCTGACTGTCTGTTGTCTACAGATTATGCCAATTTCT  
TACCGGGGATTTCTGCTTCTTACACCTCAATTTATGCAGAAAACATCAACACTACATCTTTAACTTGCTCTTCT  
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGCTTTTAACTCTAATGGGAATAACTTGCAACTAAAA  
GACCCAACTTGACAGACAAAATTATCAAATGTTGTGGAATTTTCTGTCCCTCTTAATGGATGTGGTACAATCAGA  
AAGGTAGAAGATCAGTCAATTACTTACACCAATATAATCACCTTTTCTGCATCCTCAACTTCTGAAGTGATCACC  
CGTCAGAAACAACTCCAGATTATTGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATACATAACA  
GAAGATGATGTAATACAAAGTCAAAATGCACTGGGCAAATATAACACCAGCATGGCTCTTTTGAATCCAATTCA  
TTTGAAAAGACTATACTTGAATCACCATATTATGTGGATTGAAACCAAACTCTTTTGTTCAGTTAGTCTGCAC  
ACCTCAGATCCAAATTTGGTGGTGTCTTGTGATACTGTAGAGCCTCTCCACCTCTGACTTGTGATCTCCAACC  
TACGACCTAATCAAGAGTGGATGTAGTGCAGATGAACTTGTAAAGGTGTATCCCTTATTTGGACACTATGGGAGA  
TTCCAGTTTAAATGCCTTTAAATTTCTTGAGAAGTATGAGCTCTGTGTATCTGCAGTGTAAGTTTGTATATGTGAT  
AGCAGTGACCACAGTCTCGCTGCAATCAAGGTTGTGTCTCCAGAAGCAAACGAGACATTTCTCATATAAATGG  
AAAACAGATTCATCATAGGACCCATTCTGTGAAAAGGGATCGAAGTGCAAGTGGCAATTCAGGATTTTCAGCAT  
GAAACACATGCGGAAGAACTCCAAACCAGCCTTTCAACAGTGTGCATCTGTTTCTTTCATGTTTCTAGCTCTG  
AATGTGGTGAATGTAGCGCAATCAGAGTGAAGCATTTTGTAAATCAACGGGCAGACTACAAATACCAGAAGCTG  
CAGAATATTAACTAACAGGTCCAACCCTAAGTGAGACATGTTTCTCCAGGATGCCAAAGGAAATGCTACCTCGT  
GGCTACACATATTATGAATAAATGAGGAAGGCCCTGAAAGTGACACACAGGCCTGCATGTAAAAAAA

**FIGURE 344**

MELVRRMLPLTLLILSCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTIE  
RPENKSIRIIFSIVQLDPDGSCSENIKVFDGTSSNGPLLQGVCSKNDYVPVFESSSTLTFQ  
IVTDSARIQRTVFVFFYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQVEKD  
YKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCGRVTPTFESSNSLTVVLSTDYA  
NSYRGFSASYTSIYAENINTTSLTCSSDRMRVIIISKSYLEAFNSNGNNLQLKDPTCRPKLSNV  
VEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQQLQIIVKCEMGHNSTVEIIYI  
TEDDVIQSQNALGKYNTSMALFESNSFEKTIKESPPYYVDLNQTLFVQVSLHTSDPNLVVFLDT  
CRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYLQCKVLICD  
SSDHQSRCNQGCVSRSKRDISSYKWKTDIIIGPIRLKRDRSASGNSGFQHETHAEETPNQPFN  
SVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

**Important features:**

**Signal sequence:**

amino acids 1-24

**Transmembrane domain:**

amino acids 571-586

**N-glycosylation site.**

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,  
394-398, 419-423

**Casein kinase II phosphorylation site.**

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,  
408-412, 463-467, 520-524, 556-560

**Tyrosine kinase phosphorylation site.**

amino acids 172-180, 407-415, 407-416, 519-528

**N-myristoylation site.**

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

# FIGURE 345

TGGGGGCCCCCAGGCTCGCGCTGGAGCGAAGCAGCATGGGCAGTCGGTGCGCGCTGGCCCTGGCGGTGCTCTC  
GGCCTTGCTGTGTAGGCTCTGGAGCTCTGGGGTGTTCGAACTGAAGCTGCAGGAGTTCGTCAACAAGAGGGGCT  
GCTGGGGAACCGCAATTGCTGCCGCGGGGGCGCGGGGCCACCGCGTGCCTGCCGGACCTTCTTCGCGGTGTG  
CCTCAAGCACTACCAGGCCAGCGTGTCCCCGAGCCGCCCTGCACCTACGGCAGCGCCGTACCCCCGTGCTGGG  
CGTCGACTCCTTCAGTCTGCCCGACGGCGGGGGCGCCGACTCCGCGTTTCAGCAACCCCATCCGCTTCCCCCTCGG  
CTTCACCTGGCCGGGCACCTTCTCTCTGATTATTGAAGCTCTCCACACAGATTCTCCTGATGACCTCGCAACAGA  
AAACCCAGAAAGACTCATCAGCCGCTGGCCACCCAGAGGCACCTGACGGTGGGGCAGGAGTGGTCCCAGGACCT  
GCACAGCAGCGCCGCGACGGACCTCAAGTACTCTTACCGCTTCGTGTGTGACGAACACTACTACGGAGAGGGCTG  
CTCCGTTTTCGCGCTCCCCGGGACGATGCCTTCGGCCACTTCACCTGTGGGGAGCGTGGGGAGAAAGTGTGCAA  
CCCTGGCTGGAAGGGCCCTACTGCACAGAGCCGATCTGCCTGCCTGGATGTGATGAGCAGCATGGATTTTGTGA  
CAAACAGGGGAATGCAAGTGCAGAGTGGGCTGGCAGGGCCGGTACTGTGACGAGTGTATCCGCTATCCAGGCTG  
TCTCCATGGCACCTGCCAGCAGCCCTGGCAGTGCAACTGCCAGGAAGGCTGGGGGGCCCTTTCTGCAACCAAGGA  
CCTGAACTACTGCACACACCATAAGCCCTGCAAGAATGGAGCCACCTGCACCAACACGGGCCAGGGGAGCTACAC  
TTGCTCTTGCCGGCCTGGGTACACAGGTGCCACCTGCGAGCTGGGGATTGACGAGTGTGACCCAGCCCTTGTA  
GAACGGAGGGAGCTGCACGGATCTCGAGAACAGTACTCCTGTACCTGCCACCCCGCTTCTACGGCAAAATCTG  
TGAATTGAGTGCCATGACCTGTGCGGACGGCCCTTGCTTTAACGGGGGTCCGCTGTGACAGACGCCCGATGGAGG  
GTACAGCTGCCGCTGCCCGTGGGCTACTCCGGCTTCAACTGTGAGAAGAAAATTGACTACTGCAGCTCTTCACC  
CTGTTCTTAATGTTGCCAAGTGTGTGGACCTCGGTGATGCCCTACCTGTGCCGCTGCCAGGCCGGCTTCTCGGGGAG  
GCACTGTGACGACAACGTGGACGACTGCGCCTCCTCCCCGTGCCCAACGGGGGCACCTGCCGGGATGGCTGAA  
CGACTTCTCCTGCACCTGCCCGCCTGGCTACACGGGCAGGAACCTGCAGTGCCCCGTGACGAGGTGCGAGCACGC  
ACCTTGCACCAATGGGGCCACCTGCCACGAGAGGGGCCACCGCTATGTGTGCGAGTGTGCCGAGGCTACGGGGG  
TCCCAACTGCCAGTTCTCTGCTCCCCGAGCTGCCCGGGGCCAGCGGTGGTGGACCTCACTGAGAAGCTAGAGGG  
CCAGGGCGGGCCATTCCCTGGGTGGCCGTGTGCGCCGGGGTCACTCTTGTCTCATGCTGTCTGGGCTGTGC  
CGCTGTGGTGGTCTGCGTCCGGCTGAGGCTGCAGAAGCACCGGCCCCAGCCGACCCCTGCCGGGGGAGACGGA  
GACCATGAACAACCTGGCCAACCTGCCAGCGTGCAGAAGGACATCTCAGTCAGCATCATCGGGGCCACGCAGATCAA  
GAACACCAACAAGAAGGCGGACTTCCACGGGGACCACAGCGCCGACAAGAATGGCTTCAAGGCCCGCTACCCAGC  
GGTGGACTATAACCTCGTGAGGACCTCAAGGGTGACGACACCGCCGTGAGGGACGCGCACAGCAAGCGTGACAC  
CAAGTGCCAGCCCCAGGCTCCTCAGGGGAGGAGAAGGGGACCCCGACCACACTCAGGGGTGGAGAAGCATCTGA  
AAGAAAAAGGCCGACTCGGGCTGTTCAACTTCAAAAGACACCAAGTACAGTCGGTGTACGTATATCCGAGGA  
GAAGGATGAGTGCCTCATAGCAACTGAGGTGTTAAAAATGGAAGTGAGATGGCAAGACTCCGTTTCTCTTAAATA  
AGTAAATTCCAAGGATATATGCCCCAACGAATGCTGCTGAAGAGGAGGGAGGCCCTCGTGGACTGCTGCTGAGAA  
ACCGAGTTCAGACCGAGCAGGTCTCTCCTGAGGTCTCGACGCCTGCCGACAGCCTGTGCGCGCCCGCGCGCC  
TGCGGCACTGCCCTTCCGTGACGTGCGCGTTGCACTATGGACAGTTGCTCTTAAGAGAATATATATTTAAATGGGT  
GAACTGAATTACGCATAAGAAGCATGCACTGCCTGAGTGTATATTTGGATTCTTATGAGCCAGTCTTTTCTTGA  
ATTAGAAACACAACACTGCCTTTATTGTCTTTTGTATACGAAGATGTGCTTTTTCTAGATGGAAAAGATGTGT  
GTTATTTTTTGGATTGTAAAAATATTTTTCATGATATCTGTAAAGCTTGAGTATTTTTGTATATAAATGTAT  
TAATTTAAATTTGGTAAATATGTACAAAGGCACCTTCGGGTCTATGTGACTATATTTTTTGTATATAAATGTAT  
TTATGGAATATTTGTCAAATGTTATTTGAGTTTTTACTGTTTTGTTAATGAAGAAATTCCTTTTTTAAATATTT  
TTCCAAAATAAATTTTATGAATGACAAAAA  
AAAAAA

### **FIGURE 346**

MGSRCALALAVLSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGAGPPPCACRTFFFRVC  
LKHYQASVSPEPPCTYGS AVTPVLGVDSFSLPDGGGADSAFSNPIRFPFGFTWPGTFSLIIEA  
LHTDSPDDLATENPERLISR LATQRHLTVGEEWSQDLHSSGRTDLKYSYRFVCD EHYH YEGGCS  
VF CRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFC DKPGECKCRVGVWQGR  
YCD ECI RYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPKNGATCTNTGQGSYTCS  
CRPGYTGATCELGIDECDPSPCKNGGSCTDLENSYSCTCPPGFYGKICELSAMTCADGPCFNG  
GRCS DSPDGGYSCRCPVGYSGFNC EKKIDYCSSSPCSNGAKCVDLGDAYLCRCQAGFSGRHCD  
DNVDDCASSPCANGGTCRDGVNDFSC TCPPGYTGRNCSAPVSRCEHAPCHNGATCHERGHRYV  
CECARGYGGPNCQFLLPELPPGPAVVDL TEKLEGQGGPFPWVAVCAGVILVLM LLLGCAAVV  
CVRLRLQKHRPPADPCRGETETMNNLANCQREKDISVSIIGATQIKNTNKKADFHGDHSADKN  
GFKARYPAVDYNLVQDLKGDDTAVRDAHSKRDTKCQPQGSSGEEKGTPTTLRGGEASERKRPD  
SGCSTSKDTKYQSVYVISEEKDECVIATEV

**Important features:**

**Signal sequence:**

Amino acids 1-21

**Transmembrane domain:**

Amino acids 546-566

**N-glycosylation site:**

Amino acids 477-481

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 660-664

**Tyrosine kinase phosphorylation sites:**

Amino acids 176-185;252-261

**N-myristoylation sites:**

Amino acids 2-8;37-43;40-46;98-104;99-105;262-268;281-287;  
282-288;301-307;310-316;328-334;340-344;378-384;387-393;512-518;  
676-682;683-689;695-701

**Aspartic acid and asparagine hydroxylation sites:**

Amino acids 343-355;420-432;458-470

**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 552-563

**EGF-like domain cysteine pattern signature:**

Amino acids 243-255;274-286;314-326;352-364;391-403;429-441;  
467-479;505-517



**FIGURE 347**

CCCACGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTTCGGTCAACA  
TCGTAGTCCACCCCCTCCCCATCCCCAGCCCCGGGGATTTCAGGCTCGCCAGCGCCAGCCAG  
GGAGCCGGCCGGGAAGCGCGATGGGGGCCCCAGCCGCCTCGCTCCTGCTCCTGCTCCTGCTGT  
TCGCCTGCTGCTGGGCGCCCGGCGGGGCCAACCTCTCCAGGACGACAGCCAGCCCTGGACAT  
CTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGCTCAAGTGCCAAGTGAAAGATCACGAGG  
ACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGAGAGCCC  
TTCGAGATAATCGAATTTCAGCTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGCATCAGCA  
ATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCTGTGCGAACTG  
CCAAGTCCCTCGTCACTGTGCTAGGAATTCACAGAAGCCCATCATCACTGGTTATAAATCTT  
CATTACGGGAAAAAGACACAGCCACCCCTAAACTGTTCAGTCTTCTGGGAGCAAGCCTGCAGCCC  
GGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCATACAGGAAGATC  
CCAATGGTAAACCTTCACTGTTCAGCAGCTCGGTGACATTCCAGGTTACCCGGGAGGATGATG  
GGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGACAGATCCACCTCTC  
AACGCATTGAAGTTTTATACACACCAACTGCGATGATTAGGCCAGACCCTCCCCATCCTCGTG  
AGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCCCCCAGCAGTACCTAT  
GGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGTGCCCTGATCTTCCCTT  
TCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAGCAACATGGGCAGCTACA  
AGGCCTACTACACCCTCAATGTTAATGACCCAGTCCGGTGCCCTCCTCCTCCAGCACCTACC  
ACGCCATCATCGGTGGGATCGTGGCTTTCATTGTCTTCTGCTGCTCATCATGCTCATCTTCC  
TTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACATGAGGCAAAAGGCTCCGACG  
ATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCGGGCAGTCAGGAGGGGACGACA  
AGAAGGAATATTTTCATCTAGAGGCGCTGCCCACTTCTGCGCCCCCAGGGGCCCTGTGGGG  
ACTGCTGGGGCCGTACCAACCCGACTTGTACAGAGCAACCGCAGGGCCGCCCTCCCGCTT  
GCTCCCCAGCCCAACCCCTGTACAGAATGTCTGCTTTGGGTGCGGTTTTGTACTCGGT  
TTGGAATGGGGAGGGAGGAGGGCGGGGGAGGGGAGGGTTGCCCTCAGCCCTTCCGTGGCTT  
CTCTGCATTTGGGTTATTATTATTTTGTAAACAATCCCAAATCAAATCTGTCTCCAGGCTGGA  
GAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAACAAACAAAAACA

**FIGURE 348**

MGAPAASLLLLLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQWS  
NPAQQTLYFGEKRALRDNRIQLVTSTPHELSSISISNVALADEGEYTC SIFTMPVRTAKSLVTV  
LGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFT  
VSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQKLLL  
HCEGRGNPVPQQYLWEKEGSPPLKMTQESALIFPFLNKSDSGTYGCTATSNMG SYKAYYTLN  
VNDPSPVPSSSSSTYHAIIGGIVAFIVFLLLLIMLIFLGHYLIRHKGTYLTHEAKGSDDAPDADT  
AIINAEGGQSGGDDKKEYFI

**Important features:**

**Signal sequence:**

amino acids 1-20

**Transmembrane domain:**

amino acids 331-352

**N-glycosylation site.**

amino acids 25-29, 290-294

**Casein kinase II phosphorylation site.**

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

**N-myristoylation site.**

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,  
306-310, 334-340, 360-364, 385-389, 386-390

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

# **FIGURE 349**

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAGGACAGCAGCAAAG  
 AGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTACCATACGCCCTCAGGACGTTCCCTCTA  
 GCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGTCATTTTGATTTTGCTGTTTATTTTTTTTTTCTTTTCTT  
 TTTCACCACCATTTGTATTTTATTTCCGTACTTTCAGAAATGGGGCTACAGACCACAAAGTGGCCAGCCATGGGG  
 CTTTTTTCCTGAAGTCTTGGCTTATCATTTCCCTGGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCTGCCCTA  
 GTGTGTGCCGCTGCGACAGGAACCTTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTGCCTCTTGGGATCCCGG  
 AGGGCGTAACCGTACTCTACCTCCACAACAACCAAAATTAATAATGCTGGATTTCCTGCAGAACTGCACAATGTAC  
 AGTCGGTGCACACGGTCTACCTGTATGGCAACCAACTGGACGAATCCCCATGAACCTTCCCAAGAAATGTCAGAG  
 TTCTCCATTGTCAGGAAAACAATATTCAGACCATTTCACGGGCTGCTCTTGCCAGCTCTTGAAGCTTGAAGAGC  
 TGCACCTGGATGACAACCTCCATATCCACAGTGGGGGTGGAAGACGGGGCCTTCGGGAGGCTATTAGCCTCAAAT  
 TGTGTGTTTTGTCTAAGAAATCACCTGAGCAGTGTGCTGTTGGGCTTCTGTGGACTTGCAAGAGCTGAGAGTGG  
 ATGAAAAATCGAATTGCTGTCTATCCGACATGGCCTTCCAGAATCTCACAGAGCTTGGAGCGCTTATTGTGGACG  
 GGAACCTCCTGACCAACAAGGGTATCGCCGAGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTTCAATTG  
 TACGTAATTCGCTGTCCACCTCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTTGCAGGACAACC  
 AGATAAACACCATTCCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCAACAACCAAC  
 TGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACCTGAAGCAGCTCACTGCTCGGAATAACCTTGGT  
 TTTGTGACTGCAGTATTAAATGGGTACAGAAATGGCTCAAATATATCCCTTCATCTCTCAACGTGCGGGGTTTCA  
 TGTGCCAAGGTCCTGAACAAGTCCGGGGGATGGCCGTGAGGAATTAATATGAATCTTTTGTCTGTCCCACCA  
 CGACCCCGGCTGCTCTCTTCAACCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCACCCCTCTCTA  
 TTCCAAACCTTAGCAGAAGCTACACGCCTCCAACTCCTACCACATCGAAACTTCCCACGATTCCTGACTGGGATG  
 GCAGAGAAAGAGTGACCCACCTATTTCTGAACGGATCCAGCTCTCTATCCATTTTGTGAATGATACTTCCATTCT  
 AAGTCAGCTGGCTCTCTCTTTCACCGTGATGGCATACAAACCTCACATGGGTGAAAATGGGCCACAGTTTAGTAG  
 GGGGCATCGTTCAGGAGCGCATAGTCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCA  
 CCTATCGGATTTGTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTTGTTTCAAGGCCA  
 CCACCCATGCTCTCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGACGTCCACAGCATGG  
 GCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTTGTGCTGGTGGTCTTGCTCAGCGTCTTTT  
 GCTGGCATATGCACAAAAAGGGGCGTACACCTCCAGAAAGTGGAAATACAACCGGGGCGGCGGAAAGATGATT  
 ATTGCGAGGCAGGCACCAAGAAGGACAACCTCCATCCTGGAGATGACAGAAACAGTTTTTCAGATCGTCTCCTTAA  
 ATAACGATCAACTCCTTAAAGGAGATTTCAGACTGCAGCCCATTTACACCCCAAATGGGGGATTAATTACACAG  
 ACTGCCATATCCCCAACACATGCGTACTGCAACAGCAGCGTGCCAGACCTGGAGCACTGCCATACGTCAGCAGC  
 CAGAGGCCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAACACACTCGTGTGTGCACATAAAGACACGCAG  
 ATTACATTTGATAAATGTTACACAGATGCATTTGTGCATTTGAATACTCTGTAATTTATACGGGTGACTATATAA  
 TGGGATTTAAAAAAGTGCTATCTTTTCTATTTCAAGTTAATTACAAACAGTTTTGTAACTCTTGTCTTTTAAAT  
 TCTT

## **FIGURE 350**

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIPE  
GVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTISR  
AALAQLLKLEELHLDNSISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELRVDE  
NRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLT KLKEFSIVRNSLSHPPPDLPGT  
HLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNNPWFCD  
CSIKWVTEWLKYIPSSLNVRGFMCGQPEQVRGMAVRELNMNLLSCPTTTPGLPLFTPAPSTAS  
PTTQPPTLSIPNPSRSYTPPTPTTSKLPTIPDWDGRERVTTPISERIQLSIHFVNDTSIQVSW  
LSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPLDAFNRYRAV  
EDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVLLSVFCWHMH  
KKGRYTSQKWKYNRGRRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKGD FRLQPIYTP  
NGGINYTDCHIPNNMRYCNSSVPDLEHCHT

**Important features:**

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 542-561

**N-glycosylation site.**

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

**Casein kinase II phosphorylation site.**

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

**Tyrosine kinase phosphorylation site.**

amino acids 319-328

**N-myristoylation site.**

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,  
522-528, 545-551, 633-639

**Amidation site.**

amino acids 581-585

**Leucine zipper pattern.**

amino acids 164-186

**Phospholipase A2 aspartic acid active site.**

amino acids 39-50

**FIGURE 351**

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTTCGGTTTCCCTCCTGCTGTTTGGGGGCA  
 TGAAGAGGCTTCGCCGCCGGGAGTAAAGAAGGAATTGACCGGGCAGCGCGAGGGAGGAGCGCGCACGCGACCGC  
 GAGGCGGGCGTGCACCTTCGGCTGGAAGTTTGTGCCGGGCCCCGAGCGCGCGCGGCTGGGAGCTTCGGGTAGA  
 GACCTAGGCGCGCTGGACCGCGATGAGCGCGCCGAGCCTCCGTGCGCGCGCGCGGGGTTGGGGCTGCTGCTGTGC  
 GCGGTGCTGGGGCGCGCTGGCCGGTCCGACAGCGCGCGCTCGCGGGGAACCGGGGAGCCCTCTGGGGTAGCCGCC  
 GAGCGCCCATGCCCCACTACCTGCCGCTGCCCTCGGGACCTGCTGGACTGCAGTCGTAAGCGGCTAGCGCGTCTT  
 CCCGAGCCACTCCCCTCCTGGGTGCTCGGCTGGACTTAAGTCACAACAGATTATCTTTTCATCAAGGCAAGTTCC  
 ATGAGCCACCTTCAAAGCCTTCGAGAAGTGAACCTGAACAACAAATGAATTGGAGACCATTCCAAATCTGGGACCA  
 GTCTCGGCAAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGAACATCTGAAAGAG  
 TTTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTTCAGAGCTCCAACTGCATTTCCAGCCCTACAG  
 CTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACA  
 CTCCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCACCCAAAGTGTGTTAAACCTGCCCACTGCAA  
 CATCTCGAATTTGAACCGAAACAAGATTAAAAATGTAGATGGACTGCATTCCAAGGCCCTTGGTGCTCTGAAGTCT  
 CTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTTTGGGGGCTGAGCAACATGGAATTTTG  
 CAGCTGGACCATAACACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTTGCTGATGCTGCAGGAACCTTCAT  
 CTGAGCAAAATCGGATCCATCAACAGGATCAGCCCTGATGCCCTGGGAGTTCTGCCAGAACTCAGTGAGCTGACCTA  
 ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCTTGGCTAAGCTTACTAAATACACTGCACATTGGG  
 AACACAGAGTCAGCTACATTTGCTGATTGTGCTTCCGGGGGCTTTCAGTTTAAAGACTTTGGATCTGAAGAAC  
 AATGAAATTTCTGGACTATTGAAGACATGAATGGTGCTTTCTCTGGGCTTGACAACTGAGGCGACTGATATCT  
 CAAGGAAATCGGATCCGTTCTATTACTAAAAAAGCCTTCACTGGTTTGGATGCCATCTAGACCTGAGT  
 GACAACGCAATCATGTCTTTACAAGGCAATGCATTTTTCACAAATGAAGAACTGCAACAATTCATTTAAATACA  
 TCAAGCCTTTTGTGCGATTGCCAGCTAAATGGCTCCACAGTGGGTGGCGGAAACAACTTTCAGAGCTTTGT  
 AATGCCAGTTGTGCCCATCTCAGCTGCTAAAGGAAGAAGCATTTTGTCTGTAGCCAGATGGCTTTGTGTGT  
 GATGATTTTCCCAAAACCCAGATCAGGTTCCAGCCAGAAACACAGTCGGCAATAAAGGTTCCAATTTGAGTTTC  
 ATCTGCTCAGCTGCCAGCAGCAGTGATTTCCCAATGACTTTTGTCTGGAAAAAGACAATGAACACTGTCATGAT  
 GCTGAAATGGAATTTATGCACACCTCCGGGCCCAAGGTGGCGAGGTGATGGAGTATACCACTCCTTCCGGCTG  
 CGCGAGGTGGAATTTGCCAGTGAGGGGAAATATCAGTGTGTCTCTCAATCACTTTGGTTCTATCTGACTCTGT  
 AAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTCACCAAGACCCCATGGATCTCACCATCCGAGCTGGGGCC  
 ATGGCACGCTTGGAGTGTGCTGCTGTGGGGCAGCCCGCCAGATAGCTGGCAGAAGGATGGGGGCACAGAC  
 TTCCAGCTGCACGGGAGAGACGCATGTCATGTCAGGAGATGACGTGTTCTTTATCGTGGATGTGAAGATA  
 GAGGACATTTGGGTATACAGCTGCACAGCTCAGAACAGTGCAAGAGTATTTTCAGCAAAATGCAACTCTGACTGTC  
 CTAGAAACACCATCATTTTTCGGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAAACAGCCGCTCTACAGTGC  
 ATTGCTGGAGGAAGCCTCCCCCTAAACTGAACTGGACCAAGATGATAGCCCATTTGGTGTAAACCGAGAGGCAC  
 TTTTTCGACGAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTCAGTGATGCTGGGAAATACACATGTGAG  
 ATGCTAACACCCCTTGGCACTGAGAGAGGAAACGTCGCCCTCAGTGATGATCCCACTCCAACCTGCGACTCCCCT  
 CAGATGACAGCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCGTGATCATAGCCGTGGTTTGTCTGT  
 GTGTGGGACGTCATCTCGTGTGGGTGTCATCATATACCACACAAGGCGGAGGAATGAAGATTGCAGCATTACC  
 AACACAGATGAGACCAACTTGGCCAGCAGATATTCCTAGTTATTTGTCTCATCTCAGGGAACGTTAGCTGACAGGCAG  
 GATGGGTACGTGTCTTCAGAAAGTGGAAGCCACCACAGTTTGTACATCTTCAGGTGCTGGATTTTTCTTACCA  
 CAACATGACAGTAGTGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTTC  
 CTTTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTGAAGGGAAATGTGTATGGCTCAGATCCTTTTGAAACA  
 TATCATACAGGTTGCAGTCTTGACCAAGAACAGTTTAAATGGACCCTATGAGCCAGTTACATAAAGAAAAAG  
 GAGTGCTACCCATGTTCTCATCTTCAGAAAGATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACAT  
 GTGAGGAAGCTACTTAACACTAGTTACTCTCACAATGAAGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCC  
 TCTTTAGATTTTAGTGCAATCCAGAGCCAGCGTCGGTTGCCCTCGAGTAATTTCTTTTCATGGGTACCTTTGGAAAA  
 GCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAGCCATCAGATTGTGAGCCAAGAGCCTTTTAT  
 TTGAAAGCTCATTCTTCCCGAGACTTGGACTCTGGGTGAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAA  
 GAAATCACATTTGTACCTTTAAACAGACTTTAGAAAACTACAGGACTCCAAATTTTCAGTCTTATGACTTGGAC  
 ACATAGACTGAATGAGACCAAGGAAAGCTTAACATACTACCTCAAGTGAACCTTTTATTTAAAGAGAGAGAAT  
 CTTATGTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAGATGCTTTATTTATACAGATGAACCAAAATTAC  
 AAAAGTTTATGAAATTTTTTACTGGGAATGATGCTCATATAAGAATACCTTTTTTAACTATTTTTTAACTTTG  
 TTTTATGCAAAAAGTATCTTACGTAAATTAATGATATAAATCATGATATTTTTATGATTTTTTATAATGCCAGA  
 TTTCTTTTTATGGAAATGAGTTACTAAAGCATTTTAAATAATACCTGCTTGTACCATTTTTTAAATAGAAGTT  
 ACTTCATTATATTTTGCACATTATATTTAATAAATGTGTCAATTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## FIGURE 352

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAERPCPTTCRCLGDLDCSRKRLARLPEPLPSW  
VARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANITLLSLAGNRIVEILPEHLKEFQSLCTL  
DLSSNNISELQTAFAPALQLKYLYLNSNRVTSMEPGYFDNLANTLLVLKLNRRNRI SAIPPKMFKL PQHQHLELNRRN  
KIKNVDGLTFQGLGALKSLKMQRNGVT KLMDGAFWGLSNMEILQLDHNLTETITKGWLYGLLMLQELHLSQNAIN  
RISPDWEFCQKLSLEDLTFNHL SRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSSLKTLDLKNNIEISWTI  
EDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMKKLQQLHLNTSSLLCDC  
QLKWLPQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCDDFPKPQITVQPETQSAIKGSNLSFICSAASS  
SDSPMTFAWKDNEELLHDAEMENYAHLEAQQGGEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVN  
MLPSFTKTPMDLTIRAGAMARLECAAVGHPAPQIAWQKDGTDFFAARERRMHVMPEDDVFFIVDVKIEDIGVYS  
CTAQNSAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKLNWTKDDSPLVVTERHFFAAGNQ  
LLIIVDSVDSDAGKYTCESNTLGTTERGNVRLSVIPTPTCDSPQMTAPSLDDDGWATVGVVIIAVVCCVVGTSLV  
WVVIYHTRRRNEDCSITNTDETNLPA DIPSYLSSQGT LADRQDGYVSSSESGSHHQFVTSSGAGFFLPQHDSSGT  
CHIDNSSEADVEAATDLFLCPFLGSTGPMYLGKNGVYSGDPFFETYHTGCSPPDRTVLMHDHYEPSYIKKKECYPCSH  
PSEESCERSFSNISWPSHVRKLLNTSYSHNEGPGMKNLCLNKSSLD FSANPEPASVASSNSFMGTFGKALRRPHL  
DAYSSFGQPSDCQPRAFY LKAHSSPDLDGSEEDGKERTDFQENHICTFKQTLNRYRTPNFQSYDLDT

**Important features:**

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 808-828

**N-glycosylation site.**

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,  
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

**Glycosaminoglycan attachment site.**

amino acids 886-890

**Casein kinase II phosphorylation site.**

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,  
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,  
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,  
1073-1077, 1079-1083, 1081-1085

**Tyrosine kinase phosphorylation site.**

amino acids 667-675

**N-myristoylation site.**

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,  
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

**Leucine zipper pattern.**

amino acids 58-80, 65-87

# **FIGURE 353**

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTTTCTTCTCCTTTCTGGCTTCGGACATTGG  
AGCACTAAATGAACCTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTGTTACTTTGTGATGAGATCGGGGATGA  
ATTGCTCGCTTTAAAAATGCTGCTTTGGATTCTGTTGCTGGAGACGTCTCTTTGTTTTGCCGCTGGAAACGTTAC  
AGGGGACGTTTGCAGAGAGAAGATCTGTTCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAA  
GGGCTTCACAAGTCTGCAGCGTTTCACTGCCCCGACTTCCAGTTTTACCATTTATTTCTGCATGGCAATTCCTT  
CACTCGACTTTTCCCTAATGAGTTTCGCTAACTTTTATAATGCGGTTAGTTTGCACATGGAAAACAATGGCTTGCA  
TGAAATCGTTCGGGGGCTTTTCTGGGGCTGCAGCTGGTGAAAAGGCTGCACATCAACAACAACAGATCAAGTC  
TTTTCGAAAGCAGACTTTTCTGGGGCTGGACGATCTGGAATATCTCCAGGCTGATTTTAATTTATTACGAGATAT  
AGACCCGGGGGCTTCCAGGACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCCCTACC  
TGCCAACGTGTTCCAGTATGTGCCATCACCCACCTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCCCTATGA  
GGAGGTCTTGGAGCAAATCCCTGGTATTGCGGAGATCTGCTAGAGGATAACCCCTTGGGACTGCACCTGTGATCT  
GCTCTCCCTGAAAGAATGGCTGGAACAATTTCCCAAGAATGCCCTGATCGGCCGAGTGGTCTGCGAAGCCCCAC  
CAGACTGCAGGGTAAAGACCTCAATGAAACCACCGAACAGGACTTGTGTCTTTGAAAAACCGAGTGGATTCTAG  
TCTCCCGCGCCCCCTGCCCAAGAAGAGACCTTTGCTCTGGACCCCTGCCAACTCTTTCAAGACAAATGGGCA  
AGAGGATCATGCCACACCAGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGATCAAAATCAG  
ACCCACAGCAGCGATAGCGACGGGTAGCTCCAGGAACAAACCCCTTAGCTAACAGTTTACCCTGCCCTGGGGCTG  
CAGCTGCGACCACATCCCAGGGTCGGGTTTAAAGATGAACTGCAACAACAGGAACGTGAGCAGCTTGGCTGATTT  
GAAGCCCAAGCTCTCTAACGTGACGAGCTTTTCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTT  
TGTGGATTACAAGAACCTCATCTGTTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACAACTTTCAA  
GAACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCGGAGAAATTCGCGGG  
GCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCATCTCCCGGCACCTTTCAATGCCAT  
GCCCAAACTGAGGATCCTCATTTCTCAACAACAACCTGCTGAGGTCCCTGCCTGTGGACGTGTTTCGCTGGGGTCTC  
GCTCTCTAAACTCAGCTGCACAACAATTACTTTCATGTACCTCCCGGTGGCAGGGGTGCTGGACCAGTTAACCTC  
CATCATCCAGATAGACCTCCACGGAACCCCTGGGAGTGCTCCTGCACAATTGTGCCTTTCAAGCAGTGGGCAGA  
ACGCTTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAATTTCTTTAGAAAGGATTTTAT  
GCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCTCGCCACGTTAACTTCGCACAGTAAAAA  
CAGCACTGGGTTGGCGGAGACCGGGACGCACTCCAACCTCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTT  
GGTCCCGGACTGCTGCTGGTGTGTTGTACCTCCGCCCTTACCGTGGTGGGCATGCTCGTGTATTATCCTGAGGAA  
CCGAAAGCGGTCCAAGAGACGAGATGCCAACTCCTCCGCGTCCGAGATTAATTTCCCTACAGACAGTCTGTGACTC  
TTCCTACTGGCACAATGGGCCTTACAACGCAGATGGGGCCACAGAGTGTATGACTGTGGCTCTCACTCGTCTC  
AGACTAAGACCCCCAACCCCAATAGGGGAGGGCAGAGGGAAGGCGATACATCCTTCCCCACCGCAGGCACCCCGG  
GGCTGGAGGGGCGTGTACCCAAATCCCCGCGCCATCAGCCTGGATGGGCATAAGTAGATAAATAACTGTGAGCTC  
GCACAACCGAAAGGCCTGACCCCTTACTTAGCTCCCTCCTTGAAACAAAGAGCAGACTGTGGAGAGCTGGGAGA  
GCGCAGCCAGCTCGCTCTTTGCTGAGAGCCCTTTTGACAGAAAGCCAGCACGACCTGCTGGAAGAACTGACA  
GTGCCCTCGCCCTCGGCCCGGGGCTGTGGGGTTGGATGCCGCGGTTCTATACATATATACATATATCCACATC  
TATATAGAGAGATAGATATCTATTTTTCCCTGTGGATTAGCCCCGTGATGGCTCCCTGTTGGCTACGCAGGGAT  
GGGCAGTTGCACGAAGGCATGAATGTATTGTAAATAAGTAACTTTGACTTCTGAC

## **FIGURE 354**

MLLWILLLETSLCFAAGNVTGDVCKEIKCSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYHL  
FLHGNSLTRLPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNKKIKSFRKQTF  
LGLDDLEYLQADFNLLRDIDPGAQDLNKLLEVLILNDNLISTLPANVFQYVPITHLDLRGNRL  
KTLPEYEEVLEQIPGIAEILLEDNPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQKDL  
NETTEQDLCPKLRVDSSLPAPPAQEETFAPGPLPTPFKTNGQEDHATPGSAPNGGTKIPGNW  
QIKIRPTAAIATGSSRNKPLANSRPCPGGCSCDHIPGSGLKMNCCNNRVSSSLADLKPCLSNVQ  
ELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLLDLRWLYMDSNYLDTLRSR  
KFAGLQNLEYLNVEYNAIQLILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSLSKLSLHNN  
YFMYLPVAGVLDQLTSIIQIDLHGNPWECSTIVPFKQWAERLGSEVLMSDLKCETPVNFFRK  
DFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVLVPGLLLVFVT  
SAFTVVGMLVFILRNKRKSKRRDANSSASEINSLQTVCDSSYWHNGPYNADGAHRVYDCGSHS  
LSD

**Important features:**

**Signal sequence:**  
amino acids 1-15

**Transmembrane domain:**  
amino acids 618-638

**N-glycosylation site.**  
amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**  
amino acids 122-126, 646-650

**Casein kinase II phosphorylation site.**  
amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,  
608-612, 657-661, 666-670, 693-697

**N-myristoylation site.**  
amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,  
354-360, 465-471, 493-499, 598-604, 603-609

**Prokaryotic membrane lipoprotein lipid attachment site.**  
amino acids 337-348



# **FIGURE 355**

AGTCGACTGCGTCCCCTGTACCCGGCGCCAGCTGTGTTCCCTGACCCCAGAATAACTCAGGGCTGCACCGGGCCTG  
GCAGCGCTCCGCACACATTTCTGTGCGCGCCTAAGGGAACTGTTGGCCGCTGGGCCCCGGGGGGATTCTTGG  
CAGTTGGGGGGTCCGTGCGGAGCGAGGGCGGAGGGGAAGGGAGGGGGAACCGGGTTGGGGAAGCCAGCTGTAGAG  
GGCGGTGACCGCGCTCCAGACACAGCTCTGCGTCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGC  
GGGGCCTCAGAGAAATGAGGCCGGCGTTCGCCCTGTGCCTCCTCTGGCAGGCGCTCTGGCCCCGGGCCGGCGCGG  
CGAACACCCCACTGCCGACCGTGTGCTGCGCCTCGGGGCGCTGCTACAGCCTGCACCACGCTACCATGAA  
GCGGCAGGCGGCCGAGGAGGCTGCATCCTGCGAGGTGGGGCGCTCAGCACCGTGCCTGCGGGCGCCGAGCTGCG  
CGCTGTGCTCGCGCTCCTGCGGGCAGGCCCCAGGGCCCCGAGAGGGGCTCCAAAGACCTGCTGTTCTGGGTGCGCACT  
GGAGCGCAGGCGTTCCCACTGCACCTGGAGAACGAGCCTTTGCGGGGTTTCTCCTGGCTGTCTCCGACCCCGG  
CGGTCTCGAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGCGGAGATGCGCGGTACT  
CCAGGCCACCGTGGGGTTCGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGCGCGCCAACGGCTACCTGTG  
CAAGTACCAGTTTGTAGGTCTGTGTCTGCGCGCGCCCCGGGGCCGCTCTAACTTGAGCTATCGCGCGCCCTT  
CCAGCTGCACAGCGCCGCTCTGGACTTCAGTCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGGACAGCTCCC  
GATCTCAGTTACTTGCATCGCGGACGAAATCGGCGCTCGCTGGGACAACTCTCGGGCGATGTGTTGTGTCCCTG  
CCCCGGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAACTGCCTAGACGACTTGGGAGGCTTTGCGCTG  
CGAATGTGTACGGGCTTCGAGCTGGGGAAGGACGGCCGCTCTTGTGTGACCAGTGGGGAAGGACAGCCGACCTT  
TGGGGGGACCGGGGTGCCCCACCAGGCGCCCCCGGCCACTGCAACCAGCCCCGTGCCGAGAGAACATGGCCAAAT  
CAGGGTCGACGAGAAGCTGGGAGAGACACCACTTGTCCCTGAACAAGACAATTCAGTAACATCTATTCTGAGAT  
TCCTCGATGGGGATCACAGAGCACGATGTCTACCCCTTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCACTATCAC  
CCCATCAGGGAGCGTGATTTCCAAGTTTAATTTACGACTTCCTCTGCCACTCCTCAGGCTTTGACTCCTCCTC  
TGCCGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTGGTGATCTTGACCATGACAGTACTGGGGCTTGT  
CAAGCTCTGCTTTCACGAAAGCCCCCTCTTCCAGCCAAGGAAGGAGTCTATGGGCCCGCCGGGCCTGGAGAGTGA  
TCCTGAGCCCGTGCTTTGGGCTCCAGTTCTGCACATTGCACAAACAATGGGGTGAAAGTCGGGGACTGTGATCT  
GCGGGACAGAGCAGAGGGTGCTTGTGCGGAGTCCCTCTTGGCTCTAGTGATGCATAGGGAAACAGGGGACA  
TGGGCACTCCTGTGAACAGTTTTTCACTTTTGTGATAACGGGGAAACCAAGAGGAACCTTACTTGTGTAACTGACAA  
TTTCTGCAGAAATCCCCCTTCTCTAAATTCCTTTTACTCCACTGAGGAGCTAAATCAGAACTGCACACTCCTTC  
CCTGATGATAGAGGAAGTGGAAGTGCCTTTAGGATGGTGATACTGGGGACCGGGTAGTGCTGGGGAGAGATATT  
TTCTTATGTTTATTCGAGAATTTGGAGAAGTGATTGAACTTTTCAAGACATTGGAAACAAATAGAACACAATAT  
AATTTACATTAAAAATAATTTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTTTCAAGGCTAGGAGTATATTGG  
TTCGAAATCCCAGGGAAAAAATAAAAAATAAAAAATTAAAGGATTGTTGAT

**FIGURE 356**

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAEEACILRGGALST  
VRAGAE LRAVLALLRAGPGPGGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSSDPGGLESD  
TLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLC PAPRPGAASN  
LSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPGRYLR  
AGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTS GEGQPTLGGTGVPTRRPPATATSPVP  
QRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITPSGSVIS  
KFNSTTSSATPQAFDSSSAVVFI FVSTAVVVLVILMTVLGLVKLCFHESPSSQPRKESMGPP  
GLESDPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

**Important features:**

**Signal sequence:**  
amino acids 1-16

**Transmembrane domain:**  
amino acids 399-418

**N-glycosylation site.**  
amino acids 189-193, 381-385

**Glycosaminoglycan attachment site.**  
amino acids 289-293

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**  
amino acids 98-102, 434-438

**Casein kinase II phosphorylation site.**  
amino acids 275-279, 288-292, 342-346, 445-449

**N-myristoylation site.**  
amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,  
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,  
477-483

**Aspartic acid and asparagine hydroxylation site.**  
amino acids 262-274

**FIGURE 357**

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTCTTCAACCAGACCTCTACATTCATTTTGAAGA  
AGACTAAAAATGGTGTTCCTAATGTGGACACTGAAGAGACAAATTCCTATCCTTTTAAACATAATCCTAATTTCC  
AACTCCTTGGGGCTAGATGGTTTCTAAACCTCTGCCTGTGATGTCACTCTGGATGTTCCAAAGAACCATGTG  
ATCGTGGACTGCACAGACAAGCATTGACAGAAATTCCTGGAGGTATCCACGAACACCACGAACCTCACCTC  
ACCATTAACCACATACCAGACATCTCCCCAGCGTCTTTTACAGACTGGACCATCTGGTAGAGATCGATTTTCA  
TGCAACTGTGTACCTATTCCACTGGGGTCAAAAAACAACATGTGCATCAAGAGGCTGCAGATTAAACCCAGAAGC  
TTTAGTGGACTCACTTATTTAAATCCCTTTACCTGGATGGAACACAGCTACTAGAGATACCGCAGGGCCTCCCG  
CCTAGCTTACAGCTTCTCAGCCTTGAGGCCAACACATCTTTTCCATCAGAAAAGAGAATCTTACAGAACTGGCC  
AACATAGAAAATACTCTACCTGGGCCAAAACCTGTTATTATCGAAATCCTTGTATGTTTCATATTCAATAGAGAAA  
GATGCCTTCTAACTTGACAAAGTTAAAGTGCTCTCCCTGAAAGATAACATGTGCAGCCCTCCCTACTGTT  
TTGCCATCTACTTTAACAGAACTATATCTCTACAACAACATGATTGCAAAAATCCAAGAAGATGATTTTAATAAC  
CTCAACCAATTACAATTTGACCTTAAGTGGAATTCCTCGTGTATATAATGCCATTTCTTCACTGAAAAGCGCG  
TGTAATAATAATTTCTCCCTACAGATCCCTGTAAATGCTTTTGATGCGCTGACAGAAATTAAGTTTACGCTCTA  
CACAGTAACCTCTCTCAGCATGTGCCCAAGATGGTTTAAAGACATCAACAACTCCAGGAACCTGGATCTGTCC  
CAAACTTCTTGGCCAAAGAAATGGGGATGCTAAATTTCTGCATTTTCTCCCGCCTCATCCAATTGGATCTG  
TCTTTCAATTTGAACCTTCAAGTCTAGCTGATCTATGAATCTATCAAGCATTTTCTTCACTGAAAAGCGCTG  
AAAATCTGCGGATCAGAGGATATGTCTTTAAAGAGTTGAAAAGCTTTAACCTCTCGCCATTACATAATCTTCAA  
AATCTTGAAGTTCTTGATCTGGCACTAACTTTATAAAAATTGTAACTCAGCATGTTTAAACAATTTAAAGA  
CTGAAAGCTATAGATCTTTCAGTGAATAAAATATCACCTTCAGGAGATTCAAGTGAAGTTGGCTTCTGCTCAA  
GCCAGAACTTCTGTAGAAAGTTATGAACCCGAGTCTGGAACAATTACATTATTTTCAAGATATGATAAGTATGCA  
AGGAGTTGCAGATTCAAAAACAAGAGGCTTCTTTCATGTCTGTTAATGAAAGCTGCTACAAGTATGGGCAGACC  
TTGGATCTAAGTAAAAATAGTATATTTTGTCAAGTCTCTGATTTTTCAGCATCTTTCTTCTCAAATGCCTG  
AATCTGTCAGGAAATCTCATTAGCCAACTCTTAATGGCAGTGAATCCAACCTTTAGCAGAGCTGAGATATTTG  
GACTTCTCCAACAACCGGCTTGATTTACTCCATTCAACAGCATTTGAAGAGCTTCAAAAACCTGGAAGTTCTGGAT  
ATAAGCAGTAATAGCCATTATTTTCAATCAGAAGGAATTACTCATATGCTAACTTTACCAAGAACCTAAAGGTT  
CTGCAGAACTGATGATGAACGACAATGACATCTCTTCTCCACCAGCAGGACCATGGAGAGTGAGTCTCTTAGA  
ACTCTGGAATTCAAGGAAATCACTTAGATGTTTATGGAGAGAAGGTGATAACAGATACTTACAATTATTTCAAG  
AATCTGCTAAAATTAGAGGAATTAGACATCTCTAAAAATTCCTAAGTTTCTTGCCTTCTGGAGTTTGTATGGT  
ATGCCTCCAAATCTAAGAATCTCTCTTTGGCCAAAAATGGGCTCAAATCTTTCAGTTGGAAGAACTCCAGTGT  
CTAAAGAACCCTGGAACTTTGGACCTCAGCCACAACCACTGACCACTGTCCCTGAGAGATTATCCAACCTGTTCC  
AGAAGCCTCAAGAATCTGATCTTAAAGATAATCAAATCAGGAGTCTGACGAAGTATTTTCTACAAGATGCCTTC  
CAGTTGCGATATCTGGATCTCAGCTCAAAATAAATCCAGATGATCCAAAAGACCAGCTTCCAGAAAATGTCTC  
AACAACTGAAGATGTTGCTTTTGCATCATAATCGGTTTCTGTGCACCTGTGATGCTGTGTGGTTTGTCTGGTGG  
GTTAACCATACGGAGGTGACTATTCCTTACCTGGCCACAGATGTGACTTGTGTGGGGCCAGGAGCACACAGGGC  
CAAAGTGTGATCTCCCTGGATCTGTACACCTGTGAGTTAGATCTGACTAACCTGATTCTGTTCTCACTTTCCATA  
TCTGTATCTCTCTTTCTCATGGTGATGATGACAGCAAGTCACCTCTATTTCTGGGATGTGTGGTATATTTACCAT  
TTCTGTAAGGCCAAGATAAAGGGGTATCAGCGTCTAATATCACCAGACTGTTGCTATGATGCTTTTATTGTGAT  
GACACTAAAGACCCAGCTGTGACCGAGTGGGTTTGGCTGAGCTGGTGGCCAACTGGAAGACCCAAGAGAGAAA  
CATTTTAATTTATGTCTCGAGGAAGGGACTGGTTACCAGGGCAGCCAGTTCTGGAACCTTTCCAGAGCATA  
CAGCTTAGCAAAAAGACAGTGTGTTGTGATGACAGACAAGTATGCAAGACTGAAAATTTTAAGATAGCATTTTAC  
TTGTCCCATCAGAGGCTCATGGATGAAAAGTTGATGTGATTATCTTGATATTTCTTGAGAAGCCCTTTTCAAGAA  
TCCAAGTTCTCCAGCTCCGGAAGGCTCTGTGGGAGTTCTGTCTTGTAGTGGCCAAACCCGCAAGCTCAC  
CCATACTTCTGGCAGTGTCTAAGAACGCCCTGGCCACAGACAATCATGTGGCCTATAGTCAGGTGTTCAAGGAA  
ACGGTCTAGCCCTTCTTTGCAAAACACAACCTGCTAGTTTACCAAGGAGAGGCTGGC

**FIGURE 358**

MVFPMTLKRQILILFNIILISKLLGARWFPKTLPCDVTLDVPKNHVIVDCTDKHLTEIPGGI  
PTNTTNLTTLTINHIPDISPASFHRLDHLVEIDFRCNCVPIPLGSKNNMCIKRLQIKPRSFSGL  
TYLKSLYLDGNQLLEIPQGLPPSLQLLSLEANNIFSIRKENLTELANIEILYLGNQCYRNP  
YVSYSIEKDAFLNLTKLKVLSLKDNVNTAVPTVLPSTLTLEYLYNNMIAKIQEDDFNNLNQLQ  
ILDLSGNCPRCYNAPFPCAPCKNNSPLQIPVNAFDALTELKVLRLHSNSLQHVPFRWFKNINK  
LQELDLSQNFLAKEIGDAKFLHFLPSLIQLDLSFNFELQVYRASMNLSQAFSSLSKSLKILRIR  
GYVFKELKSFNLSPLHNLQNLVLDLGTNFIKIANLSMFKQFKRLKVIDLSVNKISPSGDSSE  
VGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGQTLDLKNS  
IFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNRLDLLHSTAFEELHK  
LEVLDISSNSHYFQSEGITHMLNFTKNLKVLOKLMMNDNDISSSTSRTMESESLRTLEFRGNH  
LDVLWREGDNRYLQLFKNLLKLEELDISKNLSFLPSGVFDGMPNPNLKNLSLAKNGLKSFSWK  
KLQCLKNLETDLDSHNQLTTVPERLSNCSRSLKNLILKNNQIRSLTKYFLQDAFQLRYLDLSS  
NKIQMIQKTSFPENVLNNLKMLLLHHNRFLCTDAVWFVWVWNHTEVTIPYLATDVTVCVPGA  
HKGQSVISLDLYTCELDLTNLILFSLSISVSLFLMVMMTASHLYFWDVWYIYHFCKAKIKGYQ  
RLISPDCCYDAFIVYDTKDPVTEWVLAELVAKLEDPREKHFNLCEERDWLPGQPVLNLSQ  
SIQLSKKTVMFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVILIFLEKPFQKSKFLQLRKRLC  
GSSVLEWPTNPQAHFYFWQCLKNALATDNHVAYSQVFKETV

**Important features:**

**Signal sequence:**

amino acids 1-26

**Transmembrane domain:**

amino acids 840-860

# **FIGURE 359**

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTTCCTGATGCTTCTGCTGCCGCTACTGCTAC  
TGCTGGTGGCCACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGTATGGTGG  
AGCTGCACAACCTCTACCGGGCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGAGAT  
GGGACGAGGAGCTGGCCGCCTTCGCCAAGGCCTACGCACGGCAGTGCGTGTGGGGCCACAACA  
AGGAGCGCGGGCGCCGCGGCGAGAATCTGTTGCCATCACAGACGAGGGCATGGACGTGCCGC  
TGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCTGCAGCC  
CAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATCGGCTGTG  
GTTCCCACTTCTGTGAGAAGCTCCAGGGTGGTGGAGGAGACCAACATCGAATTACTGGTGTGCA  
ACTATGAGCCTCCGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGACTCCGTGCTCCC  
AATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGCCCGGAAGATG  
CTCAGGATTTGCCTTACCTGGTAAGTGAAGGGCCCATCCTTCCGGGCGACTGAAGCATCAGACT  
CTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCTTGGTAACAGAGG  
TCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCAGGCCCCAACTTCCTTAG  
CAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCGTAACAAGTGAAGTCCCTT  
CCATTTTGGCAGCTCACAGCCTGCCCTCCTTGGATGAGGAGCCAGTTACCTTCCCCAAATCGA  
CCCATGTTCTATCCCAAATCAGCAGACAAAGTGACAGACAAAACAAAAGTGCCCTCTAGGA  
GCCCAGAGAACTCTCTGGACCCCCAAGATGTCCCTGACAGGGGCAAGGGAACCTCTACCCCATG  
CCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTTCCAGTGAGGTCTTGGCCTCAGTTT  
TTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGACCACACGGGGCACACCTCCT  
CCAAGTCCCTGCCCAATTTCCCCAATACTCTGCCACCGCTAATGCCACGGGTGGGCGTGCCC  
TGGCTCTGCAGTCGTCTTGCCAGGTGCAGAGGGCCCTGACAAGCCTAGCGTTGTGTCAGGGC  
TGAAGTCGGGCCCTGGTCATGTGTGGGGCCCTCTCCTGGGACTACTGCTCCTGCCTCCTCTGG  
TGTGGCTGGAATCTTCTGAATGGGATAACCACTCAAAGGGTGAAGAGGTGAGCTGTCTCCTG  
TCATCTTCCCCACCCTGTCCCCAGCCCCCTAAACAAGATACTTCTTGGTTAAGGCCCTCCGGAA  
GGGAAAGGCTACGGGGCATGTGCCTCATCACACCATCCATCCTGGAGGCACAAGGCCTGGCTG  
GCTGCGAGCTCAGGAGGCCGCCTGAGGACTGCACACCGGGCCACACCTCTCCTGCCCCCTCCC  
TCCTGAGTCCTGGGGGTGGGAGGATTTGAGGGAGCTCACTGCCTACCTGGCCTGGGGCTGTCT  
GCCCACACAGCATGTGCGCTCTCCCTGAGTGCTGTGTAGCTGGGGATGGGGATTCTTAGGGG  
CAGATGAAGGACAAGCCCCACTGGAGTGGGGTTCTTTGAGTGGGGGAGGCAGGGACGAGGGAA  
GGAAAGTAACCTCTGACTCTCCAATAAAAACCTGTCCAACCTGTGAAA

**FIGURE 360**

MHGSCSFLMLLLPLLLLLLVATTGPVGALTDEEKRLMVELHNLRYAQVSPTASDMLHMRWDEEL  
AAFAKAYARQCVWGHNKERRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQMC  
GHYTQVWAKTERIGCGSHFCEKLGQVEETNIELLVVCNYEPPGNVKGKRPYQEGTPCSQCPSG  
YHCKNSLCEPIGSPEDAQDLPLYLVTEAPSFRAEASDSRKMGTTPSSLATGIPAFVLVTEVSGSL  
ATKALPAVETQAPTSLATKDPSPMATEAPPCVTTEVPSILAAHSLPSLDEEPVTFPKSTHVPI  
PKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEELPPSSEVLASVFPAQD  
KPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVVVSGLN SGP  
GHVWGPLLGLLLLLPPLVLGIF

**Important features:**

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 114-118, 403-407, 409-413

**Glycosaminoglycan attachment site.**

amino acids 439-443

**Casein kinase II phosphorylation site.**

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

**N-myristoylation site.**

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237, 250-256

**Amidation site.**

amino acids 82-86, 172-176

**Peroxidases proximal heme-ligand signature.**

amino acids 287-298

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.**

amino acids 127-138

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.**

amino acids 160-172

**FIGURE 361**

GACTAGTTCTCTTGGAGTCTGGGAGGAGGAAAGCGGAGCCGGCAGGGAGCGAACCAGGACTGG  
GGTGACGGCAGGGCAGGGGGCGCCTGGCCGGGGAGAAGCGCGGGGGCTGGAGCACCACCAACT  
GGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGGGGGACTGCG  
AGAGGACCCCGGCGTCCGGGCTCCCGGTGCCAGCGCTATGAGGCCACTCCTCGTCCTGCTGCT  
CCTGGGCCTGGCGGCCGGCTCGCCCCACTGGACGACAACAAGATCCCCAGCCTCTGCCCCGG  
GCACCCCGGCCTTCAGGCACGCCGGGCCACCATGGCAGCCAGGGCTTGCCGGGCCGCGATGG  
CCGCGACGGCCGCGACGGCGCGCCCGGGGCTCCGGGAGAGAAAGGCGAGGGCGGGAGGCCGGG  
ACTGCCGGGACCTCGAGGGGACCCGGGCCGCGAGGAGAGGCGGGACCCGCGGGGCCACCGG  
GCCTGCCGGGGAGTGCTCGGTGCCTCCGCGATCCGCCTTCAGCGCCAAGCGCTCCGAGAGCCG  
GGTGCTCCGCCGTCTGACGCACCCCTTGCCCTTCGACCGCGTGCTGGTGAACGAGCAGGGACA  
TTACGACGCCGTCACCGGCAAGTTCACCTGCCAGGTGCCTGGGGTCTACTACTTCGCCGTCCA  
TGCCACCGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGAATGGCGAATCCATTGCCTC  
TTTCTTCCAGTTTTTTCGGGGGTGGCCCAAGCCAGCCTCGCTCTCGGGGGGGGCCATGGTGAG  
GCTGGAGCCTGAGGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTACATTGGCATCTATGC  
CAGCATCAAGACAGACAGCACCTTCTCCGGATTTCTGGTGTACTCCGACTGGCACAGCTCCCC  
AGTCTTTGCTTAGTGCCCACTGCAAAGTGAGCTCATGCTCTCACTCCTAGAAGGAGGGTGTGA  
GGCTGACAACCAGGTATCCAGGAGGGCTGGCCCCCTGGAATATTGTGAATGACTAGGGAGG  
TGGGGTAGAGCACTCTCCGTCTGTGCTGGCAAGGAATGGGAACAGTGGCTGTCTGCGATCA  
GGTCTGGCAGCATGGGGCAGTGGCTGGATTTCTGCCCAAGACCAGAGGAGTGTGCTGTGCTGG  
CAAGTGTAAGTCCCCAGTTGCTCTGGTCCAGGAGCCACGGTGGGGTGCTCTCTTCCTGGTC  
CTCTGCTTCTCTGGATCCTCCCCACCCCTCTGCTCCTGGGGCCGGCCCTTTTCTCAGAGAT  
CACTCAATAAACCTAAGAACCCTCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 362**

MRPLLVLALLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPG  
EKGEGRPGPLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLPFD  
RVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWPKPA  
SLSGGAMVRLEPEDQVWVQVGVDYIGIYASIKTDSTFSGFLVYSDWHSSPVFA

**Important features:**

**Signal sequence.**

amino acids 1-15

**N-myristoylation sites.**

amino acids 11-17, 68-74, 216-222

**Cell attachment sequence.**

amino acids 77-80



**FIGURE 363**

[illegible]

**FIGURE 364**

MMWRPSVLLLLLLLLLRHGAQGKPSPDAGPHGQGRVHQAPLSDAPHDDAHGNFQYDHEAFLGRE  
VAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDTYD  
TDRDGRVGEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSMATREELT  
AFLHPPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPAWVQTERQQFRDF  
RDINKDGHLDGSEVGHVWLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFVGSQAT  
NYGEDLTRHHDEL

**Important features:**

**Signal sequence:**

amino acids 1-20

**N-glycosylation site.**

amino acids 140-144

**Casein kinase II phosphorylation site.**

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,  
291-295, 298-302

**N-myristoylation site.**

amino acids 263-269, 311-317

**Endoplasmic reticulum targeting sequence.**

amino acids 325-330

# **FIGURE 365**

GTCTGTTCCAGGAGTCCTTCGGCGGCTGTTGTGTCA GTGGCCTGATCGCGATGGGGACAAAG  
GCGCAAGTCGAGAGGAAACTGTTGTGCCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGGCA  
TTGGGCAGTGTTACAGTGCACTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCTGTG  
AAGTTGTCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAGTTTGACCAAGGA  
GACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGGTGACC  
TTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATACACTTGT  
ATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGTGCTTGTG  
CCTCCATCCAAGCCTACAGTTAACATCCCCCTCTCTGCCACCATTGGGAACCGGGCAGTGCTG  
ACATGCTCAGAAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGATGGGATAGTG  
ATGCCTACGAATCCCAAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCTGAATCCACA  
ACAGGAGAGCTGGTCTTTGATCCCCGTGCAGCCTCTGATACTGGAGAATACAGCTGTGAGGCA  
CGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCTGTGGAGCGGAAT  
GTGGGGGTCACTCGTGGCAGCCGTCCTTGTAACCCTGATTCTCCTGGGAATCTTGGTTTTTGGC  
ATCTGGTTTGCCCTATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGGACTTCGAGTAAGAAG  
GTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAGACCTCGTCATTCTCTG  
GTGTGAGCCTGGTTCGGCTCACCGCCTATCATCTGCATTTGCCCTTACTCAGGTGCTACCGGACT  
CTGGCCCCCTGATGTCTGTAGTTTACAGGATGCCTTATTTGTCTTCTACACCCACAGGGCCC  
CCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCCATCCTCCTTCATGCCCTC  
CCTCCCTTTCTTACCCTGCTGAGTGGCCTGGAACCTTGTTTAAAGTGTTTATTCCCCATTTCT  
TTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCCCTCTAAGTAGACAGCAAAAA  
TGGCGGGGGTTCGCAGGAATCTGCACTCAACTGCCCACCTGGCTGGCAGGGATCTTTGAATAGG  
TATCTTGAGCTTGGTTCTGGGCTCTTCTCTTGTGTACTGACGACCAGGGCCAGCTGTTCTAGA  
GCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGGTGATGACACTGGGGTCTTCCAT  
CTCTGGGGCCCCTCTCTTCTGTCTTCCCATGGGAAGTGCCACTGGGATCCCTCTGCCCTGTC  
CTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGTGGAAAATGGGAGCTCTTGTTGTGGA  
GAGCATAGTAAATTTTCAGAGAACTGAAGCCAAAAGGATTTAAAACCGCTGCTCTAAAGAAA  
AGAAAACCTGGAGGCTGGGCGCAGTGGCTCACGCCTGTAATCCCAGAGGCTGAGGCAGGCGGAT  
CACCTGAGGTCGGGAGTTTCGGGATCAGCCTGACCAACATGGAGAAACCCTACTGGAAATACAA  
AGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTCCCAGCTGCTCAGGAGCCTGGCAACAAGAG  
CAAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

**FIGURE 366**

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRI PENNPVKLS CAYSGFSSPRVEWK  
FDQGD TTRLVCYNNKITASYEDRVTF LPTGITFKSVTREDTGTYTCMVSEEGNSYGEVKVKL  
IVLVPPSKPTVNI PSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNSSYV  
LNPTTGELVFDPLSASDTGEYSCEARNGYGT PMTSNAVRMEAVERNVGVIVA AVLVTLLILGI  
LVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

**Important features:**

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 238-255

**N-glycosylation site.**

amino acids 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 270-274

**Casein kinase II phosphorylation site.**

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,  
193-197, 203-207, 287-291

**N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

**FIGURE 367**

GGGGAGAGGAATTGACCATGTAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAAATG  
 AAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGAAC  
 GAAGCTTTTTCTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA  
 TAAACCAGAGTTAGACCCCGGGGGTGGTGTGTTCTGACATAAATAAATAATCTTAAAGCAGCTGTTCCCTCC  
 CCACCCCAAAAAAAGGATGATTGGAATGAAGAACCAGGATTACAAAAGAAAAAGTATGTTCAATTTTTCTC  
 TATAAAGGAGAAAGTGAGCCAAGGAGATATTTTTGGAATGAAAAGTTTGGGGCTTTTTAGTAAAGTAAAGAACT  
 GGTGTGGTGGTGTTCCTTTCTTTTGAATTTCCACAAGAGGAGAGGAAATTAATAATACATCTGCAAGAAAA  
 TTTGAGAGAAGAAAAGTTGACCGCGCAGATTGAGGCATTGATTGGGGGAGAGAAAACAGCAGAGCACAGTTGGA  
 TTTGTGCTATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTCCTTCAACCTCCTTTTTTTTAAAT  
 TTTTATTCCTTTTGGTATCAGATCATGCGTTTCTCTTGTCTTAACCACTGGATTCCATCTGGATGTTGCT  
 GTGATCAGCTGAAAATACAACCTGTTGAATTCAGAAGGACCAACACCAGATAAATTATGAATGTTGAACAAGAT  
 GACCTTACATCCACAGCAGATAATGATAGGTCCTAGGTTTAAACAGGGCCCTATTGACCCCTGCTTGTGGTGCT  
 GCTGGCTCTTCAACTTCTGTGGTGGCTGGTCTGGTGGGGCTCAGACCTGCCCTTCTGTGTGCTCCTGCAGCAA  
 CCAGTTGAGCAAGGTGATTGTGTTGCGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCCACCAACACACGGCT  
 GCTGAACCTCCATGAGAACCATAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAGGCATTGGAATCCT  
 ACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTGGGGCTTTCAATGGTCTGGCGAACCTCAACACTCTGGA  
 ACTCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTGTATACTTGTCTAACTGAAGGAGCTCTGGT  
 GCGAAACAACCCCATTTGAAGCATCCCTTCTATGCTTTTAAACAGAATTCTTCTTTGCGCGACTAGACTTAGG  
 GGAATTGAAAAGACTTTTCATACATCTCAGAAGGTGCCCTTGAAGGTCTGTCCAACTTGAGGTATTTGAACCTTGC  
 CATGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAACTAGATGAGCTGGATCTTTCTGGGAATCA  
 TTTATCTGCCATCAGGCCTGGCTCTTTCCAGGGTTGATGCACCTTCAAAAAGTGTGGATGATACAGTCCCAGAT  
 TCAAGTGATTGAACGGAATGCCCTTGACAACCTTCAGTCACTAGTGGAGATCAACCTGGCACACAATAATCTAAC  
 ATTAATGCTCATGACCTCTCACTCCCTTGCACTCATCTAGAGCGGATACATTTACATCACAACCTTGGAACCTG  
 TAACTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCTCGAACACAGCTGTTGTGCCCCGGTG  
 TAACTCTCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCACATGCTATGCTCCGGT  
 GATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCTGAGCTGAAATGTGCGGCCCTCCACATC  
 CCTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTCATGACACATGGGGCGTACAAAGTGCGGATAGCTGT  
 GCTCAGTGATGGTACGTTAAATTTCAAAATGTAAGTGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAA  
 TTCCGTTGGGAATACTACTGCTTCAGCCACCTGAATGTTACTGCAGCAACCACTACTCCTTTCTCTTACTTTTC  
 AACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGGACCAAGATAAATGTGGGTCCCCTCC  
 AGTGGTCGACTGGGAGACCACCAATGTGACCACCTCTCTCACACCACAGAGCACAAGGTCGACAGAGAAAACCTT  
 CACCATCCCAGTGACTGATATAAACAGTGGGATCCAGGAATTGATGAGGTCATGAAGACTACCAAAATCATCAT  
 TGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTCTACAAGATGAGGAAGCAGCACC  
 TCGGCAAAACCATCAGCCCCAACAGGACTGTTGAAATTATTAATGTGGATGATGAGATTACGGGAGACACACC  
 CATGGAAGCCACCTGCCCTGCTATCGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTT  
 CAACCACACAACAAGTTAACACAATAAATCAATACACAGTTCAGTGCATGAACCGTTATTGATCCGAATGAA  
 CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTTACAGAGTTACAAAAACAACAATCAAAAAAAA  
 GACAGTTTATTAATAATGACACAATGACTGGCTAAATCTACTGTTTCAAAAAAGTGTCTTTACAAAAAACAA  
 AAAAGAAAAGAAATTTATTTATTAATAATCTATTGTGATCTAAAGCAGACAAAA

**FIGURE 368**

MLNKMTLHPQQIMIGPRFNRAFDPLLVVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVICVRKNLREVPDGIS  
TNTRLLNLHENQIQIIVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKL  
KELWLRNNPIBSIPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYNLNLAMCNLREIPNLTPLIKLDDEL  
LSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLH  
NPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAELKC  
RASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVDQTMGMYTCMVSNVSGNTTASATLNVTAATTP  
FSYFSTVTVETMEPSQDEARTDNNVGPTPVVDWETTNVTTSLTPQSTRSTEKTFITPVDINSGIPGIDEVMKT  
TKIIIGCFVAITLMAAVMLVIFYKMRKQHRQNHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYS  
YKSPFNHTTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI

**Important features:**

**Signal sequence:**

amino acids 1-44

**Transmembrane domain:**

amino acids 523-543

**N-glycosylation site.**

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438, 442-446,  
488-492, 606-610

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

**Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

**N-myristoylation site.**

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243, 391-397,  
422-428, 433-439, 531-537

**FIGURE 369**

CAAACTTGCCTGCGGAGAGCGCCAGCTTGACTTGAATGGAAGGAGCCCGAGCCCGCGGAGCGCAGCTGAGAC  
TGGGGGAGCGCTTCGGCCTGTGGGGCGCCGCTCGGCCCGGGGCGCAGCAGGGAAGGGGAAGCTGTGGTCTGCC  
CTGCTCCACGAGGCGCACTGGTGTGAACCGGGAGAGCCCTTGGGTGGTCCCGTCCCTTATCCCTCCTTTATATA  
GAAACCTTCCACACTGGGAAGGCAGCGCGAGGCAGGAGGGCTCATGGTGAAGCAAGGAGGCCGCTGATCTGCAG  
GCGCACAGCATTCGAGTTTACAGATTTTACAGATACCAAAATGGAAGGCGAGGAGGCAGAACAGCCTGCCTGGT  
TCCATCAGCCCTGGCGCCAGGCGCATCTGACTCGGCACCCCTGCAGGCACCATGGCCAGAGCCGGGTGCTGC  
TGCTCCTGCTGCTGCTGCCGCCACAGCTGCACCTGGGACCTGTGCTTGCCTGAGGGCCCCAGGATTTGGCCGAA  
GTGGCGGCCACAGCCTGAGCCCCGAAGAGAACGAATTTGCGGAGGAGGAGCCGGTGTGGTACTGAGCCCTGAGG  
AGCCCCGGCCTGGCCAGCCGCGGTGAGCTGCCCCGAGACTGTGCTGTTCAGGAGGGCGTGTGGACTGTG  
GCGGTATTGACCTGCGTGAGTTCCCGGGGACCTGCTGAGCACACCAACCACTATCTCTGCAGAACCAACGAGC  
TGGAAAAGATCTACCTTGAGGAGCTCTCCCGGTGCACCGGTGAGAGACACTGAACCTGCAAAACAACGCTGGA  
CTTCCGAGGGCTCCAGAGAAAGCGTTTGAAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAATAACAAGC  
TGACCTTGGCACCCCGCTTCTGCCCCAACGCGCTGATCAGTGTGGACTTTGCTGCCAATATCTCACCAAGATCT  
ATGGGCTCACCTTTGGCCAGAAGCCAACTTGAGGTCTGTGTACCTGCACAACAACAAGCTGGCAGACGCCGGGC  
TGCCGGACAACATGTTCAACGGCTCCAGCAACGTGAGGTCTCATCTGTCCAGCAACTTCTGCGCCACGTGC  
CCAAGCACTGCGCCTGCCCTGTACAAGCTGCACCTCAAGAACAACAGCTGGAGAAGATCCCCCGGGGGCCT  
TCAGCGAGCTGAGCAGCTGCGCGAGCTATACCTGCAGAACCACTACCTGACTGACGAGGGCCTGGACAACGAGA  
CCTTCTGGAACTCTCCAGCCTGGAGTACCTGGATCTGTCCAGCAACAACCTGTCTCGGGTCCAGCTGGGCTGC  
CGCGCAGCCTGGTGTGCTGCACTTGGAGAAGAAGCCATCCGAGCGTGGACGCGAATGTGCTGACCCCCATCC  
GCAGCTGGAGTACCTGCTGTGCACAGCAACCAAGCTGCGGGAGCAGGGCATCCACCACTGGCCTTCCAGGGCC  
TCAAGCGGTTGCACACGGTGCACCTGTACAACAACGCGCTGGAGCGCGTGGCAGTGGCCTGCGCCGCTGTC  
GCACCTCATGATCTGCACAACCAAGTACAGGCATTGGCCGCGAAGACTTTGCCACCACTACTTCTGAGAGG  
AGCTCAACCTCAGCTACAACCGCATCACAGCCACAGGTGCACCGCGAGCCTTCCGCAAGCTGCGCCTGCTGC  
GCTCGCTGGACCTGTGCGGCAACCGGCTGCACACGCTGCCACCTGGGCTGCTCGAAATGTCCATGTGCTGAAGG  
TCAAGCGCAATGAGCTGGCTGCCTTGGCACGAGGGGCGCTGGCGGCATGGCTCAGCTGCGTGAGCTGTACCTCA  
CCAGCAACCGACTGCGCAGCCGAGCCCTGGGCCCCGCTGCTGGGTGGACCTGCCCCATCTGCAGCTGCTGGACA  
TCGCCGGGAATCAGCTCACAGAGATCCCCGAGGGGCTCCCCGAGTCACTTGAGTACCTGTACCTGCAGAACACA  
AGATTAGTGCGGTGCCCGCCAATGCCTTCGACTCCACGCCCAACCTCAAGGGGATCTTTCTCAGGTTTAAACAAGC  
TGGCTGTGGGCTCCGTGGTGACAGTGCCCTTCCGGAGGCTGAAGCACTGCAGGTCTTGACATTGAAGGCAACT  
TAGAGTTTGGTGACATTTCCAAGGACCGTGGCCGCTTGGGGAAGGAAAGGAGGAGGGAAGAGGAGGAGGAGG  
AGGAAGAGGAAACAAGATAGTGACAAGGTGATGCAGATGTGACCTAGGATGATGGACCGCCGGACTCTTTCTGTC  
AGCACACGCTGTGTGCTGTGAGCCCCCACTCTGCCGTGCTCACACAGACACACCCAGCTGCACACATGAGGCA  
TCCCACATGACACGGGCTGACACAGTCTCATATCCCCACCCCTTCCACGGCGTGTCCACGGCCAGACACATGC  
ACACACATCACACCTCAAAACACCCAGCTCAGCCACACACAACCTCCAAACCAACACAGTCTCTGTACAC  
CCCCACTACCGCTGCCACGCCCTCTGAATCATGCAGGGAAGGGTCTGCCCCCTGCCCTGGCACACACAGGACCCCA  
TTCCCTCCCCCTGCTGACATGTGTATGCGTATGCATACACACACACACACACATGCACAAGTCATGTGCGAA  
CAGCCCTCCAAGCCTATGCCACAGACAGCTCTTGCCCCAGCCAGAATCAGCCATAGCAGCTCGCGTCTGCCCT  
GTCCATCTGTCCGTCCGTTCCCTGGAGAAGACACAAGGATCCATGCTCTGTGGCCAGGTGCTGCCACCCCTCT  
GGAAGTCAAAAAGCTGGCTTTTATTCTTTCCATCCTATGGGGACAGGAGCCTTCAGGACTGCTGGCCTGGCC  
TGGCCACCCCTGCTCCTCAGGTGCTGGGCGTCACTCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA  
CAGGCACTTTTCCAATGGGCAAGCCAGTGAGGCAGGATGGGAGAGCCCCCTGGGTGCTGTGGGGCCTTGGGG  
CAGGAGTGAAGCAGAGGTGATGGGGCTGGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGACACCTTT  
GTTCTTCAGGCCTGTGGGGGAAGTTCCGGGTGCCCTTTATTTTATTCTTTTCTAAGGAAAAAATGATAAAAAAT  
CTCAAGCTGATTTTCTTGTATAGAAAACTAATATAAAGCATTATCCCTATCCCTGCAAAAAA

**FIGURE 370**

MEGEEAEQPAWFHQPWPGASDSAPPAGTMAQSRVLLLLLLLLLPPQLHLGPFVLAVRAPGFGRSG  
GHSLSPREENEFAEEEPVLVLSPPEPGPGPAAVSCPRDCACSQEGVDCGGIDLREFPGDLPEH  
TNHLSLQNNQLEKIYPEELSRHRLETNLQNNRLTSRGLPEKAFEHLTNLNYLYLANNKLT  
APRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNVEVLI  
LSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDNETFWK  
LSSLEYLDLSSNNLSRVFAGLPRSLVLLHLEKNAIRSVDANVLTPIRSLEYLLLHNSQLREQG  
IHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMLHNQITGIGREDFATTYFLEELNLS  
YNRITSPQVHRDAFRKLRLRLSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAALARGALAGMA  
QLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYLQNNKISAVP  
ANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKDRGLGKEKEE  
EEEEEEEEETR

**Important features:**

**Signal sequence:**

amino acids 1-48

**N-glycosylation site.**

amino acids 243-247, 310-314, 328-332, 439-443

**Casein kinase II phosphorylation site.**

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

**N-myristoylation site.**

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,  
477-483, 498-502, 539-545, 548-554

**Leucine zipper pattern.**

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,  
535-557



# **FIGURE 371**

CACTTTCTCCCTCTCTTCTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTCGCAGAGACCTCGGAGACCGCG  
 CCGGGGAGACGGAGGTGCTGTGGGTGGGGGGACCTGTGGCTGCTCGTACCGCCCCCACCCTCCTCTTCTGCAC  
 TGCCGTCTCCGGAAGACCTTTTCCCTGCTCTGTTTCTTACCGAGTCTGTGCATCGCCCCGACCTGGCCGG  
 GAGGAGGCTTGGCCGGCGGAGATGCTCTAGGGGCGGCGGGAGGAGCGGCCGGCGGGAGCGGAGGGCCCGGCAG  
 GAAGATGGGCTCCCGTGGACAGGGACTCTTGTGGCGTACTGCCTGCTCCTTGCTTCTGGCTTGGCTCTGCTCT  
 GAGTCGTGTGCCCCATGTCCAGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGCCGTCGCCCTCCGACCA  
 TGCCGAGAGGGCTGAAGAACAACATGAAAAATACAGGCCAGTCAGGACCAGGGGCTCCCTGCTTCCGGGTGCTT  
 GCGTCTGTGTGACCCCGGTACCTCCATGTACCCGGCGACCGCGGTGCCCCAGATCAACATCACTATCTTGAAAGG  
 GGAGAAGGGTGACCGCGAGATCGAGGCCTCCAAGGGAAATATGGCAAAACAGGCTCAGCAGGGGCCAGGGGCCA  
 CACTGGACCCAAAGGGCAGAAGGGCTCCATGGGGGCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGCTTTTC  
 GGTGGGCGGAAGAAGCCCATGCACAGCAACCACTACTACCAGACGGTGATCTTCGACACGGAGTTCTGTAACCT  
 CTACGACCACTTCAACGATGTTTACCGGCAAGTTCTACTGCTACGTGCCCGGCTCTACTTCTTCAGCTCAACGT  
 GCACACCTGGAACAGAAGGAGACCTACCTGCACATCATGAAGAACAGGAGGAGGTGGTGATCTTGTTCGCGCA  
 GGTGGGCGACCGCAGCATCATGCAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACCAGGTGTGGGTACG  
 CCTCTACAAGGGCGAACGTGAGAAGCCCATCTTCAGCGAGGAGCTGGACACCTACATCACCTTCAGTGGCTACCT  
 GGTCAAGCAACGCCACCGAGCCCTAGCTGGCCGGCCACCTCCTTCTCTGCCACCTTCCACCCCTGCGCTGTGC  
 TGACCCACCGCTCTTCCCCGATCCCTGGACTCCGACTCCCTGGCTTTGGCATTAGTGAGACGCCCTGCACAC  
 ACAGAAAGCCAAAGCGATCGGTGCTCCCGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAG  
 GCGGGGCGACCCGCGAGAACCCTCTGGGACCTTCCGCGGCCCTCTCTGCACACATCCTCAAGTGACCCCGCACGG  
 CGAGACGCGGTGGCGCGCAGGGCGTCCAGGGTGGCGCACCGCGGCTCCAGTCTTGGAAATAATTAGGCAAATT  
 CTAAAGGTCTCAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAAGGGTGTATTTTTGTCTTTCCAGCCAG  
 CCTGCTGGCTCCCAAGAGAGAGGCTTTTTCAGTTGAGACTCTGCTTAAGAGAAGATCCAAAGTTAAAGCTCTGGG  
 GTCAGGGGAGGGGCGGGGGCAGGAACTACCTCTGGCTTAATTCTTTTAAGCCACGTAGGAACTTTCTTGAGGG  
 ATAGGTGAGCCCTGACATCCTGTGGCTTGCCCAAGGGCTCTGCTGGTCTTTCTGAGTCACAGCTGCGAGGTGA  
 TGGGGGCTGGGGCCCCAGGCGTCAGCCTCCAGAGGGACAGCTGAGCCCCCTGCCTTGGCTCCAGGTTGGTAGAA  
 GCAGCCGAAGGGCTCTGACAGTGGCCAGGGACCCCTGGGTCCCCCAGGCTGCAGATGTTCTATGAGGGGCGAG  
 AGCTCCTTGGTACATCCATGTGTGGCTCTGCTCCACCCCTGTGCCACCCAGAGCCCTGGGGGGTGGTCTCCATG  
 CTGCGACCCCTGGCATCGCTTTCTGTGCGGCTCCCAACAATCAGCCCCAGAAGGCCCGGGGCTTGGCTT  
 CTGTTTTTTATAAAACACCTCAAGCAGCACTGCAGTCTCCCATCTCCTCGTGGGCTAAGCATCACCGCTTCCAG  
 TGTGTTGTGTTGGTTGGCAGCAAGGCTGATCCAGACCCCTTCTGCCCCACTGCCCTCATCCAGGCTCTGACCA  
 GTAGCCTGAGAGGGGCTTTTCTAGGCTTCAGAGCAGGGGAGAGCTGGAAGGGGCTAGAAAGCTCCCGCTTGTCT  
 GTTCTCAGGCTCCTGTGAGCCTCAGTCTGAGACCAGAGTCAAGAGGAAGTACACGTCCCAATCACCGTGTCA  
 GGATTCACTCTCAGGAGCTGGGTGGCAGGAGAGGCAATAGCCCCCTGTGGCAATTGCAGGACCAGCTGGAGCAGGG  
 TTGCGGTGTCTCCAGGTGCTCTCGCCCTGCCCATGGCCACCCAGACTCTGATCTCCAGGAACCCCATAGCCCC  
 TCTCCACCTCACCCATGTTGATGCCAGGGTCACTCTTGCTACCCGCTGGGCCCCCAAACCCCGCTGCCTCTC  
 TTCCCTTCCCCCATCCCCACCTGGTTTTGACTAATCCTGCTTCCCTCTCTGGGCTGGCTGCCGGGATCTGGGG  
 TCCCTAAGTCCCTCTCTTTAAAGAACTTCTGCGGGTCAGACTCTGAAGCCGAGTTGCTGTGGGCGTGCCCGGAAG  
 CAGAGCGCCACACTCGCTGCTTAAGTCCCCCAGCTCTTTCAGAAAACATTAAACTCAGAATTGTGTTTTCAA

**FIGURE 372**

MGSRGQG LLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEEQHEKYRPS  
QDQGLPASRCLRCCDPGTSMPATAVPQINITILKGEKGDRGDRGLQGKYGKTGSAGARGHTG  
PKGQKGS MGAPGERCKSHYAAFSVGRKKPMHSNHYYQTVIFDTEFVNLYDHFMFTGKFYCYV  
PGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDRSIMQSQSLMLELREQDQVWVRLYK  
GERENAIFSEELDTYITFSGYLVKHATEP

**Important features:**

**Signal sequence.**

amino acids 1-25

**N-glycosylation site.**

amino acids 93-97

**N-myristoylation sites.**

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

**Amidation site.**

amino acids 150-154

**Cell attachment sequence.**

amino acids 104-107

**FIGURE 373**

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGCTGCGCTTTCTGTCCCCAAGCCG  
TTCTAGACGCGGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTTGAAGGGTGTGATGCTTGGAA  
GCATTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAATGC  
ACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAATTTAGAGG  
ATGAGCGCATGGAGCTCAGTAAGAGCTTTGAGTATACTGTATTATCCTTGTA AAAACCCAAAG  
ATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACACTGTGACAAAGCAGAGTTCT  
TCAGTTCTGAAAATGTTAAAGTGTGTTGAGTCAATTAATATGGACACAAATGACATGTGGTTAA  
TGATGAGAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACA ACTGGTTCTTCC  
TTGCACGCCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTGT TAAAAAAGGATC  
CATCACAGCCTTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATATGTGGGTATGG  
AAGGAGGAATTGCTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCTCAATATCCCAG  
AAAAGTGTCTGTAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAAACAGCTAGCAGTTT  
GCCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGAAAAGATGTATTTA  
ATACCAAATCTGTTGGGCTTTCTATTAAAGAGGCAATGACTTATCACCCCAACCAGGTAGTAG  
AAGGCTGTTGTTT CAGATATGGCTGTTACTTTTAATGGACTGACTCCAAATCAGATGCATGTGA  
TGATGTATGGGGTATACCGCCTTAGGGCATTG GGCATATTTTCAATGATGCATTGGTTTTCT  
TACCTCCAAATGGTTCTGACAATGACTGAGAGAGTG GTAGAAAAGCGTGAATATGATCTTTGTA  
TAGGACGTGTGTTGTCATTATTTGTAGTAGTA ACTACATATCCAATACAGCTGTATGTTTCTT  
TTTCTTTTCTAATTTGGTGGCACTGGTATAACCACACATTAAAGTCAGTAGTACATTTTTAAA  
TGAGGGTGGTTTTTTTTCTTTAAAACACATGAACATTGTAAATGTGTTGGAAAAGAAGTGTTTTA  
AGAATAATAATTTTGCAAATAAACTATTAATAAATATTATATGTGATAAATTTCTAAATTATGA  
ACATTAGAAATCTGTGGGGCACATATTTTGTCTGATTGGTTAAAAAATTTTAACAGGTCTTTA  
GCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATTTGTGATTAAAGTAAACTTTTAG  
CTGTGTGTTCCCTTTACTTCTAATACTGATTTATGTTCTAAGCCTCCCCAAGTTCCAATGGAT  
TTGCCTTCTCAAATGTACA ACTAAGCAACTAAAGAAAATTAAGTGAAAGTTGAAAAAT

**FIGURE 374**

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERMELSKSFRVYCIILV  
KPKDVSLWAAVKETWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRKAYKYAFDKYRDQYNWFFLARPTTFAI  
IENLKYFLLKKDPSQPPFYLGHITIKSGDLEYVGMEGGIVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAV  
CLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFG  
HIFNDALVFLPPNGSDND

**Important features:**

**Signal sequence:**

amino acids 1-33

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389, 399-403,  
409-413, 473-477, 729-733, 748-752

**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550, 558-564,  
651-657, 657-663, 672-672

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

# **FIGURE 375**

GTTGTGTCTTCAGCAAAACAGTGGATTTAAATCTCCTTGACACAAGCTTGAGAGCAACACAAT  
CTATCAGGAAAAGAAAAGAAAAAACCGAACCTGACAAAAAGAAGAAAAAGAAGAAGAAA  
AAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGG  
GCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAA  
AGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAA  
CCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTG  
GTGCCTGGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCA  
GAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA  
GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTGTAGAGATTTCTTCAGATAT  
CTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTAC  
GGTTACTTGGAGACACATCTCTCCCAAAGCGTTGGCTTTGTGAGTGAAGACGAATACTTGGA  
AATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGC  
CGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTTCAGAAGCCAA  
GGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCCTC  
AGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGT  
GGAAAACAGACCTTTCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAA  
CTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCC  
AGGCGCCGTCAGCGAGGTGAGCAACGGCACGTGAGGAGGGCAGGCTGCGTCTGGCTGCTGCC  
TCTTCTGGTCTTGACACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAG  
GCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA  
TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAACAAA  
GAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATATTTAGG  
TACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGACCCACTGCA  
AGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTCTCTGCCCACAGA  
GTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCATCAGTCCATAGAGACGAA  
CAGAATGAGACCTTCCGGCCCCAAGCGTGGCGCTGCGGGCACTTTGGTAGACTGTGCCACCACG  
GCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAA

**FIGURE 376**

MKTIQPKMHNSISWAI FTGLAALCLFQGV PVRSGDATFPKAMD NVTVRQGESATLRCTIDNRV  
TRVAWLNRSTILYAGNDKWCLDPRV VLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTS  
RVHLIVQVSPKIVEISSDISINEGNNISLT CIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQ  
GITREQSGDYEC SASNDVAAPVRRVKVT VNYPPYISEAKGTGVPVGQKGT LQCEASAVPSAE  
FQWYKDDKRLIEGKKGVKVENRPFLSKLI FFNVSEHDYGN YTCVASNKLGH TNASIMLFGPGA  
VSEVSNGTSRRAGCVWLLPLLVLHLLLKF

**Important features:**

**Signal peptide:**

amino acids 1-28

# **FIGURE 377**

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTTGCCCTTTAGATTGTGAA  
**ATGTGGCTCAAGGTCTTCACAACTTTCCCTTTCCCTTTGCAACAGGTGCTTGCTCGGGGCTGAAG**  
 GTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAGGCCCTCTACCTACCCGTCCAC  
 TATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCACACA  
 ATGCCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCCCTGACTTGGAATACCAACAC  
 AAGTTCACCATGATGCCACCCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCTTGATGAA  
 GGCAATTACATCGTGAAGGTCAACATTCAGGGAAATGGAACTCTATCTGCCAGTCAGAAGATA  
 CAAGTCACGGTTGATGATCCTGTCACAAAGCCAGTGGTGCAGATTATCCTCCCTCTGGGGCT  
 GTGGAGTATGTGGGGAACATGACCCTGACATGCCATGTGGAAGGGGGCACTCGGCTAGCTTAC  
 CAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTCTCCCCAAAC  
 AATACCTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCTGCCCTGGTGAGG  
 AACCTGTGAGTGAATGGAAGTGATATCATTATGCCCATCATATATTATGGACCTTATGGA  
 CTTCAAGTGAATTCTGATAAAGGGCTAAAAAGTAGGGGAAGTGTTTACTGTTGACCTTGGAGAG  
 GCCATCCTATTTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACTCCTGGATTAGGAGG  
 ACTGACAATACTACATATATCATTAAGCATGGGCCCTCGCTTAGAAGTTGCATCTGAGAAAGTA  
 GCCCAGAAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAACCGGCAGGCAAGATGAA  
 ACTCATTTACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTGACAGAAAGGAAAATCA  
 TTGTCACCTTTAGCAAGTATAACTGGAATATCACTATTTTTGATTATATCCATGTGTCTTCTC  
 TTCTATGGAAAAAATATCAACCCTACAAAGTTATAAAACAGAAACTAGAAGGCAGGCCAGAA  
 ACAGAATACAGGAAAGCTCAAAACATTTTCAGGCCATGAAGATGCTCTGGATGACTTCGGAATA  
 TATGAATTTGTTGCTTTTCCAGATGTTTCTGGTGTTCAGGATTCCAAGCAGGTCTGTTCCA  
 GCCTCTGATTGTGTATCGGGGCAAGATTTGCACAGTACAGTGTATGAAGTTATTCAGCACATC  
 CCTGCCCAGCAGCAAGACCATCCAGAGTGA**ACTTT**CATGGGCTAAACAGTACATTTCAGTGAA  
 ATTCTGAAGAAACATTTTAAGGAAAAACAGTGGAAAAAGTATATTAATCTGGAATCAGTGAAGA  
 AACCAGGACCAACACCTCTTACTCATTATTCCTTTACATGCAGAATAGAGGCATTTATGCAAA  
 TTGAACTGCAGGTTTTTTCAGCATATACACAATGTCTTGTGCAACAGAAAAACATGTTGGGGAA  
 ATATTCCTCAGTGGAGAGTCGTTCTCATGCTGACGGGGGAGAACGAAAGTGACAGGGGTTTCCT  
 CATAAGTTTTGTATGAAATATCTCTACAAACCTCAATTAGTTCTACTCTACACTTTCACATATC  
 ATCAACACTGAGACTATCCTGTCTCACCTACAAATGTGGAACTTTACATTGTTTCGATTTTTTC  
 AGCAGACTTTGTTTTATTAAATTTTTATTAGTGTTAAGAATGCTAAATTTATGTTTCAATTTT  
 ATTTCCAAATTTCTATCTTGTATTTGTACAACAAAGTAATAAGGATGGTTGTCACAAAAACA  
 AAATATGCCTTCTCTTTTTTTCAATCACCAGTAGTATTTTTGAGAAGACTTGTGAACACTT  
 AAGGAAATGACTATTAAAGTCTTATTTTTATTTTTTTCAAGGAAAGATGGATTCAAATAAATT  
 ATTCTGTTTTTGCTTTTTAAAAAAAAAAAAAA

## **FIGURE 378**

MWLKVFTTFLSFATGACSGLKVTVPSTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPHTMPKYLLGSVNKS  
VVPDLEYQHKFTMPPNASLLINPLQFPDEGNYIVKVNIQNGTLSASQKIQVTVDDPVTKPVVQIHPPSGAVEY  
VGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFSPQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPII  
YYGPYGLQVNSDKGLKVGEVFTVDLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMD  
YVCCAYNNITGRQDETHFTVIITSVGLEKLAQKGKSLSPASITGISLFLIISMCLLFLWKKYQPYKVIKQKLEG  
RPETEYRKAQTFSGHEDALDDFGIYEFVAFPPDVSGVSRIPSRSPASDCVSGQDLHSTVYEVIQHIIPAQQQDHPE

**Important features:**

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 341-359

**N-glycosylation site.**

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208, 276-280, 308-312

**Casein kinase II phosphorylation site.**

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

**Tyrosine kinase phosphorylation site.**

amino acids 272-280

**N-myristoylation site.**

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237, 239-245

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18



**FIGURE 379**

ATAGTAGAAGAATGTCTCTGAAATTACTGGATGAGTTTCAGTCATACTTTTCACATGGGCACAA  
TTTCACATTCAAGCTCCTTATCCTAGGCTAATTTTATATTATGTTAAATCACTTGTTTTTGT  
CTCACGGCTTCCTGCCTGCTATAGGCATAATTACGAGGAAGCAGAACTTCTCCAGAAGCAAGC  
GCACATGCGTTCCAAAATAAGAGCAAATTCGCTCTAAACACAGGAAAAGACCTGAAGCTTTAA  
TTAAGGGGTTACATCCAACCCAGAGCGCTTTTGTGGGCACTGATTGCTCCAGCTTCTGCGTC  
ACTGCGCGAGGGAAGAGGGAAGAGGATCCAGGCGTTAGACATGTATAGACACAAAAACAGCTG  
GAGATTGGGCTTAAAATACCCACCAAGCTCCAAAGAAGAGACCCCAAGTCCCCAAAAACATTGAT  
TTCAGGGCTGCCAGGAAGGAAGAGCAGCAGCAGGGTGGGAGAGAAGCTCCAGTCAGCCCACAA  
GATGCCATTGTCCCCCGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCT  
GCCCCTGAGGGTGGCCCCACCGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAATAAG  
GAAAAGCAGCCTCCTGACTTTCCTCGCTTGGTGGTTTGAGTGGACCTCCAGGCCAGTGCCGG  
GCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGGCGCACCCCCCAGCA  
ATCCGCGCGCCGGGACAGAATGCCCTGCAGGAACCTTCTTCTGGAAGACCTTCTCCTCCTGCAA  
ATAG

**FIGURE 380**

MYRHKNSWRLGLKYPPSSKEETQVPKTLISGLPGRKSSSRVGEKLQSAHKMPLSPGLLLLLLS  
GATATAALPLEGGPTGRDSEHMQEAAAGIRKSSLLTFLAWWFEWTSQASAGPLIGEEAREVARR  
QEGAPPQQSARRDRMPCRNFFWKTFSSCK

**Important features:**

**Transmembrane domain:**

amino acids 51-69

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 35-39, 92-96

**N-myristoylation sites.**

amino acids 64-70, 75-81, 90-96

**Amidation site.**

amino acids 33-37

# **FIGURE 381**

GGCGCCGGTGCACCGGGCGGGCTGAGCGCCTCCTGCGGCCCGGCCTGCGCGCCCCGGCCCCGCC  
GCGCCGCCACGCCCCAACCCCGGCCCGCGCCCCCTAGCCCCCGCCCGGGCCCCGCGCCCCGCGC  
CCGCGCCAGGTGAGCGCTCCGCCCGCGCGAGGCCCGCCCCCGCCCCCGCCCCCGCCCCGCC  
CGGCCGGCGGGGAACCGGGCGGATTCTCGCGCGTCAAACCACCTGATCCCATAAAAACATTC  
ATCCTCCCGCGGCCCGCGCTGCGAGCGCCCCGCCAGTCCGCGCCCGCGCCCGCTCGCCCTG  
TGCGCCCTGCGCGCCCTGCGCACCCGCGGCCCGAGCCAGCCAGAGCCGGCGGAGCGGAGCG  
CGCCGAGCCTCGTCCCGCGGCCCGGGCCGGGGCCGGGCCGTAGCGCGGCGCCTGGATGCGGAC  
CCGGCCCGGGGAGACGGGCGCCCGCCCCGAAACGACTTTCAGTCCCCGACGCGCCCCGCCCA  
ACCCCTACGATGAAGAGGGCGTCCGCTGGAGGGAGCCGGCTGCTGGCATGGGTGCTGTGGCTG  
CAGGCCTGGCAGGTGGCAGCCCCATGCCAGGTGCTGCGTATGCTACAATGAGCCCCAAGGTG  
ACGACAAGCTGCCCCCAGCAGGGCCTGCAGGCTGTGCCCGTGGGCATCCCTGCTGCCAGCCAG  
CGCATCTTCTGACAGGCAACCGCATCTCGCATGTGCCAGCTGCCAGCTTCCGTGCTGCGC  
AACCTCACCATCCTGTGGCTGCACTCGAATGTGCTGGCCCGAATTGATGCGGCTGCTTCACT  
GGCCTGGCCCTCCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCCGGTCTGTGGACCCT  
GCCACATTCCACGGCCTGGGCGGCCTACACACGCTGCACCTGGACCGCTGCGGCCTGCAGGAG  
CTGGGCCCCGGGGCTGTTCCGCGGCCTGGCTGCCCTGCAGTACCTCTACCTGCAGGACAACGCG  
CTGCAGGCACTGCCTGATGACACCTTCCGCGACCTGGGCAACCTCACACACCTCTTCTGCAC  
GGCAACCGCATCTCCAGCGTGCCCGAGCGCGCCTTCCGTGGGCTGCACAGCCTCGACCGTCTC  
TACTGCAACAGAACCGCGTGGCCCATGTGCACCCGCATGCCTTCCGTGACCTTGGCCGCCTC  
ATGACACTCTATCTGTTTGGCAACAATCTATCAGCGCTGCCCACTGAGGCCCTGGCCCCCCTG  
CGTGCCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTGTGTGACTGCCGGGCACGCCCA  
CTCTGGGCTGGCTGCAGAAGTTCCGCGGCTCCTCCTCCGAGGTGCCCTGCAGCCTCCCGCAA  
CGCCTGGCTGGCCGTGACCTCAAACGCCTAGCTGCCAATGACCTGCAGGGCTGCGCTGTGGCC  
ACCGGCCCTTACCATCCCATCTGGACCGGCAGGGCCACCGATGAGGAGCCGCTGGGGCTTCCC  
AAGTGCTGCCAGCCAGATGCCGCTGACAAGGCCTCAGTACTGGAGCCTGGAAGACCAGCTTCG  
GCAGGCAATGCGCTGAAGGGACGCGTGCCGCCCGGTGACAGCCCGCCGGGCAACGGCTCTGGC  
CCACGGCACATCAATGACTCACCTTTGGGACTCTGCCCTGGCTCTGCTGAGCCCCCGCTCACT  
GCAGTGCGGCCCCGAGGGCTCCGAGCCACCAGGGTTCCCCACCTCGGGCCCTCGCCGGAGGCCA  
GGCTGTTACGCAAGAACCGCACCCGCAGCCACTGCCGTCTGGGCCAGGCAGGCAGCGGGGT  
GGCGGGACTGGTGACTCAGAAGGCTCAGGTGCCCTACCCAGCCTCACCTGCAGCCTCACCCCC  
CTGGGCCTGGCGCTGGTGCTGTGGACAGTGCTTGGGCCCTGCTGACCCCCAGCGGACACAAGA  
GCGTGCTCAGCAGCCAGGTGTGTGTACATACGGGGTCTCTCTCCACGCCGCCAAGCCAGCCGG  
GCGGCCGACCCGTGGGGCAGGCCAGGCCAGGTCTCCCTGATGGACGCTGCCGCCCGCCACC  
CCCATCTCCACCCCATCATGTTTACAGGGTTCCGCGGCAGCGTTTGTTCAGAACGCCGCTC  
CCACCCAGATCGCGGTATATAGAGATATGCATTTTATTTTACTTGTGTAAAAATATCGGACGA  
CGTGGAATAAAGAGCTCTTTTCTTAAAAAA

**FIGURE 382**

MKRASAGGSRLLAWLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRIF  
LHG NRISHVPAASFRA CRNL TILWLHSNVLARIDAAFTGLALLEQLDLSDNAQLRSVDPATF  
HGLGRLHTLHLDRCLQE LGGPGLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLHG NR  
ISSVPERAFRGLHSLDRLLLHQNRVAHVHPHA FRDLGRLMTLYLFANNLSALPTEALAPLRAL  
QYLRLNDNPWVCD CRARPLWAWLQKFRGSSSEVP CSLPQRLAGRDLKRLAANDLQGCAVATGP  
YHPIWTGRATDEEPLGLPKCCQPDAA DKASVLEPGRPASAGNALKGRVPPGDSPPGNGSGPRH  
INDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQAGSGGGGT  
GDSEGS GALPSLTCSLTPLGLALVLWTVLGPC

**Important features:**

**Signal peptide:**

amino acids 1-26

**Leucine zipper pattern.**

amino acids 135-156

**Glycosaminoglycan attachment site.**

amino acids 436-439

**N-glycosylation site.**

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

**VWFC domain**

amino acids 411-425

# **FIGURE 383**

TTCGTGACCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCTTCTAAGAAGGGGAGTCCTGAACTTGTCTG  
 AAGCCCTTGTCGTAAGCCTTGAACACGTTCTTAAATCTATGAAGTCGAGGGACCTTTTCGCTGCTTTTGTAGGG  
 ACTTCTTTCCCTTGCTTCAGCAACATGAGGCTTTTCTTGTGGAACGCGGTCTTGACTCTGTTTCGTCACTTCTTTGA  
 TTGGGGCTTTGATCCCTGAACCAGAAGTGAAAATTGAAGTTCTCCAGAAGCCATTCACTGCCATCGCAAGACCA  
 AAGGAGGGGATTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTTATTTCACTCCACTCACA  
 AACATAACAATGGTCAGCCCATTGTTGTTTACCCTGGGCATCCTGGAGGCTCTCAAAGGTTGGGACCAGGGCTTGA  
 AAGGAATGTGTGTAGGAGAGAAGAGAAAGCTCATCATTCCTCCTGCTCTGGGCTATGGAAGAAGGAAAAGGTA  
 AAATTCCCCCAGAAAGTACACTGATATTTAATATTGATCTCCTGGAGATTGGAATGGACCAAGATCCCATGAAT  
 CATTCCAAGAAATGGATCTTAATGATGACTGGAACTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGT  
 TTGAAAACATGGTGCCTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTGTATAAGAAGATG  
 AAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTATAGAGATACATCTACCCCTT  
 TTAATATAGCACTCATCTTTCAAGAGAGGGCAGTCATCTTTAAAGAACATTTTATTTTTATACAATGTTCTTTCT  
 TGCTTTGTTTATTTTATATATTTTTCTGACTCCTATTTTAAAGAACCCTTAGGTTTCTAAGTACCCATTT  
 CTTTCTGATAAGTTATTTGGGAAGAAAAGCTAATTGGTCTTTGAATAGAAGACTTCTGGACAATTTTCACTTTC  
 ACAGATATGAAGCTTTGTTTTACTTTCTCACTTATAAATTTAAATGTTGCAACTGGGAATATACCACGACATGA  
 GACCAGGTTATAGCACAAATTAGCACCCCTATATTTCTGCTTCCCTCTATTTTCTCCAAGTTAGAGGTCAACATTT  
 GAAAAGCCTTTTGCAATAGCCCAAGGCTTGCTATTTTTCATGTTATAATGAAATAGTTTATGTGTAAGTGGCTCTG  
 AGTCTCTGCTTGAGGACCAGAGGAAAATGGTTGTTGGACCTGACTTGTTAATGGCTACTGCTTTACTAAGGAGAT  
 GTGCAATGCTGAAGTTAGAAAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGA  
 GGCTGAGGCGGGCGGATCACCTGAGGTTGGGAGTTCGAGACCAGCCTGACCAACACGGAGAAACCCTATCTCTAC  
 TAAAAATACAAAGTAGCCCGGCGTGGTGATGCGTGCTGTAATCCAGCTACCCAGGAAGGCTGAGGCGGCAGAA  
 TCACTTGAACCCGAGGCGGAGGTTGCGGTAAGCCGAGATCACCTNCAGCCTGGACACTCTGTCTCGAAAAAAGAA  
 AAGAACACGGTTAATACCATATNAATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGCTTGG  
 CTCTAGTGATTGGTGGCCTATTATGATAAATAGGACAAATCATTTATGTGTGAGTTTCTTTGTAATAAAATGTA  
 TCAATATGTTATAGATGAGGTAGAAAGTTATATTTATATTCAATATTTACTTCTTAAGGCTAGCGGAATATCCTT  
 CCTGGTTCTTTAATGGGTAGTCTATAGTATATTATACTACAATAACATTGTATCATAGATAAAGTAGTAAACCA  
 GTCTACATTTTCCCATTTCTGTCTCATCAAAAACCTGAAGTTAGCTGGGTGTGGTGGCTCATGCCTGTAATCCCAG  
 CACTTTGGGGGCCAAGGAGGGTGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAACCT  
 TGTCTCTACTAAAAATACAAAAATTAGCCAGGCGTGGTGGTGACACCTGTAGTCCCAGCTACTCGGGAGGCTGA  
 GACAGGAGATTTGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAGATTGTGCCACTGCACTCCAGCCTGGG  
 TGACAGAGCAAGACTCCATCTCAAAAAAAAAAAAAAGAAGCAGACCTACAGCAGCTACTATTGAATAAATACCTA  
 TCCTGGATTTT

**FIGURE 384**

MRLFLWNAVLTFLFVTSLIGALIPPEVKIEVLQKPFICHRKTKGGDLMLVHYEGYLEKDGS  
SLFHSTHKHNNNGQPIWFTLGILEALKGWDQGLKGMCVGEKRKLIIPPALGYGKEGKGI  
PPESTLI  
FNIDLLEIRNGPRSHESFQEMDLNDDWKLSKDEVKAYLKKEFEKKGAVVNESHHDAL  
VEDIFD  
KEDEDKDGFI  
SAREFTYKHDEL

**Important features:**

**Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 176-179

**Casein kinase II phosphorylation site.**

amino acids 143-146, 156-159, 178-181 and 200-203

**Endoplasmic reticulum targeting sequence.**

amino acids 208-211

**FKBP-type peptidyl-prolyl cis-trans isomerase**

amino acids 78-114 and 118-131

**EF-hand calcium-binding domain.**

amino acids 191-203, 184-203 and 140-159

**S-100/ICaBP type calcium binding domain**

amino acids 183-203

# **FIGURE 385**

CTCCACGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCCGTATGGGGTTGCCTGCTGCTC  
 CCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGTCC  
 CTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGTGGG  
 ATCCTCTTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGAAGGCCAGGAGACAATGAAG  
 GGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCTGTGGAACCTC  
 ACCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAGTCTTTA  
 CTGATCTCTCTGTTCGTCTTTCCAGGACCCTGCTGTCTCTCCCTCCCCCTTCTCCACCTTCCAG  
 CCTCTGGCTACAACACGCCTGCAGCCCAAGGCAAAAGCTCAGCAAACCCAGCCCCCAGGATTG  
 ACTTCTCCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGGGCTGAGGCC  
 CCTCCATTGCCAGGGAATTTCCAGTACGGGCACGAAAGGACTTCTCAGTACACAGGAACCTCT  
 CCTCACCAGCGACCTCTCCTCCTGCAGGGAGCTCCCGCCCCCATGCAGCTGGACTCCACC  
 TCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGGGTGTCCATCCCG  
 ATGGTCCGCATACTGGCCCCAGTCTTGGTGTGCTGAGCCTTCTGTGAGCCGAGGCCTGATC  
 GCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCACGGAGACACAGAGG  
 AACGAGAAGTTCTGGCTCTCACGCTTGACTGCGGAGGAAAAGGAAGCCCTTCCCAGGCCCT  
 GAGGGGGACGTGATCTCGATGCCTCCCCTCCACACATCTGAGGAGGAGCTGGGCTTCTCGAAG  
 TTTGTCTCAGCGTAGGGCAGGAGGCCCTCCTGGCCAGGCCAGCAGTGAAGCAGTATGGCTGGC  
 TGGATCAGCACCGATTCCCGAAAGCTTTCCACCTCAGCCTCAGAGTCCAGCTGCCCGGACTCC  
 AGGGCTCTCCCCACCCTCCCAGGCTCTCCTCTTGATGTTCCAGCCTGACCTAGAAGCGTTT  
 GTCAGCCCTGGAGCCAGAGCGGTGGCCTTGCTCTTCCGGCTGGAGACTGGGACATCCCTGAT  
 AGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCTCAGCAGGGCCAGACAAGGCTCAG  
 TGGATCTGGTCTGAGTTTCAATCTGCCAGGAACTCCTGGGCCTCATGCCAGTGTGCGACCCCT  
 GCCTTCTCCCACTCCAGACCCACCTTGCTCTTCCCTCCCTGGCGTCCCTCAGACTTAGTCCCA  
 CGGTCTCCTGCATCAGCTGGTGATGAAGAGGAGCATGCTGGGGTGAGACTGGGATTCTGGCTT  
 CTCTTTGAACCACCTGCATCCAGCCCTTCAGGAAGCCTGTGAAAAACGTGATTCTTGCCCCCA  
 CCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAGGACTCTGAATTTCTAACATGCCAGT  
 GACTGTGCACTTGAGTTTGAGGGCCAGTGGGCCTGATGAACGCTCACACCCCTTCAGCTTAG  
 AGTCTGCATTTGGGCTGTGACGTCTCCACCTGCCCAATAGATCTGCTCTGTCTGCGACACCA  
 GATCCACGTGGGGACTCCCCTGAGGCCTGCTAAGTCCAGGCCTTGGTCAGGTGAGTGCACAT  
 TGCAGGATAAGCCCAGGACCGGCACAGAAGTGGTTGCCTTTNCCATTTGCCCTCCCTGGNCCA  
 TGCCTTCTTGCTTTGGAAAAATGATGAAGAAAACCTTGGCTCCTTCTTGTCTGGAAAGGG  
 TTACTTGCCTATGGGTTCTGGTGGCTAGAGAGAAAAGTAGAAAACAGAGTGCACGTAGGTGT  
 CTAACACAGAGGAGAGTAGGAACAGGGCGGATACCTGAAGGTGACTCCGAGTCCAGCCCCCTG  
 GAGAAGGGGTGCGGGGTGGTGGTAAAGTAGCACAACTACTATTTTTTTTCTTTTTCCATTATT  
 ATTGTTTTTTAAGACAGAATCTCGTGCTGCTGCCAGGCTGGAGTGCAGTGGCAGATCTGCA  
 AACTCCGCCTCTGGGTTCAAGTGATTCTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAG  
 GCACGCACCACCACACCTGGCTAATTTTTGTACTTTTAGTAGAGATGGGGTTTACCATGTTG  
 GCCAGGCTGGTCTTGAACCTCCTGACCTCAAATGAGCCTCCTGCTTCACTCTCCCAAATTGCCG  
 GGATTACAGGCATGAGCCACTGTGTCTGGCCCTATTTCTTTTAAAAAGTGAATTAAGAGTTG  
 TTCAGTATGCAAACTTGGAAGATGGAGGAGAAAAAGAAAAGGAAGAAAAAATGTCACCCA  
 TAGTCTCACCAGAGACTATCATTATTTTCTGTTTTGTGTACTTCTTCCACTCTTTTCTTCTTC  
 ACATAATTTGCCGGTGTCTTTTTACAGAGCAATTATCTTGTATATACAACCTTTGTATCCTGC  
 CTTTTCCACCTTATCGTTCATCACTTTATTCCAGCACTTCTCTGTGTTTTACAGACCTTTTT  
 ATAAATAAAATGTTTCATCAGCTGCATAAAAAAAAAAAAAA

**FIGURE 386**

MRLLVLLWGCLLLPGYEALGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCSG  
TIYAEEEGQETMKGRVSIRDSRQELSLIVTLWNLTLDAGEYWCGVEKRGPDSELLISLFVFP  
GPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPGTSQ  
YGHERTSQYTGTSPHPATSPFAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIPMVRILAPV  
LVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLSRLTAEKEAPSQAPEGDVISM  
PLHTSEEEELGFSKFVSA

**Important features:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 248-269

**N-glycosylation site.**

amino acids 96-99

**Fibrinogen beta and gamma chains C-terminal domain.**

amino acids 104-113

**Ig like V-type domain:**

amino acids 13-128



# **FIGURE 387**

GCGCCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGCGGGGCCGGCTCCCGCCCGGCACATG  
GCTGCAGCCACCTCGCGCGCACCCCGAGGCGCCGCGCCAGCTCGCCCGAGGTCCGTCCGAGG  
CGCCCGGGCCCGCCCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCTCCGGGGATCGGG  
**ATGT**CCCTCCTCCTTCTCCTCTTGCTAGTTTCTACTATGTTGGAACCTTGGGGACTCACACT  
GAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTTGCCCTGCCACCATCAACTGGGGCTTCCA  
GAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGGAACCAAAAAGTGGTG  
ATCACTTACTCCAGTCGTCATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCGAGTGGCC  
TTTGCTTCCAATTTCCTGGCAGGAGATGCCTCCTTGAGATTGAACCTCTGAAGCCCAGTGAT  
GAGGGCCGGTACACCTGTAAGGTAAAGAATTACGGGCGCTACGTGTGGAGCCATGTCATCTTA  
AAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGACAGAAGGAAGT  
GACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTGTGTATTACTGGCAGCGA  
ATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCTCCCAAATCTAGGATTGACTACAACCAC  
CCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCTTACTCTGGACTGTACCAGTGCACAGCA  
GGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAACGTGACAGTATGTACAAAGCATC  
GGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTGATTTTCTCTTGGTG  
TGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGAGAGACCTAATGAAATT  
CGAGAAGATGCTGAAGCTCCAAAGCCCGTCTTGTGAAACCCAGCTCCTCTTCTCAGGCTCT  
CGGAGCTCACGCTCTGGTTCTTCTCCACTCGCTCCACAGCAAATAGTGCCTCACGCAGCCAG  
CGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCACCCAGGCATACAGCCTAGTG  
GGGCCAGAGGTGAGAGTTCTGAACCAAAGAAAGTCCACCATGCTAATCTGACCAAAGCAGAA  
ACCACACCCAGCATGATCCCCAGCCAGAGCAGAGCCTTCCAAACGGTCT**TGA**ATTACAATGGAC  
TTGACTCCCACGCTTTCTTAGGAGTCAGGGTCTTTGGACTCTTCTCGTCAATTGGAGCTCAAGT  
CACCAGCCACACAACCAGATGAGAGGTCACTAAGTAGCAGTGAGCATTGCACGGAACAGATT  
CAGATGAGCATTTTCTTTATACAAATACCAAACAAGCAAAAGGATGTAAGCTGATTCACTGTGA  
AAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGGAAAGCAGGAGTCCAAATCTATTTGT  
TGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTGAGGTGAATATACCTAAAACTTTTAAT  
GTGGGATATTTGTATCAGTGCCTTTGATTACAAATTTTCAAGAGGAAATGGGATGCTGTTTGT  
AAATTTTCTATGCATTTCTGCAAACTTATTGGATTATTAGTTATTTCAGACAGTCAAGCAGAAC  
CCACAGCCTTATTACACCTGTCTACACCATGTACTGAGCTAACCACTTCTAAGAACTCCAAA  
AAAGGAAACATGTGTCTTCTATTCTGACTTAACTTCATTTGTCATAAGGTTTGGATATTAATT  
TCAAGGGGAGTTGAAATAGTGGGAGATGGAGAAGAGTGAATGAGTTTCTCCCACTCTATACTA  
ATCTCACTATTTGTATTGAGCCCAAATAACTATGAAAGGAGACAAAATTTGTGACAAAGGA  
TTGTGAAGAGCTTTCCATCTTCATGATGTTATGAGGATTGTTGACAAACATTAGAAATATATA  
ATGGAGCAATTGTGGATTTCCCCTCAAATCAGATGCCTCTAAGGACTTTCTCTGCTAGATATTT  
CTGGAAGGAGAAAATACAACATGTCATTTATCAACGTCCTTAGAAAGAATTCTTCTAGAGAAA  
AAGGGATCTAGGAATGCTGAAAGATTACCCAACATACCATTATAGTCTCTTCTTCTGAGAAA  
ATGTGAAACCAGAATTGCAAGACTGGGTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTA  
ATATGTCAAGGAAGGTAGCCGGGCATGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAG  
GTTGCAGTGAGCCGAGATTATGCCATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

**FIGURE 388**

MSLLLLLLLLVSYYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV  
ITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHVIL  
KVLVRPSKPKCELEGELETEGSDLTLCESSSGTEPIVYYWQRIREKEGEDERLPPKSRIDYNH  
PGRVLLQNLTMSYSGLYQCTAGNEAGKESCVRVTQYVQSIGMVAGAVTGIVAGALLIFLLV  
WLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANSASRSQ  
RTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFTV

**Important freatures:**

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 232-251

**FIGURE 389**

GCGGCACCTGGAAGATGCGCCCATTTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTCG  
CCTCCTTTGTGTGCCTGGTATTTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCTGT  
CCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCCTCAAAGCTCCAGTCCCCA  
AAAGGCAAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTACTCA  
GCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGGAGAAC  
AGCTGGGAAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAAGTGGGAATGTGA  
CAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAGTTTATTC  
AGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCACAAAGACTGA  
ATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACATGAAATTCA  
GGTCTAGCTGGGTATTTATTGCAGCAAAAGGCTTGGAACCTCCCTTCCGAAATTCAGAGAGAAA  
AGATCAACCACTCTGATGCTAAGAACAACAGATATTCTGGCTGGCCTGCAGAGATCCAGATAG  
AAGGCTGCATACCCAAAGAACGAAGCTTGACACTGCAGGGTCCTGAGTAAATGTGTTCTGTATA  
AACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTTCTAAATCCAACAGCCCATATTTGAT  
GAGTATTTTTGGGTTTGTGTAAACCAATGAACATTTGCTAGTTGTATCAAATCTTGGTACGCA  
GTATTTTTATACCAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGAACTAAAATGAATGG  
AAATTCCTTAAAAAAAAA

**FIGURE 390**

MRPLAGGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERFVLKAPVPKRQKC  
DHWTFCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTATRC  
FDMYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDKNAIEALGSKEIRNMKFRSSWV  
FIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPKERS

**Important features:**

**Signal sequence.**

amino acids 1-20

**N-glycosylation sites.**

amino acids 120-124, 208-212

**Glycosaminoglycan attachment site.**

amino acids 80-84

**N-myristoylation sites.**

amino acids 81-87, 108-114, 119-125

# **FIGURE 391**

GGGGGCTTTCTTGGGCTTGGCTGCTTGAACACCTGCCTCCAAGGACCGGCCTCGGAGGGGTGCGCGGGAAGGG  
AGGGAAGAAGGAAGGGCGGGGCGGGCCCCCTGCGCCCCGCGCCCTCTGCGCGCCCCCTGTCCGCCCCGGGCC  
AGCCAGCCAGCCCCGCGGGCGGGTACACGCGCAGCCAGCCGCGCCCTCCGCGCCCAAGCGCGCCGCTGTG  
CTGTGCCCTGCGCCCTTGCCCCGCGCCAGCTTCTGCGCCCGCAGCCCGCCCGGCGCCCCCGGTGACCGTGACCT  
GCCTGGGCGCGGGGCGGAGCAGGCATGTCGCCCGGGGACCGCTACCCAGCGCTGGCCCTGGTGCTCCTGGC  
AGTGACCTTGGCCGGGTGCGAGCCAGGGCGCAGCCCTCGAGGACCTGATTATTACGGGCAGGAGATCTGGAG  
CCGGGAGCCCTACTACGCGCGCCCGGAGCCGAGCTCGAGACCTTCTCTCCGCGCTGCCTGCGGGGCGGGGA  
GGAGTGGGAGCGGCGCCCGCAGGAGCCAGGCCGCCAAGAGGGCCACCAAGCCCAAGAAAGCTCCCAAGAGGGA  
GAAGTCGGCTCCGAGCCGCTCCACCAGTAAACACAGCAACAAAAAGTTATGAGAACCAAGAGCTCTGAGAA  
GGCTGCCAACGATGATCACAGTGTCCGTGTGGCCCGTGAAGATGTGAGAGAGTGGCCACCTCTTGGTCTGGA  
AACCTTAAAAATCACAGACTTCCAGCTCCATGCTTCCACGGTGAAGCGCTATGGCCTGGGGGCACATCGAGGGAG  
ACTCAACATCCAGGCGGGCATTAAATGAAAATGATTTTTATGACGGAGCGTGGTGCGCGGGAAGAAATGACCTCCA  
GCAGTGGATTGAAGTGGATGCTCGGCGCCTGACCAGATTCACTGGTGTCTCACTCAAGGGAGGAACCTCCCTCTG  
GCTGAGTGAAGTGGTGGATCCTATAAGGTGATGGTGAGCAATGACAGCCACAGTGGGTCACTGTTAAGAAATGG  
ATCTGGAGACATGATATTTGAGGGAAACAGTGAAGAGAGATCCCTGTTCTCAATGAGCTACCCGTCCTCATGGT  
GGCCCGCTACATCCGCATAAACCTCAGTCTGGTGTGATAATGGGAGCATCTGCATGAGAATGGAGATCCTGGG  
CTGCCACTGCGAGATCCTAATAATTATTATACCGCCGGAACGAGATGACCACCACTGATGACCTGGATTTTAA  
GCACCACAATTATAAGGAAATGCGCCAGTTGATGAAAGTTGTGAATGAAATGTGTCCCAATATCACCAGAATTTA  
CAACATTGGAAGAAATGAGGCGCTGAGCTGTATGCTGTGAGATCTCAGATCACCTGGGGAGCATGAAGT  
CGGTGAGCCCGAGTTCCACTACATCGCGGGGGCCACGGCAATGAGGTGCTGGGCGGGAGCTGCTGCTGCTGCT  
GGTGAGTTCGTGTGTCAGGAGTACTTGGCCCGGAATGCGCGCATCGTCCACCTGGTGAGGAGACGCGGATTCA  
CGTCTCCCTCCCTCAACCCCGATGGCTACGAGAAGGCCCTACGAAGGGGCTCGGAGCTGGGAGGCTGGTCCCT  
GGGACGCTGGACCCACGATGGAATTGACATCAACAACACTTTCCTGATTTAAACACGCTGCTCTGGGAGGCGAGA  
GGATCGACAGAATGTCCCAGGAAAGTTCCTCAATCACTATATTGCAATCCCTGAGTGGTTCCTGTGCGAAAATGC  
CACGGTGGCTGCCAGACCAGAGCAGTATAGCCTGGATGGAAGAAATCCCTTTTGTGCTGGGCGGCAACCTGCA  
GGGCGGCGAGCTGGTGGTGGCGTATCCCTACGACCTGGTGCGGTCCCCCTGGAAGACGCGAGGAACACACCCCCAC  
CCCCGATGACCACGTGTTCCGCTGGCTGGCTACTCCTATGCTCCACACACCGCTCATGACAGAGCCCGGAG  
GAGGTGTGCGCACACGGAGGACTTCCAGAAGGAGGGGCACTGTCAATGGGGCTCCTGGCACACCGTCTGCTGG  
AAGTCTGAACGATTTTCACTACCTTCATACAACTGCTTCGAACGTGTCATCTACGTGGGCTGTGATAAATACCC  
ACATGAGAGCCAGCTGCCCGAGGAGTGGGAGAATAACCGGGAATCTCTGATCGTGTTCATGGAGCAGGTTTATCG  
TGGCATTAAAGGCTTGGTGAGAGATTACATGGAAGGAATCCCAAACGCCATTATCTCCGTAGAAGGCATTAA  
CCATGACATCCGAACAGCCAACGATGGGGATTACTGGCGCTCCTGAACCTTGAGAGTATGTGGTTCACAGCAAA  
GGCCGAAGGTTTCACTGCATCCACCAAGAACTGTATGGTGGCTATGACATGGGGGCCACAAGGTGTGACTTCAC  
ACTTAGCAAAACCAACATGGCCAGGATCCGAGAGATCATGGAGAAGTTGGGAAGCAGCCCGTCAGCTGCCAGC  
CAGGCGGCTGAAGCTGCGGGGCGGAAGAGACGACGCTGGGTGACCCCTCCTGGGCGCTTGAGACTCGTCTGGG  
ACCCATGCAAATTAACCAACCTGGTAGTAGCTCCATAGTGGACTCACTCACTGTTTCTCTCTGTAATTCAG  
AAGTGCTGGAAGAGAGGGTGCATTGTGAGGCAGGTCCCAAAGGGAAGGCTGGAGGCTGAGGCTGTTTTCTTTT  
CTTTGTTCCCATTTATCCAAATAACTTGGACAGAGCAGCAGAGAAAAGCTGATGGGAGTGAGAGAACTCAGCAAG  
CCAACTGGGAATCAGAGAGAGAAGGAGAAGGAGGGGAGCCTGTCCGTTTCAAGAGCTCTGGCTGCATAGAAAAG  
ATTCTGGTGTCTCCCTGTTTGGCTGGCAGCAAGGGTTCACAGTGCATTTGCAATTTGCACAGCTAAAATTGCAG  
CATTTCCCCAGCTGGGCTGTCCCAAATGTTACCATTTGAGATGCTCCAGGCGTCTTAAGAGAATCCACCTCTC  
TGGCCCTGGGACATTGCAAGCTGCTACAAATAAATTCTGTGTTCTTTTGACAAATAGCGTCATTGCCAAGTGCACA  
TCAGTGAGCCTCTTGAATCTGTTTAGTCTCTTTTCAACAAGGAGTGTGTTTCAAGAAAGGAGAGAGAGGCTGA  
GATCATTCAAGAGTTTGTGGGAGCAAGCATGGAGCTTCTGCAACAATTCTGGGTCCATAAAACACCCCCAAA  
GTCCCTGCTGATCCAGTAGCCCTGGAGGTTCCCCAGGTAGGGAGAGCCAGAGGTGCCAGCCTTCTTGAAGGGCCA  
GAAAATTTAGCCTGGATCTCTCTTTTACCTGCTAGGACTGGAAGAGCCAGAAGTGGGTGGCCTGAAGCCCTC  
TCTCTGCTTGAGGTATTGCCCTGTGTGGAATTGAGTGTCTATGGGTTGGCCTCATATCAGCCTGGGAGTTATTT  
TTGATATGTAGAATGCCAGATCTTCCAGATTAGGCTAAATGTAATGAAAACCTCTTAGGATTATCTGTGGAGCAT  
CAGTTTGGGAAGAATTATTGAATTATCTTGCAAGAAAAAGTATGTCTCACTTTTTGTAAATGTTGCTGCCTCAT  
TGACCTGGGAAAAATGAAAAAATAAAGCAAATGGTAAGACCTTAAAAAATAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAA

**FIGURE 392**

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPYYPARPEPELETFSPPPLPA  
GPGEWEERRPQEP RPPK RATKPKKAPKREKSAPEPPPPGKHSNKKVMRTKSSEKAANDDHSVR  
VAREDVRESCPPLGLETLKITDFQLHASTVKRYGLGAHRGRLNIQAGINENDFYDGAWCAGR  
DLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSTWVTVKNGSGDMIFEGNS  
EKEIPVLNELPVPVMVARYIRINPQSWFDNGSICMRMEILGCPLPDPNNYYHRRNEMTTTDDL  
FKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEFHYIAGA  
HGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLP SLNPDGYEKAYEGGSELGGWS  
LGRWTHDGIDINNNFIDLNTLLWEAEDRQNVPRKVPNHYIAIPEWFLSENATVAAETRAVIAW  
MEKIPFVLGGNLQGGELVVAYPYDLVRSPWKTQEHTPTPDDHVFRWLAYSYASTHRLMTDARR  
RVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHESQLPEEWENNR  
ESLIVFMEQVHRGIKGLVRDSHGKGIPNAIISVEGINHDIRTANDGDYWRLLNPGEYVVTAKA  
EGFTASTKNCMVGYDMGATRCDFTL SKTNMARIREIMEKFGKQPVSLPARRLKLGRKRRQRC

**FIGURE 393**

GTCCACATCCTGCTCAACTGGGTCAAGTCCCTCTTAGACAGAGCTCTTGTCCATCATTTGCTGAAGTGGACCAAC  
TAGTTCCCCAGTAGAGGGGTTCTCCCTGGCAATTCTTGATCGGCGTTTGGACATCTCAGATCGCTTCCAATGAAGA  
TGGCCTTGCCTTGGGGTCTGCTTGTTCATAATCATCTAACATATGGGACAAGGTTGTGCCGGCAGCTCTGGGGG  
AAGGAGCACGGGGCTGATCAAGCCATCCAGGAAACATCGGAGGACTTGTCCAGCCTTGAAGAACTCTAGTGGTT  
TCTGAATCTAGCCCACTTGGCGGTGAAGCAATGATGCAACTTCTGCAACTTCTGCTGGGGCTTTTGGGGCCAGGTGG  
CTACTTATTTCTTTTAGGGGATGTGACGAGGTGACCACTCTCACGGTGAATACCAAGTGTTCAGAGGAAGTGCC  
ATCTGGTACAGTGTATCGGGAAGCTGTCCAGGAACCTGGGCCGGGAGGAGAGGCGGAGGCAAGCTGGGGCCGCTT  
CCAGGTGTTGCAGCTGCCTCAGGCGCTCCCCATTAGGTGGACTCTGAGGAAGGTTGCTCAGCACAGGCAGGCG  
GCTGGATCGAGAGCAGCTGTGCCGACAGTGGGATCCCTGCCTGTTTCTTTTGATGTGCTTGGCACAGGGGATT  
GGCTCTGATCCATGTGGAGATCCAAGTGTGACATCAATGACACCAAGCCAGCTTTCCCAAGGCGAGGAGGA  
GTACGAAATCTCAGAGCGCTCTGTGCGAACCCGGATCCCCCTGGACAGAGCTTTGACCCAGACACAGGCC  
TAACCCCTGCACACTTACTCTGTCTCCAGTGAGCACTTTGCCTTGGATGTCTATTGTGGGCCCTGATGAGAC  
CAACATGCAGAACTCATAGTGGTGAAGGAGCTGGACAGGGAAATCCATTCATTTTTGTATCTGGTGTAACTGC  
CTATGACAATGGGAACCCCCCAAGTCAGGTACCACTTGGTCAAGGTCAACGCTTGTGGACTCCAATGACAATAG  
CCCTGCGGTTTGTGAGAGTCTGAGACTTCACTGGCACTGGAATCCAGAAGATGCTGCATCTGGTACGTTTCTATAAACT  
GACCGCCATCAGACCTGATGACCAAGGCCCAATGGGGAGGTGGAGTTCTTCTCAGTAAGCATGCTTCCAGAGGT  
GCTGGACACCTTCAGTATTGATGCCAAGACAGGCCAGGTCACTTCTGCGTCGACCTTAGACTATGAAAGAACCC  
TGCTTACGAGGTGGATGTTTCAAGCAAGGACCTGGGTCCCAATCCTATCCAGCCCATGCAAGTTCTCATCAA  
GGTCTCGATGTCAATGACAACATCCCAAGCATCCAGCTCACGTACATGGGCTTCCAGCCCATCACTGGTGTCAAGA  
TCTTTCCCAAGGACAGTTTATTGCTCTTGTCTGTCGAGATGACTTGGATTGAGGACAATGGTTTGTGCTCACTG  
CTGCTTGAGCCCAAGCTGGGCCACTTCAGGCTGAAAAGAACTAATGGCAACACATACATGTTGCTAACCAATGC  
CACACTGGACAGAGAGCAGTGGCCCAATATACCTCACTCTGTTAGCCCAAGACCAGGACTCCAGCCCTTATC  
AGCCAGAAACAGCTCAGCATTCAGATCAGTGACATCAACGACAATGCACCTGTGTTTGAGAAAGCAGGTATGA  
AGTCTCCACGCGGGAAAAACAATTACCTCTCTTCACTTACCTTACCTCAAGGCTCATGATGACAGCTTGGGCAT  
TAATGGAAGTCTCATACCGCATCCAGACTCCCGAGTTGCTCACTTAGTACTGTTGACTCCAACACAGGAGA  
GGTCAAGTCTCAGAGGCTCACTGAACTATGAAGAGATGGCCGGCTTTGAGTTCAGGTGATCGCAGAGGACAGCGG  
GCAACCCATGCTTGCATCCAGTGTCTCTGTGTGGGTGAGCCTCTTGGATGCCAATGATAATGCCCGAGAGGTGGT  
CCAGCCTGTGCTCAGCGATGGAAGGCCAGCCTCTCCGTGCTTGTGATGCTTCCAGGCCACTGCTGCTGTC  
CATCGAGACTCCCAATGGCTTGGGGCCAGCGGGCACTGACACACTTCACTTGGCCACTCAGAGCTCCCGGCTT  
CCTTTTGACAACCATTTGTGGCAAGAGATCGAGACTCGGGGGCAAATGGAGAGCCCTCTACAGCATCCGCAATGG  
AAATGAAGCCACCTCTTCATCTCAACCTCATACGGGGCAGCTGTTCTGTCAATGTACCAATGCCAGCAGCCT  
CATTGGGAGTGAGTGGGAGCTGGAGATAGTAGTAGAGGACAGGGAAGCCCCCTTACAGACCCGAGCCCTGTT  
GAGGCTCATGTTTGTCAACAGTGTGAGACCACTGAGGAGCTCAGCCCGAACGCTTGGGCCCTTGAGACTGTGAT  
GCTGACGGTGATCTGCCTGGCTGACTGTTGGGCATCTTCGGTGTGCTTCTGCTTGTGTCATGTCCATCTGCCG  
GACCAAAAGAGAGCAACAGGGCCTACAACCTGTGCGGAGGCGGAGTCCACCTACCGCCAGCAGCCCAAGAGGCC  
CCAGAAACACATTCAGAAGGCAGACATCCACCTCGTGCTGTGCTCAGGGGTGAGGAGGTGAGCCTTGTGAAGT  
CGGGCAGTCCCAAAAGATGTGGACAAGGAGCGATGATGGAAGCAGGCTGGGACCCCTGCTGAGGCCCTT  
CCACCTCACCCCGACCTGTACAGGACGCTGCTAATCAAGGCAACAGGAGGACCCGCGAGAGCCGAGGAGGT  
GCTGCAAGACACGCTCAACCTCCTTTTCAACCATCCAGGCAGAGGAATGCCTCCCGGGAGAACCTGAACCTTCC  
CGAGCCCAGCCTGCCACAGGCCAGCCACGTTCCAGGCCCTTGAAGGTTGCAGGCAGCCCAAGGGAGGCTGG  
TGGAGACCAGGCGAGTGAGGAAGCCCCACAGAGGCCACAGCCTCTCTGCAACCTTGAGACGGCAGCGACATCT  
CAATGGCAAGGTGTCCCTGAGAAAGAATCAGGGCCCGTGCATCTCGGAGCCTGGTCCGGCTGTCTGTGCT  
TGCCTTGCCTGCGGAGCGGAACCCGTGGAGGAGTCACTGTGATTCTCCTCTGTTTTCAGCAAACTCTCCAGCTGCT  
GCTCTTGTGCTCATCAGGGCCAAATTCAGCCCAAACCAAACACCCAGGAAATAAGTACTTGGCCAAGCCAGGAGG  
CAGCAGGAGTGCAATCCAGACACAGATGGCCCAAGTGAAGGCTGGAGGCGACAGACCCAGAACAGGAGGA  
AGGGCCTTTGGATCTGAAAGAGGACCTCTCTGTGAAGCAACTGCTAGAAGAGAGCTGTCAAGTCTGTCTGACCC  
CAGCACAGGTCTGGCCCTTGACCGGCTGAGCGGCCCTGACCCGGCCTGGATGGCGAGACTCTCTTGGCCCCC  
CAACCAACTACCGTGACATGTGATCTCCCCGAGTCTGCAGCCAGGAGGAGCCAGGAGCTTCCAGACGTTCCG  
CAAGGCAGAGGCCACAGAGCTGAGCCCAACAGGCACGAGGCTGGCCAGCACCTTTGTCTCGGAGATGAGCTCACT  
GCTGGAGATGCTGCTGGAACAGCGCTCCAGCATGCCCGTGGAGGCCGCTCCGAGGCGCTGCGGCGGCTCTCGGT  
CTGCGGAGGAGCCCTCAGTTTACACTTGGCCACAGTGCAGCCTCAGGCATGAAAGTGCAGGGGACCCAGGTG  
AAAGACGGGGAGTAGGGGCAAGAGCAGAGGCAGCAGCAGCAGGTCAGTGCCTGAGCAATACCTCAGACGCT  
CTGGATCCAAGAACCGGGCCTGAGATCTGTGACCAAGAGCTGGTTTCTAAAATCTTGAACCTACTAGCTAG  
CGGCGGCTTGAGAACTTTAGGGTGACTGATGCTACCCCCACAGAGGAGGCAAGAGCCCGAGCTAACAGCTGAC  
TGACCAAAAGCAGCCCTTGTAAAGCAGCTCTGAGTCTTTTGGAGGACAGGGACGTTTGTGCTGAGATAAGTGT  
TCCTGGCAAAACATATGTGGAGCAAAAGGTCAGTCTCTTGGCAGAACAGATGCCACGGAGTATCACAGGCAGG  
AAAGGCTGGCCTTCTTGGGTAGCAGGAGTCAGGGGCTTACCCTGGGGGTGCCAGGAAATGCTCTCTGACCTAT  
CAATAAAGGAAAAGCAGTAAAAAATAAAAAAAAAA

**FIGURE 394**

MMQLLQLLLGLLGPGGYLFLLGDCQEVTTLTVKYQVSEEVPSGTVIGKLSQELGREERRRQAG  
AAFQVLQLPQALPIQVDSEEGLLSTGRRLDREQLCRQWDPCLVSFDVLATGDLALIHVEIQVL  
DINDHQPRFPKGEQELEISESASLRTRIPLDRALDPDTGPNTLHTYTLSPSEHFALDVIVGPD  
ETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSDNSPFAESSLALE  
IQEDAAPGTLLIKLTATDPDQGPNGEVEFFLSKHPPEVLDTFSIDAKTGQVILRRPLDYEKN  
PAYEVDVQARDLGPNPIPAHCKVLIKVLVDVNDNIPSIHVTWASQPSLVSEALPKDSFIALVMA  
DDLD SGHNLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLLAQDQGLQPLS  
AKKQLSIQISDINDNAPVFEKSRYEVSTRENNLPSLHLITIKAHADALGINGKVSYRIQDSPV  
AHLVAIDSNTGEVTAQRSLN YEEMAGFEFQVIAEDSGQPMLASSVS VWVSLLDANDNAPEVVQ  
PVLSDGKASLSVLVNA STGHLLVPIETPNGLGPAGTDT PPLATHSSRPFLLT TIVARDADSGA  
NGEPLYSIRNGNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEI VVEDQGSPPLOTRALLRV  
MFVTSVDHLRDSARKPGALSMSMLTVICLAVLLGIFGLILALFMSICRTEKKDNRAYNCREAE  
STYRQQPKRPQKH I QKADIHLVPVLRGQAGEPCEVGQSHKDVDKEAMMEAGWDPCLOAPFHLT  
PTLYRTLNRNQGNGAPAESREVLQDTVNLLFNHPRQRNASRENLN LPEPQPATGQPRSRPLKV  
AGSPTGRLAGDQGS EEPQRPPASSATLRRQRHLNGKVSPEKESGPRQILRSLVRLSVAFAE  
RNPVEELTVDSPPVQQISQLLSLLHQGFQPKPNHRGNKYLAKPGGSRSAIPD TDGPSARAGG  
QTDPEQE EGPLDPEEDLSVKQLLEEELSSLLDPSTGLALDRLSAPDPAWMARLSLPLTTNYRD  
NVISPDAAATEEPRTFQTFTGKAEAPELSPTGTRLASTFVSEMSSLLEMLLEQRSSMPVEAASE  
ALRRLSVCGRTLSLDLATS AASGMKVQGD PGGKTGTEGKSRGSSSSSRCL

**Important features:**

**Signal peptide:**

amino acids 1-13

**Transmembrane domain:**

amino acids 719-739

**N-glycosylation site.**

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

**Cadherins extracellular repeated domain signature.**

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563



**FIGURE 395**

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCCCAGTTAAAAGG  
CTCCAGAATCGTGTACCAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAATC  
AGTAGGTGACCCCGCCCTGGATTCTGGAAGACCTCACCATGGGACGCCCCGACCTCGTGCG  
GCCAAGACGTGGATGTTCTTGCTGGGGGGAGCCTGGGCAGGACACTCCAGGGCACAG  
GAGGACAAGGTGCTGGGGGGTCATGAGTGCCAACCCCATTCGCAGCCTTGGCAGGCGGCCTTG  
TTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGTAAGTGGCAACTGGGTCTTACAGCT  
GCCCCAGAGCAAGAAATACCTGTGGTTCAGTCCATCCACACCCCTGCTACAACAGCAGCGAT  
GTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCCCTGGGGTCC  
AAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCCAGAAGTGCACCGTCTCA  
GGCTGGGGCACTGTCACCAGTCCCCGAGAGAATTTTCTGACACTCTCAACTGTGCAGAAGTA  
AAAATCTTTCCCCAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACAGATGGCATGGTC  
TGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCCAGGGCGATTCTGGAGGCCCCCTGGTGTGT  
GATGGTGACTCCAGGGCATCACATCCTGGGGCTCAGACCCCTGTGGGAGGTCCGACAAACCT  
GGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATCATAGGCAGCAAGGGC  
TGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACTCTCTGGTTC

**FIGURE 396**

MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVLV  
GGNWVLTAAHCKKPKYTVRLGDHSLQNKDGPEQEIPVVQSI PHPCYNSSDVEDHNHDLMLLQL  
RDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCEDAYP  
GQITDGMVCAGSSKGADTCQGDSGGPLVCDGALQGITSWGSDPCGRSDKPGVYTNICRYLDWI  
KKIIGSKG

**Important Features:**

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 51-71

**N-glycosylation site.**

amino acids 110-113

**Serine proteases, trypsin family, histidine active site.**

amino acids 69-74 and 207-217

**Tyrosine kinase phosphorylation site.**

amino acids 182-188

**Kringle domain proteins motif**

amino acids 205-217

**FIGURE 397**

GGCGGCTGCTGAGCTGCCTTGAGGTGCAGTGTTGGGGATCCAGAGCCATGTCGGACCTGCTAC  
TACTGGGCCTGATTGGGGGCCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGGGT  
ACTCAGGGCTACTGGCTGGGGTGGAAGTGAGTGCTGGGTCACCCCCATCCGCAACGTCACTG  
TGGCCTACAAGTTCCACATGGGGCTCTATGGTGAGACTGGGCGGCTTTTCACTGAGAGCTGCA  
GCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCCCCCTG  
ATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCCCTGAGC  
TCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGCCATGTGG  
TGACAGCCACCTTCCCCTACACCACCATTCTGTCCATCTGGCTGGCTACCCGCCGTGTCCATC  
CTGCCTTGGACACCTACATCAAGGAGCGGAAGCTGTGTGCCTATCCTCGGCTGGAGATCTACC  
AGGAAGACCAGATCCATTTTCAATGTGCCCCACTGGCACGGCAGGGAGACTTCTATGTGCCTGAGA  
TGAAGGAGACAGAGTGGAATGGCGGGGGCTTGTGGAGGCCATTGACACCCAGGTGGATGGCA  
CAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGGAAGTGAGCCCTGGCAGCCGGG  
AGACTTCAGCTGCCACACTGTCACTGGGGCGAGCAGCCGTGGCTGGGATGACGGTGACACCC  
GCAGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGAGGAGCTGGACTTGG  
AGGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGACCCTGGGACTGAGCCCCTGGGGACTACCA  
AGTGGCTCTGGGAGCCCACTGCCCCCTGAGAAGGGCAAGGAGTAACCCATGGCCTGCACCCCTCC  
TGCAGTGCAGTTGCTGAGGAACTGAGCAGACTCTCCAGCAGACTCTCCAGCCCTCTTCTCCT  
TCCTCTGGGGGAGGAGGGGTTCTGAGGGACCTGACTTCCCCTGCTCCAGGCCTCTTGCTAAG  
CCTTCTCCTCACTGCCCTTTAGGCTCCCAGGGCCAGAGGAGCCAGGGACTATTTTCTGCACCA  
GCCCCCAGGGCTGCCGCCCCTGTTGTGTCTTTTTTTCAGACTCACAGTGGAGCTTCCAGGACC  
CAGAATAAAGCCAATGATTTACTTGTTCACCTGGAAAAAAAAAAAAAAAAAAAA

**FIGURE 398**

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGLYGETGRL  
FTESCSISPKLRSIAVYYDNPHMVPPDKCRCAVGSILSEGEESPSPELIDLYQKFGFKVFSFP  
APSHVVTATFPYTTILSIWLATRRVHPALDTYIKERKLCAYPRLEIYQEDQIHFMCPARQGD  
FYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETSAAATLSPGASSRGW  
DDGDTRSEHSYSESGASGSSFEELDLEGEGLGESRLDPGTEPLGTTKWLWEPTAPEKGKE



**FIGURE 400**

MSNSVPLLCFWSLCYCFAAGSPVPFGPEGRLEDKLHKPKATQTEVKPSVRFNLRRTSKDPEHEG  
CYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHKLVSALHTREKDANVVVVDWLPL  
AHQLYTDAVNNTRVVGHSIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGTVGRI  
TGLDPAGPMFEGADIAHKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDFQPGC  
GLNDVLGSIAYGTITEVVKCEHERAVHLFVDSL VNQDKPSFAFQCTDSNRFKKGICLSCKNR  
CNSIGYNAKKMRNKRNSKMYLKTRAGMPFRGNLQSLECP

**Important features:**

**Signal peptide:**

amino acids 1-16

**Lipases, serine active site.**

amino acids 163-172

**N-glycosylation sites.**

amino acids 80-83 and 136-139

**FIGURE 401**

CTTCCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCTG  
CCTCCCTGCCTCTGGCCATGGCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGGACCTTCCTGT  
CAGTTTCCCAGACAGTCCTGGCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGGCTC  
AACTCTCCTGCACGCTCAGCCCCAGCACGTCAACATCAGGGACTACGGTGTGTCTTGGTACC  
AGCAGCGGGCAGGCAGTGCCCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCACCACC  
GGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCCACAATGCCTGTGTCC  
TCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGCTACGGCT  
TTAGTCCCTAGGGGTGGGGTGTGAGATGGGTGCCTCCCCCTCTGCCTCCCATTTCTGCCCCCTGA  
CCTTGGGTCCCTTTTAAACTTTCTCTGAGCCTTGCTTCCCCCTCTGTAAAATGGGTTAATAATA  
TTCAACATGTCAACAAC

**FIGURE 402**

MACRCLSFLMGTFLSVSQTVLAQLDALLVFPQVAQLSCTLSPQHVTIRDYGVSWYQQRAGS  
APRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVPEDDADYYCSVGYGFSF



# **FIGURE 403**

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGCGGTGCAGCAGCTCCAGAAAGCAGCGAGTTG  
GCAGAGCAGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGCTGGCTCACAACAAGATGCTCAAGGTGTCAGC  
CGTACTGTGTGTGTGTGCAGCCGCTTGGTGAGTCAGTCTCTCGCAGCTGCCGCGGCGGTGGCTGCAGCCGGGG  
GCGGTGCGACGGCGGTAATTTCTGGATGATAACAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGG  
ACAGTGGAAACAAATTCGAGACGAAGTAGAGGATGATTATTTCCGCACCTTGGAGTCCAGGAAAACCTTCGATCA  
GGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTATGCATTGCTCAAGATTC  
TCAGACTGCAGTCTGCATTAGTCACCGGAGGCTTACACACAGGATGAAAGAAGCAGGAGTAGACCATAGGCAGTG  
GAGGGGTCCCATATTATCCACCTGCAAGCAGTGCCAGTGGTCTATCCAGCCCTGTTTGTGGTTTCAGATGGTCA  
TACCTACTCTTTTCAGTGCAAACTAGAATATCAGGCATGTGTCTTAGGAAAACAGATCTCAGTCAAATGTGAAGG  
ACATTGCCCATGTCTTCAGATAAGCCACCAGTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCTGGAGTT  
CAGGGAAGTGGCAACAGATTGCGGGACTGGTTCAAGGCCCTTCATGAAAGTGAAGTCAAAACAAGAAGACAAA  
AACATTGCTGAGGCCCTGAGAGAAGCAGATTGATACAGCATCTTGCCAATTGCAAGGACTCACTTGGCTGGAT  
GTTTAACAGACTTGATACAACTATGACCTGCTATTGGACCAGTCAGAGCTCAGAAGCATTTACCTTGATAAGAA  
TGAACAGTGTACCAAGGCATTCTTCAATTCTTGTGACACATACAAGGACAGTTTAATATCTAATAATGAGTGGTG  
CTACTGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTGAGAAGCGGCAAGGGGTAAA  
GAAGCTCCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGCCAACACAATGTCATGGCAGTGT  
TGGACAGTGTGGTGTGTTGACAGATATGGAAATGAAGTCATGGGATCCAGAATAAATGGTGTTCAGATTGTGC  
TATAGATTTTGAGATCTCCGAGATTTTGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGA  
CGATATTATGAATGATGAAGATGAAATTGAAGATGATGATGAAGATGAAGGGATGATGATGATGGTGGTGATGA  
CCATGATGTATACATTGATTGATGACAGTTGAAATCAATAAATCTACATTTCTAATATTTACAAAAATGATAG  
CCTATTTAAAATTATCTTCTTCCCCAATAACAAAATGATTCTAAACCTCACATATATTTGTATAATTATTTGAA  
AAATTGCAGCTAAAGTTATAGAATTTATGTTTAAATAAGAATCATTGCTTTGAGTTTTTATATTCTTACACA  
AAAAGAAAATACATATGCAGTCTAGTCAGACAAAATAAAGTTTGAAGTGCTACTATAATAAATTTTTACAGAG  
ACAAACTTTGTAAATCTTCCATAAGCAAAATGACAGCTAGTGCTTGGGATCGTACATGTTAATTTTTTGAAAGAT  
AATTCTAAGTGAATTTAAATAAATAAATTTTAAATGACCTGGGTCTTAAGGATTTAGGAAAAATATGCATGCT  
TTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAGGATAACAGAGAGATACCATGACTCCA  
AAAAAAAAAAAAA

**FIGURE 404**

MLKVSAVLCVCAAAWCSQSLAAAAVAAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFRD  
EVEDDYFRTWSPGKPFQALDPAKDPCLKMKCSRHKVCIAQDSQTAVCISHRRLTHRMKEAGV  
DHRQWRGPILSTCKQCPVVYPSPVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCPGPSDK  
PTSTSRNVKRACSDLEFREVANRLRDWFKALHESGSQNKKTKTLRPERSRFDTSILPICKDS  
LGWMFNRLDTNYDLLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNNEWCYCFQRQQDP  
PCQTELSNIQKRQGVKLLGQYIPLCDEDGYYKPTQCHGSVGQCWCVDRYGNEVMGSRINGVA  
DCAIDFEISGDFASGDFHEWTDDEDEDDIMNDEDEIEDDEDEGDDDDGGDDHDVYI

**Important features:**

**Signal peptide:**

amino acids 1-16

**Leucine zipper pattern.**

amino acids 246-267

**N-myristoylation sites.**

amino acids 357-362, 371-376 and 376-381

**Thyroglobulin type-1 repeat proteins**

amino acids 353-365 and 339-352

**FIGURE 405**

[illegible]

## **FIGURE 406**

MTPQSLLQTTLFLLSLLFLVQGAHGRGHREDFRFCSQRNQTHRSSLHYKPTPDLRISIENSEE  
ALTVHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRDFLSDKASSLLCFQHQE  
ESLAQGPPLLATSVTSWSPQNISLPSAASFTHSFHSPHTAAHNASVDMCELKRDQLLSQF  
LKHPQKASRRPSAAPASQQQLQSLESKLTSVRFMGDMVSFEEDRINATVWKLQPTAGLQDLHIH  
SRQEEEQSEIMEYSVLLPRTLQRTKGRSGEAEKRLLLVDFFSSQALFQDKNSSQVLGEKVLGI  
VVQNTKVANLTEPVVLTFFQHQLQPKNVTLQCVFVVEDPTLSSPGHWSSAGCETVRRETQTSCF  
CNHLTYFAVLMVSSVEVDAVHKHYLSLLSYVGCVVVSALACLVTIAAYLCSRVPPLPCRKRPRDY  
TIKVHMLLLAVFLLDTSFLLSEPVALTGSEAGCRASAIPLHFSLLTCLSWMGLEGYNLYRLV  
VEVFGTYVPGYLLKLSAMGWGFPIFLVTLVALVDVDNYGPIILAVHRTPEGVIYPSMCWIRDS  
LVSYITNLGLFSLVFLFNMAMLATMVVQILRLRPHTQKWSHVLTLGLSLVLGLPWALIFFSF  
ASGTFQLVVLVLFISIITSFQGFILFIWYWSMRLQARGGPSPLKSNSDSARLPISSGSTSSSRI

**Important features:**

**Signal peptide:**

amino acids 1-25

**Putative transmembrane domains:**

amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590  
and 634-657

**Microbodies C-terminal targeting signal.**

amino acids 691-693

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 198-201 and 370-373

**N-glycosylation sites.**

amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327  
and 341-344

**G-protein coupled receptors family 2 proteins**

amino acids 475-504

**FIGURE 407**

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGAG  
CCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTCGC  
TCTGTTGCCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCTGGA  
CTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAAGCCC  
TGTTTTCTTCTCCTTCTGTGAGTGGACCACGGAGGCTGGTGAGCTGCCTGTTCATCCCAAAGCTC  
AGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCCGGCATAGAAGCCAGGAGCAGGGC  
TCTCAGAAGGCGGTGGTGCCAGCTGGGATCATGTTGTTGGCCCTGGTCTGTCTGCTCAGCTG  
CCTGCTACCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACTGGCCAGAGTGCTACATGA  
CTTCGGGGCTGGACGGATAACGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGCTTATTTTAC  
AAGCGGTTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACAACGGGATCTT  
CCAGATCAACAGCCGGAGGTGGTGCAGCAACCTCACCCGAACGTCCCCAACGTGTGCCGGAT  
GTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGCCATGAAGATAAC  
CCAAGAGCCTCAGGGTCTGGGTTACTGGGAGGCCTGGAGGCATCACTGCCAGGGAAAAGACCT  
CACTGAATGGGTGGATGGCTGTGACTTCTAGGATGGACGGAACCATGCACAGCAGGCTGGGAA  
ATGTGGTTTGTTTCCTGACCTAGGCTTGGGAAGACAAGCCAGCGAATAAAGGATGGTTGAACG  
TGAAA

**FIGURE 408**

MLLALVCLLSCLLPSSSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALDY  
EADGSTNNGIFQINSRRWCSNLTPNVPNVCRMYCSDLLNPNLKDTVICAMKITQEPQGLGYWE  
AWRHHCQGKDLTEWVDGCDF

**Important features:**

**Signal peptide:**

amino acids 1-18

**N-myristoylation site.**

amino acids 67-72

**Homologous region to Alpha-lactalbumin / lysozyme C proteins.**

amino acids 34-58 (catalytic domain), 111-132 and 66-107

**FIGURE 409**

CAGACTCCAGATTTCCTGTCAACCACGAGGAGTCCAGAGAGGAAACGCGAGCGGAGACAACAGTACCTGACGC  
 CTCTTTTCAGCCCGGATCGCCCGAGCAGGGATGGGCGACAAGATCTGGCTGCCCTTCCCGTGCTCCTTCTGGCC  
 GCTCTGCCCTCCGGTGTCTGCTGCTGGGGCGGGGCTTACACCTTCCCTCGATAGCGACTTACCTTTACCCCTT  
 CCCGCCGGCCAGAAGGAGTGCCTTCTACCAGCCCATGCCCTGAAGGCCTCGCTGGAGATCGAGTACCAAGTTTTA  
 GATGGAGCAGGATTAGATATTGATTTCCATCTTGCCTCTCCAGAAGGCAAAACCTTAGTTTTTGAACAAAGAAAA  
 TCAGATGGAGTTACACTGTAGAGACTGAAGTTGGTGATTACATGTTCTGCTTTGACAATACATTAGCACCATT  
 TCTGAGAAGGTGATTTTCTTTGAATTAATCTGGATAATATGGGAGAACAGGCACAAGAACAAGATTGGAAG  
 AAATATATTACTGGCAGATATATTGGATATGAACTGGAAGACATCTGGAATCCATCAACAGCATCAAGTCC  
 AGACTAAGCAAAAGTGGGCACATACAAATCTGCTTAGAGCATTTGAAGCTCGTGATCGAAACATACAAGAAAGC  
 AACTTTGATAGAGTCAATTTCTGGTCTATGGTTAAATTTAGTGGTCTATGGTGGTGTGAGCCATTCAAGTTTAT  
 ATGCTGAAGAGTCTGTTTGAAGATAAGAGGAAAAGTAGAACTTAAACTCCAAACTAGAGTACGTAACATTGAAA  
 AATGAGGCATAAAATGCAATAAACTGTTACAGTCAAGACCATTAAATGGTCTTCTCCAAATATTTTGAGATATA  
 AAAGTAGGAAACAGGTATAATTTAATGTGAAAATTAAGTCTTCACTTTCTGTGCAAGTAATCTGCTGATCCAG  
 TTGTACTTAAGTGTGTAACAGGAATATTTGCAAGATATAGGTTAACTGAATGAAGCCATATTAATACTGAT  
 TTTCTTAACCTTTGAAAATTTTGCAATGTCTTAGTGATTTAAATAAATGAGTATTGGGCTTAATTGCAACACC  
 AGTCTGTTTTTAAACAGGTTCTATTACCCAGAACTTTTTTGTAATGCGGCAGTTACAAATTAAGTGTGAAGTTT  
 TCAGTTTTAAGTTATAAATCACCTGAGAATTACCTAATGATGGATTGAATAAATCTTTAGACTACAAAAGCCCAA  
 CTTTTCTCTATTTACATATGCATCTCTCTATAATGTAAATAGAATAATAGCTTTGAAATACAATTAGGTTTTTG  
 AGATTTTATAACCAATACATTTCAAGTGAACATATTAGCAGAAAGCATTAGTCTTTGTACTTTGCTTACATT  
 CCAAAAGCTGACATTTTACGATTCTTAAACACAAAGTTACACTTACTAAAATTAGGACATGTTTTCTCTTTG  
 AAATGAAGAATATAGTTTAAAGCTTCTCTCCATAGGGACACATTTTCTTAACCTTAACTAAAGTGTAGGA  
 TTTTAAATTAATAGTGAAGTAAATAAGTTTATTTTAAATAGTATCTGTCAAGTTAATATCTGTCAACAGTTAA  
 TAATCATGTTATGTTAATTTAATCATGATTGCTGACTTGGATAATTCAATTATACCCAGCAGTTATGAAGGAAATA  
 TTGCTAAAATGATCTGGGCTTACCATAAATAAATATCTCTTTTCTGAGCTCTAAGAATTATCAGAAAACAGGAA  
 AGAATTTAGAAAACCTTGAAGAACTAATCCAAATAAATTTCACTTAAAGTAGAATATAAATAAATATCTAGA  
 ATCTGACTGGCTCATCATGACATCTACTCATAACATAAATCAAAGGAGATGATTAATTTCCAGTTAGCTGGAAG  
 AAACCTTTGGCTGTAGGTTTTATTTTCTACAAGAATTCTGGTTTGAATTATTTTGTGAAGCAGGTACATTTTATA  
 AAATGTAAGCCCTACTGTAAAGTTTAGCACTGGGTGTACATATTTATTAAAAATTTTATTATAACAACCTTTTAT  
 TAAATGGCCTTTCTGAACACTTTATTTATGATGTTGAAGTAAAGATTAGAAAACATAGACTCCCAAGTTTAAAA  
 CACCTAAATGTGAATAACCCATATATACAACAAAGTTTCTGCCATCTAGCTTTTGAAGTCTATGGGGGTCTTAC  
 TCAAGTACTAGTAATTTAACTTTCATCATGAATGAACATAAATTTTAAAGTTATGCCCATTTATAACGTTGTTTAT  
 GACTACATTTGTGAGTTAGAAAACAACTTAAAAATTTGGGGTATAGAACCCCTCAACAGGTTAGTAATGCTGGAATT  
 CTTGATGAGCAATAATGATAACAGAGAGTGATTTCAATTACACTCATAGTAGTATAAAAAGAGATACATTTCCC  
 TCTTAGGCCCTTGGGAGAAGAGCAGCTTAGATTTCCCTACTGGCAAGGTTTTTAAAAATGAGGTAAATGCCGTAT  
 ATGATCAATTACCTTAATTTGGCCAAGAAAATGCTTCAGGTGTCTAGGGGTATCCTCTGCAACACTTGCAGAACAA  
 AGGTCAATAAGATCCTTGCTATGAATACCCCTCCCTTTTGGCGTGTTAAATTTGCAATGAGAAGCAAAATTTACA  
 GTACCATAACTAATAAAGCAGGGTACAGATATAAACTACTGCATCTTTCTATAAACTGTGATTAAGAATTTCTA  
 CCTCTCCTGTATGGCTGTACTGTACTGTACTCTCTGACTCCTTACCTAACAAATGAATTTGTTACATAATCTTCT  
 ACATGTATGATTTGTGCCACTGATCTTAAACCTATGATTCAAGTAACTTCTTACCATATAAAAACGATAAATGCTT  
 TATTTGGAAAAGAATTTAGGAATACTAAGGACAATTATTTTTATAGACAAAGTAAAAAGACAGATATTTAAGAGG  
 CATAACCAAAAAGCAAACTTGTAAACAGAGTAAAAATCTTTAATATTCTAAAGACATACTGTTTATCTGCTT  
 CATATGCTTTTTTTAATTTCACTATTCCATTTCTAAATTAAGTTATGCTAAATGAGTAAGCTGTTTATCACTT  
 AACAGCTCATTTTGTCTTTTCAATATACAAATTTTAAAAATACTACAATATTAACTAAGGCCCAACCGATTTT  
 CATAATGTAGCAGTTACCGTGTTACCTCACACTAAGGCCTAGAGTTTGCTCTGATATGCATTTGGATGATTAAT  
 GTTATGCTGTTCTTTTATGTGAATGTCAAGACATGGAGGGTGTGTAATTTTATGGTAAAATTAATCCTTCTTA  
 CACATAATGGTGTCTTAAATTTGACAAAAATGAGCACTTACAATTTGTATGTCTCTCAAATGAAGATTTCTTAT  
 GTGAAATTTTAAAGACATTGATTCGCATGTAAGGATTTTTCATCTGAAGTACAATAATGCACAATCAGTGTTG  
 CTCAAACCTGCTTTATACTTATAAACAGCCATCTTAAATAAGCAACGTATTGTGAGTACTGATATGTATATAATAA  
 AAATATCAAAGGAAAA

**FIGURE 410**

MGDKIWLPPFVLLLAALPPVLLPGAAGFTPSLDSDFTFLLPAGQKECFYQPMPLKASLEIEYQ  
VLDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCDNTFSTISEKVIFFELIL  
DNMGEQAQEQEDWKKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDRNIQE  
SNFDRVNFWSMVNLVVMVVVSAIQVYMLKSLFEDKRKSRT

**Important features:**

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 195-217

**N-myristoylation site.**

amino acids 43-48

**Tyrosine kinase phosphorylation site.**

amino acids 55-62



**FIGURE 411**

CCCAGCTGAGGAGCCCTGCTCAAGACACGGTCACTGGATCTGAGAACTTCCCAGGGGACCGCATTCCAGAGTCA  
 GTGACTCTGTGAAGCACCCACATCTACCTCTTGCCACGTTCCCACGGGCTTGGGGGAAAGATGGTGGGGACCAAG  
 GCCTGGGTGTTCTCCTTCTGGTCTGGAAGTCACATCTGTGTTGGGGAGACAGACGATGCTCACCCAGTCAGTA  
 AGAAGAGTCCAGCCTGGGAAGAAGAACCCAGCATCTTTGCCAAGCCTGCCGACACCCTGGAGAGCCCTGGTGAG  
 TGGACAACATGGTTCAACATCGACTACCCAGGCGGGAAAGGGCGACTATGAGCGGCTGGACGCCATTGCTTCTAC  
 TATGGGGACCGTGATGTGCCCCCTCCCCTGCGGCTAGAGGCTCGGACCCTGACTGGACACCTGCGGGCAGCACT  
 GGCCAGGTGGTCCATGTTAGTCCCCGTGAGGGTTTCTGGTGCCCTCAACAGGAGCAGCGGCTGGCCAGAACTGC  
 TCTAATTACACCGTACGCTTCTCTGCCCCACAGGATCCCTGCGCCGAGACACAGAGCGCATCTGGAGCCCATGG  
 TCTCCCTGGAGCAAGTGCTCAGCTGCCCTGTGGTCAGACTGGGGTCCAGACTCGCACACGCATTGCTTGGCAGAG  
 ATGGTGTGCTGTGCACTGAGGCGAGCGAAGAGGGTCAGCACTGCATGGGCGAGGACTGTACAGCCCTGTGACCTG  
 ACCTGCCCAATGGGCGCAGGTGAATGCTGACTGTGATGCCCTGCATGTGCCAGGACTTCATGCTTCATGGGGCTGTC  
 TCCCTTCCCGGAGTGCCCCAGCCCTCAGGGGCTGCTATCTACCTCCTGACCAAGACGCCGAAGCTGCTGACCCAG  
 ACAGACAGTGTATGGGAGATTCCGAATCCCTGGCTTGTGCCCTGATGGCAAAAGCATCCTGAAGATCAAAAGGTC  
 AAGTTTGGCCCCATGTACTCACAATGCCAAGACTAGCCCTGAAGGCAGCCACCCTCAAGGCAGAGTTTGTGAGG  
 GCAGAGACTCCATACATGGTGTGAACCTTGAGACAAAAGCAGCGAGAGCTGGGCGAGGCGTGTCTGTGTCTGT  
 AAGGCCACAGGGAAGCCAGGCCAGACAAGTATTTTGGTATCATAATGACACATTGCTGGATCCTTCCCTCTAC  
 AAGCATGAGAGCAAGCTGGTGCTGAGGAACTGCAGCAGCAGGCTGGGGAGTACTTTTGCAAGGCCAGAGT  
 GATGTGGGGCTGTGAAGTCCAAGTTGCCAGCTGATTGTACAGCATCTGATGAGACTCCTTGCAACCCAGT  
 CCTGAGAGCTATCTTATCCGGCTGCCCCATGATTCTTTTCAAGATGCCACCACTCCTTCTACTATGACGTGGGA  
 CGCTGCCCTGTAAAGACTTGTGACGGGCGAGCAGGATAATGGGATCAGGTGCCGTGATGCTGTGCAGAACTGCTGT  
 GGCATCTCCAAGACAGAGGAAAGGAGATCCAGTGCACTGGCTACACGCTACCCACCAAGGTGGCCAAAGGATGC  
 AGCTTCCAGCGGTGTACGGAACCTCGGAGCATCGTGCGGGGCCGTGTGAGTGTCTGACAAATGGGGAGCCCATG  
 CGCTTTGGCCATGTGTACATGGGGACAGCCGTGTAAGCATGACTGGCTACAAGGGCACTTTACCCCTCCATGTG  
 CCCCAGGACACTGAGAGGCTGGTCTCACATTGTGGAGGCTGCAGAACTTGTCAACACCAACCAAGTGTCTA  
 CCTTTCAACAAGAAGGGGAGTGCCGTGTTCCATGAATCAAGATGCTTCGTGCGAAAGAGCCCATCACTTTGGAA  
 GCCATGGAGACCAACATCATCCCCCTGGGGGAAGTGGTGGTGAAGACCCCATGGCTGAACTGGAGATTCCATCC  
 AGGAGTTTCTACAGGCAGAAATGGGGAGCCCTACATAGGAAAAGTGAAGGCCAGTGTGACCTTCTGGATCCCCGG  
 AATATTTCCACAGCCACAGCTGCCAGACTGACCTGAACTTCATCAATGACGAAGAGAGCACTTTCCCCCTTCGG  
 ACGTATGGCATGTTCTCTGTGACTTTCAGAGATGAGGTCACTCAGAGCCACTTAATGCTGGCAAGTGAAGGTG  
 CACCTTGACTCGACCCAGGTCAGATGCCAGAGCACATATCCACAGTGAAACTCTGGTCACTCAATCCAGACACA  
 GGGCTGTGGGAGGAGGAGGAGTGAATTTCAAAATTTGAAAAATCAAAGGAGGAACAAAAGAGAGACAGAACTTCTGT  
 GTGGGCAACTGGAGATTCTGTGAGAGGAGGCTCTTTAACTGGATGTTCTGAAAGCAGGCGGTGCTTTGTTAAG  
 GTGAGGGCCTACCGAGTGTGAGAGTTCTTGCCCTAGTGAGCAGATCCAGGGGGTGTGATCTCGGTGATTAACTG  
 GAGCCTAGAACTGGCTTCTGTCCAACCCTAGGGCCTGGGGCCGCTTTGACAGTGTCTACACAGGCCCAACGGG  
 GCCTGTGTGCTGCTTCTGTGATGACCACTCCCTGATGCTTACTCTGCTATGCTTGGCAAGCCTGGCTGGG  
 GAGGAATCGAAGCAGTGGAGTCTTCTCCTAAATTAACCCAAATGCAATTGGCGTCCCTCAGCCCTATCTCAAC  
 AAGCTCAACTACCGTCGGACGGACCATGAGGATCCACGGGTAAAGAACAGAGCTTCCAGATTAGCATGGCCAAAG  
 CCAAGGCCCAACTCAGCTGAGGAGAGCAATGGGCCATCTATGCCCTTGAGAACCTCCGGGCATGTGAAGAGGCA  
 CCACCCAGTGCAGCCCACTTCCGGTCTACAGATTGAGGGGGATCGATATGACTACAACACAGTCCCTTCAAC  
 GAAGATGACCCTATGAGCTGGACTGAAGACTATCTGGCATGGTGGCCAAAGCCGATGGAATTCAGGGCCTGCTAT  
 ATCAAGGTGAAGATTGTGGGGCCACTGGAAGTGAATGTGCGATCCCGCAACATGGGGGGCACTCATCGCGGACA  
 GTGGGGAAGCTGTATGGAATCCGAGATGTGAGGAGCACTCGGGACAGGGACAGCCCAATGTCTCAGCTGCCTGT  
 CTGGAGTTCAAGTGCAGTGGGATGCTCTATGATCAGGACCGTGTGGACCGCACCTGTTGAAGGTCACTCCCCAG  
 GGCAGCTGCCGTGAGGCCAGTGTGAACCCCATGCTGCATGAGTACCTGGTCAACCACTTGCCACTTGCAGTCAAC  
 AACGACACCAGTGAATACCATGCTGGCACCCCTGGACCCACTGGGCCACAACATATGGCATCTACACTGTCACT  
 GACCAGGACCTCTGCACGGCCAAGGAGATCGCGCTCGGCCGGTGTCTTGTATGGACATCCGATGGCTCCTCCAGA  
 ATCATGAAGAGCAATGTGGGAGTAGCCCTCACCTTCACTGTGTAGAGAGGCAAGTAGGCCGCGCAGAGTGCCTTC  
 CAGTACCTCCAAGCACCCAGCCAGTCCCTGCTGCAGGCACCTGTCCAAGGAAGAGTGCCTCGAGGAGGCAG  
 CAGCGAGCGAGCAGGGGTGGCCAGCGCCAGGGTGGAGTGGTGGCTCTCTGAGATTTCTAGAGTTGCTCAACAG  
 CCCCTGATCAACTAAGTTTGTGGTACTTCAACCCTTCTGCCCCATTTTCACTGTGACAGCCATTGTGAGACTGA  
 TGCACAAACTGTCACTTGGTTAATTTAAGCACTTCTGTTTCTGTAATTTGCTTGTGTTTCTTTCATGCCTTTA  
 CTTACTTTGTCCCATGCTACTGATTGGCAGTGGCCCCACAATGGCACAATAAAGCCCTTTGTGAAACTGTTT  
 TTTAAATGAAACACAAGAAATTTGGCCACTGGTAAAACTGTCAGCTTCACTGTACTTTATTTAATGCCATTAAT  
 GCAAATATACTTCTCTTCTTTTGTGATGTTTGGCCACCTCTGCAATAGTGATAATCTGATGCTGAAGATCAA  
 ATAACCAATATAAAGCATATTTCTGGCCTTGTCCACAGGACATAGGCAAGCCCTGATCATAGTTTCATACATAT  
 AAATGGTGGTGAATAAAGAAATAAAACACAATACTTTTACTTGAATGTAAATAACTTATTTATTTCTTGTCTA  
 AATTTGGAATTTCTAGTGACATTTCAAAGTTAAGCTATTAAATATAGGGTGATCATAGTTCTCTACCAAGTCTGG  
 AAAGAACATCTCCTGGTATCCACAATTACACAGGTTGCTAACTGTATTTGTACATTTCCCTTGGCATTGCTTT  
 TGTCTTGTGTAAGAACCCAGTGTAGCCAGGGCAGATGTCAATAATGCATACTCTGTATTTGAAAAA

**FIGURE 412**

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPSIFAKPADTLES PGEWTTWFNID  
YPGGKGDYERLDAIRFYYGDRVCARPLRLEARTTDWTPAGSTGQVVHGSPREGFWCLNREQRP  
GQNCSNYTVRFLCPPGSLRRDTERIWSPWSPWSKCSAACGQTGVQTRTRICLAEMVSLCSEAS  
EEGQHCMGQDCTACDLTCPMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAAIYLLTKTPKL  
LTQTDSDGRFRIPGLCPDGKSILKITKVKFAPIVLTM PKTSLKAATIKAEFVRAETPYMVMNP  
ETKARRAGQSVSLCCKATGKPRPDKYFWYHNDTLLDPSLYKHESKLVLRLKQQHQAGEYFCKA  
QSDAGAVKSKVAQLIVTASDETPCNFPVPESYLIRLPHDCFQ NATNSFYDVGRCVPKTCAGQQ  
DNGIRCRDAVQNCCGISKTEEREIQCSGYTLPTKVAKESCQRCTETRSIVRGRVSAADNGEP  
MRFGHVYMGNSRVSM TGYKGTFTLHVPQDTERLVLT FVDRLQKFVNTTKVLPFNKKGS AVFHE  
IKMLRRKEPITLEAMETNIIPLGEVVGEDPMAELEIPSR SFYRQNGEPYIGVKKASVTFLDPR  
NISTATAAQTDLNF INDEGDTFPLRTYGMFSVDFRDEVTSEPLNAGKVKVHLDSTQVKMPEHI  
STVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLFNLDPESRRCFVKV  
RAYRSE RFLPSEQIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGPN GACVPAFCDDQSPDA  
YSAYVLASLAGEELQAVESSPKFNPNAIGVPQPYLNKLN YRRTDHEDPRVKKTAFQISMAKPR  
PNSAEESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDYN TVPFNEDDPMSWTEDYLAWW  
PKPMEFRACYIKVKIVGPLEVNVRSRNMGGTHRRTVGKLYGIRDVRSTRDRDQPNVSAACLEF  
KCSGMLYDQDRVDRTL VKVIPQGS CRRASVNPMLHEYLVNHLPLAVNNDTSEYTMLAPLDPLG  
HNYGIYTVTDQDPRTAKEIALGRCFDGTSDGSSRIMKSNVGVALT FNCVERQVGRQSAFQYLQ  
STPAQSPAAGTVQGRVPSRRQQRASRGQRQGGVVASLRFP RVAQQPLIN

**FIGURE 413**

GCCACGTTGTCTTCTTTCTTCACCAACCAACCCAGGAGCTCAGAGATCTAAGCTGCTTTCCATC  
TTTTCTCCCAGCCCCAGGACACTGACTCTGTACAGGATGGGGCCGTCCTCTTGCCTCCTTCTC  
ATCCTAATCCCCCTTCTCCAGCTGATCAACCCGGGGAGTACTCAGTGTTCCTTAGACTCCGTT  
ATGGATAAGAAGATCAAGGATGTTCTCAACAGTCTAGAGTACAGTCCCTCTCCTATAAGCAAG  
AAGCTCTCGTGTGCTAGTGTCAAAGCCAAGGCAGACCGTCCTCCTGCCCTGCTGGGATGGCT  
GTCAGTGGCTGTGCTTGTGGCTATGGCTGTGGTTCGTGGGATGTTTCAGCTGGAAACCACTGC  
CACTGCCAGTGCAGTGTGGTGGACTGGACCACTGCCCCGCTGCTGCCACCTGACCTGACAGGGA  
GGAGGCTGAGAACTCAGTTTTGTGACCATGACAGTAATGAAACCAGGGTCCCAACCAAGAAAT  
CTAACTCAAACGTCCCACTTCATTTGTTCCATTCTTGATTCTTGGGTAATAAAGACAACTTT  
GTACCTCAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 414**

MGPSSCLLLILIPLLQLINPGSTQCSLDSVMDKKIKDVLNSLEYSPSPISKKLSCASVKS  
QGRPSSCPAGMAVTGCACGYGCGSWDVQLETTCHCQCSVVDWTTARCCHLT

**FIGURE 415**

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCGCGCCCCCGGTGTG  
AGGCGGCCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGGCGGCGGAGGAGGCTGTGAGGA  
GTGTGTGGAACAGGACCCGGGACAGAGGAACCAATGGCTCCGCAGAACCTGAGCACCTTTTGCC  
TGTTGCTGCTATACCTCATCGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTGGGGG  
TGCCTCGAAGTGCCTCTATAAAGGATATTAAAAAGGCTATAGGAACTAGCCCTGCAGCTTC  
ATCCCGACCGGAACCCCTGATGATCCACAAGCCCAGGAGAAATTCAGGATCTGGGTGCTGCTT  
ATGAGGTTCTGTGAGATAGTGAGAAACGGAACAGTACGATACTTATGGTGAAGAAGGATTAA  
AAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTTCACACTTCTTTGGGGATTTTGGTTTCA  
TGTTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCCAAGAGGAAGTGATATTATGTAG  
ATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTTAGAAAACAAAC  
CTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTGTCGGCAAGAGATGCGGACCACCC  
AGCTGGGCCCCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAATGCCCTAATGTCA  
AACTAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTGAGAGACGGCATGG  
AGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGGAGATTTACGGTTCC  
GAATCAAAGTTGTCAAGCACCCAATATTTGAAAGGAGAGGAGATGATTTGTACACAAATGTGA  
CAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACTCACTTGGATGGTCACA  
AGGTACATATTTCCCGGGATAAGATCACCAGGCCAGGAGCGAAGCTATGGAAGAAAGGGGAAG  
GGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAATCACTTTTGATGTGGATT  
TTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAACAGCTACTGAAACAAGGGT  
CAGTGCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTGAATAAAATGGACTTTGTTT  
AAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTTTTTGTGTGTGTTTTTGTTTTTA  
TTTTCAATATGCAAGTTAGGCTTAATTTTTTTTATCTAATGATCATCATGAAATGAATAAGAGG  
GCTTAAGAATTTGTCCATTTGCATTTCGGAAAAGAATGACCAGCAAAAGGTTTACTAATACCTC  
TCCCTTTGGGGATTTAATGTCTGGTGCTGCCGCCTGAGTTTCAAGAATTAAAGCTGCAAGAGG  
ACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGAGTTGTTAGCAATTTTCATTCAAATG  
CCAACCTGGAGAAGTCTGTTTTTAAATACATTTTGTGTATTTTTTTA

## **FIGURE 416**

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYE  
VLSDSEKRKQYDITYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGGTTPRQQDRNIPRGSDIIVDLEVTLEEVYAGNF  
VEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQMTQEVVCECPNVKLVNEERTLEVEIEPGVRDGMETPFPI  
GEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLW  
KKGEGLPNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

**Important features:**

**Signal peptide:**

amino acids 1-22

**Cell attachment sequence.**

amino acids 254-257

**Nt-dnaJ domain signature.**

amino acids 67-87

**Homologous region to Nt-dnaJ domain proteins.**

amino acids 26-58

**N-glycosylation site.**

amino acids 5-9, 261-265

**Tyrosine kinase phosphorylation site.**

amino acids 253-260

**N-myristoylation site.**

amino acids 18-24, 31-37, 93-99, 215-221

**Amidation site.**

amino acids 164-168

**FIGURE 417**

CGGCGGCGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCCCAGCAGGA  
TGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGCCCAGCCCGCCGGGGCAG  
GATGACCAAGGCCCGGCTGTTCCGGCTGTGGCTGGTGCTGGGGTCGGTGTTTCATGATCCTGCT  
GATCATCGTGTA TGGGACAGCGCAGGCGCCGCGCACTTCTACTTGACACGTCTTCTCTAG  
GCCGCACACGGGGCCGCGCTGCCCACGCCCGGGCCGGACAGGGACAGGGAGCTCACGGCCGA  
CTCCGATGTCGACGAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGACCTTCC  
CAGAAAGGAGACGGAGCAGCCGCTGCGCCGGGAGCATGGAGGAGAGCGTGAGAGGCTACGA  
CTGGTCCCCGCGCGACGCCCGGCGCAGCCAGACCAGGGCCGGCAGCAGGCGGAGCGGAGGAG  
CGTGCTGCGGGGCTTCTGCGCCAACCTCCAGCCTGGCCTTCCCCACCAAGGAGCGCGCATTCGA  
CGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGACGACCGGCACGGGGCCATCTACTG  
CTACGTGCCCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTGAGCGGAAGCCT  
GCTGCACCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCCGCGCGAGCACGTGCACAACGC  
CAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCCGCTACGGGAAGCTCTCCCGCCACCTCAT  
GAAGGTCAAGCTCAAGAAGTACACCAAGTTCTCTTCGTGCGCGACCCCTTCGTGCGCCTGAT  
CTCCGCCCTTCCGCAGCAAGTTCGAGCTGGAGAACGAGGAGTTCTACCGCAAGTTCGCCGTGCC  
CATGCTGCGGCTGTACGCCAACCACACAGCCTGCCCCGCTCGGCGCGCGAGGCCTTCCGCGC  
TGGCCTCAAGGTGTCTTTCGCCAACTTCATCCAGTACCTGCTGGACCCGCACACGGAGAAGCT  
GGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTCTGCCACCCGTGCCAGATCGACTA  
CGACTTCGTGGGGGAAGCTGGAGACTCTGGACGAGGACGCCGCGCAGCTGCTGCAGCTACTCCA  
GGTGGACCGGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGGACCGCCAGCAGCTGGGAGGA  
GGACTGGTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCTGTATAAACTCTACGAGGCCGA  
CTTTGTTCCTTCGGCTACCCCAAGCCCCGAAAACCTCCTCCGAGACTTGAAAGCTTTCGCGTTG  
CTTTTTCTCGCGTGCTGGAACCTGACGCACGCGCACTCCAGTTTTTTTTATGACCTACGATTT  
TGCAATCTGGGCTTCTTGTTCACTCCACTGCCTCTATCCATTGAGTACTGTATCGATATTGTT  
TTTAAAGATTAATATATTTTCAGGTATTTAATACGA

**FIGURE 418**

MTKARLFRLWLVLGVSFEMILLIIVYWDSAGAAHFYLHTSF SRPHTGPPLPTPGPDRDREL TAD  
SDVDEF LDKFLSAGVKQSDLPRKETEQPPAPGSMEE SVRGYDWSPRDARRSPDQGRQQAERRS  
VLRGFCANSSLAFP TKERAFDDIPNSEL SHLIVDDRHGAIYCYVPKVACTNWK RVMIVLSGSL  
LHRGAPYRDPLRIPREHVHNASAH LTFNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPFVRLI  
SAFRSKFELENEEFYRKFAVPMLRLYANHTSLPASAREAFRAGLKV SFANFIQYLLDPHTEKL  
APFNEHWRQVYRLCHPCQIDYDFVGKLET LDEDAQAQLLQLLQVDRQLRFPPSYRNRTASSWEE  
DWF AKIPLAWRQQLYKLYEADFVLF GYPKPENLLRD

**Important features:**

**Signal peptide:**

amino acids 1-31

**N-glycosylation sites.**

amino acids 134-137, 209-212, 280-283 and 370-373

**TNFR/NGFR family cysteine-rich region protein**

amino acids 329-332



**FIGURE 419**

GGCACGAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAAG  
GCTGCCAGGAAGGAGACGCCTTCCTGAGTCCTGGATCTTTCTTCCTTCTGGAAATCTTTGACT  
GTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATCATGGACCTCGCGGGACTGCTGA  
AGTCTCAGTTCCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGCCTCAGGGCTAATCATCA  
ACACCATTACAGCTCTTCACTCTCCTCCTCTGGCCCATTAACAAGCAGCTCTTCCGGAAGATCA  
ACTGCAGACTGTCCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGTTCGGGCA  
CGGAATGCACCATCTTCACGGACCCGCGCGCTACCTCAAGTATGGGAAGGAAAATGCCATCG  
TGGTTCTCAACCACAAGTTTGAAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGAACGCTTTG  
GGCTGTTAGGGGGCTCCAAGGTCTGGCCAAGAAAGAGCTGGCCTATGTCCCAATTATCGGCT  
GGATGTGGTACTTCACCGAGATGGTCTTCTGTTTCGCGCAAGTGGGAGCAGGATCGCAAGACGG  
TTGCCACCAGTTTGCAGCACCTCCGGGACTACCCCGAGAAGTATTTTTTCTGATTCACTGTG  
AGGGCACACGGTTCACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCCCGGGCCAAGGGGC  
TGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATCACCGTGAGGAGCT  
TGAGAAATGTAGTTTTCAGCTGTATATGACTGTACACTCAATTTCAGAAATAATGAAAATCCAA  
CACTGCTGGGAGTCTTAAACGGAAAGAAATACCATGCAGATTTGTATGTTAGGAGGATCCAC  
TGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCTGGCTGCACAAGCTCTACCAGGAGA  
AGGATGCCTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCCAGAGACGCCCATGGTGCCCC  
CCCGGCGGCCCTGGACCCTCGTGAAGTGGCTGTTTTTGGGCCTCGCTGGTGCTCTACCCTTTCT  
TCCAGTTCCTGGTCAGCATGATCAGGAGCGGGTCTTCCCTGACGCTGGCCAGCTTCATCCTCG  
TCTTCTTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGTGACGGAATTGACAAGGGCT  
CTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACTGACTCAGGGAGGTGTCACCAT  
CCGAAGGGAACCTTGGGGAAGTGGTGGCCTCTGCATATCCTCCTTAGTGGGACACGGTGACAA  
AGGCTGGGTGAGCCCCCTGCTGGGCACGGCGGAAGTCACGACCTCTCCAGCCAGGGAGTCTGGT  
CTCAAGGCCGGATGGGGAGGAAGATGTTTTGTAATCTTTTTTTTCCCATGTGCTTTAGTGGGC  
TTTGTTTTTCTTTTTGTGCGAGTGTGTGTGAGAATGGCTGTGTGGTGAGTGTGAACTTTGTTC  
TGTGATCATAGAAAGGGTATTTTAGGCTGCAGGGGAGGGCAGGGCTGGGGACCGAAGGGGACA  
AGTTCCCCTTTCATCCTTTGGTGCTGAGTTTTCTGTAACCTTGGTTGCCAGAGATAAAGTGA  
AAAGTGCTTTAGGTGAGATGACTAAATTATGCCTCCAAGAAAAAAAATTAAAGTGCTTTTCT  
GGGTCAAAAAAAAAAAAA

**FIGURE 420**

MDLAGLLKSQFLCHLVFCYVFIASGLIINTIQLFTLLLWPINKQLFRKINCRLSYCISSQLVM  
LLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHNKFEIDFLCGWSLSEFGLLGGSKVLAKKEL  
AYVPIIGWMWYFTEMVFCSRKWEQDRKTVATSLQHLDYPEKYFFLIHCEGTRFTEKKHEISM  
QVARAKGLPRLKHHLLPRTKGFAITVRSLRNVVSAVYDCTLNFRNNENPTLLGVLNGKKYHAD  
LYVRRIPLEDIPEDDDECSAWLHKLYQEKDAFQEEYYRTGTFFPETPMVPPRRPWTLVNWLFWA  
SLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVRRMIGVTEIDKGSAYGNSDSKQKLND

**FIGURE 421**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCATC  
GCCATGGACACCACCAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCCGAGGGCCC  
TGGGGACGCTGGGTGCACCTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCCTGGTCACC  
ACAGTCCTTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGGAGCGCGCGGCCG  
CTGCTTGACGGCCACGACCTGCTGAGGACAAACGCCTCGAAGCAGACGGCGGCGCTGGGTGCC  
CTGAAGGAGGAGGTTCGGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTGCAGACC  
ACGCGCGCGGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCTGCGGGAA  
CTGCGTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGCCGTGAGGACGTCCGCACCT  
GAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACTCCTGCGAGCCGTGCCCCACG  
TCGTGGCTGTCTTCGAGGGCTCCTGCTACTTTTTCTCTGTGCCAAAGACGACGTGGGCGGCCG  
GCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCCTGGATGAGCAG  
GGCTTCCTCACTCGGAACACGCGTGGCCGTGGTTACTGGCTGGGCCCTGAGGGCTGTGCGCCAT  
CTGGGCAAGGTTTCAGGGCTACCACTGGGTGGACGGAGTCTCTCTCAGCTTCAGCCACTGGAAC  
CAGGGAGAGCCCAATGACGCTTGGGGGCGCGAGAACTGTGTTCATGATGCTGCACACGGGGCTG  
TGGAACGACGCACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAGAAAAGGCACAACCTGC  
TGACCCCGCCCAGTGCCCTGGAGCCGCGCCCATTCGAGCATGTCGTATCCTGGGGGCTGCTCA  
CCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTCTTCCTCATCCACCGCTGCTGAG  
TCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCCAGTGCCTGGGCTCTGGGACCTCCA  
TGCCGACCTCATCCTAACTCCACTCACGCAGACCCAACCTAACCTCCACTAGCTCCAAAATCC  
CTGCTCCTGCGTCCCCGTGATATGCCTCCACTTCTCTCCCTAACCAAGGTTAGGTGACTGAGG  
ACTGGAGCTGTTTGGTTTTCTCGCATTTTCCACCAAACCTGGAAGCTGTTTTTGCAGCCTGAGG  
AAGCATCAATAAATATTTGAGAAATGAAAAA

**FIGURE 422**

MDTTRYSKWGGSSSEVPGGPWGRVHWSRRPLFLALAVLVTTVLWAVILSILLSKASTERAAL  
LDGHDLLRTNASKQTAALGALKKEEVGDCHSCCSGTQAQLQTTRAELGEAQAKLMEQESALREL  
RERVTOGLAEAGRGREDVRTELFRALAEAVRLQNNSCPCPTSWLSFEGSCYFFSVPKTTWAAA  
QDHCADASAHLVIVGGLDEQGFLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLSFSHWNQ  
GEPNDAWGRENVCVMMMLHTGLWNDAPCDSEKDGWICEKRHNC

**Important features:**

**Type II transmembrane domain:**

amino acids 31-54

**N-glycosylation sites.**

amino acids 73-76 and 159-162

**Leucine zipper pattern.**

amino acids 102-123

**N-myristoylation sites.**

amino acids 18-23, 133-138 and 242-247

**C-type lectin domain signature.**

amino acids 264-287

**FIGURE 423**

GCGCCGCCAGGCGTAGGCGGGGTGGCCCTTGCGTCTCCCGCTTCCTTGAAAAACCCGGCGGGC  
GAGCGAGGCTGCGGGCCGGCCGCTGCCCTTCCCCACACTCCCCGCCGAGAAGCCTCGCTCGGC  
GCCCAACATGCGCGGTGGGCGCTGCGGCCCGCAGCTAACGGCGCTCCTGGCCGCTTGATCGC  
GGCTGTGGCGGCGACGGCAGGCCCCGAGGAGGCCGCGCTGCCGCCGGAGCAGAGCCGGGTCCA  
GCCCATGACCGCTCCAACCTGGACGCTGGTGATGGAGGGCGAGTGATGCTGAAATTTTACGC  
CCCATGGTGTCCATCCTGCCAGCAGACTGATTGAGAATGGGAGGCTTTTGCAAAGAATGGTGA  
AATACTTCAGATCAGTGTGGGGAAGGTAGATGTCATTCAAGAACCAGGTTTGAGTGGCCGCTT  
CTTTGTCACTCTCTCCAGCATTTTTTCATGCAAAGGATGGGATATTCCGCCGTTATCGTGG  
CCCAGGAATCTTCGAAGACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATCAGTCGAGCC  
TCTGACTGGCTGGAAATCCCAGCTTCTCTAACGATGCTCTGGAATGGCTGGTCTTTTTCAGCAT  
CTCTGGCAAGATATGGCATCTTCACAACATATTTACAGTGAATCTTGGAAATTCCTGCTTGGTG  
TTCTTATGTGTTTTTCGTATAGCCACCTTGGTTTTTGGCCTTTTTATGGGTCTGGTCTTGGT  
GGTAATATCAGAATGTTTCTATGTGCCACTTCCAAGGCATTTATCTGAGCGTTCTGAGCAGAA  
TCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATGCGGAGGAGGAAAAAGATGA  
TTCAAATGAAGAAGAAAAACAAAGACAGCCTTGTTAGATGATGAAGAAGAGAAAGAAGATCTTG  
CGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGGACAACCTGGCTGCTGGTGTGGATGAGGA  
GAGAAGTGAGGCCAATGATCAGGGGCCCCCAGGAGAGGACGGTGTGACCCGGGAGGAAGTAGA  
GCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCCTGCCAGCTGACACAGAGGTGGTGA  
AGACTCCTTGAGGCAGCGTAAAGTCAGCATGCTGACAAGGGACTGTAGATTTAATGATGCGT  
TTTCAAGAATACACACCAAAACAATATGTGAGCTTCCCTTTGGCCTGCAGTTTGTACCAATC  
CTTAATTTTTCTGAATGAGCAAGCTTCTCTTAAAGATGCTCTCTAGTCATTTGGTCTCATG  
GCAGTAAGCCTCATGTATACTAAGGAGAGTCTTCCAGGTGTGACAATCAGGATATAGAAAAAC  
AAACGTAGTGTGGGATCTGTTTGGGAGCTGGGATGGGAACAAGTTCATTTACTTAGGGGTCA  
GAGAGTCTCGACCAGAGGAGGCCATTCCCAGTCTTAATCAGCACCTTCCAGAGACAAGGCTGC  
AGGCCCTGTGAAATGAAAGCCAAGCAGGAGCCTTGGCTCCTGAGCATCCCCAAAGTGTAACTG  
AGAAGCCTTGCATCCTTTTCTGTGTAAAGTATTTATTTTGTCAAATTCAGGAAACATCAG  
GCACCACAGTGCATGAAAAATCTTTTCAGCTAGAAAATTGAAAGGGCCTTGGGTATAGAGAGC  
AGCTCAGAAAGTCATCCCAGCCCTCTGAATCTCCTGTGCTATGTTTTATTTCTTACCTTTAAT  
TTTCCAGCATTTCCACCATGGGCATTGAGGCTCTCCACACTCTTCACTATTATCTCTTGGTCA  
GAGGACTCCAATAACAGCCAGGTTTACATGAAGTGTGTTTGTTCATTCTGACCTAAGGGGTTT  
AGATAATCAGTAACCATAACCCCTGAAGCTGTGACTGCCAAACATCTCAAATGAAATGTTGTG  
GCCATCAGAGACTCAAAAGGAAGTAAGGATTTTACAAGACAGATTAATAAAAAAATGTTTTGT  
CCAAAATATAGTTGTTGTTGATTTTTTTTTTAAGTTTTCTAAGCAATATTTTTCAAGCCAGAAG  
TCCTCTAAGTCTTGCCAGTACAAGGTAGTCTTGTGAAGAAAAGTTGAATACTGTTTTGTTTTT  
ATCTCAAGGGGTTCCTGGGTCTTGAAGTACTTTAATAATAACTAAAAAACCACTTCTGATTT  
TCCTTCAGTGATGTGCTTTTGGTGAAAGAATTAATGAAGTCCAGTACCTGAAAGTGAAAGATT  
TGATTTTTGTTTCCATCTTCTGTAATCTTCCAAGAATTATATCTTTGTAAATCTCTCAATACT  
CAATCTACTGTAAGTACCCAGGAGGCTAATTTCTTT

**FIGURE 424**

MAGGRCGPQLTALLAAWIAAVAATAGPEEAALPPEQSRVQPMTASNWTLVMEGEWMLKIFYAPW  
CPSCQQTDSEWEAFKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGI FRRYRGPG  
IFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNYFTVTLGIPAWCSY  
VFFVIATLVFGLFMGLVLVVISSECFYVPLPRHLSESEQNRRSEEAHRAEQLQDAEEEEKDDSN  
EEENKDSLVDDEEEKEDLGDEDEAEEEEEDNLAAGVDEERSEANDQGPPGEDGVTTREEVEPE  
EAEEGISEQPCPADTEVVEDSLRQRKSKHADKGL

**Important features:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 191-211

**N-glycosylation site.**

amino acids 46-49

**Thioredoxin family proteins.** (homologous region to disulfide isomerase)

amino acids 56-72

**Flavodoxin proteins**

amino acids 173-187

# **FIGURE 425**

GAGGAACCTACCGGTACCGGCCGCGCTGGTAGTCGCCGCTGGCTGCACCTCACCACCTCCCGTGCGCCGCGG  
 CTGGGCCGTCCGAGAGTGCCTGTCTTCTCTCCTGCACGCGGTGCTTGGGCTCGGCCAGGCGGGGTCGCCGCCA  
 GGGTTTGAGGATGGGGGAGTAGCTACAGGAAGCGACCCCGGATGGCAAGGTATATTTTGTGGAATGAAAAGGA  
 AGTATTAGAAAATGAGCTGAAGACCATTCACAGATTAAATATTTTGGGGACAGATTTGTGATGCTTGATTCACCT  
 TGAAGTAATGTAGACAGAAGTTCTCAAATTTGCATATTACATCAACTGGAACAGCAGTGAATCTTAATGTTTAC  
 TTAAATCAGAACTTGCAATAGAAAGAGAAATGGGAGTCTGGTTAAATAAAGATGACTATATCAGAGACTTGAAAAG  
 GATCATTCTCTGTTTTCTGATAGTGTATATGGCCATTTTAGTGGGCACAGATCAGGATTTTACAGTTTACTTGG  
 AGTGTCAAAAACCTGCAAGCAGTAGAGAAAATAAGACAAGCTTCAAGAAATTGGCATTGAAGTTACATCCTGATAA  
 AAACCCGAATAACCCAAATGCACATGGCGATTTTTTAAAAATAAATAGAGCATATGAAGTACTCAAAGATGAAGA  
 TCTACGGAAAAAGTATGACAAATATGGAGAAAAGGACTTGAGGATAATCAAGGTGGCCAGTATGAAAGCTGGAA  
 CTATTATCGTTATGATTTTGGTATTTATGATGATGATCCTGAAATCATAACATTGGAAAGAAGAGAAATTTGATGC  
 TGCTGTTAATTTCTGGAGAACTGTGGTTTGTAAATTTTACTCCCCAGGCTGTTTACACTGCCATGATCTTACCTCC  
 CACATGGAGAGACTTTGCTAAAGAAGTGGATGGGTTACTTCAATTTGGAGCTGTTAACTGTGGTGTATAGAAT  
 GCTTTGCCGAATGAAAGGAGTCAACAGCTATCCAGTCTCTTCATTTTTCGGTCTGGAATGGCCCCAGTGAAATA  
 TCATGGAGACAGATCAAAGGAGAGTTTAGTGAGTTTGTCAATGCAGCATGTTAGAAGTACAGTGACAGAACTTTG  
 GACAGGAAATTTTGTCAACTCCATACAACTGCTTTTGTGCTGGTATTGGCTGGCTGATCACTTTTGTTCAAA  
 AGGAGGAGATTGTTTGTACTTACAGACACGACTCAGGCTTAGTGGCATGTTGTTTCTCACTCATTGGATGCTAA  
 AGAAATATATTTGGAAGTAATACATAATCTTCCAGATTTTGAACACTTTCGGCAAAACACTAGAGGATCGTTT  
 GGCTCATCATCGGTGGCTGTTATTTTTTCAATTTTGAAAAAATGAAATTCAAATGATCCTGAGCTGAAAAAAT  
 ACCAGAGTTACGAAGAGCATCAAATCTTCTTTATGGTCAGCTTAAGTTTGGTACACTAGATTGTACAGTTTCTGA  
 TCTGTATGTTTTTTCAGCCGTCTCTAGCAGTATTTAAAGGACAAGGAACCAAAGAATATGAAATTCATCATGGAAA  
 GAAGATTCTATATGATATACTTGCCTTTGCCAAAGAAAGTGTGAATTCATGTTACCACGCTTGGACCTCAAAA  
 TTTTCTGCCAATGACAAAGAACCATGGCTTGTGATTTCTTTGCCCCCTGGTGTCCACCATGTGAGCTTTACT  
 ACCAGAGTTACGAAGAGCATCAAATCTTCTTTATGGTCAGCTTAAGTTTGGTACACTAGATTGTACAGTTTCTGA  
 GGGACTCTGTAAACATGTATAACATTGAGCTTATCCAACAACAGTGGTATTCAACCAGTCCAACATTTCATGAGTA  
 TGAAGGACATCACTCTGCTGAACAAATCTTGGAGTTTATAGAGGATCTTATGAATCCTTCAGTGGTCTCCCTTAC  
 ACCACCACCTTCAACGAAGTAGTTACACAAAGAAAACACAACGAAGTCTGGATGGTGGATTTCTATTCTCCGTG  
 GTGTATCTTCCCTTCCAAAGTCTTAATGCCAGAAATGGAAGAAATGGCCCGGACATTAACTGGATCAACGTTGG  
 CAGTATAGATTGCCAACAGTATCATTCTTTTGTGCCAGGAAAACGTTCAAAGATACCTGAGATAAGATTTTTT  
 TCCCCCAAATCAAATAAGCTTATCAGTATCAGAGTTACAATGGTTGGAATAGGGATGCTTATTCCTTGAGAA  
 CTGGGGTCTAGGATTTTTACCTCAAGTATCCACAGATCTAACCTCAGACTTTTCACTGAAAAAGTTCTACAAGG  
 GAAAAATCATTTGGGTGATTGATTTCTATGCTCCTTGGTGTGACCTTCCAGAAATTTTGTCCAGAAATTTGAGCT  
 CTTGGCTAGGATGATTAAAGGAAAAGTGAAGCTGGAAGTAGACTGTGAGGCTTATGCTCAGACATGCCAGAA  
 AGCTGGGATCAGGGCTTATCCAATCTTAAAGTTTATTTCTACGAAAGAGCAAAAGAGAAATTTTCAAGAGAGCA  
 GATAAATACCAGAGATGCAAAAGCAATCGCTGCCCTTAATAAGTGAAAAATTTGGAACCTCTCCGAAATCAAGGCCAA  
 GAGGAATAAGGATGAACCTTGAATAATGTTGAAGATGAAGAAAAAGTTAAAAAGAAATTTGACAGATGACATCAG  
 AAGACACCTATTTAGAATGTTACATTTATGATGGGAATGAATGAACATTATCTTAGACTTCAGTTGTACTGCCA  
 GAATATCTACAGCACTGGTGTAAGAAGGGTCTGCAAACTTTTCTGTAAAGGGCCGGTTTATAAATATTTTA  
 GACTTTGCAGGCTATAATATATGTTTACACATGAGAACAAGAATAGAGTCATCATGTTATTTCTTTGTTATTTGCT  
 TTTAAACACCTTTAAAAAATATTAAGGATTTCTAGCTCAGAGCCATACAAAGTAGGCTGGATTCAGTCCATG  
 GACCATAGATTGCTGTCCCCCTGACGGACTTATAATGTTTTCAGGTGGCTGGCTTGAACATGAGTCTGCTGTGCT  
 ATCTACATAAATGTCTAAGTTGTATAAAGTCCACTTTCCCTTCACGTTTTCCTGGCTGACCTGAAAAGAGGTA  
 TAGTTTTTGGTCACTTGTCTCTTAAAAATGCTATCCCTAACCATATATTTATATTTTCGTTTAAAAACACCCAT  
 GATGTGGCACAGTAACAAACCTGTTATGCTGTATTATTATGAGGAGATTCTTCATTGTTTTCTTTCTTCTCA  
 AAGGTTGAAAAAATGCTTTTAAATTTTTCACAGCCGAGAAACAGTGCAGCAGTATATGTGCACACAGTAAGTACAC  
 AAATTTGAGCAACAGTAAAGTGACAAATTTCTGTAGTTTGTCTGTATCATCCAGGAAAACCTGAGGGAAAAAATTA  
 TAGCAATTAAGTGGGCTTGTAGAGTATCTAAATATGTTTATCAAGTATTTAGAGTTCTATATTTTAAAGATATA  
 TGTGTTTCATGTATTTTCTGAAATTTGCTTTTATAGAAATTTTCCCACTGATAGTTGATTTTGGAGCATCTAATAT  
 TTACATATTTGCTTCTGAACTTTGTTTTGACCTGTATCCTTTATTTACATTGGGTTTTTCTTTTATAGTTTGG  
 TTTTTCACCTCTGTCAGTCTATTTATTTTCAATAGGAAAAATTTACTTTACAGGTTGTTTTTACTGTAGCTTAT  
 AATGATAGTGTAGTTATTTCCAGTTACTAGTTTACTGTGAGGGGCTGCCCTTTTCAGATAAATATTTGACATAATA  
 ACTGAAGTTATTTTATAAGAAATCAAGTATATAAATCTAGGAAAGGGATCTTCTAGTTTCTGTGTTGTTTGA  
 CTCAAGAATCAAAATTTGTGAGTAAATGATGTTGTTTATGTTTATTAATTCAGAGTGTACAGAAATGGTAAAAAT  
 CCAATCAGTCAAAAGAGGTCATGAATTAAGGCTTGCAACTTTTCAAAAAAATTTTTT

**FIGURE 426**

MGVWLNKDDYIRDLKRIILCFLIVYMAILVGTDQDFYSLLGVSKTASSREIRQAFKKLALKLH  
PDKNPNNPNAHGDFLKINRAYEVLKDEDLRKKYDKYGEKLEDNQGGQYESWNYRYDFGIYD  
DDPEIITLERREFDAAVNSGELWVFVNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNCGDD  
RMLCRMKGVNSYPSLFIFRSGMAPVKYHGDRSKESLVSFAMQHVRSTVTELWTGNFVNSIQTA  
FAAGIGWLITFCSKGGDCLTSQTRLRLSGMLFLNSLDAKEIYLEVIHNLPDFELLSANTLEDR  
LAHHRWLLFFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICSPLYVFQPSLAVFK  
GQGTKEYEIIHHGKKILYDILAFAKESVNSHVTTTLPQNFNPANDKEPWLVDFFAPWCPPCRALL  
PELRRASNLLYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVVFNQSNIEHEGHHSAEQILEFI  
EDLMNPSVSLTPTTFNELVTQRKHNEVWMVDFYSPWCHPCQVLMPEWKRMARTLTGLINVGS  
IDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYSLRIWGLGLFPQVSTDLT  
PQTFSEKVLQGKNHWVIDFYAPWCGPCQNFAPFELLARMIKGKVKAGKVDCAQAYATCQKAG  
IRAYPTVKFYFYERAKRNFQEEQINTRDAKAIKALISEKLETLRNQGRNKDEL

**Important features:**

**Endoplasmic reticulum targeting sequence.**

amino acids 744-747

**Cytochrome c family heme-binding site signature.**

amino acids 158-163

**Nt-dnaJ domain signature.**

amino acids 77-96

**N-glycosylation site.**

amino acids 484-487



**FIGURE 427**

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGGACCCTGACTCTGCAGCCGAACCGGCA  
CGGTTTCGTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTCTTTCTTTCTCCCTCTTGA  
GTCCTTCTGAGATGATGGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTGCGGATGGTAG  
CGGCGGCTCTCGGCGGCCACCTCTGCTGGGAGTGAGCGCCACCTTGAACCTCGGTTCTCAATT  
CCAACGCTATCAAGAACCTGCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTCTGCAG  
TCAGCGCCGCGCCGGAATCCTGTACCCGGGCGGAATAAGTACCAGACCATTGACAACCTACC  
AGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGTCCCACCC  
GCGGAGGGGACGCAGGCGTGCAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAACGCTGCATGC  
GTCACGCTATGTGCTGCCCCGGAATTACTGCAAAAATGGAATATGTGTGTCTTCTGATCAAA  
ATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGATCATAGCACCT  
TGGATGGGTATTCCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAAAGGACAAGAAG  
GTTCTGTTTGTCTCCGGTCATCAGACTGTGCCCTCAGGATTGTGTTGTGCTAGACACTTCTGGT  
CCAAGATCTGTAAACCTGTCTTGAAAGAAGGTCAAGTGTGTACCAAGCATAGGAGAAAAGGCT  
CTCATGGACTAGAAATATTCAGCGTTGTTACTGTGGAGAAGGTCTGTCTTGCCGGATACAGA  
AAGATCACCATCAAGCCAGTAATTCTTCTAGGCTTCACACTTGTGAGAGACACTAAACCAGCT  
ATCCAAATGCAGTGAACCTCTTTTATATAATAGATGCTATGAAAACCTTTTATGACCTTCATC  
AACTCAATCCTAAGGATATACAAGTTCTGTGGTTTCAGTTAAGCATTCCAATAACACCTTCCA  
AAAACCTGGAGTGTAAGAGCTTTGTTTCTTTATGGAACCTCCCTGTGATTGCAGTAAATTACT  
GTATTGTAAATTCTCAGTGTGGCACTTACCTGTAAATGCAATGAACTTTTAATTATTTTTCT  
AAAGGTGCTGCACTGCCTATTTTTCTCTGTATGTAAATTTTGTACACATTGATTGTTAT  
CTTGACTGACAAATATTCTATATTGAACTGAAGTAAATCATTTTCAGCTTATAGTTCTTAAAG  
CATAACCCTTTACCCATTTAATTCTAGAGTCTAGAACGCAAGGATCTCTGGAATGACAAAT  
GATAGGTACCTAAAATGTAACATGAAAATACTAGCTTATTTTCTGAAATGTACTATCTTAATG  
CTTAAATTATATTTCCCTTTAGGCTGTGATAGTTTTTTGAAATAAAATTTAACATTTAAAAAA  
AAAAAA

**FIGURE 428**

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSAA  
PGILYPGGNKYQTTIDNYQPYPCAEDEECGTDEYCASPTRGGDAGVQICLACRKRRKRCMRHAM  
CCPGNYCKNGICVSSDQNHFRGEIEETITESFGNDHSTLDGYSRRTTLSSKMYHTKGQEGSVC  
LRSSDCASGLCCARHFWSKICKPVLKEGQVCTKHRRKGSHGLEIFQRCYCGEGLSCRIQKDDH  
QASNSSRLHTCQRH

**Important features:**

**Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 256-259

**Fungal Zn(2)-Cys(6) binuclear cluster domain**

amino acids 110-126

**FIGURE 429**

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCCGCTCCCGGAGCCCAGCCC  
TTTCCTAACCCAACCCAACCTAGCCAGTCCCAGCCGCCAGCGCCTGTCCCTGTCACGGACCC  
CAGCGTTACCATGTCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCT  
CCTGGTAACCTTGGGTTTTTACTCCTGTAACAACTGAAATAACAAGTCTTGCTACAGAGAATAT  
AGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTTATGCTGACTGGTGTCTGTTT  
CAGTCAGATGTTGCATCCAATTTTTGAGGAAGCTTCCGATGTCATTAAAGGAAGAATTTCCAAA  
TGAAATCAAGTAGTGTGTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCCAGAGATA  
CAGGATAAGCAAATACCCAACCCCTCAAATTGTTTCGTAATGGGATGATGATGAAGAGAGAATA  
CAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAAAAGTGACCCCAT  
TCAAGAAATTCGGGACTTAGCAGAAATCACCCTCTTGATCGCAGCAAAAGAAATATCATTTGG  
ATATTTTGTAGCAAAAGGACTCGGACAACTATAGAGTTTTTGAACGAGTAGCGAATATTTTGCA  
TGATGACTGTGCCTTCTTCTGTCATTTGGGGATGTTTCAAAACCGGAAAGATATAGTGGCGA  
CAACATAATCTACAAACCACCAGGGCATTCTGCTCCGGATATGGTGTACTTGGGAGCTATGAC  
AAATTTTGATGTGACTTACAATTGGATTCAAGATAAATGTGTTCTCTTGTCCGAGAAATAAC  
ATTTGAAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTTCTCATACTCTTTCACATGAA  
AGAAGATACAGAAAGTTTAGAAATATTCCAGAATGAAGTAGCTCGGCAATTAATAAGTGAAAA  
AGGTACAATAAACTTTTTACATGCCGATTGTGACAAATTTAGACATCCTCTTCTGCACATACA  
GAAACTCCAGCAGATTGTCTGTAAATCGCTATTGACAGCTTTAGGCATATGTATGTGTTTGG  
AGACTTCAAAGATGTATTAATTCCTGGAAAACTCAAGCAATTCGTATTTGACTTACATTCTGG  
AAAAC TGACAGAGAATTCCATCATGGACCTGACCCAACTGATACAGCCCCAGGAGAGCAAGC  
CCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAACTAGCACCCAGTGAATATAG  
GTATACTCTATTGAGGGATCGAGATGAGCTTTTAAAAAACTTGAAAAACAGTTTGTAAGCCTTTC  
AACAGCAGCATCAACCTACGTGGTGAAATAGTAAACCTATATTTTCATAATTCTATGTGTAT  
TTTTATTTTGAATAAACAGAAAGAAATTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAA

**FIGURE 430**

MHPAVFLSLPDLRCSLLLLVTWVFTPVTTEITSLATENIDEILNNADVALVNFYADWCRFSQM  
LHPIFEEASDVIKEEFPNENQVVFARVDCDQHS DIAQRYRISKYPTLKLFRNGMMMKREYRGQ  
RSVKALADYIRQQKSDPIQEIRDLAEITTLDRSKRNIIIGYFEQKSDSNYRVFERVANILHDDC  
AFLSAFGDVSKPERYSGDNIIYKPPGHSAPDMVYLGAMTNFDVTYNWIQDKCVPLVREITFEN  
GEELTEEGLPFLILFHMKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLHIQKTP  
ADCPVIAIDSFRHMYVFGDFKDVLI PGKLKQFVFDLHSGKLHREFHHGPDPTDTAPGEQAQDV  
ASSPPESSFQKLAPSEYRYTLLRDRDEL

**Important features:**

**Signal peptide:**

amino acids 1-29

**Endoplasmic reticulum targeting sequence.**

amino acids 403-406

**Tyrosine kinase phosphorylation site.**

amino acids 203-211

**Thioredoxin family proteins**

amino acids 50-66

**FIGURE 431**

GAGCAGGACGGAGCCATGGACCCCGCCAGGAAAGCAGGTGCCCAGGCCATGATCTGGACTGCA  
GGCTGGCTGCTGCTGCTGCTGCTTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCGTG  
CAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGCGCGCCGGGCGTG  
GACGTCTGCACCGAGGCCGTGGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGCAGTG  
CGGGGTTGCGGTTTCGGGACTCCCCGGCAAGAATGACCGCGGCCTGGATCTTCACGGGCTTCTG  
GCGTTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTCACCTCG  
CGGGCGCTCGACCCGGCAGGTAATGAGAGTGCATACCCGCCCAACGGCGTGGAGTGCTACAGC  
TGTGTGGGCCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCCGCTCGTGAGCTGCTACAAC  
GCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTCACCTTGACGGCAGCTAATGTG  
ACTGTGTCTTGCCTGTCCGGGGCTGTGTCCAGGATGAATTCTGCACTCGGGATGGAGTAACA  
GGCCCAGGGTTACGCTCAGTGGCTCCTGTTGCCAGGGGTCCCGCTGTAACTCTGACCTCCGC  
AACAAAGACCTACTTCTCCCCCTCGAATCCCACCCCTTGTCCGGCTGCCCCCTCCAGAGCCCACG  
ACTGTGGCCTCAACCACATCTGTCACTTCTACCTCGGCCCCAGTGAGACCCACATCCACC  
ACCAAACCCATGCCAGCGCCAACCAGTCAGACTCCGAGACAGGGAGTAGAACACGAGGCCTCC  
CGGGATGAGGAGCCCAGGTTGACTGGAGGCGCCGCTGGCCACCAGGACCGCAGCAATTCAGGG  
CAGTATCCTGCAAAAGGGGGGCCCCAGCAGCCCCATAATAAAGGCTGTGTGGCTCCACAGCT  
GGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTTACTGTGAGACTTCTCCACCTGGA  
AATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCTCATCACTTCTGTTCCCA  
CCACTGGACTGGGCTGGCCAGCCCCTGTTTTTCCAACATTCCCCAGTATCCCCAGCTTCTGC  
TGCGCTGGTTTGCGGCTTTGGGAAATAAAATACCGTTGTATATATTCTGCCAGGGGTGTTCTA  
GCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTTGTCTCTCCGCTTGTCCTCTTGTGATG  
TTAGGACAGAGTGAGAGAAGTCAGCTGTCACGGGAAGGTGAGAGAGAGGATGCTAAGCTTCC  
TACTCACTTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGGGGTGGGTGGGACAATGGCTCCCC  
ACTCTAAGCACTGCCTCCCCTACTCCCCGCATCTTTGGGGAATCGGTTCCCCATATGTCTTCC  
TTACTAGACTGTGAGCTCCTCGAGGGGGGGCCCCGTACCCAATTGCGCCTATAGTGAGTCGTA

**FIGURE 432**

MDPARKAGAQAMIWTAGWLLLLLLLRGGAQALECYSCVQKADDGCSPNKMKTVKCAPGVDVCTE  
AVGAVETIHGQFSLAVRGCGSGLPGKNDRGLDLHGLLAFIQLQOCAQDRCNAKLNLTSRALDP  
AGNESAYPPNGVECYSCVGLSREACQGTSPFVVSCYNASDHVYKGCFDGNVTLTAAANVTVSLP  
VRGCVQDEFCTRDGVTGPGFTLSGSCCQGSRCNSDLRNKTYFSPRIPLVRLPPPEPTTVAST  
TSVTTSTSAFVRPTSTTKPMPAPTSQTPRQGEHEASRDEEPRLTGGAAGHQDRSNSGQYPAK  
GGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

**FIGURE 433**

CGGGACTCGGCGGGTCCTCCTGGGAGTCTCGGAGGGGACCGGCTGTGCAGACGCCATGGAGTT  
GGTGCTGGTCTTCCTCTGCAGCCTGCTGGCCCCCATGGTCCTGGCCAGTGCAGCTGAAAAGGA  
GAAGGAAATGGACCCTTTTCATTATGATTACCAGACCCTGAGGATTGGGGGACTGGTGTTCGC  
TGTGGTCTCTCTCGGTTGGGATCCTCCTTATCCTAAGTCGCAGGTGCAAGTGCAGTTTCAA  
TCAGAAGCCCCGGGCCCCAGGAGATGAGGAAGCCCAGGTGGAGAACCCTCATCACCGCCAATGC  
AACAGAGCCCCAGAAGCAGAGAACTGAAGTGCAGCCATCAGGTGGAAGCCTCTGGAACCTGAG  
GCGGCTGCTTGAAACCTTTGGATGCAAATGTCGATGCTTAAGAAAAACCGGCCACTTCAGCAACA  
GCCCCTTTCCCAGGAGAAGCCAAGAACTTGTGTGTCCCCCACCCTATCCCCTCTAACACCATT  
CCTCCACCTGATGATGCAACTAACACTTGCCCTCCCCACTGCAGCCTGCGGTCTGCCCACCTC  
CCGTGATGTGTGTGTGTGTGTGTGTGTGACTGTGTGTGTTTGCTAACTGTGGTCTTTGTGG  
CTACTTGTGTTGTGGATGGTATTGTGTTGTGTTAGTGAACTGTGGACTCGCTTTCCAGGCAGGG  
GCTGAGCCACATGGCCATCTGCTCCTCCCTGCCCCGTGGCCCTCCATCACCTTCTGCTCCTA  
GGAGGCTGCTTGTGCCCCGAGACCAGCCCCCTCCCCCTGATTTAGGGATGCGTAGGGTAAGAGC  
ACGGGCAGTGGTCTTCAGTCGTCTTGGGACCTGGGAAGGTTTGACGACCTTTGTATCATTTCT  
TCATGGACTCCTTTCACTCCCTTTAACAAAAACCTTGCTTCCTTATCCCACCTGATCCCAGTCT  
GAAGGTCTCTTAGCAACTGGAGATACAAAGCAAGGAGCTGGTGAGCCCAGCGTTGACGTCAGG  
CAGGCTATGCCCTTCCGTGGTTAATTTCTTCCCAGGGGCTTCCACGAGGAGTCCCCATCTGCC  
CCGCCCCCTTACAGAGCGCCCGGGGATTCCAGGCCCAGGGCTTCTACTCTGCCCCCTGGGGAAT  
GTGTCCCCTGCATATCTTCTCAGCAATAACTCCATGGGCTCTGGGACCTTACCCCTTCCAACC  
TTCCCTGCTTCTGAGACTTCAATCTACAGCCCAGCTCATCCAGATGCAGACTACAGTCCCTGC  
AATTGGGTCTCTGGCAGGCAATAGTTGAAGGACTCCTGTTCCGTTGGGGCCAGCACACCGGGA  
TGGATGGAGGGAGAGCAGAGGCCCTTTGCTTCTCTGCCCTACGTCCCCCTTAGATGGGCAGCAGAG  
GCAACTCCCGCATCCTTTGCTCTGCCCTGTCGGTGGTCAGAGCGGTGAGCGAGGTGGGTGGAG  
ACTCAGCAGGCTCCGTGCAGCCCTTGGGAACAGTGAGAGGTTGAAGGTCATAACGAGAGTGGG  
AACTCAACCCAGATCCCGCCCCCTCTGTCTCTGTGTTCCCGCGGAAACCAACCAACCGTGC  
GCTGTGACCCATTGCTGTTCTCTGTATCGTGATCTATCCTCAACAACAACAGAAAAAAGGAAT  
AAAAATATCCTTTGTTTCCT

**FIGURE 434**

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLF SVGILLILSRCKC  
SFNQKPRAPGDDEEAQVENLITANATEPQKQRTQVQPSGGSLWNLRRLLLEPLDANVDA



**FIGURE 435**

GGTCCTTAATGGCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTGC  
TGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGTCA  
TCCCTAAGTTTCAAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGACTT  
TTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCCCTGGGGAAGAACTAA  
ATGTCACAACGGCCTGGAAAGCACAGAACCAGTACTGAGAGAGGTGGTGGACATACTTACAG  
AGCAACTGCGTGACATTCAGCTGGAGAATTACACACCCCAAGGAACCCCTCACCTGCGAGGCAA  
GGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTTCACTTTCGATG  
GGCAGATCTTCCCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTTCATCCTGGAGCCA  
GAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCTTCCATTACTTCTCAA  
TGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACCCCTGGAGCCAA  
GTGCAGGAGCACCCTCGCCATGTCTCAGGCACAACCCAACTCAGGGCCACAGCCACCACCC  
TCATCCTTTGCTGCCTCCTCATCATCCTCCCCTGCTTCATCCTCCCTGGCATCTGAGGAGAGT  
CCTTTAGAGTGACAGGTTAAAGCTGATACAAAAGGCTCCTGTGAGCACGGTCTTGATCAAAAC  
TCGCCCTTCTGTCTGGCCAGCTGCCCACGACCTACGGTGTATGTCCAGTGGCCTCCAGCAGAT  
CATGATGACATCATGGACCCAATAGCTCATTCACCTGCCTTGATTCCCTTTTGCCAACAATTTTA  
CCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACCTGATGGAATTCCTGCA  
CTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTCTCTTTTGTTTGGAAAA  
TCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAATGATATTGTCAAGTAAAAATAATCACG  
TTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCTTGAAAGAGAAATTTTAAATATTTAAT  
AAGAAAAAATTTATATTAATGATTGTTTCTTTAGTAATTTATTGTTCTGTACTGATATTTAA  
ATAAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAAAAA

**FIGURE 436**

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTFLH  
YDCGNKTVTPVSPLGKKLNVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQARMS  
CEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFSMGD  
CIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

# **FIGURE 437**

GTTCTCCTTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACCATGAAGCTCTTGTGGCAGG  
 TAACTGTGCACCACCACACCTGGAATGCCATCCTGCTCCCGTTCTGTCTACCTCACGGCGCAAGTGTGGATTCTGT  
 GTGCAGCCATCGCTGCTGCCGCCTCAGCCGGGGCCCCAGAACTGCCCCCTCCGTTTGTCTCGTGCAGTAACCAGTTCA  
 GCAAGGTGGTGTGCACGCGCCGGGGCCTCTCCGAGGTCCCGCAGGGTATTCCCTCGAACACCCGGTACCTCAACC  
 TCATGGAGAACAACTCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACCTGGAGGTCCTGCAGTTGG  
 GCAGGAACCTCCATCCGCGCAGATTGAGGTGGGGGCCCTTCAACGGCCTGGCCAGCCTCAACACCCCTGGAGCTGTTG  
 ACAACTGGCTGACAGTCATCCCTAGCGGGGCCCTTTGAATACCTGTCCAAGCTGCGGGAGCTCTGGCTTCGCAACA  
 ACCCATCGAAAGCATCCCCCTTTACGCCCTTCAACCGGGTCCCTCCCTCATGCGCCTGGACTTGGGGGAGCTCA  
 AGAAGCTGGAGTATATCTCTGAGGGAGCTTTTGAGGGGCTGTTCAACCTCAAGTATCTGAACCTTGGGCATGTGCA  
 ACATTAAAGACATGCCCAATCTCACCCCCCTGGTGGGGCTGGAGGAGCTGGAGATGTGAGGAACCACTTCCCTG  
 AGATCAGGCCTGGCTCCTTCCATGGCCTGAGCTCCCTCAAGAAGCTCTGGGTCTGAACCTCACAGGTCAGCCTGA  
 TTGAGCGGAATGCTTTTGACGGGCTGGCTTCACTTGTGGAACCTCAACTTGGCCCAATAACCTCTCTTCTTTGC  
 CCCATGACCTCTTTACCCCGCTGAGGTACCTGGTGGAGTTGCATCTACACCACAACCCCTTGAACCTGTGATTGTG  
 ACATTCTGTGGCTAGCCTGTGGCTTCGAGAGTATATACCCACCAATTCCACCTGCTGTGGCCGCTGTCTATGCTC  
 CCATGCACATGCGAGGCCGCTACCTCGTGGAGGTGGACCAGGCCTCCTTCCAGTGTCTGCCCCCTTCATCATGG  
 ACGCACCTCGAGACCTCAACATTTCTGAGGGTCGGATGGCAGAACTTAAGTGTGGACTCCCCCTATGTCTCCG  
 TGAAGTGGTTGCTGCCCAATGGGACAGTGTCTCAGCCAGCCTCCCGCCACCCAAGGATCTCTGTCTCAACGACG  
 GCACCTTGAACCTTTCCACGTGCTGCTTTGAGACACTGGGGGTGACACATGCATGGTGACCAATGTTGCAGGCA  
 ACTCCAACGCCTCGGCCTACCTCAATGTGAGCACGGCTGAGCTTAACACCTCCAACCTACAGCTTCTTCACCACAG  
 TAACAGTGGAGACCACGGAGATCTCGCCTGAGGACACAACGCGAAAGTACAAGCCTGTTCTACCACGTCCACTG  
 GTTACCAGCCGCATATACCACCTCTACCACGGTGTCTATTGAGACTACCCGTGTGCCCAAGCAGGTGGCAGTAC  
 CCGCGACAGACACCACTGACAAGATGCAGACCAGCCTGGATGAAGTCATGAAGACCACCAAGATCATCATTTGGCT  
 GCTTTGTGGCAGTGAATCTGCTAGCTGCCGCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCACCAGCAGC  
 GGAGTACAGTCACAGCCGCCGACTGTTGAGATAATCCAGGTGGACGAAGACATCCAGCAGCAACATCCGCAG  
 CAGCAACAGCAGCTCCGTCCGGTGTATCAGGTGAGGGGGCAGTAGTGTGCCCACAATTGATGACCATATTAAC  
 ACAACACCTACAAACCAGCACATGGGGCCCACTGGACAGAAAACAGCCTGGGGAACTCTCTGCACCCACAGTCA  
 CCCTATCTCTGAACCTTATATAATTCAGACCCATACCAAGGACAAGGTACAGGAACTCAAATATGAACCTCCCT  
 CCCCCAAAAAATTATAAAATGCAATAGAATGCACACAAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTT  
 TTCTTGATATGCTTATATATTAAGTCTATGGGCTGGTTAAAAAAAACAGATTATATTAATTTAAAGACAAAA  
 AGTCAAAACA

**FIGURE 438**

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAAASAGPQNCPSVCSCSNQFSKVVCTR  
RGLSEVPQGIPSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLASLN  
TLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRDLGELKKLEYISE  
GAFEGLFNLKYLNLGMCNIKDMPNLTPLVGLEELEMMSGNHFPFIRPGSFHGLSSLKKLWVMNS  
QVSLIERNAFDGLASLVELNLAHNNLSSLPHDLFTPLRYLVELHLHNPWNCDLWLAWWL  
REYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAELKCRTPP  
MSSVKWLLPNGTVLSHASRHPRISVLNDGTLNFSHVLLSDTGVTTCMVTVAGNSNASAYLNV  
STAE LN TSNYSF FTTVTVETTEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQTTRVPKQV  
AVPATD TTDKMQTS LDEVMKTTKIIIGCFVAVTLLAAAMLIVFYKLKRHQQRSTVTAARTVE  
IIQVDEDIPAATSAAATAAPSGVSGEGAVVLPTIHDHINYNTYKPAHGAHW TENS LGNSLHPT  
VTTISEPYIIQTHTKDKVQETQI

**FIGURE 439**

GTCGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCTG  
TCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCTGC  
CCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTCCAA  
GTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGACAGCCAAGTTGGAAGTGAAGCACTGCACC  
GATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGGAATAGTGAAAAAAT  
GTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTTCACGACACCCTGATC  
TTCATAAAAAATTGTAAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

**FIGURE 440**

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLOVAKLNPPPEALAAKLEVK  
HCTDQISFKKRLSLKKSWWK

**FIGURE 441**

GAACATTTTTAGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGATG  
GGGTTGCTGGTTTAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCACC  
ACCTCCGCCAGGAAGTGCAGGCCCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCCCCAGG  
GACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCTCCAG  
CTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCAGCCAA  
GCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCCGGAAGATGGAGGTCAAGCAGAAGGGGC  
AGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGTCAGGGGT  
TCAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGGGAAGAGGC  
CAAAGAGGCCCCAGCCGACAAGTGATCGCCCACAAGCCTTACTCACCTCTCTCTAAGTTTATA  
AGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTACAAGCTCAGG  
AGGCGAATAAATGTTCAAAGTGA

**FIGURE 442**

MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDGG  
QAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO



**FIGURE 443**

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCCTCGTCCAGTACCTCG  
TGAACCCCGGGGTGCTCCGCACGGACCCAGATGTCAAGAATATGAACACGTGGCTGCTGTTTC  
CTCCCCCTGTTCCCGGTGCAGGTGCAGACCCTGATAGTCGTGATCATCGGGATGCTCGTGCTC  
CTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCTGAGT  
ATGTCCCCCACCCTAAGCCCCGATCCCCCAAGGCTGGGTGGTCAGAGCTGCTCATCTTACA  
CCTCTACTTGAGTATGTCCCTAACCCCTGAGCCCCCACGCCTGGGGCCAGAGTCTTTGTCCCC  
CGTGTGCGCATGTGTTCAGGGTCAGCCTCTCCAGAAGTGAGATCATGGACAAAAGGGCAAA  
TCACAGGAAGAAATTAAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAATCACGCCG  
AGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAAATGTTCAGAGACAATGGA  
ATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTTCCAAAAACAC  
AAGTAGAAATTCTAACAATGAAATATATTACAGGCAGGTCACCCCTAACCAACAACCTGAAG  
CGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGTGAGTCATGTTGCT  
GAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGTAACAACAACCTCC  
CTGCTCCTGGCACCAGCCGTTTTTGGTCATGGTGGGCCAGCTGCAAAGCGTCTTCCATTCTCTG  
GGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGGTTTCTGTGGACACGGGCAGCAGAGTG  
TGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCAACCCCTGGTCAGGGCA  
GAGGGAGTTGGGTGGGTGAGGCTCTGGGCTCACCTCCATCTCCAGAGCATCCCCTGCCTGCAG  
TTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCCCACCAAGAGCCTCCTTGTTTATAACC  
ACAGGTTACCCTACAAACCACTGTCCCCACACAACCTGGGGATGTTTTTAAACACACACCTC  
TAACGCATATCTTACAGTCACTGTTGTCTTGCTGAGGGTTGAATTTTTTTTAAATGAAAGTGC  
AATGAAAATCACTGGATTAAATCCTACGGACACAGAGCTGAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAA

**FIGURE 444**

MNTWLLFLPLFPVQVQTLIVVIIGMLVLLLDLGLVHLGQLLI FHIYLSMSPTLS PRSPQGWV  
VRAAHLTPLLEYVPNPEPPTPGARVFVPRVRMCSGSASPRSEIMDKKGKSQEEIKSMRTQQAQ  
QEAELTPRPAGVVPGA

**FIGURE 445**

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGAATGGACTGGCCTCACAACTGC  
TGTTTCTTCTTACCATTTCATCTTCCTGGGGCTGGGCCAGCCCAGGAGCCCCAAAAGCAAGA  
GGAAGGGGCAAGGGCGGCCTGGGCCCCCTGGCCCCCTGGCCCTCACCAGGTGCCACTGGACCTGG  
TGTACGGATGAAACCGTATGCCCGCATGGAGGAGTATGAGAGGAACATCGAGGAGATGGTGG  
CCCAGCTGAGGAACAGCTCAGAGCTGGCCCAGAGAAAGTGTGAGGTCAACTTGCAGCTGTGGA  
TGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCCAGCCGTATCC  
CCGTGGACCTGCCGGAGGCACGGTGCCCTGTGTCTGGGCTGTGTGAACCCCTTCACCATGCAGG  
AGGACCGCAGCATGGTGAGCGTGCCGGTGTTCAGCCAGGTTCTGTGCGCCGCCGCCTCTGCC  
CGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGAGTCATGGAGACCATCGCTGTGGGCT  
GCACCTGCATCTTCTGAATCACCTGGCCCAGAAGCCAGGCCAGCAGCCCCGAGACCATCCTCCT  
TGCACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAAGCAAG

**FIGURE 446**

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRPGPLAPGPHQVPLDLVSRMKPYARMEEYE  
RNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPRI PVDLPEARCLCLGC  
VNPFTMQEDRSMVSVPVFSQVPVRRRLCPPPPRTGPCRQRAVMETIAVGCTCIF

**Important features:**

**Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 75-78

**Homologous region to IL-17**

amino acids 96-180.

**FIGURE 447**

GGAGTGCAGATGGCATCCTTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACCATGGCCAAGA  
TGGAGCTCTCGAAGGCCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCTAT  
CACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGGTGC  
CCAAGCCCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCCTGGATG  
GAGATACCAACACATCCACCCAGGAGGTGGTACAATACAACTGGGAGACTGGGGATGACCGGT  
TCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAAACTGTGGAAGAACCAG  
GGGAGAGGTGCCGAAGTTTCATTGAACTTACACCACCAGCCAAGAGAGGTGAGAAAGGACTAC  
TGGAATTTGCCACGTTGCAAGGCCCATGTCACCCCACTCTCCGATTTGGAGGGAAGCGGTTGA  
TGGAGAAGGCTTCCCTCCCCCTCCCCTCCCCTTGGGGCTTTGTGGCAAAAATCCTATGGTTATCC  
CTGGGAACGCAGATCACCTACATCGGACTTCAATTCATCAGCTTCCTCCTGCTACTAACAGAC  
TTGCTACTCACTGGGAACCCTGCCTGTGGGCTCAAACCTGAGCGCCTTTGCTGCTGTTTCCTCT  
GTCCTGTCAGGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAAGTCTTCCAAGCGACT  
GTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGGGAATTATGGCTGGGCCTTCTACATG  
GCCTGGCTCTCCTTCACCTGCTGCATGGCGTCGGCTGTCACCACCTTCAACACGTACACCAGG  
ATGGTGCTGGAGTTCAAGTGCAAGCATAGTAAGAGCTTCAAGGAAAACCCGAACCTGCCTACCA  
CATCACCATCAGTGTTTCCCTCGGCGGCTGTCAAGTGCAGCCCCCACCCTGGGTCTTTTGACC  
AGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGGGAGTCGACTTCTACTCC  
GAGCTGCGGAACAAGGGATTTCAAAGAGGGGCCAGCCAGGAGCTGAAAGAAGCAGTTAGGTCA  
TCTGTAGAGGAAGAGCAGTGTTAGGAGTTAAGCGGGTTTGGGGAGTAGGCTTGAGCCCTACCT  
TACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCGTCTCTTGAGCATGGTTTTTA  
GAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTCCTAAGGGATTCTGGGTGCCA  
CTGCTCTCTTTTCCCTCTACAGCTCCATCTTGTTTCACCCACCCACATCTCACACATCCAGAA  
TTCCCTTCTTTACTGATAGTTTCTGTGCCAGGTTCTGGGCTAAACCATGGAGATAAAAAGAAG  
AGTAAAATACACTTCCCGACCTTAAGGATCTGAAA

**FIGURE 448**

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMPV  
SLDGDNTNTSTQEVVQYNWETGDDRFSSFRSFRSGMWLSCEETVEEPGERCRSFIELTPPAKRG  
KGLLEFATLQGPCHPTLRFGGKRLMEKASLPSPLGLCGKNPMVIPGNADHLHRTSIHQLP  
TNRLATHWEPCLWAQTERLCCCFLCPVRSPGDGGPHDVFTSLPSCQLGSRRLCTTCLELWLG  
LLHGLALLHLLHGVCCHLQHVVHODGAGVQVQA

**FIGURE 449**

CCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCC  
ACGCGTCCGGTGCAAGCTCGCGCCGCACACTGCCTGGTGGAGGGAAGGAGCCCGGGCGCTCTCGCGCTCCCG  
CGCGCGCTCCGCACCTCCCCACCGCCCGCGCCCGCGCCCGCGCCGCAAGCATGAGTGAGCCCGCTCTCT  
GCAGCTTGCCTGGGCGCGCAATGGCAGGCTGTTTCCGCGGAGTAAAAGGTGGCGCGCTCAGTGGTCTGTTTCCAAT  
GACGGACATTAAACGAGCTGTGAGATCTTGGGGAGTTCGCGAGCCCCGAGTTTGGAGTTTTCCTCCCCACACGT  
CACAGTCCGAACCTGCAGAGGGAAGGCGGCGAGGAAGGCGAAGCTCGGGCTCCGGCACGTAGTTGGGAACT  
TGCGGGTCTAGAACTGCCTCCCCGCTTGCCTGGCGCGCTTGCAGCCCCGAGCGAGCAGCAAGTGAGACAT  
TGTGCGCTTGCAGATCCGCGCGCGCGGACCGGGCTGCCTCGGAAACACAGAGGGGTCTTCTCTCGCCCTGCA  
TATAATTAGCCTGCACACAAAGGGAGCAGCTGAATGGAGGTTGTCACTCTCTGGAAAAGGATTCTGACCGAGCG  
CTTCCAATGGACATTCTCAGTCTCTCTGGAAGATTCTCGTAATGGATTTCTGCTGCTCGTCTCTGTCTAT  
ACTGCTGCTGAGGAGCCCTCGGGGTGGTCTTGTGTCTGCTGGGGCTGCTTTCAGATGCTGCCCGCGCGCC  
CCAGCGGTGCTCCGAGCTGTGCGGTGCGAGGGGCGGTGCTGTACTGCGAGGCGCTCAACCTCACCGAGGCGC  
CCCACACCTGTCCGGCTGTGCTGGCTTGTCCCTGCGCTACAACAGCTCTCGGAGCTGCGCGCGCGGCGAGTTCA  
CGGGTTAATGCAGTCACTGGCTCTATCTGGATCAAAATCACATCTGCTCCGTGAGGGGACGCTTTCAGA  
AACTGCGCGGAGTTAAGGAACCTCACGTGAGTTCCAACAGATCACCAACTGCCAACACACCTTCCGGCCCA  
TGCCCAACCTGCGCAGCTGGACCTCTCGTACAACAAGCTGCAGGCGCTCGCGCCGACCTCTTCCACGGGCTGC  
GGAAGCTCACACGCTGCATATGCGGGCCAAAGCCATCCAGTTTGTGCGCGTCCGAGCTCTCCAGGACTGCGCA  
GCCTCAAGTTTTCGACATCGGATACAATCAGCTCAAGAGTCTGGCGCGCACTCTTTCGCGCGCTTGTTTAAGC  
TCACCGAGCTGCACCTCGAGCACAAAGCTTGGTGAAGTGAACCTTCCGCCACTTCCGCGGCTCTCTCCCTGC  
ACTCGCTCTGCTGCGGAGGAACAAGGTGGCCATTGTGGTCACTCGCTGGAGTGGGTTTGGAACTGGAGAAAA  
TGGAGTTGTGCGGCAACGAGATCGAGTACATGGAGCCCCATGTGTTGAGACCGTGGCGCACCTGCGAGTCCCTGC  
AGCTGGACTCCAACCGCTCACTACATCGAGCCCCGATCCTCAACTCTTGGAAAGTCCCTGACAAAGCATCACCC  
TGGCGGGAACCTGTGGGATTGCGGGCGCAAGTGTGTGCCCTAGCCTCGTGGCTCAGCAACTCCAGGGGCGCT  
ACGATGGCAACTGCGAGTGCAGCCGCGAGTACGCACAGGCGGAGGACGTCTGAGCGCTGTATCGCTTCC  
ACCTTGGCAGGATGGGGCCGAGCCACAGCGGCCACTGCTCTCGGCGCTCACCAACCGCATGTATCTGGGGC  
CCCCTGCCAGCTCGGCCACACGCTCGCGGACGGCGGGGAGGGGACGACAGCGGACATTCGAGCCTGCCACCG  
TGGCTCTTCCAGGCGGAGACGCGGAGAACGCGGTGCAGATCCACAAGGTGGTCAAGGGCACCATGGCCCTCA  
TCTTCTCTCTCATCGTGGTCTGTGCTCTACGTGTCTTGAAGTGTTCACAGCCAGCTCAGGCGCTCA  
GACAGTGTCTTGTACGCGAGCGCAGGAAGCAAAAGCAGAAACAGACCATGCATCAGATGGCTGCCATGTCTGCCC  
AGGAATACTATCTGATTACAAACCGAACCATTTGAGGGAGCCCTGGTGATCATCAACGAGTATGGCTCGTGTA  
CCTGCCACAGCAGCCCGGAGGAATGCGAGGTGTGATTGTCCAGTGGCTCTCAACCCATGCGCTACCAATA  
CGCTTGGGCGAGCCGGGACGGGCGGCGGCGGCGGCGGCTGCTCTGTCTGTGCTCTGATATGCTCTCTTAC  
TGAACTTTAAGGGGATCTCTCCAGAGACTTGACATTTTAGCTTTATTTGTGTCTTAAAAACAAAAGCAATTAA  
AACACAACAAAAACCCACCCACACCTTTCAGGACAGTCTATCTTAAATTTTATATGAGAACTCTTCTCTCC  
TTTGAAGATCTGTCCATATTCAGGAATCTGAGAGTGTAAAAAAGGTGGCCATAAGACAGAGAGAGAATAATCGTG  
CTTTGTTTTATGCTACTCTCCACCTTGCCTATGATTAACATCATGTATGTAGAAGATCTTAAAGTCCATACGC  
ATTTATGAAGAACCATTGGAAAGAGGAATCTGCAATCTGGGAGCTTAAGAGCAAATGATGACCATAGAAAGCTA  
TGTTCTTACTTTGTGTGTGTGTCTGTATGTTTCTGCGTTGTGTGCTTTTGTAGGCAAGCAAACGTTGTCTACACA  
AACGGGAATTTAGCTCACATCATTTTATGCCCCCTGTGCTCTAGCTCTGGAGATTGGTGGGGGAGGTGGGGGA  
AACGGCAGGAATAAGGGAAAGTGGTAGTTTAACTAAGGTTTTGTAACACTTGAATCTTTCTTCTCAAATTA  
ATTATCTTTAAGCTTCAAGAACTTGCTCTGACCCCTTAAGCAAACCTAAGCAATTTAAAGAGAATCTAAT  
TTTAAAGGTGTAGACCTTTTTTTTATCTTCCCACAGAGGGTGCTAATCTCATTATGCTGTGCTATCTGAAA  
GAACCTAAGGCCACAATTCACGTCTCGTCTGGGCATTTGTGATGGATTGACCTCCATTTGCGATACCTTCCAG  
CTGATTTAAAGTTTCAGCAGTGGTATTGAGGTTTTTCGAATATTTATATAGAAAAAAGTCTTTTTCACATGACAAAT  
GACACTCTCACACAGTCTTAGCCCTAGTAGTTTTTATAGTTTGACAGAGGAAGCAGGTTAAATGAGACCTGTC  
CTCTGCTGCACTCAGAAAAATAGGCAGTCCCTGATGCTCAGATCTTAGCCTTGATATTAATAGTTGAGACCACT  
TACCCCAATGCAGCTTACTCCCAAGACTACAAGTTACCATCGCAAGGAAAGGTTATTCAGTAAAGGAA  
ATAGTTTTCTCAACCATTTAAAAATATCTTCTGAACCTCATCAAAAGTAGAAGAGCCCCAACCTTTTCTCTGTC  
CTTCAAGAAAGGCAGACATTTGGTATGATTTAGCATCAACAACATTTATGAGTATATGTAAGTAAATCAGAGGGG  
CAAAATGCCACTTGTATTCTCCCAAGTTTTTCAAGCAAGTACACACAGATCTCTGGTAGGATTAGGGGCCACTT  
GTGTTTCCGGCTTATTTTAGTCTGCTGTCAGCAAGTTTGTGCTAGTCTATCTGACATGGCCCCAGTAGAACAG  
GGCATTTGATGGATCACATGAGATGGTAGAAGGAACATCATCACATACCCCTCTCACAGAGAAAAATTAAGAA  
CCAGAAATTTATCTGTTTTGGAGCAAGAGTGTATAATGTTTCAGGGTAGTCAAAATAAACAATAAATATCTCC  
TCTAGATGAGTGGGATGTTGGCTGATTGGGTCTGCCATTGACAGAATGTCAAATAAAGGAATTAGCTAGAA  
TATGACCATTAAATGTGCTTCTGAAATATATTTTGAATAGGTTTGAATGTCA

**FIGURE 450**

MDFLLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPHN  
LSGLLGLSLRYNSLSELRAGQFTGLMQLTWLYLDHNHICSVQGDAFQKLRRVKELTLSSNQIT  
QLPNTTFRPMPNLRSDLSYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRIFQDCRSLKF  
LDIGYNQLKSLARNSFAGLFKLTELHLEHNDLVKVNFAHFPRLLISLHSLCLRRNKVAIVVSSL  
DWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDNRPTYIEPRILNSWKSLSITLAGNL  
WDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDVYAFHLCEDGAEPTSGHLLSAV  
TNRSDLGPPASSATTLADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMALIFSFLI  
VVLVLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNHIEGALV I  
NEYGSCTCHQQPARECEV



# **FIGURE 451**

TTGAGCGCAGGTGAGCTCCTGCGCGTTCCGGGGGCGTTCCTCCAGTCACCCTCCCGCCGTTAC  
 CCGCGGCGCGCCCCGAGGGAGTCTCCTCCAGACCCTCCCTCCCGTTGCTCCAACTAATACGGA  
 CTGAACGGATCGCTGCGAGGGTGGGAGAGAAAATTAGGGGGAGAAAGGACAGAGAGAGCAACT  
 ACCATCCATAGCCAGATAGATTATCTTACACTGAAGTATCAAGTACTTTGAAAATGACTTCG  
 AAATTTATCTTGGTGTCTTCATACCTTGCTGCACTGAGTCTTTCAACCACCTTTTCTCTCCAA  
 CTAGACCAGCAAAAGGTTCTACTAGTTTCTTTTGATGGATTCCGTTGGGATTACTTATATAAA  
 GTTCCAACGCCCCATTTTCATTTATATATGAAATATGGTGTTCACGTGAAGCAAGTTACTAAT  
 GTTTTTATTACAAAAACCTACCCTAACCATTTATACCTTTGGTAACTGGCCTCTTTGCAGAGAAT  
 CATGGGATTGTTGCAAAATGATATGTTTGATCCTATTCCGGAACAAATCTTTCTCCTTGGATCAC  
 ATGAATATTTATGATTCCAAGTTTGGGAAGAGCGACACCAATATGGATCACAAACCAGAGG  
 GCAGGACATACTAGTGGTGCAGCCATGTGGCCCGGAACAGATGTAAAAATACATAAGCGCTTT  
 CCTACTCATTTACATGCCCTTACAATGAGTCACTTTTCATTTGAAGATAGAGTTGCCAAAATTGTT  
 GAATGGTTTACGTCAAAAGAGCCCATAAATCTTGGTCTTCTCTATTGGGAAGACCCTGATGAC  
 ATGGGCCACCATTGTTGGGACCTGACAGTCCGCTCATGGGGCCTGTCAATTCAGATATTGACAAG  
 AAGTTAGGATATCTCATACAAATGCTGAAAAAGGCAAGTTGTGGAACACTCTGAACCTAATC  
 ATCACAAGTGATCATGGAATGACGCACTGCTCTGAGGAAAGGTTAATAGAAGTTGACCACTAC  
 CTGGATAAAGACCCTATACCCTGATTGATCAATCTCCAGTAGCAGCCATCTTGCCAAAAGAA  
 GGTAATTTGATGAAGTCTATGAAGCACTAACTCACGCTCATCCTAATCTTACTGTTTACAAA  
 AAAGAAGACGTTCCAGAAAGGTGGCATTACAAAATACAACAGTCGAATTCACCAATCATAGCA  
 GTGGCTGATGAAGGGTGGCACATTTTACAGAATAAGTCAGATGACTTTCTGTTAGGCAACCAC  
 GGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTTTAGCCCATGGTCTGCCTTCAGA  
 AAGAATTTCTCAAAAGAAGCCATGAACCTCCACAGATTTGTACCCACTACTATGCCACCTCCTC  
 AATATCACTGCCATGCCACACAATGGATCATTTCTGGAATGTCCAGGATCTGCTCAATTCAGCA  
 ATGCCAAGGGTGGTCCCTTATACACAGAGTACTATACCTCCTCCCTGGTAGTGTAAACCAGCA  
 GAATATGACCAAGAGGGGTATACCCTTATTTATAGGGGTCTCTCTTGGCAGCATTATAGTG  
 ATTGTATTTTTTTGTAATTTTCATTAAGCATTTAATTCACAGTCAAATACCTGCCTTACAAGAT  
 ATGCATGCTGAAATAGCTCAACCATTATTACAAGCCTAATGTTACTTTGAAGTGGATTTGCAT  
 ATTTGAAGTGGAGATTCCATAATTATGTCACTGTTTAAAGGTTTCAAATCTGGGAAACCAGTT  
 CCAAACATCTGCAGAAACCATTAAGCAGTTACATATTTAGGTATACACACACACACACACA  
 CACATACACACACACGACCAAAATACTTACACCTGCAAAGGAATAAAGATGTGAGAGTATGT  
 CTCCATTGTTCACTGTAGCATAGGGATAGATAAGATCCTGCTTTATTTGGACTTGGCGCAGAT  
 AATGTATATATTTAGCAACTTTGCACTATGTAAAGTACCTTATATATTGCACTTTAAATTTCT  
 CTCCTGATGGGTACTTTAATTTGAAATGCACCTTATGGACAGTTATGTCTTATAACTTGATTG  
 AAAATGACAACTTTTTCACCCCATGTACAGAAATACCTTGTACGCATTGTTCAAACCTGAAGGA  
 AATTTCTAATAATCCCGAATAATGAACATAGAAATCTATCTCCATAAATTGAGAGAAGAAGAA  
 GGTGATAAGTGTGAAAAATTAATGTGATAACCTTTGAACCTTGAATTTTGGAGATGTATTCC  
 CAACAGCAGAAATGCAACTGTGGGCATTTCTTGTCTTATTTCTTTCCAGAGAACGTGGTTTTCA  
 TTTATTTTTTCCCTCAAAAGAGAGTCAAATACTGACAGATTCGTTCTAAATATATTGTTTCTGT  
 CATAAAATTTATGTGATTTCTTGATGAGTCATATTACTGTGATTTTCATAATAATGAAGACAC  
 CATGAATATACTTTTCTTCTATATAGTTTCAGCAATGGCCTGAATAGAAGCAACCAGGCACCAT  
 CTCAGCAATGTTTTCTTGTGTTTGTAAATTTTGTCTCCTTTGAAAATTAATCACTATTAATT  
 ACATTAATAAATCAAAATTGGATAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 452**

MTSKFILVSFILAALSLSTTFSLQLDQQKVLVVSFDGFRWDYLYKVPTPHFHYIMKYGVHVKQ  
VTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEEATPIWIT  
NQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPINLGLLYWED  
PDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIIITSDHGMTQCSEERLIEL  
DQYLDKDHYTLDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYNRIQP  
IIA VADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTDLYPLLC  
HLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPYFIGVSLGS  
IIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

**Important features:**

**Signal Peptide:**

amino acids 1-22

**Transmembrane Domain:**

amino acids 429-452

**N-glycosylation sites:**

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372,  
382-385, 389-392

**Somatomedin B Domain:**

amino acids 69-85

**Sulfatase protein Region:**

amino acids 212-241

**FIGURE 453**

GGCCGCCTGGAATTGTGGGAGTTGTGTCTGCCACTCGGCTGCCGGAGGCCGAAGGTCCGTGAC  
**TATGG**GCTCCCCAGAGCCTGCCTTCATCTAGGATGGCTCCTCTGGGCATGCTGCTTGGGCTGCT  
GATGGCCGCCTGCTTCACCTTCTGCCTCAGTCATCAGAACCTGAAGGAGTTTGGCCCTGACCAA  
CCCAGAGAAGAGCAGCACCAAAGAAACGGAGAGAAAAGAAACCAAAGCCGAGGAGGAGCTGGA  
TGCCGAAGTCCTGGAGGTGTTCCACCCGACGCATGAGTGGCAGGCCCTTCAGCCAGGGCAGGC  
TGTCCTTGCAGGATCCCACGTACGGCTGAATCTTCAGACTGGGGAAAGAGAGGCCAAAACCTCCA  
ATATGAGGACAAGTTCGAAATAATTTGAAAGGCAAAAGGCTGGATATCAACACCAACACCTA  
CACATCTCAGGATCTCAAGAGTGCCTGGCAAATTCAGGAGGGGGCAGAGATGGAGAGTTT  
AAAGGAAGACAAGGCAAGGCAGGCTGAGGTAAAGCGGCTCTTCGCCCCATTGAGGAACTGAA  
GAAAGACTTTTGATGAGCTGAATGTTGTCAATTGAGACTGACATGCAGATCATGGTACGGCTGAT  
CAACAAGTTCAATAGTTCCAGCTCCAGTTTGGGAAGAGAAGATTGCTGCGCTCTTTGATCTTGA  
ATATTATGTCCATCAGATGGACAATGCGCAGGACCTGCTTTCCTTTGGTGGTCTTCAAGTGGT  
GATCAATGGGCTGAACAGCACAGAGCCCCTCGTGAAGGAGTATGCTGCGTTTGTGCTGGGCGC  
TGCTTTTCCAGCAACCCCAAGGTCCAGGTGGAGGCCATCGAAGGGGGAGCCCTGCAGAAGCT  
GCTGGTCATCCTGGCCACGGAGCAGCCGCTCACTGCAAAGAAGAAGGTCTGTTTGCCTGTG  
CTCCCTGCTGCGCCACTTCCCCTATGCCAGCGGCAGTTCCTGAAGCTCGGGGGGCTGCAGGT  
CCTGAGGACCTGGTGCAGGAGAAGGGCACGGAGGTGCTCGCCGTGCGCGTGGTCACACTGCT  
CTACGACCTGGTCACGGAGAAGATGTTTCGCCGAGGAGGAGGCTGAGCTGACCCAGGAGATGTC  
CCCAGAGAAGCTGCAGCAGTATCGCCAGGTACACCTCCTGCCAGGCCTGTGGGAACAGGGCTG  
GTGCGAGATCACGGCCCACCTCCTGGCGCTGCCCGAGCATGATGCCCGTGAGAAGGTGCTGCA  
GACACTGGGCGTCCTCCTGACCACCTGCCGGGACCGCTACCGTCAGGACCCCCAGCTCGGCAG  
GACACTGGCCAGCCTGCAGGCTGAGTACCAGGTGCTGGCCAGCCTGGAGCTGCAGGATGGTGA  
GGACGAGGGCTACTTCCAGGAGCTGCTGGGCTCTGTCAACAGCTTGCTGAAGGAGCTGAGAT**GA**  
**AGG**CCCCACACCAGGACTGGACTGGGATGCCGCTAGTGAGGCTGAGGGGTGCCAGCGTGGGTG  
GGCTTCTCAGGCAGGAGGACATCTTGGCAGTGCTGGCTTGGCCATTAAATGGAACCTGAAGG  
CCAA  
AA

## **FIGURE 454**

MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPEKSSTKETERKETKAEELD  
AEVLEVFHPTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLOYEDKFRNNLKGKRLDINTNTY  
TSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMVRLI  
NKFNSSSSSLEEKIAALFDLEYVHQM DNAQDLLSFGGLQVVINGLNSTEPLVKEYA AFVLGA  
AFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKLGGLQV  
LRTL VQEKGT EVLAVRVV TLLYDLVTEKMFAEEEEAE LTQEMSPEKLQQYRQVHLLPGLWEQGW  
CEITAHLLALPEHDAREKVLQTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLASLELQDGE  
DEGYFQELLGSVNSLLKELR

**Important features:**

**Signal peptide:**

amino acids 1-29

**Hypothetical YJL126w/YLR351c/yhcX family protein.**

amino acids 364-373

**N-glycosylation site.**

amino acids 193-197, 236-240

**N-myristoylation site.**

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

**Homologous region SLS1 protein.**

amino acids 68-340

**FIGURE 455**

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCCAGAGCCCAGGAGGAGGCAGT  
GGCCAGGAAGGCACAGGCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCCTA  
CCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAGGAGAGGTGT  
CTGTGCGTCCTGCACCCACATCTTTCTCTGTCCCCCTCCTTGCCCTGTCTGGAGGCTGCTAGAC  
TCCTATCTTCTGAATTCTATAGTGCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGTCCCTTG  
TGGTTCCTCTCTACCTGGGGAAATAAGGTGCAGCGGCCATGGCTACAGCAAGACCCCCCTGGA  
TGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTACAGAGCATGTTCTCGCCA  
ACAATGATGTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCAGGACCTGG  
GAGCTGGGGCCGGGAAGACGCCCCGGTCGGATGACAGCAGCAGCCGCATCATCAATGGATCCG  
ACTGCGATATGCACACCCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCCCAACCAGCTCTACT  
GCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCACGGCCGCCACTGCAGGAAGAAAGTTT  
TCAGAGTCCGTCTCGGCCACTACTCCCTGTCAACAGTTTATGAATCTGGGCAGCAGATGTTCC  
AGGGGGTCAAATCCATCCCCACCCCTGGCTACTCCCACCCCTGGCCACTCTAACGACCTCATGC  
TCATCAAACCTGAACAGAAGAATTCTGTCCTAAAGATGTCAGACCCATCAACGTCTCCTCTC  
ATTGTCCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGGACAACCAAGAGCCCCCAAG  
TGCACTTCCCTAAGGTCTCCAGTGCTTGAATATCAGCGTGCTAAGTCAGAAAAGGTGCGAGG  
ATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGACAAAGCAGGTAGAGACT  
CCTGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCCTGCAGGGACTCGTGTCTT  
GGGGAGATTACCTTGTGCCCCGGCCCAACAGACCGGTGTCTACACGAACCTCTGCAAGTTCA  
CCAAGTGGATCCAGGAAACCATCCAGGCCAACTCCTGAGTCATCCCAGGACTCAGCACACCCG  
CATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTTCAGACCCCTCATTCCTTCCCAGAGA  
TGTGAGAATGTTTCATCTCTCCAGCCCCTGACCCCATGTCTCCTGGACTCAGGGTCTGCTTCC  
CCCACATTGGGCTGACCGTGTCTCTCTAGTTGAACCTGGGAACAATTTCCAAAACCTGTCCAG  
GGCGGGGGGTGCGTCTCAATCTCCCTGGGGCACTTTTCATCCTCAAGCTCAGGGCCCATCCCCTT  
CTCTGCAGCTCTGACCCAAATTTAGTCCCAGAAATAAACTGAGAAGTGGAACCAAAAAA

**FIGURE 456**

MATARPPMMWVLCALITALLLGVT EHVLANNDVSCDHPSNTVPSGSNQDLGAGAGEDARSDDS  
SSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLSPV  
YESGQQMFQGVKSI PHPGYSHPGHSNDLMLIKLNRRIRPTKDVRPINVSSHCP SAGTKCLVSG  
WGTTKSPQVHF PKVLQCLNISVLSQKRCEDAYPRQIDDTMFCAGDKAGRDSCQGD SGGPVVCN  
GSLQGLVSWG DYPCARPNRPGVYT NLCKFTKWIQETIQANS

**FIGURE 457**

GCAGTCAGAGACTTCCCCCTGCCCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCCTTGCTTCTGAACT  
 AGCTCACAGTAGCCCGGCGGCCAGGGCAATCCGACCACATTTCACTCTCACCGCTGTAGGAATCCAGATGCAGG  
 CCAAGTACAGCAGCACGAGGGACATGCTGGATGATGATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTG  
 CCACAACTCGGCATCCAGAGCCCCGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGA  
 CCCTGCTGACTTTGTGCTTGGTCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTACTACCAGC  
 TCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATACGTCCCAAGAGTTGCAATCTC  
 TTCAAGTCCAGAAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAACTCTGTGCTGAGCTGTATAACA  
 AAGCTGGAGCACACAGGTGCAGCCCTTGTACAGAACAATGGAATGGCATGGAGACAATTGCTACCAGTTCTATA  
 AAGACAGCAAAAGTTGGGAGGACTGTAAATATTTCTGCCTTAGTGAAACTCTACCATGCTGAAGATAAACAAAC  
 AAGAAGACCTGGAATTTGCCGCTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTTTGGCC  
 CTGACAGTGGCAAGGCCCTGGCTGTGGATGGATGGAACCCCTTTCACTTCTGAACTGTTCCATATTATAATAGATG  
 TCACCAGCCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGGGATGATCTTCTCAAAGGACTGCAAAGAATTGA  
 AGCGTTGTGTCTGTGAGAGAAGGGCAGGAATGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCG  
 AAGGTGACTGATTTCGCCCTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAG  
 ACATTGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTTCTCGTGTTTCTGT  
 CAGGATCACCAGCATTTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACAAGAAGTCTTATTTACATGCCAC  
 CAACCAACCTCAGAAACCCATAATGTCATCTGCCTTCTTGGCTTAGAGATAACTTTTAGCTCTCTTCTTCTCAA  
 TGTCTAATATCACCTCCCTGTTTTTCATGTCTTCCTTCACTTGGTGGAAATAAGAACTTTTGAAGTAGAGGAAA  
 TACATTGAGGTAACATCCTTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACITCCCAGATTGTAC  
 CAGCAATACACAAGGAATTCTTTTGTGTTTGTTCAGTTCATACTAGTCCCTTCCCAATCCATCAGTAAAGACCC  
 CATCTGCCTTGTCCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAGAATCTCAAATCTCAATGCCTTATAA  
 GCATTCTTCTGTGTCCATTAAAGACTCTGATAATTGTCTCCCTCCATAGGAATTTCTCCAGGAAAGAAATAT  
 ATCCCCATCTCCGTTTCATATCAGAACTACCGTCCCCGATATTCCCTTCAGAGAGATTAAAGACCAGAAAAAGT  
 GAGCCTCTTCATCTGCACCTGTAATAGTTTCAGTTCCTATTTTCTTCATTGACCCATATTATACCTTTTCAGGT  
 ACTGAAGATTTAATAATAATAAATGTAAATACTGTGAAAAA

**FIGURE 458**

MQAKYSSTRDMLDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCLVLLI  
GLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRELY  
NKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAASQSY  
SEFFYSYWTGLLRPD SGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMIFSKDCKEL  
KRCVCERRAGMVKPESLHVPPETLGEGD



**FIGURE 459**

GTTGATGGCAAACCTTCCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCAC  
TGGCGGCGCGCAACACTCCGTCTCACCTCTGGGCCCCTGCATCTAGAGGAGGGCCGTCTGT  
GAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTGAGAAGCTGGCCCAGGGTGGTGGT  
CAGCTGGGTGAGGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAGGGAA  
GTGGGAGCCTCGAGCCCTCGGGTGGAAGCTGACCCCAAGCCACCCTTCACCTGGACAGGATGA  
GAGTGTGAGGTGTGCTTCGCCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGATGTTTA  
TTCGAAGCTACATGAGCTTCAGCATGAAAAACCATCCGTCTGCCACGCTGGCTGGCAGCCTCGC  
CCACCAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCCAGCCAACT  
ACTTTGCGTTTAAATCTGCAGTGGGGCCGCCAACGTCGTGGGCCCTACTATGTGCTTTGAAG  
ACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGGCAGAGGCCATAACATCGCCCTGGTGA  
ATGGAACCACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGGAGATGTTATGC  
ACCTAGTGAAATTCCTTAAAGAAATTCGGGGGGTGCACTGGTGCTGGTGGCCTCCTACGACG  
ATCCAGGGACCAAAATGAACGATGAAAGCAGGAACTCTTCTCTGACTTGGGGAGTTCTTACG  
CAAAACAACCTGGGCTTCGGGACAGCTGGGTCTTCATAGGAGCCAAAGACCTCAGGGGTAAAA  
GCCCCTTTGAGCAGTTCTTAAAGAACAGCCAGACACAAACAAATACGAGGGATGGCCAGAGC  
TGCTGGAGATGGAGGGCTGCATGCCCCGAAGCCATTTTAGGGTGGCTGTGGCTCTTCTCAG  
CCAGGGGCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCGGCAGGGGCTGAGGAGGA  
GGAGCAGGGGGTGTGCGTGGAAGGTGCTGCAGGTCTTGCACGCTGTGTGCGCCTCTCCTC  
CTCGGAAACAGAACCCTCCACAGCACATCCTACCCGGAAGACCAGCCTCAGAGGGTCTTCT  
GGAACCAGCTGTCTGTGAGAGAATGGGGTGCTTTTCGTCAGGGACTGCTGACGGCTGGTCCTG  
AGGAAGGACAACTGCCAGACTTGAGCCCAATTAAATTTTATTTTGTGCTGGTTTGAAGAAA  
AAAAAAAAAAAAA

**FIGURE 460**

MRVSGVLRLLALIFAIVTTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCPA  
NYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSGDV  
MHLVKFLKEIPGGALVLVASYYDDPGTKMNDESRLKLFSDLGSSYAKQLGFRDSWVFIGAKDLRG  
KSPFEQFLKNSPDTNKEYEGWPELLEMEGCMPPKPF

**Important features:**

**Signal peptide:**

amino acids 1-15

**ATP/GTP-binding site motif A (P-loop).**

amino acids 184-191

**N-glycosylation site.**

amino acids 107-110

# **FIGURE 461**

AAACTCAGCACTTGCCGGAGTGGCTCATTGTTAAGACAAAGGGTGTGCACTTCCTGGCCAGGA  
AACCTGAGCGGTGAGACTCCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACCTTCCTC  
TAGAACCCGACCCACCACCATGAGGTCTGCTGTGGAGATGCAGGCACCTGAGCCAAGGCGT  
CCAGTGGTCCTTGCTTCTGGCTGTCTGCTCTTCTTTCTCTTCGCTTGCCCTCTTTTATTAA  
GGAGCCTCAAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAAGAAAGGTCTCTACA  
GTCCCTGGCAAAGCCTAAGTCCAGGCACCCACAAGGGCGAGGAGGACAACCATCTATGCAGA  
GCCAGCGCCAGAGAACAATGCCCTCAACACACAAACCCAGCCCAAGGCCCACACCACCGGAGA  
CAGAGGAAAGGAGGCCAACCCAGGCACCGCCGGAGGAGCAGGACAAGGTGCCCCACACAGCACA  
GAGGGCAGCATGGAAGAGCCCAGAAAAAGAGAAAACCATGGTGAACACACTGTCACCCAGAGG  
GCAAGATGCAGGGATGGCCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCCAGGACACAAA  
GACGACCCAAGGAAATGGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGACGGTGTGAGAGAA  
GCACCAGGGCAAAGCGGCAACCACAGCCAAGACGCTCATTCCCAAAGTCAGCACAGAATGCT  
GGCTCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCACAGCAGTCATCCC  
ACCTAAGGAGAAGAAACCTCAGGCCACCCACCCCTGCCCCCTTCCAGAGCCCCACGACGCA  
GAGAAACCAAAGACTGAAGGCCGCCAACTTCAAATCTGAGCCTCGGTGGGATTTTGAGGAAAA  
ATACAGCTTCGAAATAGGAGGCCCTTCAGACGACTTGCCCTGACTCTGTGAAGATCAAAGCCTC  
CAAGTCGCTGTGGCTCCAGAACTCTTTCTGCCCAACCTCACTCTCTTCTGGACTCCAGACA  
CTTCAACCAGAGTGAGTGGGACCGCTGGAACACTTTGCACCACCTTTGGCTTCATGGAGCT  
CAACTACTCCTTGGTGCAGAAGGTCGTGACACGCTTCCCTCCAGTGCCCCAGCAGCAGCTGCT  
CCTGGCCAGCCTCCCCGCTGGGAGCCTCCGGTGCATCACCTGTGCCGTGGTGGGCAACGGGGG  
CATCCTGAACAACCTCCACATGGGCCAGGAGATAGACAGTCACGACTACGTGTTCCGATTGAG  
CGGAGCTCTATTAAAGGCTACGAACAGGATGTGGGGACTCGGACATCCTTCTACGGCTTTAC  
CGCCTTCTCCCTGACCCAGTCACTCCTTATATTGGGCAATCGGGGTTTCAAGAAGTGCCTCT  
TGGGAAGGACGTCCGCTACTTGCACCTCCTGGAAGGCACCCGGGACTATGAGTGGCTGGAAGC  
ACTGCTTATGAATCAGACGGTGATGTCAAAAAACCTTTTCTGGTTTCAGGCACAGACCCCAGGA  
AGCTTTTCGGGAAGCCCTGCACATGGACAGGTACCTGTTGCTGCACCCAGACTTTCTCCGATA  
CATGAAGAACAGGTTTCTGAGGTCTAAGACCCCTGGATGGTGCCCACTGGAGGATATACCGCCC  
CACCCTGGGGCCCTCCTGCTGCTCACTGCCCTTCAGCTCTGTGACCAGGTGAGTGCTTATGG  
CTTCATCACTGAGGGCCATGAGCGCTTTTCTGATCACTACTATGATACATCATGGAAGCGGCT  
GATCTTTTACATAAAACCATGACTTCAAGCTGGAGAGAGAAGTCTGGAAGCGGCTACACGATGA  
AGGGATAATCCGGCTGTACCAGCGTCTGGTCCCGGAACTGCCAAAGCCAAGAACTGACCGGG  
GCCAGGGCTGCCATGGTCTCCTTGCTGCTCCAAGGCACAGGATACAGTGGGAATCTTGAGAC  
TCTTTGGCCATTTCCCATGGCTCAGACTAAGCTCCAAGCCCTTCAGGAGTTCCAAGGGAACAC  
TTGAACCATGGACAAGACTCTCTCAAGATGGCAAATGGCTAATTGAGGTCTGAAGTTCTTCA  
GTACATTGCTGTAGGTCTGAGGCCAGGGATTTTAAATTAAATGGGGTGATGGGTGGCCAATA  
CCACAATTCTGCTGAAAAACACTCTTCCAGTCCAAAAGCTTCTTGATACAGAAAAAGAGCC  
TGGATTTACAGAAACATATAGATCTGTTTGAATTCCAGATCGAGTTTACAGTTGTGAAATCT  
TGAAGGTATTACTTAACTTCACTACAGATTGTCTAGAAGACCTTTCTAGGAGTTATCTGATTC  
TAGAAGGGTCTATACTTGTCTTGTCTTTAAGCTATTTGACAACTCTACGTGTGTAGAAAAAC  
TGATAATAATACAAATGATTGTTGTCCATGGAAAGGCAAATAAATTTTCTACAGTGAAAAAAA  
AAAAAAA

**FIGURE 462**

MRSC LWRCRHLSQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHQRTENIKERSLQSLAKPK  
SQAPTRARRTTIYAEPAPENNALNTQTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAWKS  
PEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTQTQGNCGQTRKLTASRTVSEKHQGKAA  
TTAKTLIPKSQLRMLAPTGA VSTRTRQKGVTTAVIPPKEKKPQATPPPAPFQSP TTTQRNQR LK  
AANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFLPNLTFLDSRHFNQSEW  
DRLEHFAPPFGFMELNYSLVQKV VTRFPVPVQQQLLLASLPAGSLRCITCAVVGNGGILNNSH  
MGQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGF TAFSLTQSL LILGNRGFKNVPLGKD VRY  
LHFLEGTRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFREALHMDRYLLLHPDFLRYMKNRFL  
RSKTL DGAHWRIYRPTTGALLLLTALQLCDQVSAYGFITEGHERFSDHYDTSWKRLIFYINH  
DFKLEREVWKRLHDEGIIRLYQRPGPGTAKAKN

**Important features:**

**Cytoplasmic Domain:**

amino acids 1-10

**Type II Transmembrane Domain:**

amino acids 11-35

**Lumenal catalytic Domain:**

amino acids 36-600

**Ribonucleotide Reductase small subunit Signature:**

amino acids 481-496

**N-glycosylation Sites:**

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

# FIGURE 463

GGGGGAGCTAGGCCGGCGGCAGTGGTGGTGGCGGCGCAAGGGTGAGGGCGGCCCCAGAAC  
 CCCAGGTAGGTAGAGCAAGAAGATGGTGTCTTCTGCCCCCTCAAATGGTCCCTTGCAACCATGTC  
 ATTTCTACTTTTCTCTCACTGTTGGCTCTCTTAACTGTGTCCACTCCTTCATGGTGTGAGAGCAC  
 TGAAGCATCTCCAAAACGTAGTAGTGATGGGACACCATTTCTTTGGAATAAAAATACGACTTCCTGA  
 GTACGTCAATCCCAAGTTCATTATGATCTCTTGATCCATGCAAACCTTACCACGCTGACCTTCTG  
 GGGAAACCACGAAAGTAGAAATCACAGCCAGTCAGCCCACCAGCACCATCATCTGTCATAGTCA  
 CCACCTGTCAGATATCTAGGGCCACCCTCAGGAAGGGAGCTGGAGAGAGGCTATCGGAAGAACC  
 CCTGCAAGTCTCTGGAACACCCCCCTCAGGAGCAAATTTGCACTGCTGGCTCCCGAGCCCCCTCT  
 TGTGGGCTCCCGTACACAGTTTGTCACTTCACTATGCTGGCAATCTTTGGAGACTTTCCACGG  
 ATTTTACAAAAGCACCTACAGAACCAAGGAAGGGGAACTGAGGATAGCTAGCATCAACACAATTT  
 TGAACCCACTGCAGCTAGAATGGCCTTTCCCTGCTTTGATGAACCTGCTTCAAAGCAAGTTT  
 CTCAATCAAAATTAGAAGAGAGCCAAAGCCACTAGCCATCTCCAATATGCCATTGGTGAAATC  
 TGTGACTGTTGCTGAAGGACTCATAGAAGACCATTTTGTATGCTCACTGTGAAGATGAGCACCTA  
 TCTGGTGGCCTTCATCATTTTCAAGTTTGTGAGTCTGTGAGCAAGATAACCAAGAGTGGAGTCAA  
 GGTCTCTGTTTATGCTGTGCCAGACAAGATAAATCAAGCAGATTATGCACTGGATGCTGCGGT  
 GACTCTTCTAGAATTTTATGAGGATTATTTTCAAGTATACCGTATCCCTTACCACCAAGATCT  
 TGCTGCTATTCCCGACTTTTCACTCTGGTGTATGGAACCTGGGGACTGACACATATAGAGA  
 ATCTGCTCTGTTGTTGATGCAGAAAAGTCTTCTGCATCAAGTAAGCTTGGCATCACAGTGAC  
 TGTGGCCCATGAACCTGGCCACCAGTGGTTTGGGAACCTGGTCACTATGGAATGGTGGAATGA  
 TCTTTGGCTAAATGAAGGATTTGCCAAATTTATGGAGTTTGTGTCTGTCACTGTGACCCATCC  
 TGAAGTGAAAGTTGGAGATTATTTCTTTGGCAAAATGTTTGTACGCAATGGAGGTAGATGCTTT  
 AAATTCCTCACACCCTGTGTCTACACCTGTGGAAAATCCTGCTCAGATCCGGGAGATGTTTGA  
 TGATGTTTCTTATGATAAGGGAGCTTGTATTTCTGAATATGCTAAGGGAGTATCTTAGCGCTGA  
 CGCATTTAAAAGTGGTATTGTACAGTATCTCCAGAAAGCATAGCTATAAAAAATACAAAAACGA  
 GGACCTGTGGGATAGTATGGCAAGTATTTGCCCTACAGATGGTGTAAAAGGGATGGATGGCTT  
 TTGCTCTAGAAGTCAACATTCATCTTCACTCCTCACATTGGCATCAGGAAGGGGTGGATGTGAA  
 AACCATGATGAACACTTGGACACTGCAGAGGGGTTTTCCCTAATAACCATCACAGTGAGGGG  
 GAGGAATGTACACATGAAGCAAGAGCACTACATGAAGGGCTCTGACGGCGCCCCGGACACTGG  
 GTACCTGTGGCATGTTCCATTGACATTCATCACCAGCAAATCCAACATGGTCCATCGATTTTTT  
 TCAAGCTCTGAGCATTTGGGAAGCTGTCCATTGAAAAGGCCCTTGGATTTATCCCTGTACTTGA  
 GGGCATGAATGGCTATTACATTGTGCATTACGAGGATGATGGATGGGACTCTTTGACTGGCCT  
 TTTAAAAGGAACACACACAGCAGTCAGCAGTAATGATCGGGCAAGTCTCATTAAACAATGCATT  
 TTTAAAAGGAACACACACAGCAGTCAGCAGTAATGATCGGGCAAGTCTCATTAAACAATGCATT  
 ACATGAAACTGAAATTATGCCCGTGTTCAGGTTTTGAATGAGCTGATTCCCTATGTATAAGTT  
 AATGGAGAAAAGAGATATGAATGAAGTGGAAACTCAATTCAAGGCCCTTCTCATCAGGCTGCT  
 AAGGGACCTCATTGATAAGCAGACATGGACAGACGAGGGCTCAGTCTCAGAGCAAATGCTGCG  
 GAGTGAACCTACTCTCCTCGCCTGTGTGCACAACTATCAGCCGTGCGTACAGAGGGCAGAAGG  
 CTATTTTCAAGAAAGTGAAGGAATCCAATGGAAACTTGAGCCTGCCTGTGACGCTGACCTTGGC  
 AGTGTCTGTGCTGTGGGGGCCAGAGCACAGAAGGCTGGGATTTTCTTTATAGTAAATATCAGTT  
 TTCTTTGTCCAGTACTGAGAAAAGCCAAATTGAATTTGCCCTCTGCAGAACCCAAAATAAGGA  
 AAAGCTTCAATGGCTACTAGATGAAAGCTTTAAGGGAGATAAAAATAAAACTCAGGAGTTTCC  
 ACAAATTTTACACTCATTGGCAGGAACCCAGTAGGATACCCACTGGCCTGGCAATTTCTGAG  
 GAAAACTGGAACAACTTTGTACAAAAGTTTGAACCTTGGCTCATCTTCCATAGCCCACATGGT  
 AATGGGTACAACAAATCAATTTCCACAAGAACACGGCTTGAAGAGGTAAAAGGATTCTTCAG  
 CTCTTTTGAAGAAAATGGTTCTCAGCTCCGTTGTGTCCAACAGACAATTGAAACCATTGAAGA  
 AAACATCGGTTGGATGGATAAGAATTTTGATAAAATCAGAGTGTGGCTGCAAAGTGAAGAGCT  
 TGAACGTATGTAATAAATTCCTCCCTTGGCCGTTTCTGTTATCTCTAATCACCACATTTTGT  
 TGAGTGTATTTTCAAACCTAGAGATGGCTGTTTTGGCTCCAACCTGGAGATACTTTTTTCCCTTC  
 AACTCATTTTTTGAATATCCCTGTGAAAAGAAATAGCTGTTAGTTTTTTCATGAATGGGCTTTTT  
 CATGAATGGGCTATCGCTACCATGTGTTTTGTTTCACTACAGGTGTTGCCCTGCAACGTAAACC  
 CAAGTGTGGGTTCCCTGCCACAGAAGAATAAAGTACCTTATTCTTCTCAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAA

**FIGURE 464**

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVHY  
DLLIHANLTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPLQVLEHP  
PQEQIALLAPEPLLVLGYPTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTAARM  
AFPCFDEPAFKASFSIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVAFIIS  
DFESVSKITKSGVKVSVYAVPDKINQADYALDAAVTLLEFYEDYFSIPYPLPKQDLAAIPDFQ  
SGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVVAHELHQWFGNLVTMEWWNDLWLNELF  
AKFMEFVSVSVTHPELVKVDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFDDVSYDKG  
ACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKGMDFGCSRSQHS  
SSSSHWHQEGVDVKTMMNTWTTLQRGFPLITITVGRNVHMKQEHYMKGSDGAPDTGYLWHVPL  
TFITSKSNMVHRFLLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSLTGLLKGTHTA  
VSSNDRASLINNAFQLVSIKLSIEKALDLSLYLKHETEIMPVFQGLNELIPMYKLMKRD MN  
EVETQFKAFLIRLLRDLIDKQTTWDEGSVSEQMLRSELLLLACVHNYQPCVQRAEGYFRKWKE  
SNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSSSTEKSQIEFALCRTCQNKEKLQWLLD  
ESFKGDKIKTQEFPPQILTIGRNPVGYPLAWQFLRKNWNKLVQKFELGSSSIAHVMVGT'TNQF  
STRTRLEE VKGFFSSLKENGSQLRCVQQTITETIEENIGWMDKNFDKIRVWLQSEKLERM

**Important features:**

**Signal peptide:**

amino acids 1-34

**N-glycosylation sites:**

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

**Neutral zinc metallopeptidases, zinc-binding region signature:**

amino acids 350-360

**FIGURE 465**

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCACT  
GCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCCGA  
CCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCCGACAGCGGCTTGGGGTGCCAGGACAC  
GTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGGAGGC  
CAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTA  
CACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGC  
CCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGGAAGGCTG  
TCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACTGTTATGATGGCCTCCT  
CAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGG  
TTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCCGTGGGTATGACTGAGAACTGCAATAG  
GAAAGATTTTCTGACCTGTCTATCGGGGGACCACCATTTATGACACACGGAACTTGGCTCAAGA  
ACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCTAGGAGAC  
GCTGCTGCTCATAGATGTAGGACTCACATCAACCCCTGGTGGGGACAAAAGGCTGCAGCACTGT  
TGGGGCTCAAAATTTCCAGAAGACCACCATCCACTCAGCCCCCTCCTGGGGTGCTTGTGGCCTC  
CTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAA  
CTCCCTCCCTCCTCAAGCTGCCCCCTGTCCCAGGAGACCGGCAGTGTCTACCTGTGTGCAGCC  
CCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTA  
TGATGGGTACATTCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTGAGGGCTGCGT  
GGCCCAACCTTCCAGCTTCTTGTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGA  
GAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC  
TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGGCCCTC  
CTGCTTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACCTCCCTC  
TGACCTCATAACCTAATGGCCTTGACACCAGATTCTTTCCCATTCTGTCCATGAATCATCTT  
CCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGAGCCTGGAGCATC  
CGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTATCTGATAATACAGAC  
CCTGTCCTTTCA

**FIGURE 466**

MSAVLLLLALLGFILPLPGVQALLCQFGTVQHVKVSDLPQWTPKNTSCDSGLGCQDTLMLIE  
SGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQPPA  
DPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRGRGGIFSNLRVQGCMPPQPGCNLLN  
GTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETLLLLID  
VGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLNCSASSSSVLLNSLPPQ  
AAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGCVAQPSS  
FLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGVGLALAPALWWGVVCPSC



# FIGURE 467

GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGAGCCCTTGAGACATCCTTG  
 AGAAGAGCCACAGCATAAGAGACTGCCCTGCTTGGTGTTCCTGTCAGGATGATGGTGGCCCTTCG  
 AGGAGCTTCTGCATTGCTGGTTCTGTTCTTGCAGCTTTCTGCCCCCGCCGAGTGTACCCA  
 GGACCCAGCCATGGTGCATTACATCTACCAGCGCTTCGAGTCTTGGAGCAAGGGCTGGAAAA  
 ATGTACCCCAAGCAACGAGGGCATAACATTCAGAATTCGAAGATTCTCAAAAAATATATCTGT  
 CATGCTGGGAAGATGTCAGACCTACACAAGTGAGTACAAGAGTGCAGTGGGTAACCTTGGCACT  
 GAGAGTTGAACGTGCCAACGGGAGATTGACTACATACAATACCTTCGAGAGGCTGACGAGTG  
 CATCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAAGAGAAAAA  
 GATCCGGACTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTCTTTGAAAAAT  
 AGTGAAGAAGATGATGGACACACATGGCTCTTGGATGAAAGATGCTGTCTATAACTCTCCAAA  
 GGTGTACTTATTAATTGGATCCAGAAACAACACTGTTTGGGAATTTGCAAACATACGGGCATT  
 CATGGAGGATAACACCAAGCCAGCTCCCCGGAAGCAAATCCTAACACTTTCTGGCAGGGAAC  
 AGGCCAAGTGATCTACAAAGGTTTTCTATTTTTTTCATAACCAAGCAACTTCTAATGAGATAAT  
 CAAATATAACCTGCAGAAGAGGACTGTGGAAGATCGAATGCTGCTCCAGGAGGGGTAGGCCG  
 AGCATTGGTTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGTGGATGAGCATGGGCT  
 CTGGGCCATCCACTCTGGGCCAGGCACCCATAGCCATTTGGTCTCACAAAGATTGAGCCGGG  
 CACACTGGGAGTGGAGCATTCATGGGATACCCCATGCAGAAGCCAGGATGCTGAAGCCTCATT  
 CCTCTTGTGTGGGTTCTCTATGTGGTCTACAGTACTGGGGGCCAGGGCCCTCATCGCATCAC  
 CTGCATCTATGATCCACTGGGCACTATCAGTGAGGAGGACTTGCCCAACTTGTTCTTCCCCAA  
 GAGACCAAGAAGTCACTCCATGATCCATTACAACCCAGAGATAAGCAGCTCTATGCCTGGAA  
 TGAAGGAAACCAGATCATTTACAAACTCCAGACAAAGAGAAAGCTGCCTCTGAAGTAATGCAT  
 TACAGCTGTGAGAAAGAGCACTGTGGCTTTGGCAGCTGTTCTACAGGACAGTGAGGCTATAGC  
 CCCTTCACAATATAGTATCCCTCTAATCACACACAGGAAGAGTGTGTAGAAGTGGAATACGT  
 ATGCCTCCTTTCCCAAATGTCACTGCCTTAGGTATCTTCCAAGAGCTTAGATGAGAGCATATC  
 ATCAGGAAAGTTTCAACAATGTCATTACTCCCCAAACCTCCTGGCTCTCAAGGATGACCAC  
 ATTCTGATACAGCCTACTTCAAGCCTTTTGTCTTTTACTGCTCCCCAGCATTTACTGTAACCTCTG  
 CCATCTTCCCTCCCACAATTAGAGTTGTATGCCAGCCCCCTAATATTCACCACTGGCTTTTCTC  
 TCCCTGGCCTTTTGCTGAAGCTCTTCCCTCTTTTTTCAAATGTCTATPGATATTCTCCATTTT  
 CACTGCCCAACTAAAATACTATTAATATTTCTTTCTTTTCTTTTCTTTTCTTTTGGAGACAAGGT  
 CTCATATGTTGGCCAGGCTGGTCTCAAACCTCCAGAGCTCAAGAGATCCTCCTGCCTCAGCCT  
 CCTAAGTACCTGGGATTACAGGCATGTGCCACCACACCTGGCTTAAATACTATTTCTTATTG  
 AGGTTTAACCTCTATTTCCCTAGCCCTGTCCTTCCACTAAGCTTGGTAGATGTAATAATAAAA  
 GTGAAAATATTAACATTTGAATATCGCTTTCCAGGTGTGGAGTGTTCACATCATTGAATTC  
 TCGTTTTACCTTTGTGAAACATGCACAAGTCTTTACAGCTGTCAATTCTAGAGTTTAGGTGAGT  
 AACACAATTACAAAGTGAAAGATACAGCTAGAAAATACTACAAATCCCATAGTTTTTCCATTG  
 CCCAAGGAAGCATCAAATACGTATGTTTGTTCACCTACTCTTATAGTCAATGCGTTTCATCGTT  
 TCAGCCTAAAAATAATAGTCTGTCCCTTTAGCCAGTTTTTCATGTCTGCACAAGACCTTTCAAT  
 AGGCCTTTCAAATGATAATTCTCCAGAAAACAGTCTAAGGGTGAGGACCCCAACTCTAGCC  
 TCCTCTTGTCTTGTCTGTCTCTTCTCTCTTTCTGCTTTAAATTCAATAAAGTGACACTG  
 AGCAAAAAAAAAAAAAA

**FIGURE 468**

MMVALRGASALLVLFLLAAFLPPPQCTQDPAMVHYIYQRFVRVLEQGLEKCTQATRAYIQEFQEF  
SKNISVMLGRCQTYTSEYKSAVGNLALRVERAQREIDYIQYLREADECIVSEDKTLAEMLLQE  
AEEKKIRTLNLNASCDNMLMGIKSLKIVKKMMDTHGSWMKDAVYNSPKVYLLIGSRNNTVWEF  
ANIRAFMEDNTKPAPRKQILTLWQGTGQVIYKGFLFFHNQATSNEIIKYNLQKRTVEDRMLL  
PGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEPGTLGVEHSWDTPCRSQ  
DAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFFPKRPRSHSMIHYNPRDK  
QLYAWNEGNQIIYKLQTKRKLPLK

**FIGURE 469**

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGGC  
AGTGTTTTGCCTTCACCCCAAGTGACCATGAGAGGTGCCACGCGAGTCTCAATCATGCTCCTC  
CTAGTAACTGTGTCTGACTGTGCTGTGATCACAGGGGCCTGTGAGCGGGATGTCCAGTGTGGG  
GCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGCACCCCGCTGGGG  
CGGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCCCTTCTTCAGGAAACGCAAGCAC  
CACACCTGTCCTTGCTTGCCCAACCTGCTGTGCTCCAGGTTCCCGACGGCAGGTACCGCTGC  
TCCATGGACTTGAAGAACATCAATTTTTTAGGCGCTTGCCTGGTCTCAGGATACCCACCATCCT  
TTTCTGAGCACAGCCTGGATTTTTATTTCTGCCATGAAACCCAGCTCCCATGACTCTCCAG  
TCCCTACACTGACTACCCTGATCTCTCTTGTCTAGTACGCACATATGCACACAGGCAGACATA  
CCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTACAGCTTGAGGCTGTGGTGTG  
AAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTAAATGGCAGAAA  
GGACATTCCCCCTCCCCTCCCCAGGTGACCTGCTCTTTTCTGGGCCCTGCCCTCTCCCCA  
CATGTATCCCTCGGTCTGAATTAGACATTCTGGGCACAGGCTCTTGGGTGCATTGCTCAGAG  
TCCCAGGTCCTGGCCTGACCCTCAGGCCCTTCACGTGAGGTCTGTGAGGACCAATTTGTGGGT  
AGTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGACTCAAGATTGGCTCTT  
CCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCAGGGAGGCCAATCAGCC  
CCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTTGTGGCCTGTGACCTGTGACCTTCTGCCA  
GAATTGTCATGCCTCTGAGGCCCCCTCTTACCACACTTTACCAGTTAACCCTGAAGCCCCCA  
ATTCCCACAGCTTTTCCATTAAAAATGCAAATGGTGGTGGTTCAATCTAATCTGATATTGACAT  
ATTAGAAGGCAATTAGGGTGTTCCTTAAACAACTCCTTTCCAAGGATCAGCCCTGAGAGCAG  
GTTGGTGACTTTGAGGAGGGCAGTCCTCTGTCCAGATTGGGGTGGGAGCAAGGGACAGGGAGC  
AGGGCAGGGGCTGAAAGGGGCACTGATTACAGACCAGGGAGGCAACTACACACCAACATGCTGG  
CTTTAGAATAAAAGCACCAACTGAAAAAA

**FIGURE 470**

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPG  
SHKVPFFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

**Important feratures:**

**Signal peptide:**

amino acids 1-19

**Tyrosine kinase phosphorylation site:**

amino acids 88-95

**N-myristoylation sites:**

amino acids 33-39, 35-41, 46-52

**FIGURE 471**

AGCGCCCGGGCGTCGGGGCGGTAAAAGGCCGGCAGAAGGGAGGCACTTGAGAAATGTCTTTCC  
TCCAGGACCCCAAGTTTCTTCACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGCTG  
CTGCCTTGGCATGTGCTGCTTGCCAACACAGACGTGTTTCTGTCCAAGCCCCAGAAAGCGGCCC  
TGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAAAGCAA  
AGGAGCTATGGGAAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTTCCTCT  
GTCGAGAGGAAGCTGCGGATCTGTCCTCCCTGAAAAGCATGTTGGACCAGCTGGGCGTCCCCC  
TCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTATTTCAAAG  
GAGAAATCTTCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGGCGGAAGATGATGTTTA  
TGGGATTTATCCGTCTGGGAGTGTGGTACAACTTCTTCCGAGCCTGGAACGGAGGCTTCTCTG  
GAAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTTCGTGGTGGGATCAGGAAAGCAGG  
GCATTCTTCTTGAGCACCGAGAAAAAGAATTTGGAGACAAAGTAAACCTACTTTCTGTTCTGG  
AAGCTGCTAAGATGATCAAACCACAGACTTTGGCCTCAGAGAAAAAATGATTGTGTGAAACTG  
CCCAGCTCAGGGATAACCAGGGACATTCACCTGTGTTTATGGGATGTATTGTTTCCACTCGTG  
TCCCTAAGGAGTGAGAAACCCATTTATACTCTACTCTCAGTATGGATTATTAATGTATTTTAA  
TATTCTGTTTAGGCCCACCTAAGGCAAAATAGCCCCAAAACAAGACTGACAAAAATCTGAAAAA  
CTAATGAGGATTATTAAGCTAAAACCTGGGAAATAGGAGGCTTAAAATTGACTGCCAGGCTGG  
GTGCAGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCAAGGTGAGCAAGTCACTTGAG  
GTCGGGAGTTTCGAGACCAGCCTGAGCAACATGGCGAAACCCGTCTCTACTAAAAATACAAAA  
ATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCGGGAGGCTGAGGCAGGAGAA  
TCACTTGAACCTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCACACCACTGTATTCCAGCCTG  
GGTGACTGAGACTCTAACTAA

**FIGURE 472**

MSFLQDPSFFTGMWSIGAGALGAAALALLLANTDVFLSKPQKALEYLEDIDLKTLEKEPRT  
FKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDFQP  
YFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGEGBFILGGVFVVG  
GKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

**FIGURE 473**

AATATATCATCTATTTATCATTAATCAATAATGTATTCTTTTATTCCAATAACATTTGGGTTT  
TGGGATTTTAATTTTCAAACACAGCAGAATGACATTTTTCTGTCACTATTATTATTGTTGGT  
ATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCTATC  
AAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTCCTAC  
CAAAGCTGTCAAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGAGGGTT  
AATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATGATTGTA  
AATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATATATACAA  
TAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACTTTATTAAT  
TTTTAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGATCATATAAT  
TTGATACAAATAAAAGAAAAGTGTCTCTCCCTTACAGAATTGACATTTTAAATGCCATACA  
GTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAAAGAAGCGAAAA  
TGTTGCCAAGGAAAAAAAAA

**FIGURE 474**

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGKG  
IVKGRNLDSRGLILGAEEAWGRGVKKNT





**FIGURE 476**

MAPLALHLLVLPILLSLVSQDWKAERSQDPFEKCMQDPDYEQLLKVVWTWGLNRTLKPQRVI  
VVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSSHRILHK  
LCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPEKLGIALRPQEKGHSPEDIYQMALNQ  
ALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMSDGGFFYLSFAEALRAHSC  
LSDRLQYSRIVGGWDLPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPPARNLKVKA  
DVVLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFRPPFWREEHIEGGHSNTDR  
PSRMIFYPPPREGALLASYTWSDAFAAGLSREEALRLALDDVAALHGPVVRQLWDGTGVV  
KRWAEQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKSALRAAIKI  
NSRKGPASDTASPEGHASDMEGQGHVHGVAASSPSHDLAKEEGSHPPVQQLSLQNTTHTRTSH

**Important features:**

**Signal peptide:**

amino acids 1-21

# **FIGURE 477**

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCCGGCCTTCTGCTGCAAT  
GGACGCTCTGAAGCCACCCTGTCTCTGGAGGAACCAAGAGCGAGGGGAAGAAGGACAGGGACTCGTGTGGCAGGAA  
GAACTCAGAGCCGGGAAGCCCCATTCACTAGAGCACTGAGAGATGCGGGCCCCCTCGCAGGGTCTGAATTTCTT  
GCTGCTGTTTCAAAAGATGCTTTTATCTTTAACTTTTGTGTTTCCCACTTCCGACCCCGCGGTGATCTGCAT  
CCTGACATTTGGAGCTGCCATCTTCTGTGGCTGATCACCAGACCTCAACCCGTCTTACCTCTTCTTGACCTGAA  
CAATCAGTCTGTGGGAATTGAGGGAGGAGCACGGAAGGGGGTTTCCAGAGAACAATGACCTAAACAAGTTGCTG  
CTTCTCAGATGCCAAGACTATGTATGAGGTTTCCAAAGAGGACTCGCTGTGTCTGACAATGGGCCCTGCTTGGG  
ATATAGAAAACCAAACAGCCCTACAGATGGCTATCTTACAAACAGGTGTCTGATAGAGCAGAGTACCTGGGTTT  
CTGTCTCTTGCAATAAGGTTATAAATCATCACCAGACCACTTGTGCGCATCTTTGCTCAGAAATAGGCCAGAGTG  
GATCATCTCCGAATTGGCTTGTACAGTACTCTATGGTAGCTGTACCTCTGTATGACACCTTGGGACCAGAAGC  
CATCGTACATATTGTCAACAAGGCTGATATCGCCATGGTGATCTGTGACACACCCCAAAAGGCATTGGTGCTGAT  
AGGGAATGTAGAGAAGGCTTCAACCCGAGCCTGAAGGTGATCATCCTTATGGACCCCTTGTATGATGACCTGAA  
GCAAGAGGGGAGAGAAGTGGAAATTGAGATCTTATCCCTATATGATGCTGAGAACCCTAGGCCAAAGAGCACTCAG  
AAAACCTGTGCCTCCTAGCCCAAGACCTGAGCGTCATCTGCTTACCAGTGGGACCACAGGTGACCCCAAGG  
AGCCATGATAACCCATCAAAATATTGTTTCAAATGCTGCTGCCCTTCTCAAATGTGTGGAGCATGCTTATGAGCC  
CACTCCTGATGATGTGGCCATATCCTACCTCCCTCTGGCTCATATGTTTGAGAGGATTGTACAGGCTGTTGTGTA  
CAGCTGTGGAGCCAGAGTTGGATTCTTCCAAGGGGATATTTCGGTTGCTGGCTGACGACATGAAGACTTTGAAGCC  
CACATTGTTTCCCGCGGTGCTCGACTCCTTAACAGGATCTACGATAAGGTACAAATGAGGCCAAGACACCCCTT  
GAAGAAGTTCTTGTGAAGCTGGCTGTTTCCAGTAAATTCAAAGAGCTTCAAAGGGTATCATCAGGCATGATAG  
TTTCTGGGACAAAGCTCATCTTTGCAAGATCCAGGACAGCCTGGGCGGAAGGGTTCTGTAAATTGTCACTGGAGC  
TGCCCCCATGTCCACTTCAGTCATGACATTCTTCCGGGCAGCAATGGGATGTCAGGTGTATGAAGCTTATGGTCA  
AACAGAATGCACAGGTGGCTGTACATTTACATTACCTGGGACTGGACATCAGGTACGTTGGGGTGGCCCTGGC  
TTGCAATTACGTGAAGCTGGAAGATGTGGCTGACATGAACACTTTTACAGTGAATAATGAAGGAGAGGTCTGCAT  
CAAGGTACAAACGTTTCAAAGGATACCTGAAGGACCTTGAGAAGACACAGGAAGCCCTGGACAGTGATGGCTG  
GCTTCACACAGGAGACATTGGTTCGCTGGCTCCCGAATGGAATCTGAAGATCATCGACCGTAAAAAGAACATTTT  
CAAGCTGGCCCCAAGGAGAATACATTGCACCAGAGAAGATAGAAAATATCTACAACAGGAGTCAACCACTGTTACA  
AATTTTTGTACACGGGGAGAGCTTACGGTCATCCTTAGTAGGAGTGGTGGTTCTTGACACAGATGTACTTCCCTC  
ATTTGCAGCCAAGCTTGGGGTGAAGGGCTCCTTTGAGGAATGTGCCAAAACCAAGTTGTAAGGGAAGCCATTTT  
AGAAGACTTGAGAAAATTGGGAAAGAAAGTGGCCCTTAAACTTTTGAACAGGTCAAAGCCATTTTCTTCACTCC  
AGAGCCATTTTCCATTGAAAATGGGCTCTTGACACCAACATTGAAAGCAAAGCGAGGAGAGCTTTCCAAATACTT  
TCGGACCCAAATTGACAGCCTGTATGAGCACATCCAGGATTAGGATAAGGTACTTAAGTACCTGCCGGCCCACTG  
TGCACCTGCTTGTGAGAAAATGGATTAAAACTATTCTTACATTGTTTTGCTTCTCCTATTTTTTTTAAACC  
TGTTAAACTCTAAAGCCATAGCTTTTGTGTTTATATTGAGACATATAATGTGTAACTTAGTTCCTCAATAAATCA  
ATCCTGTCTTTCCCATCTTCGATGTTGCTAATATTAAAGGCTTCAGGGCTACTTTTATCAACATGCCTGTCTTCAA  
GATCCAGTTTATGTTCTGTGCTTCTCCTCATGATTTCACCTTAATACTATTAGTAACCACAAGTTCAAGGGT  
CAAAGGACCCCTCTGTGCCTTCTTCTTGTGTTTGTGATAAACATAACTTGCCAACAGTCTCTATGCTTATTTACA  
TCTTCTACTGTTCAAACCTAAGAGATTTTAAATCTGAAAACTGCTTACAATTCATGTTTTCTAGCCACTCCAC  
AAACCACTAAAATTTTAGTTTTAGCCTATCACTCATGTCAATCATATCTATGAGACAAATGTCTCCGATGCTCTT  
CTGCGTAAATTAAATTGTGTACTGAAGGGAAAAGTTTGATCATACCAAACATTTCCTAACTCTCTAGTTAGATA  
TCTGACTTGGGAGTATTAATAATGGGTCTATGACATACTGTCCAAAAGGAATGCTGTTCTTAAAGCATTATTTA  
CAGTAGGAACCTGGGAGTAAATCTGTTCCCTACAGTTTGTGCTGAGCTGGAAGCTGTGGGGGAAGGAGTTGACA  
GGTGGGCCCAGTGAACCTTTCCAGTAAATGAAGCAAGCACTGAATAAAAACCTCCTGAAGTGGGAACAAAGATCT  
ACAGGCAAGCAAGATGCCACACAACAGGCTTATTTTCTGTGAAGGAACCACTGATCTCCCCCACCCTTGGATT  
AGAGTCTCTGCTCTACCTTACCCACAGATAACACATGTTGTTTCTACTTGTAAATGTAAGTCTTTAAATAAAC  
TATTACAGATAAAAAA

**FIGURE 478**

MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNLLLLFTKMLFI FNF  
LFSPLPTPALICILTFGAAIFLWLITRPQPVLPLLDLNNQSVGIEGGARKGVSQKNNDLTSCC  
FSDAKTMYEVFQRLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSSPDQ  
FVGIFAQNRPEWIISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKALVLIG  
NVEKGFTPSLKVIIILMDPFDDDLKQGEKSGIEILSLYDAENLGKEHFRKPVPPSPEDLSVIC  
FTSGTTGDPKGAMITHQNIIVSNAAFLKCVEHAYEPTPDDVAISYLPLAHMFERIVQAVVYSC  
GARVGFFQGDIRLLADDMMKTLKPTLFPAPVRLNRIYDKVQNEAKTPLKKFLLKLAVSSKFKE  
LQKGIIRHDSFWDKLIFAKIQDSLGGVRVIVTGAAPMSTSVMTFFRAAMGCQVYEAYGQTEC  
TGGCTFTLPGDWTSGHVGVPACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFKGYLKDPEKT  
QEALDSDGWLHTGDIGRWLPNGTLKIIDRKKNIFKLAQGEYIAPEKIENIYNRSQPVLQIFVH  
GESLRSSSLVGVVVPTDVLPSFAAKLGVKGSFEELCQNVVREAILEDLQKIGKESGLKTFEQ  
VKAIFLHPEPFSIENGLLTPTLKAKRGELSKYFRTQIDSLYEHIQD

**Important features:**

**Type II transmembrane domain:**

amino acids 61-80

**Putative AMP-binding domain signature.**

amino acids 314-325

**N-glycosylation site.**

amino acids 102-105, 588-591 and 619-622

# **FIGURE 479**

GGAGGCGGAGGCCGCGGCGAGCCGGGCGGAGCAGTGAGGGCCCTAGCGGGGCGGAGCGGGG  
 CCGGGGCCCCCTAAGCCATTCTGAAGTCATGGGCTGGCCAGGACATTGGTGACCCGCCAATCC  
 GGTATGGACGACTGGAAGCCAGCCCCCTCATCAAGCCCTTTGGGGCTCGGAAGAAGCGGAGC  
 TGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTGCGGAGATTCTGTGAGACA  
 GGGGCCGTGCTTTTCTGTGCTGGTGACTGTCTATTGTCAATATCAAGTTGATCCTGGACACTCGG  
 CGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCCCTAGGC  
 CGCCTGGAGCCCCACGGCGCAGAGGCAGTGGTCCCCGGCGGGTCTTGAGCGTAGAGGTGTAT  
 TCAAGTCGCAGCAAAGTATATGTGCGCAGTGGATGGCACCACGGTGTGGAGGATGAGGCCCGG  
 GAGCAGGGCCGGGCATCCATGTCTATTGTCTCAACCAGGCCACGGGCCACGTGATGGCAAAA  
 CGTGTGTTTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTGTCTATTCTCAACATGGTA  
 GCGCCCGGCGGAGTGCTCATCTGCACTGTCAAGGATGAGGGCTCCTTCCACCTCAAGGACACA  
 GCCAAGGCTCTGCTGAGGAGCCTGGGCAGCCAGGCTGGCCCTGCCCTGGGCTGGAGGGACACA  
 TGGGCCTTCGTGGGACGAAAAGGAGGTCTGTCTTCGGGGAGAAACATTCTAAGTCACCTGCC  
 CTCTCTTCTGGGGGACCCAGTCTGTCTGAAGACAGATGTGCCATTGAGCTCAGCAGAAGAG  
 GCAGAGTGCCACTGGGCAGACACAGAGCTGAACCGTCGCCGCCGGCGCTTCTGCAGCAAAGTT  
 GAGGGCTATGGAAGTGTATGCAGCTGCAAGGACCCACACCCATCGAGTTCAGCCCTGACCCA  
 CTCCAGACAACAAGGTCTCAATGTGCCTGTGGCTGTCTATTGCAGGGAACCGACCCAATTAC  
 CTGTACAGGATGCTGCGCTCTCTGTCTTCAGCCCAGGGGGTGTCTCCTCAGATGATAACAGTT  
 TTCATTGACGGCTACTATGAGGAACCCATGGATGTGGTGGCACTGTTTGGTCTGAGGGGCATC  
 CAGCATACTCCCATCAGCATCAAGAATGCCCGCGTGTCTCAGCACTACAAGGCCAGCCTCACT  
 GCCACTTTCAACCTGTTTTCCGGAGGCCAAGTTTGTCTGTGGTTCTGGAAGAGGACCTGGACATT  
 GCTGTGGATTTTTCTGAGTTTCTGAGCCAATCCATCCACTACTGGAGGAGGATGACAGCCTG  
 TACTGCATCTCTGGCCTGGAATGACCAGGGGTATGAACACACGGCTGAGGACCCAGCACTACTG  
 TACCGTGTGGAGACCATGCCCTGGGCTGGGCTGGGTGCTCAGGAGGTCTTGTACAAGGAGGAG  
 CTTGAGCCCAAGTGGCCTACACCGGAAAAGCTCTGGGATTGGGACATGTGGATGCGGATGCCCT  
 GAACAACGCCGGGGCGGAGAGTGCAATCATCCCTGACGTTTTCCCGATCTACCACTTTGGCATC  
 GTCGGCCTCAACATGAATGGCTACTTTACAGAGGCCTACTTCAAGAAGCACAAAGTTCAACACG  
 GTTCCAGGTGTCCAGCTCAGGAATGTGGACAGTCTGAAGAAAGAAGCTTATGAAGTGGAAGTT  
 CACAGGCTGCTCAGTGAGGCTGAGGTTCTGGACCACAGCAAGAACCCTTGTGAAGACTCTTTC  
 CTGCCAGACACAGAGGGCCACACCTACGTGGCCTTTATTTCGAATGGAGAAAGATGATGACTTC  
 ACCACCTGGACCCAGCTTGCCAAGTGCCTCCATATCTGGGACCTGGATGTGCGTGGCAACCAT  
 CGGGGCTGTGGAGATTGTTTTCGGAAGAAGAACCCTTCTGGTGGTGGGGTCCCCGGCTTCC  
 CCTACTCAGTGAAGAAGCCACCCTCAGTCACCCCAATTTTTCTGGAGCCACCCCCAAAGGAG  
 GAGGGAGCCCCAGGAGCCCCAGAACAGACATGAAGACCTCCTCCAGGACCCGCGGGGCTGGGT  
 ACTGTGTACCCCCAGGCTGGCTAGCCCTTCCCTCCATCCTGTAGGATTTTGTAGATGCTGGTA  
 GGGGCTGGGGCTACCTTGTTTTTAACATGAGACTTAATTACTAATCCAAGGGGAGGGTTCCC  
 CTGCTCCAACACCCCGTTCCCTGAGTTAAAAGTCTATTTATTTACTTCTTGTGGAGAAGGGC  
 AGGAGAGTACCTGGGAATCATTACGATCCCTAGCAGCTCATCCTGCCCTTTGAATACCCTCAC  
 TTTCCAGGCCTGGCTCAGAATCTAACCTATTTATTGACTGTCTGAGGGCCTTGAAACAGGC  
 CGAACCTGGAGGGCCTGGATTTCTTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTC  
 TTAATCAGGAACTGCTGTGCCCAACCCATGGACAGGCCCAGCTGGGGCCACATGCTGACAC  
 AGACTCACTCAGAGACCTTAGACACTGGACCAGGCCTCCTCTCAGCCTTCTCTTTGTCCAGA  
 TTTCCAAAGCTGGATAAGTTGGTCATTGATTAAAAAAGGAGAAGCCCTCTGGGAAAAAAAAA  
 AAAAAAAAAAAAAAAAAA

**FIGURE 480**

MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQRALRRFCQTGAVLFLLVTIVIVNIKLILDTRR  
AISEANEDPEPEQDYDEALGRLEPPRRRGSGPRRVLDVEVYSSRSKVYVAVDGTTVLEDEARE  
QGRGIHVIVLNQATGHVMAKRVFDTYSPHEDEAMVLFNLMVAPGRVLICTVKDEGSFHLKDTA  
KALLRSLGSQAGPALGWRDTWAFVGRKGGPVFGEKHSKSPALSSWGDPVLLKTDVPLSSAEEA  
ECHWADTELNRRRRRRFC SKVEGYGSVCCKDPTPIEFSPDPLPDNKVLNVPVAVIAGNRPNYL  
YRMLRSLLSAQGVSPQMITV FIDGYEPM DVVALFGLRGIQHTPISIKNARVSQHYKASLTA  
TFNLFPEAKFAVVLEEDLDIAVDFFSFLSQSIHLLLEEDDSLVCISAWNDQGYEHTAEDPALLY  
RVETMPGLGWVLRRLSLYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECIIPDVSRSYHFGIV  
GLNMNGYFHEAYFKKHKFNTVPGVQLRNVD SLKKEAYEVEVHRL LSEAEVLDH SKNPCEDSFL  
PDTEGHTYVAFIRMEKDDDDFTTWTQLAKCLHIWDL DVRGNHRGLWRLFRKKNHFLVGV PASP  
YSVKKPPSVTPIFLEPPPKEEGAPGAPEQT

**Important features:**

**Transmembrane domain:**

amino acids 38-55

**Homologous region to Mouse GNT1**

amino acids 229-660

**FIGURE 481**

GAAAGAAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCA  
GGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT  
GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTT  
CCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGTATCA  
TTCTGGTTTGTGGTTACAGACCCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGCAATCA  
GCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACCTCTGGAA  
TTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATT  
ATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATC  
TGGCAACGTAGAAGAAAGAACAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAA  
AACATGATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGGGGGCATATTA  
ATGATGCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTC  
CTCAAGAAATTAAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGAT  
CATATATTTTGTTCACCATTCCTTCTTTTGTAAATAAATTTTGAATGTGCTTGAAAGTGAAAAG  
CAATCAATTATACCCACCAACACCAC'TGAAATCATAAGCTATTACGACTCAAATATTTCTAA  
AATATTTTCTGACAGTATAGTGATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAA  
GCATTTTGTAGAAATAAGATCAGGCATATGTATATATTTTCACTTCAAAGACCTAAGGAAAA  
ATAAATTTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTT  
TGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTA  
AATGGATGGATAAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCA  
ACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCATT  
TCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTTTTAA  
AAAAAAAAAAAAAAAAAAAAA

**FIGURE 482**

MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVPN  
REATEISHVLLCNVTQRVSFVFWVTDPSKNHTLPAVEVQSAIRMNKNRINNAFFLNDQTLLEFL  
KIPSTLAPPMDSVPWIIFGVIFCIIIVAIALLILSGIWQRRRKNEPSEVDDAEDKCENM  
ITIENGIPSDPLDMKGGILMMPS



# **FIGURE 483**

CGTCTCTGCGTTTCGCCATGCGTCCCCGGGGCGCCAGGGCCACTCTGGCCTCTGCCCTGGGGGGC  
 CCTGGCTTGGGCGGTGGGCTTCGTGAGCTCCATGGGCTCGGGGAACCCCGCGCCCGGTGGTGT  
 TTGCTGGCTCCAGCAGGGCCAGGAGGCCACCTGCAGCCTGGTGCTCCAGACTGATGTCAACCG  
 GGCCGAGTGCTGTGCCTCCGGCAACATTGACACCGCCTGGTCCAACCTCACCCACCCGGGGAA  
 CAAGATCAACCTCCTCGGCTTCTTGGGCCTTGTCCACTGCCTTCCCTGCAAAGATTTCGTGCGA  
 CGGCGTGGAGTGCGGGCCCGGGCAAGGCGTGCCGCATGCTGGGGGGCCGCCCGCGCTGCGAGTG  
 CGCGCCCGACTGCTCGGGGCTCCCGGCGCGGCTGCAGGTCTGCGGCTCAGACGGCGCCACCTA  
 CCGCGACGAGTGCGAGCTGCGCGCCGCGCGCTGCCGCGGCCACCCGACCTGAGCGTCATGTA  
 CCGGGGCCGCTGCCGCAAGTCTGTGAGCACGTGGTGTGTGAGCGGGCGCCCTGCCCTGTGCCCTCCAG  
 GGACCAGACGGGCAGCGCCCACTGCGTGGTGTGTGAGCGGGCGCCCTGCCCTGTGCCCTCCAG  
 CCCCAGGCGAGGCTTTGCGGCAACAACAACGTACCTACATCTCCTCGTGCCACATGCGCCA  
 GGCCACCTGCTTCTTGGGCCGCTCCATCGGCGTGCGCCACGCGGGCAGCTGCGCAGGCACCCC  
 TGAGGAGCCGCCAGGTGGTGAAGTCTGCAGAAGAGGAAGAGAACTTCGTGTGAAGCCTGCAGGAC  
 AGGCCTGGGCCTGGTGCCCGAGGCCCCCATCATCCCCTGTTATTTATTGCCACAGCAGAGTC  
 TAATTTATATGCCACGGACACTCCTTAGAGCCCGGATTTCGGACCACTTGGGGATCCCAGAAC  
 TCCCTGACGATATCCTGGAAGGACTGAGGAAGGGAGGCCTGGGGGCCGGCTGGTGGGTGGGAT  
 AGACCTGCGTTCCGGACACTGAGCGCCTGATTTAGGGCCCTTCTCTAGGATGCCCCAGCCCC  
 ACCCTAAGACCTATTGCGGGGAGGATTCCACACTTCCGCTCCTTTGGGGATAAACCTATTAA  
 TTATTGCTACTATCAAGAGGGCTGGGCATTCTCTGCTGGTAATTCTGAAGAGGCATGACTGC  
 TTTTCTCAGCCCCAAGCCTCTAGTCTGGGTGTGTACGGAGGGTCTAGCCTGGGTGTGTACGGA  
 GGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGT  
 GAGTACGGAGGGTCTAGCCTGGGTGTGTATGGAGGATCTAGCCTGGGTGAGTATGGAGGGTCT  
 AGGAGGTCTAGCCTGGGTGTGTATGGAGGGTCTAGCCTGGGTGTGTATGGAGGGTCTAGCCTGGGTGAGTAT  
 GGAGGGTCTAGCCTGGGTGTGTATGGAGGGTCTAGCCTGGGTGAGTATGGAGGGTCTAGCCTG  
 GGTGTGTACGGAGGGTCTAGTCTGAGTGCGTGTGGGGACCTCAGAACACTGTGACCTTAGCCC  
 AGCAAGCCAGGCCCTTCATGAAGGCCAAGAAGGCTGCCACCATTCCCTGCCAGCCCAAGAACT  
 CCAGCTTCCCCACTGCCTCTGTGTGCCCCCTTTGCGTCTGTGAAGGCCATTGAGAAATGCCCA  
 GTGTGCCCCCTGGGAAAGGGCACGGCCTGTGCTCCTGACACGGGCTGTGCTTGGCCACAGAAC  
 CACCCAGCGTCTCCCCCTGCTGCTGTCCACGTGAGTTCATGAGGCAACGTCGCGTGGTCTCAGA  
 CGTGGAGCAGCCAGCGGCAGCTCAGAGCAGGGCACTGTGTCCGGCGGAGCCAAGTCCACTCTG  
 GGGGAGCTCTGGCGGGGACACGGGCCACTGCTCACCCACTGGCCCCGAGGGGGGTGTAGACG  
 CCAAGACTCACGCATGTGTGACATCCGGAGTCTGGAGCCGGGTGTCCAGTGGCACCCTAG  
 GTGCCTGCTGCCTCCACAGTGGGGTTACACCCAGGGCTCCTTGGTCCCCCACAACCTGCCCC  
 GGCCAGGCCTGCAGACCCAGACTCCAGCCAGACCTGCCTCACCCACCAATGCAGCCGGGGCTG  
 GCGACACCAGCCAGGTGCTGGTCTTGGGCCAGTTCTCCACGACGGCTCACCCCTCCCTCCAT  
 CTGCGTTGATGCTCAGAATCGCCTACCTGTGCCTGCGTGTAAACCACAGCCTCAGACCAGCTA  
 TGGGGAGAGGACAACACGGAGGATATCCAGCTTCCCCGGTCTGGGGTGAGGAATGTGGGGAGC  
 TTGGGCATCCTCCTCCAGCCTCCTCCAGCCCCCAGGCAGTGCCCTTACCTGTGGTGCCAGAAA  
 AGTGCCCCCTAGGTTGGTGGGTCTACAGGAGCCTCAGCCAGGCAGCCACCCACCCCTGGGGCC  
 CTGCCTCACCAAGGAAATAAAGACTCAAGCCATAAAAAAAAA

**FIGURE 484**

MRPGAPGPLWPLPWGALAWAVGFVSSMSGGNPAPGGVCWLQQGQEATCSLVLQTDVTRAEC  
CA  
SGNIDTAWSNLTHPGNKINLLGFLGLVHCLPCKDSCDGVCEGPGKACRMLGGRPRCECAPDCS  
GLPARLQVCGSDGATYRDECELRAARCRGHPDLSVMYRGRCRKSCEHVVCPRPQSCVVDQTGS  
AHCVVCRAAPCPVPSSPGQELCGNNNVITYISSCHMRQATCFLGRSIGVRHAGSCAGTPEEPPG  
GESAEEEENFV

**Important features:**

**Signal peptide:**

amino acids 1-20

**N-glycosylation sites.**

amino acids 73-77, 215-219

**Osteonectin domain proteins.**

amino acids 97-130, 169-202

**FIGURE 485**

GCTCGAGGCCGGCGGGCGGGAGAGCGACCCGGGCGGCCTCGTAGCGGGGCCCCGGATCCCC  
GAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAGATGATGGGCTTGGGA  
AACGGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGCTGGCCGCCCTGGTGGCCTGCATCATC  
GTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGGAGCGTGGACCTCCAGACACGGATCATG  
GAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGGCGCCGTGGAGCTGAAGAAGAAC  
GAGTTCCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGCCACAAC  
TTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTTTGGTGAATAACATC  
ACCACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCTGCAGAGGAATTAC  
GGCAGGCTGCAGCAGGATGTCTCCAGTTTCAGAAGAACCAGACCAACCTGGAGAGGAAGTTC  
TCCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTGTGAGGAGCGA  
ATAGAAGAGGTACCAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGAGTGAAAACAAC  
GACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAGGCAGCAGGCCTG  
CCACACACAGAGGTGCCACAAGGGAAGGGAAACGTGCTTGGTAACAGCAAGTCCCAGACACCA  
GCCCCCAGTTCGGAAGTGGTTTTTGGATTCAAAGAGACAAGTTGAGAAAGAGGAAACCAATGAG  
ATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAGCCAGGCCGGGAGCAG  
GTGGTGGAAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGGAGAACTGGGCCAGACC  
CCACAGGTGCAGGCTGCCCTGTCACTGAGCCAGGAAAATCCAGAGATGGAGGGCCCTGAGCGA  
GACCAGCTTGTTCATCCCCGACGGACAGGAGGAGGAGCAGGAAGCTGCCGGGAAGGGAGAAAC  
CAGCAGAACTGAGAGGAGAAGATGACTACAACATGGATGAAAATGAAGCAGAATCTGAGACA  
GACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATGTTTTTAATGTTGAAGATCAG  
AAAAGAGACACCATAAATTTACTTGATCAGCGTGAAAAGCGGAATCATACACTCTGAATTGAA  
CTGGAATCACATATTTCAACAACAGGGCCGAAGAGATGACTATAAAATGTTTCATGAGGGACTGA  
ATACTGAAAACGTGAAATGTACTAAATAAAATGTACATCTGA

**FIGURE 486**

MMGLGNRRSMKSPPLVLAALVACIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAAERGAV  
ELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQLKT  
LQRYNYGRLQQDVLQFQKNQTNLERKFSDLSQCINQMKEVKEQCEERIEEVTKKGNEAVASRD  
LSENNDQRQQLQALSEPQPRQLQAAGLPHTTEVPQGKGNVLGNSKSQTPAPSSEVVLDSCRQVEK  
EETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQVQAALSVSQENPEM  
EGPERDQLVIPDGQEEEQEAAGEGRNQKLRGEDDYNMDENEAESETDKQAALAGNDRNIDVF  
NVEDQKRDTINLLDQREKRNHTL

**Important features:**

**Signal peptide:**

amino acids 1-29

**FIGURE 487**

AACTCAAACCTCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGGAGTGGCCTTGGCAGGG  
TGTTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTCATGTAT  
GGCAAGAGCTCTACTCGTGCGGTGCTTCTTCTCCTTGGCATAACAGCTCACAGCTCTTTGGCCT  
ATAGCAGCTGTGGAAATTTATACCTCCCGGGTGCTGGAGGCTGTTAATGGGACAGATGCTCGG  
TTAAAATGCACTTTCTCCAGCTTTGCCCCCTGTGGGTGATGCTCTAACAGTGACCTGGAATTTT  
CGTCCTCTAGACGGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTCCAACCC  
ATGAGTGGGCGGTTTAAGGACCGGGTGCTTGGGATGGGAATCCTGAGCGGTACGATGCCTCC  
ATCCTTCTCTGGAACTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGAAGAACCCA  
CCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTACGCTTCTCT  
GAGATCCACTTCCTGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCATAATAGTAATT  
GTAGTGGTCCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTCATAAAGTGGTG  
GAGATAAAATCAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCTGTTTATTTAGAA  
GACACAGACTTACAATTTTAGATGGAAGCTGAGATGATTTCCAAGAACAAGAACCCTAGTATT  
TCTTGAAGTTAATGGAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGTTTTTCCAACCAGTTC  
TGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCACAGTGCTCCTCCATAT  
CACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTTTCAAGAGTGAAATTTTTTCAA  
GTGCTCATTAGGTTTTTATAACAAGAAGCTACATTTTTTGCCCTTAAGACACTACTTACAGTGT  
TATGACTTGTATACACATATATTGGTATCAAAGGGGATAAAAGCCAATTTGTCTGTTACATTT  
CCTTTCACGTATTTCTTTTAGCAGCACTTCTGCTACTAAAGTTAATGTGTTTACTCTCTTTCC  
TTCCACATTCTCAATTAAGGTGAGCTAAGCCTCCTCGGTGTTTCTGATTAACAGTAAATC  
CTAAATTCAAACGTGTTAAATGACATTTTTATTTTTATGTCTCTCCTTAACTATGAGACACATC  
TTGTTTTACTGAATTTCTTTCAATATTCAGGTGATAGATTTTTGTGCG

**FIGURE 488**

MYGKSSTRAVLLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVTW  
NFRPLDGGPEQFVFYYHIDPFQPMGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQVK  
NPPDVDGVIGEIRLSVVHTVRFSEIHFLALAIGSACALMIIIVIVVVLFOHYRKKRWAERAHK  
VVEIKSKEEERLNQEKKVSVYLEDTD

**FIGURE 489**

[illegible]

**FIGURE 490**

MLLLWVSVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFDGRLLTFHPGSQVVKLPFINFM  
KTRGTSFLNAYTNSPICCPRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQKF  
GKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPVNLIRNRTKVRVMERDWQNTDKAVNWLK  
EAINYTEPFVIYLG LNLPHYPSPSSGENFGSSTFHTSLYWLEKVS HDAIKIPKWSPLSEMHP  
VDYYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVYSSDHG  
ELAMEHRQFYKMSMYEASAHVPLLMMGPGIKAGLQVSNVSLVDIYPTMLDIAGIPLPQNLSG  
YSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYS DGASILPQLFD  
LSSDPDELTVNAVVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIGQYNSNVIA  
NLRWHQDWQKEPRKYENAIQWLKTHMNPRAV

**Important features:**

**Signal peptide:**

amino acids 1-15

**N-glycosylation sites.**

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,  
498-501

**Sulfatases proteins:**

amino acids 286-315, 359-369, 78-97



**FIGURE 491**

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGA  
GCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATGGC  
CTCTCTTGGCCTCCAACCTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACTGGT  
TGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTGCGGTGCCAGCATTTGTGACAGCAGT  
TGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAGTGTGA  
CATCTATAGCACCCCTTCTGGGCCTGCCCCTGACATCCAGGCTGCCCAGGCCATGATGGTGAC  
ATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCACAGTCTTT  
CTGCCAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTCATCCTTGG  
AGGCCTCCTGGGATTCAATCCTGTTGCCTGGAATCTTCATGGGATCCTACGGGACTTCTACTC  
ACCACTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGGGCATTATTTCT  
TTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCTCTGCTCATCCCAGAGAAATCG  
CTCCAACTACTACGATGCCACCAAGCCCAACCTCTTGCCACAAGGAGCTCTCCAAGGCCTGG  
TCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCCCTACAGCCTGACAGGGTATGTGTGAAAGAAC  
CAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCA  
CAGGTGAGGGACACTACCACTGGATCGTGTGAGAAGGTGCTGCTGAGGATAGACTGACTTTGG  
CCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAACAGCATGCAGGTTGAATTGCCAA  
GGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCTCACCTTGCTGCTCCCCTGCCCTAAGTCCCC  
AACCCTCAACTTGAAACCCCATTCCTTAAGCCAGGACTCAGAGGATCCCTTTGCCCTCTGGT  
TTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCCTGACTGACCCTCTGTGATCAA  
AGACCCTCTCTCTGGCTGAGGTGGCTCTTAGCTCATTGCTGGGGATGGGAAGGAGAAGCAGT  
GGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCCTCCAAAGAACTGATTGGCCC  
TGGAACCTCCATCCCCTCTTGTATGACTCCACAGTGTCCAGACTAATTTGTGCATGAACTG  
AAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAGGATGCAGGATGGGAGGACAGGAA  
GGCAGCCTGGGACATTTAAAAAATA

**FIGURE 492**

MASLGLQLVGYILGLLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQ  
CDIYSTLLGLPADIQAAQAMMVTSSAIISSLACIISVGMRCTVFCQESRAKDRVAVAGGVFFI  
LGGLLGFIPIVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSSQR  
NRSNYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV

**Important features:**

**Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

**N-glycosylation site.**

amino acids 190-193

**PMP-22 / EMP / MP20 family proteins.**

amino acids 46-59

**FIGURE 493**

GCACTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCCATGGTGCCCAGAATCTTCGCTCCTGCT  
TATGTGTCACTCTGTCTCCTCCTCTTGTGTCCAAGGGAAGTCATCGCTCCCGCTGGCTCAGAA  
CCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAGTGC  
TGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCTGCACCTTC  
TGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCTTTGGCCTCACAAACGATTTTGTGTGAAG  
CTGAAGGTTCAAGGTGTGAATTCCCAGTGCCACTCATCTCCCATCTCCAGTAAATGTGAAAGC  
AGAAGACGTTTTCCCTGAGGAAGACATAGAAAAGAAAATCAACTTTCACTAAGGCATCTCAGAAA  
CATAGGCTAAGGTAATATGTGTACCAGTAGAGAAAGCCTGAGGAATTTACAAAATGATGCAGCT  
CCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGTAGATTATCA  
GGAAATAAATAAAGTGGTTTTTTCCAATGTACACACCTGTAAAA

**FIGURE 494**

MVPRIFAPAYVSVCLLLLCPREVIAPAGSEPWLCQPAPRCGDKIYNPLEQCCYNDAIVSLSET  
RQCGPPCTFWPCFELCCLDSFGLTNDVFVKLVQGVNSQCHSSPISSKCESRRRFP

**Important features:**

**Signal peptide:**

amino acids 1-25

**FIGURE 495**

CTCCACTGCAACCACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATTT  
TCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCTGA  
TGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCCCTGCAGCACTGTTGCT  
ATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGAAACTGCACCTTCAGAGTCT  
GCTTTGAGCAGTGCTGCCCCCTGGACCTTCATGGTGAAGCTGATAAACCAGAACTGCCACTCAG  
CCCGGACCTCGGATGACAGGCTTTGTCTGAGTGTCTAGCTTAATGGAACATCAGGGGAACGATGA  
CTCCTGGATTCTCCTTCCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTACCTGAGATCTGGGA  
TGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCCACTTCATTCTGTGACC  
TGTCTGAGGCCCCACCTGCAGCTGCCCTGAGGAGGCCCCACAGGTCCCCCTTCTAGAATTCTGGA  
CAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCTCCTGATGACCCCTATG  
GCCAACATCAACCCGGCACCACCCCAAGGCTGGCTGGGGAACCCCTTCACCCCTTCTGTGAGATT  
TTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAATAAATTTATGTA  
CTTTATAAATGAAAA

**FIGURE 496**

MAPRGCI VAVFAIFCISRL LCSHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVPL  
ARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCD SARTSDDRLCRSVS

**Important features:**

**Signal peptide:**

amino acids 1-24

# **FIGURE 497**

TGAAGGACTTTTCCAGGACCCAAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGGCACTC  
 CTTGGCCTCCGCAGCCGATCACATGAAGGTGGTGCCAAGTCTCCTGCTCTCCGTCTCCTGGC  
 ACAGGTGTGGCTGGTACCCGGCTTGGCCCCCAGTCTCAGTCGCCAGAGACCCCAGCCCCTCA  
 GAACCAGACCAGCAGGGTAGTGCAGGCTCCCAGGGAGGAAGAGGAAGATGAGCAGGAGGCCAG  
 CGAGGAGAAGGCCGGTGAGGAAGAGAAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTTGCCAA  
 GGAGACTTCAAACCTTCGGATTTCAGCCTGCTGCGAAAGATCTCCATGAGGCACGATGGCAACAT  
 GGTCTTCTCTCCATTTGGCATGTCTTGGCCATGACAGGCTTGATGCTGGGGGCCACAGGGCC  
 GACTGAAACCCAGATCAAGAGAGGGCTCCACTTGCAGGCCCTGAAGCCCACCAAGCCCGGGCT  
 CCTGCCTTCCCTCTTTAAGGGACTCAGAGAGACCCTCTCCCGCAACCTGGAAGTGGGCCTCTC  
 ACAGGGGAGTTTTGCCTTCATCCACAAGGATTTTGATGTCAAAGAGACTTTCTTCAATTTATC  
 CAAGAGGTATTTTGATACAGAGTGCGTGCCTATGAATTTTCGCAATGCCTCACAGGCCAAAAG  
 GCTCATGAATCATTACATTAACAAAGAGACTCGGGGGAAAATTCCCAAAGTGTGATGAGAT  
 TAATCCTGAAACCAAATTAATTCCTTGTGGATTACATCTTGTTCAAAGGGAAAATGGTTGACCCC  
 ATTTGACCCTGTCTTCACCGAAGTCGACACTTTCACCTGGACAAGTACAAGACCATTAAAGGT  
 GCCCATGATGTACGGTGCAGGCAAGTTTGCCTCCACCTTGGACAAGAATTTTCGTTGTCTATGT  
 CCTCAAACCTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCTCATGGAGAAAATGGGTGA  
 CCACCTCGCCCTTGAAGACTACCTGACCACAGACTTGGTGGAGACATGGCTCAGAAACATGAA  
 AACCAGAAACATGGAAGTTTTCTTTCCGAAGTTCAGCTAGATCAGAAGTATGAGATGCATGA  
 GCTGCTTAGGCAGATGGGAATCAGAAGAATCTTCTCACCTTTGCTGACCTTAGTGAACCTCTC  
 AGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTTACGAAGAACAGTGATTGAAGTTGATGA  
 AAGGGGCACTGAGGCAGTGGCAGGAATCTTGTGAGAAATTAAGTCTTATTCCATGCCTCCTGT  
 CATCAAAGTGGACCGGCCATTTCAATTCATGATCTATGAAGAAACCTCTGGAATGCTTCTGTT  
 TCTGGGCAGGGTGGTGAATCCGACTCTCCTATAATTCAGGACATGCATAAGCACTTCGTGCTG  
 TAGTAGATGCTGAATCTGAGGTATCAAACACACACAGGATACCAGCAATGGATGGCAGGGGAG  
 AGTGTTCTTTTGTCTTAACTAGTTTAGGGTGTCTCAAATAAATACAGTAGTCCCCACTTA  
 TCTGAGGGGGATACATTCAAAGACCCCCAGCAGATGCCTGAAACGGTGGACAGTGCTGAACCT  
 TATATATATTTTTTCTACACATACATACCTATGATAAAAGTTTAATTTATAAATTAGGCACAG  
 TAAGAGATTAAACAATAATAACAACATTAAAGTAAATGAGTTACTTGAACGCAAGCACTGCAAT  
 ACCATAACAGTCAAACCTGATTATAGAGAAGGCTACTAAGTGACTCATGGGCGAGGAGCATAGA  
 CAGTGTGGAGACATTGGGCAAGGGGAGAATTCACATCCTGGGTGGGACAGAGCAGGACGATGC  
 AAGATTCCATCCCACTACTCAGAATGGCATGCTGCTTAAGACTTTTAGATTGTTTATTTCTGG  
 AATTTTTTCATTTAATGTTTTTGGACCATGGTTGACCATGGTTAACTGAGACTGCAGAAAGCAA  
 AACCATGGATAAGGGAGGACTACTACAAAAGCATTAATTTGATACATATTTTTTAAAAAAA  
 AAAAAAAA

**FIGURE 498**

MKVVPSLLLSVLLAQVWLVPG LAPSPQSPETPAPQNQTSRVVQAPREEEDEQEASEEKAGEE  
EKAWLMASRQQ LAKETSNFGFSLLRKISMRHDGNMVFSFPGMSLAMTGLMLGATGPTETQIKR  
GLHLQALKPTKPGLLPSLFKGLRETL SRNLELGLSQGSFAFIHKDFDVKETFFNLSKRYFDTE  
CVP MNFRNASQAKRL MNHYINKETR GKIPKLFDEINPETKLILVDYILFKGKWLTPFDPVFTE  
VDTFHLDKYKTIKVPM MYGAGKFASTFDKNFRCHVLKLPYQGNATMLVVLMEKMGDHLALEDY  
LTTDLVETWLRNMKTRNMEVFFPKFKLDQKYEMHELLRQMGIRRI FSPFADLSELSATGRNLQ  
VSRVLRRTVIEVDERGTEAVAGILSEITAYSMPPVIKVDRPFHFMIYEETSGMLLFLGRVVNP  
TLL



**FIGURE 499**

[illegible]

**FIGURE 500**

MDSLRLKMLISVAMLGAGAGVGYALLVIVTPGERRRKQEMLKEMPLQDPRSREEAARTQQLLLAT  
LQEAATTQENVAWRKNWMVGEGGASGRSP

**Important features:**

**Signal peptide:**

amino acids 1-18

**FIGURE 501**

[illegible]

**FIGURE 502**

MGPSTPLLILFLLSWGPLQGQHHLVEYMERRLAALAEERLAQCQDQSSRHAAELRDFKNKML  
PLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGRN  
EKYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRLRDF  
TLAMAARKASRVRVPFPWVGTLVYGGFLYFARRPPGRPGGGGEMENTLQLIKFHLANRTVV  
DSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCLAKLDPQTLDTQQWDTP  
CPRENAEAAFVICGTLYVVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAHASLRYN  
PRERQLYAWDDGYQIVYKLEMRKKEEV

**Important features:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 177-180, 248-251

**FIGURE 503**

TGCGGCGCAGTGTAGACCTGGGAGGAATGGGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGGT  
CTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCTGAGCAGCTTCTTGGGCC  
CTGGTACGTGCTTGCGGTGGCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAAGAA  
CGTCGTGGGGGTGGTGGTGACCTCACTCCAGAAAAACAACCTGCGGACGCTGTCCTCTCAGCA  
CGGGCTGGGAGGGTGTGACCAGAGTGTGATGGACCTGATAAAGCGAACTCCGGATGGGTGTT  
TGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGACTATGC  
CATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGTACAGTCT  
GACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTCACCAAGTGGAGCAGGAGCCTGGGCTT  
CCTGTACAGTAGCAGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAGATCCTTCTGTG  
AGTGCTGCGTCCCCAGTAGGGATGGCGCCACAGGGTCCTGTGACCTCGGCCAGTGTCCACCC  
ACCTCGCTCAGCGGCTCCCGGGGCCCAGCACCAGCTCAGAATAAAGCGATTCCACAGCA

**FIGURE 504**

MGGLLLAFLALVSVPRQAVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVTL  
TPENNLRTLSSQHGLGGCDQSVMDLIKRNSGWVFENPSIGVLELWVLATNFRDYAIIFTQLEF  
GDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

**Important features:**

**Signal peptide:**

amino acids 1-20

**FIGURE 505**

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCACA  
GCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCCATGAGGATTCTGCAGTTAATC  
CTGCTTGCTCTGGCAACAGGGCTTGTAGGGGGAGAGACCAGGATCATCAAGGGGTTTCGAGTGC  
AAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTTCGAGAAGACGCGGCTACTCTGTGGGGCG  
ACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCCGCTACATAGTT  
CACCTGGGGCAGCACAACCTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCCACTGAG  
TCCTTCCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGACATCATG  
CTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCTCTCCTCA  
CGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCCAGCCCCAG  
TTACGCCTGCCTCACACCTTGCGATGCGCCAACATCACCATCATTGAGCACCAGAAGTGTGAG  
AACGCCTACCCCGGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGGAAGGGGGCAAG  
GACTCCTGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGTAACCAGTCTCTTCAAGGCATTATC  
TCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACACGAAAGTCTGCAAA  
TATGTGGACTGGATCCAGGAGACGATGAAGAACAATTAGACTGGACCCACCCACCACAGCCCA  
TCACCCTCCATTTCCACTTGGTGTTTGGTTCCTGTTCACCTCTGTTAATAAGAAACCCTAAGCC  
AAGACCCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATGCTGTCACTTAATAATC  
AACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATTCTGCCTTGAAATATTGTGACTCTG  
GGAATGACAACACCTGGTTTGTCTCTGTTGTATCCCCAGCCCCAAAGACAGCTCCTGGCCAT  
ATATCAAGGTTTCAATAAATATTTGCTAAATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAA

**FIGURE 506**

MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAHC  
LKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITWAV  
RPLTLSSRCVTAGTSC LISGWGSTSSPQLRLPHTLRCANITIIIEHQKCENAYPGNITDTMVCA  
SVQEGGKDSCQGDSSGGLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN

**Important features:**

**Signal peptide:**

amino acids 1-18

**Serine proteases, trypsin family, histidine active site.**

amino acids 58-63

**N-glycosylation sites.**

amino acids 99-102, 165-168, 181-184, 210-213

**Glycosaminoglycan attachment site.**

amino acids 145-148

**Kringle domain proteins.**

amino acids 197-209, 47-64

**Serine proteases, trypsin family, histidine protein**

amino acids 199-209, 47-63, 220-243

**Apple domain proteins**

amino acids 222-249, 189-222



**FIGURE 507**

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCAGACATGAGG  
AGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAGCA  
CCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAGGCC  
TGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGCTGTTCCCTGTC  
CAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTCAGGGCAGGGGCCCCATCCTT  
CCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCCTGGGCCGTGTCCTGAGTCCCGAGCCC  
GACCATGACAGCCTGTACCACCCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCCCCGGTTG  
TGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACATCTACCAC  
CCCCAGTAGGGCTCCAGGGGCCATCACTGCCCCGCCCCTGTCCCAAGGCCCAGGCTGTTGGGA  
CTGGGACCCCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCAGCAGGCAAAAAAAAAAAAAA  
AAAAAA

**FIGURE 508**

MRRLLLVTSLVVVLLWEAGAVPAPKVPIKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVLF  
PVQKPKLLTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQGEERP  
RLWVMPNHQVLLGPEEDQDHIYHPQ

**FIGURE 509**

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCCC  
ACGAGGCTGCCGCATCCTGCCCTCGGAACAATGGGACTCGGCGCGCGAGGTGCTTGGGCCGCG  
CTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGGCCGCCCATGAAAGCGCAGCCATG  
GCGGCATCTGCAAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAACAGAG  
ACTCTCCAACATGTGCCTTCTGACCATACAAATGAACTTCCAACAGTACTGTGAAACCACCA  
ACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCGGCATCT  
AATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTCTACACCC  
AAAACAACAAGTGTTCACAGAACACATCTCAGATATCAACATCCACAATGACCGTAACCCAC  
AATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAACCTATGCATTCTGAAGCA  
AAGAAAGGATCAAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAAAGCTGGGAGTT  
TTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTGCGGTATCGAACC  
ATAGATGAACATGATGCCATCATTTAAGGGAAATCCATGGACCAAGGATGGAATACAGATTGAT  
GCTGCCCTATCAATTAAATTTTGGTTTATTAATAGTTTAAAACAATATTCTCTTTTTTGAAAATA  
GTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTAAAGATTCTTCAAGG  
TAACAAGGGTTTGGGTTTGAATAAACATCTGGATCTTATAGACCGTTCATACAATGGTTTT  
AGCAAGTTCATAGTAAGACAAACAAGTCCTATCTTTTTTTTTTGGCTGGGGTGGGGGCATTGG  
TCACATATGACCAGTAATTGAAAGACGTCATCACTGAAAGACAGAATGCCATCTGGGCATACA  
AATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTGTAGCTCACATAAAGAACTT  
CAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACACAGAAATTATACAATCAAA  
CTAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTGTGCTTTAACTGTAGTAGTT  
GGTCTAGAAACAAAATACTCC

**FIGURE 510**

MGLGARGAWAALLLGTQLQVLALLGAAHESAAMAASANIENSGLPHNSSANSTETLQHVPSDHT  
NETSNSTVKPPTSVASDSSNTTVTTMKPTAASNTPGMVSTNMTSTTLKSTPKTTSVSQNTS  
QISTSTMTVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTLGVLSILYIGCKM  
YYSRRGIRYRTIDEHDAII

**FIGURE 511**

GACTTTGCTTGAATGTTTACATTTTCTGCTCGCTGTCCTACATATCACAAATAGTGTTTACGTTTTGTTAAAC  
 TTTGGGGTGTGAGGAGTTGAGCTTGCTCAGCAAGCCAGCATGGCTAGGATGAGCTTTGTTATAGCAGCTTGCCAA  
 TTGGTGCTGGGCCTACTAATGACTTCATTAACCGAGTCTTCCATACAGAATAGTGAGTGTCACAACTTTGCGTA  
 TGTGAAATTCGTCCTCGTTTACCCACAGTCAACTTACAGAGAAGCCACCACTGTTGATTGCAATGACCTCCGC  
 TTAACAAGGATTCCAGTAACCTCTCTAGTGACACACAAGTGCTTCTCTTACAGAGCAATAACATCGCGAAGACT  
 GTGGATGAGCTGCAGCAGCTTTTCAACTTGACTGAACTAGATTTCTCCAAAACAACTTTACTAACATTAAGGAG  
 GTCGGGCTGGCAAACCTAACCCAGCTCACAAAGCTGCATTGGAGGAAAATCAGATTACCGAGATGACTGATTAC  
 TGTCTACAAGACCTCAGCAACCTTCAAGAACTCTACATCAACCACAACCAAATTAGCACTATTTCTGCTCATGCT  
 TTTGCAGGCTTAAAAAATCTATTAAGGCTCCACCTGAACTCCAACAAATTGAAAGTTATTGATAGTCGCTGGTTT  
 GATTCTACACCCAACCTGGAATTTCTCATGATCGGAGAAAACCTGTGATTGGAATTCTGGATATGAACCTCAAA  
 CCCCTCGCAAATTTGAGAAGCTTAGTTTTGGCAGGAATGTATCTCACTGATATTCCTGGAAATGCTTTGGTGGGT  
 CTGGATAGCCTTGAGAGCCTGTCTTTTATGATAACAACTGGTTAAAGTCCCTCAACTTGCCCTGCAAAAAGTT  
 CCAAATTTGAAATTTCTAGACCTCAACAAAAACCCATTCAAAAATCCAAGAAGGGGACTTCAAAAATATGCTT  
 CGGTTAAAGAAGCTGGGAATCAACAATATGGGCGAGCTCGTTTCTGTCGACCGCTATGCCCTGGATAACTTGCCCT  
 GAACTCACAAAGCTGGAAGCCACCAATAACCTTAACTCTCTTACATCCACCGCTTGGCTTTCCGAAGTGTCCCT  
 GCTCTGGAAGCTTGATGCTGAACAACAATGCCCTTGAATGCCATTTACCAAAGACAGTCGAATCCCTCCCCAAT  
 CTGCGTGAGATCAGTATCCATAGCAATCCCTCAGGTGTGACTGTGTGATCCACTGGATTAACCTCAACAAAACC  
 AACATCCGCTTCATGAGCCCTGTCCATGTTCTGTGCCATGCCGCCGAATATAAAGGGCACCAGGTGAAGGAA  
 GTTTTAAATCCAGGATTCGAGTGAACAGTGCCTCCCAATGATATCTCACGACAGCTTCCCAATCGTTTAAACGTG  
 GATATCGGCACGACGGTTTTCTTAGACTGTGAGCCATGGCTGAGCCAGAACCTGAAATTTACTGGGTCACTCCC  
 ATTGGAAATAAGATAACTGTGGAACCCCTTTTCAAGATAAATAAGCTAAGTAGCGAAGGTACCTTGGAAATATCT  
 AACATACAAATTGAAGACTCAGGAAGATACACATGTGTGCCCAGAATGTCCAAGGGGCAGACACTCGGGTGGCA  
 ACAATTAAGGTTAACGGGACCCCTTCTGGATGGTACCCAGGTGCTAAAAATATACGTCAAGCAGACAGAATCCCAT  
 TCCATCTTAGTGCTCTGGAAGTTAATTCCAATGTCATGACGTCAAACCTTAAATGGTCTGCTGCCACCATGAAG  
 ATTGATAACCTCACATAACATATACTGCCAGGGTCCAGTCGATGTCCATGAATACAACCTAACGCATCTGCAG  
 CCTTCCACAGATTATGAAGTGTGTCTCACAGTGTCCAATATTCATCAGCAGACTCAAAAGTCATGCGTAAATGTC  
 ACAACCAAAATGCCGCCCTTCGCAGTGGACATCTCTGATCAAGAAACAGTACAGCCCTTGCTGCAAGTAAATGGG  
 TCTATGTTTGCCGTCATTAGCCTTGCGTCCATTGCTGTGTAATTTGCCAAAAGATTTAAGAGAAAAAATACCAC  
 CACTCATTTAAAAAGTATATGCAAAAAACCTCTTCAATCCCACTAAATGAGCTGTACCCACCACTCATTAACCTC  
 TGGGAAGGTGACAGCGAGAAAGACAAAGATGGTTCTGCAGACACCAAGCCAACCCAGGTGACACATCCAGAAGC  
 TATTACATGTGTTAACTCAGAGGATATTTTGCTTCTGGTAGTAAGGAGCACAAAGACGTTTTTGTCTTTATTCTGC  
 AAAAGTGAACAAGTTGAAGACTTTTGTATTTTGTACTTTGCTAGTTTGTGGCAGAGTGGAGAGGACGGGTGGATA  
 TTTCAAATTTTTTAGTATAGCGTATCGCAAGGGTTTGACACGGCTGCCAGCGACTCTAGGCTTCCAGTCTGTGT  
 TTGGTTTTTATTCTTATCATTATTATGATTGTTATTATATTATTATTTTATTAGTTGTTGTGCTAAACTCAAT  
 AATGCTGTTCTAACTACAGTGCTCAATAAATGATTAAATGACAGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AA

**FIGURE 512**

MARMSFVIAACQLVLGLLMTSLTESSIONSECPQLCVCEIRPWFTPQSTYREATTVDCNDLRL  
TRIPSNLSSDTQVLLQLSQNNIAKTVDLQQLFNLTELDIFSQNNFTNIKEVGLANLTQLTTLHL  
EENQITEMTDYCLQDLSNLQELYINHNIQISTISAHAFAGLKNLLRLHLNSNKLKVIDSRWFDS  
TPNLEILMIGENPVIGILDMNFKPLANLRSLVLAGMYLTDIPGNALVGLDSLESLSFYDNKLV  
KVPQLALQKVPNLKFLDLNKNPIHKIQEGDFKNMLRLKELGINNMGELVSVDRYALDNLPELT  
KLEATNNPKLSYIHRLAFRSVPALESMLNNNALNAIYQKTVESLPNLREISIHNSPLRCDCV  
IHWINSNKTNIRFMEPLSMFCAMPPEYKGHQVKEVLIQDSSEQCLPMISHDSFPNRLNVDIGT  
TVFLDCRAMAEPEPEIYWVTPIGNKITVETLSDKYKLSSEGTLEISNIQIEDSGRYTCVAQNV  
QGADTRVATIKVNGTLLDGTQVLKIYVKQTESHSLVSWKVNSNVMTSNLKWSSATMKIDNPH  
ITYTARVPVDVHEYNLTHLQPSTDYEVCLTVSNIHQQTQKSCVNVTTKNAFAVDISDQETST  
ALAAVMGSMFAVISLASIAVYFAKRFRKKNYHSLKKYMQKTSSIPLNELYPPLINLWEGDSE  
KDKDGSADTKPTQVDTSRSYYMW

**Important features:**

**Signal peptide:**

Amino acids 1-25

**Transmembrane domain:**

Amino acids 508-530

**N-glycosylation sites:**

Amino acids 69-73;96-100;106-110;117-121;385-389;517-521;  
582-586;611-615

**Tyrosine kinase phosphorylation site:**

Amino acids 573-582

**N-myristoylation sites:**

Amino acids 16-22;224-230;464-470;637-643;698-704

**FIGURE 513**

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTCC  
CAGCAATATGCATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCCCCT  
GTCTGGATGGGCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGGGCT  
GAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGAATCACGCATGC  
CGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGCAAGGA  
GTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGATCAACCA  
TGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACGCTGCTGG  
ACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCACACTGGGGTCCACCAGGCTGG  
GAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGGAAAGGAAGT  
GGAGAAGCTTGGCCAAGGTGCCCAACCATGCTGCTGGCCAGGCCGGGAAGGAGCTGCAGAATGC  
TCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGCAACCATCAAAG  
CGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGGGGCCTCAGTCAA  
CACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCATGCCCTTAAACTGG  
CATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTACATCAGCTGACATGACCTGGAGGGG  
TTGGGGGTGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTACTGGGATTTGTGAATAAA  
CTTGATACACCA

**FIGURE 514**

MHLARLVGSCSLLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVKGALDGINSGITHAGR  
EVEKVFNGLSNMGSHGTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAGQA  
GKEADKAVQGFTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQNAHN  
GVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP

**Important features:**

**Signal peptide:**

amino acids 1-25

**Homologous region to circumsporozoite (CS) repeats:**

amino acids 35-225



**FIGURE 515**

CCCACGCGTCCGCCCACGCGTCCGGGTGCCACTCGCGCGCCGGCCGCGCTCCGGGCTTCTCTT  
TTCCCTCCGACGCGCCACGGCTGCCCAGACATTCCGGCTGCCGGGTCTGGAGAGCTCCCCGAA  
CCCCTCCGCGGAGAGGAGCGAGGCGCGCCAGGGTGGCCCCCGGGGCGCGCTTGGTCTCGGAG  
AAGCGGGACGAGGCCGAGGATGAGCGACTGAGGGCGACGCGGGCACTGACGCGAGTTGGGG  
CCGCGACTACCGGCAGCTGACAGCGCGATGAGCGACTCCCCAGAGACGCCCTAGCCCCGTGTG  
CGCGCCAGGCGGAGCGCGCAGGTGGGGCTGGGCTGTAGTGGTCCGCCCCACGCGGGTCCGCC  
GCCGGCCCAGGATGGGCGCTGGCAACCCGGGCCCCGCGCCCCGCGCTGCTACCCCTGCGCCCCG  
TGCGAGCCCGGCGTCCGGCCCCGCGCCTGCGCTCATGGACGGCGGCTCCCGGCTGGCGGCGGC  
GCGCCCCCGGGCTGTGAATGCGACTCGCCCCTCGGCCGCGCTCCCCGCCCGCCCGCCCGG  
GACGTGGTAGGGGATGCCAGCTCCACTGCGATGGCAGTTGGCGCGCTCTCCAGTTCCCTCCT  
GGTCACCTGCTGCCTGATGGTGGCTCTGTGCAGTCCGAGCATCCCGCTGGAGAAGCTGGCCCA  
GGCACCAGAGCAGCCGGGCCAGGAGAAGCGTGAGCACGCCACTCGGGACGGCCCGGGGCGGGT  
GAACGAGCTCGGGCGCCCGGCGAGGGACGAGGGCGGCGAGCGCCGGGACTGGAAGAGCAAGAG  
CGGCCGTGGGCTCGCCGGCCGTGAGCCGTGGAGCAAGCTGAAGCAGGCCTGGGTCTCCAGGG  
CGGGGGCGCCAAGGCCGGGGATCTGCAGGTCCGGCCCCGCGGGACACCCCGCAGGCGGAAGC  
CCTGGCCCGCAGCCGCCCAGGACGCGATTGGCCCCGAACTCGCGCCCACGCCCGAGCCACCCGA  
GGAGTACGTGTACCCGGACTACCGTGGCAAGGGCTGCGTGACGAGAGCGGCTTCGTGTACGC  
GATCGGGGAGAAGTTTCGCGCCGGGCCCCCTCGGCCTGCCGTGCTGTGCACCGAGGAGGGGCC  
GCTGTGCGCGCAGCCCGAGTGCCCGAGGCTGCACCCGCGTGCATCCACGTGACACGAGCCA  
GTGCTGCCCCGAGTGCAAGGAGAGGAAGAATACTGCGAGTTCGGGGCAAGACCTATCAGAC  
TTTGAGGAGTTCGTGGTGTCTCCATGCGAGAGGTGTCGCTGTGAAGCCAACGGTGAGGTGCT  
ATGCACAGTGTGAGCGTGTCCCCAGACGGAGTGTGTGGACCCCTGTGTACGAGCCTGATCAGTG  
CTGTCCCATCTGCAAAAATGGTCCAACTGCTTTGCAGAAACCGCGGTGATCCCTGCTGGCAG  
AGAAGTGAAGACTGACGAGTGCACCATATGCCACTGTACTTATGAGGAAGGCACATGGAGAAT  
CGAGCGGCAGGCCATGTGCACGAGACATGAATGCAGGCAAATGTAGACGCTTCCAGAACACA  
AACTCTGACTTTTTCTAGAACATTTTACTGATGTGAACATTCTAGATGACTCTGGGAACTATC  
AGTCAAAGAAGACTTTTGATGAGGAATAATGGAAAATTGTTGGTACTTTTCCTTTTCTTGATA  
ACAGTTACTACAACAGAAGGAAATGGATATATTTCAAACATCAACAAGAACTTTGGGCATAA  
AATCCTTCTCTAAATAAATGTGCTATTTTCACAGTAAGTACACAAAAGTACACTATTATATAT  
CAAATGTATTTCTATAATCCCTCCATTAGAGAGCTTATATAAGTGTTTTCTATAGATGCAGAT  
TAAAAATGCTGTGTGTCAACCGTCAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 516**

MPSSTAMAVGALSSSLLVTCCLMVALCSPSIPLEKLAQAPEQPGQEKREHATRDGPGRVNELG  
RPARDEGGSGRDWKSksGRGLAGREPWSKLKQAWVSQGGGAKAGDLQVRPRGDTQAEALAAA  
AQDAIGPELAPTPEPPPEEYVYPDYRGKGCVDSESGFVYAIGKFAFGPSACPCLCTEEGPLCAQ  
PECPRLHPRCIHVDTSQCCPQCKERKNYCEFRGKTYQTLEEFVVSPCERCRCCEANGEVLCTVS  
ACPQTECVDPVYEPDQCCPICKNGPNCFAETAVIPAGREVKTDECTICHCTYEETWRIERQA  
MCTRHECRQM

**Important features:**

**Signal peptide:**

amino acids 1-27

**Transmembrane domain:**

amino acids 11-30

**Glycosaminoglycan attachment site.**

amino acids 80-83

**N-myristoylation sites.**

amino acids 10-15, 102-107, 103-108

**Cell attachment sequence.**

amino acids 114-117

**EGF-like domain cysteine pattern signature.**

amino acids 176-187

**FIGURE 517**

GGACAACCGTTGCTGGGTGTCCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCCT  
TTCGGCCTTGAGGTTCCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCTAC  
GGACGACGCCTATGAAGCCCTTAGTCCTTCTAGTTGCGCTTTTGCTATGGCCTTCGTCTGTGC  
CGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATACAAG  
TTTTAGAGAACCTAGTACGAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAATCTAACT  
CTCCAAAACATGTTTATTCTATAGCATCAAAGGGATCAAATTTAAGGAGCTAGTTACACATG  
GAGACGCTTCAACTGAGAATGATGTTTTAACCAATCCTATCAGTGAAGAACTACAACCTTCC  
CTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAAACACACGGAAGTACCCCATTTCTGGT  
CGATCAAACCAAACAATGTTTCCATTGTTTTGCATGCAGAGGAACCTTATATTGAAAAATGAAG  
AGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATGTTGCCAGTTG  
TTACTGAATCATCTACAAGTCCATATGTTACCTCATACAAGTCACCTGTCACCACTTTAGATA  
AGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCTCAGGTGAAACTG  
CGATAGAAAAACCCGAAGAGTTTGGAAAGCACCCAGAGAGTTGGAATAATGATGACATTTTGA  
AAAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACTTCCTTAGTGACACCAGCAACCCAG  
CATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCCTTGCTCTAGCAGCAG  
CAGCAGAACATAAATTA AAAACAATGTATAAGTCCCAGTTATTGCCAGTAGGACGAACAAGTA  
ATAAAATTGATGACATCGAACTGTTATTAACATGCTGTGTAATTC TAGATCTAACTCTATG  
AATATTTAGATATTA AATGTGTTCCACCAGAGATGAGAGAAAAAGCTGCTACAGTATTCAATA  
CATTA AAAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA AAAGTTTATTAAACAATAA  
TATAAAAATTTTAAACCTACTTGATATTCCATAACAAAGCTGATTTAAGCAAACCTGCATTTTT  
TCACAGGAGAAATAATCATATTCGTAATTTCAAAGTTGTATAAAAATATTTTCTATTGTAGT  
TCAAATGTGCCAACATCTTTATGTGT CATGTGTATGAACAATTTTCATATGCACTAAAAACC  
TAATTTAAAATAAAATTTTGGTTCAGGAAAAAA

**FIGURE 518**

MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRSVPSGEPGREKKSNSPKH  
VYSIASKGSKFKELVTHGDASTENDVLTNPISEETTTFTGGFTPEIGKKKHTESTPFWSIKP  
NNVSIVLHAEFPYIENEEPEPEPEPAAKQTEAPRMLPVVTSSTSPYVTSYKSPVTTLDKSTG  
IEISTESEDVPQLSGETAIEKPEEFGKHPESWNDDILKKILDINSQVQQALLSDTSNPAYRE  
DIEASKDHLKRSLALAAAAEHKLKTMYSQLLPVGRTSNKIDDIE TVINMLCNSRSKLYEYLD  
IKCVPPEMREKAATVFNTLKNMCRSRRVTALLKVY

**Important features:**

**Signal peptide:**

amino acids 1-19

**FIGURE 519**

CGGCTCGAGTGCAGCTGTGGGGAGATTTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATCTTG  
GATTTGAAAAGTTGAGAGCAGCATGTTTTTGCCCACTGAAACTCATCCTGCTGCCAGTGTTACTG  
GATTATTCCTTGGGCCTGAATGACTTGAATGTTTTCCCCGCCTGAGCTAACAGTCCATGTGGGT  
GATTCAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATATTCAAGATAGAC  
TGGACTCTGTCAACCAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCAATCTC  
AGTGTGCCTATTGGGCGCTTCCAGAACCGGTACACTTGATGGGGGACATCTTATGCAATGAT  
GGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGAAATCCGC  
CTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAGAGGAGCCC  
AAAGAGCTCATGGTCCATGTGGGTGGATTGATTGAGATGGGATGTGTTTTCCAGAGCACAGAA  
GTGAAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGAGGAGATTGTA  
TTTCGTTACTACCACAACTCAGGATGTCTGTGGAGTACTCCAGAGCTGGGGCCACTTCCAG  
AATCGTGTGAACCTGGTGGGGGACATTTTCCGCAATGACGGTTCATCATGCTTCAAGGAGTG  
AGGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACCTGGTGTTCAGAAA  
ACCATTGTGCTGCATGTGAGCCCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGG  
CCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTCTGTGCCACAATCCTG  
CTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAAATAAGAGTTCAGTGAATTCT  
ACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAGAAAAACCCTGCCATTTT  
GAAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTACGGGAGGTGATCGAGGAA  
GAAGAACCAAGTAAAAAATCAGAGGCCACCTACATGACCATGCACCCAGTTTGGCCTTCTCTG  
AGGTGAGATCGGAACAACTCACTTGAAAAAAGTCAGGTGGGGGAATGCCAAAAACACAGCAA  
GCCTTTTGAGAAGAATGGAGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCCTGTGTGT  
GTCCTGGGCCACTCTACCAAGTGATTTTCAGACTCCCGCTCTCCAGCTGTCTCTCTGTCTCATT  
GTTTGGTCAATACTGAAGATGGAGAATTTGGAGCCTGGCAGAGAGACTGGACAGCTCTGGA  
GGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGCCTCTGGAGTGGGACACTGGCCCTG  
GGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCCGTTGGATCAGACCCTCCTGTGGGCAGGG  
TTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATAAAAAACCAACCCAAATCAA

**FIGURE 520**

MFCPLKLILLPVLLDYSGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLSPE  
HAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEQADQGTYYICEIRLKGESQV  
FKKAVVLHVLPEEPKELMVHVGGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYYHKL  
RMSVEYSQSWGHFQNRVNLVGDI FRNDGSIMLQGVRES DGGNYTCSIHLGNLVFKKTIVLHVS  
PEEPRTLVT PAALRPLVLGGNQLV IIVGIVCATILLPVLLILIVKKTCGNKSSVNSTVLVKNT  
KKTNP EIKEKPC HFERCEGEKHIYSPII VREVIEEEEPSEKSEATYMTMHPVWPSLRSDRNNS  
LEKKSGGGMPKTQQAF

**FIGURE 521**

CTATGAAGAAGCTTCCTGGAAAACAATAAGCAAAGGAAAACAAATGTGTCCCATCTCACATGG  
TTCTACCCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGGAA  
ACTACATTTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCCATGCAGGA  
TGAAGATGGATACATCACCTTAAATATTAAAACTCGGAAACCAGCTCTCGTCTCCGTTGGCCC  
TGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGGATGGT  
TGTCGGGCTGGTGGCTCTGGGGATTGGTCTGTGCATGCAGCGCAATTACCTACAAGATGAGAA  
TGAAAATCGCACAGGAACTCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGGTAAAAACA  
ATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCCTGTGACACAACTGGAGATA  
TTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACTTAACATGGGAAGAGAGTAAGCAGTA  
CTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGGAGTACATCAA  
AGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAATGAGGTCTGGAA  
GTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGAAGATGAAAAGGAAA  
TATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCCTACCTTCTGTGAGAACAAACATTA  
TTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCTTAATGCAAAGAGGT  
GGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAAGATATGTATGAATGCATCAGTA  
GCTGAAAAAAAAAAAAAA

**FIGURE 522**

MQDEDGYITLNIKTRKPALVSVGPASSSWWRVMALILLILCVGMVVGLVALGIWSVMQRNYLQ  
DENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSYGFRRHNLTWEEES  
KQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEFLEDG  
KGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP



**FIGURE 523**

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGGC  
AAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCCAA  
GAAAATATGTAAATCACTTAAGATTGTGGAAGTGGTGTGGTATCCTGGCCCTAACTCTAAT  
TGTCTGTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACATGGA  
GCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTACATGGAAATTGATCCTGTGACCAG  
AACTGAAATATTGAGAAGCGGAAATGGCACTGATGAAACATTGGAAAGTGCACGACTTTAAAAA  
CGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTATCAAAACTCAGATTAAAGT  
GATTCCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACCACAACCTTT  
CTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGATTTTCTTAA  
AAATTCCAAATTTCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATCCCACTCTAAT  
ATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGAGAAGATCTTCACTTTCTGCCAACGA  
AAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGTAGAGAAGACCCG  
TCACGCCAGACAAGCAAGTGAGGAAGAACTTCCAATAAATGACTATACTGAAAATGGAATAGA  
ATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGTGAGGCAACCGCTA  
TTGCCGCCGCTCTGTGAACCTTTACTAGGCTACTACCCATATCCATACTGCTACCAAGGAGG  
ACGAGTCATCTGTCGTGTCATCATGCCTTGTAAGTGGTGGGTGGCCCGCATGCTGGGGAGGGT  
CTAATAGGAGGTTTGAGCTCAAATGCTTAAACTGCTGGCAACATATAATAAATGCATGCTATT  
CAATGAATTTCTGCCTATGAGGCATCTGGCCCTGGTAGCCAGCTCTCCAGAATTACTTGTAG  
GTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACCAAAAAAAAAAAAAAAAAA

## **FIGURE 524**

MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPPKAYD  
MEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIIYFVGLQKCFIKTQI  
KVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKN SKILEICDNVTMYWINPT  
LISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDYTENG  
IEFDPMLDERGYCCIIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWVARMLGRV

**Important features:**

**Signal peptide:**

amino acids 1-40

**Transmembrane domain:**

amino acids 25-47 (type II)

**N-glycosylation sites.**

amino acids 94-97, 180-183

**Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-  
242

**N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 315-317

**Cytochrome c family heme-binding site signature.**

amino acids 9-14

**FIGURE 525**

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGCATGAAGATCACTGGGGGTC  
TCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCCAA  
AAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCACAT  
ACCTACCAGTTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCACTTGTGTACCGAGA  
GCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGCTAAATTCTCCATGGAC  
ATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTGAGTTTC  
TTTCAGTTTTTACTGATGTTCTGGGTGGGGGACAGAGCCAGATTCAGAGTAATCTTGACTGAAT  
GGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCATTTTTTTTTT  
TAACACGTCAATAAAAAAATAATCTCCAGA

**FIGURE 526**

MKITGGLLLLCTVVYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGNE  
CHLCTESLKSNQVQFLHDGSC

**Important features:**

**Signal peptide:**

amino acids 1-19

**FIGURE 527**

CGACGATGCTACGCGCGCCCGGCTGCCTCCTCCGGACCTCCGTAGCGCCTGCCGCGGCCCTGG  
 CTGCGGCGCTGCTCTCGTCTGCGCGCTGCTCTCTTCTAGAGCCGAGGGACCCGGTGGCCT  
 CGTCGCTCAGCCCCCTATTTCCGGCACCAAGACTCGCTACGAGGATGTCAACCCCGTGCCTATTGT  
 CGGGCCCCGAGGCTCCGTGGCGGGACCTGAGCTGCTGGAGGGGACCTGCACCCCGGTGCAGC  
 TGGTCGCCCCCTATTCCGCCACGGCACCCGCTACCCACGGTCAAACAGATCCGCAAGCTGAGGC  
 AGCTGCACGGGTTGCTGCAGGCCCCGGGTCAGGGATGGCGGGGCTAGTAGTACCGGCAGCC  
 GCGACCTGGGTGCAGCGCTGGCCGACTGGCCTTTGTGGTACGCGGACTGGATGGACGGGCAGC  
 TAGTAGAGAAGGGACGGCAGGATATGCGACAGCTGGCGCTGCGTCTGGCCTCGCTCTTCCCGG  
 CCCTTTTCAGCCGTGAGAACTACGGCCGCTGCGGCTCATCACCAGTTCCAAGCACCGTGCA  
 TGGATAGCAGCGCCGCTTCTTGCAGGGGCTGTGGCAGCACTACCACCTGGCTTGCCCGCGC  
 CGGACGTCGCAGATATGGAGTTTGGACCTCCAACAGTTAATGATAAACTAATGAGATTTTGTG  
 ATCACTGTGAGAAGTTTCTTAAGTAGAAAAAATGCTACAGCTCTTTATCAGTGGGAG  
 CCTTCAAACTGGACCAGAAATGCAGAACATTTTAAAAAAGTTGCAGCTACTTTGCAAGTGC  
 CAGTAAATGATTTAAATGCAGATTTAATTCAAGTAGCCTTTTTCACCTGTTTATTGACCTGG  
 CAATTAAAGGTGTTAAATCTCCTTGGTGTGATGTTTTGACATAGATGATGCAAGGTATTAG  
 AATATTTAAATGATCTGAAACAATATGGAAAAGAGGATATGGGTATACTATTAACAGTCGAT  
 CCAGCTGCACCTTGTGTTTCAGGATATCTTTCAGCACTTGGACAAAGCAGTTGAACAGAAACAAA  
 GGTCTCAGCCAATTTCTTCTCCAGTCATCTCCAGTTTGGTCATGCAGAGACTCTTCTCCAC  
 TGCTTTCTCTCATGGGCTACTTCAAAGACAAGGAACCCCTAACAGCGTACAATTACAAAAAC  
 AAATGCATCGGAAGTTCCGAAGTGGTCTCATTGTACCTTATGCCCTCGAACCTGATATTTGTGC  
 TTTACCACTGTGAAAATGCTAAGACTCTAAAGAAACAATTCGAGTGCAGATGTTATTAATG  
 AAAAGGTGTTACCTTTGGCTTACTCACAAGAACTGTTTCATTTTATGAAGATCTGAAGAACC  
 ACTACAAGGACATCCTTCAGAGTTGTCAAACAGTGAAGAATGTGAATTAGCAAGGGTAACA  
 GTACATCTGATGAACTATGAGTAAGTGAAGAACATTTTAAATCTTTAGGAATCTGCAATGAG  
 TGATTACATGCTTGTAATAGGTAGGCAATTCCTTGATTACAGGAAGCTTTTATATTACTTGAG  
 TATTTCTGTCTTTTCACAGAAAAACATTGGGTTTCTCTCTGGGTTTGGACATGAAATGTAAGA  
 AAAGATTTTTCAGTGGAGCAGCTCTCTTAAGGAGAAACAAATCTATTTAGAGAAACAGCTGGC  
 CCTGCAATGTTTACAGAAATGAAATCTTCTTACTTATATAAGAAATCTCACACTGAGATAG  
 AATTGTGATTTTATAATAACACTTGAAAAGTGCTGGAGTAACAAAATATCTCAGTTGGACCAT  
 CCTTAACTTGATTGAACTGTCTAGGAACTTTACAGATTGTTCTGCAGTTCTCTCTTCTTTCC  
 TCAGGTAGGACAGCTCTAGCATTTTCTTAATCAGGAATATTGTGGTAAGCTGGGAGTATCACT  
 CTGGAAGAAAGTAACATCTCCAGATGAGAATTTGAAACAAGAAACAGAGTGTTGTAAGGAC  
 ACCTTCACTGAAGCAAGTCGGAAAGTACAATGAAAATAAATATTTTGGTATTTATTTATGAA  
 ATATTTGAACATTTTTTCAATAATTCCTTTTTACTTCTAGGAAGTCTCAAAGACCATCTTAA  
 ATTATTTATATGTTTGGACAATTAGCAACAAGTCAGATAGTTAGAATCGAAGTTTTTCAAATCC  
 ATTGCTTAGCTAACTTTTTTCACTTCTGTCACTTGGCTTCGATTTTTATATTTTCTATATATG  
 AAATGTATCTTTTGGTTGTTTGATTTTTCTTCTTCTTGTGAAATAGTTCTGAGTCTGTCA  
 AATGCCGTGAAAGTATTTGCTATAATAAGAAAATTCCTGTGACTTTAAAAAAA

**FIGURE 528**

MLRAPGCLLRTSVAPAAALAAALLSSLARCSLLEPRDPVASSLSPTYFGTKTRYEDVNFVLLSG  
PEAPWRDPELLEGTCTPVQLVALIRHGTRYPTVKQIRKLRQLHGLLQARGSRDGGASSTGSRD  
LGAALADWPLWYADWMDGQLVEKGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHRCMD  
SSAAFLQGLWQHYHPGLPPPDVADMEFGPPTVNDKLMRFFDHCEKFLTEVEKNATALYHVEAF  
KTGPEMQNILKKVAATLQVPVNDLNADLIQVAFFTCSEFDLAIKGVKSPWCDVFDIDDAKVLEY  
LNDLKQYWKRQYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGHAETLLPLL  
SLMGYFKDKEPLTAYNYKKQMRKFRSGLIVPYASNLI FVLYHCENAKTPKEQFRVQMLLNEK  
VLPLAYSQETVSFYEDLKNHYKDILQSCQTSEECELARANSTSEDEL

**Important features:**

**Signal sequence**

amino acids 1-30

**N-glycosylation sites.**

amino acids 242-246, 481-485

**N-myristoylation sites.**

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

**Endoplasmic reticulum targeting sequence.**

amino acids 484-489

**FIGURE 529**

GGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGGCGTGGAGGTGCCACCCGGCGCGGGTGC  
CGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGGGA  
CGCGGCGGCGGCGGCGGCGGCGACTGCAGTGGCTGGACGATGGCAGCGTCCGCCGGAGCCGGGGCG  
GTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTTCGGTGTCTGGCGGCGGCGCTTGGGCTC  
TTGACAGCTGGAGTATCAGCCTTGGAGTATATACGCCAAAAGAAATCTTCGTGGCAAATGGT  
ACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACCTCAGT  
TCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTCTGTTTTTCCACTACTCCCAAGGG  
CAAGTGTACCTTGGGAATTATCCACCATTAAAGACAGAATCAGCTGGGCTGGAGACCTTGAC  
AAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACAAATGGCACCTATATCTGT  
GATGTCAAAAACCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTATGTCTGTAGAA  
AAAGAGAATTTGCCTGTGTTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTGCTGTGTTCTTA  
GGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCCCTCTATAGAAGGAAAAAAGCTCTAAACCG  
GATTACACTGGCTGCAGTACATCAGAGAGTTTGTCCACCGTTAAGCAGGCTCCTCGGAAGTCC  
CCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCCTTCTGGATCTCACCAGGGCCCAGTCATA  
TATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAACAAGTCAGAGTCTGTG  
GTGTATGCGGATATCCGAAAGAATTAAAGAGAATACCTAGAACATATCCTCAGCAAGAAACAAA  
ACCAAAGTGGACTCTCGTGCAGAAAATGTAGCCATTACCACATGTAGCCTTGGAGACCCAGG  
CAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGTACAAAGGATATGTATAAA  
TATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTTCATGATGAAAAGATGGTATGATTC  
TACATATGTACCCATTGTCTTGCTGTTTTTGTACTTTCTTTTCAGGTCAATTTACAATTGGGAG  
ATTTTCAGAAACATTCCTTTACCATCATTTAGAAATGGTTTTGCCTTAATGGAGACAATAGCAG  
ATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAAATCTAAGGGCTTAAGACTGATTAGTCTTA  
GCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAAGCATACCCAGGGTGGCCTTTAGC  
ACAGTATCAGTACCATTTATTTGTCTGCCGCTTTTAAAAAATACCCATTGGCTATGCCACTTG  
AAAACAATTTGAGAAGTTTTTTTGAAGTTTTTCTCACTAAAAATGGGGCAATTGTAGCCTT  
ACATGTTGTGTAGACTTACTTTAAGTTTGCACCTTTGAAATGTGTATATCAATTTCTGGATT  
CATAATAGCAAGATTAGCAAAGGATAAATGCCGAAGGTCACCTTCATTCTGGACACAGTTGGAT  
CAATACTGATTAAGTAGAAAAATCCAAGCTTTGCTTGAGAACTTTTGTAAACGTGGAGAGTAAAA  
AGTATCGGTTTTTA

**FIGURE 530**

MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKST  
STTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKSDASINIENMQ  
FIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVVGIVTAVVLGLTLLISMILAV  
LYRRKNSKRDTGCGSTSESLSPVKQAPRKSPDTEGLVKSLPSGSHQGPVIYAQLDHSGGHHS  
DKINKSESVVYADIRKN

**Important features:**

**Signal peptide:**

amino acids 1-37

**Transmembrane domain:**

amino acids 161-183



**FIGURE 531**

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGCTCGA  
GGCTGGTGGGAAGAAGCCGAGATGCGCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGCTC  
TTGCTGATGGCGGTAGCAGCGCCAGTTCGAGCCCGGGGCAGCGGCTGCCGGGCCGGGACTGGT  
GCGCGAGGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCCCTGTGGCACGGTGGGGCTGCTGCTG  
GAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCTGGAAC  
CAGCAGGATGGTACCTTGTCCCTGTACAGCGGCAGCTCAGCGAGGAGGAGCGGGGCCGACTC  
CGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGGGGCCCTG  
GATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGGTGGAGTCG  
CACCTGTCCGACCAGCTGACCCTGACGTGGATGTGGCCGGCAACGTGGTGGGCGTGTCCGTG  
GTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACC'TGGAGCTGTTCAAC  
ACCTCGGTGCAGCTGCAGCCGCCCACCACAGCCCCAGGCCCTGAGACGGCGGCCTTCATTGAG  
CGCCTGGAGATGGAACAGGCCCAGAAGGCCAAGAACCCCCAGGAGCAGAAGTCCTTCTTCGCC  
AAATACTGGATGTACATCATTCCCGTCGTCCTGTTCCCTCATGATGTCAGGAGCGCCAGACACC  
GGGGGCCAGGGTGGGGTGGGGTGGGGTGGTGGTGGGGTAGTGGCCTTTGCTGTGTGCCA  
CCCTCCCTGTAAGTCTATTTAAAAACATCGACGATACATTGAAATGTGTGAACGTTTTGAAAA  
GCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGGTCCCTGATGTACAAGCT  
TGATTGAAATTCAC'TGCTCAC'TTGATACGTTATTCAGAAACCCAAGGAATGGCTGTCCCCATC  
CTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTATTAAACTGTCCCCAGATC  
GACACGCAAAAAAAAAA

**FIGURE 532**

MAAASAGATRLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEID  
DSANFRKRGSLLWNQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRIIPRRPGALDGLEAGG  
YVSSFVPACSLVESHLSDQLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFNTSVQLQP  
PTTAPGPETAAFIERLEMEQAQKAKNPQEQKSFFAKYWMIIPVVLFLMSGAPDTGGQGGGG  
GGGGGGGSGLCVPPSL

**Important features:**

**Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 226-243



**FIGURE 534**

MELALLCGLVVMAGVPIQGGIILNLNKMVKQVTGKMPILSYWPGCHCGLGGRGQPKDATDWC  
CQTHDCCYDHLKTQGCGIYKDNNKSSIHCMDSLQRYCLMAVFNVIIYLENEDSE

**Important features:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 1-24

**N-glycosylation site.**

amino acids 86-89

**N-myristoylation sites.**

amino acids 20-25, 45-50

**Phospholipase A2 histidine active site.**

amino acids 63-70

**FIGURE 535**

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCTG  
 AACTGGGTGCTCATCACGGGAAGTCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAGCC  
 CCAAATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATGTAGGATCCAGTTTTT  
 TTTTAAACGCCCCCTCCCCACCCCCCAAAAACTGTAAAGATGCAAAAACGTAATATCCAT  
 GAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATTTATTT  
 GTTCTTGGAGTGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCTCCCAAG  
 GGTCCAATTTTTCTTCTGGGTGTGAGCGAGCCCTGACTCACTACAGTGCAGCTGACAGGGG  
 CTGTCATGCAACTGGCCCCTAAGCCAAAGCAAAAGACCTAAGGACGACCTTTGAACAATACAA  
 AGGATGGGTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTTATAGCCCC  
 ACTGTCTTACTGACAATGCTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTGTAGGTGTGAA  
 GGCAAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCCTCAAGTATATCTGCTGGT  
 TGCTTAGGTTTTGTCCCTTCGCTATAACAGCCTTCAAAAACCTAAGTATAATCAATTTAAAGGG  
 CTCACCAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATATTGACGAAAATGCT  
 TTTAATGGAATACGCAGACTCAAAGAGCTGATTCTTAGTTCCAATAGAAATCTCCTATTTTCTT  
 AACATACCTTCAGACCTGTGACAAATTTACGGAACCTGGATCTGTCTATAATCAGCTGCAT  
 TCTCTGGGATCTGAACAGTTTCGGGGCTTGCGGAAGCTGCTGAGTTTACATTTACGGTCTAAC  
 TCCCTGAGAACCATCCCTGTGCGAATATTCCAAGACTGCCGCAACCTGGAACTTTTGGACCTG  
 GGATATAACCGGATCCGAAGTTTAGCCAGGAATGCTTTTGCTGGCATGATCAGACTCAAAGAA  
 CTTACCTGGAGCACAATCAATTTTCCAAGCTCAACCTGGCCCTTTTCCAAGGTTGGTCAGC  
 CTTCAGAACCTTTACTTGCAGTGGAATAAAATCAGTGTATAGGACAGACCATGTCTTGACC  
 TGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGATCGAAGCTTTCAGTGGACCCAGT  
 GTTTTCCAGTGTGTCCGAATCTGCAGCGCCTCAACCTGGATTCCAACAGCTCACATTTATT  
 GGTCAAGAGATTTTGGATTCTTGATATCCCTCAATGACATCAGTCTTGCTGGGAATATATGG  
 GAATGCAGCAGAAATATTTGCTCCCTTGTAAGTGGCTGAAAAGTTTTAAAGGTCTAAGGGAG  
 AATACAATTATCTGTGCCAGTCCCAAGAGCTGCAAGGAGTAAATGTGATCGATGCAGTGAAG  
 AACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGTTTGATCTGGCCAGGGCTCTCCCAAAG  
 CCGACGTTTAAAGCCCAAGCTCCCCAGGCCGAAGCATGAGAGCAAACCCCCCTTTGCCCCGACG  
 GTGGGAGCCACAGAGCCCGGCCAGAGACCGATGCTGACGCCGAGCACATCTTTCCATAAA  
 ATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCGTGCTCGTCATCTGCTGGTTATCTACGTG  
 TCATGGAAGCGGTACCCTGCGAGCATGAAGCAGCTGCAGCAGCGCTCCCTCATGCGAAGGCAC  
 AGGAAAAAGAAAAGACAGTCCCTAAAGCAAATGACTCCAGCACCCAGGAATTTTATGTAGAT  
 TATAAACCCACCAACACGGAGACCAGCGAGATGCTGCTGAATGGGACGGGACCTGCACCTAT  
 AACAAATCGGGCTCCAGGGAGTGTGAGGTATGAACCATTGTGATAAAAAGAGCTCTTAAAAGC  
 TGGGAAATAAGTGGTGCTTTATTGAACTCTGGTGACTATCAAGGGAACGCGATGCCCCCCTC  
 CCCTTCCCTCTCCCTCTCACTTTGGTGGCAAGATCCTTCTTGTCCGTTTTAGTGCATTCTATA  
 ATACTGGTCATTTTCTCTCATACATAATCAACCCATTGAAATTTAAATACCACAATCAATGT  
 GAAGCTTGAATCCGGTTTAATATAATACCTATTGTATAAGACCCTTTACTGATTCCATTAAT  
 GTCGCATTTGTTTTAAGATAAAACTTCTTTCATAGGTAAAAA

## **FIGURE 536**

MGFNVIRLLSGSAVALVIAPT VLLTMLSSAERGCPKGCRCEGKMVYCESQKLQEIPSSISAGC  
LGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNHISNIDENAFNGIRRLKELILSSNRISYFLN  
NTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLR TIPVRIFQDCRNLELLDLG  
YNRIRSLARNVFAGMIRLKEHLHLEHNQFSKLNALFPRLVSLQONLYLOWNKISVIGQTMSTW  
SSLQRLDLSGNEIEAFSGPSVFQCVPNLQRLNLDNKLTFIGQEILDSWISLNDISLAGNIWE  
CSRNICSLVNWLKSFKGLRENTI ICASPKELQGVNVIDAVKNYSICGKSTTERFDLARALPKP  
TFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKI IAGSVALFLSVLVILLVIYVS  
WKRYPASMQLQQRSLMRRHRKKRQSLKQMTPTSTQEFYVDYKPTNTETSEMLLNGTGPCTYN  
KSGSRECEV

**Important features:**

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 420-442

**N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

**Tyrosine kinase phosphorylation site.**

amino acids 136-142

**N-myristoylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

**FIGURE 537**

GGGACTACAAGCCGCGCCGCTGCCGCTGGCCCTCAGCAACCTCGACATGGCGCTGAGGCGGCCACCGCGAC  
TCCGGCTCTGCGCTCGGCTGCCCTGACTTCTTCCTGCTGCTGCTTTTCAGGGGCTGCCTGATAGGGGCTGTAAATC  
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTTGAAAGTGTGGAACGTCTTGTCATCATTACGGATTTCG  
AGACAAGTGACCCAGGATCGAGTGGAAGAAAATTCAAGATGAACAAACCATATGTGTTTTTGACAACAAAA  
TTCAGGGAGACTTGGCGGGTCGTGCAGAAATACTGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG  
ACTCAGCCCTTTATCGCTGTGAGGTCTGTGCTCGAAATGACCGCAAGGAAATTGATGAGATTGTGATCGAGTTAA  
CTGTGCAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGGTTCTGGTTGTCCTTGCTGTACTGGCCCTGA  
TCAGCTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA  
ACCCAGGAAACAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCGACTTCAGACACAAGTCATCGTTTG  
TGATCTGAGACCCGCGGTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCTGTCAA  
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTAGAAAGCTTTTCGTTTGGCCAAAGTTGACCA  
CTACTCTTCTTACTCTAACAAGCCACATGAATAGAAGAATTTTCTCAAGATGGACCCGGTAAATATAACCACAA  
GGAAGCGAAACTGGGTGCGTTCACTGAGTTGGGTTCCTAATCTGTTTCTGGCCTGATTCGCCCATGAGTATTAGG  
GTGATCTTAAAGAGTTTGCTACGTAAACGCCCCGTGCTGGGCCCTGTGAAGCCAGCATGTTCAACCTGGTCTGT  
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACACGACGCGCATCCCGCGGGAACCCA  
GAAAAGGCTTCTTACACAGCAGCCTTACTTCATCGGCCACAGACACCACCGCAGTTTCTTCTTAAAGGCTCTGC  
TGATCGGTGTTGCAGTGTCCATGTGTGAGAAGCTTTTGGATCAGCATTTTGTAAAAACAACCAAAATCAGGAAG  
GTAAATTTGGTTGCTGGAAGAGGGATCTTGCCCTGAGGAACCTGCTTGTCCAACAGGGTGTGAGGATTTAAGGAA  
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTGTTTATTTTATAAAATTT  
TACATCTAAATTTTGTCTAAGGATGTATTTTGATTATTGAAAAGAAAATTTCTATTTAACTGTAAATATATTGT  
CATACAATGTTAAATAACCTATTTTTTAAAAAGTTCAACTTAAGGTAGAAGTTCCAAGTACTAGTGTAAAT  
TGGAAAAATATCAATAATTAAGAGTATTTTACCCAGGAATCCTCTCATGGAAGTTTACTGTGATGTTCTTTTCT  
CACACAAGTTTTAGCCTTTTTCACAAGGGAACCTCATGCTACACATCAGACCATAGTTGCTTAGGAAACCTT  
TAAAAATTCAGTTAAGCAATGTTGAAATCAGTTGTCATCTCTTCAAAAGAAACCTCTCAGGTTAGCTTTGAACT  
GCCTCTTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACACAGATG  
CCAGTCAGCTCCTGGGGTTGCGCCAGGCGCCCCGCTCTAGCTCACTGTTGCTCGCTGCTGCTGCCAGGAGGCCCT  
GCCATCCTTGGGCCCTGGCAGTGGCTGTGTCCAGTGAGCTTTACTCAGTGCGCCTTGCTTCTATCCAGCACAGC  
TCTCAGGTGGGCACTGCAGGGACACTGGTGTCTTCCATGTAGCGTCCAGCTTTGGGCTCCTGTAACAGACCTCT  
TTTTGGTTATGGATGGCTCACAAAATAGGGCCCCAATGCTATTTTTTTTTTTTAAAGTTTGTTTAATTATTTGTT  
AAGATTGTCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTTTAAAGAAAATGGAT  
CCCAGTGTTCCTCTTTGCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTGCGATTTCAAAACAAACCATGAT  
GGAGTGGCGGCCAGTCCAGCCTTTTAAAGAACGTGAGGTGGAGCAGCCAGGTGAAAGGCCCTGGCGGGGAGGAAAG  
TGAAACGCCCTGAATCAAAGCAGTTTTCTAATTTTGACTTTAAATTTTTCATCCGCCGAGACACTGCTCCCATT  
TGTGGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT  
GCCGTGCTGGACTCAGGACTGAAGTGTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCTTGGGA  
GAATGGCTCTCACTACTCACCTTGTCTTTCAGCTTCCAGTGTCTTGGGTTTTTTTATACTTTGACAGCTTTTTTTT  
AATTGCATACATGAGACTGTGTGACTTTTTTTAGTTATGTGAAACACTTTGCCGCGAGGCCCTGGCAGAGGCA  
GGAAATGCTCCAGCAGTGGCTCAGTGCTCCCTGGTGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTC  
CCTCCATCATTGCCACCTTGGTAGAGAGGGATGGCTCCCCACCCTCAGCGTTGGGGATTACGCTCCAGCCTCCT  
TCTTGGTTGTCTAGTGTATAGGGTAGCCTTATTGCCCCCTCTTCTTATACCCCTAAACCTTCTACACTAGTGCCA  
TGGGAACCAGGTCTGAAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA  
CGGAAAAGGAATACTCGTGTATTTTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT  
GCCTTTGGATGGATGTGCTGTACACAGATGCTACAGACTGTACTAACACACCGTAATTTGGCATTGTGTTTAAAC  
CTCATTTATAAAAGCTTCAAAAAACCCA

**FIGURE 538**

MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS DP  
RIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTS LKIWNVTRRDSALYRCEVVARNDRKEI  
DEIVIELTVQVKPVPVPCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPR  
FRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDLNIGGIIGGVLV  
LAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

**Important features:**

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 243-263

**N-glycosylation sites.**

amino acids 104-107, 192-195

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

**Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

**Tyrosine kinase phosphorylation site.**

amino acids 69-77

**N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267



# **FIGURE 539**

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTGTCAGAGGCCGGGGAAGAGAAGCAAAGC  
GCAACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCCTCTAGGACATACACGGGACCCCTAA  
CTTCAGTCCCCCAAACGCGCACCTCGAAGTCTTGAATCCAGCCCCGCACATCCACGCGCGG  
CACAGGCGCGGCAGGCGGCAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGCTCGGGCAGCTGG  
GCTCGGGCGCGGGAGTAGGGCCCCGGCAGGGAGGCAGGGAGGCTGCATATTAGAGTTCGCGGG  
CTGCGCCCTGGGCAGAGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCGCCGCGA  
TGAGCCGCGTGGTCTCGCTGCTGCTGGGCGCCGCGCTGCTCTGCGGCCACGGAGCCTTCTGCC  
GCCGCGTGGTCAGCGGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTACAAAATGG  
CCTACTTCCATGAACTGTCCAGCCGAGTGAGCTTTAGGAGGCACGCCTGGCTTGTGAGAGTG  
AGGGAGGAGTCCCTCCTCAGCCTTGAGAATGAAGCAGAACAGAAGTTAATAGAGAGCATGTTGC  
AAAACCTGACAAAACCCGGGACAGGGATTTCTGATGGTGATTTCTGGATAGGGCTTTGGAGGA  
ATGGAGATGGGCAAACATCTGGTGCTGCCAGATCTCTACCAAGTGTGATGGAAGCAATT  
CCCAGTACCGAACTGGTACACAGATGAACCTTCCCTGCGGAAGTGAAAAGTGTGTTGTGATGT  
ATCACCACCAACTGCCAATCCTGGCCTTGGGGGTCCCTACCTTTACCAAGTGGAAATGATGACA  
GGTGTAAACATGAAGCACAAATTATTTGCAAGTATGAACCAGAGATTAATCCAACAGCCCCCTG  
TAGAAAAGCCTTATCTTACAAATCAACCAGGAGACACCCATCAGAATGTGGTTGTTACTGAAG  
CAGGTATAATTCCCAATCTAATTTATGTTGTTATACCAACAATACCCCTGCTCTTACTGATAC  
TGTTGCTTTTGGAACTGTGTTTCCAGATGCTGCATAAAAGTAAAGGAAGAACAAAACTA  
GTCCAAACCAGTCTACACTGTGGATTTCAAAGAGTACCAGAAAAGAAAGTGGCATGGAAAGTAT  
AATAACTCATTGACTTGGTTCCAGAATTTGTAAATTCTGGATCTGTATAAGGAATGGCATCAG  
AACAAATAGCTTGGAAATGGCTTGAATCACAAAGGATCTGCAAGATGAAGTGAAGTCCCCCT  
TGAGGCAAATATTAAAGTAATTTTATATGTCTATTATTTCAATTAAGAATATGCTGTGCTA  
ATAATGGAGTGAGACATGCTTATTTTGCTAAAGGATGCACCCAACTTCAAACCTCAAGCAAA  
TGAAATGGACAATGCAGATAAAGTTGTATCAACACGTCGGGAGTATGTGTGTTAGAAGCAAT  
TCCTTTTATTTCTTTCACCTTTCATAAGTTGTTATCTAGTCAATGTAATGTATATTGTATGA  
AATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAAGTGTGTTGATAAAATGAAGTGTCTA  
ATATTTATTTTATGGCATCTCATTTTCAATACATGCTCTTTTGATTAAGAACTTATTAC  
TGTTGTCAACTGAATTCACACACACACAAATATAGTACCATAGAAAAAGTTTGTCTCTCGAA  
ATAATTCATCTTTCAGCTTCTCTGCTTTTGGTCAATGTCTAGGAAATCTCTTCAGAAATAAGA  
AGCTATTTTCAATTAAGTGTGATATAAACCTCCTCAAACATTTTACTTAGAGGCAAGGATTGTCT  
AATTTCAATTGTGCAAGACATGTGCCTTATAATTATTTTACTTAAATTAACAGATTTTG  
TAATAATGTAACCTTTGTTAATAGGTGCATAAACTAATGCAGTCAATTTGAACAAAAGAGT  
GACATACACAATATAAATCATATGTCTTCACACGTTGCCATATAATGAGAAGCAGCTCTCTG  
AGGGTTCTGAAATCAATGTGGTCCCTCTCTTGCCCACTAAACAAAGATGGTTGTTTCGGGGTTT  
GGGATTGACACTGGAGGCAGATAGTTGCAAAGTTAGTCTAAGGTTTCCCTAGCTGTATTTAGC  
CTCTGACTATATTAGTATACAAAGAGGTGATGTGGTTGAGACCAGGTGAATAGTCACTATCAG  
TGTGGAGACAAGCACAGCACACAGACATTTTAGGAAGGAAAGGAACTACGAAATCGTGTGAAA  
ATGGGTTGGAACCCATCAGTGATCGCATATTCAATTGATGAGGGTTTGCTTGAGATAGAAAATG  
GTGGCTCCTTTCTGTCTTATCTCCTAGTTTCTTCAATGCTTACGCCTTGTCTCTCAAGAGA  
AAGTTGTAACCTCTGGTCTTCATATGTCCCTGTGCTCCTTTTAAACCAATAAAGAGTTCTTG  
TTTCTGGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 540**

MSRVVSLLLGAALLCGHGAFRRVVSQGQKVCFADFKHPCYKMAYFHELSSRVSFQEARLACES  
EGGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDGFWIGLWRNGDGQTSGACPDLYQWSDGSN  
SQYRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINPTAP  
VEKPYLTNQPGDTHQNVVTEAGIIPNLIYVVIPTIPLLLLLILVAFGTCCFQMLHKS KGRTKT  
SPNQSTLWISKSTRKESGMEV

**Important features:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 214-235

**N-glycosylation sites.**

amino acids 86-89 and 255-258

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 266-269

**N-myristoylation sites.**

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145  
and 212-217

**FIGURE 541**

GGAGAAATGGAGAGAGCAGTGAGAGTGGAGTCCGGGGTCTGGTCCGGGGTGGTCTGTCTGCTCCTGGCATGCCCTG  
 CCACAGCCACTGGGCCCGAAGTTGCTCAGCCTGAAGTAGACACCACCCTGGGTCGTGTGCCAGGCCGGCAGGTGG  
 GCGTGAAGGGCACAGACCGCCTTGTGAATGTCTTTCTGGGCATTCCATTGCCCAGCCGCCACTGGGCCCTGACC  
 GGTTCACAGCCCCACACCCAGCACAGCCCTGGGAGGGTGTGCGGGATGCCAGCACTGCGCCCCCAATGTGCCCTAC  
 AAGACGTGGAGAGCATGAACAGCAGCAGATTGTCTCTCAACGGAAACAGCAGATCTTCTCCGTTTCAGAGGACT  
 GCCTGGTCTCAACGTCTATAGCCAGCTGAGGTCCCCGAGGGTCCGGTAGGCCGGTCATGGTATGGGTCCATG  
 GAGGCGCTCTGATAACTGGCGCTGCCACCTCCTACGATGGATCAGCTCTGGCTGCCCTATGGGGATGTGGTCTGTGG  
 TTACAGTCCAGTACCGCCTTGGGGTCTTGGCTTCTTCAGCACTGGAGATGAGCATGCACCTGGCAACCAGGGCT  
 TCCTAGATGTGGTAGCTGCTTTGCGCTGGGTGCAAGAAAACATCGCCCCCTTCGGGGGTGACCTCAACTGTGTCA  
 CTGTCTTTGGTGGATCTGCCGGTGGGAGCATCATCTCTGGCCTGGTCTGTCCCCAGTGGCTGCAGGGCTGTTC  
 ACAGAGCCATCACACAGAGTGGGGTTCATCACCCCCAGGGATCATCGACTCTCACCTTGGCCCCCTAGCTCAGA  
 AAATCGCAAAACACCTTGGCCTGACGCTCCAGCTCCCCGGCTGAGATGGTGCAGTGCCTTCAGCAGAAAGAAGGAG  
 AAGAGCTGGTCTTAGCAAGAAGCTGAAAAATACTATCTATCTCTCACCGTTGATGGCACTGTCTTCCCCAAAA  
 GCCCCAAGGAACCTCTGAAGGAGAAGCCCTTCCACTCTGTGCCCTTCTCATGGGTGTCAACAACCATGAGTTCA  
 GCTGGCTCATCCCCAGGGGCTGGGGTCTCTGGATACAATGGAGCAGATGAGCCGGGAGGACATGTGGCCATCT  
 CAACACCCGTCTTGACCACTCTGGATGTGCCCCCTGAGATGATGCCACCGTCATAGATCAATACCTAGGAAGCA  
 ACTCGGACGCACAAGCCAAATGCCAGGCGTTCCAGGAATTATGGGTGACGTATTCAATGTTCCACCGTCA  
 GTTTTTCAAGATACCTTCGAGATTCTGGAAGCCCTGTCTTTTCTATGAGTTCAGCATCGACCCAGTTCTTTTG  
 CGAAGATCAAACCTGCTGGGTGAAGGCTGATCATGGGGCCGAGGGTGCTTTTGTGTTTCGGAGGTCCCTTCCTCA  
 TGGACGAGAGCTCCCGCTGGCCTTTCAGAGGCCACAGAGGAGGAGAAGCAGCTAAGCCCTACCATGATGGCCCC  
 AGTGGACCCACTTTTGGCCGACAGGGGACCCCAATAGCAAGGCTCTGCCTCTTGGCCCCAAATCAACCAGGCGG  
 AACAATATCTGGAGATCAACCCAGTGCCACGGGCCGACAGAAGTTCAGGGAGGCCCTGGATGCAGTTCTGGTCAG  
 AGACGCTCCCCAGCAAGATACAACAGTGGCACCAGAAGCAGAAGAACAGGAAGGCCAGGAGGACCTCTGAGGCC  
 AGGCCTGAACCTTCTTGGCTGGGGCAAACCACTCTTCAAGTGGTGGCAGAGTCCACAGCAGCCGACGCCCTCTC  
 CCCCTGCTGAGACTTTAATCTCCACAGCCCTTAAAGTGTTCGGCCGCTCTGTGACTGGAGTTATGCTCTTTTGAA  
 ATGTCAAAAGGCCCGCCTCCACCTCTGGGGCATTGTACAAGTTCTTCCCTCTCCCTGAAGTGCCTTTCTGCTTT  
 CTTGCTGGTAGGTTCTAGCACATTCTCTAGCTTCTGGAGGACTCACTCCCCAGGAAGCCTTCCCTGCCTTCTC  
 TGGGCTGTGCGGCCCGGAGTCTGCGTCCATTAGAGCACAGTCCACCCGAGGCTAGCACCGTGTCTGTCTGTCT  
 CCCCTCAGAGGAGCTCTCTCAAATGGGGATTAGCCTAACCCCACTCTGTCAACCACACAGGATCGGGTGGGA  
 CTGGAGCTAGGGGGTGTGCTGAGTGAGTGAGTGAAACACAGAATATGGGAATGGCAGCTGCTGAACCTTGAAC  
 CCAGAGCCTTCAGGTGCCAAAGCCATACTCAGGCCCCACCGACATTGTCCACCTTGGCCAGAGGGGTGCATGCC  
 AATGGCAGAGACCTGGGATGGGAGAAGTCTCGGGGCGCCAGGGGATCCAGCCTAGAGCAGACCTTAGCCCCGTGAC  
 TAAGGCCTCAGACTAGGGCGGGAGGGGTCTCTCTCTCTGTGCTGCCAGTCTGCCCCCTGCACAAGACAACAGA  
 ATCCATCAGGGCCATGAGTGTACCCAGACCTGACCCCTCACCAATTCAGCCCCCTGACCCCTCAGGACGCTGGATG  
 CCAGCTCCCAGCCCCAGTGCCGGGTCTCTCTCTCTCTGCTGCCAGTCTGCCCCCTGCACAAGACAACAGA  
 AGCACCACCAAGACACAGCAGGACAGGCCAGGGGAGGGCATCTGGACCAGGGCATCCGTCCGGCTATTGTCA  
 GAGAAAAGAAGAGACCCACCCACTCGGGCTGCAAAAGGTGAAAAGCACCAGAGGTTTTCAGATGGAAGTGAGAG  
 GTGACAGTGTGTGGCAGCCCTCACAGCCCTCGCTTGTCTCTCTGCGCCTCTGCTGGGCTCCCACTTTGGCA  
 GCACTTGAGGAGCCCTTCAACCCGCCCTGCACTGTAGGAGCCCTTTCTGGGCTGGCCAAGGCCGAGCCAGCT  
 CCCTCAGCTTGCGGGGAGGTGCGGAGGGAGAGGGGCGGGCAGGAACCGGGCTGCGCGCAGCGCTTGCGGGCCAG  
 AGTGAGTTCGGGTGGGCGTGGGCTCGGCGGGGCCCACTCAGAGCAGCTGGCCGGCCCCAGGCAGTGAGGGCT  
 TAGCACTGGGCCAGCAGCTGCTGTGCTCGATTCTCGCTGGGCCTTAGCTGCCTCCCCGCGGGCAGGGCTCGG  
 GACCTGCAGCCCTCCATGCTGACCCCTCCCCACCCCCGTGGGCTCTGTGCGGCCGAGCCTCCCCAAGGAG  
 CGCCGCCCTCTGCTCCACAGCGCCAGTCCCATCGACCACCAAGGGCTGAGGAGTGCGGGTGCACAGCGCGGGA  
 CTGGCAGGCAGCTCCACCTGCTGCCCCAGTGTGGATCCACTGGGTGAAGCCAGCTGGGCTCTGAGTCTGGTGG  
 GGACTTGGAGAACCTTTATGTCTAGCTAAGGGATTGTAAATACACCGATGGGCATCTGTATCTAGCTCAAGGTT  
 TGTAAACACACCAATCAGCACCTGTGTCTAGCTCAGTGTGTTGTGAATGCACCAATCCACACTCTGTATCTGGCT  
 ACTCTGGTGGGGACTTGGAGAACCTTTGTGTCCACACTCTGTATCTAGCTAATCTAGTGGGGATGTGGAGAACCT  
 TTGTGTCTAGCTCAGGGATCGTAAACGCACCAATCAGCACCTGTCAAAACAGACCCTTGACTCTCTGTAAAT  
 GGACCAATCAGCAGGATGTGGGTGGGGCGAGACAAGAGAATAAAAGCAGGCTGCCTGAGCCAGCAGTGACAACCC  
 CCTCGGGTCCCCTCCCAGCCGTGGAAGCTTTGTTCTTTCGCTCTTGTCAATAAATCTTGCTACTGCCCAAA

**FIGURE 542**

MERAVRVESGVLVGVVCLLLACPATATGPEVAQPEVDTTLGRVVRGRQVGKGTDRLVNVFLGI  
PFAQPPLGPDRFSAPHPAQPWEGVRDASTAPPMCLQDVESMNSSRFVLNGKQQIFSVSEDCLV  
LNVYSPAIEVPAGSGRPVMVWVHGGALITGAATSYDGSALAAYGDVVVVTVQYRLGVLGFFSTG  
DEHAPGNQGFLLDVVAALRWVQENIAPFGGDLNCVTVFSGSAGGSIISGLVLSFVAAGLFHRAI  
TQSGVITTPGIIDSHPWPLAQKIANLACSSSSPAEMVQCLOQKEGEEELVLSKKLKNTIYPLT  
VDGTVFPKSPKELLKEKPFHSVPFLMGVMNHEFSWLIPRGWGLLDTMEQMSREDMLAISTPVL  
TSLDVPPEMMPTVIDEYLGSNSDAQAKCQAFQEFMGDVFINVPTVSFSRYLRDSGSPVFFYEF  
QHRPSSFAKIKPAWVKADHGAEGAFVFGGPFLMDESSRLAFPEATEEEKQLSLTMMAQWTHFA  
RTGDPNSKALPPWPQFNQAEQYLEINPVPRAGQKFREAWMQFWSETLPSKIQQWHQKQ?NRKA  
QEDL

**Important features:**

**Signal peptide:**

amino acids 1-27

**Transmembrane domain:**

amino acids 226-245

**N-glycosylation site.**

amino acids 105-109

**N-myristoylation sites.**

amino acids 10-16, 49-55, 62-68, 86-92, 150-156, 155-161,  
162-168, 217-223, 227-233, 228-234, 232-238, 262-268, 357-363,  
461-467

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 12-23

**Carboxylesterases type-B serine active site.**

amino acids 216-232

FIGURE 543

TTGTCGCTTGGCCCTTCGCAATGCGAGACCCCGAGCGTCCCCCCCCCGCCCTCTGCTTCTGCTGCTGCTA  
 CTGGGGGGCGCCACCGGCTCTTTCTGAGGAGCCGCCCGCTTAGCGTGGCCCCCAGGGACTACCTGAACCCAC  
 TATCCGCTGTTTTGTGGGCAGCGGCCCGACGCCTGACCCCGCAGAGGTGTGACGACCTCAACATCCACGGA  
 GTCTCTCGGGCTCAACGAGACGCTGTTCTATTTGGGACAGGACAACCTTACCGCGTAGAGCTGGAGCCCCACG  
 TCCACGGAGCTGCGTACAGGATACAGGAACTGACTGGAGATCTAACCCACGCGACATAAACGTTGTGTCGGATGAAG  
 GCGAAACAGGAGGGCGAGTGTGCAAACTTCGTAAGGTGCTGCTCCTTCGGGACGAGTCCACGCTCTTTGTGTGC  
 GGTTCACACGCCTTCAACCCTGTGTGCGCAACTACAGCATAGACACCCCTGCAGCCGCTCGGAGCAACATCAGC  
 GGTATGCCCCGCTGCCCTGACGACCCCAAGCAGCCCAATGTTGCCCTCTTCTCTGACGGGATGCTCTTACAGCT  
 AACTGTTACCGACTTCCCTAGCACTTATGCTGTCTGATCTACCGCAGCTCGGGGACAGGCCACCCTGCGCACCGTG  
 AACATGATGCTCAAAGTGGTTCAAAGAGCCTTACTTTGTCCATGCGGTGGAGTGGGGCAGCCATGTCTACTTCTTC  
 TTCGGGAGATTGCGATGGAGTTTAACTACCTGGAGAGAGGTGGTGGTGTCCCGCGTGGCCCCGAGTGTGCAAGAAG  
 GACGTGGGAGGCTCCCCCGCGTGTGGAGAAGCAGTGGACGCTCTTCTGAAGCGCGGCTCAACTCTGTTGTA  
 CCGCGAGACTCCCTTTTACTTCAAAGTGTGACGCTGTACGCGGTGGTGCAGCTCGGGGCCGCTGCTGAGCTT  
 FTCTGTGCGCTTTTTTTCACGCCACAGCAACAGCATCCCTGGCTCGGCTGTCTGCGCCTTTGACCTGACACAGGTG  
 GCAGCTGTGTTTGAAGGCCGCTTCCGAGAGCAGAAGTCCCCGAGTCCATCTGGAACGCGGCTGCCGAGGATCAG  
 GTGCCTCGACCCCCGCGCGGTGCTGCGCAGCCCCGGATGCACTCAATGCTCCAGCGCTTCCCGATGAC  
 ATCCTCAACTTTGTCAAGACCCACCTCTGATGGACGAGCGGTGCCCTCGCTGGGCCATGCGCCTTGGATCCTG  
 CGGACCTGATGAGGACACAGCTGACTCGAGTGGCTGTGGACGTGGGAGCCGGCCCCCTGGGGCAACCAGACCGTT  
 GTCTTCTGGGTTCTGAGGCGGGACGCTCTCAAGTTCTCTGCTCCGGCCCAATGCCAGCACTCAGGACCGTCT  
 GGGCTCAGTGTCTTCTCTGGAGGAGTTTGAGACTACCCGCGGACAGGTGTGGACCGCGCCGCTGGCGAGACA  
 GGGCAGCGGCTGCTGAGCTTTGAGCTGGACGCACTCTCGGGGGCTGCTGGCTGCTTCCCCCGCTGCGTGGT  
 CGAGTGCCTGTGGCTGCTGCGTGCAGCAGTACTCGGGGTGTATGAAGAACTGTATCGGCAGTCAAGACCCCTACTGC  
 GGGTGGGCCCCCAGCGCTCTGTCATCTTCTCAGCCCGGACACAGAGCCGCTTTGAGCAGGACGTTGTCGGG  
 GCCAGCACTCAGGCTTAGGGGATGTCACAGGACTCTCTGCGGGCCAGCCTCTCGAGGACCGCGCGGGCTGGT  
 TCGGTGAACCTGCTGGTAACCTGCTCGGTGCGCGCTCTCGTGTGGGAGCCCTGCTGCTGCTTCCGCTTCAAGCTGGG  
 TGGTTCTGGGGCTTCGTGAGCGCGCGGAGCTGGCCCCGGCGCAAGGACAAGGAGGCCATCTGGCGCACGGGGCG  
 GCGAGGCGGTGCTGAGCGTCAAGCGCTGGGCGAGCGCAGGGCGCAGGGTCCCCGGGGGCGGGGCGGAGGCGGT  
 GCGGTGGCGCGGGGTTCCCCCGGAGGCCCTGCTGGCGCCCTGATGCGCCCTGATGCAACGCTGGGCAAGCCGCTG  
 CTGCAAGGGCGGGCCCCACGACTGGACTCGGGCTGCTGCCACGCCGAGCAGCGCCGCTGCCAGCGAGAAGCGC  
 CTGCCCATCTCGCACCCCGCACCCCCACCGCTGGGGCCCCCGCGCTGGGACCAAGGCCACCCCTGCTCCCGGCC  
 TCCGCTTATCTCTCTCTGCTGCTGGCGCCCGCGGGCCCCCGAGCAGCCCCCGCGCTGGGGGAGCGGAC  
 CCGCAGCGCGCCTCTATGCTGCGCGCCCGCGCGCTCCACCGGCACTTCCGCTACCCCCACCGCCAG  
 CCGGACCGCGCGGGTGGTGTCCCGGCCACCGGCCCTTTGACACCGACTCAGCGCGGATGGGCTCCCGCG  
 CCTGGAGAGCCGCCCGCAGCGGCAGCTGAGGAGGCCACTGGGCCCCACGCCCTCCGGCGCCACCTGCGC  
 CGCACCCACAGTTCAACAGCGCGCAGGCCCGGCTGGGACGCCACCGCGGCTGCCACGCCCGCGGGGACA  
 GACTTGGCCCACTCTCTCCCTATGGGGGGCGGACAGGACTCGCCCGCTGCCCCCTAGCGCGGGGGCCCCCG  
 ATGCTTGGCAGTGCCAGCCACGAGGACGAGACGTTGCCAGAACGCGGGCGGGGCGGCAACTCG  
 AGTGGGTGCTCAAGTCCCCCGGACCCACCGCGGAGTGGGGGGCCCCCTCCGCCACAAGGAAGCACACCAG  
 CTCGCCCTCCCCCTACCCGGGGCGCAGGACGCTGAGACGTTTGGGGGTGGGTGGGCGGAGGACTTTGCTATG  
 GATTTGAGTTGACCTTATGCGGTAGGTTTGGTTTTTTTGTGACGTTTTGGTTTTCTTTTCGGTTTTCTAAC  
 AATTGACAACTCCGTTCTCGGGTGGCGGACGAGCAGGGAGGCTTGGACCCGCTGGGAATGGGGGGCACAG  
 CTCGACACCTAAGCCCTCCCCACCCCTGAAAGGTCCCTCCCCAACCCAGGCCCTTGGCGTGTGTGGTGTGCG  
 TGGTGTGCGTGCCGTGTTCTGTGCAAGGGGCGGGGAGTGGGCGTGTGTGTGCTGCCAGAGGCTGCTG  
 TGGCGGTGTGTGATGCTGGGCCACGCGTGCAGGTTGTGTGTCACGAGCAGCATCTGTGGTGGCCCGCGCGC  
 TGGCGCTTGGCTGAGCCAGCTGCGGCTTCCAGAAGGCCGGGGTCTCCGAGGTGCGGTTAGAGATTGAAC  
 CCCCCCACTCTCGACAGGGAAGCGGGACAATGCCGGGGTTTTCAGGCAGGAGACACGAGGAGGGCCTGCCGGA  
 AGTCACATCGGCAGCAGCTGTCTAAAGGCTTGGGGGCGTGGGGGCGCGAGAGTGGTGGGGCCCCCTGTGTAA  
 ATACGGCCCCAGGGTGTGAGAGGATCCCATGCCACCCCTCCCTTTGTGACCTCCCCCTATGACCTCCAGCTGA  
 CCATGTCATGCCACGTGGCTGGTGGGTTCTCTGCTCTTTGGAGTTTTGCTCTCCCCGAGCCCCCTCCCATCAAT  
 AAAACTCTGTTTTACAACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 544**

MQTPRASPPRPALLLLLLLLGGAGHLFPPEEPPPLSVAPRDYLNHYPVFVGS GPGRLTPAEGAD  
DLNIQRVLRVNRTLFIGDRDNLRYVELEPPTSTELRYQRKLTWRSNPSDINVCRMKGKQEGEC  
RNFVKVLLLLRDESTLFVCGSNAFNPVCANYSIDTLQPVGDNISGMARCPYDPKHANVALFSDG  
MLFTATVTDFLAIDAVIYRSLGDRPTLRTVKHDSKWFKEPYFVHAVEWGS HVYFFFREIAMEF  
NYLEKVVVSRVARVCKNDVGGSPRVLEKQWTSFLKARLNCSVPGDSHFYFNVLQAVTG VVSLG  
GRPVLAVFSTPSNSIPGSAVCAFDLTQVAAVFEGRFREQKSPESI WTPVPEDQVPRPRPGCC  
AAPGMQYNASSALPDDILNFVKTHPLMDEAVPSLG HAPWILRTLMRHQLTRVAVDVGAGPWGN  
QTVVFLGSEAGTVLKFLVRPNASTSGTSGLSVFLEEFETYRDPDRCGRP GGGETGQRLLSLELD  
AASGGLLA AFPRCVVRVPVARCQQYSGCMKNCIGSQDPYCGWAPD GSCIFLSPGTRAAFEQDV  
SGASTSGLGDC TGLLRASLSEDRAGLVSVNLLVTSSVAAFVVGAVVSGFSV GWFVGLRERREL  
ARRKDKEAILAHGAGEAVLSVSR LGERRAQGPGRGGGGGGGAGVPPEALLAPLMQNGWAKAT  
LLQGGPHDLDSGLLPTPEQTPLPQKRLPTPHPHPHALGPRAWDHGHP LLLPASASSSLLLLAPA  
RAPEQPPAPGEPTPDGRLYAARPGRASHGDFPLTPHASPDRRRVVSAPTGPLDPASAADGLPR  
PWSPPTGSLRRPLGPHAPPAATLRRTHTFNSGEARPGDRHRGCHARPGTDLAHLLPYGGADR  
TAPPVP

**Important features:**

**Signal peptide:**

amino acids 1-25

**Transmembrane domains:**

amino acids 318-339, 598-617

**N-glycosylation sites.**

amino acids 74-78, 155-159, 167-171, 291-295, 386-390, 441-445,  
462-466

**Glycosaminoglycan attachment sites.**

amino acids 51-55, 573-577

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 102-106

**N-myristoylation sites.**

amino acids 21-27, 50-56, 189-195, 333-339, 382-388, 448-454,  
490-496, 491-497, 508-514, 509-515, 531-537, 558-564, 569-575,  
574-580, 580-586, 610-616, 643-649, 663-669, 666-672, 667-673,  
668-674, 669-675, 670-676, 868-874, 879-885

**FIGURE 545**

GATGGCGCAGCCACAGCTTCTGTGAGATTCTGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGGG  
GACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCAAA  
ACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTT  
CCAGGCCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACG  
ACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCACGGGAG  
GCTTGGCAGTTTTTTCTTACTCCTGTGGTCTCCAGATTTTCAGGCCTAAGATGAAAGCCTCTAGT  
CTTGCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAG  
ACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCT  
GAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACT  
GAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTC  
TATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGC  
AGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACA  
TGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG  
GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATGGAG  
GAGACAGAATTAGGAGGAAAGTGATGCTGCTGCTAAGAATATTTCGAGGTCAAGAGCTCCAGTCT  
TCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACTGTACTAGTCTTGTGCT  
GGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCATGATTGTCTTTATGCATCCCC  
AATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAATATCTTTCTGCTATTGGATATATT  
TATTAGTTAATATATTTATTTATTTTTTGCTATTTAATGTATTTATTTTTTTACTTGGACATG  
AACTTTAAAAAAATTACAGATTATATTTATAACCTGACTAGAGCAGGTGATGTATTTTTAT  
ACAGTAAAAAATAAACCTTGTAATCTAGAAGAGTGGCTAGGGGGGTATTTCATTTGTAT  
TCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGATATTTGAAATTGAACCAATGAC  
TACTTAGGATGGGTTGTGGAATAAGTTTTGATGTGGAATTGCACATCTACCTTACAATTACTG  
ACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTATCTTCCAGCCAGGAATCCTACACGG  
CCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATACCAAAAAAAAAAAAAAAAAAAAA

**FIGURE 546**

MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNGATTTCATNSHSDSELRPE  
IFSSREAWQFFLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQE  
IRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHY  
TLRKISSLANSFLTICKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDI  
LLQWMEETE

**Important features:**

**Signal peptide:**

amino acids 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 192-195, 225-228

**N-myristoylation sites.**

amino acids 42-47, 46-51, 136-141



**FIGURE 547**

AGCAACTCAAGTTCATCATTGTCCTGAGAGAGAGGAGCAGCGCGGTTCTCGGCCGGGACAGCA  
 GAACGCCAGGGGACCTTCACCTGGGCGCGCCGGGGCACGGGCTTTGATTGTCTGGGGTCGCG  
 GAGACCCGCGCGCCTGCCCTGCACGCCGGGCGGCAACCTTTGCAGTCGCGTTGGCTGCTGCGA  
 TCGGCCGGGCGGGTCCCTGCCGAAGGCTCGGCTGCTTCTGTCCACCTCTTACACTTCTTCATTT  
 ATCGGTGGATCATTTTCGAGAGTCCGTCTTGTAATGTTTGGCACTTTGCTACTTTATTGCTTC  
 TTTCTGGCGACAGTTCAGCACTCGCCGAGACCGGCGGAGAAAGGCAGCTGAGCCCGGAGAAG  
 AGCGAAATATGGGGACCCGGGCTAAAAGCAGACGTCGTCCTTCCCGCCCGCTATTTCTATATT  
 CAGGCAGTGGATACATCAGGGAATAAATTCACATCTTCTCCAGGCGAAAAGGTCTTCCAGGTG  
 AAAGTCTCAGCACCAGAGGAGCAATTCAGTAGAGTTGGAGTCCAGGTTTTAGACCGAAAAGAT  
 GGGTCCTTCATAGTAAGATACAGAATGTATGCAAGCTACAAAAATCTGAAGGTGGAAATTAAA  
 TTCCAAGGGCAACATGTGGCCAAATCCCATATATTTTTAAAAGGGCCGGTTTACCATGAGAAC  
 TGTGACTGTCTCTGCAAGATAGTGCAGCCTGGCTACGGGAGATGAACTGCCCTGAAACCATT  
 GCTCAGATTTCAGAGAGATCTGGCACATTTCCCTGCTGTGGATCCAGAAAAGATTGCAGTAGAA  
 ATCCCAAAAAGATTTGGACAGAGGCAGAGCCTATGTCACTACACCTTAAAGGATAACAAGGTT  
 TATATCAAGACTCATGGTGAACATGTAGGTTTTAGAAATTTTCATGGATGCCATACTACTTTCT  
 TTGACTAGAAAAGGTGAAGATGCCAGATGTGGAGCTCTTTGTTAATTTGGGAGACTGGCCTTTG  
 GAAAAAAGAAATCCAATTCAAACATCCATCCGATCTTTTCTGCTGTGGCTCCACAGATTCC  
 AAGGATATCGTGATGCCTACGTACGATTTGACTGATTCTGTTCTGGAAACCATGGGCCGGGTA  
 AGTCTGGATATGATGTCCGTGCAAGCTAACACGGGTCTCCCTGGGAAAGCAAAAATTCACCT  
 GCCGTCTGGAGAGGGCGAGACAGCCGCAAAGAGAGACTCGAGCTGGTTAAACTCAGTAGAAAA  
 CACCCAGAACTCATAGACGCTGCTTTCACCAACTTTTTCTTCTTTAAACACGATGAAAACCTG  
 TATGGTCCCATTTGTGAAACATATTTTCAATTTTTGATTTCTTCAAGCATAAGTATCAAATAAAT  
 ATCGATGGCACTGTAGCAGCTTATCGCCTGCCATATTTGCTAGTTGGTGACAGTGTTGTGCTG  
 AAGCAGGATTCATCTACTATGAACATTTTTACAATGAGCTGCAGCCCTGGAAACACTACATT  
 CCAGTTAAGAGCAACCTGAGCGATCTGCTAGAAAACTTAAATGGGCGAAAGATCACGATGAA  
 GAGGCCAAAAAGATAGCAAAAGCAGGACAAGAATTTGCAAGAAATAATCTCATGGGCGATGAC  
 ATATTCTGTTATTATTTCAAACCTTTTCCAGGAATATGCCAATTTACAAGTGAGTGAGCCCCAA  
 ATCCGAGAGGGCATGAAAAGGGTAGAACCACAGACTGAGGACGACCTCTTCCCTTGTAATTGC  
 CATAGGAAAAAGACCAAAGATGAACCTGATATGCAAAATAACTTCTATTAGAATAATGGTGC  
 TCTGAAGACTCTTCTTAATAAAAAGAAGAATTTTTTTAAGTATTAATTCATGGACAATATA  
 AAATCTGTGTGATTGTTTGCAGTATGAAGACACATTTCTACTTATGCAGTATTCTCATGACTG  
 TACTTTAAAGTACATTTTGTAGAAATTTTATAATAAAACCACCTTTATTTTAAAGGAAAAAAA

## **FIGURE 548**

MFGTLLLYCFFLATVPALAE TGGERQLSPEKSEIWGPGLKADVLPARYFYIQAVDTSGNKFT  
SSPGEKVFQVKVSAPEEQFTRVG VQVLDRKDGSFIVRYRMYASYKNLKVEIKFQGQHVAKSPY  
ILKGPVYHENCDCPLQDSAAWLREMNCPETIAQIQRD LAHFPAVDPEKIAVEIPKRFGQRQSL  
CHYTLKDNKVYIKTHGEHVGFRI FMDAILLSLTRKVKMPDVELFVNLGDWPLEKKKSNSNIHP  
IFSWCGSTDSKDIVMPTYDLTDSVLETMGRVSLDMMSVQANTGPPWESKNSTAVWRGRDSRKE  
RLELVKLSRKHP ELIDAAFTNFFFFKH DENLYGPVKHISFFDFFKH KYQINIDGTVAAYRLP  
YLLVGDSVVLKQDSIYYEHFYNELQPWKHYIPVKS NLSDLLEK LKWAKDHDEEAKKIAKAGQE  
FARNNLMGDDIFCYYFKLFQ EYANLQVSEPQIREGMKRVEPQTEDDLFPCTCHRKKTKDEL

**Important features:**

**Signal peptide:**

amino acids 1-17

**N-glycosylation sites.**

amino acids 302-306, 414-418

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 243-247, 495-499

**Tyrosine kinase phosphorylation site.**

amino acids 341-348

**N-myristoylation sites.**

amino acids 59-65, 118-124, 184-190, 258-264, 370-376, 439-445

**Endoplasmic reticulum targeting sequence.**

amino acids 499-504

**FIGURE 549**

GGGTGATTGAACTAAACCTTCGCCGCACCGAGTTTGCAGTACGGCCGTACCCGCACCGCTGC  
CTGCTTGCGGTTGGAGAAATCAAGGCCCTACCGGGCCTCCGTAGTCACCTCTCTATAGTGGGC  
GTGGCCGAGGCCGGGGTGACCCTGCCGGAGCCTCCGCTGCCAGCGACATGTTCAAGGTAATTC  
AGAGGTCCGTGGGGCCAGCCAGCCTGAGCTTGCTCACCTTCAAAGTCTATGCAGCACCAAAAA  
AGGACTCACCTCCCAAAAATTCCGTGAAGGTTGATGAGCTTTCACCTACTCAGTTCCTGAGG  
GTCAATCGAAGTATGTGGAGGAGGCAAGGAGCCAGCTTGAAGAAAGCATCTCACAGCTCCGAC  
ACTATTGCGAGCCATACACAACCTGGTGTCAGGAAACGTACTCCCAAACTAAGCCCAAGATGC  
AAAGTTTGGTTCAATGGGGGTTAGACAGCTATGACTATCTCCAAAATGCACCTCCTGGATTTT  
TTCCGAGACTTGGTGTTATTGGTTTTGCTGGCCTTATTGGACTCCTTTTGGCTAGAGGTTCAA  
AAATAAAGAAGCTAGTGTATCCGCCTGGTTTCATGGGATTAGCTGCCTCCCTCTATTATCCAC  
AACAAGCCATCGTGTTTGCCCAGGTGAGTGGGGAGAGATTATATGACTGGGGTTTACGAGGAT  
ATATAGTCATAGAAGATTTGTGGAAGGAGAACTTTCAAAGCCAGGAAATGTGAAGAATTCAC  
CTGGAACTAGTAGAAAACCTCCATGCTCTGCCATCTTAATCAGTTATAGGTAAACATTGGAAA  
CTCCATAGAATAAATCAGTATTTCTACAGAAAAATGGCATAGAAGTCAGTATTGAATGTATTA  
AATTGGCTTTCTTCTTCAGGAAAACTAGACCAGACCTCTGTTATCTTCTGTGAAATCATCCT  
ACAAGCAAACCTAAGTGGAAATCCCTTACCTAGAGATAATGTACAAGCCTTAGAACTCCTCAT  
TCTCATGTTGCTATTTATGTACCTAATTAAAACCCAAGTTTAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAA

**FIGURE 550**

MFKVIQRSVGPASLSLLTFKVYAAPKKDSPPKNSVKVDELSLYSVPEGQSKYVEEARSQLEES  
ISQLRHYCEPYTTWCQETYSQTKPKMQSLVQWGLDSYDYLQNAPPGFFPRLGVIGFAGLIGLL  
LARGSKIKKLVYPPGFMGLAASLYYPQQAIVFAQVSGERLYDWGLRGYIVIEDLWKENFQKPG  
NVKNSPGTK

**Important features:**

**Signal peptide:**

Amino acids 1-23

**Transmembrane domain:**

Amino acids 111-130

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 26-30

**Tyrosine kinase phosphorylation site:**

Amino acids 36-44

**N-myristoylation sites:**

Amino acids 124-130;144-150;189-195

## SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

### FIELD OF THE INVENTION

[0001] The present invention relates generally to the identification and isolation of novel DNA and to the recombinant production of novel polypeptides.

### BACKGROUND OF THE INVENTION

[0002] Extracellular proteins play important roles in, among other things, the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation, migration, differentiation, or interaction with other cells, is typically governed by information received from other cells and/or the immediate environment. This information is often transmitted by secreted polypeptides (for instance, mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and hormones) which are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins. These secreted polypeptides or signaling molecules normally pass through the cellular secretory pathway to reach their site of action in the extracellular environment.

[0003] Secreted proteins have various industrial applications, including as pharmaceuticals, diagnostics, biosensors and bioreactors. Most protein drugs available at present, such as thrombolytic agents, interferons, interleukins, erythropoietins, colony stimulating factors, and various other cytokines, are secretory proteins. Their receptors, which are membrane proteins, also have potential as therapeutic or diagnostic agents. Efforts are being undertaken by both industry and academia to identify new, native secreted proteins. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel secreted proteins. Examples of screening methods and techniques are described in the literature [see, for example, Klein et al., *Proc. Natl. Acad. Sci.* 93:7108-7113 (1996); U.S. Pat. No. 5,536,637].

[0004] Membrane-bound proteins and receptors can play important roles in, among other things, the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation, migration, differentiation, or interaction with other cells, is typically governed by information received from other cells and/or the immediate environment. This information is often transmitted by secreted polypeptides (for instance, mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and hormones) which are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins. Such membrane-bound proteins and cell receptors include, but are not limited to, cytokine receptors, receptor kinases, receptor phosphatases, receptors involved in cell-cell interactions, and cellular adhesion molecules like selectins and integrins. For instance, transduction of signals that regulate cell growth and differentiation is regulated in part by phosphorylation of various cellular proteins. Protein tyrosine kinases, enzymes that catalyze that process, can also act as growth factor receptors. Examples include fibroblast growth factor receptor and nerve growth factor receptor.

[0005] Membrane-bound proteins and receptor molecules have various industrial applications, including as pharma-

ceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be employed as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction.

[0006] Efforts are being undertaken by both industry and academia to identify new, native receptor or membrane-bound proteins. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel receptor or membrane-bound proteins.

### SUMMARY OF THE INVENTION

[0007] In one embodiment, the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence that encodes a PRO polypeptide.

[0008] In one aspect, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule encoding a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

[0009] In other aspects, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about

90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule comprising the coding sequence of a full-length PRO polypeptide cDNA as disclosed herein, the coding sequence of a PRO polypeptide lacking the signal peptide as disclosed herein, the coding sequence of an extracellular domain of a transmembrane PRO polypeptide, with or without the signal peptide, as disclosed herein or the coding sequence of any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

**[0010]** In a further aspect, the invention concerns an isolated nucleic acid molecule comprising a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule that encodes the same mature polypeptide encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein, or (b) the complement of the DNA molecule of (a).

**[0011]** Another aspect the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence encoding a PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated, or is complementary to such encoding nucleotide sequence, wherein the transmembrane domain(s) of such polypeptide are disclosed herein. Therefore, soluble extracellular domains of the herein described PRO polypeptides are contemplated.

**[0012]** Another embodiment is directed to fragments of a PRO polypeptide coding sequence, or the complement thereof, that may find use as, for example, hybridization probes, for encoding fragments of a PRO polypeptide that may optionally encode a polypeptide comprising a binding site for an anti-PRO antibody or as antisense oligonucleotide

probes. Such nucleic acid fragments are usually at least about 10 nucleotides in length, alternatively at least about 15 nucleotides in length, alternatively at least about 20 nucleotides in length, alternatively at least about 30 nucleotides in length, alternatively at least about 40 nucleotides in length, alternatively at least about 50 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 70 nucleotides in length, alternatively at least about 80 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 100 nucleotides in length, alternatively at least about 110 nucleotides in length, alternatively at least about 120 nucleotides in length, alternatively at least about 130 nucleotides in length, alternatively at least about 140 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 160 nucleotides in length, alternatively at least about 170 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 190 nucleotides in length, alternatively at least about 200 nucleotides in length, alternatively at least about 250 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 350 nucleotides in length, alternatively at least about 400 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 500 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 700 nucleotides in length, alternatively at least about 800 nucleotides in length, alternatively at least about 900 nucleotides in length and alternatively at least about 1000 nucleotides in length, wherein in this context the term "about" means the referenced nucleotide sequence length plus or minus 10% of that referenced length. It is noted that novel fragments of a PRO polypeptide-encoding nucleotide sequence may be determined in a routine manner by aligning the PRO polypeptide-encoding nucleotide sequence with other known nucleotide sequences using any of a number of well known sequence alignment programs and determining which PRO polypeptide-encoding nucleotide sequence fragment(s) are novel. All of such PRO polypeptide-encoding nucleotide sequences are contemplated herein. Also contemplated are the PRO polypeptide fragments encoded by these nucleotide molecule fragments, preferably those PRO polypeptide fragments that comprise a binding site for an anti-PRO antibody.

**[0013]** In another embodiment, the invention provides isolated PRO polypeptide encoded by any of the isolated nucleic acid sequences hereinabove identified.

**[0014]** In a certain aspect, the invention concerns an isolated PRO polypeptide, comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93%

amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein.

[0015] In a further aspect, the invention concerns an isolated PRO polypeptide comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to an amino acid sequence encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein.

[0016] In a specific aspect, the invention provides an isolated PRO polypeptide without the N-terminal signal sequence and/or the initiating methionine and is encoded by a nucleotide sequence that encodes such an amino acid sequence as hereinbefore described. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

[0017] Another aspect the invention provides an isolated PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

[0018] In yet another embodiment, the invention concerns agonists and antagonists of a native PRO polypeptide as

defined herein. In a particular embodiment, the agonist or antagonist is an anti-PRO antibody or a small molecule.

[0019] In a further embodiment, the invention concerns a method of identifying agonists or antagonists to a PRO polypeptide which comprise contacting the PRO polypeptide with a candidate molecule and monitoring a biological activity mediated by said PRO polypeptide. Preferably, the PRO polypeptide is a native PRO polypeptide.

[0020] In a still further embodiment, the invention concerns a composition of matter comprising a PRO polypeptide, or an agonist or antagonist of a PRO polypeptide as herein described, or an anti-PRO antibody, in combination with a carrier. Optionally, the carrier is a pharmaceutically acceptable carrier.

[0021] Another embodiment of the present invention is directed to the use of a PRO polypeptide, or an agonist or antagonist thereof as hereinbefore described, or an anti-PRO antibody, for the preparation of a medicament useful in the treatment of a condition which is responsive to the PRO polypeptide, an agonist or antagonist thereof or an anti-PRO antibody.

[0022] In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the herein described polypeptides. Host cell comprising any such vector are also provided. By way of example, the host cells may be CHO cells, *E. coli*, or yeast. A process for producing any of the herein described polypeptides is further provided and comprises culturing host cells under conditions suitable for expression of the desired polypeptide and recovering the desired polypeptide from the cell culture.

[0023] In other embodiments, the invention provides chimeric molecules comprising any of the herein described polypeptides fused to a heterologous polypeptide or amino acid sequence. Example of such chimeric molecules comprise any of the herein described polypeptides fused to an epitope tag sequence or a Fc region of an immunoglobulin.

[0024] In another embodiment, the invention provides an antibody which binds, preferably specifically, to any of the above or below described polypeptides. Optionally, the antibody is a monoclonal antibody, humanized antibody, antibody fragment or single-chain antibody.

[0025] In yet other embodiments, the invention provides oligonucleotide probes which may be useful for isolating genomic and cDNA nucleotide sequences, measuring or detecting expression of an associated gene or as antisense probes, wherein those probes may be derived from any of the above or below described nucleotide sequences. Preferred probe lengths are described above.

[0026] In yet other embodiments, the present invention is directed to methods of using the PRO polypeptides of the present invention for a variety of uses based upon the functional biological assay data presented in the Examples below.

#### BRIEF DESCRIPTION OF THE DRAWINGS

[0027] FIG. 1 shows a nucleotide sequence (SEQ ID NO:1) of a native sequence PRO177 cDNA, wherein SEQ ID NO:1 is a clone designated herein as "DNA16438-1387".

[0028] FIG. 2 shows the amino acid sequence (SEQ ID NO:2) derived from the coding sequence of SEQ ID NO:1 shown in FIG. 1.

[0029] FIG. 3 shows a nucleotide sequence (SEQ ID NO:3) of a native sequence PRO3574 cDNA, wherein SEQ ID NO:3 is a clone designated herein as "DNA19360-2552".

[0030] FIG. 4 shows the amino acid sequence (SEQ ID NO:4) derived from the coding sequence of SEQ ID NO:3 shown in FIG. 3.

[0031] FIG. 5 shows a nucleotide sequence (SEQ ID NO:5) of a native sequence PRO1280 cDNA, wherein SEQ ID NO:5 is a clone designated herein as "DNA33455-1548".

[0032] FIG. 6 shows the amino acid sequence (SEQ ID NO:6) derived from the coding sequence of SEQ ID NO:5 shown in FIG. 5.

[0033] FIG. 7 shows a nucleotide sequence (SEQ ID NO:7) of a native sequence PRO4984 cDNA, wherein SEQ ID NO:7 is a clone designated herein as "DNA37155-2651".

[0034] FIG. 8 shows the amino acid sequence (SEQ ID NO:8) derived from the coding sequence of SEQ ID NO:7 shown in FIG. 7.

[0035] FIG. 9 shows a nucleotide sequence (SEQ ID NO:9) of a native sequence PRO4988 cDNA, wherein SEQ ID NO:9 is a clone designated herein as "DNA38269-2654".

[0036] FIG. 10 shows the amino acid sequence (SEQ ID NO:10) derived from the coding sequence of SEQ ID NO:9 shown in FIG. 9.

[0037] FIG. 11 shows a nucleotide sequence (SEQ ID NO:11) of a native sequence PRO305 cDNA, wherein SEQ ID NO:11 is a clone designated herein as "DNA40619-1220".

[0038] FIG. 12 shows the amino acid sequence (SEQ ID NO:12) derived from the coding sequence of SEQ ID NO:11 shown in FIG. 11.

[0039] FIG. 13 shows a nucleotide sequence (SEQ ID NO:13) of a native sequence PRO1866 cDNA, wherein SEQ ID NO:13 is a clone designated herein as "DNA44174-2513".

[0040] FIG. 14 shows the amino acid sequence (SEQ ID NO:14) derived from the coding sequence of SEQ ID NO:13 shown in FIG. 13.

[0041] FIG. 15 shows a nucleotide sequence (SEQ ID NO:15) of a native sequence PRO4996 cDNA, wherein SEQ ID NO:15 is a clone designated herein as "DNA44675-2662".

[0042] FIG. 16 shows the amino acid sequence (SEQ ID NO:16) derived from the coding sequence of SEQ ID NO:15 shown in FIG. 15.

[0043] FIG. 17 shows a nucleotide sequence (SEQ ID NO:17) of a native sequence PRO4406 cDNA, wherein SEQ ID NO:17 is a clone designated herein as "DNA45408-2615".

[0044] FIG. 18 shows the amino acid sequence (SEQ ID NO:18) derived from the coding sequence of SEQ ID NO:17 shown in FIG. 17.

[0045] FIG. 19 shows a nucleotide sequence (SEQ ID NO:19) of a native sequence PRO1120 cDNA, wherein SEQ ID NO:19 is a clone designated herein as "DNA48606-1479".

[0046] FIG. 20 shows the amino acid sequence (SEQ ID NO:20) derived from the coding sequence of SEQ ID NO:19 shown in FIG. 19.

[0047] FIG. 21 shows a nucleotide sequence (SEQ ID NO:21) of a native sequence PRO4990 cDNA, wherein SEQ ID NO:21 is a clone designated herein as "DNA52753-2656".

[0048] FIG. 22 shows the amino acid sequence (SEQ ID NO:22) derived from the coding sequence of SEQ ID NO:21 shown in FIG. 21.

[0049] FIG. 23 shows a nucleotide sequence (SEQ ID NO:23) of a native sequence PRO738 cDNA, wherein SEQ ID NO:23 is a clone designated herein as "DNA53915-1258".

[0050] FIG. 24 shows the amino acid sequence (SEQ ID NO:24) derived from the coding sequence of SEQ ID NO:23 shown in FIG. 23.

[0051] FIG. 25 shows a nucleotide sequence (SEQ ID NO:25) of a native sequence PRO3577 cDNA, wherein SEQ ID NO:25 is a clone designated herein as "DNA53991-2553".

[0052] FIG. 26 shows the amino acid sequence (SEQ ID NO:26) derived from the coding sequence of SEQ ID NO:25 shown in FIG. 25.

[0053] FIG. 27 shows a nucleotide sequence (SEQ ID NO:27) of a native sequence PRO1879 cDNA, wherein SEQ ID NO:27 is a clone designated herein as "DNA54009-2517".

[0054] FIG. 28 shows the amino acid sequence (SEQ ID NO:28) derived from the coding sequence of SEQ ID NO:27 shown in FIG. 27.

[0055] FIG. 29 shows a nucleotide sequence (SEQ ID NO:29) of a native sequence PRO1471 cDNA, wherein SEQ ID NO:29 is a clone designated herein as "DNA56055-1643".

[0056] FIG. 30 shows the amino acid sequence (SEQ ID NO:30) derived from the coding sequence of SEQ ID NO:29 shown in FIG. 29.

[0057] FIG. 31 shows a nucleotide sequence (SEQ ID NO:31) of a native sequence PRO1114 cDNA, wherein SEQ ID NO:31 is a clone designated herein as "DNA57033-1403".

[0058] FIG. 32 shows the amino acid sequence (SEQ ID NO:32) derived from the coding sequence of SEQ ID NO:31 shown in FIG. 31.

[0059] FIG. 33 shows a nucleotide sequence (SEQ ID NO:33) of a native sequence PRO1076 cDNA, wherein SEQ ID NO:33 is a clone designated herein as "DNA57252-1453".

[0060] FIG. 34 shows the amino acid sequence (SEQ ID NO:34) derived from the coding sequence of SEQ ID NO:33 shown in FIG. 33.

[0061] FIG. 35 shows a nucleotide sequence (SEQ ID NO:35) of a native sequence PRO1483 cDNA, wherein SEQ ID NO:35 is a clone designated herein as "DNA58799-1652".



[0062] FIG. 36 shows the amino acid sequence (SEQ ID NO:36) derived from the coding sequence of SEQ ID NO:35 shown in FIG. 35.

[0063] FIG. 37 shows a nucleotide sequence (SEQ ID NO:37) of a native sequence PRO4985 cDNA, wherein SEQ ID NO:37 is a clone designated herein as "DNA59770-2652".

[0064] FIG. 38 shows the amino acid sequence (SEQ ID NO:38) derived from the coding sequence of SEQ ID NO:37 shown in FIG. 37.

[0065] FIG. 39 shows a nucleotide sequence (SEQ ID NO:39) of a native sequence PRO5000 cDNA, wherein SEQ ID NO:39 is a clone designated herein as "DNA59774-2665".

[0066] FIG. 40 shows the amino acid sequence (SEQ ID NO:40) derived from the coding sequence of SEQ ID NO:39 shown in FIG. 39.

[0067] FIG. 41 shows a nucleotide sequence (SEQ ID NO:41) of a native sequence PRO1881 cDNA, wherein SEQ ID NO:41 is a clone designated herein as "DNA60281-2518".

[0068] FIG. 42 shows the amino acid sequence (SEQ ID NO:42) derived from the coding sequence of SEQ ID NO:41 shown in FIG. 41.

[0069] FIG. 43 shows a nucleotide sequence (SEQ ID NO:43) of a native sequence PRO4314 cDNA, wherein SEQ ID NO:43 is a clone designated herein as "DNA60736-2559".

[0070] FIG. 44 shows the amino acid sequence (SEQ ID NO:44) derived from the coding sequence of SEQ ID NO:43 shown in FIG. 43.

[0071] FIG. 45 shows a nucleotide sequence (SEQ ID NO:45) of a native sequence PRO4987 cDNA, wherein SEQ ID NO:45 is a clone designated herein as "DNA61875-2653".

[0072] FIG. 46 shows the amino acid sequence (SEQ ID NO:46) derived from the coding sequence of SEQ ID NO:45 shown in FIG. 45.

[0073] FIG. 47 shows a nucleotide sequence (SEQ ID NO:47) of a native sequence PRO4313 cDNA, wherein SEQ ID NO:47 is a clone designated herein as "DNA62312-2558".

[0074] FIG. 48 shows the amino acid sequence (SEQ ID NO:48) derived from the coding sequence of SEQ ID NO:47 shown in FIG. 47.

[0075] FIG. 49 shows a nucleotide sequence (SEQ ID NO:49) of a native sequence PRO4799 cDNA, wherein SEQ ID NO:49 is a clone designated herein as "DNA62849-1604".

[0076] FIG. 50 shows the amino acid sequence (SEQ ID NO:50) derived from the coding sequence of SEQ ID NO:49 shown in FIG. 49.

[0077] FIG. 51 shows a nucleotide sequence (SEQ ID NO:51) of a native sequence PRO4995 cDNA, wherein SEQ ID NO:51 is a clone designated herein as "DNA66307-2661".

[0078] FIG. 52 shows the amino acid sequence (SEQ ID NO:52) derived from the coding sequence of SEQ ID NO:51 shown in FIG. 51.

[0079] FIG. 53 shows a nucleotide sequence (SEQ ID NO:53) of a native sequence PRO1341 cDNA, wherein SEQ ID NO:53 is a clone designated herein as "DNA66677-2535".

[0080] FIG. 54 shows the amino acid sequence (SEQ ID NO:54) derived from the coding sequence of SEQ ID NO:53 shown in FIG. 53.

[0081] FIG. 55 shows a nucleotide sequence (SEQ ID NO:55) of a native sequence PRO1777 cDNA, wherein SEQ ID NO:55 is a clone designated herein as "DNA71235-1706".

[0082] FIG. 56 shows the amino acid sequence (SEQ ID NO:56) derived from the coding sequence of SEQ ID NO:55 shown in FIG. 55.

[0083] FIG. 57 shows a nucleotide sequence (SEQ ID NO:57) of a native sequence PRO3580 cDNA, wherein SEQ ID NO:57 is a clone designated herein as "DNA71289-2547".

[0084] FIG. 58 shows the amino acid sequence (SEQ ID NO:58) derived from the coding sequence of SEQ ID NO:57 shown in FIG. 57.

[0085] FIG. 59 shows a nucleotide sequence (SEQ ID NO:59) of a native sequence PRO1779 cDNA, wherein SEQ ID NO:59 is a clone designated herein as "DNA73775-1707".

[0086] FIG. 60 shows the amino acid sequence (SEQ ID NO:60) derived from the coding sequence of SEQ ID NO:59 shown in FIG. 59.

[0087] FIG. 61 shows a nucleotide sequence (SEQ ID NO:61) of a native sequence PRO1754 cDNA, wherein SEQ ID NO:61 is a clone designated herein as "DNA76385-1692".

[0088] FIG. 62 shows the amino acid sequence (SEQ ID NO:62) derived from the coding sequence of SEQ ID NO:61 shown in FIG. 61.

[0089] FIG. 63 shows a nucleotide sequence (SEQ ID NO:63) of a native sequence PRO1906 cDNA, wherein SEQ ID NO:63 is a clone designated herein as "DNA76395-2527".

[0090] FIG. 64 shows the amino acid sequence (SEQ ID NO:64) derived from the coding sequence of SEQ ID NO:63 shown in FIG. 63.

[0091] FIG. 65 shows a nucleotide sequence (SEQ ID NO:65) of a native sequence PRO1870 cDNA, wherein SEQ ID NO:65 is a clone designated herein as "DNA77622-2516".

[0092] FIG. 66 shows the amino acid sequence (SEQ ID NO:66) derived from the coding sequence of SEQ ID NO:65 shown in FIG. 65.

[0093] FIG. 67 shows a nucleotide sequence (SEQ ID NO:67) of a native sequence PRO4329 cDNA, wherein SEQ ID NO:67 is a clone designated herein as "DNA77629-2573".

[0094] FIG. 68 shows the amino acid sequence (SEQ ID NO:68) derived from the coding sequence of SEQ ID NO:67 shown in FIG. 67.

[0095] FIG. 69 shows a nucleotide sequence (SEQ ID NO:69) of a native sequence PRO4979 cDNA, wherein SEQ ID NO:69 is a clone designated herein as "DNA77645-2648".

[0096] FIG. 70 shows the amino acid sequence (SEQ ID NO:70) derived from the coding sequence of SEQ ID NO:69 shown in FIG. 69.

[0097] FIG. 71 shows a nucleotide sequence (SEQ ID NO:71) of a native sequence PRO1885 cDNA, wherein SEQ ID NO:71 is a clone designated herein as "DNA79302-2521".

[0098] FIG. 72 shows the amino acid sequence (SEQ ID NO:72) derived from the coding sequence of SEQ ID NO:71 shown in FIG. 71.

[0099] FIG. 73 shows a nucleotide sequence (SEQ ID NO:73) of a native sequence PRO1882 cDNA, wherein SEQ ID NO:73 is a clone designated herein as "DNA79865-2519".

[0100] FIG. 74 shows the amino acid sequence (SEQ ID NO:74) derived from the coding sequence of SEQ ID NO:73 shown in FIG. 73.

[0101] FIG. 75 shows a nucleotide sequence (SEQ ID NO:75) of a native sequence PRO4989 cDNA, wherein SEQ ID NO:75 is a clone designated herein as "DNA80135-2655".

[0102] FIG. 76 shows the amino acid sequence (SEQ ID NO:76) derived from the coding sequence of SEQ ID NO:75 shown in FIG. 75.

[0103] FIG. 77 shows a nucleotide sequence (SEQ ID NO:77) of a native sequence PRO4323 cDNA, wherein SEQ ID NO:77 is a clone designated herein as "DNA80794-2568".

[0104] FIG. 78 shows the amino acid sequence (SEQ ID NO:78) derived from the coding sequence of SEQ ID NO:77 shown in FIG. 77.

[0105] FIG. 79 shows a nucleotide sequence (SEQ ID NO:79) of a native sequence PRO1886 cDNA, wherein SEQ ID NO:79 is a clone designated herein as "DNA80796-2523".

[0106] FIG. 80 shows the amino acid sequence (SEQ ID NO:80) derived from the coding sequence of SEQ ID NO:79 shown in FIG. 79.

[0107] FIG. 81 shows a nucleotide sequence (SEQ ID NO:81) of a native sequence PRO4395 cDNA, wherein SEQ ID NO:81 is a clone designated herein as "DNA80840-2605".

[0108] FIG. 82 shows the amino acid sequence (SEQ ID NO:82) derived from the coding sequence of SEQ ID NO:81 shown in FIG. 81.

[0109] FIG. 83 shows a nucleotide sequence (SEQ ID NO:83) of a native sequence PRO1782 cDNA, wherein SEQ ID NO:83 is a clone designated herein as "DNA80899-2501".

[0110] FIG. 84 shows the amino acid sequence (SEQ ID NO:84) derived from the coding sequence of SEQ ID NO:83 shown in FIG. 83.

[0111] FIG. 85 shows a nucleotide sequence (SEQ ID NO:85) of a native sequence PRO4338 cDNA, wherein SEQ ID NO:85 is a clone designated herein as "DNA81228-2580".

[0112] FIG. 86 shows the amino acid sequence (SEQ ID NO:86) derived from the coding sequence of SEQ ID NO:85 shown in FIG. 85.

[0113] FIG. 87 shows a nucleotide sequence (SEQ ID NO:87) of a native sequence PRO4341 cDNA, wherein SEQ ID NO:87 is a clone designated herein as "DNA81761-2583".

[0114] FIG. 88 shows the amino acid sequence (SEQ ID NO:88) derived from the coding sequence of SEQ ID NO:87 shown in FIG. 87.

[0115] FIG. 89 shows a nucleotide sequence (SEQ ID NO:89) of a native sequence PRO5990 cDNA, wherein SEQ ID NO:89 is a clone designated herein as "DNA96042-2682".

[0116] FIG. 90 shows the amino acid sequence (SEQ ID NO:90) derived from the coding sequence of SEQ ID NO:89 shown in FIG. 89.

[0117] FIG. 91 shows a nucleotide sequence (SEQ ID NO:91) of a native sequence PRO3438 cDNA, wherein SEQ ID NO:91 is a clone designated herein as "DNA82364-2538".

[0118] FIG. 92 shows the amino acid sequence (SEQ ID NO:92) derived from the coding sequence of SEQ ID NO:91 shown in FIG. 91.

[0119] FIG. 93 shows a nucleotide sequence (SEQ ID NO:93) of a native sequence PRO4321 cDNA, wherein SEQ ID NO:93 is a clone designated herein as "DNA82424-2566".

[0120] FIG. 94 shows the amino acid sequence (SEQ ID NO:94) derived from the coding sequence of SEQ ID NO:93 shown in FIG. 93.

[0121] FIG. 95 shows a nucleotide sequence (SEQ ID NO:95) of a native sequence PRO4304 cDNA, wherein SEQ ID NO:95 is a clone designated herein as "DNA82430-2557".

[0122] FIG. 96 shows the amino acid sequence (SEQ ID NO:96) derived from the coding sequence of SEQ ID NO:95 shown in FIG. 95.

[0123] FIG. 97 shows a nucleotide sequence (SEQ ID NO:97) of a native sequence PRO1801 cDNA, wherein SEQ ID NO:97 is a clone designated herein as "DNA83500-2506".

[0124] FIG. 98 shows the amino acid sequence (SEQ ID NO:98) derived from the coding sequence of SEQ ID NO:97 shown in FIG. 97.

[0125] FIG. 99 shows a nucleotide sequence (SEQ ID NO:99) of a native sequence PRO4403 cDNA, wherein SEQ ID NO:99 is a clone designated herein as "DNA83509-2612".

[0126] FIG. 100 shows the amino acid sequence (SEQ ID NO:100) derived from the coding sequence of SEQ ID NO:99 shown in FIG. 99.

[0127] FIG. 101 shows a nucleotide sequence (SEQ ID NO:101) of a native sequence PRO4324 cDNA, wherein SEQ ID NO:101 is a clone designated herein as "DNA83560-2569".

[0128] FIG. 102 shows the amino acid sequence (SEQ ID NO:102) derived from the coding sequence of SEQ ID NO:101 shown in FIG. 101.

[0129] FIG. 103 shows a nucleotide sequence (SEQ ID NO:103) of a native sequence PRO4303 cDNA, wherein SEQ ID NO:103 is a clone designated herein as "DNA84139-2555".

[0130] FIG. 104 shows the amino acid sequence (SEQ ID NO:104) derived from the coding sequence of SEQ ID NO:103 shown in FIG. 103.

[0131] FIG. 105 shows a nucleotide sequence (SEQ ID NO:105) of a native sequence PRO4305 cDNA, wherein SEQ ID NO:105 is a clone designated herein as "DNA84141-2556".

[0132] FIG. 106 shows the amino acid sequence (SEQ ID NO:106) derived from the coding sequence of SEQ ID NO:105 shown in FIG. 105.

[0133] FIG. 107 shows a nucleotide sequence (SEQ ID NO:107) of a native sequence PRO4404 cDNA, wherein SEQ ID NO:107 is a clone designated herein as "DNA84142-2613".

[0134] FIG. 108 shows the amino acid sequence (SEQ ID NO:108) derived from the coding sequence of SEQ ID NO:107 shown in FIG. 107.

[0135] FIG. 109 shows a nucleotide sequence (SEQ ID NO:109) of a native sequence PRO1884 cDNA, wherein SEQ ID NO:109 is a clone designated herein as "DNA84318-2520".

[0136] FIG. 110 shows the amino acid sequence (SEQ ID NO:110) derived from the coding sequence of SEQ ID NO:109 shown in FIG. 109.

[0137] FIG. 111 shows a nucleotide sequence (SEQ ID NO:111) of a native sequence PRO4349 cDNA, wherein SEQ ID NO:111 is a clone designated herein as "DNA84909-2590".

[0138] FIG. 112 shows the amino acid sequence (SEQ ID NO:112) derived from the coding sequence of SEQ ID NO:111 shown in FIG. 111.

[0139] FIG. 113 shows a nucleotide sequence (SEQ ID NO:113) of a native sequence PRO4401 cDNA, wherein SEQ ID NO:113 is a clone designated herein as "DNA84912-2610".

[0140] FIG. 114 shows the amino acid sequence (SEQ ID NO:114) derived from the coding sequence of SEQ ID NO:113 shown in FIG. 113.

[0141] FIG. 115 shows a nucleotide sequence (SEQ ID NO:115) of a native sequence PRO1867 cDNA, wherein SEQ ID NO:115 is a clone designated herein as "DNA84925-2514".

[0142] FIG. 116 shows the amino acid sequence (SEQ ID NO:116) derived from the coding sequence of SEQ ID NO:115 shown in FIG. 115.

[0143] FIG. 117 shows a nucleotide sequence (SEQ ID NO:117) of a native sequence PRO4319 cDNA, wherein SEQ ID NO:117 is a clone designated herein as "DNA84928-2564".

[0144] FIG. 118 shows the amino acid sequence (SEQ ID NO:118) derived from the coding sequence of SEQ ID NO:117 shown in FIG. 117.

[0145] FIG. 119 shows a nucleotide sequence (SEQ ID NO:119) of a native sequence PRO4991 cDNA, wherein SEQ ID NO:119 is a clone designated herein as "DNA84932-2657".

[0146] FIG. 120 shows the amino acid sequence (SEQ ID NO:120) derived from the coding sequence of SEQ ID NO:119 shown in FIG. 119.

[0147] FIG. 121 shows a nucleotide sequence (SEQ ID NO:121) of a native sequence PRO4398 cDNA, wherein SEQ ID NO:121 is a clone designated herein as "DNA86592-2607".

[0148] FIG. 122 shows the amino acid sequence (SEQ ID NO:122) derived from the coding sequence of SEQ ID NO:121 shown in FIG. 121.

[0149] FIG. 123 shows a nucleotide sequence (SEQ ID NO:123) of a native sequence PRO4346 cDNA, wherein SEQ ID NO:123 is a clone designated herein as "DNA86594-2587".

[0150] FIG. 124 shows the amino acid sequence (SEQ ID NO:124) derived from the coding sequence of SEQ ID NO:123 shown in FIG. 123.

[0151] FIG. 125 shows a nucleotide sequence (SEQ ID NO:125) of a native sequence PRO4350 cDNA, wherein SEQ ID NO:125 is a clone designated herein as "DNA86647-2591".

[0152] FIG. 126 shows the amino acid sequence (SEQ ID NO:126) derived from the coding sequence of SEQ ID NO:125 shown in FIG. 125.

[0153] FIG. 127 shows a nucleotide sequence (SEQ ID NO:127) of a native sequence PRO4318 cDNA, wherein SEQ ID NO:127 is a clone designated herein as "DNA87185-2563".

[0154] FIG. 128 shows the amino acid sequence (SEQ ID NO:128) derived from the coding sequence of SEQ ID NO:127 shown in FIG. 127.

[0155] FIG. 129 shows a nucleotide sequence (SEQ ID NO:129) of a native sequence PRO4340 cDNA, wherein SEQ ID NO:129 is a clone designated herein as "DNA87656-2582".

[0156] FIG. 130 shows the amino acid sequence (SEQ ID NO:130) derived from the coding sequence of SEQ ID NO:129 shown in FIG. 129.

[0157] FIG. 131 shows a nucleotide sequence (SEQ ID NO:131) of a native sequence PRO4400 cDNA, wherein SEQ ID NO:131 is a clone designated herein as "DNA87974-2609".

[0158] FIG. 132 shows the amino acid sequence (SEQ ID NO:132) derived from the coding sequence of SEQ ID NO:131 shown in FIG. 131.

[0159] FIG. 133 shows a nucleotide sequence (SEQ ID NO:133) of a native sequence PRO4320 cDNA, wherein SEQ ID NO:133 is a clone designated herein as "DNA88001-2565".

[0160] FIG. 134 shows the amino acid sequence (SEQ ID NO:134) derived from the coding sequence of SEQ ID NO:133 shown in FIG. 133.

[0161] FIG. 135 shows a nucleotide sequence (SEQ ID NO:135) of a native sequence PRO4409 cDNA, wherein SEQ ID NO:135 is a clone designated herein as "DNA88004-2575".

[0162] FIG. 136 shows the amino acid sequence (SEQ ID NO:136) derived from the coding sequence of SEQ ID NO:135 shown in FIG. 135.

[0163] FIG. 137 shows a nucleotide sequence (SEQ ID NO:137) of a native sequence PRO4399 cDNA, wherein SEQ ID NO:137 is a clone designated herein as "DNA89220-2608".

[0164] FIG. 138 shows the amino acid sequence (SEQ ID NO:138) derived from the coding sequence of SEQ ID NO:137 shown in FIG. 137.

[0165] FIG. 139 shows a nucleotide sequence (SEQ ID NO:139) of a native sequence PRO4418 cDNA, wherein SEQ ID NO:139 is a clone designated herein as "DNA89947-2618".

[0166] FIG. 140 shows the amino acid sequence (SEQ ID NO:140) derived from the coding sequence of SEQ ID NO:139 shown in FIG. 139.

[0167] FIG. 141 shows a nucleotide sequence (SEQ ID NO:141) of a native sequence PRO4330 cDNA, wherein SEQ ID NO:141 is a clone designated herein as "DNA90842-2574".

[0168] FIG. 142 shows the amino acid sequence (SEQ ID NO:142) derived from the coding sequence of SEQ ID NO:141 shown in FIG. 141.

[0169] FIG. 143 shows a nucleotide sequence (SEQ ID NO:143) of a native sequence PRO4339 cDNA, wherein SEQ ID NO:143 is a clone designated herein as "DNA91775-2581".

[0170] FIG. 144 shows the amino acid sequence (SEQ ID NO:144) derived from the coding sequence of SEQ ID NO:143 shown in FIG. 143.

[0171] FIG. 145 shows a nucleotide sequence (SEQ ID NO:145) of a native sequence PRO4326 cDNA, wherein SEQ ID NO:145 is a clone designated herein as "DNA91779-2571".

[0172] FIG. 146 shows the amino acid sequence (SEQ ID NO:146) derived from the coding sequence of SEQ ID NO:145 shown in FIG. 145.

[0173] FIG. 147 shows a nucleotide sequence (SEQ ID NO:147) of a native sequence PRO6014 cDNA, wherein SEQ ID NO:147 is a clone designated herein as "DNA92217-2697".

[0174] FIG. 148 shows the amino acid sequence (SEQ ID NO:148) derived from the coding sequence of SEQ ID NO:147 shown in FIG. 147.

[0175] FIG. 149 shows a nucleotide sequence (SEQ ID NO:149) of a native sequence PRO3446 cDNA, wherein SEQ ID NO:149 is a clone designated herein as "DNA92219-2541".

[0176] FIG. 150 shows the amino acid sequence (SEQ ID NO:150) derived from the coding sequence of SEQ ID NO:149 shown in FIG. 149.

[0177] FIG. 151 shows a nucleotide sequence (SEQ ID NO:151) of a native sequence PRO4322 cDNA, wherein SEQ ID NO:151 is a clone designated herein as "DNA92223-2567".

[0178] FIG. 152 shows the amino acid sequence (SEQ ID NO:152) derived from the coding sequence of SEQ ID NO:151 shown in FIG. 151.

[0179] FIG. 153 shows a nucleotide sequence (SEQ ID NO:153) of a native sequence PRO4381 cDNA, wherein SEQ ID NO:153 is a clone designated herein as "DNA92225-2603".

[0180] FIG. 154 shows the amino acid sequence (SEQ ID NO:154) derived from the coding sequence of SEQ ID NO:153 shown in FIG. 153.

[0181] FIG. 155 shows a nucleotide sequence (SEQ ID NO:155) of a native sequence PRO4348 cDNA, wherein SEQ ID NO:155 is a clone designated herein as "DNA92232-2589".

[0182] FIG. 156 shows the amino acid sequence (SEQ ID NO:156) derived from the coding sequence of SEQ ID NO:155 shown in FIG. 155.

[0183] FIG. 157 shows a nucleotide sequence (SEQ ID NO:157) of a native sequence PRO4371 cDNA, wherein SEQ ID NO:157 is a clone designated herein as "DNA92233-2599".

[0184] FIG. 158 shows the amino acid sequence (SEQ ID NO:158) derived from the coding sequence of SEQ ID NO:157 shown in FIG. 157.

[0185] FIG. 159 shows a nucleotide sequence (SEQ ID NO:159) of a native sequence PRO3742 cDNA, wherein SEQ ID NO:159 is a clone designated herein as "DNA92243-2549".

[0186] FIG. 160 shows the amino acid sequence (SEQ ID NO:160) derived from the coding sequence of SEQ ID NO:159 shown in FIG. 159.

[0187] FIG. 161 shows a nucleotide sequence (SEQ ID NO:161) of a native sequence PRO5773 cDNA, wherein SEQ ID NO:161 is a clone designated herein as "DNA92253-2671".

[0188] FIG. 162 shows the amino acid sequence (SEQ ID NO:162) derived from the coding sequence of SEQ ID NO:161 shown in FIG. 161.

[0189] FIG. 163 shows a nucleotide sequence (SEQ ID NO:163) of a native sequence PRO5774 cDNA, wherein SEQ ID NO:163 is a clone designated herein as "DNA92254-2672".

[0190] FIG. 164 shows the amino acid sequence (SEQ ID NO:164) derived from the coding sequence of SEQ ID NO:163 shown in FIG. 163.

[0191] FIG. 165 shows a nucleotide sequence (SEQ ID NO:165) of a native sequence PRO4343 cDNA, wherein SEQ ID NO:165 is a clone designated herein as "DNA92255-2584".

[0192] FIG. 166 shows the amino acid sequence (SEQ ID NO:166) derived from the coding sequence of SEQ ID NO:165 shown in FIG. 165.

[0193] FIG. 167 shows a nucleotide sequence (SEQ ID NO:167) of a native sequence PRO4325 cDNA, wherein SEQ ID NO:167 is a clone designated herein as "DNA92269-2570".

[0194] FIG. 168 shows the amino acid sequence (SEQ ID NO:168) derived from the coding sequence of SEQ ID NO:167 shown in FIG. 167.

[0195] FIG. 169 shows a nucleotide sequence (SEQ ID NO:169) of a native sequence PRO4347 cDNA, wherein SEQ ID NO:169 is a clone designated herein as "DNA92288-2588".

[0196] FIG. 170 shows the amino acid sequence (SEQ ID NO:170) derived from the coding sequence of SEQ ID NO:169 shown in FIG. 169.

[0197] FIG. 171 shows a nucleotide sequence (SEQ ID NO:171) of a native sequence PRO3743 cDNA, wherein SEQ ID NO:171 is a clone designated herein as "DNA92290-2550".

[0198] FIG. 172 shows the amino acid sequence (SEQ ID NO:172) derived from the coding sequence of SEQ ID NO:171 shown in FIG. 171.

[0199] FIG. 173 shows a nucleotide sequence (SEQ ID NO:173) of a native sequence PRO4426 cDNA, wherein SEQ ID NO:173 is a clone designated herein as "DNA93012-2622".

[0200] FIG. 174 shows the amino acid sequence (SEQ ID NO:174) derived from the coding sequence of SEQ ID NO:173 shown in FIG. 173.

[0201] FIG. 175 shows a nucleotide sequence (SEQ ID NO:175) of a native sequence PRO4500 cDNA, wherein SEQ ID NO:175 is a clone designated herein as "DNA93020-2642".

[0202] FIG. 176 shows the amino acid sequence (SEQ ID NO:176) derived from the coding sequence of SEQ ID NO:175 shown in FIG. 175.

[0203] FIG. 177 shows a nucleotide sequence (SEQ ID NO:177) of a native sequence PRO4389 cDNA, wherein SEQ ID NO:177 is a clone designated herein as "DNA94830-2604".

[0204] FIG. 178 shows the amino acid sequence (SEQ ID NO:178) derived from the coding sequence of SEQ ID NO:177 shown in FIG. 177.

[0205] FIG. 179 shows a nucleotide sequence (SEQ ID NO:179) of a native sequence PRO4337 cDNA, wherein SEQ ID NO:179 is a clone designated herein as "DNA94833-2579".

[0206] FIG. 180 shows the amino acid sequence (SEQ ID NO: 180) derived from the coding sequence of SEQ ID NO:179 shown in FIG. 179.

[0207] FIG. 181 shows a nucleotide sequence (SEQ ID NO:181) of a native sequence PRO4992 cDNA, wherein SEQ ID NO:181 is a clone designated herein as "DNA94838-2658".

[0208] FIG. 182 shows the amino acid sequence (SEQ ID NO:182) derived from the coding sequence of SEQ ID NO:181 shown in FIG. 181.

[0209] FIG. 183 shows a nucleotide sequence (SEQ ID NO:183) of a native sequence PRO5996 cDNA, wherein SEQ ID NO:183 is a clone designated herein as "DNA94844-2686".

[0210] FIG. 184 shows the amino acid sequence (SEQ ID NO:184) derived from the coding sequence of SEQ ID NO:183 shown in FIG. 183.

[0211] FIG. 185 shows a nucleotide sequence (SEQ ID NO:185) of a native sequence PRO4345 cDNA, wherein SEQ ID NO:185 is a clone designated herein as "DNA94854-2586".

[0212] FIG. 186 shows the amino acid sequence (SEQ ID NO:186) derived from the coding sequence of SEQ ID NO:185 shown in FIG. 185.

[0213] FIG. 187 shows a nucleotide sequence (SEQ ID NO:187) of a native sequence PRO4978 cDNA, wherein SEQ ID NO:187 is a clone designated herein as "DNA95930".

[0214] FIG. 188 shows the amino acid sequence (SEQ ID NO:188) derived from the coding sequence of SEQ ID NO:187 shown in FIG. 187.

[0215] FIG. 189 shows a nucleotide sequence (SEQ ID NO:189) of a native sequence PRO5780 cDNA, wherein SEQ ID NO:189 is a clone designated herein as "DNA96868-2677".

[0216] FIG. 190 shows the amino acid sequence (SEQ ID NO:190) derived from the coding sequence of SEQ ID NO:189 shown in FIG. 189.

[0217] FIG. 191 shows a nucleotide sequence (SEQ ID NO:191) of a native sequence PRO5992 cDNA, wherein SEQ ID NO:191 is a clone designated herein as "DNA96871-2683".

[0218] FIG. 192 shows the amino acid sequence (SEQ ID NO:192) derived from the coding sequence of SEQ ID NO:191 shown in FIG. 191.

[0219] FIG. 193 shows a nucleotide sequence (SEQ ID NO:193) of a native sequence PRO4428 cDNA, wherein SEQ ID NO:193 is a clone designated herein as "DNA96880-2624".

[0220] FIG. 194 shows the amino acid sequence (SEQ ID NO:194) derived from the coding sequence of SEQ ID NO:193 shown in FIG. 193.

[0221] FIG. 195 shows a nucleotide sequence (SEQ ID NO:195) of a native sequence PRO4994 cDNA, wherein SEQ ID NO:195 is a clone designated herein as "DNA96986-2660".

[0222] FIG. 196 shows the amino acid sequence (SEQ ID NO:196) derived from the coding sequence of SEQ ID NO:195 shown in FIG. 195.

[0223] FIG. 197 shows a nucleotide sequence (SEQ ID NO:197) of a native sequence PRO5995 cDNA, wherein SEQ ID NO:197 is a clone designated herein as "DNA96988-2685".

[0224] FIG. 198 shows the amino acid sequence (SEQ ID NO:198) derived from the coding sequence of SEQ ID NO:197 shown in FIG. 197.

[0225] FIG. 199 shows a nucleotide sequence (SEQ ID NO:199) of a native sequence PRO6094 cDNA, wherein SEQ ID NO:199 is a clone designated herein as "DNA96995-2709".

[0226] FIG. 200 shows the amino acid sequence (SEQ ID NO:200) derived from the coding sequence of SEQ ID NO:199 shown in FIG. 199.

[0227] FIG. 201 shows a nucleotide sequence (SEQ ID NO:201) of a native sequence PRO4317 cDNA, wherein SEQ ID NO:201 is a clone designated herein as "DNA97004-2562".

[0228] FIG. 202 shows the amino acid sequence (SEQ ID NO:202) derived from the coding sequence of SEQ ID NO:201 shown in FIG. 201.

[0229] FIG. 203 shows a nucleotide sequence (SEQ ID NO:203) of a native sequence PRO5997 cDNA, wherein SEQ ID NO:203 is a clone designated herein as "DNA97005-2687".

[0230] FIG. 204 shows the amino acid sequence (SEQ ID NO:204) derived from the coding sequence of SEQ ID NO:203 shown in FIG. 203.

[0231] FIG. 205 shows a nucleotide sequence (SEQ ID NO:205) of a native sequence PRO5005 cDNA, wherein SEQ ID NO:205 is a clone designated herein as "DNA97009-2668".

[0232] FIG. 206 shows the amino acid sequence (SEQ ID NO:206) derived from the coding sequence of SEQ ID NO:205 shown in FIG. 205.

[0233] FIG. 207 shows a nucleotide sequence (SEQ ID NO:207) of a native sequence PRO5004 cDNA, wherein SEQ ID NO:207 is a clone designated herein as "DNA97013-2667".

[0234] FIG. 208 shows the amino acid sequence (SEQ ID NO:208) derived from the coding sequence of SEQ ID NO:207 shown in FIG. 207.

[0235] FIG. 209 shows a nucleotide sequence (SEQ ID NO:209) of a native sequence PRO6001 cDNA, wherein SEQ ID NO:209 is a clone designated herein as "DNA98380-2690".

[0236] FIG. 210 shows the amino acid sequence (SEQ ID NO:210) derived from the coding sequence of SEQ ID NO:209 shown in FIG. 209.

[0237] FIG. 211 shows a nucleotide sequence (SEQ ID NO:211) of a native sequence PRO6013 cDNA, wherein SEQ ID NO:211 is a clone designated herein as "DNA98561-2696".

[0238] FIG. 212 shows the amino acid sequence (SEQ ID NO:212) derived from the coding sequence of SEQ ID NO:211 shown in FIG. 211.

[0239] FIG. 213 shows a nucleotide sequence (SEQ ID NO:213) of a native sequence PRO4502 cDNA, wherein SEQ ID NO:213 is a clone designated herein as "DNA98575-2644".

[0240] FIG. 214 shows the amino acid sequence (SEQ ID NO:214) derived from the coding sequence of SEQ ID NO:213 shown in FIG. 213.

[0241] FIG. 215 shows a nucleotide sequence (SEQ ID NO:215) of a native sequence PRO6007 cDNA, wherein SEQ ID NO:215 is a clone designated herein as "DNA98593-2694".

[0242] FIG. 216 shows the amino acid sequence (SEQ ID NO:216) derived from the coding sequence of SEQ ID NO:215 shown in FIG. 215.

[0243] FIG. 217 shows a nucleotide sequence (SEQ ID NO:217) of a native sequence PRO6028 cDNA, wherein SEQ ID NO:217 is a clone designated herein as "DNA98600-2703".

[0244] FIG. 218 shows the amino acid sequence (SEQ ID NO:218) derived from the coding sequence of SEQ ID NO:217 shown in FIG. 217.

[0245] FIG. 219 shows a nucleotide sequence (SEQ ID NO:219) of a native sequence PRO100 cDNA, wherein SEQ ID NO:219 is a clone designated herein as "DNA99333".

[0246] FIG. 220 shows the amino acid sequence (SEQ ID NO:220) derived from the coding sequence of SEQ ID NO:219 shown in FIG. 219.

[0247] FIG. 221 shows a nucleotide sequence (SEQ ID NO:221) of a native sequence PRO4327 cDNA, wherein SEQ ID NO:221 is a clone designated herein as "DNA99391-2572".

[0248] FIG. 222 shows the amino acid sequence (SEQ ID NO:222) derived from the coding sequence of SEQ ID NO:221 shown in FIG. 221.

[0249] FIG. 223 shows a nucleotide sequence (SEQ ID NO:223) of a native sequence PRO4315 cDNA, wherein SEQ ID NO:223 is a clone designated herein as "DNA99393-2560".

[0250] FIG. 224 shows the amino acid sequence (SEQ ID NO:224) derived from the coding sequence of SEQ ID NO:223 shown in FIG. 223.

[0251] FIG. 225 shows a nucleotide sequence (SEQ ID NO:225) of a native sequence PRO5993 cDNA, wherein SEQ ID NO:225 is a clone designated herein as "DNA100276-2684".

[0252] FIG. 226 shows the amino acid sequence (SEQ ID NO:226) derived from the coding sequence of SEQ ID NO:225 shown in FIG. 225.

[0253] FIG. 227 shows a nucleotide sequence (SEQ ID NO:227) of a native sequence PRO4503 cDNA, wherein SEQ ID NO:227 is a clone designated herein as "DNA100312-2645".

[0254] FIG. 228 shows the amino acid sequence (SEQ ID NO:228) derived from the coding sequence of SEQ ID NO:227 shown in FIG. 227.

[0255] FIG. 229 shows a nucleotide sequence (SEQ ID NO:229) of a native sequence PRO4976 cDNA, wherein SEQ ID NO:229 is a clone designated herein as "DNA100902-2646".

[0256] FIG. 230 shows the amino acid sequence (SEQ ID NO:230) derived from the coding sequence of SEQ ID NO:229 shown in FIG. 229.

[0257] FIG. 231 shows a nucleotide sequence (SEQ ID NO:231) of a native sequence PRO5798 cDNA, wherein SEQ ID NO:231 is a clone designated herein as "DNA102899-2679".

[0258] FIG. 232 shows the amino acid sequence (SEQ ID NO:232) derived from the coding sequence of SEQ ID NO:231 shown in FIG. 231.

[0259] FIG. 233 shows a nucleotide sequence (SEQ ID NO:233) of a native sequence PRO6242 cDNA, wherein SEQ ID NO:233 is a clone designated herein as "DNA104875-2720".

[0260] FIG. 234 shows the amino acid sequence (SEQ ID NO:234) derived from the coding sequence of SEQ ID NO:233 shown in FIG. 233.

[0261] FIG. 235 shows a nucleotide sequence (SEQ ID NO:235) of a native sequence PRO6095 cDNA, wherein SEQ ID NO:235 is a clone designated herein as "DNA105680-2710".

[0262] FIG. 236 shows the amino acid sequence (SEQ ID NO:236) derived from the coding sequence of SEQ ID NO:235 shown in FIG. 235.

[0263] FIG. 237 shows a nucleotide sequence (SEQ ID NO:237) of a native sequence PRO6093 cDNA, wherein SEQ ID NO:237 is a clone designated herein as "DNA105779-2708".

[0264] FIG. 238 shows the amino acid sequence (SEQ ID NO:238) derived from the coding sequence of SEQ ID NO:237 shown in FIG. 237.

[0265] FIG. 239 shows a nucleotide sequence (SEQ ID NO:239) of a native sequence PRO6012 cDNA, wherein SEQ ID NO:239 is a clone designated herein as "DNA105794-2695".

[0266] FIG. 240 shows the amino acid sequence (SEQ ID NO:240) derived from the coding sequence of SEQ ID NO:239 shown in FIG. 239.

[0267] FIG. 241 shows a nucleotide sequence (SEQ ID NO:241) of a native sequence PRO6027 cDNA, wherein SEQ ID NO:241 is a clone designated herein as "DNA105838-2702".

[0268] FIG. 242 shows the amino acid sequence (SEQ ID NO:242) derived from the coding sequence of SEQ ID NO:241 shown in FIG. 241.

[0269] FIG. 243 shows a nucleotide sequence (SEQ ID NO:243) of a native sequence PRO6181 cDNA, wherein SEQ ID NO:243 is a clone designated herein as "DNA107698-2715".

[0270] FIG. 244 shows the amino acid sequence (SEQ ID NO:244) derived from the coding sequence of SEQ ID NO:243 shown in FIG. 243.

[0271] FIG. 245 shows a nucleotide sequence (SEQ ID NO:245) of a native sequence PRO6097 cDNA, wherein SEQ ID NO:245 is a clone designated herein as "DNA107701-2711".

[0272] FIG. 246 shows the amino acid sequence (SEQ ID NO:246) derived from the coding sequence of SEQ ID NO:245 shown in FIG. 245.

[0273] FIG. 247 shows a nucleotide sequence (SEQ ID NO:247) of a native sequence PRO6090 cDNA, wherein SEQ ID NO:247 is a clone designated herein as "DNA107781-2707".

[0274] FIG. 248 shows the amino acid sequence (SEQ ID NO:248) derived from the coding sequence of SEQ ID NO:247 shown in FIG. 247.

[0275] FIG. 249 shows a nucleotide sequence (SEQ ID NO:249) of a native sequence PRO7171 cDNA, wherein SEQ ID NO:249 is a clone designated herein as "DNA108670-2744".

[0276] FIG. 250 shows the amino acid sequence (SEQ ID NO:250) derived from the coding sequence of SEQ ID NO:249 shown in FIG. 249.

[0277] FIG. 251 shows a nucleotide sequence (SEQ ID NO:251) of a native sequence PRO6258 cDNA, wherein SEQ ID NO:251 is a clone designated herein as "DNA108688-2725".

[0278] FIG. 252 shows the amino acid sequence (SEQ ID NO:252) derived from the coding sequence of SEQ ID NO:251 shown in FIG. 251.

[0279] FIG. 253 shows a nucleotide sequence (SEQ ID NO:253) of a native sequence PRO9820 cDNA, wherein SEQ ID NO:253 is a clone designated herein as "DNA108769-2765".

[0280] FIG. 254 shows the amino acid sequence (SEQ ID NO:254) derived from the coding sequence of SEQ ID NO:253 shown in FIG. 253.

[0281] FIG. 255 shows a nucleotide sequence (SEQ ID NO:255) of a native sequence PRO6243 cDNA, wherein SEQ ID NO:255 is a clone designated herein as "DNA108935-2721".

[0282] FIG. 256 shows the amino acid sequence (SEQ ID NO:256) derived from the coding sequence of SEQ ID NO:255 shown in FIG. 255.

[0283] FIG. 257 shows a nucleotide sequence (SEQ ID NO:257) of a native sequence PRO6182 cDNA, wherein SEQ ID NO:257 is a clone designated herein as "DNA110700-2716".

[0284] FIG. 258 shows the amino acid sequence (SEQ ID NO:258) derived from the coding sequence of SEQ ID NO:257 shown in FIG. 257.

[0285] FIG. 259 shows a nucleotide sequence (SEQ ID NO:259) of a native sequence PRO6079 cDNA, wherein SEQ ID NO:259 is a clone designated herein as "DNA11750-2706".

[0286] FIG. 260 shows the amino acid sequence (SEQ ID NO:260) derived from the coding sequence of SEQ ID NO:259 shown in FIG. 259.

[0287] FIG. 261 shows a nucleotide sequence (SEQ ID NO:261) of a native sequence PRO7434 cDNA, wherein SEQ ID NO:261 is a clone designated herein as "DNA123430-2755".

[0288] FIG. 262 shows the amino acid sequence (SEQ ID NO:262) derived from the coding sequence of SEQ ID NO:261 shown in FIG. 261.

[0289] FIG. 263 shows a nucleotide sequence (SEQ ID NO:263) of a native sequence PRO9865 cDNA, wherein SEQ ID NO:263 is a clone designated herein as "DNA125154-2785".

[0290] FIG. 264 shows the amino acid sequence (SEQ ID NO:264) derived from the coding sequence of SEQ ID NO:263 shown in FIG. 263.

[0291] FIG. 265 shows a nucleotide sequence (SEQ ID NO:265) of a native sequence PRO9828 cDNA, wherein SEQ ID NO:265 is a clone designated herein as "DNA142238-2768".

[0292] FIG. 266 shows the amino acid sequence (SEQ ID NO:266) derived from the coding sequence of SEQ ID NO:265 shown in FIG. 265.

[0293] FIG. 267 shows a nucleotide sequence (SEQ ID NO:267) of a native sequence PRO196 cDNA, wherein SEQ ID NO:267 is a clone designated herein as "DNA22779-1130".

[0294] FIG. 268 shows the amino acid sequence (SEQ ID NO:268) derived from the coding sequence of SEQ ID NO:267 shown in FIG. 267.

[0295] FIG. 269 shows a nucleotide sequence (SEQ ID NO:269) of a native sequence PRO197 cDNA, wherein SEQ ID NO:269 is a clone designated herein as "DNA22780-1078".

[0296] FIG. 270 shows the amino acid sequence (SEQ ID NO:270) derived from the coding sequence of SEQ ID NO:269 shown in FIG. 269.

[0297] FIG. 271 shows a nucleotide sequence (SEQ ID NO:271) of a native sequence PRO195 cDNA, wherein SEQ ID NO:271 is a clone designated herein as "DNA26847-1395".

[0298] FIG. 272 shows the amino acid sequence (SEQ ID NO:272) derived from the coding sequence of SEQ ID NO:271 shown in FIG. 271.

[0299] FIG. 273 shows a nucleotide sequence (SEQ ID NO:273) of a native sequence PRO187 cDNA, wherein SEQ ID NO:273 is a clone designated herein as "DNA27864-1155".

[0300] FIG. 274 shows the amino acid sequence (SEQ ID NO:274) derived from the coding sequence of SEQ ID NO:273 shown in FIG. 273.

[0301] FIG. 275 shows a nucleotide sequence (SEQ ID NO:275) of a native sequence PRO182 cDNA, wherein SEQ ID NO:275 is a clone designated herein as "DNA27865-1091".

[0302] FIG. 276 shows the amino acid sequence (SEQ ID NO:276) derived from the coding sequence of SEQ ID NO:275 shown in FIG. 275.

[0303] FIG. 277 shows a nucleotide sequence (SEQ ID NO:277) of a native sequence PRO188 cDNA, wherein SEQ ID NO:277 is a clone designated herein as "DNA28497-1130".

[0304] FIG. 278 shows the amino acid sequence (SEQ ID NO:278) derived from the coding sequence of SEQ ID NO:277 shown in FIG. 277.

[0305] FIG. 279 shows a nucleotide sequence (SEQ ID NO:279) of a native sequence PRO183 cDNA, wherein SEQ ID NO:279 is a clone designated herein as "DNA28498".

[0306] FIG. 280 shows the amino acid sequence (SEQ ID NO:280) derived from the coding sequence of SEQ ID NO:279 shown in FIG. 279.

[0307] FIG. 281 shows a nucleotide sequence (SEQ ID NO:281) of a native sequence PRO184 cDNA, wherein SEQ ID NO:281 is a clone designated herein as "DNA28500".

[0308] FIG. 282 shows the amino acid sequence (SEQ ID NO:282) derived from the coding sequence of SEQ ID NO:281 shown in FIG. 281.

[0309] FIG. 283 shows a nucleotide sequence (SEQ ID NO:283) of a native sequence PRO185 cDNA, wherein SEQ ID NO:283 is a clone designated herein as "DNA28503".

[0310] FIG. 284 shows the amino acid sequence (SEQ ID NO:284) derived from the coding sequence of SEQ ID NO:283 shown in FIG. 283.

[0311] FIG. 285 shows a nucleotide sequence (SEQ ID NO:285) of a native sequence PRO200 cDNA, wherein SEQ ID NO:285 is a clone designated herein as "DNA29101-1122".

[0312] FIG. 286 shows the amino acid sequence (SEQ ID NO:286) derived from the coding sequence of SEQ ID NO:285 shown in FIG. 285.

[0313] FIG. 287 shows a nucleotide sequence (SEQ ID NO:287) of a native sequence PRO202 cDNA, wherein SEQ ID NO:287 is a clone designated herein as "DNA30869".

[0314] FIG. 288 shows the amino acid sequence (SEQ ID NO:288) derived from the coding sequence of SEQ ID NO:287 shown in FIG. 287.

[0315] FIG. 289 shows a nucleotide sequence (SEQ ID NO:289) of a native sequence PRO214 cDNA, wherein SEQ ID NO:289 is a clone designated herein as "DNA32286-1191".

[0316] FIG. 290 shows the amino acid sequence (SEQ ID NO:290) derived from the coding sequence of SEQ ID NO:289 shown in FIG. 289.

[0317] FIG. 291 shows a nucleotide sequence (SEQ ID NO:291) of a native sequence PRO215 cDNA, wherein SEQ ID NO:291 is a clone designated herein as "DNA32288-1132".

[0318] FIG. 292 shows the amino acid sequence (SEQ ID NO:292) derived from the coding sequence of SEQ ID NO:291 shown in FIG. 291.



[0319] **FIG. 293** shows a nucleotide sequence (SEQ ID NO:293) of a native sequence PRO219 cDNA, wherein SEQ ID NO:293 is a clone designated herein as "DNA32290-1164".

[0320] **FIG. 294** shows the amino acid sequence (SEQ ID NO:294) derived from the coding sequence of SEQ ID NO:293 shown in **FIG. 293**.

[0321] **FIG. 295** shows a nucleotide sequence (SEQ ID NO:295) of a native sequence PRO211 cDNA, wherein SEQ ID NO:295 is a clone designated herein as "DNA32292-1131".

[0322] **FIG. 296** shows the amino acid sequence (SEQ ID NO:296) derived from the coding sequence of SEQ ID NO:295 shown in **FIG. 295**.

[0323] **FIG. 297** shows a nucleotide sequence (SEQ ID NO:297) of a native sequence PRO220 cDNA, wherein SEQ ID NO:297 is a clone designated herein as "DNA32298-1132".

[0324] **FIG. 298** shows the amino acid sequence (SEQ ID NO:298) derived from the coding sequence of SEQ ID NO:297 shown in **FIG. 297**.

[0325] **FIG. 299** shows a nucleotide sequence (SEQ ID NO:299) of a native sequence PRO366 cDNA, wherein SEQ ID NO:299 is a clone designated herein as "DNA33085-1110".

[0326] **FIG. 300** shows the amino acid sequence (SEQ ID NO:300) derived from the coding sequence of SEQ ID NO:299 shown in **FIG. 299**.

[0327] **FIG. 301** shows a nucleotide sequence (SEQ ID NO:301) of a native sequence PRO216 cDNA, wherein SEQ ID NO:301 is a clone designated herein as "DNA33087-1158".

[0328] **FIG. 302** shows the amino acid sequence (SEQ ID NO:302) derived from the coding sequence of SEQ ID NO:301 shown in **FIG. 301**.

[0329] **FIG. 303** shows a nucleotide sequence (SEQ ID NO:303) of a native sequence PRO221 cDNA, wherein SEQ ID NO:303 is a clone designated herein as "DNA33089-1132".

[0330] **FIG. 304** shows the amino acid sequence (SEQ ID NO:304) derived from the coding sequence of SEQ ID NO:303 shown in **FIG. 303**.

[0331] **FIG. 305** shows a nucleotide sequence (SEQ ID NO:305) of a native sequence PRO228 cDNA, wherein SEQ ID NO:305 is a clone designated herein as "DNA33092-1202".

[0332] **FIG. 306** shows the amino acid sequence (SEQ ID NO:306) derived from the coding sequence of SEQ ID NO:305 shown in **FIG. 305**.

[0333] **FIG. 307** shows a nucleotide sequence (SEQ ID NO:307) of a native sequence PRO217 cDNA, wherein SEQ ID NO:307 is a clone designated herein as "DNA33094-1131".

[0334] **FIG. 308** shows the amino acid sequence (SEQ ID NO:308) derived from the coding sequence of SEQ ID NO:307 shown in **FIG. 307**.

[0335] **FIG. 309** shows a nucleotide sequence (SEQ ID NO:309) of a native sequence PRO222 cDNA, wherein SEQ ID NO:309 is a clone designated herein as "DNA33107-1135".

[0336] **FIG. 310** shows the amino acid sequence (SEQ ID NO:310) derived from the coding sequence of SEQ ID NO:309 shown in **FIG. 309**.

[0337] **FIG. 311** shows a nucleotide sequence (SEQ ID NO:311) of a native sequence PRO224 cDNA, wherein SEQ ID NO:311 is a clone designated herein as "DNA33221-1133".

[0338] **FIG. 312** shows the amino acid sequence (SEQ ID NO:312) derived from the coding sequence of SEQ ID NO:311 shown in **FIG. 311**.

[0339] **FIG. 313** shows a nucleotide sequence (SEQ ID NO:313) of a native sequence PRO230 cDNA, wherein SEQ ID NO:313 is a clone designated herein as "DNA33223-1136".

[0340] **FIG. 314** shows the amino acid sequence (SEQ ID NO:314) derived from the coding sequence of SEQ ID NO:313 shown in **FIG. 313**.

[0341] **FIG. 315** shows a nucleotide sequence (SEQ ID NO:315) of a native sequence PRO198 cDNA, wherein SEQ ID NO:315 is a clone designated herein as "DNA33457-1078".

[0342] **FIG. 316** shows the amino acid sequence (SEQ ID NO:316) derived from the coding sequence of SEQ ID NO:315 shown in **FIG. 315**.

[0343] **FIG. 317** shows a nucleotide sequence (SEQ ID NO:317) of a native sequence PRO226 cDNA, wherein SEQ ID NO:317 is a clone designated herein as "DNA33460-1166".

[0344] **FIG. 318** shows the amino acid sequence (SEQ ID NO:318) derived from the coding sequence of SEQ ID NO:317 shown in **FIG. 317**.

[0345] **FIG. 319** shows a nucleotide sequence (SEQ ID NO:319) of a native sequence PRO261 cDNA, wherein SEQ ID NO:319 is a clone designated herein as "DNA33473-1176".

[0346] **FIG. 320** shows the amino acid sequence (SEQ ID NO:320) derived from the coding sequence of SEQ ID NO:319 shown in **FIG. 319**.

[0347] **FIG. 321** shows a nucleotide sequence (SEQ ID NO:321) of a native sequence PRO242 cDNA, wherein SEQ ID NO:321 is a clone designated herein as "DNA33785-1143".

[0348] **FIG. 322** shows the amino acid sequence (SEQ ID NO:322) derived from the coding sequence of SEQ ID NO:321 shown in **FIG. 321**.

[0349] **FIG. 323** shows a nucleotide sequence (SEQ ID NO:323) of a native sequence PRO227 cDNA, wherein SEQ ID NO:323 is a clone designated herein as "DNA33786-1132".

[0350] **FIG. 324** shows the amino acid sequence (SEQ ID NO:324) derived from the coding sequence of SEQ ID NO:323 shown in **FIG. 323**.

[0351] **FIG. 325** shows a nucleotide sequence (SEQ ID NO:325) of a native sequence PRO237 cDNA, wherein SEQ ID NO:325 is a clone designated herein as "DNA34353-1428".

[0352] **FIG. 326** shows the amino acid sequence (SEQ ID NO:326) derived from the coding sequence of SEQ ID NO:325 shown in **FIG. 325**.

[0353] **FIG. 327** shows a nucleotide sequence (SEQ ID NO:327) of a native sequence PRO241 cDNA, wherein SEQ ID NO:327 is a clone designated herein as "DNA34392-1170".

[0354] **FIG. 328** shows the amino acid sequence (SEQ ID NO:328) derived from the coding sequence of SEQ ID NO:327 shown in **FIG. 327**.

[0355] **FIG. 329** shows a nucleotide sequence (SEQ ID NO:329) of a native sequence PRO231 cDNA, wherein SEQ ID NO:329 is a clone designated herein as "DNA34434-1139".

[0356] **FIG. 330** shows the amino acid sequence (SEQ ID NO:330) derived from the coding sequence of SEQ ID NO:329 shown in **FIG. 329**.

[0357] **FIG. 331** shows a nucleotide sequence (SEQ ID NO:331) of a native sequence PRO235 cDNA, wherein SEQ ID NO:331 is a clone designated herein as "DNA35558-1167".

[0358] **FIG. 332** shows the amino acid sequence (SEQ ID NO:332) derived from the coding sequence of SEQ ID NO:331 shown in **FIG. 331**.

[0359] **FIG. 333** shows a nucleotide sequence (SEQ ID NO:333) of a native sequence PRO323 cDNA, wherein SEQ ID NO:333 is a clone designated herein as "DNA35595-1228".

[0360] **FIG. 334** shows the amino acid sequence (SEQ ID NO:334) derived from the coding sequence of SEQ ID NO:333 shown in **FIG. 333**.

[0361] **FIG. 335** shows a nucleotide sequence (SEQ ID NO:335) of a native sequence PRO245 cDNA, wherein SEQ ID NO:335 is a clone designated herein as "DNA35638-1216".

[0362] **FIG. 336** shows the amino acid sequence (SEQ ID NO:336) derived from the coding sequence of SEQ ID NO:335 shown in **FIG. 335**.

[0363] **FIG. 337** shows a nucleotide sequence (SEQ ID NO:337) of a native sequence PRO246 cDNA, wherein SEQ ID NO:337 is a clone designated herein as "DNA35639-1172".

[0364] **FIG. 338** shows the amino acid sequence (SEQ ID NO:338) derived from the coding sequence of SEQ ID NO:337 shown in **FIG. 337**.

[0365] **FIG. 339** shows a nucleotide sequence (SEQ ID NO:339) of a native sequence PRO288 cDNA, wherein SEQ ID NO:339 is a clone designated herein as "DNA35663-1129".

[0366] **FIG. 340** shows the amino acid sequence (SEQ ID NO:340) derived from the coding sequence of SEQ ID NO:339 shown in **FIG. 339**.

[0367] **FIG. 341** shows a nucleotide sequence (SEQ ID NO:341) of a native sequence PRO248 cDNA, wherein SEQ ID NO:341 is a clone designated herein as "DNA35674-1142".

[0368] **FIG. 342** shows the amino acid sequence (SEQ ID NO:342) derived from the coding sequence of SEQ ID NO:341 shown in **FIG. 341**.

[0369] **FIG. 343** shows a nucleotide sequence (SEQ ID NO:343) of a native sequence PRO257 cDNA, wherein SEQ ID NO:343 is a clone designated herein as "DNA35841-1173".

[0370] **FIG. 344** shows the amino acid sequence (SEQ ID NO:344) derived from the coding sequence of SEQ ID NO:343 shown in **FIG. 343**.

[0371] **FIG. 345** shows a nucleotide sequence (SEQ ID NO:345) of a native sequence PRO172 cDNA, wherein SEQ ID NO:345 is a clone designated herein as "DNA35916-1161".

[0372] **FIG. 346** shows the amino acid sequence (SEQ ID NO:346) derived from the coding sequence of SEQ ID NO:345 shown in **FIG. 345**.

[0373] **FIG. 347** shows a nucleotide sequence (SEQ ID NO:347) of a native sequence PRO258 cDNA, wherein SEQ ID NO:347 is a clone designated herein as "DNA35918-1174".

[0374] **FIG. 348** shows the amino acid sequence (SEQ ID NO:348) derived from the coding sequence of SEQ ID NO:347 shown in **FIG. 347**.

[0375] **FIG. 349** shows a nucleotide sequence (SEQ ID NO:349) of a native sequence PRO265 cDNA, wherein SEQ ID NO:349 is a clone designated herein as "DNA36350-1158".

[0376] **FIG. 350** shows the amino acid sequence (SEQ ID NO:350) derived from the coding sequence of SEQ ID NO:349 shown in **FIG. 349**.

[0377] **FIG. 351** shows a nucleotide sequence (SEQ ID NO:351) of a native sequence PRO326 cDNA, wherein SEQ ID NO:351 is a clone designated herein as "DNA37140-1234".

[0378] **FIG. 352** shows the amino acid sequence (SEQ ID NO:352) derived from the coding sequence of SEQ ID NO:351 shown in **FIG. 351**.

[0379] **FIG. 353** shows a nucleotide sequence (SEQ ID NO:353) of a native sequence PRO266 cDNA, wherein SEQ ID NO:353 is a clone designated herein as "DNA37150-1178".

[0380] **FIG. 354** shows the amino acid sequence (SEQ ID NO:354) derived from the coding sequence of SEQ ID NO:353 shown in **FIG. 353**.

[0381] **FIG. 355** shows a nucleotide sequence (SEQ ID NO:355) of a native sequence PRO269 cDNA, wherein SEQ ID NO:355 is a clone designated herein as "DNA38260-1180".

[0382] **FIG. 356** shows the amino acid sequence (SEQ ID NO:356) derived from the coding sequence of SEQ ID NO:355 shown in **FIG. 355**.

[0383] FIG. 357 shows a nucleotide sequence (SEQ ID NO:357) of a native sequence PRO285 cDNA, wherein SEQ ID NO:357 is a clone designated herein as "DNA40021-1154".

[0384] FIG. 358 shows the amino acid sequence (SEQ ID NO:358) derived from the coding sequence of SEQ ID NO:357 shown in FIG. 357.

[0385] FIG. 359 shows a nucleotide sequence (SEQ ID NO:359) of a native sequence PRO328 cDNA, wherein SEQ ID NO:359 is a clone designated herein as "DNA40587-1231".

[0386] FIG. 360 shows the amino acid sequence (SEQ ID NO:360) derived from the coding sequence of SEQ ID NO:359 shown in FIG. 359.

[0387] FIG. 361 shows a nucleotide sequence (SEQ ID NO:361) of a native sequence PRO344 cDNA, wherein SEQ ID NO:361 is a clone designated herein as "DNA40592-1242".

[0388] FIG. 362 shows the amino acid sequence (SEQ ID NO:362) derived from the coding sequence of SEQ ID NO:361 shown in FIG. 361.

[0389] FIG. 363 shows a nucleotide sequence (SEQ ID NO:363) of a native sequence PRO272 cDNA, wherein SEQ ID NO:363 is a clone designated herein as "DNA40620-1183".

[0390] FIG. 364 shows the amino acid sequence (SEQ ID NO:364) derived from the coding sequence of SEQ ID NO:363 shown in FIG. 363.

[0391] FIG. 365 shows a nucleotide sequence (SEQ ID NO:365) of a native sequence PRO301 cDNA, wherein SEQ ID NO:365 is a clone designated herein as "DNA40628-1216".

[0392] FIG. 366 shows the amino acid sequence (SEQ ID NO:366) derived from the coding sequence of SEQ ID NO:365 shown in FIG. 365.

[0393] FIG. 367 shows a nucleotide sequence (SEQ ID NO:367) of a native sequence PRO331 cDNA, wherein SEQ ID NO:367 is a clone designated herein as "DNA40981-1234".

[0394] FIG. 368 shows the amino acid sequence (SEQ ID NO:368) derived from the coding sequence of SEQ ID NO:367 shown in FIG. 367.

[0395] FIG. 369 shows a nucleotide sequence (SEQ ID NO:369) of a native sequence PRO332 cDNA, wherein SEQ ID NO:369 is a clone designated herein as "DNA40982-1235".

[0396] FIG. 370 shows the amino acid sequence (SEQ ID NO:370) derived from the coding sequence of SEQ ID NO:369 shown in FIG. 369.

[0397] FIG. 371 shows a nucleotide sequence (SEQ ID NO:371) of a native sequence PRO353 cDNA, wherein SEQ ID NO:371 is a clone designated herein as "DNA41234-1242".

[0398] FIG. 372 shows the amino acid sequence (SEQ ID NO:372) derived from the coding sequence of SEQ ID NO:371 shown in FIG. 371.

[0399] FIG. 373 shows a nucleotide sequence (SEQ ID NO:373) of a native sequence PRO310 cDNA, wherein SEQ ID NO:373 is a clone designated herein as "DNA43046-1225".

[0400] FIG. 374 shows the amino acid sequence (SEQ ID NO:374) derived from the coding sequence of SEQ ID NO:373 shown in FIG. 373.

[0401] FIG. 375 shows a nucleotide sequence (SEQ ID NO:375) of a native sequence PRO337 cDNA, wherein SEQ ID NO:375 is a clone designated herein as "DNA43316-1237".

[0402] FIG. 376 shows the amino acid sequence (SEQ ID NO:376) derived from the coding sequence of SEQ ID NO:375 shown in FIG. 375.

[0403] FIG. 377 shows a nucleotide sequence (SEQ ID NO:377) of a native sequence PRO346 cDNA, wherein SEQ ID NO:377 is a clone designated herein as "DNA44167-1243".

[0404] FIG. 378 shows the amino acid sequence (SEQ ID NO:378) derived from the coding sequence of SEQ ID NO:377 shown in FIG. 377.

[0405] FIG. 379 shows a nucleotide sequence (SEQ ID NO:379) of a native sequence PRO350 cDNA, wherein SEQ ID NO:379 is a clone designated herein as "DNA44175-1314".

[0406] FIG. 380 shows the amino acid sequence (SEQ ID NO:380) derived from the coding sequence of SEQ ID NO:379 shown in FIG. 379.

[0407] FIG. 381 shows a nucleotide sequence (SEQ ID NO:381) of a native sequence PRO526 cDNA, wherein SEQ ID NO:381 is a clone designated herein as "DNA44184-1319".

[0408] FIG. 382 shows the amino acid sequence (SEQ ID NO:382) derived from the coding sequence of SEQ ID NO:381 shown in FIG. 381.

[0409] FIG. 383 shows a nucleotide sequence (SEQ ID NO:383) of a native sequence PRO381 cDNA, wherein SEQ ID NO:383 is a clone designated herein as "DNA44194-1317".

[0410] FIG. 384 shows the amino acid sequence (SEQ ID NO:384) derived from the coding sequence of SEQ ID NO:383 shown in FIG. 383.

[0411] FIG. 385 shows a nucleotide sequence (SEQ ID NO:385) of a native sequence PRO846 cDNA, wherein SEQ ID NO:385 is a clone designated herein as "DNA44196-1353".

[0412] FIG. 386 shows the amino acid sequence (SEQ ID NO:386) derived from the coding sequence of SEQ ID NO:385 shown in FIG. 385.

[0413] FIG. 387 shows a nucleotide sequence (SEQ ID NO:387) of a native sequence PRO363 cDNA, wherein SEQ ID NO:387 is a clone designated herein as "DNA45419-1252".

[0414] FIG. 388 shows the amino acid sequence (SEQ ID NO:388) derived from the coding sequence of SEQ ID NO:387 shown in FIG. 387.

[0415] FIG. 389 shows a nucleotide sequence (SEQ ID NO:389) of a native sequence PRO365 cDNA, wherein SEQ ID NO:389 is a clone designated herein as "DNA46777-1253".

[0416] FIG. 390 shows the amino acid sequence (SEQ ID NO:390) derived from the coding sequence of SEQ ID NO:389 shown in FIG. 389.

[0417] FIG. 391 shows a nucleotide sequence (SEQ ID NO:391) of a native sequence PRO1310 cDNA, wherein SEQ ID NO:391 is a clone designated herein as "DNA47394-1572".

[0418] FIG. 392 shows the amino acid sequence (SEQ ID NO:392) derived from the coding sequence of SEQ ID NO:391 shown in FIG. 391.

[0419] FIG. 393 shows a nucleotide sequence (SEQ ID NO:393) of a native sequence PRO731 cDNA, wherein SEQ ID NO:393 is a clone designated herein as "DNA48331-1329".

[0420] FIG. 394 shows the amino acid sequence (SEQ ID NO:394) derived from the coding sequence of SEQ ID NO:393 shown in FIG. 393.

[0421] FIG. 395 shows a nucleotide sequence (SEQ ID NO:395) of a native sequence PRO322 cDNA, wherein SEQ ID NO:395 is a clone designated herein as "DNA48336-1309".

[0422] FIG. 396 shows the amino acid sequence (SEQ ID NO:396) derived from the coding sequence of SEQ ID NO:395 shown in FIG. 395.

[0423] FIG. 397 shows a nucleotide sequence (SEQ ID NO:397) of a native sequence PRO536 cDNA, wherein SEQ ID NO:397 is a clone designated herein as "DNA49142-1430".

[0424] FIG. 398 shows the amino acid sequence (SEQ ID NO:398) derived from the coding sequence of SEQ ID NO:397 shown in FIG. 397.

[0425] FIG. 399 shows a nucleotide sequence (SEQ ID NO:399) of a native sequence PRO719 cDNA, wherein SEQ ID NO:399 is a clone designated herein as "DNA49646-1327".

[0426] FIG. 400 shows the amino acid sequence (SEQ ID NO:400) derived from the coding sequence of SEQ ID NO:399 shown in FIG. 399.

[0427] FIG. 401 shows a nucleotide sequence (SEQ ID NO:401) of a native sequence PRO619 cDNA, wherein SEQ ID NO:401 is a clone designated herein as "DNA49821-1562".

[0428] FIG. 402 shows the amino acid sequence (SEQ ID NO:402) derived from the coding sequence of SEQ ID NO:401 shown in FIG. 401.

[0429] FIG. 403 shows a nucleotide sequence (SEQ ID NO:403) of a native sequence PRO771 cDNA, wherein SEQ ID NO:403 is a clone designated herein as "DNA49829-1346".

[0430] FIG. 404 shows the amino acid sequence (SEQ ID NO:404) derived from the coding sequence of SEQ ID NO:403 shown in FIG. 403.

[0431] FIG. 405 shows a nucleotide sequence (SEQ ID NO:405) of a native sequence PRO1083 cDNA, wherein SEQ ID NO:405 is a clone designated herein as "DNA50921-1458".

[0432] FIG. 406 shows the amino acid sequence (SEQ ID NO:406) derived from the coding sequence of SEQ ID NO:405 shown in FIG. 405.

[0433] FIG. 407 shows a nucleotide sequence (SEQ ID NO:407) of a native sequence PRO862 cDNA, wherein SEQ ID NO:407 is a clone designated herein as "DNA52187-1354".

[0434] FIG. 408 shows the amino acid sequence (SEQ ID NO:408) derived from the coding sequence of SEQ ID NO:407 shown in FIG. 407.

[0435] FIG. 409 shows a nucleotide sequence (SEQ ID NO:409) of a native sequence PRO733 cDNA, wherein SEQ ID NO:409 is a clone designated herein as "DNA52196-1348".

[0436] FIG. 410 shows the amino acid sequence (SEQ ID NO:410) derived from the coding sequence of SEQ ID NO:409 shown in FIG. 409.

[0437] FIG. 411 shows a nucleotide sequence (SEQ ID NO:411) of a native sequence PRO1188 cDNA, wherein SEQ ID NO:411 is a clone designated herein as "DNA52598-1518".

[0438] FIG. 412 shows the amino acid sequence (SEQ ID NO:412) derived from the coding sequence of SEQ ID NO:411 shown in FIG. 411.

[0439] FIG. 413 shows a nucleotide sequence (SEQ ID NO:413) of a native sequence PRO770 cDNA, wherein SEQ ID NO:413 is a clone designated herein as "DNA54228-1366".

[0440] FIG. 414 shows the amino acid sequence (SEQ ID NO:414) derived from the coding sequence of SEQ ID NO:413 shown in FIG. 413.

[0441] FIG. 415 shows a nucleotide sequence (SEQ ID NO:415) of a native sequence PRO1080 cDNA, wherein SEQ ID NO:415 is a clone designated herein as "DNA56047-1456".

[0442] FIG. 416 shows the amino acid sequence (SEQ ID NO:416) derived from the coding sequence of SEQ ID NO:415 shown in FIG. 415.

[0443] FIG. 417 shows a nucleotide sequence (SEQ ID NO:417) of a native sequence PRO1017 cDNA, wherein SEQ ID NO:417 is a clone designated herein as "DNA56112-1379".

[0444] FIG. 418 shows the amino acid sequence (SEQ ID NO:418) derived from the coding sequence of SEQ ID NO:417 shown in FIG. 417.

[0445] FIG. 419 shows a nucleotide sequence (SEQ ID NO:419) of a native sequence PRO1016 cDNA, wherein SEQ ID NO:419 is a clone designated herein as "DNA56113-1378".

[0446] FIG. 420 shows the amino acid sequence (SEQ ID NO:420) derived from the coding sequence of SEQ ID NO:419 shown in FIG. 419.

[0447] FIG. 421 shows a nucleotide sequence (SEQ ID NO:421) of a native sequence PRO792 cDNA, wherein SEQ ID NO:421 is a clone designated herein as "DNA56352-1358".

[0448] FIG. 422 shows the amino acid sequence (SEQ ID NO:422) derived from the coding sequence of SEQ ID NO:421 shown in FIG. 421.

[0449] FIG. 423 shows a nucleotide sequence (SEQ ID NO:423) of a native sequence PRO938 cDNA, wherein SEQ ID NO:423 is a clone designated herein as "DNA56433-1406".

[0450] FIG. 424 shows the amino acid sequence (SEQ ID NO:424) derived from the coding sequence of SEQ ID NO:423 shown in FIG. 423.

[0451] FIG. 425 shows a nucleotide sequence (SEQ ID NO:425) of a native sequence PRO1012 cDNA, wherein SEQ ID NO:425 is a clone designated herein as "DNA56439-1376".

[0452] FIG. 426 shows the amino acid sequence (SEQ ID NO:426) derived from the coding sequence of SEQ ID NO:425 shown in FIG. 425.

[0453] FIG. 427 shows a nucleotide sequence (SEQ ID NO:427) of a native sequence PRO1008 cDNA, wherein SEQ ID NO:427 is a clone designated herein as "DNA57530-1375".

[0454] FIG. 428 shows the amino acid sequence (SEQ ID NO:428) derived from the coding sequence of SEQ ID NO:427 shown in FIG. 427.

[0455] FIG. 429 shows a nucleotide sequence (SEQ ID NO:429) of a native sequence PRO1075 cDNA, wherein SEQ ID NO:429 is a clone designated herein as "DNA57689-1385".

[0456] FIG. 430 shows the amino acid sequence (SEQ ID NO:430) derived from the coding sequence of SEQ ID NO:429 shown in FIG. 429.

[0457] FIG. 431 shows a nucleotide sequence (SEQ ID NO:431) of a native sequence PRO1007 cDNA, wherein SEQ ID NO:431 is a clone designated herein as "DNA57690-1374".

[0458] FIG. 432 shows the amino acid sequence (SEQ ID NO:432) derived from the coding sequence of SEQ ID NO:431 shown in FIG. 431.

[0459] FIG. 433 shows a nucleotide sequence (SEQ ID NO:433) of a native sequence PRO1056 cDNA, wherein SEQ ID NO:433 is a clone designated herein as "DNA57693-1424".

[0460] FIG. 434 shows the amino acid sequence (SEQ ID NO:434) derived from the coding sequence of SEQ ID NO:433 shown in FIG. 433.

[0461] FIG. 435 shows a nucleotide sequence (SEQ ID NO:435) of a native sequence PRO791 cDNA, wherein SEQ ID NO:435 is a clone designated herein as "DNA57838-1337".

[0462] FIG. 436 shows the amino acid sequence (SEQ ID NO:436) derived from the coding sequence of SEQ ID NO:435 shown in FIG. 435.

[0463] FIG. 437 shows a nucleotide sequence (SEQ ID NO:437) of a native sequence PRO1111 cDNA, wherein SEQ ID NO:437 is a clone designated herein as "DNA58721-1475".

[0464] FIG. 438 shows the amino acid sequence (SEQ ID NO:438) derived from the coding sequence of SEQ ID NO:437 shown in FIG. 437.

[0465] FIG. 439 shows a nucleotide sequence (SEQ ID NO:439) of a native sequence PRO812 cDNA, wherein SEQ ID NO:439 is a clone designated herein as "DNA59205-1421".

[0466] FIG. 440 shows the amino acid sequence (SEQ ID NO:440) derived from the coding sequence of SEQ ID NO:439 shown in FIG. 439.

[0467] FIG. 441 shows a nucleotide sequence (SEQ ID NO:441) of a native sequence PRO1066 cDNA, wherein SEQ ID NO:441 is a clone designated herein as "DNA59215-1425".

[0468] FIG. 442 shows the amino acid sequence (SEQ ID NO:442) derived from the coding sequence of SEQ ID NO:441 shown in FIG. 441.

[0469] FIG. 443 shows a nucleotide sequence (SEQ ID NO:443) of a native sequence PRO1185 cDNA, wherein SEQ ID NO:443 is a clone designated herein as "DNA59220-1514".

[0470] FIG. 444 shows the amino acid sequence (SEQ ID NO:444) derived from the coding sequence of SEQ ID NO:443 shown in FIG. 443.

[0471] FIG. 445 shows a nucleotide sequence (SEQ ID NO:445) of a native sequence PRO1031 cDNA, wherein SEQ ID NO:445 is a clone designated herein as "DNA59294-1381".

[0472] FIG. 446 shows the amino acid sequence (SEQ ID NO:446) derived from the coding sequence of SEQ ID NO:445 shown in FIG. 445.

[0473] FIG. 447 shows a nucleotide sequence (SEQ ID NO:447) of a native sequence PRO1360 cDNA, wherein SEQ ID NO:447 is a clone designated herein as "DNA59488-1603".

[0474] FIG. 448 shows the amino acid sequence (SEQ ID NO:448) derived from the coding sequence of SEQ ID NO:447 shown in FIG. 447.

[0475] FIG. 449 shows a nucleotide sequence (SEQ ID NO:449) of a native sequence PRO1309 cDNA, wherein SEQ ID NO:449 is a clone designated herein as "DNA59588-1571".

[0476] FIG. 450 shows the amino acid sequence (SEQ ID NO:450) derived from the coding sequence of SEQ ID NO:449 shown in FIG. 449.

[0477] FIG. 451 shows a nucleotide sequence (SEQ ID NO:451) of a native sequence PRO1107 cDNA, wherein SEQ ID NO:451 is a clone designated herein as "DNA59606-1471".

[0478] FIG. 452 shows the amino acid sequence (SEQ ID NO:452) derived from the coding sequence of SEQ ID NO:451 shown in FIG. 451.

[0479] FIG. 453 shows a nucleotide sequence (SEQ ID NO:453) of a native sequence PRO836 cDNA, wherein SEQ ID NO:453 is a clone designated herein as "DNA59620-1463".

[0480] FIG. 454 shows the amino acid sequence (SEQ ID NO:454) derived from the coding sequence of SEQ ID NO:453 shown in FIG. 453.

[0481] FIG. 455 shows a nucleotide sequence (SEQ ID NO:455) of a native sequence PRO1132 cDNA, wherein SEQ ID NO:455 is a clone designated herein as "DNA59767-1489".

[0482] FIG. 456 shows the amino acid sequence (SEQ ID NO:456) derived from the coding sequence of SEQ ID NO:455 shown in FIG. 455.

[0483] FIG. 457 shows a nucleotide sequence (SEQ ID NO:457) of a native sequence PRO1131 cDNA, wherein SEQ ID NO:457 is a clone designated herein as "DNA59777-1480".

[0484] FIG. 458 shows the amino acid sequence (SEQ ID NO:458) derived from the coding sequence of SEQ ID NO:457 shown in FIG. 457.

[0485] FIG. 459 shows a nucleotide sequence (SEQ ID NO:459) of a native sequence PRO1130 cDNA, wherein SEQ ID NO:459 is a clone designated herein as "DNA59814-1486".

[0486] FIG. 460 shows the amino acid sequence (SEQ ID NO:460) derived from the coding sequence of SEQ ID NO:459 shown in FIG. 459.

[0487] FIG. 461 shows a nucleotide sequence (SEQ ID NO:461) of a native sequence PRO844 cDNA, wherein SEQ ID NO:461 is a clone designated herein as "DNA59839-1461".

[0488] FIG. 462 shows the amino acid sequence (SEQ ID NO:462) derived from the coding sequence of SEQ ID NO:461 shown in FIG. 461.

[0489] FIG. 463 shows a nucleotide sequence (SEQ ID NO:463) of a native sequence PRO1154 cDNA, wherein SEQ ID NO:463 is a clone designated herein as "DNA59846-1503".

[0490] FIG. 464 shows the amino acid sequence (SEQ ID NO:464) derived from the coding sequence of SEQ ID NO:463 shown in FIG. 463.

[0491] FIG. 465 shows a nucleotide sequence (SEQ ID NO:465) of a native sequence PRO1181 cDNA, wherein SEQ ID NO:465 is a clone designated herein as "DNA59847-1511".

[0492] FIG. 466 shows the amino acid sequence (SEQ ID NO:466) derived from the coding sequence of SEQ ID NO:465 shown in FIG. 465.

[0493] FIG. 467 shows a nucleotide sequence (SEQ ID NO:467) of a native sequence PRO1126 cDNA, wherein SEQ ID NO:467 is a clone designated herein as "DNA60615-1483".

[0494] FIG. 468 shows the amino acid sequence (SEQ ID NO:468) derived from the coding sequence of SEQ ID NO:467 shown in FIG. 467.

[0495] FIG. 469 shows a nucleotide sequence (SEQ ID NO:469) of a native sequence PRO1186 cDNA, wherein SEQ ID NO:469 is a clone designated herein as "DNA60621-1516".

[0496] FIG. 470 shows the amino acid sequence (SEQ ID NO:470) derived from the coding sequence of SEQ ID NO:469 shown in FIG. 469.

[0497] FIG. 471 shows a nucleotide sequence (SEQ ID NO:471) of a native sequence PRO1198 cDNA, wherein SEQ ID NO:471 is a clone designated herein as "DNA60622-1525".

[0498] FIG. 472 shows the amino acid sequence (SEQ ID NO:472) derived from the coding sequence of SEQ ID NO:471 shown in FIG. 471.

[0499] FIG. 473 shows a nucleotide sequence (SEQ ID NO:473) of a native sequence PRO1159 cDNA, wherein SEQ ID NO:473 is a clone designated herein as "DNA60627-1508".

[0500] FIG. 474 shows the amino acid sequence (SEQ ID NO:474) derived from the coding sequence of SEQ ID NO:473 shown in FIG. 473.

[0501] FIG. 475 shows a nucleotide sequence (SEQ ID NO:475) of a native sequence PRO1265 cDNA, wherein SEQ ID NO:475 is a clone designated herein as "DNA60764-1533".

[0502] FIG. 476 shows the amino acid sequence (SEQ ID NO:476) derived from the coding sequence of SEQ ID NO:475 shown in FIG. 475.

[0503] FIG. 477 shows a nucleotide sequence (SEQ ID NO:477) of a native sequence PRO1250 cDNA, wherein SEQ ID NO:477 is a clone designated herein as "DNA60775-1532".

[0504] FIG. 478 shows the amino acid sequence (SEQ ID NO:478) derived from the coding sequence of SEQ ID NO:477 shown in FIG. 477.

[0505] FIG. 479 shows a nucleotide sequence (SEQ ID NO:479) of a native sequence PRO1475 cDNA, wherein SEQ ID NO:479 is a clone designated herein as "DNA61185-1646".

[0506] FIG. 480 shows the amino acid sequence (SEQ ID NO:480) derived from the coding sequence of SEQ ID NO:479 shown in FIG. 479.

[0507] FIG. 481 shows a nucleotide sequence (SEQ ID NO:481) of a native sequence PRO1312 cDNA, wherein SEQ ID NO:481 is a clone designated herein as "DNA61873-1574".

[0508] FIG. 482 shows the amino acid sequence (SEQ ID NO:482) derived from the coding sequence of SEQ ID NO:481 shown in FIG. 481.

[0509] FIG. 483 shows a nucleotide sequence (SEQ ID NO:483) of a native sequence PRO1308 cDNA, wherein SEQ ID NO:483 is a clone designated herein as "DNA62306-1570".

[0510] FIG. 484 shows the amino acid sequence (SEQ ID NO:484) derived from the coding sequence of SEQ ID NO:483 shown in FIG. 483.

[0511] **FIG. 485** shows a nucleotide sequence (SEQ ID NO:485) of a native sequence PRO1326 cDNA, wherein SEQ ID NO:485 is a clone designated herein as "DNA62808-1582".

[0512] **FIG. 486** shows the amino acid sequence (SEQ ID NO:486) derived from the coding sequence of SEQ ID NO:485 shown in **FIG. 485**.

[0513] **FIG. 487** shows a nucleotide sequence (SEQ ID NO:487) of a native sequence PRO1192 cDNA, wherein SEQ ID NO:487 is a clone designated herein as "DNA62814-1521".

[0514] **FIG. 488** shows the amino acid sequence (SEQ ID NO:488) derived from the coding sequence of SEQ ID NO:487 shown in **FIG. 487**.

[0515] **FIG. 489** shows a nucleotide sequence (SEQ ID NO:489) of a native sequence PRO1246 cDNA, wherein SEQ ID NO:489 is a clone designated herein as "DNA64885-1529".

[0516] **FIG. 490** shows the amino acid sequence (SEQ ID NO:490) derived from the coding sequence of SEQ ID NO:489 shown in **FIG. 489**.

[0517] **FIG. 491** shows a nucleotide sequence (SEQ ID NO:491) of a native sequence PRO1356 cDNA, wherein SEQ ID NO:491 is a clone designated herein as "DNA64886-1601".

[0518] **FIG. 492** shows the amino acid sequence (SEQ ID NO:492) derived from the coding sequence of SEQ ID NO:491 shown in **FIG. 491**.

[0519] **FIG. 493** shows a nucleotide sequence (SEQ ID NO:493) of a native sequence PRO1275 cDNA, wherein SEQ ID NO:493 is a clone designated herein as "DNA64888-1542".

[0520] **FIG. 494** shows the amino acid sequence (SEQ ID NO:494) derived from the coding sequence of SEQ ID NO:493 shown in **FIG. 493**.

[0521] **FIG. 495** shows a nucleotide sequence (SEQ ID NO:495) of a native sequence PRO1274 cDNA, wherein SEQ ID NO:495 is a clone designated herein as "DNA64889-1541".

[0522] **FIG. 496** shows the amino acid sequence (SEQ ID NO:496) derived from the coding sequence of SEQ ID NO:495 shown in **FIG. 495**.

[0523] **FIG. 497** shows a nucleotide sequence (SEQ ID NO:497) of a native sequence PRO1358 cDNA, wherein SEQ ID NO:497 is a clone designated herein as "DNA64890-1612".

[0524] **FIG. 498** shows the amino acid sequence (SEQ ID NO:498) derived from the coding sequence of SEQ ID NO:497 shown in **FIG. 497**.

[0525] **FIG. 499** shows a nucleotide sequence (SEQ ID NO:499) of a native sequence PRO1286 cDNA, wherein SEQ ID NO:499 is a clone designated herein as "DNA64903-1553".

[0526] **FIG. 500** shows the amino acid sequence (SEQ ID NO:500) derived from the coding sequence of SEQ ID NO:499 shown in **FIG. 499**.

[0527] **FIG. 501** shows a nucleotide sequence (SEQ ID NO:501) of a native sequence PRO1294 cDNA, wherein SEQ ID NO:501 is a clone designated herein as "DNA64905-1558".

[0528] **FIG. 502** shows the amino acid sequence (SEQ ID NO:502) derived from the coding sequence of SEQ ID NO:501 shown in **FIG. 501**.

[0529] **FIG. 503** shows a nucleotide sequence (SEQ ID NO:503) of a native sequence PRO1273 cDNA, wherein SEQ ID NO:503 is a clone designated herein as "DNA65402-1540".

[0530] **FIG. 504** shows the amino acid sequence (SEQ ID NO:504) derived from the coding sequence of SEQ ID NO:503 shown in **FIG. 503**.

[0531] **FIG. 505** shows a nucleotide sequence (SEQ ID NO:505) of a native sequence PRO1279 cDNA, wherein SEQ ID NO:505 is a clone designated herein as "DNA65405-1547".

[0532] **FIG. 506** shows the amino acid sequence (SEQ ID NO:506) derived from the coding sequence of SEQ ID NO:505 shown in **FIG. 505**.

[0533] **FIG. 507** shows a nucleotide sequence (SEQ ID NO:507) of a native sequence PRO1195 cDNA, wherein SEQ ID NO:507 is a clone designated herein as "DNA65412-1523".

[0534] **FIG. 508** shows the amino acid sequence (SEQ ID NO:508) derived from the coding sequence of SEQ ID NO:507 shown in **FIG. 507**.

[0535] **FIG. 509** shows a nucleotide sequence (SEQ ID NO:509) of a native sequence PRO1271 cDNA, wherein SEQ ID NO:509 is a clone designated herein as "DNA66309-1538".

[0536] **FIG. 510** shows the amino acid sequence (SEQ ID NO:510) derived from the coding sequence of SEQ ID NO:509 shown in **FIG. 509**.

[0537] **FIG. 511** shows a nucleotide sequence (SEQ ID NO:511) of a native sequence PRO1338 cDNA, wherein SEQ ID NO:511 is a clone designated herein as "DNA66667-1596".

[0538] **FIG. 512** shows the amino acid sequence (SEQ ID NO:512) derived from the coding sequence of SEQ ID NO:511 shown in **FIG. 511**.

[0539] **FIG. 513** shows a nucleotide sequence (SEQ ID NO:513) of a native sequence PRO1343 cDNA, wherein SEQ ID NO:513 is a clone designated herein as "DNA66675-1587".

[0540] **FIG. 514** shows the amino acid sequence (SEQ ID NO:514) derived from the coding sequence of SEQ ID NO:513 shown in **FIG. 513**.

[0541] **FIG. 515** shows a nucleotide sequence (SEQ ID NO:515) of a native sequence PRO1434 cDNA, wherein SEQ ID NO:515 is a clone designated herein as "DNA68818-2536".

[0542] **FIG. 516** shows the amino acid sequence (SEQ ID NO:516) derived from the coding sequence of SEQ ID NO:515 shown in **FIG. 515**.

[0543] FIG. 517 shows a nucleotide sequence (SEQ ID NO:517) of a native sequence PRO1418 cDNA, wherein SEQ ID NO:517 is a clone designated herein as "DNA68864-1629".

[0544] FIG. 518 shows the amino acid sequence (SEQ ID NO:518) derived from the coding sequence of SEQ ID NO:517 shown in FIG. 517.

[0545] FIG. 519 shows a nucleotide sequence (SEQ ID NO:519) of a native sequence PRO1387 cDNA, wherein SEQ ID NO:519 is a clone designated herein as "DNA68872-1620".

[0546] FIG. 520 shows the amino acid sequence (SEQ ID NO:520) derived from the coding sequence of SEQ ID NO:519 shown in FIG. 519.

[0547] FIG. 521 shows a nucleotide sequence (SEQ ID NO:521) of a native sequence PRO1384 cDNA, wherein SEQ ID NO:521 is a clone designated herein as "DNA71159-1617".

[0548] FIG. 522 shows the amino acid sequence (SEQ ID NO:522) derived from the coding sequence of SEQ ID NO:521 shown in FIG. 521.

[0549] FIG. 523 shows a nucleotide sequence (SEQ ID NO:523) of a native sequence PRO1565 cDNA, wherein SEQ ID NO:523 is a clone designated herein as "DNA73727-1673".

[0550] FIG. 524 shows the amino acid sequence (SEQ ID NO:524) derived from the coding sequence of SEQ ID NO:523 shown in FIG. 523.

[0551] FIG. 525 shows a nucleotide sequence (SEQ ID NO:525) of a native sequence PRO1474 cDNA, wherein SEQ ID NO:525 is a clone designated herein as "DNA73739-1645".

[0552] FIG. 526 shows the amino acid sequence (SEQ ID NO:526) derived from the coding sequence of SEQ ID NO:525 shown in FIG. 525.

[0553] FIG. 527 shows a nucleotide sequence (SEQ ID NO:527) of a native sequence PRO1917 cDNA, wherein SEQ ID NO:527 is a clone designated herein as "DNA76400-2528".

[0554] FIG. 528 shows the amino acid sequence (SEQ ID NO:528) derived from the coding sequence of SEQ ID NO:527 shown in FIG. 527.

[0555] FIG. 529 shows a nucleotide sequence (SEQ ID NO:529) of a native sequence PRO1787 cDNA, wherein SEQ ID NO:529 is a clone designated herein as "DNA76510-2504".

[0556] FIG. 530 shows the amino acid sequence (SEQ ID NO:530) derived from the coding sequence of SEQ ID NO:529 shown in FIG. 529.

[0557] FIG. 531 shows a nucleotide sequence (SEQ ID NO:531) of a native sequence PRO1556 cDNA, wherein SEQ ID NO:531 is a clone designated herein as "DNA76529-1666".

[0558] FIG. 532 shows the amino acid sequence (SEQ ID NO:532) derived from the coding sequence of SEQ ID NO:531 shown in FIG. 531.

[0559] FIG. 533 shows a nucleotide sequence (SEQ ID NO:533) of a native sequence PRO1561 cDNA, wherein SEQ ID NO:533 is a clone designated herein as "DNA76538-1670".

[0560] FIG. 534 shows the amino acid sequence (SEQ ID NO:534) derived from the coding sequence of SEQ ID NO:533 shown in FIG. 533.

[0561] FIG. 535 shows a nucleotide sequence (SEQ ID NO:535) of a native sequence PRO1693 cDNA, wherein SEQ ID NO:535 is a clone designated herein as "DNA77301-1708".

[0562] FIG. 536 shows the amino acid sequence (SEQ ID NO:536) derived from the coding sequence of SEQ ID NO:535 shown in FIG. 535.

[0563] FIG. 537 shows a nucleotide sequence (SEQ ID NO:537) of a native sequence PRO1868 cDNA, wherein SEQ ID NO:537 is a clone designated herein as "DNA77624-2515".

[0564] FIG. 538 shows the amino acid sequence (SEQ ID NO:538) derived from the coding sequence of SEQ ID NO:537 shown in FIG. 537.

[0565] FIG. 539 shows a nucleotide sequence (SEQ ID NO:539) of a native sequence PRO1890 cDNA, wherein SEQ ID NO:539 is a clone designated herein as "DNA79230-2525".

[0566] FIG. 540 shows the amino acid sequence (SEQ ID NO:540) derived from the coding sequence of SEQ ID NO:539 shown in FIG. 539.

[0567] FIG. 541 shows a nucleotide sequence (SEQ ID NO:541) of a native sequence PRO1887 cDNA, wherein SEQ ID NO:541 is a clone designated herein as "DNA79862-2522".

[0568] FIG. 542 shows the amino acid sequence (SEQ ID NO:542) derived from the coding sequence of SEQ ID NO:541 shown in FIG. 541.

[0569] FIG. 543 shows a nucleotide sequence (SEQ ID NO:543) of a native sequence PRO4353 cDNA, wherein SEQ ID NO:543 is a clone designated herein as "DNA80145-2594".

[0570] FIG. 544 shows the amino acid sequence (SEQ ID NO:544) derived from the coding sequence of SEQ ID NO:543 shown in FIG. 543.

[0571] FIG. 545 shows a nucleotide sequence (SEQ ID NO:545) of a native sequence PRO1801 cDNA, wherein SEQ ID NO:545 is a clone designated herein as "DNA83500-2506".

[0572] FIG. 546 shows the amino acid sequence (SEQ ID NO:546) derived from the coding sequence of SEQ ID NO:545 shown in FIG. 545.

[0573] FIG. 547 shows a nucleotide sequence (SEQ ID NO:547) of a native sequence PRO4357 cDNA, wherein SEQ ID NO:547 is a clone designated herein as "DNA84917-2597".

[0574] FIG. 548 shows the amino acid sequence (SEQ ID NO:548) derived from the coding sequence of SEQ ID NO:547 shown in FIG. 547.



[0575] FIG. 549 shows a nucleotide sequence (SEQ ID NO:549) of a native sequence PRO4302 cDNA, wherein SEQ ID NO:549 is a clone designated herein as "DNA92218-2554".

[0576] FIG. 550 shows the amino acid sequence (SEQ ID NO:550) derived from the coding sequence of SEQ ID NO:549 shown in FIG. 549.

#### DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

##### [0577] 1. Definitions

[0578] The terms "PRO polypeptide" and "PRO" as used herein and when immediately followed by a numerical designation refer to various polypeptides, wherein the complete designation (i.e., PRO/number) refers to specific polypeptide sequences as described herein. The terms "PRO/number polypeptide" and "PRO/number" wherein the term "number" is provided as an actual numerical designation as used herein encompass native sequence polypeptides and polypeptide variants (which are further defined herein). The PRO polypeptides described herein may be isolated from a variety of sources, such as from human tissue types or from another source, or prepared by recombinant or synthetic methods. The term "PRO polypeptide" refers to each individual PRO/number polypeptide disclosed herein. All disclosures in this specification which refer to the "PRO polypeptide" refer to each of the polypeptides individually as well as jointly. For example, descriptions of the preparation of, purification of, derivation of, formation of antibodies to or against, administration of, compositions containing, treatment of a disease with, etc., pertain to each polypeptide of the invention individually. The term "PRO polypeptide" also includes variants of the PRO/number polypeptides disclosed herein.

[0579] A "native sequence PRO polypeptide" comprises a polypeptide having the same amino acid sequence as the corresponding PRO polypeptide derived from nature. Such native sequence PRO polypeptides can be isolated from nature or can be produced by recombinant or synthetic means. The term "native sequence PRO polypeptide" specifically encompasses naturally-occurring truncated or secreted forms of the specific PRO polypeptide (e.g., an extracellular domain sequence), naturally-occurring variant forms (e.g., alternatively spliced forms) and naturally-occurring allelic variants of the polypeptide. In various embodiments of the invention, the native sequence PRO polypeptides disclosed herein are mature or full-length native sequence polypeptides comprising the full-length amino acid sequences shown in the accompanying figures. Start and stop codons are shown in bold font and underlined in the figures. However, while the PRO polypeptide disclosed in the accompanying figures are shown to begin with methionine residues designated herein as amino acid position 1 in the figures, it is conceivable and possible that other methionine residues located either upstream or downstream from the amino acid position 1 in the figures may be employed as the starting amino acid residue for the PRO polypeptides.

[0580] The PRO polypeptide "extracellular domain" or "ECD" refers to a form of the PRO polypeptide which is essentially free of the transmembrane and cytoplasmic domains. Ordinarily, a PRO polypeptide ECD will have less

than 1% of such transmembrane and/or cytoplasmic domains and preferably, will have less than 0.5% of such domains. It will be understood that any transmembrane domains identified for the PRO polypeptides of the present invention are identified pursuant to criteria routinely employed in the art for identifying that type of hydrophobic domain. The exact boundaries of a transmembrane domain may vary but most likely by no more than about 5 amino acids at either end of the domain as initially identified herein. Optionally, therefore, an extracellular domain of a PRO polypeptide may contain from about 5 or fewer amino acids on either side of the transmembrane domain/extracellular domain boundary as identified in the Examples or specification and such polypeptides, with or without the associated signal peptide, and nucleic acid encoding them, are contemplated by the present invention.

[0581] The approximate location of the "signal peptides" of the various PRO polypeptides disclosed herein are shown in the present specification and/or the accompanying figures. It is noted, however, that the C-terminal boundary of a signal peptide may vary, but most likely by no more than about 5 amino acids on either side of the signal peptide C-terminal boundary as initially identified herein, wherein the C-terminal boundary of the signal peptide may be identified pursuant to criteria routinely employed in the art for identifying that type of amino acid sequence element (e.g., Nielsen et al., *Prot. Eng.* 10: 1-6 (1997) and von Heinje et al., *Nucl. Acids. Res.* 14:4683-4690 (1986)). Moreover, it is also recognized that, in some cases, cleavage of a signal sequence from a secreted polypeptide is not entirely uniform, resulting in more than one secreted species. These mature polypeptides, where the signal peptide is cleaved within no more than about 5 amino acids on either side of the C-terminal boundary of the signal peptide as identified herein, and the polynucleotides encoding them, are contemplated by the present invention.

[0582] "PRO polypeptide variant" means an active PRO polypeptide as defined above or below having at least about 80% amino acid sequence identity with a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Such PRO polypeptide variants include, for instance, PRO polypeptides wherein one or more amino acid residues are added, or deleted, at the N- or C-terminus of the full-length native amino acid sequence. Ordinarily, a PRO polypeptide variant will have at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity,

alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, PRO variant polypeptides are at least about 10 amino acids in length, alternatively at least about 20 amino acids in length, alternatively at least about 30 amino acids in length, alternatively at least about 40 amino acids in length, alternatively at least about 50 amino acids in length, alternatively at least about 60 amino acids in length, alternatively at least about 70 amino acids in length, alternatively at least about 80 amino acids in length, alternatively at least about 90 amino acids in length, alternatively at least about 100 amino acids in length, alternatively at least about 150 amino acids in length, alternatively at least about 200 amino acids in length, alternatively at least about 300 amino acids in length, or more.

**[0583]** “Percent (%) amino acid sequence identity” with respect to the PRO polypeptide sequences identified herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the specific PRO polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, Calif. or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

**[0584]** In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A

that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

$$100 \text{ times the fraction } X/Y$$

**[0585]** where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program’s alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. As examples of % amino acid sequence identity calculations using this method, Tables 2 and 3 demonstrate how to calculate the % amino acid sequence identity of the amino acid sequence designated “Comparison Protein” to the amino acid sequence designated “PRO”, wherein “PRO” represents the amino acid sequence of a hypothetical PRO polypeptide of interest, “Comparison Protein” represents the amino acid sequence of a polypeptide against which the “PRO” polypeptide of interest is being compared, and “X,” “Y” and “Z” each represent different hypothetical amino acid residues.

**[0586]** Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % amino acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., *Methods in Enzymology* 266:460480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span=1, overlap fraction=0.125, word threshold (T)=11, and scoring matrix=BLOSUM62. When WU-BLAST-2 is employed, a % amino acid sequence identity value is determined by dividing (a) the number of matching identical amino acid residues between the amino acid sequence of the PRO polypeptide of interest having a sequence derived from the native PRO polypeptide and the comparison amino acid sequence of interest (i.e., the sequence against which the PRO polypeptide of interest is being compared which may be a PRO variant polypeptide) as determined by WU-BLAST-2 by (b) the total number of amino acid residues of the PRO polypeptide of interest. For example, in the statement “a polypeptide comprising an the amino acid sequence A which has or having at least 80% amino acid sequence identity to the amino acid sequence B”, the amino acid sequence A is the comparison amino acid sequence of interest and the amino acid sequence B is the amino acid sequence of the PRO polypeptide of interest.

**[0587]** Percent amino acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., *Nucleic Acids Res.* 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov> or otherwise obtained from the National Institute of Health, Bethesda, Md. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask=yes, strand=all, expected occurrences=10, minimum low complexity

length=15/5, multi-pass e-value=0.01, constant for multi-pass=25, dropoff for final gapped alignment=25 and scoring matrix=BLOSUM62.

**[0588]** In situations where NCBI-BLAST2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

100 times the fraction  $X/Y$

**[0589]** where X is the number of amino acid residues scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A.

**[0590]** "PRO variant polynucleotide" or "PRO variant nucleic acid sequence" means a nucleic acid molecule which encodes an active PRO polypeptide as defined below and which has at least about 80% nucleic acid sequence identity with a nucleotide acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, a PRO variant polynucleotide will have at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity with a nucleic acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal sequence, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Variants do not encompass the native nucleotide sequence.

**[0591]** Ordinarily, PRO variant polynucleotides are at least about 30 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 120 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 210 nucleotides in length, alternatively at least about 240 nucleotides in length, alternatively at least about 270 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 900 nucleotides in length, or more.

**[0592]** "Percent (%) nucleic acid sequence identity" with respect to PRO-encoding nucleic acid sequences identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the PRO nucleic acid sequence of interest, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. For purposes herein, however, % nucleic acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, Calif. or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

**[0593]** In situations where ALIGN-2 is employed for nucleic acid sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

100 times the fraction  $W/Z$

**[0594]** where W is the number of nucleotides scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C. As examples of % nucleic acid sequence identity calculations, Tables 4 and 5, demonstrate how to calculate the % nucleic acid sequence identity of the nucleic acid sequence designated "Comparison DNA" to the nucleic acid sequence designated "PRO-DNA", wherein "PRO-DNA" represents a hypothetical

PRO-encoding nucleic acid sequence of interest, "Comparison DNA" represents the nucleotide sequence of a nucleic acid molecule against which the "PRO-DNA" nucleic acid molecule of interest is being compared, and "N", "L" and "V" each represent different hypothetical nucleotides.

**[0595]** Unless specifically stated otherwise, all % nucleic acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % nucleic acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., *Methods in Enzymology* 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span=1, overlap fraction=0.125, word threshold (T)=11, and scoring matrix=BLOSUM62. When WU-BLAST-2 is employed, a % nucleic acid sequence identity value is determined by dividing (a) the number of matching identical nucleotides between the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest having a sequence derived from the native sequence PRO polypeptide-encoding nucleic acid and the comparison nucleic acid molecule of interest (i.e., the sequence against which the PRO polypeptide-encoding nucleic acid molecule of interest is being compared which may be a variant PRO polynucleotide) as determined by WU-BLAST-2 by (b) the total number of nucleotides of the PRO polypeptide-encoding nucleic acid molecule of interest. For example, in the statement "an isolated nucleic acid molecule comprising a nucleic acid sequence A which has or having at least 80% nucleic acid sequence identity to the nucleic acid sequence B", the nucleic acid sequence A is the comparison nucleic acid molecule of interest and the nucleic acid sequence B is the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest.

**[0596]** Percent nucleic acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., *Nucleic Acids Res.* 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov> or otherwise obtained from the National Institute of Health, Bethesda, Md. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask=yes, strand=all, expected occurrences=10, minimum low complexity length=15/5, multi-pass e-value=0.01, constant for multi-pass=25, dropoff for final gapped alignment=25 and scoring matrix=BLOSUM62.

**[0597]** In situations where NCBI-BLAST2 is employed for sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

$$100 \text{ times the fraction } W/Z$$

**[0598]** where W is the number of nucleotides scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be

appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C.

**[0599]** In other embodiments, PRO variant polynucleotides are nucleic acid molecules that encode an active PRO polypeptide and which are capable of hybridizing, preferably under stringent hybridization and wash conditions, to nucleotide sequences encoding a full-length PRO polypeptide as disclosed herein. PRO variant polypeptides may be those that are encoded by a PRO variant polynucleotide.

**[0600]** "Isolated," when used to describe the various polypeptides disclosed herein, means polypeptide that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Isolated polypeptide includes polypeptide in situ within recombinant cells, since at least one component of the PRO polypeptide natural environment will not be present. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step.

**[0601]** An "isolated" PRO polypeptide-encoding nucleic acid or other polypeptide-encoding nucleic acid is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the polypeptide-encoding nucleic acid. An isolated polypeptide-encoding nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated polypeptide-encoding nucleic acid molecules therefore are distinguished from the specific polypeptide-encoding nucleic acid molecule as it exists in natural cells. However, an isolated polypeptide-encoding nucleic acid molecule includes polypeptide-encoding nucleic acid molecules contained in cells that ordinarily express the polypeptide where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

**[0602]** The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

**[0603]** Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA

sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

**[0604]** The term “antibody” is used in the broadest sense and specifically covers, for example, single anti-PRO monoclonal antibodies (including agonist, antagonist, and neutralizing antibodies), anti-PRO antibody compositions with polypeptidic specificity, single chain anti-PRO antibodies, and fragments of anti-PRO antibodies (see below). The term “monoclonal antibody” as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts.

**[0605]** “Stringency” of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured DNA to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative temperature which can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel et al., *Current Protocols in Molecular Biology*, Wiley Interscience Publishers, (1995).

**[0606]** “Stringent conditions” or “high stringency conditions”, as defined herein, may be identified by those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50° C.; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50 mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42° C.; or (3) employ 50% formamide, 5× SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5× Denhardt’s solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42° C., with washes at 42° C. in 0.2× SSC (sodium chloride/sodium citrate) and 50% formamide at 55° C., followed by a high-stringency wash consisting of 0.1× SSC containing EDTA at 55° C.

**[0607]** “Moderately stringent conditions” may be identified as described by Sambrook et al., *Molecular Cloning: A Laboratory Manual*, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and %SDS) less stringent than those described above. An example of moderately stringent conditions is overnight incubation at 37° C. in a solution comprising: 20% formamide, 5× SSC (150 mM NaCl, 15 mM trisodium citrate), 50

mM sodium phosphate (pH 7.6), 5× Denhardt’s solution, 10% dextran sulfate, and 20 mg/ml denatured sheared salmon sperm DNA, followed by washing the filters in 1× SSC at about 37-50° C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

**[0608]** The term “epitope tagged” when used herein refers to a chimeric polypeptide comprising a PRO polypeptide fused to a “tag polypeptide”. The tag polypeptide has enough residues to provide an epitope against which an antibody can be made, yet is short enough such that it does not interfere with activity of the polypeptide to which it is fused. The tag polypeptide preferably also is fairly unique so that the antibody does not substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 and 50 amino acid residues (preferably, between about 10 and 20 amino acid residues).

**[0609]** As used herein, the term “immunoadhesin” designates antibody-like molecules which combine the binding specificity of a heterologous protein (an “adhesin”) with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesins comprise a fusion of an amino acid sequence with the desired binding specificity which is other than the antigen recognition and binding site of an antibody (i.e., is “heterologous”), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin molecule typically is a contiguous amino acid sequence comprising at least the binding site of a receptor or a ligand. The immunoglobulin constant domain sequence in the immunoadhesin may be obtained from any immunoglobulin, such as IgG-1, IgG-2, IgG-3, or IgG-4 subtypes, IgA (including IgA-1 and IgA-2), IgE, IgD or IgM.

**[0610]** “Active” or “activity” for the purposes herein refers to form(s) of a PRO polypeptide which retain a biological and/or an immunological activity of native or naturally-occurring PRO, wherein “biological” activity refers to a biological function (either inhibitory or stimulatory) caused by a native or naturally-occurring PRO other than the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO and an “immunological” activity refers to the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO.

**[0611]** The term “antagonist” is used in the broadest sense, and includes any molecule that partially or fully blocks, inhibits, or neutralizes a biological activity of a native PRO polypeptide disclosed herein. In a similar manner, the term “agonist” is used in the broadest sense and includes any molecule that mimics a biological activity of a native PRO polypeptide disclosed herein. Suitable agonist or antagonist molecules specifically include agonist or antagonist antibodies or antibody fragments, fragments or amino acid sequence variants of native PRO polypeptides, peptides, antisense oligonucleotides, small organic molecules, etc. Methods for identifying agonists or antagonists of a PRO polypeptide may comprise contacting a PRO polypeptide with a candidate agonist or antagonist molecule and measuring a detectable change in one or more biological activities normally associated with the PRO polypeptide.

[0612] "Treatment" refers to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) the targeted pathologic condition or disorder. Those in need of treatment include those already with the disorder as well as those prone to have the disorder or those in whom the disorder is to be prevented.

[0613] "Chronic" administration refers to administration of the agent(s) in a continuous mode as opposed to an acute mode, so as to maintain the initial therapeutic effect (activity) for an extended period of time. "Intermittent" administration is treatment that is not consecutively done without interruption, but rather is cyclic in nature.

[0614] "Mammal" for purposes of treatment refers to any animal classified as a mammal, including humans, domestic and farm animals, and zoo, sports, or pet animals, such as dogs, cats, cattle, horses, sheep, pigs, goats, rabbits, etc. Preferably, the mammal is human.

[0615] Administration "in combination with" one or more further therapeutic agents includes simultaneous (concurrent) and consecutive administration in any order.

[0616] "Carriers" as used herein include pharmaceutically acceptable carriers, excipients, or stabilizers which are non-toxic to the cell or mammal being exposed thereto at the dosages and concentrations employed. Often the physiologically acceptable carrier is an aqueous pH buffered solution. Examples of physiologically acceptable carriers include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptide; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN<sup>TM</sup>, polyethylene glycol (PEG), and PLURONICS<sup>TM</sup>.

[0617] "Antibody fragments" comprise a portion of an intact antibody, preferably the antigen binding or variable region of the intact antibody. Examples of antibody fragments include Fab, Fab', F(ab')<sub>2</sub>, and Fv fragments; diabodies; linear antibodies (Zapata et al., *Protein Eng.* 8(10): 1057-1062 [1995]); single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

[0618] Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, a designation reflecting the ability to crystallize readily. Pepsin treatment yields an F(ab)<sub>2</sub> fragment that has two antigen-combining sites and is still capable of cross-linking antigen.

[0619] "Fv" is the minimum antibody fragment which contains a complete antigen-recognition and -binding site. This region consists of a dimer of one heavy- and one light-chain variable domain in tight, non-covalent association. It is in this configuration that the three CDRs of each variable domain interact to define an antigen-binding site on the surface of the V<sub>H</sub>-V<sub>L</sub> dimer. Collectively, the six CDRs confer antigen-binding specificity to the antibody. However,

even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

[0620] The Fab fragment also contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab fragments differ from Fab' fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. F(ab'), antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

[0621] The "light chains" of antibodies (immunoglobulins) from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains.

[0622] Depending on the amino acid sequence of the constant domain of their heavy chains, immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into subclasses (isotypes), e.g., IgG1, IgG2, IgG3, IgG4, IgA, and IgA2.

[0623] "Single-chain Fv" or "sFv" antibody fragments comprise the V<sub>H</sub> and V<sub>L</sub> domains of antibody, wherein these domains are present in a single polypeptide chain. Preferably, the Fv polypeptide further comprises a polypeptide linker between the V<sub>H</sub> and V<sub>L</sub> domains which enables the sFv to form the desired structure for antigen binding. For a review of sFv, see Pluckthun in *The Pharmacology of Monoclonal Antibodies*, vol. 113, Rosenberg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994).

[0624] The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a heavy-chain variable domain (V<sub>H</sub>) connected to a light-chain variable domain (V<sub>L</sub>) in the same polypeptide chain (V<sub>H</sub>-V<sub>L</sub>). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger et al., *Proc. Natl. Acad. Sci. USA*, 90:6444-6448 (1993).

[0625] An "isolated" antibody is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody will be purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the

antibody in situ within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

[0626] An antibody that “specifically binds to” or is “specific for” a particular polypeptide or an epitope on a particular polypeptide is one that binds to that particular polypeptide or epitope on a particular polypeptide without substantially binding to any other polypeptide or polypeptide epitope.

[0627] The word “label” when used herein refers to a detectable compound or composition which is conjugated directly or indirectly to the antibody so as to generate a “labeled” antibody. The label may be detectable by itself (e.g. radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, may catalyze chemical alteration of a substrate compound or composition which is detectable.

[0628] By “solid phase” is meant a non-aqueous matrix to which the antibody of the present invention can adhere. Examples of solid phases encompassed herein include those formed partially or entirely of glass (e.g., controlled pore glass), polysaccharides (e.g., agarose), polyacrylamides,

polystyrene, polyvinyl alcohol and silicones. In certain embodiments, depending on the context, the solid phase can comprise the well of an assay plate; in others it is a purification column (e.g., an affinity chromatography column). This term also includes a discontinuous solid phase of discrete particles, such as those described in U.S. Pat. No. 4,275,149.

[0629] A “liposome” is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug (such as a PRO polypeptide or antibody thereto) to a mammal. The components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of biological membranes.

[0630] A “small molecule” is defined herein to have a molecular weight below about 500 Daltons.

[0631] An “effective amount” of a polypeptide disclosed herein or an agonist or antagonist thereof is an amount sufficient to carry out a specifically stated purpose. An “effective amount” may be determined empirically and in a routine manner, in relation to the stated purpose.

TABLE 1

/*	
*	
* C—C increased from 12 to 15	
* Z is average of EQ	
* B is average of ND	
* match with stop is _M; stop—stop = 0; J (joker) match = 0	
*/	
#define	_M -8 /* value of a match with a stop */
int	_day[26][26] = {
/*	A B C D E F G H I J K L M N O P Q R S T U V W X Y Z */
/* A */	{2, 0, -2, 0, 0, -4, 1, -1, -1, 0, -1, -2, -1, 0, _M, 1, 0, -2, 1, 1, 0, 0, -6, 0, -3, 0},
/* B */	{0, 3, -4, 3, 2, -5, 0, 1, -2, 0, 0, -3, -2, 2, _M, -1, 1, 0, 0, 0, 0, -2, -5, 0, -3, 1},
/* C */	{-2, -4, 15, -5, -5, -4, -3, -3, -2, 0, -5, -6, -5, -4, _M, -3, -5, -4, 0, -2, 0, -2, -8, 0, 0, -5},
/* D */	{0, 3, -5, 4, 3, -6, 1, 1, -2, 0, 0, -4, -3, 2, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 2},
/* E */	{0, 2, -5, 3, 4, -5, 0, 1, -2, 0, 0, -3, -2, 1, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 3},
/* F */	{-4, -5, -4, -6, -5, 9, -5, -2, 1, 0, -5, 2, 0, -4, _M, -5, -5, -4, -3, -3, 0, -1, 0, 0, 7, -5},
/* G */	{1, 0, -3, 1, 0, -5, 5, -2, -3, 0, -2, -4, -3, 0, _M, -1, -1, -3, 1, 0, 0, -1, -7, 0, -5, 0},
/* H */	{-1, 1, -3, 1, 1, -2, -2, 6, -2, 0, 0, -2, -2, 2, _M, 0, 3, 2, -1, -1, 0, -2, -3, 0, 0, 2},
/* I */	{-1, -2, -2, -2, -2, 1, -3, -2, 5, 0, -2, 2, 2, -2, _M, -2, -2, -2, -1, 0, 0, 4, -5, 0, -1, -2},
/* J */	{0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* K */	{-1, 0, -5, 0, 0, -5, -2, 0, -2, 0, 5, -3, 0, 1, _M, -1, 1, 3, 0, 0, 0, -2, -3, 0, -4, 0},
/* L */	{-2, -3, -6, -4, -3, 2, -4, -2, 2, 0, -3, 6, 4, -3, _M, -3, -2, -3, -3, -1, 0, 2, -2, 0, -1, -2}
/* M */	{-1, -2, -5, -3, -2, 0, -3, -2, 2, 0, 0, 4, 6, -2, _M, -2, -1, 0, -2, -1, 0, 2, -4, 0, -2, -1},
/* N */	{0, 2, -4, 2, 1, -4, 0, 2, -2, 0, 1, -3, -2, 2, _M, -1, 1, 0, 1, 0, 0, -2, -4, 0, -2, 1},
/* O */	{_M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, 0, _M, _M, _M, _M, _M, _M, _M, _M, _M},
/* P */	{1, -1, -3, -1, -1, -5, -1, 0, -2, 0, -1, -3, -2, -1, _M, 6, 0, 0, 1, 0, 0, -1, -6, 0, -5, 0},
/* Q */	{0, 1, -5, 2, 2, -5, -1, 3, -2, 0, 1, -2, -1, 1, _M, 0, 4, 1, -1, -1, 0, -2, -5, 0, -4, 3},
/* R */	{-2, 0, -4, -1, -1, -4, -3, 2, -2, 0, 3, -3, 0, 0, _M, 0, 1, 6, 0, -1, 0, -2, 2, 0, -4, 0},
/* S */	{1, 0, 0, 0, 0, -3, 1, -1, -1, 0, 0, -3, -2, 1, _M, 1, -1, 0, 2, 1, 0, -1, -2, 0, -3, 0},
/* T */	{1, 0, -2, 0, 0, -3, 0, -1, 0, 0, 0, -1, -1, 0, _M, 0, -1, -1, 1, 3, 0, 0, -5, 0, -3, 0},
/* U */	{0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* V */	{0, -2, -2, -2, -2, -1, -1, -2, 4, 0, -2, 2, 2, -2, _M, -1, -2, -2, -1, 0, 0, 4, -6, 0, -2, -2},
/* W */	{-6, -5, -8, -7, -7, 0, -7, -3, -5, 0, -3, -2, -4, -4, _M, -6, -5, 2, -2, -5, 0, -6, 17, 0, 0, -6},
/* X */	{0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* Y */	{-3, -3, 0, -4, -4, 7, -5, 0, -1, 0, -4, -1, -2, -2, _M, -5, -4, -4, -3, -3, 0, -2, 0, 0, 10, -4},
/* Z */	{0, 1, -5, 2, 3, -5, 0, 2, -2, 0, 0, -2, -1, 1, _M, 0, 3, 0, 0, 0, 0, -2, -6, 0, -4, 4},
};	
/*	
*/	
#include	<stdio.h>
#include	<ctype.h>
#define	MAXJMP 16 /* max jumps in a diag */
#define	MAXGAP 24 /* don't continue to penalize gaps larger than this */
#define	JMPS 1024 /* max jmps in an path */
#define	MX 4 /* save if there's at least MX-1 bases since last jmp */
#define	DMAT 3 /* value of matching bases */

TABLE 1-continued

```
#define DMIS      0 /* penalty for mismatched bases */
#define DINS0     8 /* penalty for a gap */
#define DINS1     1 /* penalty per base */
#define PINS0     8 /* penalty for a gap */
#define PINS1     4 /* penalty per residue */
struct jmp {
    short      n[MAXJMP]; /* size of jmp (neg for dely) */
    unsigned short x[MAXJMP]; /* base no. of jmp in seq x */
                                /* limits seq to 2^16 -1 */
};
struct diag {
    int      score; /* score at last jmp */
    long     offset; /* offset of prev block */
    short    ijmp; /* current jmp index */
    struct jmp jp; /* list of jmps */
};
struct path {
    int      spc; /* number of leading spaces */
    short    n[JMPs]; /* size of jmp (gap) */
    int      x[JMPs]; /* loc of jmp (last elem before gap) */
};
char      *ofile; /* output file name */
char      *namex[2]; /* seq names: getseqs() */
char      *prog; /* prog name for err msgs */
char      *seqx[2]; /* seqs: getseqs() */
int      dmax; /* best diag: nw() */
int      dmax0; /* final diag */
int      dna; /* set if dna: main() */
int      endgaps; /* set if penalizing end gaps */
int      gapx, gapy; /* total gaps in seqs */
int      len0, len1; /* seq lens */
int      ngapx, ngapy; /* total size of gaps */
int      smax; /* max score: nw() */
int      *xbm; /* bitmap for matching */
long     offset; /* current offset in jmp file */
struct diag *dx; /* holds diagonals */
struct path pp[2]; /* holds path for seqs */
char      *calloc(), *malloc(), *index(), *strcpy();
char      *getseq(), *g_calloc();
/* Needleman-Wunsch alignment program
*
* usage: progs file1 file2
* where file1 and file2 are two dna or two protein sequences.
* The sequences can be in upper- or lower-case an may contain ambiguity
* Any lines beginning with ';', '>' or '<' are ignored
* Max file length is 65535 (limited by unsigned short x in the jmp struct)
* A sequence with 1/3 or more of its elements ACGTU is assumed to be DNA
* Output is in the file "align.out"
*
* The program may create a tmp file in /tmp to hold info about traceback.
* Original version developed under BSD 4.3 on a vax 8650
*/
#include "nw.h"
#include "day.h"
static __dbval[26] = {
    1,14,2,13,0,0,4,11,0,0,12,0,3,15,0,0,0,5,6,8,8,7,9,0,10,0
};
static __pbval[26] = {
    1, 2|(1<<('D'-'A'))|(1<<('N'-'A')), 4, 8, 16, 32, 64,
    128, 256, 0xFFFFFFF, 1<<10, 1<<11, 1<<12, 1<<13, 1<<14,
    1<<15, 1<<16, 1<<17, 1<<18, 1<<19, 1<<20, 1<<21, 1<<22,
    1<<23, 1<<24, 1<<25|(1<<('E'-'A'))|(1<<('Q'-'A'))
};
main(ac, av)
int      ac;
char      *av[];
{
    prog = av[0];
    if(ac != 3) {
        fprintf(stderr, "usage: %s file1 file2\n", prog);
        fprintf(stderr, "where file1 and file2 are two dna or two protein sequences.\n");
        fprintf(stderr, "The sequences can be in upper- or lower-case\n");
        fprintf(stderr, "Any lines beginning with ';', '>' or '<' are ignored\n");
        fprintf(stderr, "Output is in the file \"align.out\"\n");
        exit(1);
    }
}
```

main



TABLE 1-continued

---

```

    namex[0] = av[1];
    namex[1] = av[2];
    seqx[0] = getseq(namex[0], &len0);
    seqx[1] = getseq(namex[1], &len1);
    xbm = (dna)? _dbval : _pbval;
    endgaps = 0; /* 1 to penalize endgaps */
    ofile = "align.out"; /* output file */
    nw(); /* fill in the matrix, get the possible jmps */
    readjmps(); /* get the actual jmps */
    print(); /* print stats, alignment */
    cleanup(0); /* unlink any tmp files */
}
/* do the alignment, return best score: main()
* dna: values in Fitch and Smith, PNAS, 80, 1382-1386, 1983
* pro: PAM 250 values
* When scores are equal, we prefer mismatches to any gap, prefer
* a new gap to extending an ongoing gap, and prefer a gap in seqx
* to a gap in seq y.
*/
nw()
{
    char *px, *py; /* seqs and ptrs */
    int *ndely, *dely; /* keep track of dely */
    int ndelx, delx; /* keep track of delx */
    int *tmp; /* for swapping row0, row1 */
    int mis; /* score for each type */
    int ins0, ins1; /* insertion penalties */
    register id; /* diagonal index */
    register ij; /* jmp index */
    register *col0, *col1; /* score for curr, last row */
    register xx, yy; /* index into seqs */
    dx = (struct diag *)g_calloc("to get diags", len0+len1+1, sizeof(struct diag));
    ndely = (int *)g_calloc("to get ndely", len1+1, sizeof(int));
    dely = (int *)g_calloc("to get dely", len1+1, sizeof(int));
    col0 = (int *)g_calloc("to get col0", len1+1, sizeof(int));
    col1 = (int *)g_calloc("to get col1", len1+1, sizeof(int));
    ins0 = (dna)? DINS0 : PINS0;
    ins1 = (dna)? DINS1 : PINS1;
    smax = -10000;
    if (endgaps) {
        for (col0[0] = dely[0] = -ins0, yy = 1; yy <= len1; yy++) {
            col0[yy] = dely[yy] = col0[yy-1] - ins1;
            ndely[yy] = yy;
        }
        col0[0] = 0; /* Waterman Bull Math Biol 84 */
    }
    else
        for (yy = 1; yy <= len1; yy++)
            dely[yy] = -ins0;
    /* fill in match matrix
    */
    for (px = seqx[0], xx = 1; xx <= len0; px++, xx++) {
        /* initialize first entry in col
        */
        if (endgaps) {
            if (xx == 1)
                col1[0] = delx = -(ins0+ins1);
            else
                col1[0] = delx = col0[0]-ins1;
            ndelx = xx;
        }
        else {
            col1[0] = 0;
            delx = -ins0;
            ndelx = 0;
        }
    }

    for (py = seqx[1], yy = 1; yy <= len1; py++, yy++) {
        mis = col0[yy-1];
        if (dna)
            mis += (xbm[*px-'A']&xbm[*py-'A'])? DMAT : DMIS;
        else
            mis += _day[*px-'A'][*py-'A'];
        /* update penalty for del in x seq;
        * favor new del over ongoing del
        * ignore MAXGAP if weighting endgaps

```

TABLE 1-continued

---

```

    /*
    if (endgaps || ndely[yy] < MAXGAP) {
        if (col0[yy] - ins0 >= dely[yy]) {
            dely[yy] = col0[yy] - (ins0+ins1);
            ndely[yy] = 1;
        } else {
            dely[yy] -= ins1;
            ndely[yy]++;
        }
    } else {
        if (col0[yy] - (ins0+ins1) >= dely[yy]) {
            dely[yy] = col0[yy] - (ins0+ins1);
            ndely[yy] = 1;
        } else
            ndely[yy]++;
    }
    /* update penalty for del in y seq;
    * favor new del over ongoing del
    */
    if (endgaps || ndelx < MAXGAP) {
        if (col1[yy-1] - ins0 >= delx) {
            delx = col1[yy-1] - (ins0+ins1);
            ndelx = 1;
        } else {
            delx -= ins1;
            ndelx++;
        }
    } else {
        if (col1[yy-1] - (ins0+ins1) >= delx) {
            delx = col1[yy-1] - (ins0+ins1);
            ndelx = 1;
        } else
            ndelx++;
    }
    /* pick the maximum score; we're favoring
    * mis over any del and delx over dely
    */

    id = xx - yy + len1 - 1;
    if (mis >= delx && mis >= dely[yy])
        col1[yy] = mis;
    else if (delx >= dely[yy]) {
        col1[yy] = delx;
        ij = dx[id].ijmp;
        if (dx[id].jp.n[0] && (!dna || (ndelx >= MAXJMP
        && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
            dx[id].ijmp++;
            if (++ij >= MAXJMP) {
                writeimps(id);
                ij = dx[id].ijmp = 0;
                dx[id].offset = offset;
                offset += sizeof(struct jmp) + sizeof(offset);
            }
        }
        dx[id].jp.n[ij] = ndelx;
        dx[id].jp.x[ij] = xx;
        dx[id].score = delx;
    }
    else {
        col1[yy] = dely[yy];
        ij = dx[id].ijmp;
        if (dx[id].jp.n[0] && (!dna || (ndely[yy] >= MAXJMP
        && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
            dx[id].ijmp++;
            if (++ij >= MAXJMP) {
                writeimps(id);
                ij = dx[id].ijmp = 0;
                dx[id].offset = offset;
                offset += sizeof(struct jmp) + sizeof(offset);
            }
        }
        dx[id].jp.n[ij] = ndely[yy];
        dx[id].jp.x[ij] = xx;
        dx[id].score = dely[yy];
    }
    if (xx == len0 && yy < len1) {

```

...nw

TABLE 1-continued

---

```

        /* last col
        */
        if (endgaps)
            col1[yy] -= ins0+ins1*(len1-yy);
        if (col1[yy] > smax) {
            smax = col1[yy];
            dmax = id;
        }
    }
}
if (endgaps && xx < len0)
    col1[yy-1] -= ins0+ins1*(len0-xx);
if (col1[yy-1] > smax) {
    smax = col1[yy-1];
    dmax = id;
}
tmp = col0; col0 = col1; col1 = tmp;
}
(void) free((char *)ndely);
(void) free((char *)dely);
(void) free((char *)col0);
(void) free((char *)col1);
    }
}

/*
 *
 * print() -- only routine visible outside this module
 *
 * static:
 * getmat() -- trace back best path, count matches: print()
 * pr_align() -- print alignment of described in array p[]; print()
 * dumpblock() -- dump a block of lines with numbers, stars: pr_align()
 * nums() -- put out a number line: dumpblock()
 * putline() -- put out a line (name, [num], seq, [num]): dumpblock()
 * stars() -- put a line of stars: dumpblock()
 * stripname() -- strip any path and prefix from a seqname
 */
#include "nw.h"
#define SPC          3
#define P__LINE      256 /* maximum output line */
#define P__SPC        3 /* space between name or num and seq */
extern      _day[26][26];
int         olen;        /* set output line length */
FILE        *fx;         /* output file */
print()
{
    int         lx, ly, firstgap, lastgap; /* overlap */
    if ((fx = fopen(ofile, "w")) == 0) {
        fprintf(stderr, "%s: can't write %s\n", prog, ofile);
        cleanup(1);
    }
    fprintf(fx, "<first sequence: %s (length = %d)\n", namex[0], len0);
    fprintf(fx, "<second sequence: %s (length = %d)\n", namex[1], len1);
    olen = 60;
    lx = len0;
    ly = len1;
    firstgap = lastgap = 0;
    if (dmax < len1 - 1) { /* leading gap in x */
        pp[0].spc = firstgap = len1 - dmax - 1;
        ly -= pp[0].spc;
    }
    else if (dmax > len1 - 1) { /* leading gap in y */
        pp[1].spc = firstgap = dmax - (len1 - 1);
        lx -= pp[1].spc;
    }
    if (dmax0 < len0 - 1) { /* trailing gap in x */
        lastgap = len0 - dmax0 - 1;
        lx -= lastgap;
    }
    else if (dmax0 > len0 - 1) { /* trailing gap in y */
        lastgap = dmax0 - (len0 - 1);
        ly -= lastgap;
    }
    getmat(lx, ly, firstgap, lastgap);
    pr_align();
}
/*

```

TABLE 1-continued

---

```

* trace back the best path, count matches
*/
static
getmat(lx, ly, firstgap, lastgap)                                     getmat
int      lx, ly;                                           /* "core" (minus endgaps) */
int      firstgap, lastgap;                                /* leading trailing overlap */
{
    int      nm, i0, i1, siz0, siz1;
    char      outx[32];
    double    pct;
    register  n0, n1;
    register char *p0, *p1;
    /* get total matches, score
    */
    i0 = i1 = siz0 = siz1 = 0;
    p0 = seqx[0] + pp[1].spc;
    p1 = seqx[1] + pp[0].spc;
    n0 = pp[1].spc + 1;
    n1 = pp[0].spc + 1;
    nm = 0;
    while ( *p0 && *p1 ) {
        if (siz0) {
            p1++;
            n1++;
            siz0--;
        }
        else if (siz1) {
            p0++;
            n0++;
            siz1--;
        }
        else {
            if (xbm[*p0-'A']&xbm[*p1-'A'])
                nm++;
            if (n0++ == pp[0].x[i0])
                siz0 = pp[0].n[i0++];
            if (n1++ == pp[1].x[i1])
                siz1 = pp[1].n[i1++];
            p0++;
            p1++;
        }
    }
    /* pct homology:
    * if penalizing endgaps, base is the shorter seq
    * else, knock off overhangs and take shorter core
    */
    if (endgaps)
        lx = (len0 < len1)? len0 : len1;
    else
        lx = (lx < ly)? lx : ly;
    pct = 100.*(double)nm/(double)lx;
    fprintf(fx, "\n");
    fprintf(fx, "<%d match%s in an overlap of %d: %.2f percent similarity\n",
        nm, (nm == 1)? "" : "es", lx, pct);
    fprintf(fx, "<gaps in first sequence: %d", gapx);
    if (gapx) {
        (void) sprintf(outx, "(%d %s%s)",
            ngapx, (dna)? "base": "residue", (ngapx == 1)? "" : "s");
        fprintf(fx, "%s", outx);
    }
    fprintf(fx, ", gaps in second sequence: %d", gapy);
    if (gapy) {
        (void) sprintf(outx, "(%d %s%s)",
            ngapy, (dna)? "base": "residue", (ngapy == 1)? "" : "s");
        fprintf(fx, "%s", outx);
    }
    if (dna)
        fprintf(fx,
            "\n<score: %d (match = %d, mismatch = %d, gap penalty = %d + %d per base)\n",
            smax, DMAT, DMIS, DINS0, DINS1);
    else
        fprintf(fx,
            "\n<score: %d (Dayhoff PAM 250 matrix, gap penalty = %d + %d per residue)\n",
            smax, PINS0, PINS1);
    if (endgaps)
        fprintf(fx,
            "<endgaps penalized. left endgap: %d %s%s, right endgap: %d %s%s\n",

```

---

TABLE 1-continued

---

```

    firstgap, (dna)? "base" : "residue", (firstgap == 1)? "" : "s",
    lastgap, (dna)? "base" : "residue", (lastgap == 1)? "" : "s");
else
    fprintf(fx, "<endgaps not penalized\n");
}
static      nm;                /* matches in core -- for checking */
static      lmax;              /* lengths of stripped file names */
static      ij[2];             /* jmp index for a path */
static      nc[2];             /* number at start of current line */
static      ni[2];             /* current elem number -- for gapping */
static      siz[2];
static char  *ps[2];           /* ptr to current element */
static char  *po[2];           /* ptr to next output char slot */
static char  out[P_LINE];      /* output line */
static char  star[P_LINE];     /* set by stars() */
/*
 * print alignment of described in struct path pp[]
 */
static
pr_align()
{
    int      nn;                /* char count */
    int      more;
    register  i;
    for (i = 0, lmax = 0; i < 2; i++) {
        nn = stripname(name[i]);
        if (nn > lmax)
            lmax = nn;
        nc[i] = 1;
        ni[i] = 1;
        siz[i] = ij[i] = 0;
        ps[i] = seqx[i];
        po[i] = out[i];
    }
    for (nn = nm = 0, more = 1; more;) {
        for (i = more = 0; i < 2; i++) {
            /*
             * do we have more of this sequence?
             */
            if (!*ps[i])
                continue;
            more++;
            if (pp[i].spc) { /* leading space */
                *po[i]++ = ' ';
                pp[i].spc--;
            }
            else if (siz[i]) { /* in a gap */
                *po[i]++ = '-';
                siz[i]--;
            }
            else { /* we're putting a seq element
             */
                *po[i] = *ps[i];
                if (islower(*ps[i]))
                    *ps[i] = toupper(*ps[i]);
                po[i]++;
                ps[i]++;
            }
            /*
             * are we at next gap for this seq?
             */
            if (ni[i] == pp[i].x[ij[i]]) {
                /*
                 * we need to merge all gaps
                 * at this location
                 */
                siz[i] = pp[i].n[ij[i]++];
                while (ni[i] == pp[i].x[ij[i]])
                    siz[i] += pp[i].n[ij[i]++];
            }
            ni[i]++;
        }
        if (++nn == olen || !more && nn) {
            dumpblock();
            for (i = 0; i < 2; i++)
                po[i] = out[i];
        }
    }
}

```

pr\_align

...pr\_align

TABLE 1-continued

<pre>        nn = 0;     } } } } /*  * dump a block of lines, including numbers, stars: pr_align()  */ static dumpblock() {     register i;     for(i = 0; i &lt; 2; i++)         *po[i]-- = '\0';      (void) putc('\n', fx);     for (i = 0; i &lt; 2; i++) {         if (*out[i] &amp;&amp; (*out[i] != ' '    *(po[i]) != ' ')) {             if (i == 0)                 nums(i);             if (i == 0 &amp;&amp; *out[1])                 stars();             putline(i);             if (i == 0 &amp;&amp; *out[1])                 fprintf(fx, star);             if (i == 1)                 nums(i);         }     } } /*  * put out a number line: dumpblock()  */ static nums(ix) int    ix;        /* index in out[] holding seq line */ {     char    nline[P_LINE];     register    i, j;     register char    *pn, *px, *py;     for(pn = nline, i = 0; i &lt; lmax+P_SPC; i++, pn++)         *pn = ' ';     for (i = nc[ix], py = out[ix]; *py; py++, pn++) {         if (*py == ' '    *py == '-')             *pn = ' ';         else {             if (i%10 == 0    (i == 1 &amp;&amp; nc[ix] != 1)) {                 j = (i &lt; 0)? -i : i;                 for (px = pn; j /= 10, px--)                     *px = j%10 + '0';                 if (i &lt; 0)                     *px = '-';             }             else                 *pn = ' ';             i++;         }     }     *pn = '\0';     nc[ix] = i;     for (pn = nline; *pn; pn++)         (void) putc(*pn, fx);     (void) putc('\n', fx); } /*  * put out a line (name, [num], seq. [num]): dumpblock()  */ static putline(ix) int    ix; {     int    i;     register char    *px;     for (px = namex[ix], i = 0; *px &amp;&amp; *px != ':'; px++, i++)         (void) putc(*px, fx);     for (i &lt; lmax+P_SPC; i++)         (void) putc(' ', fx); }</pre>	<pre>dumpblock  ...dumpblock  nums  putline  ...putline</pre>
--	---

TABLE 1-continued

<pre>/* these count from 1:  * ni[] is current element (from 1)  * nc[] is number at start of current line  */ for (px = out[ix]; *px; px++)     (void) putc(*px&amp;0x7F, fx); (void) putc('\n', fx); } /*  * put a line of stars (seqs always in out[0], out[1]): dumpblock()  */ static stars()</pre>		stars
<pre>{     int i;     register char *p0, *p1, cx, *px;     if (!*out[0]    (*out[0] == ' ' &amp;&amp; *(p0[0]) == ' ')            !*out[1]    (*out[1] == ' ' &amp;&amp; *(p0[1]) == ' '))         return;     px = star;     for (i = lmax+P_SPC; i; i--)         *px++ = ' ';     for (p0 = out[0], p1 = out[1]; *p0 &amp;&amp; *p1; p0++, p1++) {         if (isalpha(*p0) &amp;&amp; isalpha(*p1)) {             if (xbm[*p0-'A']&amp;xbm[*p1-'A']) {                 cx = '*';                 nm++;             }             else if (!dna &amp;&amp; _day[*p0-'A'][*p1-'A'] &gt; 0)                 cx = '.';             else                 cx = ' ';         }         else             cx = ' ';         *px++ = cx;     }     *px++ = '\n';     *px = '\0'; } /*  * strip path or prefix from pn, return len: pr_align()  */ static stripname(pn)</pre>		stripname
<pre>{     char *pn; /* file name (may be path) */      register char *px, *py;     py = 0;     for (px = pn; *px; px++)         if (*px == '/')             py = px + 1;     if (py)         (void) strcpy(pn, py);     return(strlen(pn)); } /*  * cleanup() -- cleanup any tmp file  * getseq() -- read in seq, set dna, len, maxlen  * g_calloc() -- calloc() with error checkin  * readjimps() -- get the good jimps, from tmp file if necessary  * writejimps() -- write a filled array of jimps to a tmp file: nw()  */ #include "nw.h" #include &lt;sys/file.h&gt; char *jname = "/tmp/homgXXXXXX"; /* tmp file for jimps */ FILE *fj; int cleanup(); /* cleanup tmp file */ long lseek(); /*  * remove any tmp file if we blow  */ cleanup(i)</pre>		cleanup
<pre>{     int i;      if (fj)</pre>		

TABLE 1-continued

<pre>(void) unlink(jname); exit(i); } /*  * read, return ptr to seq, set dna, len, maxlen  * skip lines starting with ';', '&lt;', or '&gt;'  * seq in upper or lower case  */ char * getseq(file, len) char *file;          /* file name */ int *len;             /* seq len */ {     char line[1024], *pseq;     register char *px, *py;     int natgc, tlen;     FILE *fp;     if ((fp = fopen(file, "r")) == 0) {         fprintf(stderr, "%s: can't read %s\n", prog, file);         exit(1);     }     tlen = natgc = 0;     while (fgets(line, 1024, fp)) {         if (*line == ';'    *line == '&lt;'    *line == '&gt;')             continue;         for (px = line; *px != '\n'; px++)             if (isupper(*px)    islower(*px))                 tlen++;     }     if ((pseq = malloc((unsigned)(tlen+6))) == 0) {         fprintf(stderr, "%s: malloc() failed to get %d bytes for %s\n", prog, tlen+6, file);         exit(1);     }     pseq[0] = pseq[1] = pseq[2] = pseq[3] = '\0';      py = pseq + 4;     *len = tlen;     rewind(fp);     while (fgets(line, 1024, fp)) {         if (*line == ';'    *line == '&lt;'    *line == '&gt;')             continue;         for (px = line; *px != '\n'; px++) {             if (isupper(*px))                 *py++ = *px;             else if (islower(*px))                 *py++ = toupper(*px);             if (index("ATGCU", *(py-1)))                 natgc++;         }     }     *py++ = '\0';     *py = '\0';     (void) fclose(fp);     dna = natgc &gt; (tlen/3);     return(pseq+4); } char * g__calloc(msg, nx, sz) char *msg;           /* program, calling routine */ int nx, sz;          /* number and size of elements */ {     char *px, *calloc();     if ((px = calloc((unsigned)nx, (unsigned)sz)) == 0) {         if (*msg) {             fprintf(stderr, "%s: g__calloc() failed %s (n= %d, sz= %d)\n", prog, msg, nx, sz);             exit(1);         }     }     return(px); } /*  * get final jmps from dx[] or tmp file, set pp[], reset dmax: main()  */ readjmps() {     int fd = -1;</pre>		getseq
		...getseq
		g__calloc
		readjmps



TABLE 1-continued

---

```

int      siz, i0, i1;
register i, j, xx;
if (fj) {
    (void) fclose(fj);
    if ((fd = open(jname, O_RDONLY, 0)) < 0) {
        fprintf(stderr, "%s: can't open() %s\n", prog, jname);
        cleanup(1);
    }
}
for (i = i0 = i1 = 0, dmax0 = dmax, xx = len0; ;i++) {
    while (1) {
        for (j = dx[dmax].ijmp; j >= 0 && dx[dmax].jp.x[j] >= xx; j--)
            ;

        if (j < 0 && dx[dmax].offset && fj) {
            (void) lseek(fd, dx[dmax].offset, 0);
            (void) read(fd, (char *)&dx[dmax].jp, sizeof(struct jmp));
            (void) read(fd, (char *)&dx[dmax].offset, sizeof(dx[dmax].offset));
            dx[dmax].ijmp = MAXJMP-1;
        }
        else
            break;
    }
    if (i >= JMPS) {
        fprintf(stderr, "%s: too many gaps in alignment\n", prog);
        cleanup(1);
    }
    if (j >= 0) {
        siz = dx[dmax].jp.n[j];
        xx = dx[dmax].jp.x[j];
        dmax += siz;
        if (siz < 0) {
            /* gap in second seq */
            pp[1].n[i1] = -siz;
            xx += siz;
            /* id = xx - yy + len1 - 1
            */
            pp[1].x[i1] = xx - dmax + len1 - 1;
            gapy++;
            ngapy -= siz;
        /* ignore MAXGAP when doing endgaps */
        siz = (-siz < MAXGAP || endgaps)? -siz : MAXGAP;
        i1++;
    }
    else if (siz > 0) {
        /* gap in first seq */
        pp[0].n[i0] = siz;
        pp[0].x[i0] = xx;
        gapx++;
        ngapx += siz;
        /* ignore MAXGAP when doing endgaps */
        siz = (siz < MAXGAP || endgaps)? siz : MAXGAP;
        i0++;
    }
}
    else
        break;
}
/* reverse the order of jmps
*/
for (j = 0, i0--; j < i0; j++, i0--) {
    i = pp[0].n[j]; pp[0].n[j] = pp[0].n[i0]; pp[0].n[i0] = i;
    i = pp[0].x[j]; pp[0].x[j] = pp[0].x[i0]; pp[0].x[i0] = i;
}
for (j = 0, i1--; j < i1; j++, i1--) {
    i = pp[1].n[j]; pp[1].n[j] = pp[1].n[i1]; pp[1].n[i1] = i;
    i = pp[1].x[j]; pp[1].x[j] = pp[1].x[i1]; pp[1].x[i1] = i;
}
if (fd >= 0)
    (void) close(fd);
if (fj) {
    (void) unlink(jname);
    fj = 0;
    offset = 0;
}
}
/*
* write a filled jmp struct offset of the prev one (if any): nw()
*/

```

TABLE 1-continued

writeimps(ix)	writeimps
int ix;	
{	
char *mktemp();	
if (!fj) {	
if (mktemp(jname) < 0) {	
fprintf(stderr, "%s: can't mktemp() %s\n", prog, jname);	
cleanup(1);	
}	
if ((fj = fopen(jname, "w")) == 0) {	
fprintf(stderr, "%s: can't write %s\n", prog, jname);	
exit(1);	
}	
(void) fwrite((char *)&dx[ix].jp, sizeof(struct jmp), 1, fj);	
(void) fwrite((char *)&dx[ix].offset, sizeof(dx[ix].offset), 1, fj);	
}	

[0632]

TABLE 2

PRO	XXXXXXXXXXXXXXXXXX	(Length = 15 amino acids)
Comparison Protein	XXXXXXXXYYYYYYY	(Length = 12 amino acids)

% amino acid sequence identity = (the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) = 5 divided by 15 = 33.3%

[0633]

TABLE 3

PRO	XXXXXXXXXX	(Length = 10 amino acids)
Comparison Protein	XXXXXXXXYYYZZYZ	(Length = 15 amino acids)

% amino acid sequence identity = (the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) = 5 divided by 10 = 50%

[0634]

TABLE 4

PRO-DNA	NNNNNNNNNNNNNN	(Length = 14 nucleotides)
Comparison DNA	NNNNNNLLLLLLLL	(Length = 16 nucleotides)

% nucleic acid sequence identity = (the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) = 6 divided by 14 = 42.9%

[0635]

TABLE 5

PRO-DNA	NNNNNNNNNNNN	(Length = 12 nucleotides)
Comparison DNA	NNNNLLLVV	(Length = 9 nucleotides)

% nucleic acid sequence identity = (the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) = 4 divided by 12 = 33.3%

[0636] II. Compositions and Methods of the Invention

[0637] A. Full-Length PRO Polypeptides

[0638] The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO polypeptides. In particular, cDNAs encoding various PRO polypeptides have been identified and isolated, as disclosed in further detail in the Examples below. It is noted that proteins produced in separate expression rounds may be given different PRO numbers but the UNQ number is unique for any given DNA and the encoded protein, and will not be changed. However, for sake of simplicity, in the present specification the protein encoded by the full length native nucleic acid molecules disclosed herein as well as all further native homologues and variants included in the foregoing definition of PRO, will be referred to as "PRO/number", regardless of their origin or mode of preparation.

[0639] As disclosed in the Examples below, various cDNA clones have been deposited with the ATCC. The actual nucleotide sequences of those clones can readily be determined by the skilled artisan by sequencing of the deposited clone using routine methods in the art. The predicted amino acid sequence can be determined from the nucleotide sequence using routine skill. For the PRO polypeptides and encoding nucleic acids described herein, Applicants have identified what is believed to be the reading frame best identifiable with the sequence information available at the time.

[0640] B. PRO Polypeptide Variants

[0641] In addition to the full-length native sequence PRO polypeptides described herein, it is contemplated that PRO variants can be prepared. PRO variants can be prepared by introducing appropriate nucleotide changes into the PRO DNA, and/or by synthesis of the desired PRO polypeptide. Those skilled in the art will appreciate that amino acid changes may alter post-translational processes of the PRO, such as changing the number or position of glycosylation sites or altering the membrane anchoring characteristics.

[0642] Variations in the native full-length sequence PRO or in various domains of the PRO described herein, can be made, for example, using any of the techniques and guidelines for conservative and non-conservative mutations set forth, for instance, in U.S. Pat. No. 5,364,934. Variations may be a substitution, deletion or insertion of one or more

codons encoding the PRO that results in a change in the amino acid sequence of the PRO as compared with the native sequence PRO. Optionally the variation is by substitution of at least one amino acid with any other amino acid in one or more of the domains of the PRO. Guidance in determining which amino acid residue may be inserted, substituted or deleted without adversely affecting the desired activity may be found by comparing the sequence of the PRO with that of homologous known protein molecules and minimizing the number of amino acid sequence changes made in regions of high homology. Amino acid substitutions can be the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with a serine, i.e., conservative amino acid replacements. Insertions or deletions may optionally be in the range of about 1 to 5 amino acids. The variation allowed may be determined by systematically making insertions, deletions or substitutions of amino acids in the sequence and testing the resulting variants for activity exhibited by the full-length or mature native sequence.

[0643] PRO polypeptide fragments are provided herein. Such fragments may be truncated at the N-terminus or C-terminus, or may lack internal residues, for example, when compared with a full length native protein. Certain fragments lack amino acid residues that are not essential for a desired biological activity of the PRO polypeptide.

[0644] PRO fragments may be prepared by any of a number of conventional techniques. Desired peptide fragments may be chemically synthesized. An alternative approach involves generating PRO fragments by enzymatic digestion, e.g., by treating the protein with an enzyme known to cleave proteins at sites defined by particular amino acid residues, or by digesting the DNA with suitable restriction enzymes and isolating the desired fragment. Yet another suitable technique involves isolating and amplifying a DNA fragment encoding a desired polypeptide fragment, by polymerase chain reaction (PCR). Oligonucleotides that define the desired termini of the DNA fragment are employed at the 5' and 3' primers in the PCR. Preferably, PRO polypeptide fragments share at least one biological and/or immunological activity with the native PRO polypeptide disclosed herein.

[0645] In particular embodiments, conservative substitutions of interest are shown in Table 6 under the heading of preferred substitutions. If such substitutions result in a change in biological activity, then more substantial changes, denominated exemplary substitutions in Table 6, or as further described below in reference to amino acid classes, are introduced and the products screened.

TABLE 6		
Original Residue	Exemplary Substitutions	Preferred Substitutions
Ala (A)	val; leu; ile	val
Arg (R)	lys; gln; asn	lys
Asn (N)	gln; his; lys; arg	gln
Asp (D)	glu	glu
Cys (C)	ser	ser
Gln (Q)	asn	asn
Glu (E)	asp	asp
Gly (G)	pro; ala	ala

TABLE 6-continued		
Original Residue	Exemplary Substitutions	Preferred Substitutions
His (H)	asn; gln; lys; arg	arg
Ile (I)	leu; val; met; ala; phe; norleucine	leu
Leu (L)	norleucine; ile; val; met; ala; phe	ile
Lys (K)	arg; gln; asn	arg
Met (M)	leu; phe; ile	leu
Phe (F)	leu; val; ile; ala; tyr	leu
Pro (P)	ala	ala
Ser (S)	thr	thr
Thr (T)	ser	ser
Trp (W)	tyr; phe	tyr
Tyr (Y)	trp; phe; thr; ser	phe
Val (V)	ile; leu; met; phe; ala; norleucine	leu

[0646] Substantial modifications in function or immunological identity of the PRO polypeptide are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties:

- [0647] (1) hydrophobic: norleucine, met, ala, val, leu, ile;
- [0648] (2) neutral hydrophilic: cys, ser, thr;
- [0649] (3) acidic: asp, glu;
- [0650] (4) basic: asn, gln, his, lys, arg;
- [0651] (5) residues that influence chain orientation: gly, pro; and
- [0652] (6) aromatic: trp, tyr, phe.

[0653] Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Such substituted residues also may be introduced into the conservative substitution sites or, more preferably, into the remaining (non-conserved) sites.

[0654] The variations can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis [Carter et al., *Nucl. Acids Res.* 13:4331 (1986); Zoller et al., *Nucl. Acids Res.*, 10:6487 (1987)], cassette mutagenesis [Wells et al., *Gene*, 34:315 (1985)], restriction selection mutagenesis [Wells et al., *Philos. Trans. R. Soc. London SerA*, 317:415 (1986)] or other known techniques can be performed on the cloned DNA to produce the PRO variant DNA.

[0655] Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant [Cunningham and Wells, *Science*, 244:

1081-1085 (1989)]. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions [Creighton, *The Proteins*, (W.H. Freeman & Co., N.Y.); Chothia, *J. Mol. Biol.*, 150:1 (1976)]. If alanine substitution does not yield adequate amounts of variant, an isoteric amino acid can be used.

#### [0656] C. Modifications of PRO

[0657] Covalent modifications of PRO are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a PRO polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C-terminal residues of the PRO. Derivatization with bifunctional agents is useful, for instance, for crosslinking PRO to a water-insoluble support matrix or surface for use in the method for purifying anti-PRO antibodies, and vice-versa. Commonly used crosslinking agents include, e.g., 1,1-bis-(diazocetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propionimide.

[0658] Other modifications include deamidation of glutamyl and asparagyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the  $\alpha$ -amino groups of lysine, arginine, and histidine side chains [T. E. Creighton, *Proteins: Structure and Molecular Properties*, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

[0659] Another type of covalent modification of the PRO polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence PRO (either by removing the underlying glycosylation site or by deleting the glycosylation by chemical and/or enzymatic means), and/or adding one or more glycosylation sites that are not present in the native sequence PRO. In addition, the phrase includes qualitative changes in the glycosylation of the native proteins, involving a change in the nature and proportions of the various carbohydrate moieties present.

[0660] Addition of glycosylation sites to the PRO polypeptide may be accomplished by altering the amino acid sequence. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence PRO (for O-linked glycosylation sites). The PRO amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the PRO polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

[0661] Another means of increasing the number of carbohydrate moieties on the PRO polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such

methods are described in the art, e.g., in WO 87/05330 published Sep. 11, 1987, and in Aplin and Wriston, *CRC Crit. Rev. Biochem.*, pp. 259-306 (1981).

[0662] Removal of carbohydrate moieties present on the PRO polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., *Arch. Biochem. Biophys.*, 259:52 (1987) and by Edge et al., *Anal. Biochem.*, 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., *Meth. Enzymol.*, 138:350 (1987).

[0663] Another type of covalent modification of PRO comprises linking the PRO polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol (PEG), polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Pat. Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

[0664] The PRO of the present invention may also be modified in a way to form a chimeric molecule comprising PRO fused to another, heterologous polypeptide or amino acid sequence.

[0665] In one embodiment, such a chimeric molecule comprises a fusion of the PRO with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl-terminus of the PRO. The presence of such epitope-tagged forms of the PRO can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the PRO to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., *Mol. Cell. Biol.*, 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., *Molecular and Cellular Biology*, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., *Protein Engineering*, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., *BioTechnology*, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., *Science*, 255:192-194 (1992)]; an  $\alpha$ -tubulin epitope peptide [Skinner et al., *J. Biol. Chem.* 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., *Proc. Natl. Acad. Sci. USA*, 87:6393-6397 (1990)].

[0666] In an alternative embodiment, the chimeric molecule may comprise a fusion of the PRO with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule (also referred to as an "immunoadhesin"), such a fusion could be to the Fc region of an IgG molecule. The Ig fusions preferably include the substitution of a soluble (transmembrane domain deleted or inactivated) form of a PRO polypeptide in place of at least one variable region within an Ig molecule. In a particularly preferred embodiment, the immunoglobulin fusion includes the hinge, CH2 and CH3, or the hinge, CH1, CH2 and CH3

regions of an IgG1 molecule. For the production of immunoglobulin fusions see also U.S. Pat. No. 5,428,130 issued Jun. 27, 1995.

#### [0667] D. Preparation of PRO

[0668] The description below relates primarily to production of PRO by culturing cells transformed or transfected with a vector containing PRO nucleic acid. It is, of course, contemplated that alternative methods, which are well known in the art, may be employed to prepare PRO. For instance, the PRO sequence, or portions thereof, may be produced by direct peptide synthesis using solid-phase techniques [see, e.g., Stewart et al., *Solid-Phase Peptide Synthesis*, W.H. Freeman Co., San Francisco, Calif. (1969); Merrifield, *J. Am. Chem. Soc.*, 85:2149-2154 (1963)]. In vitro protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be accomplished, for instance, using an Applied Biosystems Peptide Synthesizer (Foster City, Calif.) using manufacturer's instructions. Various portions of the PRO may be chemically synthesized separately and combined using chemical or enzymatic methods to produce the full-length PRO.

#### 1. Isolation of DNA Encoding PRO

[0669] DNA encoding PRO may be obtained from a cDNA library prepared from tissue believed to possess the PRO mRNA and to express it at a detectable level. Accordingly, human PRO DNA can be conveniently obtained from a cDNA library prepared from human tissue, such as described in the Examples. The PRO-encoding gene may also be obtained from a genomic library or by known synthetic procedures (e.g., automated nucleic acid synthesis).

[0670] Libraries can be screened with probes (such as antibodies to the PRO or oligonucleotides of at least about 20-80 bases) designed to identify the gene of interest or the protein encoded by it. Screening the cDNA or genomic library with the selected probe may be conducted using standard procedures, such as described in Sambrook et al., *Molecular Cloning: A Laboratory Manual* (New York: Cold Spring Harbor Laboratory Press, 1989). An alternative means to isolate the gene encoding PRO is to use PCR methodology [Sambrook et al., supra; Dieffenbach et al., *PCR Primer: A Laboratory Manual* (Cold Spring Harbor Laboratory Press, 1995)].

[0671] The Examples below describe techniques for screening a cDNA library. The oligonucleotide sequences selected as probes should be of sufficient length and sufficiently unambiguous that false positives are minimized. The oligonucleotide is preferably labeled such that it can be detected upon hybridization to DNA in the library being screened. Methods of labeling are well known in the art, and include the use of radiolabels like <sup>32</sup>P-labeled ATP, biotinylation or enzyme labeling. Hybridization conditions, including moderate stringency and high stringency, are provided in Sambrook et al., supra.

[0672] Sequences identified in such library screening methods can be compared and aligned to other known sequences deposited and available in public databases such as GenBank or other private sequence databases. Sequence identity (at either the amino acid or nucleotide level) within

defined regions of the molecule or across the full-length sequence can be determined using methods known in the art and as described herein.

[0673] Nucleic acid having protein coding sequence may be obtained by screening selected cDNA or genomic libraries using the deduced amino acid sequence disclosed herein for the first time, and, if necessary, using conventional primer extension procedures as described in Sambrook et al., supra, to detect precursors and processing intermediates of mRNA that may not have been reverse-transcribed into cDNA.

#### 2. Selection and Transformation of Host Cells

[0674] Host cells are transfected or transformed with expression or cloning vectors described herein for PRO production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. The culture conditions, such as media, temperature, pH and the like, can be selected by the skilled artisan without undue experimentation. In general, principles, protocols, and practical techniques for maximizing the productivity of cell cultures can be found in *Mammalian Cell Biotechnology: a Practical Approach*, M. Butler, ed. (IRL Press, 1991) and Sambrook et al., supra.

[0675] Methods of eukaryotic cell transfection and prokaryotic cell transformation are known to the ordinarily skilled artisan, for example, CaCl<sub>2</sub>, CaPO<sub>4</sub>, liposome-mediated and electroporation. Depending on the host cell used, transformation is performed using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in Sambrook et al., supra, or electroporation is generally used for prokaryotes. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw et al., *Gene*, 23:315 (1983) and WO 89/05859 published Jun. 29, 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, *Virology*, 52:456-457 (1978) can be employed. General aspects of mammalian cell host system transfections have been described in U.S. Pat. No. 4,399,216. Transformations into yeast are typically carried out according to the method of Van Solingen et al., *J. Bact.*, 130:946 (1977) and Hsiao et al., *Proc. Natl. Acad. Sci. (USA)*, 76:3829 (1979). However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or polycations, e.g., polybrene, polyornithine, may also be used. For various techniques for transforming mammalian cells, see Keown et al., *Methods in Enzymology*, 185:527-537 (1990) and Mansour et al., *Nature*, 336:348-352 (1988).

[0676] Suitable host cells for cloning or expressing the DNA in the vectors herein include prokaryote, yeast, or higher eukaryote cells. Suitable prokaryotes include but are not limited to eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *E. coli*. Various *E. coli* strains are publicly available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325) and K5772 (ATCC 53,635). Other suitable prokaryotic host cells include Enterobacteriaceae such as *Escherichia*, e.g., *E. coli*, *Enterobacter*, *Erwinia*, *Klebsiella*, *Proteus*, *Salmonella*, e.g.,

*Salmonella typhimurium*, *Serratia*, e.g., *Serratia marcescens*, and *Shigella*, as well as *Bacilli* such as *B. subtilis* and *B. licheniformis* (e.g., *B. licheniformis* 41P disclosed in DD 266,710 published Apr. 12, 1989), *Pseudomonas* such as *P. aeruginosa*, and *Streptomyces*. These examples are illustrative rather than limiting. Strain W3110 is one particularly preferred host or parent host because it is a common host strain for recombinant DNA product fermentations. Preferably, the host cell secretes minimal amounts of proteolytic enzymes. For example, strain W3110 may be modified to effect a genetic mutation in the genes encoding proteins endogenous to the host, with examples of such hosts including *E. coli* W3110 strain 1A2, which has the complete genotype tonA; *E. coli* W3110 strain 9E4, which has the complete genotype tonA ptr3; *E. coli* W3110 strain 27C7 (ATCC 55,244), which has the complete genotype tonA ptr3 phoA E]5 (argF-lac)169 degP ompT kan<sup>r</sup>; *E. coli* W3110 strain 37D6, which has the complete genotype tonA ptr3 phoA E]5 (argF-lac)169 degP ompT rbs7 ilvG kan<sup>r</sup>; *E. coli* W3110 strain 40B4, which is strain 37D6 with a non-kanamycin resistant degP deletion mutation; and an *E. coli* strain having mutant periplasmic protease disclosed in U.S. Pat. No. 4,946,783 issued Aug. 7, 1990. Alternatively, in vitro methods of cloning, e.g., PCR or other nucleic acid polymerase reactions, are suitable.

[0677] In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for PRO-encoding vectors. *Saccharomyces cerevisiae* is a commonly used lower eukaryotic host micro-organism. Others include *Schizosaccharomyces pombe* (Beach and Nurse, *Nature*, 290: 140 [1981]; EP 139,383 published May 2, 1985); *Kluyveromyces* hosts (U.S. Pat. No. 4,943,529; Fleer et al., *Bio/Technology*, 9:968-975 (1991)) such as, e.g., *K. lactis* (MW98-8C, CBS683, CBS4574; Louvencourt et al., *J. Bacteriol.*, 154(2):737-742 [1983]), *K. fragilis* (ATCC 12,424), *K. bulgaricus* (ATCC 16,045), *K. wickerhamii* (ATCC 24,178), *K. waltii* (ATCC 56,500), *K. drosophilum* (ATCC 36,906; Van den Berg et al., *Bio/Technology*, 8:135 (1990)), *K. thermotolerans*, and *K. marxianus*; *yarrowia* (EP 402,226); *Pichia pastoris* (EP 183,070; Sreekrishna et al., *J. Basic Microbiol.*, 28:265-278 [1988]); *Candida*; *Trichoderma reesia* (EP 244,234); *Neurospora crassa* (Case et al., *Proc. Natl. Acad. Sci. USA*, 76:5259-5263 [1979]); *Schwanniomyces* such as *Schwanniomyces occidentalis* (EP 394,538 published Oct. 31, 1990); and filamentous fungi such as, e.g., *Neurospora*, *Penicillium*, *Tolypocladium* (WO 91/00357 published Jan. 10, 1991), and *Aspergillus* hosts such as *A. nidulans* (Balance et al., *Biochem. Biophys. Res. Commun.*, 112:284-289 [1983]; Tilbum et al., *Gene*, 26:205-221 [1983]; Yelton et al., *Proc. Natl. Acad. Sci. USA*, 81: 1470-1474 [1984]) and *A. niger* (Kelly and Hynes, *EMBO J.*, 4:475-479 [1985]). Methylotrophic yeasts are suitable herein and include, but are not limited to, yeast capable of growth on methanol selected from the genera consisting of *Hansenula*, *Candida*, *Kloeckera*, *Pichia*, *Saccharomyces*, *Torulopsis*, and *Rhodotorula*. A list of specific species that are exemplary of this class of yeasts may be found in C. Anthony, *The Biochemistry of Methylotrophs*, 269 (1982).

[0678] Suitable host cells for the expression of glycosylated PRO are derived from multicellular organisms. Examples of invertebrate cells include insect cells such as *Drosophila* S2 and *Spodoptera* Sf9, as well as plant cells. Examples of useful mammalian host cell lines include

Chinese hamster ovary (CHO) and COS cells. More specific examples include monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., *J. Gen. Virol.*, 36:59 (1977)); Chinese hamster ovary cells/-DHFR (CHO, Urlaub and Chasin, *Proc. Natl. Acad. Sci. USA*, 77:4216(1980)); mouse sertoli cells (T1M4, Mather, *Biol. Reprod.*, 23:243-251 (1980)); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); and mouse mammary tumor (MMT 060562, ATCC CCL51). The selection of the appropriate host cell is deemed to be within the skill in the art.

### 3. Selection and Use of a Replicable Vector

[0679] The nucleic acid (e.g., cDNA or genomic DNA) encoding PRO may be inserted into a replicable vector for cloning (amplification of the DNA) or for expression. Various vectors are publicly available. The vector may, for example, be in the form of a plasmid, cosmid, viral particle, or phage. The appropriate nucleic acid sequence may be inserted into the vector by a variety of procedures. In general, DNA is inserted into an appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence. Construction of suitable vectors containing one or more of these components employs standard ligation techniques which are known to the skilled artisan.

[0680] The PRO may be produced recombinantly not only directly, but also as a fusion polypeptide with a heterologous polypeptide, which may be a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. In general, the signal sequence may be a component of the vector, or it may be apart of the PRO-encoding DNA that is inserted into the vector. The signal sequence may be a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase, Ipp, or heat-stable enterotoxin II leaders. For yeast secretion the signal sequence may be, e.g., the yeast invertase leader, alpha factor leader (including *Saccharomyces* and *Kluyveromyces*  $\alpha$ -factor leaders, the latter described in U.S. Pat. No. 5,010, 182), or acid phosphatase leader, the *C. albicans* glucoamylase leader (EP 362,179 published Apr. 4, 1990), or the signal described in WO 90/13646 published Nov. 15, 1990. In mammalian cell expression, mammalian signal sequences may be used to direct secretion of the protein, such as signal sequences from secreted polypeptides of the same or related species, as well as viral secretory leaders.

[0681] Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the  $2\mu$  plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for cloning vectors in mammalian cells.

[0682] Expression and cloning vectors will typically contain a selection gene, also termed a selectable marker.

Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, e.g., the gene encoding D-alanine racemase for *Bacilli*.

**[0683]** An example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the PRO-encoding nucleic acid, such as DHFR or thymidine kinase. An appropriate host cell when wild-type DHFR is employed is the CHO cell line deficient in DHFR activity, prepared and propagated as described by Urlaub et al., *Proc. Natl. Acad. Sci. USA*, 77:4216 (1980). A suitable selection gene for use in yeast is the *trp1* gene present in the yeast plasmid YRp7 [Stinchcomb et al., *Nature*, 282:39 (1979); Kingsman et al., *Gene*, 7:141 (1979); Tschemper et al., *Gene*, 10:157 (1980)]. The *trp1* gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1 [Jones, *Genetics*, 85:12 (1977)].

**[0684]** Expression and cloning vectors usually contain a promoter operably linked to the PRO-encoding nucleic acid sequence to direct mRNA synthesis. Promoters recognized by a variety of potential host cells are well known. Promoters suitable for use with prokaryotic hosts include the  $\beta$ -lactamase and lactose promoter systems [Chang et al., *Nature*, 275:615 (1978); Goeddel et al., *Nature*, 281:544 (1979)], alkaline phosphatase, a tryptophan (*trp*) promoter system [Goeddel, *Nucleic Acids Res.*, 8:4057 (1980); EP 36,776], and hybrid promoters such as the *tac* promoter [deBoer et al., *Proc. Natl. Acad. Sci. USA*, 80:21-25 (1983)]. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding PRO.

**[0685]** Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase [Hitzeman et al., *J. Biol. Chem.*, 255:2073 (1980)] or other glycolytic enzymes [Hess et al., *J. Adv. Enzyme Reg.*, 7:149 (1968); Holland, *Biochemistry*, 17:4900 (1978)], such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

**[0686]** Other yeast promoters, which are inducible promoters having the additional advantage of transcription controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in EP 73,657.

**[0687]** PRO transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published Jul. 5, 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), from heterologous mammalian promoters, e.g., the actin promoter or an immunoglobulin promoter, and

from heat-shock promoters, provided such promoters are compatible with the host cell systems.

**[0688]** Transcription of a DNA encoding the PRO by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin,  $\alpha$ -fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. The enhancer may be spliced into the vector at a position 5' or 3' to the PRO coding sequence, but is preferably located at a site 5' from the promoter.

**[0689]** Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding PRO.

**[0690]** Still other methods, vectors, and host cells suitable for adaptation to the synthesis of PRO in recombinant vertebrate cell culture are described in Gething et al., *Nature*, 293:620-625 (1981); Mantei et al., *Nature*, 281:40-46 (1979); EP 117,060; and EP 117,058.

#### 4. Detecting Gene Amplification/Expression

**[0691]** Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA [Thomas, *Proc. Natl. Acad. Sci. USA*, 77:5201-5205 (1980)], dot blotting (DNA analysis), or in situ hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

**[0692]** Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of cells or tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence PRO polypeptide or against a synthetic peptide based on the DNA sequences provided herein or against exogenous sequence fused to PRO DNA and encoding a specific antibody epitope.

#### 5. Purification of Polypeptide

**[0693]** Forms of PRO may be recovered from culture medium or from host cell lysates. If membrane-bound, it can

be released from the membrane using a suitable detergent solution (e.g. Triton-X 100) or by enzymatic cleavage. Cells employed in expression of PRO can be disrupted by various physical or chemical means, such as freeze-thaw cycling, sonication, mechanical disruption, or cell lysing agents.

**[0694]** It may be desired to purify PRO from recombinant cell proteins or polypeptides. The following procedures are exemplary of suitable purification procedures: by fractionation on an ion-exchange column; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; protein A Sepharose columns to remove contaminants such as IgG; and metal chelating columns to bind epitope-tagged forms of the PRO. Various methods of protein purification may be employed and such methods are known in the art and described for example in Deutscher, *Methods in Enzymology*, 182 (1990); Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag, New York (1982). The purification step(s) selected will depend, for example, on the nature of the production process used and the particular PRO produced.

#### **[0695]** E. Uses for PRO

**[0696]** Nucleotide sequences (or their complement) encoding PRO have various applications in the art of molecular biology, including uses as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. PRO nucleic acid will also be useful for the preparation of PRO polypeptides by the recombinant techniques described herein.

**[0697]** The full-length native sequence PRO gene, or portions thereof, may be used as hybridization probes for a cDNA library to isolate the full-length PRO cDNA or to isolate still other cDNAs (for instance, those encoding naturally-occurring variants of PRO or PRO from other species) which have a desired sequence identity to the native PRO sequence disclosed herein. Optionally, the length of the probes will be about 20 to about 50 bases. The hybridization probes may be derived from at least partially novel regions of the full length native nucleotide sequence wherein those regions may be determined without undue experimentation or from genomic sequences including promoters, enhancer elements and introns of native sequence PRO. By way of example, a screening method will comprise isolating the coding region of the PRO gene using the known DNA sequence to synthesize a selected probe of about 40 bases. Hybridization probes may be labeled by a variety of labels, including radionucleotides such as <sup>32</sup>P or <sup>35</sup>S, or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems. Labeled probes having a sequence complementary to that of the PRO gene of the present invention can be used to screen libraries of human cDNA, genomic DNA or mRNA to determine which members of such libraries the probe hybridizes to. Hybridization techniques are described in further detail in the Examples below.

**[0698]** Any EST sequences disclosed in the present application may similarly be employed as probes, using the methods disclosed herein.

**[0699]** Other useful fragments of the PRO nucleic acids include antisense or sense oligonucleotides comprising a

singe-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target PRO mRNA (sense) or PRO DNA (antisense) sequences. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment of the coding region of PRO DNA. Such a fragment generally comprises at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (*Cancer Res.* 48:2659, 1988) and van der Krol et al. (*BioTechniques* 6:958, 1988).

**[0700]** Binding of antisense or sense oligonucleotides to target nucleic acid sequences results in the formation of duplexes that block transcription or translation of the target sequence by one of several means, including enhanced degradation of the duplexes, premature termination of transcription or translation, or by other means. The antisense oligonucleotides thus may be used to block expression of PRO proteins. Antisense or sense oligonucleotides further comprise oligonucleotides having modified sugar-phosphodiester backbones (or other sugar linkages, such as those described in WO 91/06629) and wherein such sugar linkages are resistant to endogenous nucleases. Such oligonucleotides with resistant sugar linkages are stable in vivo (i.e., capable of resisting enzymatic degradation) but retain sequence specificity to be able to bind to target nucleotide sequences.

**[0701]** Other examples of sense or antisense oligonucleotides include those oligonucleotides which are covalently linked to organic moieties, such as those described in WO 90/10048, and other moieties that increases affinity of the oligonucleotide for a target nucleic acid sequence, such as poly-(L-lysine). Further still, intercalating agents, such as ellipticine, and alkylating agents or metal complexes may be attached to sense or antisense oligonucleotides to modify binding specificities of the antisense or sense oligonucleotide for the target nucleotide sequence.

**[0702]** Antisense or sense oligonucleotides may be introduced into a cell containing the target nucleic acid sequence by any gene transfer method, including, for example, CaPO<sub>4</sub>-mediated DNA transfection, electroporation, or by using gene transfer vectors such as Epstein-Barr virus. In a preferred procedure, an antisense or sense oligonucleotide is inserted into a suitable retroviral vector. A cell containing the target nucleic acid sequence is contacted with the recombinant retroviral vector, either in vivo or ex vivo. Suitable retroviral vectors include, but are not limited to, those derived from the murine retrovirus M-MuLV, N2 (a retrovirus derived from M-MuLV), or the double copy vectors designated DCT5A, DCT5B and DCT5C (see WO 90/13641).

**[0703]** Sense or antisense oligonucleotides also may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell.



[0704] Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. The sense or antisense oligonucleotide-lipid complex is preferably dissociated within the cell by an endogenous lipase.

[0705] Antisense or sense RNA or DNA molecules are generally at least about 5 bases in length, about 10 bases in length, about 15 bases in length, about 20 bases in length, about 25 bases in length, about 30 bases in length, about 35 bases in length, about 40 bases in length, about 45 bases in length, about 50 bases in length, about 55 bases in length, about 60 bases in length, about 65 bases in length, about 70 bases in length, about 75 bases in length, about 80 bases in length, about 85 bases in length, about 90 bases in length, about 95 bases in length, about 100 bases in length, or more.

[0706] The probes may also be employed in PCR techniques to generate a pool of sequences for identification of closely related PRO coding sequences.

[0707] Nucleotide sequences encoding a PRO can also be used to construct hybridization probes for mapping the gene which encodes that PRO and for the genetic analysis of individuals with genetic disorders. The nucleotide sequences provided herein may be mapped to a chromosome and specific regions of a chromosome using known techniques, such as in situ hybridization, linkage analysis against known chromosomal markers, and hybridization screening with libraries.

[0708] When the coding sequences for PRO encode a protein which binds to another protein (example, where the PRO is a receptor), the PRO can be used in assays to identify the other proteins or molecules involved in the binding interaction. By such methods, inhibitors of the receptor/ligand binding interaction can be identified. Proteins involved in such binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction. Also, the receptor PRO can be used to isolate correlative ligand(s). Screening assays can be designed to find lead compounds that mimic the biological activity of a native PRO or a receptor for PRO. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates. Small molecules contemplated include synthetic organic or inorganic compounds. The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays and cell based assays, which are well characterized in the art.

[0709] Nucleic acids which encode PRO or its modified forms can also be used to generate either transgenic animals or "knock out" animals which, in turn, are useful in the development and screening of therapeutically useful reagents. A transgenic animal (e.g., a mouse or rat) is an animal having cells that contain a transgene, which transgene was introduced into the animal or an ancestor of the animal at a prenatal, e.g., an embryonic stage. A transgene is a DNA which is integrated into the genome of a cell from which a transgenic animal develops. In one embodiment, cDNA encoding PRO can be used to clone genomic DNA encoding PRO in accordance with established techniques and the genomic sequences used to generate transgenic

animals that contain cells which express DNA encoding PRO. Methods for generating transgenic animals, particularly animals such as mice or rats, have become conventional in the art and are described, for example, in U.S. Pat. Nos. 4,736,866 and 4,870,009. Typically, particular cells would be targeted for PRO transgene incorporation with tissue-specific enhancers. Transgenic animals that include a copy of a transgene encoding PRO introduced into the germ line of the animal at an embryonic stage can be used to examine the effect of increased expression of DNA encoding PRO. Such animals can be used as tester animals for reagents thought to confer protection from, for example, pathological conditions associated with its overexpression. In accordance with this facet of the invention, an animal is treated with the reagent and a reduced incidence of the pathological condition, compared to untreated animals bearing the transgene, would indicate a potential therapeutic intervention for the pathological condition.

[0710] Alternatively, non-human homologues of PRO can be used to construct a PRO "knock out" animal which has a defective or altered gene encoding PRO as a result of homologous recombination between the endogenous gene encoding PRO and altered genomic DNA encoding PRO introduced into an embryonic stem cell of the animal. For example, cDNA encoding PRO can be used to clone genomic DNA encoding PRO in accordance with established techniques. A portion of the genomic DNA encoding PRO can be deleted or replaced with another gene, such as a gene encoding a selectable marker which can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector [see e.g., Thomas and Capecchi, *Cell*, 51:503 (1987) for a description of homologous recombination vectors]. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced DNA has homologously recombined with the endogenous DNA are selected [see e.g., Li et al., *Cell*, 69:915 (1992)]. The selected cells are then injected into a blastocyst of an animal (e.g., a mouse or rat) to form aggregation chimeras [see e.g., Bradley, in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152]. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knock-out animals can be characterized for instance, for their ability to defend against certain pathological conditions and for their development of pathological conditions due to absence of the PRO polypeptide.

[0711] Nucleic acid encoding the PRO polypeptides may also be used in gene therapy. In gene therapy applications, genes are introduced into cells in order to achieve in vivo synthesis of a therapeutically effective genetic product, for example for replacement of a defective gene. "Gene therapy" includes both conventional gene therapy where a lasting effect is achieved by a single treatment, and the administration of gene therapeutic agents, which involves the one time or repeated administration of a therapeutically effective DNA or mRNA. Antisense RNAs and DNAs can be used as therapeutic agents for blocking the expression of certain genes in vivo. It has already been shown that short

antisense oligonucleotides can be imported into cells where they act as inhibitors, despite their low intracellular concentrations caused by their restricted uptake by the cell membrane. (Zamecnik et al., *Proc. Natl. Acad. Sci. USA* 83:4143-4146 [1986]). The oligonucleotides can be modified to enhance their uptake, e.g. by substituting their negatively charged phosphodiester groups by uncharged groups.

[0712] There are a variety of techniques available for introducing nucleic acids into viable cells. The techniques vary depending upon whether the nucleic acid is transferred into cultured cells in vitro, or in vivo in the cells of the intended host. Techniques suitable for the transfer of nucleic acid into mammalian cells in vitro include the use of liposomes, electroporation, microinjection, cell fusion, DEAE-dextran, the calcium phosphate precipitation method, etc. The currently preferred in vivo gene transfer techniques include transfection with viral (typically retroviral) vectors and viral coat protein-liposome mediated transfection (Dzau et al., *Trends in Biotechnology* 11,205-210 [1993]). In some situations it is desirable to provide the nucleic acid source with an agent that targets the target cells, such as an antibody specific for a cell surface membrane protein or the target cell, a ligand for a receptor on the target cell, etc. Where liposomes are employed, proteins which bind to a cell surface membrane protein associated with endocytosis may be used for targeting and/or to facilitate uptake, e.g. capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, proteins that target intracellular localization and enhance intracellular half-life. The technique of receptor-mediated endocytosis is described, for example, by Wu et al., *J. Biol. Chem.* 262,4429-4432 (1987); and Wagner et al., *Proc. Natl. Acad. Sci. U.S. Pat. No.* 87,3410-3414(1990). For review of gene marking and gene therapy protocols see Anderson et al., *Science* 256, 808-813 (1992).

[0713] The PRO polypeptides described herein may also be employed as molecular weight markers for protein electrophoresis purposes and the isolated nucleic acid sequences may be used for recombinantly expressing those markers.

[0714] The nucleic acid molecules encoding the PRO polypeptides or fragments thereof described herein are useful for chromosome identification. In this regard, there exists an ongoing need to identify new chromosome markers, since relatively few chromosome marking reagents, based upon actual sequence data are presently available. Each PRO nucleic acid molecule of the present invention can be used as a chromosome marker.

[0715] The PRO polypeptides and nucleic acid molecules of the present invention may also be used diagnostically for tissue typing, wherein the PRO polypeptides of the present invention may be differentially expressed in one tissue as compared to another, preferably in a diseased tissue as compared to a normal tissue of the same tissue type. PRO nucleic acid molecules will find use for generating probes for PCR, Northern analysis, Southern analysis and Western analysis.

[0716] The PRO polypeptides described herein may also be employed as therapeutic agents. The PRO polypeptides of the present invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby the PRO product hereof is combined in admixture with a pharmaceutically acceptable carrier vehicle. Thera-

peutic formulations are prepared for storage by mixing the active ingredient having the desired degree of purity with optional physiologically acceptable carriers, excipients or stabilizers (*Remington's Pharmaceutical Sciences* 16th edition, Osol, A. Ed. (1980)), in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone, amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN™ PLURONICS™ or PEG.

[0717] The formulations to be used for in vivo administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes, prior to or following lyophilization and reconstitution.

[0718] Therapeutic compositions herein generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

[0719] The route of administration is in accord with known methods, e.g. injection or infusion by intravenous, intraperitoneal, intracerebral, intramuscular, intraocular, intraarterial or intralesional routes, topical administration, or by sustained release systems.

[0720] Dosages and desired drug concentrations of pharmaceutical compositions of the present invention may vary depending on the particular use envisioned. The determination of the appropriate dosage or route of administration is well within the skill of an ordinary physician. Animal experiments provide reliable guidance for the determination of effective doses for human therapy. Interspecies scaling of effective doses can be performed following the principles laid down by Mordenti, J. and Chappell, W. "The use of interspecies scaling in toxicokinetics" In *Toxicokinetics and New Drug Development*, Yacobi et al., Eds., Pergamon Press, New York 1989, pp. 42-96.

[0721] When in vivo administration of a PRO polypeptide or agonist or antagonist thereof is employed, normal dosage amounts may vary from about 10 ng/kg to up to 100 mg/kg of mammal body weight or more per day, preferably about 1 µg/kg/day to 10 mg/kg/day, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature; see, for example, U.S. Pat. Nos. 4,657,760; 5,206,344; or 5,225,212. It is anticipated that different formulations will be effective for different treatment compounds and different disorders, that administration targeting one organ or tissue, for example, may necessitate delivery in a manner different from that to another organ or tissue.

[0722] Where sustained-release administration of a PRO polypeptide is desired in a formulation with release characteristics suitable for the treatment of any disease or disorder requiring administration of the PRO polypeptide, microen-

capsulation of the PRO polypeptide is contemplated. Microencapsulation of recombinant proteins for sustained release has been successfully performed with human growth hormone (rhGH), interferon-(rhIFN-), interleukin-2, and MN rgp120. Johnson et al., *Nat. Med.*, 2:795-799 (1996); Yasuda, *Biomed. Ther.*, 27:1221-1223 (1993); Hora et al., *Bio/Technology*, 8:755-758 (1990); Cleland, "Design and Production of Single Immunization Vaccines Using Polylactide Polyglycolide Microsphere Systems," in *Vaccine Design: The Subunit and Adjuvant Approach*, Powell and Newman, eds. (Plenum Press: New York, 1995), pp. 439-462; WO 97/03692, WO 96/40072, WO 96/07399; and U.S. Pat. No. 5,654,010.

[0723] The sustained-release formulations of these proteins were developed using poly-lactic-coglycolic acid (PLGA) polymer due to its biocompatibility and wide range of biodegradable properties. The degradation products of PLGA, lactic and glycolic acids, can be cleared quickly within the human body. Moreover, the degradability of this polymer can be adjusted from months to years depending on its molecular weight and composition. Lewis, "Controlled release of bioactive agents from lactide/glycolide polymer," in: M. Chasin and R. Langer (Eds.), *Biodegradable Polymers as Drug Delivery Systems* (Marcel Dekker: New York, 1990), pp.1-41.

[0724] This invention encompasses methods of screening compounds to identify those that mimic the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (antagonists). Screening assays for antagonist drug candidates are designed to identify compounds that bind or complex with the PRO polypeptides encoded by the genes identified herein, or otherwise interfere with the interaction of the encoded polypeptides with other cellular proteins. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates.

[0725] The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays, and cell-based assays, which are well characterized in the art.

[0726] All assays for antagonists are common in that they call for contacting the drug candidate with a PRO polypeptide encoded by a nucleic acid identified herein under conditions and for a time sufficient to allow these two components to interact.

[0727] In binding assays, the interaction is binding and the complex formed can be isolated or detected in the reaction mixture. In a particular embodiment, the PRO polypeptide encoded by the gene identified herein or the drug candidate is immobilized on a solid phase, e.g., on a microtiter plate, by covalent or non-covalent attachments. Non-covalent attachment generally is accomplished by coating the solid surface with a solution of the PRO polypeptide and drying. Alternatively, an immobilized antibody, e.g., a monoclonal antibody, specific for the PRO polypeptide to be immobilized can be used to anchor it to a solid surface. The assay is performed by adding the non-immobilized component, which may be labeled by a detectable label, to the immobilized component, e.g., the coated surface containing the anchored component. When the reaction is complete, the non-reacted components are removed, e.g., by washing, and

complexes anchored on the solid surface are detected. When the originally non-immobilized component carries a detectable label, the detection of label immobilized on the surface indicates that complexing occurred. Where the originally non-immobilized component does not carry a label, complexing can be detected, for example, by using a labeled antibody specifically binding the immobilized complex.

[0728] If the candidate compound interacts with but does not bind to a particular PRO polypeptide encoded by a gene identified herein, its interaction with that polypeptide can be assayed by methods well known for detecting protein-protein interactions. Such assays include traditional approaches, such as, e.g., cross-linking, co-immunoprecipitation, and co-purification through gradients or chromatographic columns. In addition, protein-protein interactions can be monitored by using a yeast-based genetic system described by Fields and co-workers (Fields and Song, *Nature (London)*, 340:245-246(1989); Chien et al., *Proc. Natl. Acad. Sci. USA*, 88:9578-9582 (1991)) as disclosed by Chevray and Nathans, *Proc. Natl. Acad. Sci. USA*, 89:5789-5793 (1991). Many transcriptional activators, such as yeast GAL4, consist of two physically discrete modular domains, one acting as the DNA-binding domain, the other one functioning as the transcription-activation domain. The yeast expression system described in the foregoing publications (generally referred to as the "two-hybrid system") takes advantage of this property, and employs two hybrid proteins, one in which the target protein is fused to the DNA-binding domain of GAL4, and another, in which candidate activating proteins are fused to the activation domain. The expression of a GAL1-lacZ reporter gene under control of a GAL4-activated promoter depends on reconstitution of GAL4 activity via protein-protein interaction. Colonies containing interacting polypeptides are detected with a chromogenic substrate for  $\beta$ -galactosidase. A complete kit (MATCHMAKER™) for identifying protein-protein interactions between two specific proteins using the two-hybrid technique is commercially available from Clontech. This system can also be extended to map protein domains involved in specific protein interactions as well as to pinpoint amino acid residues that are crucial for these interactions.

[0729] Compounds that interfere with the interaction of a gene encoding a PRO polypeptide identified herein and other intra- or extracellular components can be tested as follows: usually a reaction mixture is prepared containing the product of the gene and the intra- or extracellular component under conditions and for a time allowing for the interaction and binding of the two products. To test the ability of a candidate compound to inhibit binding, the reaction is run in the absence and in the presence of the test compound. In addition, a placebo may be added to a third reaction mixture, to serve as positive control. The binding (complex formation) between the test compound and the intra- or extracellular component present in the mixture is monitored as described hereinabove. The formation of a complex in the control reaction(s) but not in the reaction mixture containing the test compound indicates that the test compound interferes with the interaction of the test compound and its reaction partner.

[0730] To assay for antagonists, the PRO polypeptide may be added to a cell along with the compound to be screened for a particular activity and the ability of the compound to

inhibit the activity of interest in the presence of the PRO polypeptide indicates that the compound is an antagonist to the PRO polypeptide. Alternatively, antagonists may be detected by combining the PRO polypeptide and a potential antagonist with membrane-bound PRO polypeptide receptors or recombinant receptors under appropriate conditions for a competitive inhibition assay. The PRO polypeptide can be labeled, such as by radioactivity, such that the number of PRO polypeptide molecules bound to the receptor can be used to determine the effectiveness of the potential antagonist. The gene encoding the receptor can be identified by numerous methods known to those of skill in the art, for example, ligand panning and FACS sorting. Coligan et al., *Current Protocols in Immun.*, 1(2): Chapter 5 (1991). Preferably, expression cloning is employed wherein polyadenylated RNA is prepared from a cell responsive to the PRO polypeptide and a cDNA library created from this RNA is divided into pools and used to transfect COS cells or other cells that are not responsive to the PRO polypeptide. Transfected cells that are grown on glass slides are exposed to labeled PRO polypeptide. The PRO polypeptide can be labeled by a variety of means including iodination or inclusion of a recognition site for a site-specific protein kinase. Following fixation and incubation, the slides are subjected to autoradiographic analysis. Positive pools are identified and sub-pools are prepared and re-transfected using an interactive sub-pooling and re-screening process, eventually yielding a single clone that encodes the putative receptor.

[0731] As an alternative approach for receptor identification, labeled PRO polypeptide can be photoaffinity-linked with cell membrane or extract preparations that express the receptor molecule. Cross-linked material is resolved by PAGE and exposed to X-ray film. The labeled complex containing the receptor can be excised, resolved into peptide fragments, and subjected to protein micro-sequencing. The amino acid sequence obtained from micro-sequencing would be used to design a set of degenerate oligonucleotide probes to screen a cDNA library to identify the gene encoding the putative receptor.

[0732] In another assay for antagonists, mammalian cells or a membrane preparation expressing the receptor would be incubated with labeled PRO polypeptide in the presence of the candidate compound. The ability of the compound to enhance or block this interaction could then be measured.

[0733] More specific examples of potential antagonists include an oligonucleotide that binds to the fusions of immunoglobulin with PRO polypeptide, and, in particular, antibodies including, without limitation, poly- and monoclonal antibodies and antibody fragments, single-chain antibodies, anti-idiotypic antibodies, and chimeric or humanized versions of such antibodies or fragments, as well as human antibodies and antibody fragments. Alternatively, a potential antagonist may be a closely related protein, for example, a mutated form of the PRO polypeptide that recognizes the receptor but imparts no effect, thereby competitively inhibiting the action of the PRO polypeptide.

[0734] Another potential PRO polypeptide antagonist is an antisense RNA or DNA construct prepared using antisense technology, where, e.g., an antisense RNA or DNA

molecule acts to block directly the translation of mRNA by hybridizing to targeted mRNA and preventing protein translation. Antisense technology can be used to control gene expression through triple-helix formation or antisense DNA or RNA, both of which methods are based on binding of a polynucleotide to DNA or RNA. For example, the 5' coding portion of the polynucleotide sequence, which encodes the mature PRO polypeptides herein, is used to design an antisense RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription (triple helix—see Lee et al., *Nucl. Acids Res.*, 6:3073 (1979); Cooney et al., *Science*, 241: 456 (1988); Dervan et al., *Science*, 251:1360 (1991)), thereby preventing transcription and the production of the PRO polypeptide. The antisense RNA oligonucleotide hybridizes to the mRNA in vivo and blocks translation of the mRNA molecule into the PRO polypeptide (antisense—Okano, *Neurochem.*, 56:560 (1991); *Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression* (CRC Press: Boca Raton, Fla., 1988). The oligonucleotides described above can also be delivered to cells such that the antisense RNA or DNA may be expressed in vivo to inhibit production of the PRO polypeptide. When antisense DNA is used, oligodeoxyribonucleotides derived from the translation-initiation site, e.g., between about -10 and +10 positions of the target gene nucleotide sequence, are preferred.

[0735] Potential antagonists include small molecules that bind to the active site, the receptor binding site, or growth factor or other relevant binding site of the PRO polypeptide, thereby blocking the normal biological activity of the PRO polypeptide. Examples of small molecules include, but are not limited to, small peptides or peptide-like molecules, preferably soluble peptides, and synthetic non-peptidyl organic or inorganic compounds.

[0736] Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. Ribozymes act by sequence-specific hybridization to the complementary target RNA, followed by endonucleolytic cleavage. Specific ribozyme cleavage sites within a potential RNA target can be identified by known techniques. For further details see, e.g., Rossi, *Current Biology*, 4:469-471 (1994), and PCT publication No. WO 97/33551 (published Sep. 18, 1997).

[0737] Nucleic acid molecules in triple-helix formation used to inhibit transcription should be single-stranded and composed of deoxynucleotides. The base composition of these oligonucleotides is designed such that it promotes triple-helix formation via Hoogsteen base-pairing rules, which generally require sizeable stretches of purines or pyrimidines on one strand of a duplex. For further details see, e.g., PCT publication No. WO 97/33551, supra.

[0738] These small molecules can be identified by any one or more of the screening assays discussed hereinabove and/or by any other screening techniques well known for those skilled in the art.

[0739] Diagnostic and therapeutic uses of the herein disclosed molecules may also be based upon the positive functional assay hits disclosed and described below.

**[0740] F. Anti-PRO Antibodies**

**[0741]** The present invention further provides anti-PRO antibodies. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

**[0742] 1. Polyclonal Antibodies**

**[0743]** The anti-PRO antibodies may comprise polyclonal antibodies. Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the PRO polypeptide or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

**[0744] 2. Monoclonal Antibodies**

**[0745]** The anti-PRO antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, *Nature*, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro.

**[0746]** The immunizing agent will typically include the PRO polypeptide or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, *Monoclonal Antibodies: Principles and Practice*, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

**[0747]** Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to

a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, Calif. and the American Type Culture Collection, Manassas, Va. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies [Kozbor, *J. Immunol.*, 133:3001 (1984); Brodeur et al., *Monoclonal Antibody Production Techniques and Applications*, Marcel Dekker, Inc., New York, (1987) pp. 51-63].

**[0748]** The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against PRO. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, *Anal. Biochem.*, 107:220 (1980).

**[0749]** After the desired hybridoma cells are identified, the clones may be subcloned by limiting dilution procedures and grown by standard methods [Goding, *supra*]. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells may be grown in vivo as ascites in a mammal.

**[0750]** The monoclonal antibodies secreted by the subclones may be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

**[0751]** The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in U.S. Pat. No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also may be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences [U.S. Pat. No. 4,816,567; Morrison et al., *supra*] or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

**[0752]** The antibodies may be monovalent antibodies. Methods for preparing monovalent antibodies are well known in the art. For example, one method involves recom-

binant expression of immunoglobulin light chain and modified heavy chain. The heavy chain is truncated generally at any point in the Fc region so as to prevent heavy chain crosslinking. Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted so as to prevent crosslinking.

[0753] In vitro methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can be accomplished using routine techniques known in the art.

#### [0754] 3. Human and Humanized Antibodies

[0755] The anti-PRO antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')<sub>2</sub> or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., *Nature* 321:522-525(1986); Riechmann et al., *Nature*, 332:323-329(1988); and Presta, *Curr. Op. Struct. Biol.* 2:593-596 (1992)].

[0756] Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature* 332:323-327 (1988); Verhoeven et al., *Science*, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Pat. No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

[0757] Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, *J. Mol. Biol.*, 227:381

(1991); Marks et al., *J. Mol. Biol.*, 222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, p. 77 (1985) and Boerner et al., *J. Immunol.*, 147(1):86-95 (1991)]. Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Pat. Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks et al., *BioTechnology* 10, 779-783 (1992); Lonberg et al., *Nature* 368 856-859 (1994); Morrison, *Nature* 368, 812-13 (1994); Fishwild et al., *Nature Biotechnology* 14, 845-51 (1996); Neuberger, *Nature Biotechnology* 14, 826 (1996); Lonberg and Huszar, *Intern. Rev. Immunol.* 13 65-93 (1995).

[0758] The antibodies may also be affinity matured using known selection and/or mutagenesis methods as described above. Preferred affinity matured antibodies have an affinity which is five times, more preferably 10 times, even more preferably 20 or 30 times greater than the starting antibody (generally murine, humanized or human) from which the matured antibody is prepared.

#### [0759] 4. Bispecific Antibodies

[0760] Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for the PRO, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit.

[0761] Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities [Milstein and Cuello, *Nature* 305:537-539 (1983)]. Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published May 13, 1993, and in Traunecker et al., *EMBO J.*, 10:3655-3659 (1991).

[0762] Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be 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. For further details of generating bispecific antibodies see, for example, Suresh et al., *Methods in Enzymology*, 121:210 (1986).

[0763] According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

[0764] Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')<sub>2</sub> bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared can be prepared using chemical linkage. Brennan et al, *Science* 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate F(ab')<sub>2</sub> fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

[0765] Fab' fragments may be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby et al., *J. Exp. Med.* 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')<sub>2</sub> molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

[0766] Various technique for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., *J. Immunol.* 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., *Proc. Natl. Acad. Sci. USA* 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V<sub>H</sub>) connected to a light-chain variable domain (V<sub>L</sub>) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V<sub>H</sub> and V<sub>L</sub> domains of one fragment are forced to pair with the complementary V<sub>L</sub>

and V<sub>H</sub> domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (scFv) dimers has also been reported. See, Gruber et al., *J. Immunol.* 152:5368 (1994).

[0767] Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., *J. Immunol.* 147:60 (1991).

[0768] Exemplary bispecific antibodies may bind to two different epitopes on a given PRO polypeptide herein. Alternatively, an anti-PRO polypeptide arm may be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD 16) so as to focus cellular defense mechanisms to the cell expressing the particular PRO polypeptide. Bispecific antibodies may also be used to localize cytotoxic agents to cells which express a particular PRO polypeptide. These antibodies possess a PRO-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the PRO polypeptide and further binds tissue factor (TF).

#### [0769] 5. Heteroconjugate Antibodies

[0770] Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells [U.S. Pat. No. 4,676,980], and for treatment of HIV infection [WO 91/00360; WO 92/200373; EP 03089]. It is contemplated that the antibodies may be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Pat. No. 4,676,980.

#### [0771] 6. Effector Function Engineering

[0772] It may be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) may be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated may have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., *J. Exp. Med.*, 176: 1191-1195 (1992) and Shopes, *J. Immunol.*, 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity may also be prepared using heterobifunctional cross-linkers as described in Wolff et al *Cancer Research*, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and may thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., *Anti-Cancer Drug Design*. 3: 219-230 (1989).

#### [0773] 7. Immunoconjugates

[0774] The invention also pertains to immunoconjugates comprising an antibody conjugated to acytotoxic agent such

as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radio-conjugate).

[0775] Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleuritesfordii proteins, dianthin proteins, *Phytolacca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include  $^{212}\text{Bi}$ ,  $^{131}\text{I}$ ,  $^{131}\text{In}$ ,  $^{90}\text{Y}$ , and  $^{186}\text{Re}$ . Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimide HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., *Science*, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

[0776] In another embodiment, the antibody may be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is conjugated to a cytotoxic agent (e.g., a radionucleotide).

#### [0777] 8. Immunoliposomes

[0778] The antibodies disclosed herein may also be formulated as immunoliposomes. Liposomes containing the antibody are prepared by methods known in the art, such as described in Epstein et al., *Proc. Natl. Acad. Sci. USA*, 82: 3688 (1985); Hwang et al., *Proc. Natl. Acad. Sci. USA*, 77: 4030 (1980); and U.S. Pat. Nos. 4,485,045 and 4,544,545. Liposomes with enhanced circulation time are disclosed in U.S. Pat. No. 5,013,556.

[0779] Particularly useful liposomes can be generated by the reverse-phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol, and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the antibody of the present invention can be conjugated to the liposomes as described in Martin et al., *J. Biol. Chem.*, 257: 286-288 (1982) via a disulfide-interchange reaction. A chemotherapeutic agent (such as Doxorubicin) is optionally contained within the liposome. See Gabizon et al., *J. National Cancer Inst.*, 81(19): 1484 (1989).

#### [0780] 9. Pharmaceutical Compositions of Antibodies

[0781] Antibodies specifically binding a PRO polypeptide identified herein, as well as other molecules identified by the screening assays disclosed hereinbefore, can be administered for the treatment of various disorders in the form of pharmaceutical compositions.

[0782] If the PRO polypeptide is intracellular and whole antibodies are used as inhibitors, internalizing antibodies are preferred. However, lipofections or liposomes can also be used to deliver the antibody, or an antibody fragment, into cells. Where antibody fragments are used, the smallest inhibitory fragment that specifically binds to the binding domain of the target protein is preferred. For example, based upon the variable-region sequences of an antibody, peptide molecules can be designed that retain the ability to bind the target protein sequence. Such peptides can be synthesized chemically and/or produced by recombinant DNA technology. See, e.g., Marasco et al., *Proc. Natl. Acad. Sci. USA*, 90: 7889-7893 (1993). The formulation herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Alternatively, or in addition, the composition may comprise an agent that enhances its function, such as, for example, a cytotoxic agent, cytokine, chemotherapeutic agent, or growth-inhibitory agent. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

[0783] The active ingredients may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacrylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles, and nanocapsules) or in macroemulsions. Such techniques are disclosed in Remington's *Pharmaceutical Sciences*, supra.

[0784] The formulations to be used for in vivo administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes.

[0785] Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, e.g., films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and  $\gamma$  ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT<sup>TM</sup> (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods. When encapsulated antibodies remain in the body for a long time, they may denature or aggregate as a result of exposure to moisture at 37° C., resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for stabilization depending on the mechanism involved. For



example, if the aggregation mechanism is discovered to be intermolecular S—S bond formation through thio-disulfide interchange, stabilization may be achieved by modifying sulfhydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

#### [0786] G. Uses for Anti-PRO Antibodies

[0787] The anti-PRO antibodies of the invention have various utilities. For example, anti-PRO antibodies may be used in diagnostic assays for PRO, e.g., detecting its expression (and in some cases, differential expression) in specific cells, tissues, or serum. Various diagnostic assay techniques known in the art may be used, such as competitive binding assays, director indirect sandwich assays and immunoprecipitation assays conducted in either heterogeneous or homogeneous phases [Zola, *Monoclonal Antibodies: A Manual of Techniques*, CRC Press, Inc. (1987) pp. 147-158]. The antibodies used in the diagnostic assays can be labeled with a detectable moiety. The detectable moiety should be capable of producing, either directly or indirectly, a detectable signal. For example, the detectable moiety may be a radioisotope, such as  $^3\text{H}$ ,  $^{14}\text{C}$ ,  $^{32}\text{P}$ ,  $^{35}\text{S}$ , or  $^{125}\text{I}$ , a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the detectable moiety may be employed, including those methods described by Hunter et al., *Nature*, 144:945 (1962); David et al., *Biochemistry*, 13:1014 (1974); Pain et al., *J. Immunol. Meth.*, 40:219 (1981); and Nygren, *J. Histochem. and Cytochem.*, 30:407 (1982).

[0788] Anti-PRO antibodies also are useful for the affinity purification of PRO from recombinant cell culture or natural sources. In this process, the antibodies against PRO are immobilized on a suitable support, such as a Sephadex resin or filter paper, using methods well known in the art. The immobilized antibody then is contacted with a sample containing the PRO to be purified, and thereafter the support is washed with a suitable solvent that will remove substantially all the material in the sample except the PRO, which is bound to the immobilized antibody. Finally, the support is washed with another suitable solvent that will release the PRO from the antibody.

[0789] The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

[0790] All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

#### EXAMPLES

[0791] Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following examples, and throughout the

specification, by ATCC accession numbers is the American Type Culture Collection, Manassas, Va.

#### Example 1

##### Extracellular Domain Homology Screening to Identify Novel Polypeptides and cDNA Encoding Therefor

[0792] The extracellular domain (ECD) sequences (including the secretion signal sequence, if any) from about 950 known secreted proteins from the Swiss-Prot public database were used to search EST databases. The EST databases included public databases (e.g., Dayhoff, GenBank), and proprietary databases (e.g. LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, Calif.). The search was performed using the computer program BLAST or BLAST-2 (Altschul et al., *Methods in Enzymology* 266:460480 (1996)) as a comparison of the ECD protein sequences to a 6 frame translation of the EST sequences. Those comparisons with a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, Wash.).

[0793] Using this extracellular domain homology screen, consensus DNA sequences were assembled relative to the other identified EST sequences using phrap. In addition, the consensus DNA sequences obtained were often (but not always) extended using repeated cycles of BLAST or BLAST-2 and phrap to extend the consensus sequence as far as possible using the sources of EST sequences discussed above.

[0794] Based upon the consensus sequences obtained as described above, oligonucleotides were then synthesized and used to identify by PCR a cDNA library that contained the sequence of interest and for use as probes to isolate a clone of the full-length coding sequence for a PRO polypeptide. Forward and reverse PCR primers generally range from 20 to 30 nucleotides and are often designed to give a PCR product of about 100-1000 bp in length. The probe sequences are typically 40-55 bp in length. In some cases, additional oligonucleotides are synthesized when the consensus sequence is greater than about 1-1.5 kbp. In order to screen several libraries for a full-length clone, DNA from the libraries was screened by PCR amplification, as per Ausubel et al., *Current Protocols in Molecular Biology*, with the PCR primer pair. A positive library was then used to isolate clones encoding the gene of interest using the probe oligonucleotide and one of the primer pairs.

[0795] The cDNA libraries used to isolate the cDNA clones were constructed by standard methods using commercially available reagents such as those from Invitrogen, San Diego, Calif. The cDNA was primed with oligo dT containing a NotI site, linked with blunt to SalI hemikinased adaptors, cleaved with NotI, sized appropriately by gel electrophoresis, and cloned in a defined orientation into a suitable cloning vector (such as pRKB or pRKD; pRK5B is a precursor of pRK5D that does not contain the SfiI site; see, Holmes et al., *Science*, 253:1278-1280 (1991)) in the unique XhoI and NotI sites.

## Example 2

## Isolation of cDNA Clones by Amylase Screening

**[0796]** 1. Preparation of Oligo dT Primed cDNA Library

**[0797]** mRNA was isolated from a human tissue of interest using reagents and protocols from Invitrogen, San Diego, Calif. (Fast Track 2). This RNA was used to generate an oligo dT primed cDNA library in the vector pRK5D using reagents and protocols from Life Technologies, Gaithersburg, Md. (Super Script Plasmid System). In this procedure, the double stranded cDNA was sized to greater than 1000 bp and the Sall/NotI linker cDNA was cloned into XhoI/NotI cleaved vector. pRK5D is a cloning vector that has an sp6 transcription initiation site followed by an SfiI restriction enzyme site preceding the XhoI/NotI cDNA cloning sites.

**[0798]** 2. Preparation of Random Primed cDNA Library

**[0799]** A secondary cDNA library was generated in order to preferentially represent the 5' ends of the primary cDNA clones. Sp6 RNA was generated from the primary library (described above), and this RNA was used to generate a random primed cDNA library in the vector pSST-AMY.0 using reagents and protocols from Life Technologies (Super Script Plasmid System, referenced above). In this procedure the double stranded cDNA was sized to 500-1000 bp, linker with blunt to NotI adaptors, cleaved with SfiI, and cloned into SfiI/NotI cleaved vector. pSST-AMY.0 is a cloning vector that has a yeast alcohol dehydrogenase promoter preceding the cDNA cloning sites and the mouse amylase sequence (the mature sequence without the secretion signal) followed by the yeast alcohol dehydrogenase terminator, after the cloning sites. Thus, cDNAs cloned into this vector that are fused in frame with amylase sequence will lead to the secretion of amylase from appropriately transfected yeast colonies.

**[0800]** 3. Transformation and Detection

**[0801]** DNA from the library described in paragraph 2 above was chilled on ice to which was added electrocompetent DH10B bacteria (Life Technologies, 20 ml). The bacteria and vector mixture was then electroporated as recommended by the manufacturer. Subsequently, SOC media (Life Technologies, 1 ml) was added and the mixture was incubated at 37° C. for 30 minutes. The transformants were then plated onto 20 standard 150 mm LB plates containing ampicillin and incubated for 16 hours (37° C.). Positive colonies were scraped off the plates and the DNA was isolated from the bacterial pellet using standard protocols, e.g. CsCl-gradient. The purified DNA was then carried on to the yeast protocols below.

**[0802]** The yeast methods were divided into three categories: (1) Transformation of yeast with the plasmid/cDNA combined vector; (2) Detection and isolation of yeast clones secreting amylase; and (3) PCR amplification of the insert directly from the yeast colony and purification of the DNA for sequencing and further analysis.

**[0803]** The yeast strain used was HD56-5A (ATCC-90785). This strain has the following genotype: MAT alpha, ura3-52, leu2-3, leu2-112, his3-11, his3-15, MAL<sup>+</sup>, SUC<sup>+</sup>, GAL<sup>+</sup>. Preferably, yeast mutants can be employed that have deficient post-translational pathways. Such mutants may have translocation deficient alleles in sec71, sec72, sec62,

with truncated sec71 being most preferred. Alternatively, antagonists (including antisense nucleotides and/or ligands) which interfere with the normal operation of these genes, other proteins implicated in this post translation pathway (e.g., SEC61p, SEC72p, SEC62p, SEC63p, TDJ1p or SSA1p-4p) or the complex formation of these proteins may also be preferably employed in combination with the amylase-expressing yeast.

**[0804]** Transformation was performed based on the protocol outlined by Gietz et al., *Nucl. Acid. Res.*, 20:1425 (1992). Transformed cells were then inoculated from agar into YEPD complex media broth (100 ml) and grown overnight at 30° C. The YEPD broth was prepared as described in Kaiser et al., *Methods in Yeast Genetics*, Cold Spring Harbor Press, Cold Spring Harbor, N.Y., p. 207 (1994). The overnight culture was then diluted to about 2×10<sup>6</sup> cells/ml (approx. OD<sub>600</sub>=0.1) into fresh YEPD broth (500 ml) and regrown to 1×10<sup>7</sup> cells/ml (approx. OD<sub>600</sub>=0.4-0.5).

**[0805]** The cells were then harvested and prepared for transformation by transfer into GS3 rotor bottles in a Sorval GS3 rotor at 5,000 rpm for 5 minutes, the supernatant discarded, and then resuspended into sterile water, and centrifuged again in 50 ml falcon tubes at 3,500 rpm in a Beckman GS-6KR centrifuge. The supernatant was discarded and the cells were subsequently washed with LiAc/TE (10 ml, 10 mM Tris-HCl, 1 mM EDTA pH 7.5, 100 mM Li<sub>200</sub>CCH<sub>3</sub>), and resuspended into LiAc/TE (2.5 ml).

**[0806]** Transformation took place by mixing the prepared cells (100 μl) with freshly denatured single stranded salmon testes DNA (Lofstrand Labs, Gaithersburg, Md.) and transforming DNA (1 μg, vol.<10 μl) in microfuge tubes. The mixture was mixed briefly by vortexing, then 40% PEG/TE (600 μl, 40% polyethylene glycol-4000, 10 mM Tris-HCl, 1 mM EDTA, 100 mM Li<sub>200</sub>CCH<sub>3</sub>, pH 7.5) was added. This mixture was gently mixed and incubated at 30° C. while agitating for 30 minutes. The cells were then heat shocked at 42° C. for 15 minutes, and the reaction vessel centrifuged in a microfuge at 12,000 rpm for 5-10 seconds, decanted and resuspended into TE (500 μl, 10 mM Tris-HCl, 1 mM EDTA pH 7.5) followed by recentrifugation. The cells were then diluted into TE (1 ml) and aliquots (200 μl) were spread onto the selective media previously prepared in 150 mm growth plates (VWR).

**[0807]** Alternatively, instead of multiple small reactions, the transformation was performed using a single, large scale reaction, wherein reagent amounts were scaled up accordingly.

**[0808]** The selective media used was a synthetic complete dextrose agar lacking uracil (SCD-Ura) prepared as described in Kaiser et al., *Methods in Yeast Genetics*, Cold Spring Harbor Press, Cold Spring Harbor, N.Y., p.208-210 (1994). Transformants were grown at 30° C. for 2-3 days.

**[0809]** The detection of colonies secreting amylase was performed by including red starch in the selective growth media. Starch was coupled to the red dye (Reactive Red-120, Sigma) as per the procedure described by Biely et al., *Anal. Biochem.*, 172:176-179 (1988). The coupled starch was incorporated into the SCD-Ura agar plates at a final concentration of 0.15% (w/v), and was buffered with potassium phosphate to a pH of 7.0 (50-100 mM final concentration).

[0810] The positive colonies were picked and streaked across fresh selective media (onto 150 mm plates) in order to obtain well isolated and identifiable single colonies. Well isolated single colonies positive for amylase secretion were detected by direct incorporation of red starch into buffered SCD-Ura agar. Positive colonies were determined by their ability to break down starch resulting in a clear halo around the positive colony visualized directly.

[0811] 4. Isolation of DNA by PCR Amplification

[0812] When a positive colony was isolated, a portion of it was picked by a toothpick and diluted into sterile water (30  $\mu$ l) in a 96 well plate. At this time, the positive colonies were either frozen and stored for subsequent analysis or immediately amplified. An aliquot of cells (5  $\mu$ l) was used as a template for the PCR reaction in a 25  $\mu$ l volume containing: 0.5  $\mu$ l Klentaq (Clontech, Palo Alto, Calif.); 4.0  $\mu$ l 10 mM dNTP's (Perkin Elmer-Cetus); 2.5  $\mu$ l Kentaq buffer (Clontech); 0.25  $\mu$ l forward oligo 1; 0.25  $\mu$ l reverse oligo 2; 12.5  $\mu$ l distilled water. The sequence of the forward oligonucleotide 1 was:

[0813] 5'-TGTAACGACGGCCAGTTAAATAGAC-CTGCAATTATTAATCT-3' (SEQ ID NO:553)

[0814] The sequence of reverse oligonucleotide 2 was:

[0815] 5'-CAGGAAACAGCTATGACCACCTGCA-CACCTGCAAATCCATT-3' (SEQ ID NO:554)

[0816] PCR was then performed as follows:

a.		Denature	92° C.,	5 minutes
b.	3 cycles of:	Denature	92° C.,	30 seconds
		Anneal	59° C.,	30 seconds
		Extend	72° C.,	60 seconds
c.	3 cycles of:	Denature	92° C.,	30 seconds
		Anneal	57° C.,	30 seconds
		Extend	72° C.,	60 seconds
d.	25 cycles of:	Denature	92° C.,	30 seconds
		Anneal	55° C.,	30 seconds
		Extend	72° C.,	60 seconds
e.		Hold	4° C.	

[0817] The underlined regions of the oligonucleotides annealed to the ADH promoter region and the amylase region, respectively, and amplified a 307 bp region from vector pSST-AMY.0 when no insert was present. Typically, the first 18 nucleotides of the 5' end of these oligonucleotides contained annealing sites for the sequencing primers. Thus, the total product of the PCR reaction from an empty vector was 343 bp. However, signal sequence-fused cDNA resulted in considerably longer nucleotide sequences.

[0818] Following the PCR, an aliquot of the reaction (5  $\mu$ l) was examined by agarose gel electrophoresis in a 1% agarose gel using a Tris-Borate-EDTA (TBE) buffering system as described by Sambrook et al., supra. Clones resulting in a single strong PCR product larger than 400 bp were further analyzed by DNA sequencing after purification with a 96 Qiaquick PCR clean-up column (Qiagen Inc., Chatsworth, Calif.).

Example 3

Isolation of cDNA Clones Using Signal Algorithm Analysis

[0819] Various polypeptide-encoding nucleic acid sequences were identified by applying a proprietary signal

sequence finding algorithm developed by Genentech, Inc. (South San Francisco, Calif.) upon ESTs as well as clustered and assembled EST fragments from public (e.g., GenBank) and/or private (LIFESEQ®, Incyte Pharmaceuticals, Inc., Palo Alto, Calif.) databases. The signal sequence algorithm computes a secretion signal score based on the character of the DNA nucleotides surrounding the first and optionally the second methionine codon(s) (ATG) at the 5'-end of the sequence or sequence fragment under consideration. The nucleotides following the first ATG must code for at least 35 unambiguous amino acids without any stop codons. If the first ATG has the required amino acids, the second is not examined. If neither meets the requirement, the candidate sequence is not scored. In order to determine whether the EST sequence contains an authentic signal sequence, the DNA and corresponding amino acid sequences surrounding the ATG codon are scored using a set of seven sensors (evaluation parameters) known to be associated with secretion signals. Use of this algorithm resulted in the identification of numerous polypeptide-encoding nucleic acid sequences.

Example 4

Isolation of cDNA clones Encoding Human PRO Polypeptides

[0820] Using the techniques described in Examples 1 to 3 above, numerous full-length cDNA clones were identified as encoding PRO polypeptides as disclosed herein. These cDNAs were then deposited under the terms of the Budapest Treaty with the American Type Culture Collection, 10801 University Blvd., Manassas, Va. 20110-2209, USA (ATCC) as shown in Table 7 below.

TABLE 7

Material	ATCC Dep. No.	Deposit Date
DNA16438-1387	209771	Apr. 14, 1998
DNA19360-2552	203654	Feb. 9, 1999
DNA33455-1548	PTA-127	May 25, 1999
DNA37155-2651	PTA-429	Jul. 27, 1999
DNA38269-2654	PTA-432	Jul. 27, 1999
DNA40619-1220	209525	Dec. 10, 1997
DNA44174-2513	203577	Jan. 12, 1999
DNA44675-2662	PTA-430	Jul. 27, 1999
DNA45408-2615	PTA-203	Jun. 8, 1999
DNA48606-1479	203040	Jul. 1, 1998
DNA52753-2656	PTA-611	Aug. 31, 1999
DNA53915-1258	209593	Jan. 21, 1998
DNA53991-2553	203649	Feb. 9, 1999
DNA54009-2517	203574	Jan. 12, 1999
DNA56055-1643	PTA-129	May 25, 1999
DNA57033-1403	209905	May 27, 1998
DNA57252-1453	203585	Jan. 12, 1999
DNA58799-1652	203665	Feb. 9, 1999
DNA59770-2652	PTA-427	Jul. 27, 1999
DNA59774-2665	PTA-615	Aug. 31, 1999
DNA60281-2518	203582	Jan. 12, 1999
DNA60736-2559	203838	Mar. 9, 1999
DNA61875-2653	PTA-428	Jul. 27, 1999
DNA62312-2558	203836	Mar. 9, 1999
DNA62849-1604	PTA-205	Jun. 8, 1999
DNA66307-2661	PTA-431	Jul. 27, 1999
DNA66677-2535	203659	Feb. 9, 1999
DNA71235-1706	203584	Jan. 12, 1999
DNA71289-2547	PTA-126	May 25, 1999
DNA73775-1707	PTA-US	May 25, 1999
DNA76385-1692	203664	Feb. 9, 1999

TABLE 7-continued

Material	ATCC Dep. No.	Deposit Date
DNA76395-2527	203578	Jan. 12, 1999
DNA77622-2516	203554	Dec. 22, 1998
DNA77629-2573	203850	Mar. 16, 1999
DNA77645-2648	PTA-45	May 11, 1999
DNA79302-2521	203545	Dec. 22, 1998
DNA79865-2519	203544	Dec. 22, 1998
DNA80135-2655	PTA-234	Jun. 15, 1999
DNA80794-2568	203848	Mar. 16, 1999
DNA80796-2523	203555	Dec. 22, 1998
DNA80840-2605	203949	Apr. 20, 1999
DNA80899-2501	203539	Dec. 15, 1998
DNA81228-2580	203871	Mar. 23, 1999
DNA81761-2583	203862	Mar. 23, 1999
DNA82358-2738	PTA-510	Aug. 10, 1999
DNA82364-2538	203603	Jan. 20, 1999
DNA82424-2566	203813	Mar. 2, 1999
DNA82430-2557	203812	Mar. 2, 1999
DNA83500-2506	203391	Oct. 29, 1998
DNA83509-2612	203965	Apr. 27, 1999
DNA83560-2569	203816	Mar. 2, 1999
DNA84139-2555	203814	Mar. 2, 1999
DNA84141-2556	203810	Mar. 2, 1999
DNA84142-2613	PTA-22	May 4, 1999
DNA84318-2520	203580	Jan. 12, 1999
DNA84909-2590	203889	Mar. 30, 1999
DNA84912-2610	203964	Apr. 27, 1999
DNA84925-2514	203548	Dec. 22, 1998
DNA84928-2564	203817	Mar. 2, 1999
DNA84932-2657	PTA-235	Jun. 15, 1999
DNA86592-2607	203968	Apr. 27, 1999
DNA86594-2587	203894	Mar. 30, 1999
DNA86647-2591	203893	Mar. 30, 1999
DNA87185-2563	203811	Mar. 2, 1999
DNA87656-2582	203867	Mar. 23, 1999
DNA87974-2609	203963	Apr. 27, 1999
DNA88001-2565	203815	Mar. 2, 1999
DNA88004-2575	203890	Mar. 30, 1999
DNA89220-2608	PTA-130	May 25, 1999
DNA89947-2618	203970	Apr. 27, 1999
DNA90842-2574	203845	Mar. 16, 1999
DNA91775-2581	203861	Mar. 23, 1999
DNA91779-2571	203844	Mar. 16, 1999
DNA92217-2697	PTA-513	Aug. 10, 1999
DNA92219-2541	203663	Feb. 9, 1999
DNA92223-2567	203851	Mar. 16, 1999
DNA92225-2603	203950	Apr. 20, 1999
DNA92232-2589	203895	Mar. 30, 1999
DNA92233-2599	PTA-134	May 25, 1999
DNA92243-2549	203852	Mar. 16, 1999
DNA92253-2671	PTA-258	Jun. 22, 1999
DNA92254-2672	PTA-259	Jun. 22, 1999
DNA92255-2584	203866	Mar. 23, 1999
DNA92269-2570	203853	Mar. 16, 1999
DNA92288-2588	203892	Mar. 30, 1999
DNA92290-2550	203847	Mar. 16, 1999
DNA93012-2622	PTA-21	May 4, 1999
DNA93020-2642	PTA-121	May 25, 1999
DNA94830-2604	203951	Apr. 20, 1999
DNA94833-2579	203869	Mar. 23, 1999
DNA94838-2658	PTA-232	Jun. 15, 1999
DNA94844-2686	PTA-385	Jul. 20, 1999
DNA94854-2586	203864	Mar. 23, 1999
DNA96868-2677	PTA-262	Jun. 22, 1999
DNA96871-2683	PTA-381	Jul. 20, 1999
DNA96880-2624	PTA-15	May 4, 1999
DNA96986-2660	PTA-239	Jun. 15, 1999
DNA96988-2685	PTA-384	Jul. 20, 1999
DNA96995-2709	PTA-475	Aug. 3, 1999
DNA97004-2562	203854	Mar. 16, 1999
DNA97005-2687	PTA-378	Jul. 20, 1999
DNA97009-2668	PTA-257	Jun. 22, 1999
DNA97013-2667	PTA-231	Jun. 15, 1999
DNA98380-2690	PTA-388	Jul. 20, 1999
DNA98561-2696	PTA-620	Aug. 31, 1999

TABLE 7-continued

Material	ATCC Dep. No.	Deposit Date
DNA98575-2644	PTA-118	May 25, 1999
DNA98593-2694	PTA-477	Aug. 3, 1999
DNA98600-2703	PTA-488	Aug. 3, 1999
DNA99391-2572	203849	Mar. 16, 1999
DNA99393-2560	203837	Mar. 9, 1999
DNA100276-2684	PTA-380	Jul. 20, 1999
DNA100312-2645	PTA-44	May 11, 1999
DNA100902-2646	PTA-42	May 11, 1999
DNA102899-2679	PTA-123	May 25, 1999
DNA104875-2720	PTA-482	Aug. 3, 1999
DNA105680-2710	PTA-483	Aug. 3, 1999
DNA105779-2708	PTA-485	Aug. 3, 1999
DNA105794-2695	PTA-480	Aug. 3, 1999
DNA105838-2702	PTA-476	Aug. 3, 1999
DNA107698-2715	PTA-472	Aug. 3, 1999
DNA107701-2711	PTA-487	Aug. 3, 1999
DNA107781-2707	PTA-484	Aug. 3, 1999
DNA108670-2744	PTA-546	Aug. 17, 1999
DNA108688-2725	PTA-515	Aug. 10, 1999
DNA108769-2765	PTA-861	Oct. 19, 1999
DNA108935-2721	PTA-518	Aug. 10, 1999
DNA110700-2716	PTA-512	Aug. 10, 1999
DNA111750-2706	PTA-489	Aug. 3, 1999
DNA123430-2755	PTA-614	Aug. 31, 1999
DNA125154-2785	PTA-957	Nov. 16, 1999
DNA142238-2768	PTA-819	Oct. 5, 1999
DNA22779-1130	209280	Sept. 18, 1997
DNA26847-1395	209772	Apr. 14, 1998
DNA27864-1155	209375	Oct. 16, 1997
DNA27865-1091	209296	Sept. 23, 1997
DNA28497-1130	209279	Sept. 18, 1997
DNA29101-1122	209653	Mar. 5, 1998
DNA32286-1191	209385	Oct. 16, 1997
DNA32288-1132	209261	Sept. 16, 1997
DNA32290-1164	209384	Oct. 16, 1997
DNA32292-1131	209258	Sept. 16, 1997
DNA32298-1132	209257	Sept. 16, 1997
DNA33085-1110	209087	May 30, 1997
DNA33087-1158	209381	Oct. 16, 1997
DNA33089-1132	209262	Sept. 16, 1997
DNA33092-1202	209420	Oct. 28, 1997
DNA33094-1131	209256	Sept. 16, 1997
DNA33107-1135	209251	Sept. 16, 1997
DNA33221-1133	209263	Sept. 16, 1997
DNA33223-1136	209264	Sept. 16, 1997
DNA33460-1166	209376	Oct. 16, 1997
DNA33473-1176	209391	Oct. 17, 1997
DNA33785-1143	209417	Oct. 28, 1997
DNA33786-1132	209253	Sept. 16, 1997
DNA34353-1428	209855	May 12, 1998
DNA34392-1170	209526	Dec. 10, 1997
DNA34434-1139	209252	Sept. 16, 1997
DNA35558-1167	209374	Oct. 16, 1997
DNA35595-1228	209528	Dec. 10, 1997
DNA35638-1216	209265	Sept. 16, 1997
DNA35639-1172	209396	Oct. 17, 1997
DNA35663-1129	209201	Aug. 18, 1997
DNA35674-1142	209416	Oct. 28, 1997
DNA35841-1173	209403	Oct. 17, 1997
DNA35916-1161	209419	Oct. 28, 1997
DNA35918-1174	209402	Oct. 17, 1997
DNA36350-1158	209378	Oct. 16, 1997
DNA37140-1234	209489	Nov. 21, 1997
DNA37150-1178	209401	Oct. 17, 1997
DNA38260-1180	209397	Oct. 17, 1997
DNA40021-1154	209389	Oct. 17, 1997
DNA40587-1231	209438	Nov. 7, 1997
DNA40592-1242	209492	Nov. 21, 1997
DNA40620-1183	209388	Oct. 17, 1997
DNA40628-1216	209432	Nov. 7, 1997
DNA40981-1234	209439	Nov. 7, 1997
DNA40982-1235	209433	Nov. 7, 1997
DNA41234-1242	209618	Feb. 5, 1998
DNA43046-1225	209484	Nov. 21, 1997

TABLE 7-continued

Material	ATCC Dep. No.	Deposit Date
DNA43316-1237	209487	Nov. 21, 1991
DNA44167-1243	209434	Nov. 7, 1997
DNA44184-1319	209704	Mar. 26, 1998
DNA44194-1317	209808	Apr. 28, 1998
DNA44196-1353	209847	May 6, 1998
DNA45419-1252	209616	Feb. 5, 1998
DNA46777-1253	209619	Feb. 5, 1998
DNA47394-1572	203109	Aug. 11, 1998
DNA48331-1329	209715	Mar. 31, 1998
DNA48336-1309	209669	Mar. 11, 1998
DNA49142-1430	203002	Jun. 23, 1998
DNA49646-1327	209705	Mar. 26, 1998
DNA49821-1562	209981	Jun. 16, 1998
DNA49829-1346	209749	Apr. 7, 1998
DNA50921-1458	209859	May 12, 1998
DNA52187-1354	209845	May 6, 1998
DNA52196-1348	209748	Apr. 7, 1998
DNA52598-1518	203107	Aug. 11, 1998
DNA54228-1366	209801	Apr. 23, 1998
DNA56047-1456	209948	Jun. 9, 1998
DNA56112-1379	209883	May 20, 1998
DNA56113-1378	203049	Jul. 1, 1998
DNA56352-1358	209846	May 6, 1998
DNA56433-1406	209857	May 12, 1998
DNA56439-1376	209864	May 14, 1998
DNA57530-1375	209880	May 20, 1998
DNA57689-1385	209869	May 14, 1998
DNA57690-1374	209950	Jun. 9, 1998
DNA57693-1424	203008	Jun. 23, 1998
DNA57838-1337	203014	Jun. 23, 1998
DNA58721-1475	203110	Aug. 11, 1998
DNA59205-1421	203009	Jun. 23, 1998
DNA59215-1425	209961	Jun. 9, 1998
DNA59220-1514	209962	Jun. 9, 1998
DNA59294-1381	209866	May 14, 1998
DNA59488-1603	203157	Aug. 25, 1998
DNA59588-1571	203106	Aug. 11, 1998
DNA59606-1471	209945	Jun. 9, 1998
DNA59620-1463	209989	Jun. 16, 1998
DNA59767-1489	203108	Aug. 11, 1998
DNA59777-1480	203111	Aug. 11, 1998
DNA59814-1486	203359	Oct. 20, 1998
DNA59839-1461	209988	Jun. 16, 1998
DNA59846-1503	209978	Jun. 16, 1998
DNA59847-1511	203098	Aug. 4, 1998
DNA60615-1483	209980	Jun. 16, 1998
DNA60621-1516	203091	Aug. 4, 1998
DNA60622-1525	203090	Aug. 4, 1998
DNA60627-1508	203092	Aug. 4, 1998
DNA60764-1533	203452	Nov. 10, 1998
DNA60775-1532	203173	Sept. 1, 1998
DNA61185-1646	203464	Nov. 17, 1998
DNA61873-1574	203132	Aug. 18, 1998
DNA62306-1570	203254	Sept. 9, 1998
DNA62808-1582	203358	Oct. 20, 1998
DNA62814-1521	203093	Aug. 4, 1998
DNA64885-1529	203457	Nov. 3, 1998
DNA64886-1601	203241	Sept. 9, 1998
DNA64888-1542	203249	Sept. 9, 1998
DNA64889-1541	203250	Sept. 9, 1998
DNA64890-1612	203131	Aug. 18, 1998
DNA64903-1553	203223	Sept. 15, 1998
DNA64905-1558	203233	Sept. 15, 1998
DNA65402-1540	203252	Sept. 9, 1998
DNA65405-1547	203476	Nov. 17, 1998
DNA65412-1523	203094	Aug. 4, 1998
DNA66309-1538	203235	Sept. 15, 1998
DNA66667-1596	203267	Sept. 22, 1998
DNA66675-1587	203282	Sept. 22, 1998
DNA68818-2536	203657	Feb. 9, 1999
DNA68864-1629	203276	Sept. 22, 1998
DNA68872-1620	203160	Aug. 25, 1998
DNA71159-1617	203135	Aug. 18, 1998
DNA73727-1673	203459	Nov. 3, 1998

TABLE 7-continued

Material	ATCC Dep. No.	Deposit Date
DNA73739-1645	203270	Sept. 22, 1998
DNA76400-2528	203573	Jan. 12, 1999
DNA76510-2504	203477	Nov. 17, 1998
DNA76529-1666	203315	Oct. 6, 1998
DNA76538-1670	203313	Oct. 6, 1998
DNA77301-1708	203407	Oct. 27, 1998
DNA77624-2515	203553	Dec. 22, 1998
DNA79230-2525	203549	Dec. 22, 1998
DNA79862-2522	203550	Dec. 22, 1998
DNA80145-2594	PTA-204	Jun. 8, 1999
DNA83500-2506	203391	Oct. 29, 1998
DNA84917-2597	203863	Mar. 23, 1999
DNA92218-2554	203834	Mar. 9, 1999
DNA96042-2682	PTA-382	Jul. 20, 1999

[0821] These deposits were made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and the Regulations thereunder (Budapest Treaty). This assures maintenance of a viable culture of the deposit for 30 years from the date of deposit. The deposits will be made available by ATCC under the terms of the Budapest Treaty, and subject to an agreement between Genentech, Inc. and ATCC, which assures permanent and unrestricted availability of the progeny of the culture of the deposit to the public upon issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent application, whichever comes first, and assures availability of the progeny to one determined by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to 35 USC §122 and the Commissioner's rules pursuant thereto (including 37 CFR §1.14 with particular reference to 886 OG 638).

[0822] The assignee of the present application has agreed that if a culture of the materials on deposit should die or be lost or destroyed when cultivated under suitable conditions, the materials will be promptly replaced on notification with another of the same. Availability of the deposited material is not to be construed as a license to practice the invention in contravention of the rights granted under the authority of any government in accordance with its patent laws.

Example 5

Use of PRO as a Hybridization Probe

[0823] The following method describes use of a nucleotide sequence encoding PRO as a hybridization probe.

[0824] DNA comprising the coding sequence of full-length or mature PRO as disclosed herein is employed as a probe to screen for homologous DNAs (such as those encoding naturally-occurring variants of PRO) in human tissue cDNA libraries or human tissue genomic libraries.

[0825] Hybridization and washing of filters containing either library DNAs is performed under the following high stringency conditions. Hybridization of radiolabeled PRO-derived probe to the filters is performed in a solution of 50% formamide, 5× SSC, 0.1% SDS, 0.1% sodium pyrophosphate, 50 mM sodium phosphate, pH 6.8, 2× Denhardt's solution, and 10% dextran sulfate at 42° C. for 20 hours.

Washing of the filters is performed in an aqueous solution of 0.1× SSC and 0.1% SDS at 42° C.

[0826] DNAs having a desired sequence identity with the DNA encoding full-length native sequence PRO can then be identified using standard techniques known in the art.

#### Example 6

##### Expression of PRO in *E. coli*

[0827] This example illustrates preparation of an unglycosylated form of PRO by recombinant expression in *E. coli*.

[0828] The DNA sequence encoding PRO is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector. A variety of expression vectors may be employed. An example of a suitable vector is pBR322 (derived from *E. coli*; see Bolivar et al., *Gene*, 2:95 (1977)) which contains genes for ampicillin and tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. The PCR amplified sequences are then ligated into the vector. The vector will preferably include sequences which encode for an antibiotic resistance gene, a trp promoter, a polyhis leader (including the first six STII codons, polyhis sequence, and enterokinase cleavage site), the PRO coding region, lambda transcriptional terminator, and an argu gene.

[0829] The ligation mixture is then used to transform a selected *E. coli* strain using the methods described in Sambrook et al., *supra*. Transformants are identified by their ability to grow on LB plates and antibiotic resistant colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis and DNA sequencing.

[0830] Selected clones can be grown overnight in liquid culture medium such as LB broth supplemented with antibiotics. The overnight culture may subsequently be used to inoculate a larger scale culture. The cells are then grown to a desired optical density, during which the expression promoter is turned on.

[0831] After culturing the cells for several more hours, the cells can be harvested by centrifugation. The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the solubilized PRO protein can then be purified using a metal chelating column under conditions that allow tight binding of the protein.

[0832] PRO may be expressed in *E. coli* in a poly-His tagged form, using the following procedure. The DNA encoding PRO is initially amplified using selected PCR primers. The primers will contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector, and other useful sequences providing for efficient and reliable translation initiation, rapid purification on a metal chelation column, and proteolytic removal with enterokinase. The PCR-amplified, poly-His tagged sequences are then ligated into an expression vector, which is used to transform an *E. coli* host based on strain 52 (W3110 fuhA(tonA) Ion galE rpoHts(htpRts) clpP(lacIq). Transformants are first grown in LB containing 50 mg/ml carbenicillin at 30° C. with shaking until an O.D.600 of 3-5 is reached. Cultures are then diluted 50-100 fold into CRAP media (prepared by mixing 3.57 g (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>, 0.71 g sodium citrate-2H<sub>2</sub>O, 1.07 g KCl, 5.36 g Difco yeast extract,

5.36 g Sheffield hycase SF in 500 mL water, as well as 110 mM MPOS, pH 7.3, 0.55% (w/v) glucose and 7 mM MgSO<sub>4</sub>) and grown for approximately 20-30 hours at 30° C. with shaking. Samples are removed to verify expression by SDS-PAGE analysis, and the bulk culture is centrifuged to pellet the cells. Cell pellets are frozen until purification and refolding.

[0833] *E. coli* paste from 0.5 to 1 L fermentations (6-10 g pellets) is resuspended in 10 volumes (w/v) in 7 M guanidine, 20 mM Tris, pH 8 buffer. Solid sodium sulfite and sodium tetrathionate is added to make final concentrations of 0.1M and 0.02 M, respectively, and the solution is stirred overnight at 4° C. This step results in a denatured protein with all cysteine residues blocked by sulfitolization. The solution is centrifuged at 40,000 rpm in a Beckman Ultracentrifuge for 30 min. The supernatant is diluted with 3-5 volumes of metal chelate column buffer (6 M guanidine, 20 mM Tris, pH 7.4) and filtered through 0.22 micron filters to clarify. The clarified extract is loaded onto a 5 ml Qiagen Ni-NTA metal chelate column equilibrated in the metal chelate column buffer. The column is washed with additional buffer containing 50 mM imidazole (Calbiochem, Utrol grade), pH 7.4. The protein is eluted with buffer containing 250 mM imidazole. Fractions containing the desired protein are pooled and stored at 4° C. Protein concentration is estimated by its absorbance at 280 nm using the calculated extinction coefficient based on its amino acid sequence.

[0834] The proteins are refolded by diluting the sample slowly into freshly prepared refolding buffer consisting of: 20 mM Tris, pH 8.6, 0.3 M NaCl, 2.5 M urea, 5 mM cysteine, 20 mM glycine and 1 mM EDTA. Refolding volumes are chosen so that the final protein concentration is between 50 to 100 micrograms/ml. The refolding solution is stirred gently at 4° C. for 12-36 hours. The refolding reaction is quenched by the addition of TFA to a final concentration of 0.4% (pH of approximately 3). Before further purification of the protein, the solution is filtered through a 0.22 micron filter and acetonitrile is added to 2-10% final concentration. The refolded protein is chromatographed on a Poros R1/H reversed phase column using a mobile buffer of 0.1% TFA with elution with a gradient of acetonitrile from 10 to 80%. Aliquots of fractions with A280 absorbance are analyzed on SDS polyacrylamide gels and fractions containing homogeneous refolded protein are pooled. Generally, the properly refolded species of most proteins are eluted at the lowest concentrations of acetonitrile since those species are the most compact with their hydrophobic interiors shielded from interaction with the reversed phase resin. Aggregated species are usually eluted at higher acetonitrile concentrations. In addition to resolving misfolded forms of proteins from the desired form, the reversed phase step also removes endotoxin from the samples.

[0835] Fractions containing the desired folded PRO polypeptide are pooled and the acetonitrile removed using a gentle stream of nitrogen directed at the solution. Proteins are formulated into 20 mM Hepes, pH 6.8 with 0.14 M sodium chloride and 4% mannitol by dialysis or by gel filtration using G25 Superfine (Pharmacia) resins equilibrated in the formulation buffer and sterile filtered.

[0836] Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

## Example 7

## Expression of PRO in Mammalian Cells

[0837] This example illustrates preparation of a potentially glycosylated form of PRO by recombinant expression in mammalian cells.

[0838] The vector, pRK5 (see EP 307,247, published Mar. 15, 1989), is employed as the expression vector. Optionally, the PRO DNA is ligated into pRK5 with selected restriction enzymes to allow insertion of the PRO DNA using ligation methods such as described in Sambrook et al., *supra*. The resulting vector is called pRK5-PRO.

[0839] In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown to confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10  $\mu$ g pRK5-PRO DNA is mixed with about 1  $\mu$ g DNA encoding the VA RNA gene [Thimmappaya et al., *Cell*, 31:543 (1982)] and dissolved in 500  $\mu$ l of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M  $\text{CaCl}_2$ . To this mixture is added, dropwise, 500  $\mu$ l of 50 mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM  $\text{NaPO}_4$ , and a precipitate is allowed to form for 10 minutes at 25° C. The precipitate is suspended and added to the 293 cells and allowed to settle for about four hours at 37° C. The culture medium is aspirated off and 2 ml of 20% glycerol in PBS is added for 30 seconds. The 293 cells are then washed with serum free medium, fresh medium is added and the cells are incubated for about 5 days.

[0840] Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture medium (alone) or culture medium containing 200  $\mu$ Ci/ml  $^{35}\text{S}$ -cysteine and 200  $\mu$ Ci/ml  $^{35}\text{S}$ -methionine. After a 12 hour incubation, the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15% SDS gel. The processed gel may be dried and exposed to film for a selected period of time to reveal the presence of PRO polypeptide. The cultures containing transfected cells may undergo further incubation (in serum free medium) and the medium is tested in selected bioassays.

[0841] In an alternative technique, PRO may be introduced into 293 cells transiently using the dextran sulfate method described by Somparyrac et al., *Proc. Natl. Acad. Sci.*, 12:7575 (1981). 293 cells are grown to maximal density in a spinner flask and 700  $\mu$ g pRK5-PRO DNA is added. The cells are first concentrated from the spinner flask by centrifugation and washed with PBS. The DNA-dextran precipitate is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue culture medium, and re-introduced into the spinner flask containing tissue culture medium, 5  $\mu$ g/ml bovine insulin and 0.1  $\mu$ g/ml bovine transferrin. After about four days, the conditioned media is centrifuged and filtered to remove cells and debris. The sample containing expressed PRO can then be concentrated and purified by any selected method, such as dialysis and/or column chromatography.

[0842] In another embodiment, PRO can be expressed in CHO cells. The pRK5-PRO can be transfected into CHO cells using known reagents such as  $\text{CaPO}_4$  or DEAE-dextran. As described above, the cell cultures can be incubated, and the medium replaced with culture medium (alone) or

medium containing a radiolabel such as  $^{35}\text{S}$ -methionine. After determining the presence of PRO polypeptide, the culture medium may be replaced with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed PRO can then be concentrated and purified by any selected method.

[0843] Epitope-tagged PRO may also be expressed in host CHO cells. The PRO may be subcloned out of the pRK5 vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as a poly-his tag into a Baculovirus expression vector. The poly-his tagged PRO insert can then be subcloned into a SV40 driven vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells can be transfected (as described above) with the SV40 driven vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged PRO can then be concentrated and purified by any selected method, such as by  $\text{Ni}^{2+}$ -chelate affinity chromatography.

[0844] PRO may also be expressed in CHO and/or COS cells by a transient expression procedure or in CHO cells by another stable expression procedure.

[0845] Stable expression in CHO cells is performed using the following procedure. The proteins are expressed as an IgG construct (immunoadhesin), in which the coding sequences for the soluble forms (e.g. extracellular domains) of the respective proteins are fused to an IgG1 constant region sequence containing the hinge, CH2 and CH2 domains and/or is a poly-His tagged form.

[0846] Following PCR amplification, the respective DNAs are subcloned in a CHO expression vector using standard techniques as described in Ausubel et al., *Current Protocols of Molecular Biology*, Unit 3.16, John Wiley and Sons (1997). CHO expression vectors are constructed to have compatible restriction sites 5' and 3' of the DNA of interest to allow the convenient shuttling of cDNA's. The vector used expression in CHO cells is as described in Lucas et al., *Nucl. Acids Res.* 24:9 (1774-1779 (1996)), and uses the SV40 early promoter/enhancer to drive expression of the cDNA of interest and dihydrofolate reductase (DHFR). DHFR expression permits selection for stable maintenance of the plasmid following transfection.

[0847] Twelve micrograms of the desired plasmid DNA is introduced into approximately 10 million CHO cells using commercially available transfection reagents Superfect® (Quiagen), Dospoer® or Eugene® (Boehringer Mannheim). The cells are grown as described in Lucas et al., *supra*. Approximately  $3 \times 10^{-7}$  cells are frozen in an ampule for further growth and production as described below.

[0848] The ampules containing the plasmid DNA are thawed by placement into water bath and mixed by vortexing. The contents are pipetted into a centrifuge tube containing 10 mLs of media and centrifuged at 1000 rpm for 5 minutes. The supernatant is aspirated and the cells are resuspended in 10 mL of selective media (0.2  $\mu$ m filtered PS20 with 5% 0.2  $\mu$ m diafiltered fetal bovine serum). The cells are then aliquoted into a 100 mL spinner containing 90 mL of selective media. After 1-2 days, the cells are transferred into a 250 mL spinner filled with 150 mL selective growth medium and incubated at 37° C. After another 2-3

days, 250 mL, 500 mL and 2000 mL spinners are seeded with  $3 \times 10^5$  cells/mL. The cell media is exchanged with fresh media by centrifugation and resuspension in production medium. Although any suitable CHO media may be employed, a production medium described in U.S. Pat. No. 5,122,469, issued Jun. 16, 1992 may actually be used. A 3L production spinner is seeded at  $1.2 \times 10^5$  cells/mL. On day 0, the cell number pH is determined. On day 1, the spinner is sampled and sparging with filtered air is commenced. On day 2, the spinner is sampled, the temperature shifted to 33° C., and 30 mL of 500 g/L glucose and 0.6 mL of 10% antifoam (e.g., 35% polydimethylsiloxane emulsion, Dow Corning 365 Medical Grade Emulsion) taken. Throughout the production, the pH is adjusted as necessary to keep it at around 7.2. After 10 days, or until the viability dropped below 70%, the cell culture is harvested by centrifugation and filtering through a 0.22  $\mu$ m filter. The filtrate was either stored at 4° C. or immediately loaded onto columns for purification.

[0849] For the poly-His tagged constructs, the proteins are purified using a Ni-NTA column (Qiagen). Before purification, imidazole is added to the conditioned media to a concentration of 5 mM. The conditioned media is pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 ml/min. at 4° C. After loading, the column is washed with additional equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein is subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80° C.

[0850] Immunoadhesin (Fc-containing) constructs are purified from the conditioned media as follows. The conditioned medium is pumped onto a 5 ml Protein A column (Pharmacia) which had been equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column is washed extensively with equilibration buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein is immediately neutralized by collecting 1 ml fractions into tubes containing 275  $\mu$ L of 1 M Tris buffer, pH 9. The highly purified protein is subsequently desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity is assessed by SDS polyacrylamide gels and by N-terminal amino acid sequencing by Edman degradation. Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

#### Example 8

##### Expression of PRO in Yeast

[0851] The following method describes recombinant expression of PRO in yeast.

[0852] First, yeast expression vectors are constructed for intracellular production or secretion of PRO from the ADH2/GAPDH promoter. DNA encoding PRO and the promoter is inserted into suitable restriction enzyme sites in the selected plasmid to direct intracellular expression of PRO. For secretion, DNA encoding PRO can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, a native PRO signal peptide or other mammalian signal peptide, or, for example, a yeast

alpha-factor or invertase secretory signal/leader sequence, and linker sequences (if needed) for expression of PRO.

[0853] Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described above and cultured in selected fermentation media. The transformed yeast supernatants can be analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with Coomassie Blue stain.

[0854] Recombinant PRO can subsequently be isolated and purified by removing the yeast cells from the fermentation medium by centrifugation and then concentrating the medium using selected cartridge filters. The concentrate containing PRO may further be purified using selected column chromatography resins.

[0855] Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

#### Example 9

##### Expression of PRO in Baculovirus-Infected Insect Cells

[0856] The following method describes recombinant expression of PRO in Baculovirus-infected insect cells.

[0857] The sequence coding for PRO is fused upstream of an epitope tag contained within a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG). A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the sequence encoding PRO or the desired portion of the coding sequence of PRO such as the sequence encoding the extracellular domain of a transmembrane protein or the sequence encoding the mature protein if the protein is extracellular is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then digested with those selected restriction enzymes and subcloned into the expression vector.

[0858] Recombinant baculovirus is generated by co-transfecting the above plasmid and BaculoGold™ virus DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4-5 days of incubation at 28° C., the released viruses are harvested and used for further amplifications. Viral infection and protein expression are performed as described by O'Reilley et al., *Baculovirus expression vectors: A Laboratory Manual*, Oxford: Oxford University Press (1994).

[0859] Expressed poly-his tagged PRO can then be purified, for example, by  $\text{Ni}^{2+}$ -chelate affinity chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by Rupert et al., *Nature*, 362:175-179 (1993). Briefly, Sf9 cells are washed, resuspended in sonication buffer (25 mL Hepes, pH 7.9; 12.5 mM  $\text{MgCl}_2$ ; 0.1 mM EDTA; 10% glycerol; 0.1% NP40; 0.4 M KCl), and sonicated twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% glycerol, pH 7.8) and filtered through a 0.45  $\mu$ m filter. A  $\text{Ni}^{2+}$ -NTA agarose column (commercially available from Qiagen) is prepared with a bed volume of 5 mL,



washed with 25 mL of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is loaded onto the column at 0.5 mL per minute. The column is washed to baseline  $A_{280}$  with loading buffer, at which point fraction collection is started. Next, the column is washed with a secondary wash buffer (50 mM phosphate; 300 mM NaCl, 10% glycerol, pH 6.0), which elutes nonspecifically bound protein. After reaching  $A_{280}$  baseline again, the column is developed with a 0 to 500 mM Imidazole gradient in the secondary wash buffer. One mL fractions are collected and analyzed by SDS-PAGE and silver staining or Western blot with  $Ni^{2+}$ -NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted  $His_{10}$ -tagged PRO are pooled and dialyzed against loading buffer.

**[0860]** Alternatively, purification of the IgG tagged (or Fc tagged) PRO can be performed using known chromatography techniques, including for instance, Protein A or protein G column chromatography.

**[0861]** Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

#### Example 10

##### Preparation of Antibodies that Bind PRO

**[0862]** This example illustrates preparation of monoclonal antibodies which can specifically bind PRO.

**[0863]** Techniques for producing the monoclonal antibodies are known in the art and are described, for instance, in Goding, supra Immunogens that may be employed include purified PRO, fusion proteins containing PRO, and cells expressing recombinant PRO on the cell surface. Selection of the immunogen can be made by the skilled artisan without undue experimentation.

**[0864]** Mice, such as Balb/c, are immunized with the PRO immunogen emulsified in complete Freund's adjuvant and injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, Mont.) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice may also be boosted with additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing in ELISA assays to detect anti-PRO antibodies.

**[0865]** After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of PRO. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then fused (using 35% polyethylene glycol) to a selected murine myeloma cell line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and thymidine) medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

**[0866]** The hybridoma cells will be screened in an ELISA for reactivity against PRO. Determination of "positive"

hybridoma cells secreting the desired monoclonal antibodies against PRO is within the skill in the art.

**[0867]** The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti-PRO monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

#### Example 11

##### Purification of PRO Polypeptides Using Specific Antibodies

**[0868]** Native or recombinant PRO polypeptides may be purified by a variety of standard techniques in the art of protein purification. For example, pro-PRO polypeptide, mature PRO polypeptide, or pre-PRO polypeptide is purified by immunoaffinity chromatography using antibodies specific for the PRO polypeptide of interest. In general, an immunoaffinity column is constructed by covalently coupling the anti-PRO polypeptide antibody to an activated chromatographic resin.

**[0869]** Polyclonal immunoglobulins are prepared from immune sera either by precipitation with ammonium sulfate or by purification on immobilized Protein A (Pharmacia LKB Biotechnology, Piscataway, N.J.). Likewise, monoclonal antibodies are prepared from mouse ascites fluid by ammonium sulfate precipitation or chromatography on immobilized Protein A. Partially purified immunoglobulin is covalently attached to a chromatographic resin such as CnBr-activated SEPHAROSE™ (Pharmacia LKB Biotechnology). The antibody is coupled to the resin, the resin is blocked, and the derivative resin is washed according to the manufacturer's instructions.

**[0870]** Such an immunoaffinity column is utilized in the purification of PRO polypeptide by preparing a fraction from cells containing PRO polypeptide in a soluble form. This preparation is derived by solubilization of the whole cell or of a subcellular fraction obtained via differential centrifugation by the addition of detergent or by other methods well known in the art. Alternatively, soluble PRO polypeptide containing a signal sequence may be secreted in useful quantity into the medium in which the cells are grown.

**[0871]** A soluble PRO polypeptide-containing preparation is passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of PRO polypeptide (e.g., high ionic strength buffers in the presence of detergent). Then, the column is eluted under conditions that disrupt antibody/PRO polypeptide binding (e.g., a low pH buffer such as approximately pH 2-3, or a high concentration of a chaotrope such as urea or thiocyanate ion), and PRO polypeptide is collected.

#### Example 12

##### Drug Screening

**[0872]** This invention is particularly useful for screening compounds by using PRO polypeptides or binding fragment

thereof in any of a variety of drug screening techniques. The PRO polypeptide or fragment employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the PRO polypeptide or fragment. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between PRO polypeptide or a fragment and the agent being tested. Alternatively, one can examine the diminution in complex formation between the PRO polypeptide and its target cell or target receptors caused by the agent being tested.

[0873] Thus, the present invention provides methods of screening for drugs or any other agents which can affect a PRO polypeptide-associated disease or disorder. These methods comprise contacting such an agent with an PRO polypeptide or fragment thereof and assaying (i) for the presence of a complex between the agent and the PRO polypeptide or fragment, or (ii) for the presence of a complex between the PRO polypeptide or fragment and the cell, by methods well known in the art. In such competitive binding assays, the PRO polypeptide or fragment is typically labeled. After suitable incubation, free PRO polypeptide or fragment is separated from that present in bound form, and the amount of free or uncomplexed label is a measure of the ability of the particular agent to bind to PRO polypeptide or to interfere with the PRO polypeptide/cell complex.

[0874] Another technique for drug screening provides high throughput screening for compounds having suitable binding affinity to a polypeptide and is described in detail in WO 84/03564, published on Sep. 13, 1984. Briefly stated, large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. As applied to a PRO polypeptide, the peptide test compounds are reacted with PRO polypeptide and washed. Bound PRO polypeptide is detected by methods well known in the art. Purified PRO polypeptide can also be coated directly onto plates for use in the aforementioned drug screening techniques. In addition, non-neutralizing antibodies can be used to capture the peptide and immobilize it on the solid support.

[0875] This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of binding PRO polypeptide specifically compete with a test compound for binding to PRO polypeptide or fragments thereof. In this manner, the antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with PRO polypeptide.

#### Example 13

##### Rational Drug Design

[0876] The goal of rational drug design is to produce structural analogs of biologically active polypeptide of interest (i.e., a PRO polypeptide) or of small molecules with which they interact, e.g., agonists, antagonists, or inhibitors. Any of these examples can be used to fashion drugs which are more active or stable forms of the PRO polypeptide or which enhance or interfere with the function of the PRO polypeptide in vivo (c.f., Hodgson, *BioTechnology*, 9: 19-21 (1991)).

[0877] In one approach, the three-dimensional structure of the PRO polypeptide, or of an PRO polypeptide-inhibitor complex, is determined by x-ray crystallography, by computer modeling or, most typically, by a combination of the two approaches. Both the shape and charges of the PRO polypeptide must be ascertained to elucidate the structure and to determine active site(s) of the molecule. Less often, useful information regarding the structure of the PRO polypeptide may be gained by modeling based on the structure of homologous proteins. In both cases, relevant structural information is used to design analogous PRO polypeptide-like molecules or to identify efficient inhibitors. Useful examples of rational drug design may include molecules which have improved activity or stability as shown by Braxton and Wells, *Biochemistry*, 31:7796-7801 (1992) or which act as inhibitors, agonists, or antagonists of native peptides as shown by Athauda et al., *J. Biochem.*, 113:742-746 (1993).

[0878] It is also possible to isolate a target-specific antibody, selected by functional assay, as described above, and then to solve its crystal structure. This approach, in principle, yields a pharmacore upon which subsequent drug design can be based. It is possible to bypass protein crystallography altogether by generating anti-idiotypic antibodies (anti-ids) to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of the anti-ids would be expected to be an analog of the original receptor. The anti-id could then be used to identify and isolate peptides from banks of chemically or biologically produced peptides. The isolated peptides would then act as the pharmacore.

[0879] By virtue of the present invention, sufficient amounts of the PRO polypeptide may be made available to perform such analytical studies as X-ray crystallography. In addition, knowledge of the PRO polypeptide amino acid sequence provided herein will provide guidance to those employing computer modeling techniques in place of or in addition to x-ray crystallography.

#### Example 14

##### Identification of PRO Polypeptides That Stimulate TNF- $\alpha$ Release In Human Blood (Assay 128)

[0880] This assay shows that certain PRO polypeptides of the present invention act to stimulate the release of TNF- $\alpha$  in human blood. PRO polypeptides testing positive in this assay are useful for, among other things, research purposes where stimulation of the release of TNF- $\alpha$  would be desired and for the therapeutic treatment of conditions wherein enhanced TNF- $\alpha$  release would be beneficial. Specifically, 200  $\mu$ l of human blood supplemented with 50 mM Hepes buffer (pH 7.2) is aliquoted per well in a 96 well test plate. To each well is then added 300  $\mu$ l of either the test PRO polypeptide in 50 mM Hepes buffer (at various concentrations) or 50 mM Hepes buffer alone (negative control) and the plates are incubated at 37° C. for 6 hours. The samples are then centrifuged and 50  $\mu$ l of plasma is collected from each well and tested for the presence of TNF- $\alpha$  by ELISA assay. A positive in the assay is a higher amount of TNF- $\alpha$  in the PRO polypeptide treated samples as compared to the negative control samples.

[0881] The following PRO polypeptides tested positive in this assay: PRO195, PRO202, PRO215, PRO221, PRO217,

PRO222, PRO198, PRO245, PRO172, PRO265, PRO266, PRO344, PRO337, PRO322, PRO1286, PRO1279, PRO1338 and PRO1343.

#### Example 15

##### Detection of Polypeptides That Affect Glucose or FFA Uptake in Skeletal Muscle (Assay 106)

**[0882]** This assay is designed to determine whether PRO polypeptides show the ability to affect glucose or FFA uptake by skeletal muscle cells. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of disorders where either the stimulation or inhibition of glucose uptake by skeletal muscle would be beneficial including, for example, diabetes or hyper- or hypo-insulinemia.

**[0883]** In a 96 well format, PRO polypeptides to be assayed are added to primary rat differentiated skeletal muscle, and allowed to incubate overnight. Then fresh media with the PRO polypeptide and +/- insulin are added to the wells. The sample media is then monitored to determine glucose and FFA uptake by the skeletal muscle cells. The insulin will stimulate glucose and FFA uptake by the skeletal muscle, and insulin in media without the PRO polypeptide is used as a positive control, and a limit for scoring. As the PRO polypeptide being tested may either stimulate or inhibit glucose and FFA uptake, results are scored as positive in the assay if greater than 1.5 times or less than 0.5 times the insulin control.

**[0884]** The following PRO polypeptides tested positive as being capable of affecting glucose and/or FFA uptake by skeletal muscle in this assay: PRO182, PRO366, PRO198, PRO172 and PRO719.

#### Example 16

##### Chondrocyte Re-differentiation Assay (Assay 110)

**[0885]** This assay shows that certain polypeptides of the invention act to induce redifferentiation of chondrocytes, therefore, are expected to be useful for the treatment of various bone and/or cartilage disorders such as, for example, sports injuries and arthritis. The assay is performed as follows. Porcine chondrocytes are isolated by overnight collagenase digestion of articular cartilage of metacarpophalangeal joints of 4-6 month old female pigs. The isolated cells are then seeded at 25,000 cells/cm<sup>2</sup> in Ham F-12 containing 10% FBS and 4 µg/ml gentamycin. The culture media is changed every third day and the cells are then seeded in 96 well plates at 5,000 cells/well in 100 µl of the same media without serum and 100 µl of the test PRO polypeptide, 5 nM staurosporin (positive control) or medium alone (negative control) is added to give a final volume of 200 µl/well. After 5 days of incubation at 37° C., a picture of each well is taken and the differentiation state of the chondrocytes is determined. A positive result in the assay occurs when the redifferentiation of the chondrocytes is determined to be more similar to the positive control than the negative control.

**[0886]** The following polypeptide tested positive in this assay: PRO182, PRO366, PRO198 and PRO1868.

#### Example 17

##### Chondrocyte Proliferation Assay (Assay 111)

**[0887]** This assay is designed to determine whether PRO polypeptides of the present invention show the ability to

induce the proliferation and/or redifferentiation of chondrocytes in culture. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of various bone and/or cartilage disorders such as, for example, sports injuries and arthritis.

**[0888]** Porcine chondrocytes are isolated by overnight collagenase digestion of articular cartilage of the metacarpophalangeal joint of 4-6 month old female pigs. The isolated cells are then seeded at 25,000 cells/cm<sup>2</sup> in Ham F-12 containing 10% FBS and 4 µg/ml gentamycin. The culture media is changed every third day and the cells are reseeded to 25,000 cells/cm<sup>2</sup> every five days. On day 12, the cells are seeded in 96 well plates at 5,000 cells/well in 100% of the same media without serum and 100 µl of either serum-free medium (negative control), staurosporin (final concentration of 5 nM; positive control) or the test PRO polypeptide are added to give a final volume of 200 µl/well. After 5 days at 37° C., 20 µl of Alamar blue is added to each well and the plates are incubated for an additional 3 hours at 37° C. The fluorescence is then measured in each well (Ex:530 nm; Em: 590 nm). The fluorescence of a plate containing 200 µl of the serum-free medium is measured to obtain the background. A positive result in the assay is obtained when the fluorescence of the PRO polypeptide treated sample is more like that of the positive control than the negative control.

**[0889]** The following PRO polypeptides tested positive in this assay: PRO202, PRO224, PRO172 and PRO1312.

#### Example 18

##### Detection of PRO Polypeptides That Affect Glucose or FFA Uptake by Primary Rat Adipocytes (Assay 94)

**[0890]** This assay is designed to determine whether PRO polypeptides show the ability to affect glucose or FFA uptake by adipocyte cells. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of disorders where either the stimulation or inhibition of glucose uptake by adipocytes would be beneficial including, for example, obesity, diabetes or hyper- or hypo-insulinemia.

**[0891]** In a 96 well format, PRO polypeptides to be assayed are added to primary rat adipocytes, and allowed to incubate overnight. Samples are taken at 4 and 16 hours and assayed for glycerol, glucose and FFA uptake. After the 16 hour incubation, insulin is added to the media and allowed to incubate for 4 hours. At this time, a sample is taken and glycerol, glucose and FFA uptake is measured. Media containing insulin without the PRO polypeptide is used as a positive reference control. As the PRO polypeptide being tested may either stimulate or inhibit glucose and FFA uptake, results are scored as positive in the assay if greater than 1.5 times or less than 0.5 times the insulin control.

**[0892]** The following PRO polypeptides tested positive as being capable of affecting glucose and/or FFA uptake in this assay: PRO202, PRO211, PRO344 and PRO1338.

#### Example 19

##### Gene Expression in Bovine Pericytes (Assay 105)

**[0893]** This assay is designed to identify PRO polypeptides which activate gene expression in pericytes. Such

polypeptides would be expected to be useful as growth factors and/or for situations where the activation of gene expression is desired or beneficial. Bovine pericytes are plated on 60 mm culture dishes in growth media for 1 week. On day 1, various PRO polypeptides are diluted (1%) and incubated with the pericytes for 1,4 and 24 hr. timepoints. The cells are harvested and the RNA isolated using TR1-Reagent following the included instructions. The RNA is then quantified by reading the 260/280 OD using a spectrophotometer. The gene expression analysis is done by Taq-Man reactions using Perkin Elmer reagents and specially designed bovine probes and primers. Expression of the following genes is analyzed: GAPDH, beta-integrin, connective tissue growth factor (CTGF), ICAM-1, monocyte chemoattractantprotein-1 (MCP-1), osteopontin, transforming growth factor-beta (TGF-beta), TGF-beta receptor, tissue inhibitor of metalloproteinase (TIMP), tissue factor (TF), VEGF-A, thrombospondin, VEGF- $\beta$ , angiopoietin-2, and collagenase. Replicates are then averaged and the SD determined. The gene expression levels are then normalized to GAPDH. These are then normalized to the expression levels obtained with a protein (PIN32) which does not significantly induce gene expression in bovine pericytes when compared to untreated controls. Any PRO polypeptide that gives a gene expression level 2-fold or higher over the PIN32 control is considered a positive hit.

[0894] The following PRO polypeptides tested positive in this assay: PRO366.

#### Example 20

##### Identification of PRO Polypeptides That Activate Pericytes (Assay 125)

[0895] This assay shows that certain polypeptides of the invention act to activate proliferation of pericyte cells and, therefore, are useful not only as diagnostic markers for particular types of pericyte-associated tumors but also for giving rise to antagonists which would be expected to be useful for the therapeutic treatment of pericyte-associated tumors. Such PRO polypeptides also would be expected to be useful as growth factors and/or for situations where the induction of cell proliferation is desired or beneficial. Activation of pericyte proliferation also correlates with the induction of angiogenesis and, as such, PRO polypeptides capable of inducing pericyte proliferation would be expected to be useful for the treatment of conditions where induced angiogenesis would be beneficial including, for example, wound healing, and the like. Specifically, on day 1, pericytes are received from VEC Technologies, and all but 5 ml media is removed from the flask. On day 2, the pericytes are trypsinized, washed, spun and plated on 96 well plates. On day 7, the media is removed and the pericytes are treated with 100  $\mu$ l of either the specific PRO polypeptide or control treatments (positive control =DME+5% +/-PDGF @ 500 ng/ $\mu$ l; negative control=PIN32, a polypeptide determined to have no significant effect on pericyte proliferation). C-fos and GAPDH gene expression levels are then determined and the replicates are averaged and the SD is determined. The c-fos values are normalized to GAPDH and the results are expressed as fold increase over PIN32. Anything providing at least a 2-fold or higher response as compared to the negative control is considered positive for the assay.

[0896] The following polypeptides tested positive in this assay: PRO366.

#### Example 21

##### Ability of PRO Polypeptides to Stimulate the Release of Proteoglycans from Cartilage (Assay 97)

[0897] The ability of various PRO polypeptides to stimulate the release of proteoglycans from cartilage tissue was tested as follows.

[0898] The metacarpophalangeal joint of 4-6 month old pigs was aseptically dissected, and articular cartilage was removed by free hand slicing being careful to avoid the underlying bone. The cartilage was minced and cultured in bulk for 24 hours in a humidified atmosphere of 95% air, 5% CO<sub>2</sub> in serum free (SF) media (DME/F12 1:1) with 0.1% BSA and 100 U/ml penicillin and 100  $\mu$ g/ml streptomycin. After washing three times, approximately 100 mg of articular cartilage was aliquoted into micronics tubes and incubated for an additional 24 hours in the above SF media. PRO polypeptides were then added at 1% either alone or in combination with 18 ng/ml interleukin-1 $\alpha$ , a known stimulator of proteoglycan release from cartilage tissue. The supernatant was then harvested and assayed for the amount of proteoglycans using the 1,9-dimethyl-methylene blue (DMB) colorimetric assay (Farndale and Buttle, *Biochem. Biophys. Acta* 883:173-177 (1985)). A positive result in this assay indicates that the test polypeptide will find use, for example, in the treatment of sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis.

[0899] When various PRO polypeptides were tested in the above assay, the polypeptides demonstrated a marked ability to stimulate release of proteoglycans from cartilage tissue both basally and after stimulation with interleukin-1 $\alpha$  and at 24 and 72 hours after treatment, thereby indicating that these PRO polypeptides are useful for stimulating proteoglycan release from cartilage tissue. As such, these PRO polypeptides are useful for the treatment of sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis. The polypeptides testing positive in this assay are: PRO216.

#### Example 22

##### Proliferation of Rat Utricular Supporting Cells (Assay 54)

[0900] This assay shows that certain polypeptides of the invention act as potent mitogens for inner ear supporting cells which are auditory hair cell progenitors and, therefore, are useful for inducing the regeneration of auditory hair cells and treating hearing loss in mammals. The assay is performed as follows. Rat UEC-4 utricular epithelial cells are aliquoted into 96 well plates with a density of 3000 cells/well in 200  $\mu$ l of serum-containing medium at 33° C. The cells are cultured overnight and are then switched to serum-free medium at 37° C. Various dilutions of PRO polypeptides (or nothing for a control) are then added to the cultures and the cells are incubated for 24 hours. After the 24 hour incubation, <sup>3</sup>H-thymidine (1  $\mu$ Ci/well) is added and the cells are then cultured for an additional 24 hours. The cultures are then washed to remove unincorporated radiolabel, the cells harvested and Cpm per well determined. Cpm of at least

30% or greater in the PRO polypeptide treated cultures as compared to the control cultures is considered a positive in the assay.

[0901] The following polypeptides tested positive in this assay: PRO172.

#### Example 23

##### Stimulatory Activity in Mixed Lymphocyte Reaction (MLR) Assay (Assay 24)

[0902] This example shows that certain polypeptides of the invention are active as a stimulator of the proliferation of stimulated T-lymphocytes. Compounds which stimulate proliferation of lymphocytes are useful therapeutically where enhancement of an immune response is beneficial. A therapeutic agent may take the form of antagonists of the polypeptide of the invention, for example, murine-human chimeric, humanized or human antibodies against the polypeptide.

[0903] The basic protocol for this assay is described in Current Protocols in Immunology, unit 3.12; edited by J E Coligan, A M Kruisbeek, D H Marglies, E M Shevach, W Strober, National Institutes of Health, Published by John Wiley & Sons, Inc.

[0904] More specifically, in one assay variant, peripheral blood mononuclear cells (PBMC) are isolated from mammalian individuals, for example a human volunteer, by leukopheresis (one donor will supply stimulator PBMCs, the other donor will supply responder PBMCs). If desired, the cells are frozen in fetal bovine serum and DMSO after isolation. Frozen cells may be thawed overnight in assay media (37° C., 5% CO<sub>2</sub>) and then washed and resuspended to 3×10<sup>6</sup> cells/ml of assay media (RPMI; 10% fetal bovine serum, 1% penicillin/streptomycin, 1% glutamine, 1% HEPES, 1% non-essential amino acids, 1% pyruvate). The stimulator PBMCs are prepared by irradiating the cells (about 3000 Rads).

[0905] The assay is prepared by plating in triplicate wells a mixture of:

[0906] 100:1 of test sample diluted to 1% or to 0.1%,

[0907] 50:1 of irradiated stimulator cells, and

[0908] 50:1 of responder PBMC cells.

[0909] 100 microliters of cell culture media or 100 microliter of CD4-IgG is used as the control. The wells are then incubated at 37° C., 5% CO<sub>2</sub> for 4 days. On day 5, each well is pulsed with tritiated thymidine (1.0 mCi/well; Amersham). After 6 hours the cells are washed 3 times and then the uptake of the label is evaluated.

[0910] In another variant of this assay, PBMCs are isolated from the spleens of Balb/c mice and C57B6 mice. The cells are teased from freshly harvested spleens in assay media (RPMI; 10% fetal bovine serum, 1% penicillin/streptomycin, 1% glutamine, 1% HEPES, 1% non-essential amino acids, 1% pyruvate) and the PBMCs are isolated by overlaying these cells over Lympholyte M (Organon Teknika), centrifuging at 2000 rpm for 20 minutes, collecting and washing the mononuclear cell layer in assay media and resuspending the cells to 1×10<sup>7</sup> cells/ml of assay media. The assay is then conducted as described above.

[0911] Positive increases over control are considered positive with increases of greater than or equal to 180% being preferred. However, any value greater than control indicates a stimulatory effect for the test protein.

[0912] The following PRO polypeptides tested positive in this assay: PRO344.

#### Example 24

##### Pericyte c-Fos Induction (Assay 93)

[0913] This assay shows that certain polypeptides of the invention act to induce the expression of c-fos in pericyte cells and, therefore, are useful not only as diagnostic markers for particular types of pericyte-associated tumors but also for giving rise to antagonists which would be expected to be useful for the therapeutic treatment of pericyte-associated tumors. Induction of c-fos expression in pericytes is also indicative of the induction of angiogenesis and, as such, PRO polypeptides capable of inducing the expression of c-fos would be expected to be useful for the treatment of conditions where induced angiogenesis would be beneficial including, for example, wound healing, and the like. Specifically, on day 1, pericytes are received from VEC Technologies and all but 5 ml of media is removed from flask. On day 2, the pericytes are trypsinized, washed, spun and then plated onto 96 well plates. On day 7, the media is removed and the pericytes are treated with 1100 µl of PRO polypeptide test samples and controls (positive control=DME+5% serum+/-PDGF at 500 ng/ml; negative control=protein 32). Replicates are averaged and SD/CV are determined. Fold increase over Protein 32 (buffer control) value indicated by chemiluminescence units (RLU) luminometer reading verses frequency is plotted on a histogram. Two-fold above Protein 32 value is considered positive for the assay. ASY Matrix: Growth media=low glucose DMEM=20% FBS+1× pen strep+1× fungizone. Assay Media=low glucose DMEM+5% FBS. The following polypeptides tested positive in this assay: PRO301, PRO619, PRO1066 and PRO1265.

#### Example 25

##### Cytokine Release Assay (Assay 120)

[0914] This assay is designed to determine whether PRO polypeptides of the present invention are capable of inducing the release of cytokines from peripheral blood mononuclear cells (PBMCs). PRO polypeptides capable of inducing the release of cytokines from PBMCs are useful from the treatment of conditions which would benefit from enhanced cytokine release and will be readily evident to those of ordinary skill in the art. Specifically, 1×10<sup>6</sup> cells/ml of peripheral blood mononuclear cells (PBMC) are cultured with 1% of a PRO polypeptide for 3 days in complete RPMI media. The supernatant is then harvested and tested for increased concentrations of various cytokines by ELISA as compared to a human IgG treated control. A positive in the assay is a 10-fold or greater increase in cytokine concentration in the PRO polypeptide treated sample as compared to the human IgG treated control.

[0915] The following polypeptides tested positive in this assay: PRO526 and PRO1343.

## Example 26

Inhibition of A-Peptide Binding to Factor VIIA  
(Assay 118)

[0916] This assay is designed to identify PRO polypeptides which are capable of inhibiting the binding of A-peptide to factor VIIA, thereby affecting the blood coagulation cascade. PRO polypeptides testing positive in this assay are expected to be useful for the treatment of conditions where alteration of the blood coagulation cascade would be beneficial including, for example, stroke, heart attack and various coagulation disorders. These PRO polypeptides are also useful for the identification of agonist and antagonist molecules which would also be useful for treatment of those conditions.

[0917] Specifically, 384 well plates are coated with soluble factor VIIA and are incubated overnight at 4° C. The wells are then decanted and are blocked by the addition of 0.5% BSA for 1 hour. The wells are then washed and 20  $\mu$ l of biotinylated A-peptide and either various concentration of the PRO polypeptide (test) or nothing (negative control) are added to each well. The plates are then incubated for 1 hour at room temperature. The wells are again washed and then 40  $\mu$ l of streptavidin-europium is added to each well. The plates are then incubated for 30 minutes at room temperature and then washed. 40  $\mu$ l of a fluorescence enhancement solution is then added to each well, the plates incubated for 5 minutes at room temperature and each well is then read on Wallac Victor reader under europium delayed fluorescence settings. Percent inhibition of binding of the A-peptide to the factor VIIA is then determined (as compared to the negative control), wherein a positive in the assay is a percent inhibition of 30% or greater.

[0918] The following PRO polypeptides tested positive in this assay: PRO182.

## Example 27

Inhibition of Adipocyte Differentiation Assay  
(Assay 66)

[0919] This assay is designed to identify PRO polypeptides which are capable of inhibiting insulin-induced differentiation of adipocytes. PRO polypeptides testing positive in this assay would be expected to be useful for the treatment of conditions associated with obesity, diabetes, etc.

[0920] Specifically, 3T3-L1 cells are seeded into the wells of 96 well plates at  $6 \times 10^4$  cells/well and allowed to grow to confluency for 7 days. At day 7, the cells are treated with various concentrations of the PRO polypeptide (or nothing for the negative control) in the presence of 1 g/ml insulin,  $0.25 \times 10^{-6}$  M dexamethasone and 0.5 mM IBMX. The samples are then incubated at 37° C. in 7% CO<sub>2</sub> for 2 days. After the incubation, the media is removed by aspiration and the cells are washed with PBS and re-exposed to the PRO polypeptide (or nothing for the negative control) and 1  $\mu$ g/ml insulin. After 5 days, the media is removed and replaced with fresh PRO polypeptide (or nothing for the negative control) and insulin. After 5 days, the cells are lysed and the cell lysate is assayed using Sigma's Triglyceride [ $\alpha$ ]kit (Sigma procedure #336). A positive in the assay is 20% greater inhibition of adipocyte differentiation in the PRO polypeptide treated samples as compared to the negative control.

[0921] The following PRO polypeptides tested positive in this assay: PRO185 and PRO198.

## Example 28

## HUVEC Stimulation by PRO Polypeptides (Assay 131)

[0922] This assay is designed to identify PRO polypeptides which are capable of stimulating the proliferation of HUVEC cells. PRO polypeptides testing positive in this assay would be expected to be useful for inducing angiogenesis for the treatment of conditions where angiogenesis would be beneficial including, for example, wound healing, and the like. Antagonists of these PRO polypeptides would be expected to be useful for inhibiting angiogenesis for the treatment of, for example, tumors, and the like.

[0923] Specifically, COSTAR® flat bottom black plates are treated with fibronectin for 20 minutes and then washed twice with PBS. HUVEC cells are then plated at 2000 cells/well in an appropriate growth medium. The plates are then incubated overnight and then the PRO polypeptide (1% final concentration), nothing (negative control) or IL1 $\beta$  (3.3 ng/ml final concentration; positive control) is added. The plates are again incubated overnight, stained with ICAM1-Cy5 and read on FMAT. A positive in the assay is a 2-fold or greater increase in fluorescence as compared to the positive control.

[0924] The following PRO polypeptides tested positive in this assay: PRO222.

## Example 29

## Promotion of Chondrocyte Redifferentiation (Assay 129)

[0925] This assay is designed to determine whether PRO polypeptides of the present invention show the ability to induce the proliferation and/or redifferentiation of chondrocytes in culture. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of various bone and/or cartilage disorders such as, for example, sports injuries and arthritis.

[0926] Porcine chondrocytes are isolated by overnight collagenase digestion of articular cartilage of the metacarpophalangeal joint of 4-6 month old female pigs. The isolated cells are then seeded at 25,000 cells/cm<sup>2</sup> in Ham F-12 containing 10% FBS and 4  $\mu$ g/ml gentamycin. The culture media is changed every third day. On day 12, the cells are seeded in 96 well plates at 5,000 cells/well in 100  $\mu$ l of the same media without serum and 100  $\mu$ l of either serum-free medium (negative control), staurosporin (final concentration of 5 nM; positive control) or the test PRO polypeptide are added to give a final volume of 200  $\mu$ l/well. After 5 days at 37° C., 22  $\mu$ l of media containing 100  $\mu$ g/ml Hoechst 33342 and 50  $\mu$ g/ml 5-CFDA is added to each well and incubated for an additional 10 minutes at 37° C. A picture of the green fluorescence is taken for each well and the differentiation state of the chondrocytes is calculated by morphometric analysis. A positive result in the assay is obtained when the >50% of the PRO polypeptide treated cells are differentiated (compared to the background obtained by the negative control).

[0927] The following PRO polypeptides tested positive in this assay: PRO301.

Example 30

Microarray Analysis to Detect Overexpression of PRO Polypeptides in Cancerous Tumors

[0928] Nucleic acid microarrays, often containing thousands of gene sequences, are useful for identifying differentially expressed genes in diseased tissues as compared to their normal counterparts. Using nucleic acid microarrays, test and control mRNA samples from test and control tissue samples are reverse transcribed and labeled to generate cDNA probes. The cDNA probes are then hybridized to an array of nucleic acids immobilized on a solid support. The array is configured such that the sequence and position of each member of the array is known. For example, a selection of genes known to be expressed in certain disease states may be arrayed on a solid support. Hybridization of a labeled probe with a particular array member indicates that the sample from which the probe was derived expresses that gene. If the hybridization signal of a probe from a test (disease tissue) sample is greater than hybridization signal of a probe from a control (normal tissue) sample, the gene or genes overexpressed in the disease tissue are identified. The implication of this result is that an overexpressed protein in a diseased tissue is useful not only as a diagnostic marker for the presence of the disease condition, but also as a therapeutic target for treatment of the disease condition.

[0929] The methodology of hybridization of nucleic acids and microarray technology is well known in the art. In the present example, the specific preparation of nucleic acids for hybridization and probes, slides, and hybridization conditions are all detailed in U.S. Provisional Patent Application Serial No. 60/193,767, filed on Mar. 31, 2000 and which is herein incorporated by reference.

[0930] In the present example, cancerous tumors derived from various human tissues were studied for PRO polypeptide-encoding gene expression relative to non-cancerous human tissue in an attempt to identify those PRO polypeptides which are overexpressed in cancerous tumors. Two sets of experimental data were generated. In one set, cancerous human colon tumor tissue and matched non-cancerous human colon tumor tissue from the same patient (“matched colon control”) were obtained and analyzed for PRO polypeptide expression using the above described microarray technology. In the second set of data, cancerous human tumor tissue from any of a variety of different human tumors was obtained and compared to a “universal” epithelial control sample which was prepared by pooling non-cancerous human tissues of epithelial origin, including liver, kidney, and lung. mRNA isolated from the pooled tissues represents a mixture of expressed gene products from these different tissues. Microarray hybridization experiments using the pooled control samples generated a linear plot in a 2-color analysis. The slope of the line generated in a 2-color analysis was then used to normalize the ratios of (test:control detection) within each experiment. The normalized ratios from various experiments were then compared and used to identify clustering of gene expression. Thus, the pooled “universal control” sample not only allowed effective relative gene expression determinations in a simple 2-sample comparison, it also allowed multi-sample comparisons across several experiments.

[0931] In the present experiments, nucleic acid probes derived from the herein described PRO polypeptide-encoding nucleic acid sequences were used in the creation of the microarray and RNA from the tumor tissues listed above were used for the hybridization thereto. A value based upon the normalized ratio:experimental ratio was designated as a “cutoff ratio”. Only values that were above this cutoff ratio were determined to be significant. Table 8 below shows the results of these experiments, demonstrating that various PRO polypeptides of the preent invention are significantly overexpressed in various human tumor tissues as compared to a non-cancerous human tissue control. As described above, these data demonstrate that the PRO polypeptides of the present invention are useful not only as diagnostic markers for the presence of one or more cancerous tumors, but also serve as therapeutic targets for the treatment of those tumors.

TABLE 8

Molecule	is overexpressed in:	as compared to:
PRO177	breast tumor	universal normal control
PRO177	liver tumor	universal normal control
PRO177	lung tumor	universal normal control
PRO3574	breast tumor	universal normal control
PRO3574	colon tumor	matched normal colon control
PRO1280	breast tumor	universal normal control
PRO1280	lung tumor	universal normal control
PRO4984	lung tumor	universal normal control
PRO4988	colon tumor	universal normal control
PRO4988	lung tumor	universal normal control
PRO305	lung tumor	universal normal control
PRO305	colon tumor	universal normal control
PRO1866	prostate tumor	universal normal control
PRO1866	lung tumor	universal normal control
PRO1866	colon tumor	universal normal control
PRO4996	breast tumor	universal normal control
PRO4996	lung tumor	universal normal control
PRO4406	lung tumor	universal normal control
PRO4406	colon tumor	universal normal control
PRO1120	colon tumor	universal normal control
PRO1120	breast tumor	universal normal control
PRO1120	rectal tumor	universal normal control
PRO4990	lung tumor	universal normal control
PRO738	cervical tumor	universal normal control
PRO738	lung tumor	universal normal control
PRO738	breast tumor	universal normal control
PRO3577	lung tumor	universal normal control
PRO1879	breast tumor	universal normal control
PRO1879	lung tumor	universal normal control
PRO1879	colon tumor	universal normal control
PRO1471	lung tumor	universal normal control
PRO1076	prostate tumor	universal normal control
PRO1483	lung tumor	universal normal control
PRO4985	rectal tumor	universal normal control
PRO4985	colon tumor	universal normal control
PRO4985	breast tumor	universal normal control
PRO4985	lung tumor	universal normal control
PRO5000	lung tumor	universal normal control
PRO1881	liver tumor	universal normal control
PRO1881	lung tumor	universal normal control
PRO1881	breast tumor	universal normal control
PRO4314	lung tumor	universal normal control
PRO4314	breast tumor	universal normal control
PRO4987	lung tumor	universal normal control
PRO4313	lung tumor	universal normal control
PRO4313	breast tumor	universal normal control
PRO4799	colon tumor	universal normal control
PRO4995	liver tumor	universal normal control
PRO4995	colon tumor	universal normal control
PRO4995	colon tumor	matched normal colon control
PRO1341	prostate tumor	universal normal control
PRO1341	lung tumor	universal normal control

TABLE 8-continued

Molecule	is overexpressed in:	as compared to:
PRO1341	colon tumor	universal normal control
PRO1341	colon tumor	matched normal colon control
PRO1777	lung tumor	universal normal control
PRO1777	colon tumor	matched normal colon control
PRO3580	lung tumor	universal normal control
PRO3580	prostate tumor	universal normal control
PRO1779	lung tumor	universal normal control
PRO1779	colon tumor	universal normal control
PRO1779	cervical tumor	universal normal control
PRO1754	breast tumor	universal normal control
PRO1754	lung tumor	universal normal control
PRO1906	breast tumor	universal normal control
PRO1906	colon tumor	universal normal control
PRO1906	prostate tumor	universal normal control
PRO1870	breast tumor	universal normal control
PRO4329	lung tumor	universal normal control
PRO4979	colon tumor	universal normal control
PRO1885	rectal tumor	universal normal control
PRO1885	colon tumor	universal normal control
PRO1885	colon tumor	matched normal colon control
PRO1882	prostate tumor	universal normal control
PRO1882	lung tumor	universal normal control
PRO1882	colon tumor	universal normal control
PRO1882	breast tumor	universal normal control
PRO1882	cervical tumor	universal normal control
PRO4989	rectal tumor	universal normal control
PRO4989	breast tumor	universal normal control
PRO4989	colon tumor	matched normal colon control
PRO4989	colon tumor	universal normal control
PRO4323	lung tumor	universal normal control
PRO4323	liver tumor	universal normal control
PRO1886	breast tumor	universal normal control
PRO1886	lung tumor	universal normal control
PRO1886	rectal tumor	universal normal control
PRO4395	colon tumor	universal normal control
PRO4395	prostate tumor	universal normal control
PRO4395	lung tumor	universal normal control
PRO4395	cervical tumor	universal normal control
PRO1782	colon tumor	universal normal control
PRO1782	lung tumor	universal normal control
PRO4388	lung tumor	universal normal control
PRO4341	breast tumor	universal normal control
PRO4341	lung tumor	universal normal control
PRO3438	lung tumor	universal normal control
PRO4321	breast tumor	universal normal control
PRO4321	lung tumor	universal normal control
PRO4321	colon tumor	universal normal control
PRO4304	breast tumor	universal normal control
PRO4304	lung tumor	universal normal control
PRO4403	colon tumor	universal normal control
PRO4403	breast tumor	universal normal control
PRO4403	lung tumor	universal normal control
PRO4324	lung tumor	universal normal control
PRO4324	breast tumor	universal normal control
PRO4303	cervical tumor	universal normal control
PRO4303	lung tumor	universal normal control
PRO4303	breast tumor	universal normal control
PRO4303	colon tumor	universal normal control
PRO4303	prostate tumor	universal normal control
PRO4305	breast tumor	universal normal control
PRO4305	lung tumor	universal normal control
PRO4305	colon tumor	universal normal control
PRO4305	liver tumor	universal normal control
PRO4404	lung tumor	universal normal control
PRO4404	breast tumor	universal normal control
PRO4404	rectal tumor	universal normal control
PRO1884	lung tumor	universal normal control
PRO4349	colon tumor	universal normal control
PRO4349	lung tumor	universal normal control
PRO4401	colon tumor	universal normal control
PRO4401	lung tumor	universal normal control
PRO1867	lung tumor	universal normal control
PRO1867	liver tumor	universal normal control
PRO4319	breast tumor	universal normal control

TABLE 8-continued

Molecule	is overexpressed in:	as compared to:
PRO4319	lung tumor	universal normal control
PRO4991	lung tumor	universal normal control
PRO4991	colon tumor	universal normal control
PRO4398	lung tumor	universal normal control
PRO4346	lung tumor	universal normal control
PRO4350	colon tumor	universal normal control
PRO4350	prostate tumor	universal normal control
PRO4350	lung tumor	universal normal control
PRO4318	prostate tumor	universal normal control
PRO4318	lung tumor	universal normal control
PRO4340	breast tumor	universal normal control
PRO4340	lung tumor	universal normal control
PRO4400	breast tumor	universal normal control
PRO4400	lung tumor	universal normal control
PRO4320	lung tumor	universal normal control
PRO4409	lung tumor	universal normal control
PRO4409	cervical tumor	universal normal control
PRO4409	colon tumor	universal normal control
PRO4399	lung tumor	universal normal control
PRO4399	breast tumor	universal normal control
PRO4418	lung tumor	universal normal control
PRO4418	breast tumor	universal normal control
PRO4330	cervical tumor	universal normal control
PRO4330	colon tumor	matched normal colon control
PRO4339	breast tumor	universal normal control
PRO4339	colon tumor	universal normal control
PRO4326	lung tumor	universal normal control
PRO4326	colon tumor	universal normal control
PRO6014	breast tumor	universal normal control
PRO3446	colon tumor	universal normal control
PRO3446	lung tumor	universal normal control
PRO4322	lung tumor	universal normal control
PRO4322	rectal tumor	universal normal control
PRO4322	colon tumor	matched normal colon control
PRO4381	breast tumor	universal normal control
PRO4381	lung tumor	universal normal control
PRO4381	colon tumor	universal normal control
PRO4348	lung tumor	universal normal control
PRO4348	prostate tumor	universal normal control
PRO4371	breast tumor	universal normal control
PRO3742	colon tumor	universal normal control
PRO3742	lung tumor	universal normal control
PRO5773	lung tumor	universal normal control
PRO5773	colon tumor	universal normal control
PRO5773	prostate tumor	universal normal control
PRO5774	colon tumor	universal normal control
PRO4343	colon tumor	universal normal control
PRO4325	lung tumor	universal normal control
PRO4347	lung tumor	universal normal control
PRO4347	colon tumor	universal normal control
PRO4347	rectal tumor	universal normal control
PRO3743	colon tumor	universal normal control
PRO3743	lung tumor	universal normal control
PRO3743	prostate tumor	universal normal control
PRO4426	colon tumor	universal normal control
PRO4500	colon tumor	universal normal control
PRO4389	breast tumor	universal normal control
PRO4389	lung tumor	universal normal control
PRO4337	colon tumor	universal normal control
PRO4337	breast tumor	universal normal control
PRO4337	lung tumor	universal normal control
PRO4992	lung tumor	universal normal control
PRO5996	lung tumor	universal normal control
PRO4345	lung tumor	universal normal control
PRO4345	colon tumor	universal normal control
PRO5780	lung tumor	universal normal control
PRO5780	breast tumor	universal normal control
PRO5992	lung tumor	universal normal control
PRO5992	colon tumor	universal normal control
PRO5992	breast tumor	universal normal control
PRO4428	prostate tumor	universal normal control
PRO4994	lung tumor	universal normal control
PRO5995	lung tumor	universal normal control
PRO5995	colon tumor	universal normal control



TABLE 8-continued

Molecule	is overexpressed in:	as compared to:
PRO6094	lung tumor	universal normal control
PRO6094	colon tumor	universal normal control
PRO4317	lung tumor	universal normal control
PRO4317	colon tumor	universal normal control
PRO4317	liver tumor	universal normal control
PRO4317	colon tumor	matched normal colon control
PRO5997	colon tumor	universal normal control
PRO5997	lung tumor	universal normal control
PRO5005	lung tumor	universal normal control
PRO5005	colon tumor	universal normal control
PRO5004	colon tumor	universal normal control
PRO6001	breast tumor	universal normal control
PRO6013	colon tumor	universal normal control
PRO4502	lung tumor	universal normal control
PRO4502	colon tumor	universal normal control
PRO6007	breast tumor	universal normal control
PRO6028	breast tumor	universal normal control
PRO6028	colon tumor	universal normal control
PRO4327	prostate tumor	universal normal control
PRO4315	colon tumor	universal normal control
PRO5993	lung tumor	universal normal control
PRO5993	colon tumor	universal normal control
PRO4503	colon tumor	universal normal control
PRO4976	lung tumor	universal normal control
PRO5798	lung tumor	universal normal control
PRO5798	colon tumor	universal normal control
PRO6242	colon tumor	universal normal control
PRO6242	colon tumor	matched normal colon control
PRO6242	breast tumor	universal normal control
PRO6242	liver tumor	universal normal control
PRO6242	rectal tumor	universal normal control
PRO6095	breast tumor	universal normal control
PRO6095	lung tumor	universal normal control
PRO6093	colon tumor	universal normal control
PRO6093	breast tumor	universal normal control
PRO6093	lung tumor	universal normal control
PRO6093	colon tumor	matched normal colon control
PRO6012	colon tumor	universal normal control
PRO6027	lung tumor	universal normal control
PRO6027	colon tumor	universal normal control
PRO6027	rectal tumor	universal normal control
PRO6181	prostate tumor	universal normal control
PRO6181	lung tumor	universal normal control
PRO6181	colon tumor	universal normal control
PRO6097	colon tumor	universal normal control
PRO6097	lung tumor	universal normal control
PRO6090	lung tumor	universal normal control
PRO7171	lung tumor	universal normal control
PRO7171	colon tumor	universal normal control
PRO7171	breast tumor	universal normal control
PRO6258	prostate tumor	universal normal control
PRO6258	breast tumor	universal normal control
PRO6258	cervical tumor	universal normal control
PRO6258	liver tumor	universal normal control
PRO6258	colon tumor	universal normal control
PRO9820	prostate tumor	universal normal control
PRO6243	lung tumor	universal normal control
PRO6182	lung tumor	universal normal control
PRO6079	lung tumor	universal normal control
PRO6079	colon tumor	universal normal control
PRO6079	breast tumor	universal normal control
PRO6079	prostate tumor	universal normal control
PRO7434	lung tumor	universal normal control
PRO9865	colon tumor	universal normal control
PRO9828	colon tumor	universal normal control
PRO196	colon tumor	universal normal control
PRO196	lung tumor	universal normal control
PRO196	breast tumor	universal normal control
PRO197	colon tumor	universal normal control
PRO197	lung tumor	universal normal control
PRO197	breast tumor	universal normal control
PRO195	colon tumor	universal normal control
PRO195	lung tumor	universal normal control
PRO195	breast tumor	universal normal control

TABLE 8-continued

Molecule	is overexpressed in:	as compared to:
PRO187	lung tumor	universal normal control
PRO187	liver tumor	universal normal control
PRO182	colon tumor	universal normal control
PRO182	lung tumor	universal normal control
PRO182	breast tumor	universal normal control
PRO188	rectal tumor	universal normal control
PRO183	colon tumor	universal normal control
PRO183	lung tumor	universal normal control
PRO183	breast tumor	universal normal control
PRO183	rectal tumor	universal normal control
PRO184	lung tumor	universal normal control
PRO184	breast tumor	universal normal control
PRO185	lung tumor	universal normal control
PRO200	colon tumor	universal normal control
PRO200	lung tumor	universal normal control
PRO200	breast tumor	universal normal control
PRO200	rectal tumor	universal normal control
PRO202	colon tumor	universal normal control
PRO202	lung tumor	universal normal control
PRO202	breast tumor	universal normal control
PRO202	rectal tumor	universal normal control
PRO202	liver tumor	universal normal control
PRO214	colon tumor	universal normal control
PRO214	lung tumor	universal normal control
PRO215	colon tumor	universal normal control
PRO215	lung tumor	universal normal control
PRO215	breast tumor	universal normal control
PRO219	colon tumor	universal normal control
PRO219	lung tumor	universal normal control
PRO219	breast tumor	universal normal control
PRO219	liver tumor	universal normal control
PRO211	lung tumor	universal normal control
PRO211	breast tumor	universal normal control
PRO220	colon tumor	universal normal control
PRO220	lung tumor	universal normal control
PRO220	breast tumor	universal normal control
PRO366	colon tumor	universal normal control
PRO366	lung tumor	universal normal control
PRO366	breast tumor	universal normal control
PRO216	lung tumor	universal normal control
PRO221	colon tumor	universal normal control
PRO221	lung tumor	universal normal control
PRO221	breast tumor	universal normal control
PRO228	lung tumor	universal normal control
PRO228	breast tumor	universal normal control
PRO217	lung tumor	universal normal control
PRO217	breast tumor	universal normal control
PRO222	colon tumor	universal normal control
PRO222	lung tumor	universal normal control
PRO222	breast tumor	universal normal control
PRO224	colon tumor	universal normal control
PRO224	lung tumor	universal normal control
PRO224	breast tumor	universal normal control
PRO224	prostate tumor	universal normal control
PRO224	rectal tumor	universal normal control
PRO230	colon tumor	universal normal control
PRO230	lung tumor	universal normal control
PRO230	breast tumor	universal normal control
PRO230	prostate tumor	universal normal control
PRO198	colon tumor	universal normal control
PRO198	lung tumor	universal normal control
PRO198	breast tumor	universal normal control
PRO198	liver tumor	universal normal control
PRO226	lung tumor	universal normal control
PRO226	breast tumor	universal normal control
PRO261	lung tumor	universal normal control
PRO242	colon tumor	universal normal control
PRO242	lung tumor	universal normal control
PRO242	breast tumor	universal normal control
PRO227	colon tumor	universal normal control
PRO227	lung tumor	universal normal control
PRO237	colon tumor	universal normal control
PRO237	lung tumor	universal normal control
PRO237	breast tumor	universal normal control





TABLE 8-continued

Molecule	is overexpressed in:	as compared to:
PRO1693	breast tumor	universal normal control
PRO1868	lung tumor	universal normal control
PRO1868	breast tumor	universal normal control
PRO1890	colon tumor	universal normal control
PRO1890	lung tumor	universal normal control
PRO1890	breast tumor	universal normal control
PRO1890	prostate tumor	universal normal control
PRO1887	colon tumor	universal normal control
PRO1887	breast tumor	universal normal control
PRO4353	lung tumor	universal normal control
PRO4353	breast tumor	universal normal control
PRO1801	colon tumor	universal normal control
PRO1801	lung tumor	universal normal control
PRO4357	lung tumor	universal normal control
PRO4357	breast tumor	universal normal control
PRO4302	colon tumor	universal normal control
PRO4302	lung tumor	universal normal control
PRO4302	breast tumor	universal normal control
PRO4302	prostate tumor	universal normal control
PRO5990	colon tumor	universal normal control
PRO5990	lung tumor	universal normal control
PRO5990	breast tumor	universal normal control

Example 31

Identification of Receptor/Ligand Interactions

[0932] In this assay, various PRO polypeptides are tested for ability to bind to a panel of potential receptor or ligand molecules for the purpose of identifying receptor/ligand interactions. The identification of a ligand for a known receptor, a receptor for a known ligand or a novel receptor/ligand pair is useful for a variety of indications including, for example, targeting bioactive molecules (linked to the ligand or receptor) to a cell known to express the receptor or ligand, use of the receptor or ligand as a reagent to detect the presence of the ligand or receptor in a composition suspected of containing the same, wherein the composition may comprise cells suspected of expressing the ligand or receptor, modulating the growth of or another biological or immunological activity of a cell known to express or respond to the receptor or ligand, modulating the immune response of cells or toward cells that express the receptor or ligand, allowing the preparation of agonists, antagonists and/or antibodies directed against the receptor or ligand which will modulate the growth of or a biological or immunological activity of a cell expressing the receptor or ligand, and various other indications which will be readily apparent to the ordinarily skilled artisan.

[0933] The assay is performed as follows. A PRO polypeptide of the present invention suspected of being a ligand for a receptor is expressed as a fusion protein containing the Fc domain of human IgG (an immunoadhesin). Receptor-ligand binding is detected by allowing interaction of the immunoadhesin polypeptide with cells (e.g. Cos cells) expressing candidate PRO polypeptide receptors and visualization of bound immunoadhesin with fluorescent reagents directed toward the Fc fusion domain and examination by microscope. Cells expressing candidate receptors are produced by transient transfection, in parallel, of defined subsets of a library of cDNA expression vectors encoding PRO

polypeptides that may function as receptor molecules. Cells are then incubated for 1 hour in the presence of the PRO polypeptide immunoadhesin being tested for possible receptor binding. The cells are then washed and fixed with paraformaldehyde. The cells are then incubated with fluorescent conjugated antibody directed against the Fc portion of the PRO polypeptide immunoadhesin (e.g. FITC conjugated goat anti-human-Fc antibody). The cells are then washed again and examined by microscope. A positive interaction is judged by the presence of fluorescent labeling of cells transfected with cDNA encoding a particular PRO polypeptide receptor or pool of receptors and an absence of similar fluorescent labeling of similarly prepared cells that have been transfected with other cDNA or pools of cDNA. If a defined pool of cDNA expression vectors is judged to be positive for interaction with a PRO polypeptide immunoadhesin, the individual cDNA species that comprise the pool are tested individually (the pool is “broken down”) to determine the specific cDNA that encodes a receptor able to interact with the PRO polypeptide immunoadhesin.

[0934] In another embodiment of this assay, an epitope-tagged potential ligand PRO polypeptide (e.g. 8 histidine “His” tag) is allowed to interact with a panel of potential receptor PRO polypeptide molecules that have been expressed as fusions with the Fc domain of human IgG (immunoadhesins). Following a 1 hour co-incubation with the epitope tagged PRO polypeptide, the candidate receptors are each immunoprecipitated with protein A beads and the beads are washed. Potential ligand interaction is determined by western blot analysis of the immunoprecipitated complexes with antibody directed towards the epitope tag. An interaction is judged to occur if a band of the anticipated molecular weight of the epitope tagged protein is observed in the western blot analysis with a candidate receptor, but is not observed to occur with the other members of the panel of potential receptors.

[0935] Using these assays, the following receptor/ligand interactions have been herein identified:

[0936] (1) PRO1801 binds to PRO1114 and PRO4978.

[0937] (2) PRO100 binds to PRO1114.

[0938] The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by the construct deposited, since the deposited embodiment is intended as a single illustration of certain aspects of the invention and any constructs that are functionally equivalent are within the scope of this invention. The deposit of material herein does not constitute an admission that the written description herein contained is inadequate to enable the practice of any aspect of the invention, including the best mode thereof, nor is it to be construed as limiting the scope of the claims to the specific illustrations that it represents. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims.

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SEQUENCE LISTING

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The patent application contains a lengthy "Sequence Listing" section. A copy of the "Sequence Listing" is available in electronic form from the USPTO web site (<http://seqdata.uspto.gov/sequence.html?DocID=20030082759>). An electronic copy of the "Sequence Listing" will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

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What is claimed is:

1. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence that encodes an amino acid sequence selected from the group consisting of the amino acid sequence shown in **FIG. 2** (SEQ ID NO:2), **FIG. 4** (SEQ ID NO:4), **FIG. 6** (SEQ ID NO:6), **FIG. 8** (SEQ ID NO:8), **FIG. 10** (SEQ ID NO:10), **FIG. 12** (SEQ ID NO:12), **FIG. 14** (SEQ ID NO:14), **FIG. 16** (SEQ ID NO:16), **FIG. 18** (SEQ ID NO:18), **FIG. 20** (SEQ ID NO:20), **FIG. 22** (SEQ ID NO:22), **FIG. 24** (SEQ ID NO:24), **FIG. 26** (SEQ ID NO:26), **FIG. 28** (SEQ ID NO:28), **FIG. 30** (SEQ ID NO:30), **FIG. 32** (SEQ ID NO:32), **FIG. 34** (SEQ ID NO:34), **FIG. 36** (SEQ ID NO:36), **FIG. 38** (SEQ ID NO:38), **FIG. 40** (SEQ ID NO:40), **FIG. 42** (SEQ ID NO:42), **FIG. 44** (SEQ ID NO:44), **FIG. 46** (SEQ ID NO:46), **FIG. 48** (SEQ ID NO:48), **FIG. 50** (SEQ ID NO:50), **FIG. 52** (SEQ ID NO:52), **FIG. 54** (SEQ ID NO:54), **FIG. 56** (SEQ ID NO:56), **FIG. 58** (SEQ ID NO:58), **FIG. 60** (SEQ ID NO:60), **FIG. 62** (SEQ ID NO:62), **FIG. 64** (SEQ ID NO:64), **FIG. 66** (SEQ ID NO:66), **FIG. 68** (SEQ ID NO:68), **FIG. 70** (SEQ ID NO:70), **FIG. 72** (SEQ ID NO:72), **FIG. 74** (SEQ ID NO:74), **FIG. 76** (SEQ ID NO:76), **FIG. 78** (SEQ ID NO:78), **FIG. 80** (SEQ ID NO:80), **FIG. 82** (SEQ ID NO:82), **FIG. 84** (SEQ ID NO:84), **FIG. 86** (SEQ ID NO:86), **FIG. 88** (SEQ ID NO:88), **FIG. 90** (SEQ ID NO:90), **FIG. 92** (SEQ ID NO:92), **FIG. 94** (SEQ ID NO:94), **FIG. 96** (SEQ ID NO:96), **FIG. 98** (SEQ ID NO:98), **FIG. 100** (SEQ ID NO:100), **FIG. 102** (SEQ ID NO:102), **FIG. 104** (SEQ ID NO:104), **FIG. 106** (SEQ ID NO:106), **FIG. 108** (SEQ ID NO:108), **FIG. 110** (SEQ ID NO:110), **FIG. 112** (SEQ ID NO:112), **FIG. 114** (SEQ ID NO:114), **FIG. 116** (SEQ ID NO:116), **FIG. 118** (SEQ ID NO:118), **FIG. 120** (SEQ ID NO:120), **FIG. 122** (SEQ ID NO:122), **FIG. 124** (SEQ ID NO:124), **FIG. 126** (SEQ ID NO:126), **FIG. 128** (SEQ ID NO:128), **FIG. 130** (SEQ ID NO:130), **FIG. 132** (SEQ ID NO:132), **FIG. 134** (SEQ ID NO:134), **FIG. 136** (SEQ ID NO:136), **FIG. 138** (SEQ ID NO:138), **FIG. 140** (SEQ ID NO:140), **FIG. 142** (SEQ ID NO:142), **FIG. 144** (SEQ ID NO:144), **FIG. 146** (SEQ ID NO:146), **FIG. 148** (SEQ ID NO:148), **FIG. 150** (SEQ ID NO:150), **FIG. 152** (SEQ ID NO:152), **FIG. 154** (SEQ ID NO:154), **FIG. 156** (SEQ ID NO:156), **FIG. 158** (SEQ ID NO:158), **FIG. 160** (SEQ ID NO:160), **FIG. 162** (SEQ ID NO:162), **FIG. 164** (SEQ ID NO:164), **FIG. 166** (SEQ ID NO:166), **FIG. 168** (SEQ ID NO:168), **FIG. 170** (SEQ ID NO:170), **FIG. 172** (SEQ ID NO:172), **FIG. 174** (SEQ ID NO:174), **FIG. 176** (SEQ ID NO:176), **FIG. 178** (SEQ ID NO:178), **FIG. 180** (SEQ ID NO:180), **FIG. 182** (SEQ ID NO:182), **FIG. 184** (SEQ ID NO:184), **FIG. 186** (SEQ ID NO:186), **FIG. 188** (SEQ ID

NO:188), **FIG. 190** (SEQ ID NO:190), **FIG. 192** (SEQ ID NO:192), **FIG. 194** (SEQ ID NO:194), **FIG. 196** (SEQ ID NO:196), **FIG. 198** (SEQ ID NO:198), **FIG. 200** (SEQ ID NO:200), **FIG. 202** (SEQ ID NO:202), **FIG. 204** (SEQ ID NO:204), **FIG. 206** (SEQ ID NO:206), **FIG. 208** (SEQ ID NO:208), **FIG. 210** (SEQ ID NO:210), **FIG. 212** (SEQ ID NO:212), **FIG. 214** (SEQ ID NO:214), **FIG. 216** (SEQ ID NO:216), **FIG. 218** (SEQ ID NO:218), **FIG. 220** (SEQ ID NO:220), **FIG. 222** (SEQ ID NO:222), **FIG. 224** (SEQ ID NO:224), **FIG. 226** (SEQ ID NO:226), **FIG. 228** (SEQ ID NO:228), **FIG. 230** (SEQ ID NO:230), **FIG. 232** (SEQ ID NO:232), **FIG. 234** (SEQ ID NO:234), **FIG. 236** (SEQ ID NO:236), **FIG. 238** (SEQ ID NO:238), **FIG. 240** (SEQ ID NO:240), **FIG. 242** (SEQ ID NO:242), **FIG. 244** (SEQ ID NO:244), **FIG. 246** (SEQ ID NO:246), **FIG. 248** (SEQ ID NO:248), **FIG. 250** (SEQ ID NO:250), **FIG. 252** (SEQ ID NO:252), **FIG. 254** (SEQ ID NO:254), **FIG. 256** (SEQ ID NO:256), **FIG. 258** (SEQ ID NO:258), **FIG. 260** (SEQ ID NO:260), **FIG. 262** (SEQ ID NO:262), **FIG. 264** (SEQ ID NO:264), **FIG. 266** (SEQ ID NO:266), **FIG. 268** (SEQ ID NO:268), **FIG. 270** (SEQ ID NO:270), **FIG. 272** (SEQ ID NO:272), **FIG. 274** (SEQ ID NO:274), **FIG. 276** (SEQ ID NO:276), **FIG. 278** (SEQ ID NO:278), **FIG. 280** (SEQ ID NO:280), **FIG. 282** (SEQ ID NO:282), **FIG. 284** (SEQ ID NO:284), **FIG. 286** (SEQ ID NO:286), **FIG. 288** (SEQ ID NO:288), **FIG. 290** (SEQ ID NO:290), **FIG. 292** (SEQ ID NO:292), **FIG. 294** (SEQ ID NO:294), **FIG. 296** (SEQ ID NO:296), **FIG. 298** (SEQ ID NO:298), **FIG. 300** (SEQ ID NO:300), **FIG. 302** (SEQ ID NO:302), **FIG. 304** (SEQ ID NO:304), **FIG. 306** (SEQ ID NO:306), **FIG. 308** (SEQ ID NO:308), **FIG. 310** (SEQ ID NO:310), **FIG. 312** (SEQ ID NO:312), **FIG. 314** (SEQ ID NO:314), **FIG. 316** (SEQ ID NO:316), **FIG. 318** (SEQ ID NO:318), **FIG. 320** (SEQ ID NO:320), **FIG. 322** (SEQ ID NO:322), **FIG. 324** (SEQ ID NO:324), **FIG. 326** (SEQ ID NO:326), **FIG. 328** (SEQ ID NO:328), **FIG. 330** (SEQ ID NO:330), **FIG. 332** (SEQ ID NO:332), **FIG. 334** (SEQ ID NO:334), **FIG. 336** (SEQ ID NO:336), **FIG. 338** (SEQ ID NO:338), **FIG. 340** (SEQ ID NO:340), **FIG. 342** (SEQ ID NO:342), **FIG. 344** (SEQ ID NO:344), **FIG. 346** (SEQ ID NO:346), **FIG. 348** (SEQ ID NO:348), **FIG. 350** (SEQ ID NO:350), **FIG. 352** (SEQ ID NO:352), **FIG. 354** (SEQ ID NO:354), **FIG. 356** (SEQ ID NO:356), **FIG. 358** (SEQ ID NO:358), **FIG. 360** (SEQ ID NO:360), **FIG. 362** (SEQ ID NO:362), **FIG. 364** (SEQ ID NO:364), **FIG. 366** (SEQ ID NO:366), **FIG. 368** (SEQ ID NO:368), **FIG. 370** (SEQ ID NO:370), **FIG. 372** (SEQ ID NO:372), **FIG. 374** (SEQ ID NO:374), **FIG. 376** (SEQ ID NO:376), **FIG. 378** (SEQ ID NO:378), **FIG. 380** (SEQ ID NO:380), **FIG. 382** (SEQ ID NO:382), **FIG. 384** (SEQ ID NO:384), **FIG. 386** (SEQ ID NO:386), **FIG. 388** (SEQ ID NO:388), **FIG. 390** (SEQ ID NO:390), **FIG. 392** (SEQ ID

NO:392), **FIG. 394** (SEQ ID NO:394), **FIG. 396** (SEQ ID NO:396), **FIG. 398** (SEQ ID NO:398), **FIG. 400** (SEQ ID NO:400), **FIG. 402** (SEQ ID NO:402), **FIG. 404** (SEQ ID NO:404), **FIG. 406** (SEQ ID NO:406), **FIG. 408** (SEQ ID NO:408), **FIG. 410** (SEQ ID NO:410), **FIG. 412** (SEQ ID NO:412), **FIG. 414** (SEQ ID NO:414), **FIG. 416** (SEQ ID NO:416), **FIG. 418** (SEQ ID NO:418), **FIG. 420** (SEQ ID NO:420), **FIG. 422** (SEQ ID NO:422), **FIG. 424** (SEQ ID NO:424), **FIG. 426** (SEQ ID NO:426), **FIG. 428** (SEQ ID NO:428), **FIG. 430** (SEQ ID NO:430), **FIG. 432** (SEQ ID NO:432), **FIG. 434** (SEQ ID NO:434), **FIG. 436** (SEQ ID NO:436), **FIG. 438** (SEQ ID NO:438), **FIG. 440** (SEQ ID NO:440), **FIG. 442** (SEQ ID NO:442), **FIG. 444** (SEQ ID NO:444), **FIG. 446** (SEQ ID NO:446), **FIG. 448** (SEQ ID NO:448), **FIG. 450** (SEQ ID NO:450), **FIG. 452** (SEQ ID NO:452), **FIG. 454** (SEQ ID NO:454), **FIG. 456** (SEQ ID NO:456), **FIG. 458** (SEQ ID NO:458), **FIG. 460** (SEQ ID NO:460), **FIG. 462** (SEQ ID NO:462), **FIG. 464** (SEQ ID NO:464), **FIG. 466** (SEQ ID NO:466), **FIG. 468** (SEQ ID NO:468), **FIG. 470** (SEQ ID NO:470), **FIG. 472** (SEQ ID NO:472), **FIG. 474** (SEQ ID NO:474), **FIG. 476** (SEQ ID NO:476), **FIG. 478** (SEQ ID NO:478), **FIG. 480** (SEQ ID NO:480), **FIG. 482** (SEQ ID NO:482), **FIG. 484** (SEQ ID NO:484), **FIG. 486** (SEQ ID NO:486), **FIG. 488** (SEQ ID NO:488), **FIG. 490** (SEQ ID NO:490), **FIG. 492** (SEQ ID NO:492), **FIG. 494** (SEQ ID NO:494), **FIG. 496** (SEQ ID NO:496), **FIG. 498** (SEQ ID NO:498), **FIG. 500** (SEQ ID NO:500), **FIG. 502** (SEQ ID NO:502), **FIG. 504** (SEQ ID NO:504), **FIG. 506** (SEQ ID NO:506), **FIG. 508** (SEQ ID NO:508), **FIG. 510** (SEQ ID NO:510), **FIG. 512** (SEQ ID NO:512), **FIG. 514** (SEQ ID NO:514), **FIG. 516** (SEQ ID NO:516), **FIG. 518** (SEQ ID NO:518), **FIG. 520** (SEQ ID NO:520), **FIG. 522** (SEQ ID NO:522), **FIG. 524** (SEQ ID NO:524), **FIG. 526** (SEQ ID NO:526), **FIG. 528** (SEQ ID NO:528), **FIG. 530** (SEQ ID NO:530), **FIG. 532** (SEQ ID NO:532), **FIG. 534** (SEQ ID NO:534), **FIG. 536** (SEQ ID NO:536), **FIG. 538** (SEQ ID NO:538), **FIG. 540** (SEQ ID NO:540), **FIG. 542** (SEQ ID NO:542), **FIG. 544** (SEQ ID NO:544), **FIG. 546** (SEQ ID NO:546), **FIG. 548** (SEQ ID NO:548) and **FIG. 550** (SEQ ID NO:550).

2. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of the nucleotide sequence shown in **FIG. 1** (SEQ ID NO:1), **FIG. 3** (SEQ ID NO:3), **FIG. 5** (SEQ ID NO:5), **FIG. 7** (SEQ ID NO:7), **FIG. 9** (SEQ ID NO:9), **FIG. 11** (SEQ ID NO:11), **FIG. 13** (SEQ ID NO:13), **FIG. 15** (SEQ ID NO:15), **FIG. 17** (SEQ ID NO:17), **FIG. 19** (SEQ ID NO:19), **FIG. 21** (SEQ ID NO:21), **FIG. 23** (SEQ ID NO:23), **FIG. 25** (SEQ ID NO:25), **FIG. 27** (SEQ ID NO:27), **FIG. 29** (SEQ ID NO:29), **FIG. 31** (SEQ ID NO:31), **FIG. 33** (SEQ ID NO:33), **FIG. 35** (SEQ ID NO:35), **FIG. 37** (SEQ ID NO:37), **FIG. 39** (SEQ ID NO:39), **FIG. 41** (SEQ ID NO:41), **FIG. 43** (SEQ ID NO:43), **FIG. 45** (SEQ ID NO:45), **FIG. 47** (SEQ ID NO:47), **FIG. 49** (SEQ ID NO:49), **FIG. 51** (SEQ ID NO:51), **FIG. 53** (SEQ ID NO:53), **FIG. 55** (SEQ ID NO:55), **FIG. 57** (SEQ ID NO:57), **FIG. 59** (SEQ ID NO:59), **FIG. 61** (SEQ ID NO:61), **FIG. 63** (SEQ ID NO:63), **FIG. 65** (SEQ ID NO:65), **FIG. 67** (SEQ ID NO:67), **FIG. 69** (SEQ ID NO:69), **FIG. 71** (SEQ ID NO:71), **FIG. 73** (SEQ ID NO:73), **FIG. 75** (SEQ ID NO:75), **FIG. 77** (SEQ ID NO:77), **FIG. 79** (SEQ ID NO:79), **FIG. 81** (SEQ ID NO:81), **FIG. 83** (SEQ ID NO:83), **FIG. 85** (SEQ ID NO:85), **FIG. 87** (SEQ ID

NO:87), **FIG. 89** (SEQ ID NO:89), **FIG. 91** (SEQ ID NO:91), **FIG. 93** (SEQ ID NO:93), **FIG. 95** (SEQ ID NO:95), **FIG. 97** (SEQ ID NO:97), **FIG. 99** (SEQ ID NO:99), **FIG. 101** (SEQ ID NO:101), **FIG. 103** (SEQ ID NO:103), **FIG. 105** (SEQ ID NO:105), **FIG. 107** (SEQ ID NO:107), **FIG. 109** (SEQ ID NO:109), **FIG. 111** (SEQ ID NO:111), **FIG. 113** (SEQ ID NO:113), **FIG. 115** (SEQ ID NO:115), **FIG. 117** (SEQ ID NO:117), **FIG. 119** (SEQ ID NO:119), **FIG. 121** (SEQ ID NO:121), **FIG. 123** (SEQ ID NO:123), **FIG. 125** (SEQ ID NO:125), **FIG. 127** (SEQ ID NO:127), **FIG. 129** (SEQ ID NO:129), **FIG. 131** (SEQ ID NO:131), **FIG. 133** (SEQ ID NO:133), **FIG. 135** (SEQ ID NO:135), **FIG. 137** (SEQ ID NO:137), **FIG. 139** (SEQ ID NO:139), **FIG. 141** (SEQ ID NO: 141), **FIG. 143** (SEQ ID NO:143), **FIG. 145** (SEQ ID NO:145), **FIG. 147** (SEQ ID NO:147), **FIG. 149** (SEQ ID NO:149), **FIG. 151** (SEQ ID NO:151), **FIG. 153** (SEQ ID NO:153), **FIG. 155** (SEQ ID NO:155), **FIG. 157** (SEQ ID NO:157), **FIG. 159** (SEQ ID NO:159), **FIG. 161** (SEQ ID NO:161), **FIG. 163** (SEQ ID NO:163), **FIG. 165** (SEQ ID NO:165), **FIG. 167** (SEQ ID NO:167), **FIG. 169** (SEQ ID NO:169), **FIG. 171** (SEQ ID NO:171), **FIG. 173** (SEQ ID NO:173), **FIG. 175** (SEQ ID NO:175), **FIG. 177** (SEQ ID NO:177), **FIG. 179** (SEQ ID NO:179), **FIG. 181** (SEQ ID NO:181), **FIG. 183** (SEQ ID NO:183), **FIG. 185** (SEQ ID NO:185), **FIG. 187** (SEQ ID NO:187), **FIG. 189** (SEQ ID NO:189), **FIG. 191** (SEQ ID NO:191), **FIG. 193** (SEQ ID NO:193), **FIG. 195** (SEQ ID NO:195), **FIG. 197** (SEQ ID NO:197), **FIG. 199** (SEQ ID NO:199), **FIG. 201** (SEQ ID NO:201), **FIG. 203** (SEQ ID NO:203), **FIG. 205** (SEQ ID NO:205), **FIG. 207** (SEQ ID NO:207), **FIG. 209** (SEQ ID NO:209), **FIG. 211** (SEQ ID NO:211), **FIG. 213** (SEQ ID NO:213), **FIG. 215** (SEQ ID NO:215), **FIG. 217** (SEQ ID NO:217), **FIG. 219** (SEQ ID NO:219), **FIG. 221** (SEQ ID NO:221), **FIG. 223** (SEQ ID NO:223), **FIG. 225** (SEQ ID NO:225), **FIG. 227** (SEQ ID NO:227), **FIG. 229** (SEQ ID NO:229), **FIG. 231** (SEQ ID NO:231), **FIG. 233** (SEQ ID NO:233), **FIG. 235** (SEQ ID NO:235), **FIG. 237** (SEQ ID NO:237), **FIG. 239** (SEQ ID NO:239), **FIG. 241** (SEQ ID NO:241), **FIG. 243** (SEQ ID NO:243), **FIG. 245** (SEQ ID NO:245), **FIG. 247** (SEQ ID NO:247), **FIG. 249** (SEQ ID NO:249), **FIG. 251** (SEQ ID NO:251), **FIG. 253** (SEQ ID NO:253), **FIG. 255** (SEQ ID NO:255), **FIG. 257** (SEQ ID NO:257), **FIG. 259** (SEQ ID NO:259), **FIG. 261** (SEQ ID NO:261), **FIG. 263** (SEQ ID NO:263), **FIG. 265** (SEQ ID NO:265), **FIG. 267** (SEQ ID NO:267), **FIG. 269** (SEQ ID NO:269), **FIG. 271** (SEQ ID NO:271), **FIG. 273** (SEQ ID NO:273), **FIG. 275** (SEQ ID NO:275), **FIG. 277** (SEQ ID NO:277), **FIG. 279** (SEQ ID NO:279), **FIG. 281** (SEQ ID NO:281), **FIG. 283** (SEQ ID NO:283), **FIG. 285** (SEQ ID NO:285), **FIG. 287** (SEQ ID NO:287), **FIG. 289** (SEQ ID NO:289), **FIG. 291** (SEQ ID NO:291), **FIG. 293** (SEQ ID NO:293), **FIG. 295** (SEQ ID NO:295), **FIG. 297** (SEQ ID NO:297), **FIG. 299** (SEQ ID NO:299), **FIG. 301** (SEQ ID NO:301), **FIG. 303** (SEQ ID NO:303), **FIG. 305** (SEQ ID NO:305), **FIG. 307** (SEQ ID NO:307), **FIG. 309** (SEQ ID NO:309), **FIG. 311** (SEQ ID NO:311), **FIG. 313** (SEQ ID NO:313), **FIG. 315** (SEQ ID NO:315), **FIG. 317** (SEQ ID NO:317), **FIG. 319** (SEQ ID NO:319), **FIG. 321** (SEQ ID NO:321), **FIG. 323** (SEQ ID NO:323), **FIG. 325** (SEQ ID NO:325), **FIG. 327** (SEQ ID NO:327), **FIG. 329** (SEQ ID NO:329), **FIG. 331** (SEQ ID NO:331), **FIG. 333** (SEQ ID NO:333), **FIG. 335** (SEQ ID NO:335), **FIG. 337** (SEQ ID NO:337), **FIG. 339** (SEQ ID NO:339), **FIG. 341** (SEQ ID NO:341), **FIG. 343** (SEQ ID

NO:343), **FIG. 345** (SEQ ID NO:345), **FIG. 347** (SEQ ID NO:347), **FIG. 349** (SEQ ID NO:349), **FIG. 351** (SEQ ID NO:351), **FIG. 353** (SEQ ID NO:353), **FIG. 355** (SEQ ID NO:355), **FIG. 357** (SEQ ID NO:357), **FIG. 359** (SEQ ID NO:359), **FIG. 361** (SEQ ID NO:361), **FIG. 363** (SEQ ID NO:363), **FIG. 365** (SEQ ID NO:365), **FIG. 367** (SEQ ID NO:367), **FIG. 369** (SEQ ID NO:369), **FIG. 371** (SEQ ID NO:371), **FIG. 373** (SEQ ID NO:373), **FIG. 375** (SEQ ID NO:375), **FIG. 377** (SEQ ID NO:377), **FIG. 379** (SEQ ID NO:379), **FIG. 381** (SEQ ID NO:381), **FIG. 383** (SEQ ID NO:383), **FIG. 385** (SEQ ID NO:385), **FIG. 387** (SEQ ID NO:387), **FIG. 389** (SEQ ID NO:389), **FIG. 391** (SEQ ID NO:391), **FIG. 393** (SEQ ID NO:393), **FIG. 395** (SEQ ID NO:395), **FIG. 397** (SEQ ID NO:397), **FIG. 399** (SEQ ID NO:399), **FIG. 401** (SEQ ID NO:401), **FIG. 403** (SEQ ID NO:403), **FIG. 405** (SEQ ID NO:405), **FIG. 407** (SEQ ID NO:407), **FIG. 409** (SEQ ID NO:409), **FIG. 411** (SEQ ID NO:411), **FIG. 413** (SEQ ID NO:413), **FIG. 415** (SEQ ID NO:415), **FIG. 417** (SEQ ID NO:417), **FIG. 419** (SEQ ID NO:419), **FIG. 421** (SEQ ID NO:421), **FIG. 423** (SEQ ID NO:423), **FIG. 425** (SEQ ID NO:425), **FIG. 427** (SEQ ID NO:427), **FIG. 429** (SEQ ID NO:429), **FIG. 431** (SEQ ID NO:431), **FIG. 433** (SEQ ID NO:433), **FIG. 435** (SEQ ID NO:435), **FIG. 437** (SEQ ID NO:437), **FIG. 439** (SEQ ID NO:439), **FIG. 441** (SEQ ID NO:441), **FIG. 443** (SEQ ID NO:443), **FIG. 445** (SEQ ID NO:445), **FIG. 447** (SEQ ID NO:447), **FIG. 449** (SEQ ID NO:449), **FIG. 451** (SEQ ID NO:451), **FIG. 453** (SEQ ID NO:453), **FIG. 455** (SEQ ID NO:455), **FIG. 457** (SEQ ID NO:457), **FIG. 459** (SEQ ID NO:459), **FIG. 461** (SEQ ID NO:461), **FIG. 463** (SEQ ID NO:463), **FIG. 465** (SEQ ID NO:465), **FIG. 467** (SEQ ID NO:467), **FIG. 469** (SEQ ID NO:469), **FIG. 471** (SEQ ID NO:471), **FIG. 473** (SEQ ID NO:473), **FIG. 475** (SEQ ID NO:475), **FIG. 477** (SEQ ID NO:477), **FIG. 479** (SEQ ID NO:479), **FIG. 481** (SEQ ID NO:481), **FIG. 483** (SEQ ID NO:483), **FIG. 485** (SEQ ID NO:485), **FIG. 487** (SEQ ID NO:487), **FIG. 489** (SEQ ID NO:489), **FIG. 491** (SEQ ID NO:491), **FIG. 493** (SEQ ID NO:493), **FIG. 495** (SEQ ID NO:495), **FIG. 497** (SEQ ID NO:497), **FIG. 499** (SEQ ID NO:499), **FIG. 501** (SEQ ID NO:501), **FIG. 503** (SEQ ID NO:503), **FIG. 505** (SEQ ID NO:505), **FIG. 507** (SEQ ID NO:507), **FIG. 509** (SEQ ID NO:509), **FIG. 511** (SEQ ID NO:511), **FIG. 513** (SEQ ID NO:513), **FIG. 515** (SEQ ID NO:515), **FIG. 517** (SEQ ID NO:517), **FIG. 519** (SEQ ID NO:519), **FIG. 521** (SEQ ID NO:521), **FIG. 523** (SEQ ID NO:523), **FIG. 525** (SEQ ID NO:525), **FIG. 527** (SEQ ID NO:527), **FIG. 529** (SEQ ID NO:529), **FIG. 531** (SEQ ID NO:531), **FIG. 533** (SEQ ID NO:533), **FIG. 535** (SEQ ID NO:535), **FIG. 537** (SEQ ID NO:537), **FIG. 539** (SEQ ID NO:539), **FIG. 541** (SEQ ID NO:541), **FIG. 543** (SEQ ID NO:543), **FIG. 545** (SEQ ID NO:545), **FIG. 547** (SEQ ID NO:547) and **FIG. 549** (SEQ ID NO:549).

3. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of the full-length coding sequence of the nucleotide sequence shown in **FIG. 1** (SEQ ID NO:1), **FIG. 3** (SEQ ID NO:3), **FIG. 5** (SEQ ID NO:5), **FIG. 7** (SEQ ID NO:7), **FIG. 9** (SEQ ID NO:9), **FIG. 11** (SEQ ID NO:11), **FIG. 13** (SEQ ID NO:13), **FIG. 15** (SEQ ID NO:15), **FIG. 17** (SEQ ID NO:17), **FIG. 19** (SEQ ID NO:19), **FIG. 21** (SEQ ID NO:21), **FIG. 23** (SEQ ID NO:23), **FIG. 25** (SEQ ID NO:25), **FIG. 27** (SEQ ID NO:27), **FIG. 29** (SEQ ID NO:29), **FIG. 31** (SEQ ID NO:31), **FIG. 33** (SEQ ID NO:33), **FIG. 35** (SEQ ID NO:35), **FIG. 37** (SEQ ID

NO:37), **FIG. 39** (SEQ ID NO:39), **FIG. 41** (SEQ ID NO:41), **FIG. 43** (SEQ ID NO:43), **FIG. 45** (SEQ ID NO:45), **FIG. 47** (SEQ ID NO:47), **FIG. 49** (SEQ ID NO:49), **FIG. 51** (SEQ ID NO:51), **FIG. 53** (SEQ ID NO:53), **FIG. 55** (SEQ ID NO:55), **FIG. 57** (SEQ ID NO:57), **FIG. 59** (SEQ ID NO:59), **FIG. 61** (SEQ ID NO:61), **FIG. 63** (SEQ ID NO:63), **FIG. 65** (SEQ ID NO:65), **FIG. 67** (SEQ ID NO:67), **FIG. 69** (SEQ ID NO:69), **FIG. 71** (SEQ ID NO:71), **FIG. 73** (SEQ ID NO:73), **FIG. 75** (SEQ ID NO:75), **FIG. 77** (SEQ ID NO:77), **FIG. 79** (SEQ ID NO:79), **FIG. 81** (SEQ ID NO:81), **FIG. 83** (SEQ ID NO:83), **FIG. 85** (SEQ ID NO:85), **FIG. 87** (SEQ ID NO:87), **FIG. 89** (SEQ ID NO:89), **FIG. 91** (SEQ ID NO:91), **FIG. 93** (SEQ ID NO:93), **FIG. 95** (SEQ ID NO:95), **FIG. 97** (SEQ ID NO:97), **FIG. 99** (SEQ ID NO:99), **FIG. 101** (SEQ ID NO:101), **FIG. 103** (SEQ ID NO:103), **FIG. 105** (SEQ ID NO:105), **FIG. 107** (SEQ ID NO:107), **FIG. 109** (SEQ ID NO:109), **FIG. 111** (SEQ ID NO:111), **FIG. 113** (SEQ ID NO:113), **FIG. 115** (SEQ ID NO:115), **FIG. 117** (SEQ ID NO:117), **FIG. 119** (SEQ ID NO:119), **FIG. 121** (SEQ ID NO:121), **FIG. 123** (SEQ ID NO:123), **FIG. 125** (SEQ ID NO:125), **FIG. 127** (SEQ ID NO:127), **FIG. 129** (SEQ ID NO:129), **FIG. 131** (SEQ ID NO:131), **FIG. 133** (SEQ ID NO:133), **FIG. 135** (SEQ ID NO:135), **FIG. 137** (SEQ ID NO:137), **FIG. 139** (SEQ ID NO:1390), **FIG. 141** (SEQ ID NO:141), **FIG. 143** (SEQ ID NO:143), **FIG. 145** (SEQ ID NO:145), **FIG. 147** (SEQ ID NO:147), **FIG. 149** (SEQ ID NO:149), **FIG. 151** (SEQ ID NO:151), **FIG. 153** (SEQ ID NO:153), **FIG. 155** (SEQ ID NO:155), **FIG. 157** (SEQ ID NO:157), **FIG. 159** (SEQ ID NO:159), **FIG. 161** (SEQ ID NO:161), **FIG. 163** (SEQ ID NO:163), **FIG. 165** (SEQ ID NO:165), **FIG. 167** (SEQ ID NO:167), **FIG. 169** (SEQ ID NO:169), **FIG. 171** (SEQ ID NO:171), **FIG. 173** (SEQ ID NO:173), **FIG. 175** (SEQ ID NO:175), **FIG. 177** (SEQ ID NO:177), **FIG. 179** (SEQ ID NO:179), **FIG. 181** (SEQ ID NO:181), **FIG. 183** (SEQ ID NO:183), **FIG. 185** (SEQ ID NO:185), **FIG. 187** (SEQ ID NO:187), **FIG. 189** (SEQ ID NO:189), **FIG. 191** (SEQ ID NO:191), **FIG. 193** (SEQ ID NO:193), **FIG. 195** (SEQ ID NO:195), **FIG. 197** (SEQ ID NO:197), **FIG. 199** (SEQ ID NO:199), **FIG. 201** (SEQ ID NO:201), **FIG. 203** (SEQ ID NO:203), **FIG. 205** (SEQ ID NO:205), **FIG. 207** (SEQ ID NO:207), **FIG. 209** (SEQ ID NO:209), **FIG. 211** (SEQ ID NO:211), **FIG. 213** (SEQ ID NO:213), **FIG. 215** (SEQ ID NO:215), **FIG. 217** (SEQ ID NO:217), **FIG. 219** (SEQ ID NO:219), **FIG. 221** (SEQ ID NO:221), **FIG. 223** (SEQ ID NO:223), **FIG. 225** (SEQ ID NO:225), **FIG. 227** (SEQ ID NO:227), **FIG. 229** (SEQ ID NO:229), **FIG. 231** (SEQ ID NO:231), **FIG. 233** (SEQ ID NO:233), **FIG. 235** (SEQ ID NO:235), **FIG. 237** (SEQ ID NO:237), **FIG. 239** (SEQ ID NO:239), **FIG. 241** (SEQ ID NO:241), **FIG. 243** (SEQ ID NO:243), **FIG. 245** (SEQ ID NO:245), **FIG. 247** (SEQ ID NO:247), **FIG. 249** (SEQ ID NO:249), **FIG. 251** (SEQ ID NO:251), **FIG. 253** (SEQ ID NO:253), **FIG. 255** (SEQ ID NO:255), **FIG. 257** (SEQ ID NO:257), **FIG. 259** (SEQ ID NO:259), **FIG. 261** (SEQ ID NO:261), **FIG. 263** (SEQ ID NO:263), **FIG. 265** (SEQ ID NO:265), **FIG. 267** (SEQ ID NO:267), **FIG. 269** (SEQ ID NO:269), **FIG. 271** (SEQ ID NO:271), **FIG. 273** (SEQ ID NO:273), **FIG. 275** (SEQ ID NO:275), **FIG. 277** (SEQ ID NO:277), **FIG. 279** (SEQ ID NO:279), **FIG. 281** (SEQ ID NO:281), **FIG. 283** (SEQ ID NO:283), **FIG. 285** (SEQ ID NO:285), **FIG. 287** (SEQ ID NO:287), **FIG. 289** (SEQ ID NO:289), **FIG. 291** (SEQ ID NO:291), **FIG. 293** (SEQ ID

NO:293), FIG. 295 (SEQ ID NO:295), FIG. 297 (SEQ ID NO:297), FIG. 299 (SEQ ID NO:299), FIG. 301 (SEQ ID NO:301), FIG. 303 (SEQ ID NO:303), FIG. 305 (SEQ ID NO:305), FIG. 307 (SEQ ID NO:307), FIG. 309 (SEQ ID NO:309), FIG. 311 (SEQ ID NO:311), FIG. 313 (SEQ ID NO:313), FIG. 315 (SEQ ID NO:315), FIG. 317 (SEQ ID NO:317), FIG. 319 (SEQ ID NO:319), FIG. 321 (SEQ ID NO:321), FIG. 323 (SEQ ID NO:323), FIG. 325 (SEQ ID NO:325), FIG. 327 (SEQ ID NO:327), FIG. 329 (SEQ ID NO:329), FIG. 331 (SEQ ID NO:331), FIG. 333 (SEQ ID NO:333), FIG. 335 (SEQ ID NO:335), FIG. 337 (SEQ ID NO:337), FIG. 339 (SEQ ID NO:339), FIG. 341 (SEQ ID NO:341), FIG. 343 (SEQ ID NO:343), FIG. 345 (SEQ ID NO:345), FIG. 347 (SEQ ID NO:347), FIG. 349 (SEQ ID NO:349), FIG. 351 (SEQ ID NO:351), FIG. 353 (SEQ ID NO:353), FIG. 355 (SEQ ID NO:355), FIG. 357 (SEQ ID NO:357), FIG. 359 (SEQ ID NO:359), FIG. 361 (SEQ ID NO:361), FIG. 363 (SEQ ID NO:363), FIG. 365 (SEQ ID NO:365), FIG. 367 (SEQ ID NO:367), FIG. 369 (SEQ ID NO:369), FIG. 371 (SEQ ID NO:371), FIG. 373 (SEQ ID NO:373), FIG. 375 (SEQ ID NO:375), FIG. 377 (SEQ ID NO:377), FIG. 379 (SEQ ID NO:379), FIG. 381 (SEQ ID NO:381), FIG. 383 (SEQ ID NO:383), FIG. 385 (SEQ ID NO:385), FIG. 387 (SEQ ID NO:387), FIG. 389 (SEQ ID NO:389), FIG. 391 (SEQ ID NO:391), FIG. 393 (SEQ ID NO:393), FIG. 395 (SEQ ID NO:395), FIG. 397 (SEQ ID NO:397), FIG. 399 (SEQ ID NO:399), FIG. 401 (SEQ ID NO:401), FIG. 403 (SEQ ID NO:403), FIG. 405 (SEQ ID NO:405), FIG. 407 (SEQ ID NO:407), FIG. 409 (SEQ ID NO:409), FIG. 411 (SEQ ID NO:411), FIG. 413 (SEQ ID NO:413), FIG. 415 (SEQ ID NO:415), FIG. 417 (SEQ ID NO:417), FIG. 419 (SEQ ID NO:419), FIG. 421 (SEQ ID NO:421), FIG. 423 (SEQ ID NO:423), FIG. 425 (SEQ ID NO:425), FIG. 427 (SEQ ID NO:427), FIG. 429 (SEQ ID NO:429), FIG. 431 (SEQ ID NO:431), FIG. 433 (SEQ ID NO:433), FIG. 435 (SEQ ID NO:435), FIG. 437 (SEQ ID NO:437), FIG. 439 (SEQ ID NO:439), FIG. 441 (SEQ ID NO:441), FIG. 443 (SEQ ID NO:443), FIG. 445 (SEQ ID NO:445), FIG. 447 (SEQ ID NO:447), FIG. 449 (SEQ ID NO:449), FIG. 451 (SEQ ID NO:451), FIG. 453 (SEQ ID NO:453), FIG. 455 (SEQ ID NO:455), FIG. 457 (SEQ ID NO:457), FIG. 459 (SEQ ID NO:459), FIG. 461 (SEQ ID NO:461), FIG. 463 (SEQ ID NO:463), FIG. 465 (SEQ ID NO:465), FIG. 467 (SEQ ID NO:467), FIG. 469 (SEQ ID NO:469), FIG. 471 (SEQ ID NO:471), FIG. 473 (SEQ ID NO:473), FIG. 475 (SEQ ID NO:475), FIG. 477 (SEQ ID NO:477), FIG. 479 (SEQ ID NO:479), FIG. 481 (SEQ ID NO:481), FIG. 483 (SEQ ID NO:483), FIG. 485 (SEQ ID NO:485), FIG. 487 (SEQ ID NO:487), FIG. 489 (SEQ ID NO:489), FIG. 491 (SEQ ID NO:491), FIG. 493 (SEQ ID NO:493), FIG. 495 (SEQ ID NO:495), FIG. 497 (SEQ ID NO:497), FIG. 499 (SEQ ID NO:499), FIG. 501 (SEQ ID NO:501), FIG. 503 (SEQ ID NO:503), FIG. 505 (SEQ ID NO:505), FIG. 507 (SEQ ID NO:507), FIG. 509 (SEQ ID NO:509), FIG. 511 (SEQ ID NO:511), FIG. 513 (SEQ ID NO:513), FIG. 515 (SEQ ID NO:515), FIG. 517 (SEQ ID NO:517), FIG. 519 (SEQ ID NO:519), FIG. 521 (SEQ ID NO:521), FIG. 523 (SEQ ID NO:523), FIG. 525 (SEQ ID NO:525), FIG. 527 (SEQ ID NO:527), FIG. 529 (SEQ ID NO:529), FIG. 531 (SEQ ID NO:531), FIG. 533 (SEQ ID NO:533), FIG. 535 (SEQ ID NO:535), FIG. 537 (SEQ ID NO:537), FIG. 539 (SEQ ID NO:539), FIG. 541 (SEQ ID

NO:541), FIG. 543 (SEQ ID NO:543), FIG. 545 (SEQ ID NO:545), FIG. 547 (SEQ ID NO:547) and FIG. 549 (SEQ ID NO:549).

4. Isolated nucleic acid having at least 80% nucleic acid sequence identity to the full-length coding sequence of the DNA deposited under any ATCC accession number shown in Table 7.

5. A vector comprising the nucleic acid of claim 1.

6. The vector of claim 5 operably linked to control sequences recognized by a host cell transformed with the vector.

7. A host cell comprising the vector of claim 5.

8. The host cell of claim 7, wherein said cell is a CHO cell.

9. The host cell of claim 7, wherein said cell is an *E. coli*.

10. The host cell of claim 7, wherein said cell is a yeast cell.

11. A process for producing a PRO polypeptides comprising culturing the host cell of claim 7 under conditions suitable for expression of said PRO polypeptide and recovering said PRO polypeptide from the cell culture.

12. An isolated polypeptide having at least 80% amino acid sequence identity to an amino acid sequence selected from the group consisting of the amino acid sequence shown in FIG. 2 (SEQ ID NO:2), FIG. 4 (SEQ ID NO:4), FIG. 6 (SEQ ID NO:6), FIG. 8 (SEQ ID NO:8), FIG. 10 (SEQ ID NO:10), FIG. 12 (SEQ ID NO:12), FIG. 14 (SEQ ID NO:14), FIG. 16 (SEQ ID NO:16), FIG. 18 (SEQ ID NO:18), FIG. 20 (SEQ ID NO:20), FIG. 22 (SEQ ID NO:22), FIG. 24 (SEQ ID NO:24), FIG. 26 (SEQ ID NO:26), FIG. 28 (SEQ ID NO:28), FIG. 30 (SEQ ID NO:30), FIG. 32 (SEQ ID NO:32), FIG. 34 (SEQ ID NO:34), FIG. 36 (SEQ ID NO:36), FIG. 38 (SEQ ID NO:38), FIG. 40 (SEQ ID NO:40), FIG. 42 (SEQ ID NO:42), FIG. 44 (SEQ ID NO:44), FIG. 46 (SEQ ID NO:46), FIG. 48 (SEQ ID NO:48), FIG. 50 (SEQ ID NO:50), FIG. 52 (SEQ ID NO:52), FIG. 54 (SEQ ID NO:54), FIG. 56 (SEQ ID NO:56), FIG. 58 (SEQ ID NO:58), FIG. 60 (SEQ ID NO:60), FIG. 62 (SEQ ID NO:62), FIG. 64 (SEQ ID NO:64), FIG. 66 (SEQ ID NO:66), FIG. 68 (SEQ ID NO:68), FIG. 70 (SEQ ID NO:70), FIG. 72 (SEQ ID NO:72), FIG. 74 (SEQ ID NO:74), FIG. 76 (SEQ ID NO:76), FIG. 78 (SEQ ID NO:78), FIG. 80 (SEQ ID NO:80), FIG. 82 (SEQ ID NO:82), FIG. 84 (SEQ ID NO:84), FIG. 86 (SEQ ID NO:86), FIG. 88 (SEQ ID NO:88), FIG. 90 (SEQ ID NO:90), FIG. 92 (SEQ ID NO:92), FIG. 94 (SEQ ID NO:94), FIG. 96 (SEQ ID NO:96), FIG. 98 (SEQ ID NO:98), FIG. 100 (SEQ ID NO:100), FIG. 102 (SEQ ID NO:102), FIG. 104 (SEQ ID NO:104), FIG. 106 (SEQ ID NO:106), FIG. 108 (SEQ ID NO:108), FIG. 110 (SEQ ID NO:110), FIG. 112 (SEQ ID NO:112), FIG. 114 (SEQ ID NO:114), FIG. 116 (SEQ ID NO:116), FIG. 118 (SEQ ID NO:118), FIG. 120 (SEQ ID NO:120), FIG. 122 (SEQ ID NO:122), FIG. 124 (SEQ ID NO:124), FIG. 126 (SEQ ID NO:126), FIG. 128 (SEQ ID NO:128), FIG. 130 (SEQ ID NO:130), FIG. 132 (SEQ ID NO:132), FIG. 134 (SEQ ID NO:134), FIG. 136 (SEQ ID NO:136), FIG. 138 (SEQ ID NO:138), FIG. 140 (SEQ ID NO:140), FIG. 142 (SEQ ID NO:142), FIG. 144 (SEQ ID NO:144), FIG. 146 (SEQ ID NO:146), FIG. 148 (SEQ ID NO:148), FIG. 150 (SEQ ID NO:150), FIG. 152 (SEQ ID NO:152), FIG. 154 (SEQ ID NO:154), FIG. 156 (SEQ ID NO:156), FIG. 158 (SEQ ID NO:158), FIG. 160 (SEQ ID NO:160), FIG. 162 (SEQ ID NO:162), FIG. 164 (SEQ ID NO:164), FIG. 166 (SEQ ID



NO:166), **FIG. 168** (SEQ ID NO:168), **FIG. 170** (SEQ ID NO:170), **FIG. 172** (SEQ ID NO:172), **FIG. 174** (SEQ ID NO:174), **FIG. 176** (SEQ ID NO:176), **FIG. 178** (SEQ ID NO:178), **FIG. 180** (SEQ ID NO:180), **FIG. 182** (SEQ ID NO:182), **FIG. 184** (SEQ ID NO:184), **FIG. 186** (SEQ ID NO:186), **FIG. 188** (SEQ ID NO:188), **FIG. 190** (SEQ ID NO:190), **FIG. 192** (SEQ ID NO:192), **FIG. 194** (SEQ ID NO:194), **FIG. 196** (SEQ ID NO:196), **FIG. 198** (SEQ ID NO:198), **FIG. 200** (SEQ ID NO:200), **FIG. 202** (SEQ ID NO:202), **FIG. 204** (SEQ ID NO:204), **FIG. 206** (SEQ ID NO:206), **FIG. 208** (SEQ ID NO:208), **FIG. 210** (SEQ ID NO:210), **FIG. 212** (SEQ ID NO:212), **FIG. 214** (SEQ ID NO:214), **FIG. 216** (SEQ ID NO:216), **FIG. 218** (SEQ ID NO:218), **FIG. 220** (SEQ ID NO:220), **FIG. 222** (SEQ ID NO:222), **FIG. 224** (SEQ ID NO:224), **FIG. 226** (SEQ ID NO:226), **FIG. 228** (SEQ ID NO:228), **FIG. 230** (SEQ ID NO:230), **FIG. 232** (SEQ ID NO:232), **FIG. 234** (SEQ ID NO:234), **FIG. 236** (SEQ ID NO:236), **FIG. 238** (SEQ ID NO:238), **FIG. 240** (SEQ ID NO:240), **FIG. 242** (SEQ ID NO:242), **FIG. 244** (SEQ ID NO:244), **FIG. 246** (SEQ ID NO:246), **FIG. 248** (SEQ ID NO:248), **FIG. 250** (SEQ ID NO:250), **FIG. 252** (SEQ ID NO:252), **FIG. 254** (SEQ ID NO:254), **FIG. 256** (SEQ ID NO:256), **FIG. 258** (SEQ ID NO:258), **FIG. 260** (SEQ ID NO:260), **FIG. 262** (SEQ ID NO:262), **FIG. 264** (SEQ ID NO:264), **FIG. 266** (SEQ ID NO:266), **FIG. 268** (SEQ ID NO:268), **FIG. 270** (SEQ ID NO:270), **FIG. 272** (SEQ ID NO:272), **FIG. 274** (SEQ ID NO:274), **FIG. 276** (SEQ ID NO:276), **FIG. 278** (SEQ ID NO:278), **FIG. 280** (SEQ ID NO:280), **FIG. 282** (SEQ ID NO:282), **FIG. 284** (SEQ ID NO:284), **FIG. 286** (SEQ ID NO:286), **FIG. 288** (SEQ ID NO:288), **FIG. 290** (SEQ ID NO:290), **FIG. 292** (SEQ ID NO:292), **FIG. 294** (SEQ ID NO:294), **FIG. 296** (SEQ ID NO:296), **FIG. 298** (SEQ ID NO:298), **FIG. 300** (SEQ ID NO:300), **FIG. 302** (SEQ ID NO:302), **FIG. 304** (SEQ ID NO:304), **FIG. 306** (SEQ ID NO:306), **FIG. 308** (SEQ ID NO:308), **FIG. 310** (SEQ ID NO:310), **FIG. 312** (SEQ ID NO:312), **FIG. 314** (SEQ ID NO:314), **FIG. 316** (SEQ ID NO:316), **FIG. 318** (SEQ ID NO:318), **FIG. 320** (SEQ ID NO:320), **FIG. 322** (SEQ ID NO:322), **FIG. 324** (SEQ ID NO:324), **FIG. 326** (SEQ ID NO:326), **FIG. 328** (SEQ ID NO:328), **FIG. 330** (SEQ ID NO:330), **FIG. 332** (SEQ ID NO:332), **FIG. 334** (SEQ ID NO:334), **FIG. 336** (SEQ ID NO:336), **FIG. 338** (SEQ ID NO:338), **FIG. 340** (SEQ ID NO:340), **FIG. 342** (SEQ ID NO:342), **FIG. 344** (SEQ ID NO:344), **FIG. 346** (SEQ ID NO:346), **FIG. 348** (SEQ ID NO:348), **FIG. 350** (SEQ ID NO:350), **FIG. 352** (SEQ ID NO:352), **FIG. 354** (SEQ ID NO:354), **FIG. 356** (SEQ ID NO:356), **FIG. 358** (SEQ ID NO:358), **FIG. 360** (SEQ ID NO:360), **FIG. 362** (SEQ ID NO:362), **FIG. 364** (SEQ ID NO:364), **FIG. 366** (SEQ ID NO:366), **FIG. 368** (SEQ ID NO:368), **FIG. 370** (SEQ ID NO:370), **FIG. 372** (SEQ ID NO:372), **FIG. 374** (SEQ ID NO:374), **FIG. 376** (SEQ ID NO:376), **FIG. 378** (SEQ ID NO:378), **FIG. 380** (SEQ ID NO:380), **FIG. 382** (SEQ ID NO:382), **FIG. 384** (SEQ ID NO:384), **FIG. 386** (SEQ ID NO:386), **FIG. 388** (SEQ ID NO:388), **FIG. 390** (SEQ ID NO:390), **FIG. 392** (SEQ ID NO:392), **FIG. 394** (SEQ ID NO:394), **FIG. 396** (SEQ ID NO:396), **FIG. 398** (SEQ ID NO:398), **FIG. 400** (SEQ ID NO:400), **FIG. 402** (SEQ ID NO:402), **FIG. 404** (SEQ ID NO:404), **FIG. 406** (SEQ ID NO:406), **FIG. 408** (SEQ ID NO:408), **FIG. 410** (SEQ ID NO:410), **FIG. 412** (SEQ ID NO:412), **FIG. 414** (SEQ ID NO:414), **FIG. 416** (SEQ ID NO:416), **FIG. 418** (SEQ ID NO:418), **FIG. 420** (SEQ ID NO:420), **FIG. 422** (SEQ ID

NO:422), **FIG. 424** (SEQ ID NO:424), **FIG. 426** (SEQ ID NO:426), **FIG. 428** (SEQ ID NO:428), **FIG. 430** (SEQ ID NO:430), **FIG. 432** (SEQ ID NO:432), **FIG. 434** (SEQ ID NO:434), **FIG. 436** (SEQ ID NO:436), **FIG. 438** (SEQ ID NO:438), **FIG. 440** (SEQ ID NO:440), **FIG. 442** (SEQ ID NO:442), **FIG. 444** (SEQ ID NO:444), **FIG. 446** (SEQ ID NO:446), **FIG. 448** (SEQ ID NO:448), **FIG. 450** (SEQ ID NO:450), **FIG. 452** (SEQ ID NO:452), **FIG. 454** (SEQ ID NO:454), **FIG. 456** (SEQ ID NO:456), **FIG. 458** (SEQ ID NO:458), **FIG. 460** (SEQ ID NO:460), **FIG. 462** (SEQ ID NO:462), **FIG. 464** (SEQ ID NO:464), **FIG. 466** (SEQ ID NO:466), **FIG. 468** (SEQ ID NO:468), **FIG. 470** (SEQ ID NO:470), **FIG. 472** (SEQ ID NO:472), **FIG. 474** (SEQ ID NO:474), **FIG. 476** (SEQ ID NO:476), **FIG. 478** (SEQ ID NO:478), **FIG. 480** (SEQ ID NO:480), **FIG. 482** (SEQ ID NO:482), **FIG. 484** (SEQ ID NO:484), **FIG. 486** (SEQ ID NO:486), **FIG. 488** (SEQ ID NO:488), **FIG. 490** (SEQ ID NO:490), **FIG. 492** (SEQ ID NO:492), **FIG. 494** (SEQ ID NO:494), **FIG. 496** (SEQ ID NO:496), **FIG. 498** (SEQ ID NO:498), **FIG. 500** (SEQ ID NO:500), **FIG. 502** (SEQ ID NO:502), **FIG. 504** (SEQ ID NO:504), **FIG. 506** (SEQ ID NO:506), **FIG. 508** (SEQ ID NO:508), **FIG. 510** (SEQ ID NO:510), **FIG. 512** (SEQ ID NO:512), **FIG. 514** (SEQ ID NO:514), **FIG. 516** (SEQ ID NO:516), **FIG. 518** (SEQ ID NO:518), **FIG. 520** (SEQ ID NO:520), **FIG. 522** (SEQ ID NO:522), **FIG. 524** (SEQ ID NO:524), **FIG. 526** (SEQ ID NO:526), **FIG. 528** (SEQ ID NO:528), **FIG. 530** (SEQ ID NO:530), **FIG. 532** (SEQ ID NO:532), **FIG. 534** (SEQ ID NO:534), **FIG. 536** (SEQ ID NO:536), **FIG. 538** (SEQ ID NO:538), **FIG. 540** (SEQ ID NO:540), **FIG. 542** (SEQ ID NO:542), **FIG. 544** (SEQ ID NO:544), **FIG. 546** (SEQ ID NO:546), **FIG. 548** (SEQ ID NO:548) and **FIG. 550** (SEQ ID NO:550).

**13.** An isolated polypeptide having at least 80% amino acid sequence identity to an amino acid sequence encoded by the full-length coding sequence of the DNA deposited under any ATCC accession number shown in Table 7.

**14.** A chimeric molecule comprising a polypeptide according to claim 12 fused to a heterologous amino acid sequence.

**15.** The chimeric molecule of claim 14, wherein said heterologous amino acid sequence is an epitope tag sequence.

**16.** The chimeric molecule of claim 14, wherein said heterologous amino acid sequence is a Fc region of an immunoglobulin.

**17.** An antibody which specifically binds to a polypeptide according to claim 12.

**18.** The antibody of claim 17, wherein said antibody is a monoclonal antibody, a humanized antibody or a single-chain antibody.

**19.** Isolated nucleic acid having at least 80% nucleic acid sequence identity to:

- (a) a nucleotide sequence encoding the polypeptide shown in **FIG. 2** (SEQ ID NO:2), **FIG. 4** (SEQ ID NO:4), **FIG. 6** (SEQ ID NO:6), **FIG. 8** (SEQ ID NO:8), **FIG. 10** (SEQ ID NO:10), **FIG. 12** (SEQ ID NO:12), **FIG. 14** (SEQ ID NO:14), **FIG. 16** (SEQ ID NO:16), **FIG. 18** (SEQ ID NO:18), **FIG. 20** (SEQ ID NO:20), **FIG. 22** (SEQ ID NO:22), **FIG. 24** (SEQ ID NO:24), **FIG. 26** (SEQ ID NO:26), **FIG. 28** (SEQ ID NO:28), **FIG. 30** (SEQ ID NO:30), **FIG. 32** (SEQ ID NO:32), **FIG. 34** (SEQ ID NO:34), **FIG. 36** (SEQ ID NO:36), **FIG. 38** (SEQ ID NO:38), **FIG. 40** (SEQ ID NO:40), **FIG.**



(SEQ ID NO:508), **FIG. 510** (SEQ ID NO:510), **FIG. 512** (SEQ ID NO:512), **FIG. 514** (SEQ ID NO:514), **FIG. 516** (SEQ ID NO:516), **FIG. 518** (SEQ ID NO:518), **FIG. 520** (SEQ ID NO:520), **FIG. 522** (SEQ ID NO:522), **FIG. 524** (SEQ ID NO:524), **FIG. 526** (SEQ ID NO:526), **FIG. 528** (SEQ ID NO:528), **FIG. 530** (SEQ ID NO:530), **FIG. 532** (SEQ ID NO:532), **FIG. 534** (SEQ ID NO:534), **FIG. 536** (SEQ ID NO:536), **FIG. 538** (SEQ ID NO:538), **FIG. 540** (SEQ ID NO:540), **FIG. 542** (SEQ ID NO:542), **FIG. 544** (SEQ ID NO:544), **FIG. 546** (SEQ ID NO:546), **FIG. 548** (SEQ ID NO:548) or **FIG. 550** (SEQ ID NO:550), lacking its associated signal peptide;

- (b) a nucleotide sequence encoding an extracellular domain of the polypeptide shown in **FIG. 2** (SEQ ID NO:2), **FIG. 4** (SEQ ID NO:4), **FIG. 6** (SEQ ID NO:6), **FIG. 8** (SEQ ID NO:8), **FIG. 10** (SEQ ID NO:10), **FIG. 12** (SEQ ID NO:12), **FIG. 14** (SEQ ID NO:14), **FIG. 16** (SEQ ID NO:16), **FIG. 18** (SEQ ID NO:18), **FIG. 20** (SEQ ID NO:20), **FIG. 22** (SEQ ID NO:22), **FIG. 24** (SEQ ID NO:24), **FIG. 26** (SEQ ID NO:26), **FIG. 28** (SEQ ID NO:28), **FIG. 30** (SEQ ID NO:30), **FIG. 32** (SEQ ID NO:32), **FIG. 34** (SEQ ID NO:34), **FIG. 36** (SEQ ID NO:36), **FIG. 38** (SEQ ID NO:38), **FIG. 40** (SEQ ID NO:40), **FIG. 42** (SEQ ID NO:42), **FIG. 44** (SEQ ID NO:44), **FIG. 46** (SEQ ID NO:46), **FIG. 48** (SEQ ID NO:48), **FIG. 50** (SEQ ID NO:50), **FIG. 52** (SEQ ID NO:52), **FIG. 54** (SEQ ID NO:54), **FIG. 56** (SEQ ID NO:56), **FIG. 58** (SEQ ID NO:58), **FIG. 60** (SEQ ID NO:60), **FIG. 62** (SEQ ID NO:62), **FIG. 64** (SEQ ID NO:64), **FIG. 66** (SEQ ID NO:66), **FIG. 68** (SEQ ID NO:68), **FIG. 70** (SEQ ID NO:70), **FIG. 72** (SEQ ID NO:72), **FIG. 74** (SEQ ID NO:74), **FIG. 76** (SEQ ID NO:76), **FIG. 78** (SEQ ID NO:78), **FIG. 80** (SEQ ID NO:80), **FIG. 82** (SEQ ID NO:82), **FIG. 84** (SEQ ID NO:84), **FIG. 86** (SEQ ID NO:86), **FIG. 88** (SEQ ID NO:88), **FIG. 90** (SEQ ID NO:90), **FIG. 92** (SEQ ID NO:92), **FIG. 94** (SEQ ID NO:94), **FIG. 96** (SEQ ID NO:96), **FIG. 98** (SEQ ID NO:98), **FIG. 100** (SEQ ID NO:100), **FIG. 102** (SEQ ID NO:102), **FIG. 104** (SEQ ID NO:104), **FIG. 106** (SEQ ID NO:106), **FIG. 108** (SEQ ID NO:108), **FIG. 110** (SEQ ID NO:110), **FIG. 112** (SEQ ID NO:112), **FIG. 114** (SEQ ID NO:114), **FIG. 116** (SEQ ID NO:116), **FIG. 118** (SEQ ID NO:118), **FIG. 120** (SEQ ID NO:120), **FIG. 122** (SEQ ID NO:122), **FIG. 124** (SEQ ID NO:124), **FIG. 126** (SEQ ID NO:126), **FIG. 128** (SEQ ID NO:128), **FIG. 130** (SEQ ID NO:130), **FIG. 132** (SEQ ID NO:132), **FIG. 134** (SEQ ID NO:134), **FIG. 136** (SEQ ID NO:136), **FIG. 138** (SEQ ID NO:138), **FIG. 140** (SEQ ID NO:140), **FIG. 142** (SEQ ID NO:142), **FIG. 144** (SEQ ID NO:144), **FIG. 146** (SEQ ID NO:146), **FIG. 148** (SEQ ID NO:148), **FIG. 150** (SEQ ID NO:150), **FIG. 152** (SEQ ID NO:152), **FIG. 154** (SEQ ID NO:154), **FIG. 156** (SEQ ID NO:156), **FIG. 158** (SEQ ID NO:158), **FIG. 160** (SEQ ID NO:160), **FIG. 162** (SEQ ID NO:162), **FIG. 164** (SEQ ID NO:164), **FIG. 166** (SEQ ID NO:166), **FIG. 168** (SEQ ID NO:168), **FIG. 170** (SEQ ID NO:170), **FIG. 172** (SEQ ID NO:172), **FIG. 174** (SEQ ID NO:174), **FIG. 176** (SEQ ID NO:176), **FIG. 178** (SEQ ID NO:178), **FIG. 180** (SEQ ID NO:180), **FIG. 182** (SEQ ID NO:182), **FIG. 184** (SEQ ID NO:184), **FIG. 186** (SEQ ID NO:186), **FIG. 188** (SEQ ID

NO:188), **FIG. 190** (SEQ ID NO:190), **FIG. 192** (SEQ ID NO:192), **FIG. 194** (SEQ ID NO:194), **FIG. 196** (SEQ ID NO:196), **FIG. 198** (SEQ ID NO:198), **FIG. 200** (SEQ ID NO:200), **FIG. 202** (SEQ ID NO:202), **FIG. 204** (SEQ ID NO:204), **FIG. 206** (SEQ ID NO:206), **FIG. 208** (SEQ ID NO:208), **FIG. 210** (SEQ ID NO:210), **FIG. 212** (SEQ ID NO:212), **FIG. 214** (SEQ ID NO:214), **FIG. 216** (SEQ ID NO:216), **FIG. 218** (SEQ ID NO:218), **FIG. 220** (SEQ ID NO:220), **FIG. 222** (SEQ ID NO:222), **FIG. 224** (SEQ ID NO:224), **FIG. 226** (SEQ ID NO:226), **FIG. 228** (SEQ ID NO:228), **FIG. 230** (SEQ ID NO:230), **FIG. 232** (SEQ ID NO:232), **FIG. 234** (SEQ ID NO:234), **FIG. 236** (SEQ ID NO:236), **FIG. 238** (SEQ ID NO:238), **FIG. 240** (SEQ ID NO:240), **FIG. 242** (SEQ ID NO:242), **FIG. 244** (SEQ ID NO:244), **FIG. 246** (SEQ ID NO:246), **FIG. 248** (SEQ ID NO:248), **FIG. 250** (SEQ ID NO:250), **FIG. 252** (SEQ ID NO:252), **FIG. 254** (SEQ ID NO:254), **FIG. 256** (SEQ ID NO:256), **FIG. 258** (SEQ ID NO:258), **FIG. 260** (SEQ ID NO:260), **FIG. 262** (SEQ ID NO:262), **FIG. 264** (SEQ ID NO:264), **FIG. 266** (SEQ ID NO:266), **FIG. 268** (SEQ ID NO:268), **FIG. 270** (SEQ ID NO:270), **FIG. 272** (SEQ ID NO:272), **FIG. 274** (SEQ ID NO:274), **FIG. 276** (SEQ ID NO:276), **FIG. 278** (SEQ ID NO:278), **FIG. 280** (SEQ ID NO:280), **FIG. 282** (SEQ ID NO:282), **FIG. 284** (SEQ ID NO:284), **FIG. 286** (SEQ ID NO:286), **FIG. 288** (SEQ ID NO:288), **FIG. 290** (SEQ ID NO:290), **FIG. 292** (SEQ ID NO:292), **FIG. 294** (SEQ ID NO:294), **FIG. 296** (SEQ ID NO:296), **FIG. 298** (SEQ ID NO:298), **FIG. 300** (SEQ ID NO:300), **FIG. 302** (SEQ ID NO:302), **FIG. 304** (SEQ ID NO:304), **FIG. 306** (SEQ ID NO:306), **FIG. 308** (SEQ ID NO:308), **FIG. 310** (SEQ ID NO:310), **FIG. 312** (SEQ ID NO:312), **FIG. 314** (SEQ ID NO:314), **FIG. 316** (SEQ ID NO:316), **FIG. 318** (SEQ ID NO:318), **FIG. 320** (SEQ ID NO:320), **FIG. 322** (SEQ ID NO:322), **FIG. 324** (SEQ ID NO:324), **FIG. 326** (SEQ ID NO:326), **FIG. 328** (SEQ ID NO:328), **FIG. 330** (SEQ ID NO:330), **FIG. 332** (SEQ ID NO:332), **FIG. 334** (SEQ ID NO:334), **FIG. 336** (SEQ ID NO:336), **FIG. 338** (SEQ ID NO:338), **FIG. 340** (SEQ ID NO:340), **FIG. 342** (SEQ ID NO:342), **FIG. 344** (SEQ ID NO:344), **FIG. 346** (SEQ ID NO:346), **FIG. 348** (SEQ ID NO:348), **FIG. 350** (SEQ ID NO:350), **FIG. 352** (SEQ ID NO:352), **FIG. 354** (SEQ ID NO:354), **FIG. 356** (SEQ ID NO:356), **FIG. 358** (SEQ ID NO:358), **FIG. 360** (SEQ ID NO:360), **FIG. 362** (SEQ ID NO:362), **FIG. 364** (SEQ ID NO:364), **FIG. 366** (SEQ ID NO:366), **FIG. 368** (SEQ ID NO:368), **FIG. 370** (SEQ ID NO:370), **FIG. 372** (SEQ ID NO:372), **FIG. 374** (SEQ ID NO:374), **FIG. 376** (SEQ ID NO:376), **FIG. 378** (SEQ ID NO:378), **FIG. 380** (SEQ ID NO:380), **FIG. 382** (SEQ ID NO:382), **FIG. 384** (SEQ ID NO:384), **FIG. 386** (SEQ ID NO:386), **FIG. 388** (SEQ ID NO:388), **FIG. 390** (SEQ ID NO:390), **FIG. 392** (SEQ ID NO:392), **FIG. 394** (SEQ ID NO:394), **FIG. 396** (SEQ ID NO:396), **FIG. 398** (SEQ ID NO:398), **FIG. 400** (SEQ ID NO:400), **FIG. 402** (SEQ ID NO:402), **FIG. 404** (SEQ ID NO:404), **FIG. 406** (SEQ ID NO:406), **FIG. 408** (SEQ ID NO:408), **FIG. 410** (SEQ ID NO:410), **FIG. 412** (SEQ ID NO:412), **FIG. 414** (SEQ ID NO:414), **FIG. 416** (SEQ ID NO:416), **FIG. 418** (SEQ ID NO:418),

**FIG. 420** (SEQ ID NO:420), **FIG. 422** (SEQ ID NO:422), **FIG. 424** (SEQ ID NO:424), **FIG. 426** (SEQ ID NO:426), **FIG. 428** (SEQ ID NO:428), **FIG. 430** (SEQ ID NO:430), **FIG. 432** (SEQ ID NO:432), **FIG. 434** (SEQ ID NO:434), **FIG. 436** (SEQ ID NO:436), **FIG. 438** (SEQ ID NO:438), **FIG. 440** (SEQ ID NO:440), **FIG. 442** (SEQ ID NO:442), **FIG. 444** (SEQ ID NO:444), **FIG. 446** (SEQ ID NO:446), **FIG. 448** (SEQ ID NO:448), **FIG. 450** (SEQ ID NO:450), **FIG. 452** (SEQ ID NO:452), **FIG. 454** (SEQ ID NO:454), **FIG. 456** (SEQ ID NO:456), **FIG. 458** (SEQ ID NO:458), **FIG. 460** (SEQ ID NO:460), **FIG. 462** (SEQ ID NO:462), **FIG. 464** (SEQ ID NO:464), **FIG. 466** (SEQ ID NO:466), **FIG. 468** (SEQ ID NO:468), **FIG. 470** (SEQ ID NO:470), **FIG. 472** (SEQ ID NO:472), **FIG. 474** (SEQ ID NO:474), **FIG. 476** (SEQ ID NO:476), **FIG. 478** (SEQ ID NO:478), **FIG. 480** (SEQ ID NO:480), **FIG. 482** (SEQ ID NO:482), **FIG. 484** (SEQ ID NO:484), **FIG. 486** (SEQ ID NO:486), **FIG. 488** (SEQ ID NO:488), **FIG. 490** (SEQ ID NO:490), **FIG. 492** (SEQ ID NO:492), **FIG. 494** (SEQ ID NO:494), **FIG. 496** (SEQ ID NO:496), **FIG. 498** (SEQ ID NO:498), **FIG. 500** (SEQ ID NO:500), **FIG. 502** (SEQ ID NO:502), **FIG. 504** (SEQ ID NO:504), **FIG. 506** (SEQ ID NO:506), **FIG. 508** (SEQ ID NO:508), **FIG. 510** (SEQ ID NO:510), **FIG. 512** (SEQ ID NO:512), **FIG. 514** (SEQ ID NO:514), **FIG. 516** (SEQ ID NO:516), **FIG. 518** (SEQ ID NO:518), **FIG. 520** (SEQ ID NO:520), **FIG. 522** (SEQ ID NO:522), **FIG. 524** (SEQ ID NO:524), **FIG. 526** (SEQ ID NO:526), **FIG. 528** (SEQ ID NO:528), **FIG. 530** (SEQ ID NO:530), **FIG. 532** (SEQ ID NO:532), **FIG. 534** (SEQ ID NO:534), **FIG. 536** (SEQ ID NO:536), **FIG. 538** (SEQ ID NO:538), **FIG. 540** (SEQ ID NO:540), **FIG. 542** (SEQ ID NO:542), **FIG. 544** (SEQ ID NO:544), **FIG. 546** (SEQ ID NO:546), **FIG. 548** (SEQ ID NO:548) or **FIG. 550** (SEQ ID NO:550), with its associated signal peptide; or

- (c) a nucleotide sequence encoding an extracellular domain of the polypeptide shown in **FIG. 2** (SEQ ID NO:2), **FIG. 4** (SEQ ID NO:4), **FIG. 6** (SEQ ID NO:6), **FIG. 8** (SEQ ID NO:8), **FIG. 10** (SEQ ID NO:10), **FIG. 12** (SEQ ID NO:12), **FIG. 14** (SEQ ID NO:14), **FIG. 16** (SEQ ID NO:16), **FIG. 18** (SEQ ID NO:18), **FIG. 20** (SEQ ID NO:20), **FIG. 22** (SEQ ID NO:22), **FIG. 24** (SEQ ID NO:24), **FIG. 26** (SEQ ID NO:26), **FIG. 28** (SEQ ID NO:28), **FIG. 30** (SEQ ID NO:30), **FIG. 32** (SEQ ID NO:32), **FIG. 34** (SEQ ID NO:34), **FIG. 36** (SEQ ID NO:36), **FIG. 38** (SEQ ID NO:38), **FIG. 40** (SEQ ID NO:40), **FIG. 42** (SEQ ID NO:42), **FIG. 44** (SEQ ID NO:44), **FIG. 46** (SEQ ID NO:46), **FIG. 48** (SEQ ID NO:48), **FIG. 50** (SEQ ID NO:50), **FIG. 52** (SEQ ID NO:52), **FIG. 54** (SEQ ID NO:54), **FIG. 56** (SEQ ID NO:56), **FIG. 58** (SEQ ID NO:58), **FIG. 60** (SEQ ID NO:60), **FIG. 62** (SEQ ID NO:62), **FIG. 64** (SEQ ID NO:64), **FIG. 66** (SEQ ID NO:66), **FIG. 68** (SEQ ID NO:68), **FIG. 70** (SEQ ID NO:70), **FIG. 72** (SEQ ID NO:72), **FIG. 74** (SEQ ID NO:74), **FIG. 76** (SEQ ID NO:76), **FIG. 78** (SEQ ID NO:78), **FIG. 80** (SEQ ID NO:80), **FIG. 82** (SEQ ID NO:82), **FIG. 84** (SEQ ID NO:84), **FIG. 86** (SEQ ID NO:86), **FIG. 88** (SEQ ID NO:88), **FIG. 90** (SEQ ID NO:90), **FIG. 92** (SEQ ID NO:92), **FIG. 94** (SEQ ID NO:94), **FIG. 96** (SEQ ID NO:96), **FIG. 98** (SEQ ID

NO:98), **FIG. 100** (SEQ ID NO:100), **FIG. 102** (SEQ ID NO:102), **FIG. 104** (SEQ ID NO:104), **FIG. 106** (SEQ ID NO:106), **FIG. 108** (SEQ ID NO:108), **FIG. 110** (SEQ ID NO:110), **FIG. 112** (SEQ ID NO:112), **FIG. 114** (SEQ ID NO:114), **FIG. 116** (SEQ ID NO:116), **FIG. 118** (SEQ ID NO:118), **FIG. 120** (SEQ ID NO:120), **FIG. 122** (SEQ ID NO:122), **FIG. 124** (SEQ ID NO:124), **FIG. 126** (SEQ ID NO:126), **FIG. 128** (SEQ ID NO:128), **FIG. 130** (SEQ ID NO:130), **FIG. 132** (SEQ ID NO:132), **FIG. 134** (SEQ ID NO:134), **FIG. 136** (SEQ ID NO:136), **FIG. 138** (SEQ ID NO:138), **FIG. 140** (SEQ ID NO:140), **FIG. 142** (SEQ ID NO:142), **FIG. 144** (SEQ ID NO:144), **FIG. 146** (SEQ ID NO:146), **FIG. 148** (SEQ ID NO:148), **FIG. 150** (SEQ ID NO:150), **FIG. 152** (SEQ ID NO:152), **FIG. 154** (SEQ ID NO:154), **FIG. 156** (SEQ ID NO:156), **FIG. 158** (SEQ ID NO:158), **FIG. 160** (SEQ ID NO:160), **FIG. 162** (SEQ ID NO:162), **FIG. 164** (SEQ ID NO:164), **FIG. 166** (SEQ ID NO:166), **FIG. 168** (SEQ ID NO:168), **FIG. 170** (SEQ ID NO:170), **FIG. 172** (SEQ ID NO:172), **FIG. 174** (SEQ ID NO:174), **FIG. 176** (SEQ ID NO:176), **FIG. 178** (SEQ ID NO:178), **FIG. 180** (SEQ ID NO:180), **FIG. 182** (SEQ ID NO:182), **FIG. 184** (SEQ ID NO:184), **FIG. 186** (SEQ ID NO:186), **FIG. 188** (SEQ ID NO:188), **FIG. 190** (SEQ ID NO:190), **FIG. 192** (SEQ ID NO:192), **FIG. 194** (SEQ ID NO:194), **FIG. 196** (SEQ ID NO:196), **FIG. 198** (SEQ ID NO:198), **FIG. 200** (SEQ ID NO:200), **FIG. 202** (SEQ ID NO:202), **FIG. 204** (SEQ ID NO:204), **FIG. 206** (SEQ ID NO:206), **FIG. 208** (SEQ ID NO:208), **FIG. 210** (SEQ ID NO:210), **FIG. 212** (SEQ ID NO:212), **FIG. 214** (SEQ ID NO:214), **FIG. 216** (SEQ ID NO:216), **FIG. 218** (SEQ ID NO:218), **FIG. 220** (SEQ ID NO:220), **FIG. 222** (SEQ ID NO:222), **FIG. 224** (SEQ ID NO:224), **FIG. 226** (SEQ ID NO:226), **FIG. 228** (SEQ ID NO:228), **FIG. 230** (SEQ ID NO:230), **FIG. 232** (SEQ ID NO:232), **FIG. 234** (SEQ ID NO:234), **FIG. 236** (SEQ ID NO:236), **FIG. 238** (SEQ ID NO:238), **FIG. 240** (SEQ ID NO:240), **FIG. 242** (SEQ ID NO:242), **FIG. 244** (SEQ ID NO:244), **FIG. 246** (SEQ ID NO:246), **FIG. 248** (SEQ ID NO:248), **FIG. 250** (SEQ ID NO:250), **FIG. 252** (SEQ ID NO:252), **FIG. 254** (SEQ ID NO:254), **FIG. 256** (SEQ ID NO:256), **FIG. 258** (SEQ ID NO:258), **FIG. 260** (SEQ ID NO:260), **FIG. 262** (SEQ ID NO:262), **FIG. 264** (SEQ ID NO:264), **FIG. 266** (SEQ ID NO:266), **FIG. 268** (SEQ ID NO:268), **FIG. 270** (SEQ ID NO:270), **FIG. 272** (SEQ ID NO:272), **FIG. 274** (SEQ ID NO:274), **FIG. 276** (SEQ ID NO:276), **FIG. 278** (SEQ ID NO:278), **FIG. 280** (SEQ ID NO:280), **FIG. 282** (SEQ ID NO:282), **FIG. 284** (SEQ ID NO:284), **FIG. 286** (SEQ ID NO:286), **FIG. 288** (SEQ ID NO:288), **FIG. 290** (SEQ ID NO:290), **FIG. 292** (SEQ ID NO:292), **FIG. 294** (SEQ ID NO:294), **FIG. 296** (SEQ ID NO:296), **FIG. 298** (SEQ ID NO:298), **FIG. 300** (SEQ ID NO:300), **FIG. 302** (SEQ ID NO:302), **FIG. 304** (SEQ ID NO:304), **FIG. 306** (SEQ ID NO:306), **FIG. 308** (SEQ ID NO:308), **FIG. 310** (SEQ ID NO:310), **FIG. 312** (SEQ ID NO:312), **FIG. 314** (SEQ ID NO:314), **FIG. 316** (SEQ ID NO:316), **FIG. 318** (SEQ ID NO:318), **FIG. 320** (SEQ ID NO:320), **FIG. 322** (SEQ ID NO:322), **FIG. 324** (SEQ ID NO:324), **FIG. 326** (SEQ ID NO:326), **FIG. 328** (SEQ ID NO:328),

**FIG. 330** (SEQ ID NO:330), **FIG. 332** (SEQ ID NO:332), **FIG. 334** (SEQ ID NO:334), **FIG. 336** (SEQ ID NO:336), **FIG. 338** (SEQ ID NO:338), **FIG. 340** (SEQ ID NO:340), **FIG. 342** (SEQ ID NO:342), **FIG. 344** (SEQ ID NO:344), **FIG. 346** (SEQ ID NO:346), **FIG. 348** (SEQ ID NO:348), **FIG. 350** (SEQ ID NO:350), **FIG. 352** (SEQ ID NO:352), **FIG. 354** (SEQ ID NO:354), **FIG. 356** (SEQ ID NO:356), **FIG. 358** (SEQ ID NO:358), **FIG. 360** (SEQ ID NO:360), **FIG. 362** (SEQ ID NO:362), **FIG. 364** (SEQ ID NO:364), **FIG. 366** (SEQ ID NO:366), **FIG. 368** (SEQ ID NO:368), **FIG. 370** (SEQ ID NO:370), **FIG. 372** (SEQ ID NO:372), **FIG. 374** (SEQ ID NO:374), **FIG. 376** (SEQ ID NO:376), **FIG. 378** (SEQ ID NO:378), **FIG. 380** (SEQ ID NO:380), **FIG. 382** (SEQ ID NO:382), **FIG. 384** (SEQ ID NO:384), **FIG. 386** (SEQ ID NO:386), **FIG. 388** (SEQ ID NO:388), **FIG. 390** (SEQ ID NO:390), **FIG. 392** (SEQ ID NO:392), **FIG. 394** (SEQ ID NO:394), **FIG. 396** (SEQ ID NO:396), **FIG. 398** (SEQ ID NO:398), **FIG. 400** (SEQ ID NO:400), **FIG. 402** (SEQ ID NO:402), **FIG. 404** (SEQ ID NO:404), **FIG. 406** (SEQ ID NO:406), **FIG. 408** (SEQ ID NO:408), **FIG. 410** (SEQ ID NO:410), **FIG. 412** (SEQ ID NO:412), **FIG. 414** (SEQ ID NO:414), **FIG. 416** (SEQ ID NO:416), **FIG. 418** (SEQ ID NO:418), **FIG. 420** (SEQ ID NO:420), **FIG. 422** (SEQ ID NO:422), **FIG. 424** (SEQ ID NO:424), **FIG. 426** (SEQ ID NO:426), **FIG. 428** (SEQ ID NO:428), **FIG. 430** (SEQ ID NO:430), **FIG. 432** (SEQ ID NO:432), **FIG. 434** (SEQ ID NO:434), **FIG. 436** (SEQ ID NO:436), **FIG. 438** (SEQ ID NO:438), **FIG. 440** (SEQ ID NO:440), **FIG. 442** (SEQ ID NO:442), **FIG. 444** (SEQ ID NO:444), **FIG. 446** (SEQ ID NO:446), **FIG. 448** (SEQ ID NO:448), **FIG. 450** (SEQ ID NO:450), **FIG. 452** (SEQ ID NO:452), **FIG. 454** (SEQ ID NO:454), **FIG. 456** (SEQ ID NO:456), **FIG. 458** (SEQ ID NO:458), **FIG. 460** (SEQ ID NO:460), **FIG. 462** (SEQ ID NO:462), **FIG. 464** (SEQ ID NO:464), **FIG. 466** (SEQ ID NO:466), **FIG. 468** (SEQ ID NO:468), **FIG. 470** (SEQ ID NO:470), **FIG. 472** (SEQ ID NO:472), **FIG. 474** (SEQ ID NO:474), **FIG. 476** (SEQ ID NO:476), **FIG. 478** (SEQ ID NO:478), **FIG. 480** (SEQ ID NO:480), **FIG. 482** (SEQ ID NO:482), **FIG. 484** (SEQ ID NO:484), **FIG. 486** (SEQ ID NO:486), **FIG. 488** (SEQ ID NO:488), **FIG. 490** (SEQ ID NO:490), **FIG. 492** (SEQ ID NO:492), **FIG. 494** (SEQ ID NO:494), **FIG. 496** (SEQ ID NO:496), **FIG. 498** (SEQ ID NO:498), **FIG. 500** (SEQ ID NO:500), **FIG. 502** (SEQ ID NO:502), **FIG. 504** (SEQ ID NO:504), **FIG. 506** (SEQ ID NO:506), **FIG. 508** (SEQ ID NO:508), **FIG. 510** (SEQ ID NO:510), **FIG. 512** (SEQ ID NO:512), **FIG. 514** (SEQ ID NO:514), **FIG. 516** (SEQ ID NO:516), **FIG. 518** (SEQ ID NO:518), **FIG. 520** (SEQ ID NO:520), **FIG. 522** (SEQ ID NO:522), **FIG. 524** (SEQ ID NO:524), **FIG. 526** (SEQ ID NO:526), **FIG. 528** (SEQ ID NO:528), **FIG. 530** (SEQ ID NO:530), **FIG. 532** (SEQ ID NO:532), **FIG. 534** (SEQ ID NO:534), **FIG. 536** (SEQ ID NO:536), **FIG. 538** (SEQ ID NO:538), **FIG. 540** (SEQ ID NO:540), **FIG. 542** (SEQ ID NO:542), **FIG. 544** (SEQ ID NO:544), **FIG. 546** (SEQ ID NO:546), **FIG. 548** (SEQ ID NO:548) or **FIG. 550** (SEQ ID NO:550), lacking its associated signal peptide.

**20.** An isolated polypeptide having at least 80% amino acid sequence identity to:

- (a) an amino acid sequence of the polypeptide shown in **FIG. 2** (SEQ ID NO:2), **FIG. 4** (SEQ ID NO:4), **FIG. 6** (SEQ ID NO:6), **FIG. 8** (SEQ ID NO:8), **FIG. 10** (SEQ ID NO:10), **FIG. 12** (SEQ ID NO:12), **FIG. 14** (SEQ ID NO:14), **FIG. 16** (SEQ ID NO:16), **FIG. 18** (SEQ ID NO:18), **FIG. 20** (SEQ ID NO:20), **FIG. 22** (SEQ ID NO:22), **FIG. 24** (SEQ ID NO:24), **FIG. 26** (SEQ ID NO:26), **FIG. 28** (SEQ ID NO:28), **FIG. 30** (SEQ ID NO:30), **FIG. 32** (SEQ ID NO:32), **FIG. 34** (SEQ ID NO:34), **FIG. 36** (SEQ ID NO:36), **FIG. 38** (SEQ ID NO:38), **FIG. 40** (SEQ ID NO:40), **FIG. 42** (SEQ ID NO:42), **FIG. 44** (SEQ ID NO:44), **FIG. 46** (SEQ ID NO:46), **FIG. 48** (SEQ ID NO:48), **FIG. 50** (SEQ ID NO:50), **FIG. 52** (SEQ ID NO:52), **FIG. 54** (SEQ ID NO:54), **FIG. 56** (SEQ ID NO:56), **FIG. 58** (SEQ ID NO:58), **FIG. 60** (SEQ ID NO:60), **FIG. 62** (SEQ ID NO:62), **FIG. 64** (SEQ ID NO:64), **FIG. 66** (SEQ ID NO:66), **FIG. 68** (SEQ ID NO:68), **FIG. 70** (SEQ ID NO:70), **FIG. 72** (SEQ ID NO:72), **FIG. 74** (SEQ ID NO:74), **FIG. 76** (SEQ ID NO:76), **FIG. 78** (SEQ ID NO:78), **FIG. 80** (SEQ ID NO:80), **FIG. 82** (SEQ ID NO:82), **FIG. 84** (SEQ ID NO:84), **FIG. 86** (SEQ ID NO:86), **FIG. 88** (SEQ ID NO:88), **FIG. 90** (SEQ ID NO:90), **FIG. 92** (SEQ ID NO:92), **FIG. 94** (SEQ ID NO:94), **FIG. 96** (SEQ ID NO:96), **FIG. 98** (SEQ ID NO:98), **FIG. 100** (SEQ ID NO:100), **FIG. 102** (SEQ ID NO:102), **FIG. 104** (SEQ ID NO:104), **FIG. 106** (SEQ ID NO:106), **FIG. 108** (SEQ ID NO:108), **FIG. 110** (SEQ ID NO:110), **FIG. 112** (SEQ ID NO:112), **FIG. 114** (SEQ ID NO:114), **FIG. 116** (SEQ ID NO:116), **FIG. 118** (SEQ ID NO:118), **FIG. 120** (SEQ ID NO:120), **FIG. 122** (SEQ ID NO:122), **FIG. 124** (SEQ ID NO:124), **FIG. 126** (SEQ ID NO:126), **FIG. 128** (SEQ ID NO:128), **FIG. 130** (SEQ ID NO:130), **FIG. 132** (SEQ ID NO:132), **FIG. 134** (SEQ ID NO:134), **FIG. 136** (SEQ ID NO:136), **FIG. 138** (SEQ ID NO:138), **FIG. 140** (SEQ ID NO:140), **FIG. 142** (SEQ ID NO:142), **FIG. 144** (SEQ ID NO:144), **FIG. 146** (SEQ ID NO:146), **FIG. 148** (SEQ ID NO:148), **FIG. 150** (SEQ ID NO:150), **FIG. 152** (SEQ ID NO:152), **FIG. 154** (SEQ ID NO:154), **FIG. 156** (SEQ ID NO:156), **FIG. 158** (SEQ ID NO:158), **FIG. 160** (SEQ ID NO:160), **FIG. 162** (SEQ ID NO:162), **FIG. 164** (SEQ ID NO:164), **FIG. 166** (SEQ ID NO:166), **FIG. 168** (SEQ ID NO:168), **FIG. 170** (SEQ ID NO:170), **FIG. 172** (SEQ ID NO:172), **FIG. 174** (SEQ ID NO:174), **FIG. 176** (SEQ ID NO:176), **FIG. 178** (SEQ ID NO:178), **FIG. 180** (SEQ ID NO:180), **FIG. 182** (SEQ ID NO:182), **FIG. 184** (SEQ ID NO:184), **FIG. 186** (SEQ ID NO:186), **FIG. 188** (SEQ ID NO:188), **FIG. 190** (SEQ ID NO:190), **FIG. 192** (SEQ ID NO:192), **FIG. 194** (SEQ ID NO:194), **FIG. 196** (SEQ ID NO:196), **FIG. 198** (SEQ ID NO:198), **FIG. 200** (SEQ ID NO:200), **FIG. 202** (SEQ ID NO:202), **FIG. 204** (SEQ ID NO:204), **FIG. 206** (SEQ ID NO:206), **FIG. 208** (SEQ ID NO:208), **FIG. 210** (SEQ ID NO:210), **FIG. 212** (SEQ ID NO:212), **FIG. 214** (SEQ ID NO:214), **FIG. 216** (SEQ ID NO:216), **FIG. 218** (SEQ ID NO:218), **FIG. 220** (SEQ ID NO:220), **FIG. 222** (SEQ ID NO:222), **FIG. 224** (SEQ ID NO:224), **FIG. 226** (SEQ ID NO:226), **FIG. 228** (SEQ ID NO:228), **FIG. 230** (SEQ ID NO:230),

FIG. 232 (SEQ ID NO:232), FIG. 234 (SEQ ID NO:234), FIG. 236 (SEQ ID NO:236), FIG. 238 (SEQ ID NO:238), FIG. 240 (SEQ ID NO:240), FIG. 242 (SEQ ID NO:242), FIG. 244 (SEQ ID NO:244), FIG. 246 (SEQ ID NO:246), FIG. 248 (SEQ ID NO:248), FIG. 250 (SEQ ID NO:250), FIG. 252 (SEQ ID NO:252), FIG. 254 (SEQ ID NO:254), FIG. 256 (SEQ ID NO:256), FIG. 258 (SEQ ID NO:258), FIG. 260 (SEQ ID NO:260), FIG. 262 (SEQ ID NO:262), FIG. 264 (SEQ ID NO:264), FIG. 266 (SEQ ID NO:266), FIG. 268 (SEQ ID NO:268), FIG. 270 (SEQ ID NO:270), FIG. 272 (SEQ ID NO:272), FIG. 274 (SEQ ID NO:274), FIG. 276 (SEQ ID NO:276), FIG. 278 (SEQ ID NO:278), FIG. 280 (SEQ ID NO:280), FIG. 282 (SEQ ID NO:282), FIG. 284 (SEQ ID NO:284), FIG. 286 (SEQ ID NO:286), FIG. 288 (SEQ ID NO:288), FIG. 290 (SEQ ID NO:290), FIG. 292 (SEQ ID NO:292), FIG. 294 (SEQ ID NO:294), FIG. 296 (SEQ ID NO:296), FIG. 298 (SEQ ID NO:298), FIG. 300 (SEQ ID NO:300), FIG. 302 (SEQ ID NO:302), FIG. 304 (SEQ ID NO:304), FIG. 306 (SEQ ID NO:306), FIG. 308 (SEQ ID NO:308), FIG. 310 (SEQ ID NO:310), FIG. 312 (SEQ ID NO:312), FIG. 314 (SEQ ID NO:314), FIG. 316 (SEQ ID NO:316), FIG. 318 (SEQ ID NO:318), FIG. 320 (SEQ ID NO:320), FIG. 322 (SEQ ID NO:322), FIG. 324 (SEQ ID NO:324), FIG. 326 (SEQ ID NO:326), FIG. 328 (SEQ ID NO:328), FIG. 330 (SEQ ID NO:330), FIG. 332 (SEQ ID NO:332), FIG. 334 (SEQ ID NO:334), FIG. 336 (SEQ ID NO:336), FIG. 338 (SEQ ID NO:338), FIG. 340 (SEQ ID NO:340), FIG. 342 (SEQ ID NO:342), FIG. 344 (SEQ ID NO:344), FIG. 346 (SEQ ID NO:346), FIG. 348 (SEQ ID NO:348), FIG. 350 (SEQ ID NO:350), FIG. 352 (SEQ ID NO:352), FIG. 354 (SEQ ID NO:354), FIG. 356 (SEQ ID NO:356), FIG. 358 (SEQ ID NO:358), FIG. 360 (SEQ ID NO:360), FIG. 362 (SEQ ID NO:362), FIG. 364 (SEQ ID NO:364), FIG. 366 (SEQ ID NO:366), FIG. 368 (SEQ ID NO:368), FIG. 370 (SEQ ID NO:370), FIG. 372 (SEQ ID NO:372), FIG. 374 (SEQ ID NO:374), FIG. 376 (SEQ ID NO:376), FIG. 378 (SEQ ID NO:378), FIG. 380 (SEQ ID NO:380), FIG. 382 (SEQ ID NO:382), FIG. 384 (SEQ ID NO:384), FIG. 386 (SEQ ID NO:386), FIG. 388 (SEQ ID NO:388), FIG. 390 (SEQ ID NO:390), FIG. 392 (SEQ ID NO:392), FIG. 394 (SEQ ID NO:394), FIG. 396 (SEQ ID NO:396), FIG. 398 (SEQ ID NO:398), FIG. 400 (SEQ ID NO:400), FIG. 402 (SEQ ID NO:402), FIG. 404 (SEQ ID NO:404), FIG. 406 (SEQ ID NO:406), FIG. 408 (SEQ ID NO:408), FIG. 410 (SEQ ID NO:410), FIG. 412 (SEQ ID NO:412), FIG. 414 (SEQ ID NO:414), FIG. 416 (SEQ ID NO:416), FIG. 418 (SEQ ID NO:418), FIG. 420 (SEQ ID NO:420), FIG. 422 (SEQ ID NO:422), FIG. 424 (SEQ ID NO:424), FIG. 426 (SEQ ID NO:426), FIG. 428 (SEQ ID NO:428), FIG. 430 (SEQ ID NO:430), FIG. 432 (SEQ ID NO:432), FIG. 434 (SEQ ID NO:434), FIG. 436 (SEQ ID NO:436), FIG. 438 (SEQ ID NO:438), FIG. 440 (SEQ ID NO:440), FIG. 442 (SEQ ID NO:442), FIG. 444 (SEQ ID NO:444), FIG. 446 (SEQ ID NO:446), FIG. 448 (SEQ ID NO:448), FIG. 450 (SEQ ID NO:450), FIG. 452 (SEQ ID NO:452), FIG. 454 (SEQ ID NO:454), FIG. 456 (SEQ ID NO:456), FIG. 458 (SEQ ID NO:458), FIG. 460 (SEQ ID NO:460), FIG.

462 (SEQ ID NO:462), FIG. 464 (SEQ ID NO:464), FIG. 466 (SEQ ID NO:466), FIG. 468 (SEQ ID NO:468), FIG. 470 (SEQ ID NO:470), FIG. 472 (SEQ ID NO:472), FIG. 474 (SEQ ID NO:474), FIG. 476 (SEQ ID NO:476), FIG. 478 (SEQ ID NO:478), FIG. 480 (SEQ ID NO:480), FIG. 482 (SEQ ID NO:482), FIG. 484 (SEQ ID NO:484), FIG. 486 (SEQ ID NO:486), FIG. 488 (SEQ ID NO:488), FIG. 490 (SEQ ID NO:490), FIG. 492 (SEQ ID NO:492), FIG. 494 (SEQ ID NO:494), FIG. 496 (SEQ ID NO:496), FIG. 498 (SEQ ID NO:498), FIG. 500 (SEQ ID NO:500), FIG. 502 (SEQ ID NO:502), FIG. 504 (SEQ ID NO:504), FIG. 506 (SEQ ID NO:506), FIG. 508 (SEQ ID NO:508), FIG. 510 (SEQ ID NO:510), FIG. 512 (SEQ ID NO:512), FIG. 514 (SEQ ID NO:514), FIG. 516 (SEQ ID NO:516), FIG. 518 (SEQ ID NO:518), FIG. 520 (SEQ ID NO:520), FIG. 522 (SEQ ID NO:522), FIG. 524 (SEQ ID NO:524), FIG. 526 (SEQ ID NO:526), FIG. 528 (SEQ ID NO:528), FIG. 530 (SEQ ID NO:530), FIG. 532 (SEQ ID NO:532), FIG. 534 (SEQ ID NO:534), FIG. 536 (SEQ ID NO:536), FIG. 538 (SEQ ID NO:538), FIG. 540 (SEQ ID NO:540), FIG. 542 (SEQ ID NO:542), FIG. 544 (SEQ ID NO:544), FIG. 546 (SEQ ID NO:546), FIG. 548 (SEQ ID NO:548) or FIG. 550 (SEQ ID NO:550), lacking its associated signal peptide;

- (b) an amino acid sequence of an extracellular domain of the polypeptide shown in FIG. 2 (SEQ ID NO:2), FIG. 4 (SEQ ID NO:4), FIG. 6 (SEQ ID NO:6), FIG. 8 (SEQ ID NO:8), FIG. 10 (SEQ ID NO:10), FIG. 12 (SEQ ID NO:12), FIG. 14 (SEQ ID NO:14), FIG. 16 (SEQ ID NO:16), FIG. 18 (SEQ ID NO:18), FIG. 20 (SEQ ID NO:20), FIG. 22 (SEQ ID NO:22), FIG. 24 (SEQ ID NO:24), FIG. 26 (SEQ ID NO:26), FIG. 28 (SEQ ID NO:28), FIG. 30 (SEQ ID NO:30), FIG. 32 (SEQ ID NO:32), FIG. 34 (SEQ ID NO:34), FIG. 36 (SEQ ID NO:36), FIG. 38 (SEQ ID NO:38), FIG. 40 (SEQ ID NO:40), FIG. 42 (SEQ ID NO:42), FIG. 44 (SEQ ID NO:44), FIG. 46 (SEQ ID NO:46), FIG. 48 (SEQ ID NO:48), FIG. 50 (SEQ ID NO:50), FIG. 52 (SEQ ID NO:52), FIG. 54 (SEQ ID NO:54), FIG. 56 (SEQ ID NO:56), FIG. 58 (SEQ ID NO:58), FIG. 60 (SEQ ID NO:60), FIG. 62 (SEQ ID NO:62), FIG. 64 (SEQ ID NO:64), FIG. 66 (SEQ ID NO:66), FIG. 68 (SEQ ID NO:68), FIG. 70 (SEQ ID NO:70), FIG. 72 (SEQ ID NO:72), FIG. 74 (SEQ ID NO:74), FIG. 76 (SEQ ID NO:76), FIG. 78 (SEQ ID NO:78), FIG. 80 (SEQ ID NO:80), FIG. 82 (SEQ ID NO:82), FIG. 84 (SEQ ID NO:84), FIG. 86 (SEQ ID NO:86), FIG. 88 (SEQ ID NO:88), FIG. 90 (SEQ ID NO:90), FIG. 92 (SEQ ID NO:92), FIG. 94 (SEQ ID NO:94), FIG. 96 (SEQ ID NO:96), FIG. 98 (SEQ ID NO:98), FIG. 100 (SEQ ID NO:100), FIG. 102 (SEQ ID NO:102), FIG. 104 (SEQ ID NO:104), FIG. 106 (SEQ ID NO:106), FIG. 108 (SEQ ID NO:108), FIG. 110 (SEQ ID NO:110), FIG. 112 (SEQ ID NO:112), FIG. 114 (SEQ ID NO:114), FIG. 116 (SEQ ID NO:116), FIG. 118 (SEQ ID NO:118), FIG. 120 (SEQ ID NO:120), FIG. 122 (SEQ ID NO:122), FIG. 124 (SEQ ID NO:124), FIG. 126 (SEQ ID NO:126), FIG. 128 (SEQ ID NO:128), FIG. 130 (SEQ ID NO:130), FIG. 132 (SEQ ID NO:132), FIG. 134 (SEQ ID NO:134), FIG. 136 (SEQ ID NO:136), FIG. 138 (SEQ ID NO:138), FIG. 140 (SEQ ID NO: 140), FIG. 142 (SEQ ID NO:142),

**FIG. 144** (SEQ ID NO:144), **FIG. 146** (SEQ ID NO:146), **FIG. 148** (SEQ ID NO:148), **FIG. 150** (SEQ ID NO:150), **FIG. 152** (SEQ ID NO:152), **FIG. 154** (SEQ ID NO:154), **FIG. 156** (SEQ ID NO:156), **FIG. 158** (SEQ ID NO:158), **FIG. 160** (SEQ ID NO:160), **FIG. 162** (SEQ ID NO:162), **FIG. 164** (SEQ ID NO:164), **FIG. 166** (SEQ ID NO:166), **FIG. 168** (SEQ ID NO: 168), **FIG. 170** (SEQ ID NO:170), **FIG. 172** (SEQ ID NO:172), **FIG. 174** (SEQ ID NO:174), **FIG. 176** (SEQ ID NO:176), **FIG. 178** (SEQ ID NO:178), **FIG. 180** (SEQ ID NO:180), **FIG. 182** (SEQ ID NO:182), **FIG. 184** (SEQ ID NO:184), **FIG. 186** (SEQ ID NO:186), **FIG. 188** (SEQ ID NO:188), **FIG. 190** (SEQ ID NO:190), **FIG. 192** (SEQ ID NO:192), **FIG. 194** (SEQ ID NO:194), **FIG. 196** (SEQ ID NO: 196), **FIG. 198** (SEQ ID NO:198), **FIG. 200** (SEQ ID NO:200), **FIG. 202** (SEQ ID NO:202), **FIG. 204** (SEQ ID NO:204), **FIG. 206** (SEQ ID NO:206), **FIG. 208** (SEQ ID NO:208), **FIG. 210** (SEQ ID NO:210), **FIG. 212** (SEQ ID NO:212), **FIG. 214** (SEQ ID NO:214), **FIG. 216** (SEQ ID NO:216), **FIG. 218** (SEQ ID NO:218), **FIG. 220** (SEQ ID NO:220), **FIG. 222** (SEQ ID NO:222), **FIG. 224** (SEQ ID NO:224), **FIG. 226** (SEQ ID NO:226), **FIG. 228** (SEQ ID NO:228), **FIG. 230** (SEQ ID NO:230), **FIG. 232** (SEQ ID NO:232), **FIG. 234** (SEQ ID NO:234), **FIG. 236** (SEQ ID NO:236), **FIG. 238** (SEQ ID NO:238), **FIG. 240** (SEQ ID NO:240), **FIG. 242** (SEQ ID NO:242), **FIG. 244** (SEQ ID NO:244), **FIG. 246** (SEQ ID NO:246), **FIG. 248** (SEQ ID NO:248), **FIG. 250** (SEQ ID NO:250), **FIG. 252** (SEQ ID NO:252), **FIG. 254** (SEQ ID NO:254), **FIG. 256** (SEQ ID NO:256), **FIG. 258** (SEQ ID NO:258), **FIG. 260** (SEQ ID NO:260), **FIG. 262** (SEQ ID NO:262), **FIG. 264** (SEQ ID NO:264), **FIG. 266** (SEQ ID NO:266), **FIG. 268** (SEQ ID NO:268), **FIG. 270** (SEQ ID NO:270), **FIG. 272** (SEQ ID NO:272), **FIG. 274** (SEQ ID NO:274), **FIG. 276** (SEQ ID NO:276), **FIG. 278** (SEQ ID NO:278), **FIG. 280** (SEQ ID NO:280), **FIG. 282** (SEQ ID NO:282), **FIG. 284** (SEQ ID NO:284), **FIG. 286** (SEQ ID NO:286), **FIG. 288** (SEQ ID NO:288), **FIG. 290** (SEQ ID NO:290), **FIG. 292** (SEQ ID NO:292), **FIG. 294** (SEQ ID NO:294), **FIG. 296** (SEQ ID NO:296), **FIG. 298** (SEQ ID NO:298), **FIG. 300** (SEQ ID NO:300), **FIG. 302** (SEQ ID NO:302), **FIG. 304** (SEQ ID NO:304), **FIG. 306** (SEQ ID NO:306), **FIG. 308** (SEQ ID NO:308), **FIG. 310** (SEQ ID NO:310), **FIG. 312** (SEQ ID NO:312), **FIG. 314** (SEQ ID NO:314), **FIG. 316** (SEQ ID NO:316), **FIG. 318** (SEQ ID NO:318), **FIG. 320** (SEQ ID NO:320), **FIG. 322** (SEQ ID NO:322), **FIG. 324** (SEQ ID NO:324), **FIG. 326** (SEQ ID NO:326), **FIG. 328** (SEQ ID NO:328), **FIG. 330** (SEQ ID NO:330), **FIG. 332** (SEQ ID NO:332), **FIG. 334** (SEQ ID NO:334), **FIG. 336** (SEQ ID NO:336), **FIG. 338** (SEQ ID NO:338), **FIG. 340** (SEQ ID NO:340), **FIG. 342** (SEQ ID NO:342), **FIG. 344** (SEQ ID NO:344), **FIG. 346** (SEQ ID NO:346), **FIG. 348** (SEQ ID NO:348), **FIG. 350** (SEQ ID NO:350), **FIG. 352** (SEQ ID NO:352), **FIG. 354** (SEQ ID NO:354), **FIG. 356** (SEQ ID NO:356), **FIG. 358** (SEQ ID NO:358), **FIG. 360** (SEQ ID NO:360), **FIG. 362** (SEQ ID NO:362), **FIG. 364** (SEQ ID NO:364), **FIG. 366** (SEQ ID NO:366), **FIG. 368** (SEQ ID NO:368), **FIG. 370** (SEQ ID NO:370), **FIG. 372** (SEQ ID NO:372), **FIG.**

**374** (SEQ ID NO:374), **FIG. 376** (SEQ ID NO:376), **FIG. 378** (SEQ ID NO:378), **FIG. 380** (SEQ ID NO:380), **FIG. 382** (SEQ ID NO:382), **FIG. 384** (SEQ ID NO:384), **FIG. 386** (SEQ ID NO:386), **FIG. 388** (SEQ ID NO:388), **FIG. 390** (SEQ ID NO:390), **FIG. 392** (SEQ ID NO:392), **FIG. 394** (SEQ ID NO:394), **FIG. 396** (SEQ ID NO:396), **FIG. 398** (SEQ ID NO:398), **FIG. 400** (SEQ ID NO:400), **FIG. 402** (SEQ ID NO:402), **FIG. 404** (SEQ ID NO:404), **FIG. 406** (SEQ ID NO:406), **FIG. 408** (SEQ ID NO:408), **FIG. 410** (SEQ ID NO:410), **FIG. 412** (SEQ ID NO:412), **FIG. 414** (SEQ ID NO:414), **FIG. 416** (SEQ ID NO:416), **FIG. 418** (SEQ ID NO:418), **FIG. 420** (SEQ ID NO:420), **FIG. 422** (SEQ ID NO:422), **FIG. 424** (SEQ ID NO:424), **FIG. 426** (SEQ ID NO:426), **FIG. 428** (SEQ ID NO:428), **FIG. 430** (SEQ ID NO:430), **FIG. 432** (SEQ ID NO:432), **FIG. 434** (SEQ ID NO:434), **FIG. 436** (SEQ ID NO:436), **FIG. 438** (SEQ ID NO:438), **FIG. 440** (SEQ ID NO:440), **FIG. 442** (SEQ ID NO:442), **FIG. 444** (SEQ ID NO:444), **FIG. 446** (SEQ ID NO:446), **FIG. 448** (SEQ ID NO:448), **FIG. 450** (SEQ ID NO:450), **FIG. 452** (SEQ ID NO:452), **FIG. 454** (SEQ ID NO:454), **FIG. 456** (SEQ ID NO:456), **FIG. 458** (SEQ ID NO:458), **FIG. 460** (SEQ ID NO:460), **FIG. 462** (SEQ ID NO:462), **FIG. 464** (SEQ ID NO:464), **FIG. 466** (SEQ ID NO:466), **FIG. 468** (SEQ ID NO:468), **FIG. 470** (SEQ ID NO:470), **FIG. 472** (SEQ ID NO:472), **FIG. 474** (SEQ ID NO:474), **FIG. 476** (SEQ ID NO:476), **FIG. 478** (SEQ ID NO:478), **FIG. 480** (SEQ ID NO:480), **FIG. 482** (SEQ ID NO:482), **FIG. 484** (SEQ ID NO:484), **FIG. 486** (SEQ ID NO:486), **FIG. 488** (SEQ ID NO:488), **FIG. 490** (SEQ ID NO:490), **FIG. 492** (SEQ ID NO:492), **FIG. 494** (SEQ ID NO:494), **FIG. 496** (SEQ ID NO:496), **FIG. 498** (SEQ ID NO:498), **FIG. 500** (SEQ ID NO:500), **FIG. 502** (SEQ ID NO:502), **FIG. 504** (SEQ ID NO:504), **FIG. 506** (SEQ ID NO:506), **FIG. 508** (SEQ ID NO:508), **FIG. 510** (SEQ ID NO:510), **FIG. 512** (SEQ ID NO:512), **FIG. 514** (SEQ ID NO:514), **FIG. 516** (SEQ ID NO:516), **FIG. 518** (SEQ ID NO:518), **FIG. 520** (SEQ ID NO:520), **FIG. 522** (SEQ ID NO:522), **FIG. 524** (SEQ ID NO:524), **FIG. 526** (SEQ ID NO:526), **FIG. 528** (SEQ ID NO:528), **FIG. 530** (SEQ ID NO:530), **FIG. 532** (SEQ ID NO:532), **FIG. 534** (SEQ ID NO:534), **FIG. 536** (SEQ ID NO:536), **FIG. 538** (SEQ ID NO:538), **FIG. 540** (SEQ ID NO:540), **FIG. 542** (SEQ ID NO:542), **FIG. 544** (SEQ ID NO:544), **FIG. 546** (SEQ ID NO:546), **FIG. 548** (SEQ ID NO:548) or **FIG. 550** (SEQ ID NO:550), with its associated signal peptide; or

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in **FIG. 2** (SEQ ID NO:2), **FIG. 4** (SEQ ID NO:4), **FIG. 6** (SEQ ID NO:6), **FIG. 8** (SEQ ID NO:8), **FIG. 10** (SEQ ID NO:10), **FIG. 12** (SEQ ID NO:12), **FIG. 14** (SEQ ID NO:14), **FIG. 16** (SEQ ID NO:16), **FIG. 18** (SEQ ID NO:18), **FIG. 20** (SEQ ID NO:20), **FIG. 22** (SEQ ID NO:22), **FIG. 24** (SEQ ID NO:24), **FIG. 26** (SEQ ID NO:26), **FIG. 28** (SEQ ID NO:28), **FIG. 30** (SEQ ID NO:30), **FIG. 32** (SEQ ID NO:32), **FIG. 34** (SEQ ID NO:34), **FIG. 36** (SEQ ID NO:36), **FIG. 38** (SEQ ID NO:38), **FIG. 40** (SEQ ID NO:40), **FIG. 42** (SEQ ID NO:42), **FIG. 44** (SEQ ID NO:44), **FIG. 46** (SEQ ID NO:46), **FIG. 48** (SEQ ID NO:48), **FIG. 50** (SEQ ID NO:50), **FIG. 52**







**518** (SEQ ID NO:518), **FIG. 520** (SEQ ID NO:520), **FIG. 522** (SEQ ID NO:522), **FIG. 524** (SEQ ID NO:524), **FIG. 526** (SEQ ID NO:526), **FIG. 528** (SEQ ID NO:528), **FIG. 530** (SEQ ID NO:530), **FIG. 532** (SEQ ID NO:532), **FIG. 534** (SEQ ID NO:534), **FIG. 536** (SEQ ID NO:536), **FIG. 538** (SEQ ID NO:538), **FIG. 540** (SEQ ID NO:540), **FIG. 542** (SEQ ID NO:542), **FIG. 544** (SEQ ID NO:544), **FIG. 546** (SEQ ID NO:546), **FIG. 548** (SEQ ID NO:548) or **FIG. 550** (SEQ ID NO:550), lacking its associated signal peptide.

**21.** A method of detecting a PRO1801 polypeptide in a sample suspected of containing a PRO1801 polypeptide, said method comprising contacting said sample with a PRO1114 or PRO4978 polypeptide and determining the formation of a PRO 1801/PRO1114 or PRO1801/PRO4978 polypeptide conjugate in said sample, wherein the formation of said conjugate is indicative of the presence of a PRO1801 polypeptide in said sample.

**22.** The method according to claim 21, wherein said sample comprises cells suspected of expressing said PRO1801 polypeptide.

**23.** The method according to claim 21, wherein said PRO1114 or PRO4978 polypeptide is labeled with a detectable label.

**24.** The method according to claim 21, wherein said PRO1114 or PRO4978 polypeptide is attached to a solid support.

**25.** A method of detecting a PRO1114 or PRO4978 polypeptide in a sample suspected of containing a PRO1114 or PRO4978 polypeptide, said method comprising contacting said sample with a PRO1801 polypeptide and determining the formation of a PRO1801/PRO1114 or PRO1801/PRO4978 polypeptide conjugate in said sample, wherein the formation of said conjugate is indicative of the presence of a PRO1114 or PRO4978 polypeptide in said sample.

**26.** The method according to claim 25, wherein said sample comprises cells suspected of expressing said PRO1114 or PRO4978 polypeptide.

**27.** The method according to claim 25, wherein said PRO1801 polypeptide is labeled with a detectable label.

**28.** The method according to claim 25, wherein said PRO1801 polypeptide is attached to a solid support.

**29.** A method of linking a bioactive molecule to a cell expressing a PRO1801 polypeptide, said method comprising contacting said cell with a PRO1114 or PRO4978 polypeptide that is bound to said bioactive molecule and allowing said PRO1801 and said PRO1114 or PRO4978 polypeptides to bind to one another, thereby linking said bioactive molecules to said cell.

**30.** The method according to claim 29, wherein said bioactive molecule is a toxin, a radiolabel or an antibody.

**31.** The method according to claim 29, wherein said bioactive molecule causes the death of said cell.

**32.** A method of linking a bioactive molecule to a cell expressing a PRO1114 or PRO4978 polypeptide, said method comprising contacting said cell with a PRO1801 polypeptide that is bound to said bioactive molecule and allowing said PRO1801 and said PRO1114 or PRO4978 polypeptides to bind to one another, thereby linking said bioactive molecules to said cell.

**33.** The method according to claim 32, wherein said bioactive molecule is a toxin, a radiolabel or an antibody.

**34.** The method according to claim 32, wherein said bioactive molecule causes the death of said cell.

**35.** A method of modulating at least one biological activity of a cell expressing a PRO1801 polypeptide, said method comprising contacting said cell with a PRO1114 or PRO4978 polypeptide or an anti-PRO1801 polypeptide antibody, whereby said PRO1114 or PRO4978 polypeptide or anti-PRO1801 polypeptide antibody binds to said PRO1801 polypeptide, thereby modulating at least one biological activity of said cell.

**36.** The method according to claim 35, wherein said cell is killed.

**37.** A method of modulating at least one biological activity of a cell expressing a PRO1114 or PRO4978 polypeptide, said method comprising contacting said cell with a PRO1801 polypeptide or an anti-PRO1114 or anti-PRO4978 polypeptide antibody, whereby said PRO1801 polypeptide or anti-PRO1114 or anti-PRO4978 polypeptide antibody binds to said PRO1114 or PRO4978 polypeptide, thereby modulating at least one biological activity of said cell.

**38.** The method according to claim 37, wherein said cell is killed.

**39.** A method of detecting a PRO1114 polypeptide in a sample suspected of containing a PRO1114 polypeptide, said method comprising contacting said sample with a PRO100 polypeptide and determining the formation of a PRO100/PRO1114 polypeptide conjugate in said sample, wherein the formation of said conjugate is indicative of the presence of a PRO1114 polypeptide in said sample.

**40.** The method according to claim 39, wherein said sample comprises cells suspected of expressing said PRO1114 polypeptide.

**41.** The method according to claim 39, wherein said PRO100 polypeptide is labeled with a detectable label.

**42.** The method according to claim 39, wherein said PRO100 polypeptide is attached to a solid support.

**43.** A method of detecting a PRO100 polypeptide in a sample suspected of containing a PRO100 polypeptide, said method comprising contacting said sample with a PRO1114 polypeptide and determining the formation of a PRO100/PRO1114 polypeptide conjugate in said sample, wherein the formation of said conjugate is indicative of the presence of a PRO100 polypeptide in said sample.

**44.** The method according to claim 43, wherein said sample comprises cells suspected of expressing said PRO100 polypeptide.

**45.** The method according to claim 43, wherein said PRO1114 polypeptide is labeled with a detectable label.

**46.** The method according to claim 43, wherein said PRO1114 polypeptide is attached to a solid support.

**47.** A method of linking a bioactive molecule to a cell expressing a PRO100 polypeptide, said method comprising contacting said cell with a PRO1114 polypeptide that is bound to said bioactive molecule and allowing said PRO100 and said PRO1114 polypeptides to bind to one another, thereby linking said bioactive molecules to said cell.

**48.** The method according to claim 47, wherein said bioactive molecule is a toxin, a radiolabel or an antibody.

**49.** The method according to claim 47, wherein said bioactive molecule causes the death of said cell.

**50.** A method of linking a bioactive molecule to a cell expressing a PRO1114 polypeptide, said method comprising contacting said cell with a PRO100 polypeptide that is

bound to said bioactive molecule and allowing said PRO100 and said PRO1114 polypeptides to bind to one another, thereby linking said bioactive molecules to said cell.

**51.** The method according to claim 50, wherein said bioactive molecule is a toxin, a radiolabel or an antibody.

**52.** The method according to claim 50, wherein said bioactive molecule causes the death of said cell.

**53.** A method of modulating at least one biological activity of a cell expressing a PRO100 polypeptide, said method comprising contacting said cell with a PRO1114 polypeptide or an anti-PRO100 polypeptide antibody, whereby said PRO1114 polypeptide or anti-PRO100 polypeptide antibody binds to said PRO100 polypeptide, thereby modulating at least one biological activity of said cell.

**54.** The method according to claim 53, wherein said cell is killed.

**55.** A method of modulating at least one biological activity of a cell expressing a PRO1114 polypeptide, said method comprising contacting said cell with a PRO100 polypeptide or an anti-PRO1114 polypeptide antibody, whereby said PRO100 polypeptide or anti-PRO1114 polypeptide antibody binds to said PRO1114 polypeptide, thereby modulating at least one biological activity of said cell.

**56.** The method according to claim 55, wherein said cell is killed.

**57.** A method for stimulating the release of TNF- $\alpha$  from human blood, said method comprising contacting said blood with a PRO195, PRO202, PRO215, PRO221, PRO217, PRO222, PRO198, PRO245, PRO172, PRO265, PRO266, PRO344, PRO337, PRO322, PRO1286, PRO1279, PRO1338 or PRO1343 polypeptide, wherein the release of TNF- $\alpha$  from said blood is stimulated.

**58.** A method for modulating the uptake of glucose or FFA by skeletal muscle cells, said method comprising contacting said cells with a PRO182, PRO366, PRO198, PRO172 or PRO719 polypeptide, wherein the uptake of glucose or FFA by said cells is modulated.

**59.** A method for stimulating the proliferation or differentiation of chondrocyte cells, said method comprising contacting said cells with a PRO182, PRO366, PRO198, PRO1868, PRO202, PRO224, PRO172, PRO301 or PRO1312 polypeptide, wherein the proliferation or differentiation of said cells is stimulated.

**60.** A method for modulating the uptake of glucose or FFA by adipocyte cells, said method comprising contacting said cells with a PRO202, PRO211, PRO344 or PRO1338 polypeptide, wherein the uptake of glucose or FFA by said cells is modulated.

**61.** A method for stimulating the proliferation of or gene expression in pericyte cells, said method comprising contacting said cells with a PRO366 polypeptide, wherein the proliferation of or gene expression in said cells is stimulated.

**62.** A method for stimulating the release of proteoglycans from cartilage, said method comprising contacting said cartilage with a PRO216 polypeptide, wherein the release of proteoglycans from said cartilage is stimulated.

**63.** A method for stimulating the proliferation of inner ear utricular supporting cells, said method comprising contacting said cells with a PRO172 polypeptide, wherein the proliferation of said cells is stimulated.

**64.** A method for stimulating the proliferation of T-lymphocyte cells, said method comprising contacting said cells with a PRO344 polypeptide, wherein the proliferation of said cells is stimulated.

**65.** A method for stimulating the release of a cytokine from PBMC cells, said method comprising contacting said cells with a PRO526 or PRO1343 polypeptide, wherein the release of a cytokine from said cells is stimulated.

**66.** A method for inhibiting the binding of A-peptide to factor VIIA, said method comprising contacting a composition comprising said A-peptide and said factor VIIA with a PRO182 polypeptide, wherein the binding of said A-peptide to said factor VIIA is inhibited.

**67.** A method for inhibiting the differentiation of adipocyte cells, said method comprising contacting said cells with a PRO185 or PRO198 polypeptide, wherein the differentiation of said cells is inhibited.

**68.** A method for stimulating the proliferation of endothelial cells, said method comprising contacting said cells with a PRO222 polypeptide, wherein the proliferation of said cells is inhibited.

**69.** A method for detecting the presence of tumor in an mammal, said method comprising comparing the level of expression of any PRO polypeptide shown in Table 8 in (a) a test sample of cells taken from said mammal and (b) a control sample of normal cells of the same cell type, wherein a higher level of expression of said PRO polypeptide in the test sample as compared to the control sample is indicative of the presence of tumor in said mammal.

**70.** The method of claim 69, wherein said tumor is lung tumor, colon tumor, breast tumor, prostate tumor, rectal tumor, cervical tumor or liver tumor.

**71.** An oligonucleotide probe derived from any of the nucleotide sequences shown in the accompanying figures.

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