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(54) **TIE-2 LIGANDS, METHODS OF MAKING AND USES THEREOF**

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now abandoned, which is a continuation-in-part of application No. 08/348,492, filed on Dec. 2, 1994, now Pat. No. 5,879,672, which is a continuation-in-part of application No. 08/330,261, filed on Oct. 27, 1994, now Pat. No. 5,521,073, which is a continuation-in-part of application No. 08/319,932, filed on Oct. 7, 1994, now Pat. No. 5,643,755.

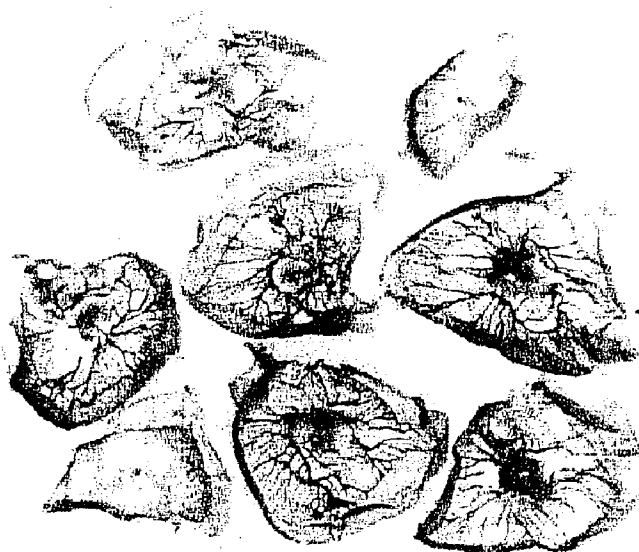
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(52) **U.S. Cl.** **530/350**; 530/388.22; 435/69.1; 435/320.1; 435/325; 424/143.1; 536/23.5

(57) **ABSTRACT**

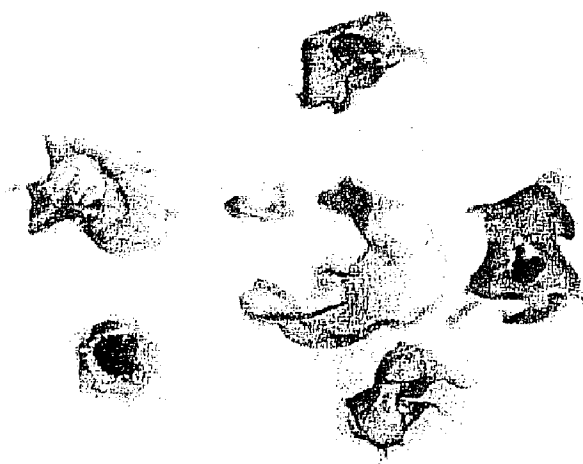
The present invention provides for an isolated nucleic acid molecule encoding a human TIE-2 ligand. In addition, the invention provides for a receptor body which specifically binds a human TIE-2 ligand. The invention also provides an antibody which specifically binds a human TIE-2 ligand. The invention further provides for an antagonist of human TIE-2. The invention also provides for therapeutic compositions as well as a method of blocking blood vessel growth, a method of promoting neovascularization, a method of promoting the growth or differentiation of a cell expressing the TIE-2 receptor, a method of blocking the growth or differentiation of a cell expressing the TIE-2 receptor and a method of attenuating or preventing tumor growth in a human.

Fig.1A



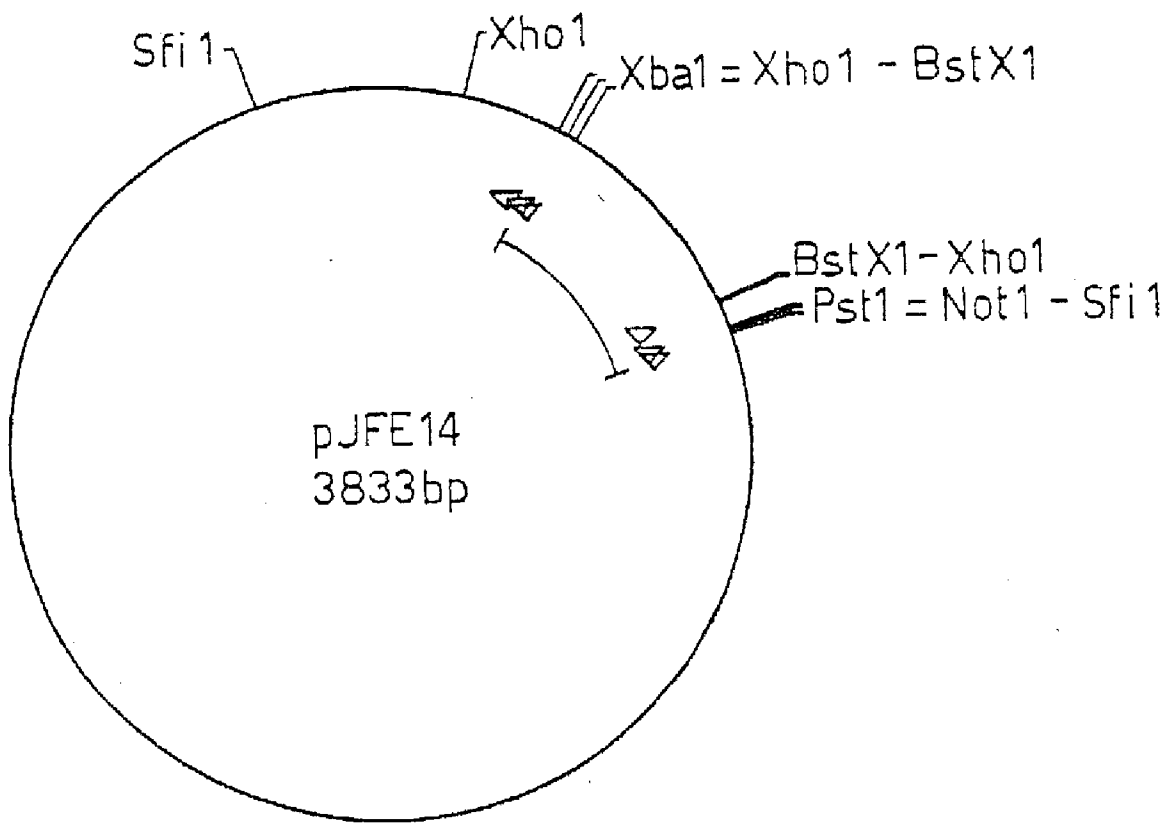
r EHK-1 ecto/h IgG1 Fc
Gelfoam (6 μ g)

Fig.1B



r TIE-2 ecto/h IgG1 Fc
Gelfoam (6 μ g)

Fig.2



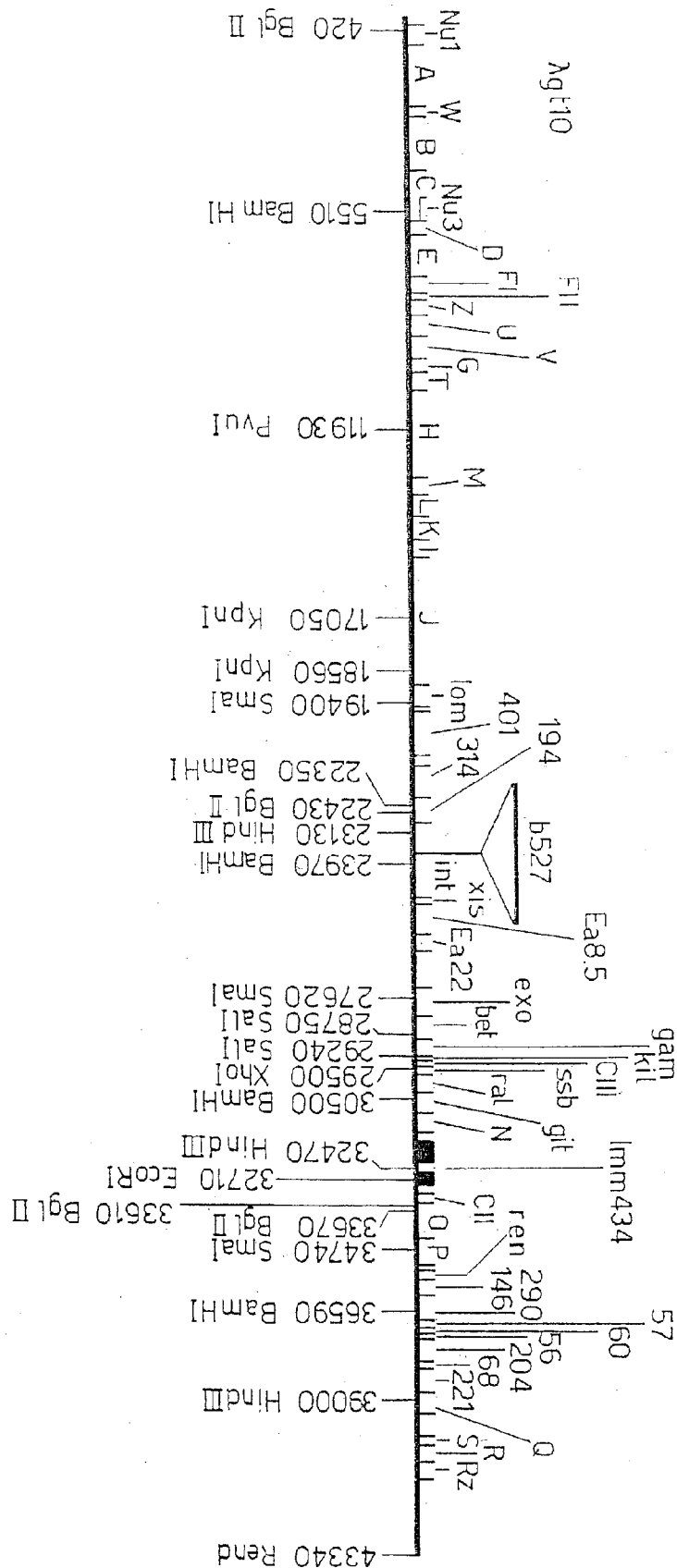


FIGURE 3

Fig. 4C

740	*	750	*	760	*	770	*	780	*	790	*								
AAG	CTG	ACA	GAT	GTT	GAG	ACC	CAG	GTA	CTA	AAT	CAA	ACT	TCT	CGA	CTT	GAG	ATA	CAG	CTG
K	L	T	D	V	E	T	Q	V	L	N	Q	T	S	R	L	E	I	Q	L>
800	*	810	*	820	*	830	*	840	*	850	*								
CTG	GAG	AAT	TCA	TTA	TCC	ACC	TAC	AAG	CTA	GAG	AAG	CAA	CTT	CTT	CAA	CAG	ACA	AAT	GAA
L	E	N	S	L	S	T	Y	K	L	E	K	Q	L	L	Q	Q	T	N	E>
860	*	870	*	880	*	890	*	900	*	910	*								
ATC	TTG	AAG	ATC	CAT	GAA	AAA	AAC	AGT	TTA	TTA	GAA	CAT	AAA	ATC	TTA	GAA	ATG	GAA	GGA
I	L	K	I	H	E	K	N	S	L	L	E	H	K	I	L	E	M	E	G>
920	*	930	*	940	*	950	*	960	*	970	*								
AAA	CAC	AAG	GAA	GAG	TTG	GAC	ACC	TTA	AAG	GAA	GAG	AAA	GAG	AAC	CTT	CAA	GGC	TTG	GTT
K	H	K	E	E	L	D	T	L	K	E	E	K	E	N	L	Q	G	L	V>
980	*	990	*	1000	*	1010	*	1020	*	1030	*								
ACT	CGT	CAA	ACA	TAT	ATA	ATC	CAG	GAG	CTG	GAA	AAG	CAA	TTA	AAC	AGA	GCT	ACC	ACC	AAC
T	R	Q	T	Y	I	I	Q	E	L	E	K	Q	L	N	R	A	T	T	N>

Fig. 4D

1040	1050	1060	1070	1080	1090
* AAC AGT GTC CTT CAG AAG CAG CAA CTG GAG CTG ATG GAC ACA GTC CAC AAC CTT GTC AAT					
N S V L Q K Q Q Q L E L M D T V H N L V N>					
1100	1110	1120	1130	1140	1150
* CTT TGC ACT AAA GAA GGT GTT TTA CTA AAG GGA GGA AAA AGA GAG GAG AAA CCA TTT					
L C T K E G V L L L K G G G K R E E K P F>					
1160	1170	1180	1190	1200	1210
* AGA GAC TGT GCA GAT GTA TAT CAA GCT GGT TTT AAT AAA AGT GGA ATC TAC ACT ATT TAT					
R D C A D V Y Q A G F N K S G I Y T I Y>					
1220	1230	1240	1250	1260	1270
* ATT AAT AAT ATG CCA GAA CCC AAA AAG GTG TTT TGC AAT ATG GAT GTC AAT GGG GGA GGT					
I N N M P E P K K K V F C N M D V N G G G>					
1280	1290	1300	1310	1320	1330
* TGG ACT GTA ATA CAA CAT CAT CGT GAA GAT GGA AGT CTA GAT TTC CAA AGA GGC TGG AAG GAA					
W T V I Q H Q H Q H R E D G S S L D F Q R G W K E>					
1340	1350	1360	1370	1380	1390
* TAT AAA ATG GGT TTT GGA AAT CCC TCC GGT GAA TAT TGG CTG GGG AAT GAG TTT ATT TTT					
Y K M G G F G N P S S G G E Y W L G N E F I F>					

Fig. 4E

1400 *	1410 *	1420 *	1430 *	1440 *	1450 *
GCC ATT ACC AGT CAG AGG CAG TAC ATG CTA AGA ATT GAG TTA ATG GAC TGG GAA GGG AAC	A I T S Q R Q Y M L R I E L M D W E G N>				
1460 *	1470 *	1480 *	1490 *	1500 *	1510 *
CGA GCC TAT TCA CAG TAT GAC AGA TTC CAC ATA GGA AAT GAA AAG CAA AAC TAT AGG TTG	R A Y S Q Y D R F H I G N E K Q N Y R L>				
1520 *	1530 *	1540 *	1550 *	1560 *	1570 *
TAT TTA AAA GGT CAC ACT GGG ACA GCA GGA AAA CAG AGC AGC CTG ATC TTA CAC GGT GCT	Y L K G G H T G T A G G K Q S S L I L H G A>				
1580 *	1590 *	1600 *	1610 *	1620 *	1630 *
GAT TTC AGC ACT AAA GAT GCT GAT AAT GAC AAC TGT ATG TGC AAA TGT GCC CTC ATG TTA	D F S T K A D N D N C M C K C A L M L>				
1640 *	1650 *	1660 *	1670 *	1680 *	1690 *
ACA GGA GGA TGG TGG TTT GAT GCT TGT GGC CCC TCC AAT CTA AAT GGA ATG TTC TAT ACT	T G G G W W F D A C G G P S N L N G M F Y T>				

Fig. 4F

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1700 *      1710 *      1720 *      1730 *      1740 *      1750 *
GCG GGA CAA AAC CAT GGA AAA CTG AAT GGG ATA AAG TGG CAC TAC TTC AAA GGG CCC AGT
A  G  Q  N  H  G  K  L  N  G  I  K  W  H  Y  F  K  G  P  S>

      1760      1770      1780      1790      1800
*      *      *      *
TAC TCC TTA CGT TCC ACA ACT ATG ATG ATT CGA CCT TTA GAT TTT TGA
Y  S  L  R  S  T  T  M  M  I  R  P  L  D  F  *>

1810 *      1820 *      1830 *      1840 *
*      *      *      *
AAGCGCAATGTCAGAAAGCGATTATGAAAGCAACA

      1850      1860 *      1870 *      1880 *      1890 *      1900 *      1910 *      1920 *
AAGAAATCCGGAGAAAGCTGCCAGGTGAGAAACTGTTTGAAAACTTCAGAAAGCAACAATATTGTCTCCCTTCCAGCAATA

      1930 *      1940 *      1950 *      1960 *      1970 *      1980 *      1990 *      2000 *
AGTGGTAGTTATGTGAAGTCACCAAGGTTCTTTGACCGTGAATCTGGAGCCGTTTGAGTTCAACAAGAGTCTCTACTTGGGG

      2010 *      2020 *      2030 *      2040 *      2050 *      2060 *      2070 *      2080 *
TGACAGTGCTCACGTGGCTCGACTATAGAAAAACTCCACTGACTGTCTGGGGCTTTAAAAAAGGGAAGAACTGCTGAGCTTGC

      2090 *      2100 *      2110 *      2120 *      2130 *      2140 *
TGTCCTTCAAACACTACTGTGGACCTTATTTTGGAACTATGGTAGCCAGATGATAAATATGGTTAATTTC
```

Fig. 5A

10	20	30	40	50	60	70	80
*	*	*	*	*	*	*	*
CAGCTGACTCAGGCAGGCTCCTCATGCTGAACGGTCCACACAGAGAGGAAACAATAAATCTCAGCTACTATGCAATAAATATC							
90	100	110	120	130	140	150	160
*	*	*	*	*	*	*	*
TCAAGTTTTAACGAAGAAAACATCATTCAGTGAAATAAAAAATTTTAAATTTTAGAACAAAAGCTAACAAAATGGCTAG							
170	180	190	200	210	220	230	240
*	*	*	*	*	*	*	*
TTTTCTATGATTCTTCAACGCTTCTTTGAGGGGAAGAGTCAAAACAACAAGCAGTTTACCTGAAATAAAGAA							
250	260	270	280	290	300	310	
*	*	*	*	*	*	*	
CTAGTTTTAGAGGTCAGAAAGGAGCAAGTTTTCGAGAGGCACGGAAGGAGTGTGCTGGCAGTACA ATG ACA GTT							
						M	T
							V>
320	330	340	350	360	370		
*	*	*	*	*	*		
TTC CTT TCC TTT GCT TTC CTC GCT GCC ATT CTG ACT CAC ATA GGG TGC AGC AAT CAG CGC							
F	L	S	F	A	F	L	T
							H
							I
							C
							S
							N
							Q
							R>
380	390	400	410	420	430		
*	*	*	*	*	*		
CGA AGT CCA GAA AAC AGT GGG AGA AGA TAT AAC CGG ATT CAA CAT GGG CAA TGT GCC TAC							
R	S	P	E	N	S	G	R
							Y
							N
							I
							Q
							H
							G
							Q
							C
							A
							Y>

Fig. 5B

440 *	450 *	460 *	470 *	480 *	490 *
ACT TTC ATT CTT CCA GAA CAC GAT GGC AAC TGT CGT GAG AGT ACG ACA GAC CAG TAC AAC	T F I A L P E H D G N C R E S T T D Q Y N>				
500 *	510 *	520 *	530 *	540 *	550 *
ACA AAC GCT CTG CAG AGA GAT GCT CCA CAC GTG GAA CCG GAT TTC TCT TCC CAG AAA CTT	T N A L Q R D A P H V E P D F S S Q K L>				
560 *	570 *	580 *	590 *	600 *	610 *
CAA CAT CTG GAA CAT GTG ATG GAA AAT TAT ACT CAG TGG CTG CAA AAA CTT GAG AAT TAC	Q H L E H V M E N Y T Q Q W L Q K L E N Y>				
620 *	630 *	640 *	650 *	660 *	670 *
ATT GTG GAA AAC ATG AAG TCG GAG ATG GCC CAG ATA CAG CAG AAT GCA GTT CAG AAC CAC	I V E N M K S E M A Q I Q Q Q N A V Q N H>				
680 *	690 *	700 *	710 *	720 *	730 *
ACG GCT ACC ATG CTG GAG ATA GGA ACC AGC CTC CTC TCT CAG ACT GCA GAG CAG ACC AGA	T A T M L E I G T S L L L S Q T A E Q T R>				
740 *	750 *	760 *	770 *	780 *	790 *
AAG CTG ACA GAT GTT GAG ACC CAG GTA CTA AAT CAA ACT TCT CGA CTT GAG ATA CAG CTG	K L T D V E T Q V L N Q Q T S R L E I Q L>				

Fig. 5C

800	810	820	830	840	850															
CTG	GAG	AAT	TCA	TTA	TCC	ACC	TAC	AAG	CTA	GAG	AAG	CAA	CTT	CTT	CAA	CAG	ACA	AAT	GAA	
L	E	N	S	L	S	L	S	T	Y	K	L	E	K	Q	L	L	Q	T	N	E>
860	870	880	890	900	910															
ATC	TTG	AAG	ATC	CAT	GAA	AAA	AAC	AGT	TTA	TTA	GAA	CAT	AAA	ATC	TTA	GAA	ATG	GAA	GGA	
I	L	K	I	H	E	K	N	S	L	L	E	H	K	I	L	E	M	E	G>	
920	930	940	950	960	970															
AAA	CAC	AAG	GAA	GAG	TTG	GAC	ACC	TTA	AAG	GAA	GAG	AAA	GAG	AAC	CTT	CAA	GGC	TTG	GTT	
K	H	K	E	E	L	D	T	L	K	E	E	K	E	N	L	Q	G	L	V>	
980	990	1000	1010	1020	1030															
ACT	CGT	CAA	ACA	TAT	ATA	ATC	CAG	GAG	CTG	GAA	AAG	CAA	TTA	AAC	AGA	GCT	ACC	ACC	AAC	
T	R	Q	T	Y	I	I	Q	E	L	E	K	Q	L	N	R	A	T	T	N>	
1040	1050	1060	1070	1080	1090															
AAC	AGT	GTC	CTT	CAG	AAG	CAG	CAA	CTG	GAG	CTG	ATG	GAC	ACA	GTC	CAC	AAC	CTT	GTC	AAT	
N	S	V	L	Q	K	Q	Q	L	E	L	M	D	T	V	H	N	L	V	N>	
1100	1110	1120	1130	1140	1150															
CTT	TGC	ACT	AAA	GAA	GTT	TTA	CTA	AAG	GGA	GGA	AAA	AGA	GAG	GAA	GAG	AAA	CCA	TTT	AGA	
L	C	T	K	E	V	L	L	K	G	G	K	R	E	E	E	K	P	F	R>	

Fig. 5D

1160	1170	1180	1190	1200	1210
* GAC TGT GCA GAT GTA TAT CAA GCT GGT TTT AAT AAA AGT GGA ATC TAC ACT ATT TAT ATT	* D C A A D V Y Q A G F N K S G I Y T I Y I>	* 1220	* 1230	* 1240	* 1250
* AAT AAT ATG CCA GAA CCC AAA AAG GTG TTT TGC AAT ATG GAT GTC AAT GGG GGA GGT TGG	* N N M P E P K K K V F C N M D V N G G G W>	* 1280	* 1290	* 1300	* 1310
* ACT GTA ATA CAA CAT CGT GAA GAT GGA AGT CTA GAT TTC CAA AGA GGC TGG AAG GAA TAT	* T V I Q H R E D G S L D F Q R G W K E Y>	* 1340	* 1350	* 1360	* 1370
* AAA ATG GGT TTT GGA AAT CCC TCC GGT GAA TAT TGG CTG GGG AAT GAG TTT ATT TTT GCC	* K M G G F G N P S G E Y W L G N E F I F A>	* 1400	* 1410	* 1420	* 1430
* ATT ACC AGT CAG AGG CAG TAC ATG CTA AGA ATT GAG TTA ATG GAC TGG GAA GGG AAC CGA	* I T S Q R Q Y M L R I E L M D W E G N R>	* 1460	* 1470	* 1480	* 1490
* GCC TAT TCA CAG TAT GAC AGA TTC CAC ATA GGA AAT GAA AAG CAA AAC TAT AGG TTG TAT	* A Y S Q Y D R F H I G N E K Q N Y R L Y>				

Fig. 5E

1520	1530	1540	1550	1560	1570	
* TTA AAA GGT CAC ACT GGG ACA GCA GGA AAA CAG AGC AGC CTG ATC TTA CAC GGT GCT GAT	* L K G G T H C A G T A G K Q S S L I L H G A D>					
1580	1590	1600	1610	1620	1630	
* TTC AGC ACT AAA GAT GCT GAT AAT GAC AAC TGT ATG TGC AAA TGT GCC CTC ATG TTA ACA	* F S T K D A D N D G A C A A C TGT ATG TGC AAA TGT GCC CTC ATG TTA ACA					
1640	1650	1660	1670	1680	1690	
* GGA GGA TGG TGG TTT GAT GCT TGT TGT GGC CCC TCC AAT CTA AAT GGA ATG TTC TAT ACT GCG	* G G W W F F D A C G G C G G C C C C P S N L L N G M F Y T A>					
1700	1710	1720	1730	1740	1750	
* GGA CAA AAC CAT GGA AAA CTG AAT GGA ATA AAG TGG CAC TAC TTC AAA GGG CCC AGT TAC	* G Q N H G G A A A C T G A A T G G A A T A A G T G G C A C T A C T T C A A A G G G C C C A G T T A C					
1760	1770	1780	1790	1800		
* TCC TTA CGT TCC ACA ACT ATG ATG ATG ATT CGA CCT TTA GAT TTT TGA	* S L R S T T A T M M M I I R P L D F *>					

Fig. 5F

1810	1820	1830	1840						
*	*	*	*						
AAGCGCAATGTCAGAAGCGATTATGAAAGCAACAAAG									
1850	1860	1870	1880	1890	1900	1910	1920		
*	*	*	*	*	*	*	*		
AAATCCGGAGAAAGCTGCCAGGTGAGAAAAGTTTGAAAACCTTCAGAAAGCAACAAATATTGTCTCCCTTCCAGCAATAAGT									
1930	1940	1950	1960	1970	1980	1990	2000		
*	*	*	*	*	*	*	*		
GGTAGTTATGTGAAGTCACCAAGGTTCTTGACCGTGAATCTGGAGCCGTTTGAGTTCAACAAGAGTCTCTACTTGGGGTGA									
2010	2020	2030	2040	2050	2060	2070	2080		
*	*	*	*	*	*	*	*		
CAGTGCTCACGTGGCTCGACTATAGAAAACCTCCACTGACTGTCTGGGCTTTAAAAAGGGAAGAACTGCTGAGCTTGCTGT									
2090	2100	2110	2120	2130	2140				
*	*	*	*	*	*				
GCTTCAAACTACTGGACCTTATTTTGGAACTATGGTAGCCAGATGATAAAATATGGTTAAATTTC									

Fig. 6C

870	880	890	900	910	920
* AAA CAG ATT TTG GAC CAG ACC AGT GAA ATA AAC AAA TTG CAA GAT AAG AAC AGT TTC CTA K Q I L D Q T S E I N K L Q D K N S F L>			*	*	*
930	940	950	960	970	980
* GAA AAG AAG GTG CTA GCT ATG GAA GAC AAG CAC ATC ATC CAA CTA CAG TCA ATA AAA GAA E K K V L A M E D K H I I Q L S I K E>			*	*	*
990	1000	1010	1020	1030	1040
* GAG AAA GAT CAG CTA CAG GTG TTA GTA TCC AAG CAA AAT TCC ATC ATT GAA GAA CTA GAA E K D Q L Q V L V S K Q N S I I E E L E>			*	*	*
1050	1060	1070	1080	1090	1100
* AAA AAA ATA GTG ACT GCC ACG GTG AAT AAT TCA GTT CTT CAA AAG CAG CAA CAT GAT CTC K K I V T A T V N N S V L Q K Q Q H D L>			*	*	*
1110	1120	1130	1140	1150	1160
* ATG GAG ACA GTT AAT AAC TTA CTG ACT ATG ATG TCC ACA TCA AAC TCA GCT AAG GAC CCC M E T V N N L L L T M M S T S N S A K D P>			*	*	*
1170	1180	1190	1200	1210	1220
* ACT GTT GCT AAA GAA GAA GAA CAA ATC AGC TTC AGA GAC TGT GCT GAA GTA TTC AAA TCA GGA T V A K E E Q I S F R D C A E E V F K S G>			*	*	*

Fig. 6D

1230	1240	1250	1260	1270	1280
*	*	*	*	*	*
CAC ACC ACA AAT GGC ATC TAC ACG TTA ACA TTC CCT AAT TCT ACA GAA GAG ATC AAG GCC					
H T T N G I Y T L T F P N S T E E I K A>					
1290	1300	1310	1320	1330	1340
*	*	*	*	*	*
TAC TGT GAC ATG GAA GCT GGA GGC GGC TGG TGG ACA ATT ATT CAG CGT GAG GAT GGC					
Y C D M E A G G G G G W T I I Q R E D G>					
1350	1360	1370	1380	1390	1400
*	*	*	*	*	*
AGC GTT GAT TTT CAG AGG ACT TGG AAA GAA TAT AAA GTG GGA TTT GGT AAC CCT TCA GGA					
S V D F Q R T W K E Y K V G G F G N P S G>					
1410	1420	1430	1440	1450	1460
*	*	*	*	*	*
GAA TAT TGG CTG GGA AAT GAG TTT GTT TCG CAA CTG ACT AAT CAG CAA CGC TAT GTG CTT					
E Y W L G N E F V S Q S Q L T N Q Q R Y V L>					
1470	1480	1490	1500	1510	1520
*	*	*	*	*	*
AAA ATA CAC CTT AAA GAC TGG GAA GGC AAT GAG GCT TAC TCA TTG TAT GAA CAT TTC TAT					
K I H L K K D W E G G N E A Y S L L Y E H F Y>					
1530	1540	1550	1560	1570	1580
*	*	*	*	*	*
CTC TCA AGT GAA GAA CTC AAT TAT AGG ATT CAC CTT AAA GGA CTT ACA GGC ACA GCC GGC					
L S S E E L N Y R I H L L K G L T G T A G>					

Fig. 6E

1590		1600		1610		1620		1630		1640											
*		*		*		*		*		*											
AAA	ATA	AGC	ATC	AGC	CAA	CCA	GGA	AAT	GAT	TTT	AGC	ACA	AAG	GAT	GGA	GAC	AAC	GAC			
K	I	S	S	I	S	Q	P	G	N	D	F	S	T	K	D	G	D	N	D>		
1650		1660		1670		1680		1690		1700											
*		*		*		*		*		*											
AAA	TGT	ATT	TGC	AAA	TGT	TCA	CAA	ATG	CTA	ACA	GGA	GGC	TGG	TGG	TTT	GAT	GCA	TGT	GGT		
K	C	I	C	K	C	S	Q	M	L	T	G	G	W	W	F	D	A	C	G>		
1710		1720		1730		1740		1750		1760											
*		*		*		*		*		*											
CCT	TCC	AAC	TTG	AAC	GGA	ATG	TAC	TAT	CCA	CAG	AGG	CAG	AAC	ACA	AAT	AAG	TTC	AAC	GGC		
P	S	N	L	N	G	M	Y	Y	P	Q	R	Q	N	T	N	K	F	N	G>		
1770		1780		1790		1800		1810		1820											
*		*		*		*		*		*											
ATT	AAA	TGG	TAC	TAC	TGG	AAA	GGC	TCA	GGC	TAT	TCG	CTC	AAG	GCC	ACA	ACC	ATG	ATG	ATC		
I	K	W	Y	Y	W	K	G	S	G	Y	S	L	K	A	T	T	M	M	I>		
1830		1840																			
*		*																			
CGA	CCA	GCA	GAT	TTC																	
R	P	A	D	F>																	
1850		1860		1870		1880		1890		1900		1910		1920							
*		*		*		*		*		*		*		*							
TAA	ACAT	CCC	AGT	CCAC	CTG	AGGA	ACTG	TCT	CGAA	CTAT	TTT	CAAA	GACT	TTA	AGCC	CCAG	TGCA	CTG	AAAG	TCA	CGG

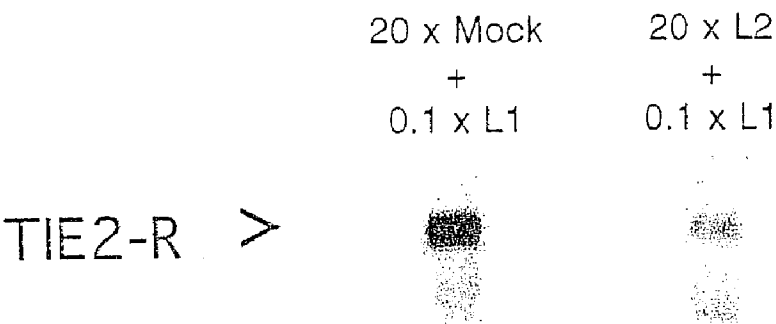
Fig. 6F

1930	1940	1950	1960	1970	1980	1990	2000
*	*	*	*	*	*	*	*
CTGCGCACGTGTCTCTTCCACACAGAGGGCGTGTGCTCGGTGCTGACGGGACCCACATGCTCCAGATTAGAGGCCCTGT							
2010	2020	2030	2040	2050	2060	2070	2080
*	*	*	*	*	*	*	*
AAACTTTATCACTTAAACTTGCATCACTTAACGGACCAAGCAAGACCCCTAAACATCCATAAATTGTGATTAGACAGAACA							
2090	2100	2110	2120	2130	2140	2150	2160
*	*	*	*	*	*	*	*
CCTATGCAAAGATGAACCCGAGGCTGAGAAATCAGACTGACAGTTTACAGACGCTGCTGTCAACAACCAAGAAATGTTATGTG							
2170	2180	2190	2200	2210	2220	2230	2240
*	*	*	*	*	*	*	*
CAAGTTTATCAGTAAATAACTGGAAAACAGAACTTATGTTATACAATACAGATCACTTGGAACTGCATTTCTTCTGAG							
2250	2260	2270	2280				
*	*	*	*				
CACTGTTTATACACTGTGTAAATACCCATATGTCCTGAATTC							

Fig. 7



Fig. 8



TIE-2 LIGANDS, METHODS OF MAKING AND USES THEREOF

[0001] This application is a continuation-in-part of copending U.S. application Ser. No. 373,579, filed Jan. 17, 1995, which is a continuation-in-part of U.S. Ser. No. 353,503, filed Dec. 9, 1994, which is a continuation-in-part of U.S. Ser. No. 348,492, filed Dec. 2, 1994, which is a continuation-in-part of U.S. Ser. No. 330,261 filed Oct. 27, 1994, which is a continuation-in-part of U.S. application Ser. No. 319,932, filed Oct. 7, 1994, the contents of each of which are hereby incorporated by reference. Throughout this application various publications are referenced. The disclosures of these publications in their entireties are hereby incorporated by reference into this application.

INTRODUCTION

[0002] The present invention relates generally to the field of genetic engineering and more particularly to genes for receptor tyrosine kinases and their cognate ligands, their insertion into recombinant DNA vectors, and the production of the encoded proteins in recipient strains of micro-organisms and recipient eukaryotic cells. More specifically, the present invention is directed to novel ligands, known as the TIE-2 ligands, that bind the TIE-2 receptor, as well as to methods of making and using the TIE-2 ligands. The invention further provides nucleic acid sequences encoding TIE-2 ligands, and methods for the generation of nucleic acids encoding TIE-2 ligands and their gene products. The TIE-2 ligands, as well as nucleic acids encoding them, may be useful in the diagnosis and treatment of certain diseases involving endothelial cells and associated TIE receptors, such as neoplastic diseases involving tumor angiogenesis, wound healing, thromboembolic diseases, atherosclerosis and inflammatory diseases. More generally, biologically active TIE-2 ligands may be used to promote the growth, survival and/or differentiation of cells expressing the TIE-2 receptor. Biologically active TIE-2 ligand may be used for the in vitro maintenance of TIE-2 receptor expressing cells in culture. Cells and tissues expressing TIE-2 receptor include, for example, cardiac and vascular endothelial cells, lens epithelium and heart epicardium. Alternatively, such ligand may be used to support cells which are engineered to express TIE-2 receptor. Further, TIE-2 ligands and their cognate receptor may be used in assay systems to identify agonists or antagonists of the TIE-2 receptor.

BACKGROUND OF THE INVENTION

[0003] The cellular behavior responsible for the development, maintenance, and repair of differentiated cells and tissues is regulated, in large part, by intercellular signals conveyed via growth factors and similar ligands and their receptors. The receptors are located on the cell surface of responding cells and they bind peptides or polypeptides known as growth factors as well as other hormone-like ligands. The results of this interaction are rapid biochemical changes in the responding cells, as well as a rapid and a long-term readjustment of cellular gene expression. Several receptors associated with various cell surfaces may bind specific growth factors.

[0004] The phosphorylation of tyrosines on proteins by tyrosine kinases is one of the key modes by which signals are transduced across the plasma membrane. Several cur-

rently known protein tyrosine kinase genes encode transmembrane receptors for polypeptide growth factors and hormones such as epidermal growth factor (EGF), insulin, insulin-like growth factor-I (IGF-I), platelet derived growth factors (PDGF-A and -B), and fibroblast growth factors (FGFs). (Heldin et al., *Cell Regulation*, 1: 555-566 (1990); Ullrich, et al., *Cell*, 61: 243-54 (1990)). In each instance, these growth factors exert their action by binding to the extracellular portion of their cognate receptors, which leads to activation of the intrinsic tyrosine kinase present on the cytoplasmic portion of the receptor. Growth factor receptors of endothelial cells are of particular interest due to the possible involvement of growth factors in several important physiological and pathological processes, such as vasculogenesis, angiogenesis, atherosclerosis, and inflammatory diseases. (Folkman, et al. *Science*, 235: 442-447 (1987)). Also, the receptors of several hematopoietic growth factors are tyrosine kinases; these include c-fms, which is the colony stimulating factor 1 receptor, Sherr, et al., *Cell*, 41: 665-676 (1985), and c-kit, a primitive hematopoietic growth factor receptor reported in Huang, et al., *Cell*, 63: 225-33 (1990).

[0005] The receptor tyrosine kinases have been divided into evolutionary subfamilies based on the characteristic structure of their ectodomains. (Ullrich, et al. *Cell*, 61: 243-54 (1990)). Such subfamilies include, EGF receptor-like kinase (subclass I) and insulin receptor-like kinase (subclass II), each of which contains repeated homologous cysteine-rich sequences in their extracellular domains. A single cysteine-rich region is also found in the extracellular domains of the eph-like kinases. Hirai, et al., *Science*, 238: 1717-1720 (1987); Lindberg, et al. *Mol. Cell. Biol.*, 10: 6316-24 (1990); Lhotak, et al., *Mol. Cell. Biol.* 11: 2496-2502 (1991). PDGF receptors as well as c-fms and c-kit receptor tyrosine kinases may be grouped into subclass III; while the FGF receptors form subclass IV. Typical for the members of both of these subclasses are extracellular folding units stabilized by intrachain disulfide bonds. These so-called immunoglobulin (Ig)-like folds are found in the proteins of the immunoglobulin superfamily which contains a wide variety of other cell surface receptors having either cell-bound or soluble ligands. Williams, et al., *Ann. Rev. Immunol.*, 6: 381-405 (1988).

[0006] Receptor tyrosine kinases differ in their specificity and affinity. In general, receptor tyrosine kinases are glycoproteins, which consist of (1) an extracellular domain capable of binding the specific growth factor(s); (2) a transmembrane domain which usually is an alpha-helical portion of the protein; (3) a juxtamembrane domain where the receptor may be regulated by, e.g., protein phosphorylation, (4) a tyrosine kinase domain which is the enzymatic component of the receptor; and (5) a carboxyterminal tail which in many receptors is involved in recognition and binding of the substrates for the tyrosine kinase.

[0007] Processes such as alternative exon splicing and alternative choice of gene promoter or polyadenylation sites have been reported to be capable of producing several distinct polypeptides from the same gene. These polypeptides may or may not contain the various domains listed above. As a consequence, some extracellular domains may be expressed as separate, secreted proteins and some forms of the receptors may lack the tyrosine kinase domain and

contain only the extracellular domain inserted in the plasma membrane via the transmembrane domain plus a short carboxyl terminal tail.

[0008] A gene encoding an endothelial cell transmembrane tyrosine kinase, originally identified by RT-PCR as an unknown tyrosine kinase-homologous cDNA fragment from human leukemia cells, was described by Partanen, et al., *Proc. Natl. Acad. Sci. USA*, 87: 8913-8917 (1990). This gene and its encoded protein are called "tie" which is an abbreviation for "tyrosine kinase with Ig and EGF homology domains." Partanen, et al. *Mol. Cell. Biol.* 12: 1698-1707 (1992).

[0009] It has been reported that tie mRNA is present in all human fetal and mouse embryonic tissues. Upon inspection, tie message has been localized to the cardiac and vascular endothelial cells. tie mRNA has been localized to the endothelia of blood vessels and endocardium of 9.5 to 18.5 day old mouse embryos. Enhanced tie expression was shown during neovascularization associated with developing ovarian follicles and granulation tissue in skin wounds. Korhonen, et al. *Blood* 80: 2548-2555 (1992). Thus tie has been suggested to play a role in angiogenesis, which is important for developing treatments for solid tumors and several other angiogenesis-dependent diseases such as diabetic retinopathy, psoriasis, atherosclerosis and arthritis.

[0010] Two structurally related rat TIE receptor proteins have been reported to be encoded by distinct genes with related profiles of expression. One gene, termed tie-1, is the rat homolog of human tie. Maisonpierre, et al., *Oncogene* 8: 1631-1637 (1993). The other gene, tie-2, may be the rat homolog of the murine tek gene, which, like tie, has been reported to be expressed in the mouse exclusively in endothelial cells and their presumptive progenitors. Dumont, et al. *Oncogene* 8: 1293-1301 (1993).

[0011] Both genes were found to be widely expressed in endothelial cells of embryonic and postnatal tissues. Significant levels of tie-2 transcripts were also present in other embryonic cell populations, including lens epithelium, heart epicardium and regions of mesenchyme. Maisonpierre, et al., *Oncogene* 8: 1631-1637 (1993).

[0012] The predominant expression of the TIE receptor in vascular endothelia suggests that TIE plays a role in the development and maintenance of the vascular system. This could include roles in endothelial cell determination, proliferation, differentiation and cell migration and patterning into vascular elements. In the mature vascular system, TIE could function in endothelial cell survival, maintenance and response to pathogenic influences.

SUMMARY OF THE INVENTION

[0013] The present invention provides for a composition comprising a TIE-2 ligand substantially free of other proteins. The invention also provides for an isolated nucleic acid molecule encoding a TIE-2 ligand. The isolated nucleic acid may be DNA, cDNA or RNA. The invention also provides for a vector comprising an isolated nucleic acid molecule encoding a TIE-2 ligand. The invention further provides for a host-vector system for the production in a suitable host cell of a polypeptide having the biological activity of a TIE-2 ligand. The suitable host cell may be bacterial, yeast, insect or mammalian. The invention also

provides for a method of producing a polypeptide having the biological activity of a TIE-2 ligand which comprises growing cells of the host-vector system under conditions permitting production of the polypeptide and recovering the polypeptide so produced.

[0014] The invention herein described of an isolated nucleic acid molecule encoding a TIE-2 ligand further provides for the development of the ligand, a fragment or derivative thereof, or another molecule which is a receptor agonist or antagonist, as a therapeutic for the treatment of patients suffering from disorders involving cells, tissues or organs which express the TIE receptor. The present invention also provides for an antibody which specifically binds such a therapeutic molecule. The antibody may be monoclonal or polyclonal. The invention also provides for a method of using such a monoclonal or polyclonal antibody to measure the amount of the therapeutic molecule in a sample taken from a patient for purposes of monitoring the course of therapy.

[0015] The present invention also provides for an antibody which specifically binds a TIE-2 ligand. The antibody may be monoclonal or polyclonal. Thus the invention further provides for therapeutic compositions comprising an antibody which specifically binds a TIE-2 ligand in a pharmaceutically acceptable vehicle. The invention also provides for a method of blocking blood vessel growth in a mammal by administering an effective amount of a therapeutic composition comprising an antibody which specifically binds a TIE-2 ligand in a pharmaceutically acceptable vehicle.

[0016] The invention further provides for therapeutic compositions comprising a TIE-2 ligand in a pharmaceutically acceptable vehicle. The invention also provides for a method of promoting neovascularization in a patient by administering an effective amount of a therapeutic composition comprising a TIE-2 ligand in a pharmaceutically acceptable vehicle. In one embodiment, the method may be used to promote wound healing. In another embodiment, the method may be used to treat ischemia.

[0017] Alternatively, the invention provides that a TIE-2 ligand may be conjugated to a cytotoxic agent and a therapeutic composition prepared therefrom. The invention further provides for a receptor body which specifically binds a TIE-2 ligand. The invention further provides for therapeutic compositions comprising a receptor body which specifically binds a TIE-2 ligand in a pharmaceutically acceptable vehicle. The invention also provides for a method of blocking blood vessel growth in a mammal by administering an effective amount of a therapeutic composition comprising a receptor body which specifically binds a TIE-2 ligand in a pharmaceutically acceptable vehicle.

[0018] The invention also provides for a TIE-2 receptor antagonist, known as TIE-2 ligand 2, as well as a method of inhibiting TIE-2 ligand biological activity in a mammal comprising administering to the mammal an effective amount of a TIE-2 antagonist. According to the invention, the antagonist may be an antibody or other molecule capable of specifically binding either TIE-2 ligand or TIE-2 receptor. For example, the antagonist may be a TIE-2 receptorbody.

BRIEF DESCRIPTION OF THE FIGURES

[0019] FIGS. 1A and 1B—TIE-2 receptorbody (TIE-2 RB) inhibits the development of blood vessels in the embry-

onic chicken chorioallantoic membrane (CAM). A single piece of resorbable gelatin foam (Gelfoam) soaked with 6 μ g of RB was inserted immediately under the CAM of 1-day chick embryos. After 3 further days of incubation, 4 day old embryos and surrounding CAM were removed and examined. **FIG. 1A:** embryos treated with EHK-1 RB (rEHK-1 ecto/h IgG1 Fc) were viable and possessed normally developed blood vessels in their surrounding CAM. **FIG. 1B:** all embryos treated with TIE-2 RB (r TIE-2 ecto/h IgG1 Fc) were dead, diminished in size and were almost completely devoid of surrounding blood vessels.

[0020] FIG. 2—Vector pJFE14.

[0021] FIG. 3—Restriction map of λ gt10.

[0022] FIG. 4—Nucleic acid and deduced amino acid (single letter code) sequences of human TIE-2 ligand from clone λ gt10 encoding htie-2 ligand 1.

[0023] FIG. 5—Nucleic acid and deduced amino acid (single letter code) sequences of human TIE-2 ligand from T98G clone.

[0024] FIG. 6—Nucleic acid and deduced amino acid (single letter code) sequences of human TIE-2 ligand from clone pBluescript KS encoding human TIE 2 ligand 2.

[0025] FIG. 7—Western blot showing activation of TIE-2 receptor by TIE-2 ligand 1 (Lane L1) but not by TIE-2 ligand 2 (Lane L2) or control (Mock).

[0026] FIG. 8—Western blot showing that prior treatment of HAEC cells with excess TIE-2 ligand 2 (Lane 2) antagonizes the subsequent ability of dilute TIE-2 ligand 1 to activate the TIE-2 receptor (TIE2-R) as compared with prior treatment of HAEC cells with MOCK medium (Lane 1).

DETAILED DESCRIPTION OF THE INVENTION

[0027] As described in greater detail below, applicants have isolated, by expression cloning, a novel ligand that binds the TIE-2 receptor. The present invention comprises a TIE-2 ligand as well as its amino acid sequence and also functionally equivalent molecules in which amino acid residues are substituted for residues within the sequence resulting in a silent change. For example, one or more amino acid residues within the sequence can be substituted by another amino acid(s) of a similar polarity which acts as a functional equivalent, resulting in a silent alteration. Substitutes for an amino acid within the sequence may be selected from other members of the class to which the amino acid belongs. For example, the class of nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan and methionine. The polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine. The positively charged (basic) amino acids include arginine, lysine and histidine. The negatively charged (acidic) amino acids include aspartic acid and glutamic acid. Also included within the scope of the invention are proteins or fragments or derivatives thereof which exhibit the same or similar biological activity and derivatives which are differentially modified during or after translation, e.g., by glycosylation, proteolytic cleavage, linkage to an antibody molecule or other cellular ligand, etc.

[0028] The present invention also encompasses the nucleotide sequence that encodes the protein described herein as TIE-2 ligand 1, as well as cells which are genetically engineered to produce the protein, by e.g. transfection, transduction, infection, electroporation, or microinjection of nucleic acid encoding the TIE-2 ligand 1 described herein in a suitable expression vector.

[0029] The present invention further encompasses the nucleotide sequence that encodes the protein described herein as TIE-2 ligand 2, as well as cells which are genetically engineered to produce the protein, by e.g. transfection, transduction, infection, electroporation, or microinjection of nucleic acid encoding the TIE-2 ligand 2 described herein in a suitable expression vector.

[0030] One skilled in the art will also recognize that the present invention encompasses DNA and RNA sequences that hybridize to a deduced TIE-2 ligand encoding sequence, under conditions of moderate stringency, as defined in, for example, Sambrook, et al. *Molecular Cloning: A Laboratory Manual*, 2 ed. Vol. 1, pp. 101-104, Cold Spring Harbor Laboratory Press (1989). Thus, a nucleic acid molecule contemplated by the invention includes one having a sequence deduced from an amino acid sequence of a TIE-2 ligand prepared as described herein, as well as a molecule having a sequence of nucleic acids that hybridizes to such a nucleic acid sequence, and also a nucleic acid sequence which is degenerate of the above sequences as a result of the genetic code, but which encodes a ligand that binds the TIE-2 receptor.

[0031] Any of the methods known to one skilled in the art for the insertion of DNA fragments into a vector may be used to construct expression vectors encoding TIE-2 ligand using appropriate transcriptional/translational control signals and the protein coding sequences. These methods may include in vitro recombinant DNA and synthetic techniques and in vivo recombinations (genetic recombination). Expression of a nucleic acid sequence encoding a TIE-2 ligand or peptide fragments thereof may be regulated by a second nucleic acid sequence so that the protein or peptide is expressed in a host transformed with the recombinant DNA molecule. For example, expression of a TIE-2 ligand described herein may be controlled by any promoter/enhancer element known in the art. Promoters which may be used to control expression of the ligand include, but are not limited to the long terminal repeat as described in Squinto et al., (*Cell* 65:1-20 (1991)); the SV40 early promoter region (Bernoist and Chambon, *Nature* 290:304-310), the CMV promoter, the M-MuLV 5' terminal repeat, the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto, et al., *Cell* 22:787-797 (1980)), the herpes thymidine kinase promoter (Wagner et al., *Proc. Natl. Acad. Sci. U.S.A.* 78:144-1445 (1981)), the adenovirus promoter, the regulatory sequences of the metallothionein gene (Brinster et al., *Nature* 296:39-42 (1982)); prokaryotic expression vectors such as the β -lactamase promoter (Villa-Kamaroff, et al., *Proc. Natl. Acad. Sci. U.S.A.* 75:3727-3731 (1978)), or the tac promoter (DeBoer, et al., *Proc. Natl. Acad. Sci. U.S.A.* 80:21-25 (1983)), see also "Useful proteins from recombinant bacteria" in *Scientific American*, 242:74-94 (1980); promoter elements from yeast or other fungi such as the Gal 4 promoter, the ADH (alcohol dehydrogenase) promoter, PGK (phosphoglycerol kinase) promoter, alkaline phosphatase promoter, and the following animal transcrip-

tional control regions, which exhibit tissue specificity and have been utilized in transgenic animals: elastase I gene control region which is active in pancreatic acinar cells (Swift et al., Cell 38:639-646 (1984); Ornitz et al., Cold Spring Harbor Symp. Quant. Biol. 50:399-409 (1986); MacDonald, Hepatology 7:425-515 (1987); insulin gene control region which is active in pancreatic beta cells (Hanahan, Nature 315:115-122 (1985)), immunoglobulin gene control region which is active in lymphoid cells (Grosschedl et al., 1984, Cell 38:647-658; Adames et al., 1985, Nature 318:533-538; Alexander et al., 1987, Mol. Cell. Biol. 7:1436-1444), mouse mammary tumor virus control region which is active in testicular, breast, lymphoid and mast cells (Leder et al., 1986, Cell 45:485-495), albumin gene control region which is active in liver (Pinkert et al., 1987, Genes and Devel. 1:268-276), alpha-fetoprotein gene control region which is active in liver (Krumlauf et al., 1985, Mol. Cell. Biol. 5:1639-1648; Hammer et al., 1987, Science 235:53-58); alpha 1-antitrypsin gene control region which is active in the liver (Kelsey et al., 1987, Genes and Devel. 1:161-171), beta-globin gene control region which is active in myeloid cells (Mogam et al., 1985, Nature 315:338-340; Kollias et al., 1986, Cell 46:89-94); myelin basic protein gene control region which is active in oligodendrocyte cells in the brain (Readhead et al., 1987, Cell 48:703-712); myosin light chain-2 gene control region which is active in skeletal muscle (Shani, 1985, Nature 314:283-286), and gonadotropin releasing hormone gene control region which is active in the hypothalamus (Mason et al., 1986, Science 234:1372-1378). The invention further encompasses the production of antisense compounds which are capable of specifically hybridizing with a sequence of RNA encoding a TIE-2 ligand to modulate its expression. (Ecker, U.S. Pat. No. 5,166,195, issued Nov. 24, 1992).

[0032] Thus, according to the invention, expression vectors capable of being replicated in a bacterial or eukaryotic host comprising a nucleic acid encoding a TIE-2 ligand as described herein, are used to transfect a host and thereby direct expression of such nucleic acid to produce the TIE-2 ligand, which may then be recovered in a biologically active form. As used herein, a biologically active form includes a form capable of binding to the TIE-2 receptor and causing a biological response such as a differentiated function or influencing the phenotype of the cell expressing the receptor. Such biologically active forms would, for example, induce phosphorylation of the tyrosine kinase domain of the TIE-2 receptor.

[0033] Expression vectors containing the gene inserts can be identified by four general approaches: (a) DNA-DNA hybridization, (b) presence or absence of "marker" gene functions, (c) expression of inserted sequences and (d) PCR detection. In the first approach, the presence of a foreign gene inserted in an expression vector can be detected by DNA-DNA hybridization using probes comprising sequences that are homologous to an inserted TIE-2 ligand encoding gene. In the second approach, the recombinant vector/host system can be identified and selected based upon the presence or absence of certain "marker" gene functions (eq., thymidine kinase activity, resistance to antibiotics, transformation phenotype, occlusion body formation in baculovirus, etc.) caused by the insertion of foreign genes in the vector. For example, if a nucleic acid encoding a TIE-2 ligand is inserted within the marker gene sequence of the vector, recombinants containing the insert can be identified

by the absence of the marker gene function. In the third approach, recombinant expression vectors can be identified by assaying the foreign gene product expressed by the recombinant. Such assays can be based, for example, on the physical or functional properties of a TIE-2 ligand gene product, for example, by binding of the ligand to the TIE-2 receptor or portion thereof which may be tagged with, for example, a detectable antibody or portion thereof or by binding to antibodies produced against the TIE-2 ligand protein or a portion thereof. Cells of the present invention may transiently or, preferably, constitutively and permanently express TIE-2 ligands as described herein. In the fourth approach, DNA nucleotide primers can be prepared corresponding to a tie-2 specific DNA sequence. These primers could then be used to PCR a tie-2 gene fragment. (PCR Protocols: A Guide To Methods and Applications, Edited by Michael A. Innis et al., Academic Press (1990)).

[0034] The recombinant ligand may be purified by any technique which allows for the subsequent formation of a stable, biologically active protein. For example, and not by way of limitation, the ligand may be recovered from cells either as soluble proteins or as inclusion bodies, from which they may be extracted quantitatively by 8M guanidinium hydrochloride and dialysis. In order to further purify the ligand, conventional ion exchange chromatography, hydrophobic interaction chromatography, reverse phase chromatography or gel filtration may be used.

[0035] In additional embodiments of the invention, a recombinant TIE-2 ligand encoding gene may be used to inactivate or "knock out" the endogenous gene by homologous recombination, and thereby create a TIE-2 ligand deficient cell, tissue, or animal. For example, and not by way of limitation, the recombinant TIE-2 ligand encoding gene may be engineered to contain an insertional mutation, for example the neo gene, which would inactivate the native TIE-2 ligand encoding gene. Such a construct, under the control of a suitable promoter, may be introduced into a cell, such as an embryonic stem cell, by a technique such as transfection, transduction, or injection. Cells containing the construct may then be selected by G418 resistance. Cells which lack an intact TIE-2 ligand encoding gene may then be identified, e.g. by Southern blotting, PCR detection, Northern blotting or assay of expression. Cells lacking an intact TIE-2 ligand encoding gene may then be fused to early embryo cells to generate transgenic animals deficient in such ligand. Such an animal may be used to define specific in vivo processes, normally dependent upon the ligand.

[0036] The present invention also provides for antibodies to the TIE-2 ligands described herein which are useful for detection of the ligands in, for example, diagnostic applications. For preparation of monoclonal antibodies directed toward TIE-2 ligand, any technique which provides for the production of antibody molecules by continuous cell lines in culture may be used. For example, the hybridoma technique originally developed by Kohler and Milstein (1975, Nature 256:495-497), as well as the trioma technique, the human B-cell hybridoma technique (Kozbor et al., 1983, Immunology Today 4:72), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole et al., 1985, in "Monoclonal Antibodies and Cancer Therapy," Alan R. Liss, Inc. pp. 77-96) and the like are within the scope of the present invention.

[0037] The monoclonal antibodies may be human monoclonal antibodies or chimeric human-mouse (or other species) monoclonal antibodies. Human monoclonal antibodies may be made by any of numerous techniques known in the art (e.g., Teng et al., 1983, Proc. Natl. Acad. Sci. U.S.A. 80:7308-7312; Kozbor et al., 1983, Immunology Today 4:72-79; Olsson et al., 1982, Meth. Enzymol. 92:3-16). Chimeric antibody molecules may be prepared containing a mouse antigen-binding domain with human constant regions (Morrison et al., 1984, Proc. Natl. Acad. Sci. U.S.A. 81:6851, Takeda et al., 1985, Nature 314:452).

[0038] Various procedures known in the art may be used for the production of polyclonal antibodies to epitopes of the TIE-2 ligands described herein. For the production of antibody, various host animals can be immunized by injection with a TIE-2 ligand, or a fragment or derivative thereof, including but not limited to rabbits, mice and rats. Various adjuvants may be used to increase the immunological response, depending on the host species, and including but not limited to Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, and potentially useful human adjuvants such as BCG (*Bacille Calmette-Guerin*) and *Corynebacterium parvum*.

[0039] A molecular clone of an antibody to a selected TIE-2 ligand epitope can be prepared by known techniques. Recombinant DNA methodology (see e.g., Maniatis et al., 1982, Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.) may be used to construct nucleic acid sequences which encode a monoclonal antibody molecule, or antigen binding region thereof.

[0040] The present invention provides for antibody molecules as well as fragments of such antibody molecules. Antibody fragments which contain the idiotype of the molecule can be generated by known techniques. For example, such fragments include but are not limited to: the F(ab')₂ fragment which can be produced by pepsin digestion of the antibody molecule; the Fab' fragments which can be generated by reducing the disulfide bridges of the F(ab')₂ fragment, and the Fab fragments which can be generated by treating the antibody molecule with papain and a reducing agent. Antibody molecules may be purified by known techniques, e.g., immunoabsorption or immunoaffinity chromatography, chromatographic methods such as HPLC (high performance liquid chromatography), or a combination thereof.

[0041] The present invention further encompasses an immunoassay for measuring the amount of a TIE-2 ligand in a biological sample by

[0042] a) contacting the biological sample with at least one antibody which specifically binds the TIE-2 ligand so that the antibody forms a complex with any TIE-2 ligand present in the sample; and

[0043] b) measuring the amount of the complex and thereby measuring the amount of the TIE-2 ligand in the biological sample

[0044] The invention further encompasses an assay for measuring the amount of TIE-2 receptor in a biological sample by

[0045] a) contacting the biological sample with at least one ligand of the invention so that the ligand forms a complex with the TIE-2 receptor; and

[0046] b) measuring the amount of the complex and thereby measuring the amount of the TIE-2 receptor in the biological sample.

[0047] The present invention also provides for the utilization of a TIE-2 ligand to support the survival and/or growth and/or differentiation of TIE-2 receptor expressing cells. Thus, the ligand may be used as a supplement to support, for example, endothelial cells in culture.

[0048] Further, the discovery by applicants of a cognate ligand for the TIE-2 receptor enables the utilization of assay systems useful for the identification of agonists or antagonists of the TIE-2 receptor. Such assay systems would be useful in identifying molecules capable of promoting or inhibiting angiogenesis. For example, in one embodiment, antagonists of the TIE-2 receptor may be identified as test molecules that are capable of interfering with the interaction of the TIE-2 receptor with a biologically active TIE-2 ligand. Such antagonists are identified by their ability to 1) block the binding of a biologically active TIE-2 ligand to the receptor as measured, for example, using BIAcore biosensor technology (BIAcore; Pharmacia Biosensor, Piscataway, N.J.); or 2) block the ability of a biologically active TIE-2 ligand to cause a biological response. Such biological responses include, but are not limited to, phosphorylation of the TIE-2 receptor or downstream components of the TIE-2 signal transduction pathway, or survival, growth or differentiation of TIE-2 receptor bearing cells.

[0049] In one embodiment, cells engineered to express the TIE-2 receptor may be dependent for growth on the addition of TIE-2 ligand. Such cells provide useful assay systems for identifying additional agonists of the TIE-2 receptor, or antagonists capable of interfering with the activity of TIE-2 ligand on such cells. Alternatively, autocrine cells, engineered to be capable of co-expressing both TIE-2 ligand and receptor, may provide useful systems for assaying potential agonists or antagonists.

[0050] Therefore, the present invention provides for introduction of the TIE-2 receptor into cells that do not normally express this receptor, thus allowing these cells to exhibit profound and easily distinguishable responses to a ligand which binds this receptor. The type of response elicited depends on the cell utilized, and not the specific receptor introduced into the cell. Appropriate cell lines can be chosen to yield a response of the greatest utility for assaying, as well as discovering, molecules that can act on tyrosine kinase receptors. The molecules may be any type of molecule, including but not limited to peptide and non-peptide molecules, that will act in systems to be described in a receptor specific manner.

[0051] One of the more useful systems to be exploited involves the introduction of the TIE-2 receptor into a fibroblast cell line (e.g., NIH3T3 cells) thus such a receptor which does not normally mediate proliferative responses can, following introduction into fibroblasts, nonetheless be assayed by a variety of well established methods to quan-

titate effects of fibroblast growth factors (e.g. thymidine incorporation or other types of proliferation assays; see van Zoelen, 1990, "The Use of Biological Assays For Detection Of Polypeptide Growth Factors" in *Progress Factor Research*, Vol. 2, pp. 131-152; Zhan and M. Goldfarb, 1986, *Mol. Cell. Biol.*, Vol. 6, pp. 3541-3544). These assays have the added advantage that any preparation can be assayed both on the cell line having the introduced receptor as well as the parental cell line lacking the receptor; only specific effects on the cell line with the receptor would be judged as being mediated through the introduced receptor. Such cells may be further engineered to express the TIE-2 ligand, thus creating an autocrine system useful for assaying for molecules that act as antagonists/agonists of this interaction. Thus, the present invention provides for host cells comprising nucleic acid encoding TIE-2 ligand and nucleic acid encoding TIE-2 receptor.

[0052] The TIE-2 receptor/TIE-2 ligand interaction also provides a useful system for identifying small molecule agonists or antagonists of the TIE-2 receptor. For example, fragments, mutants or derivatives of a TIE-2 ligand may be identified that bind the TIE-2 receptor but do not induce biological activity. Alternatively, the characterization of a TIE-2 ligand enables the determination of active portions of the molecule. Further, the identification of a ligand enables the determination of the X-ray crystal structure of the receptor/ligand complex, thus enabling identification of the binding site on the receptor. Knowledge of the binding site will provide useful insight into the rational design of novel agonists and antagonists.

[0053] The specific binding of a test molecule to the TIE-2 receptor may be measured in a number of ways. For example, the actual binding of test molecule to cells expressing tie-2 may be detected or measured, by detecting or measuring (i) test molecule bound to the surface of intact cells; (ii) test molecule cross-linked to TIE-2 protein in cell lysates; or (iii) test molecule bound to TIE-2 in vitro. The specific interaction between test molecule and TIE-2 may be evaluated by using reagents that demonstrate the unique properties of that interaction.

[0054] As a specific, nonlimiting example, the methods of the invention may be used as follows. Consider a case in which the TIE-2 ligand in a sample is to be measured. Varying dilutions of the sample (the test molecule), in parallel with a negative control (NC) containing no TIE-2 ligand activity, and a positive control (PC) containing a known amount of a TIE-2 ligand, may be exposed to cells that express tie-2 in the presence of a detectably labeled TIE-2 ligand (in this example, radioiodinated ligand). The amount of TIE-2 ligand in the test sample may be evaluated by determining the amount of ^{125}I -labeled TIE-2 ligand that binds to the controls and in each of the dilutions, and then comparing the sample values to a standard curve. The more TIE-2 ligand in the sample, the less ^{125}I -ligand that will bind to TIE-2.

[0055] The amount of ^{125}I -ligand bound may be determined by measuring the amount of radioactivity per cell, or by cross-linking the TIE-2 ligand to cell surface proteins using DSS, as described in Meakin and Shooter, 1991, *Neuron* 6:153-163, and detecting the amount of labeled protein in cell extracts using, for example, SDS polyacrylamide gel electrophoresis, which may reveal a labeled

protein having a size corresponding to TIE-2 ligand/TIE-2 receptor. The specific test molecule/TIE-2 interaction may further be tested by adding to the assays various dilutions of an unlabeled control ligand that does not bind the TIE-2 receptor and therefore should have no substantial affect on the competition between labeled TIE-2 ligand and test molecule for TIE-2 binding. Alternatively, a molecule known to be able to disrupt TIE-2 ligand/TIE-2 binding, such as, but not limited to, anti-TIE-2 antibody, or TIE-2 receptorbody as described herein, may be expected to interfere with the competition between ^{125}I -TIE-2 ligand and test molecule for TIE-2 receptor binding.

[0056] Detectably labeled TIE-2 ligand includes, but is not limited to, TIE-2 ligand linked covalently or noncovalently to a radioactive substance, a fluorescent substance, a substance that has enzymatic activity, a substance that may serve as a substrate for an enzyme (enzymes and substrates associated with calorimetrically detectable reactions are preferred) or to a substance that can be recognized by an antibody molecule that is preferably a detectably labeled antibody molecule.

[0057] Alternatively, the specific binding of test molecule to TIE-2 may be measured by evaluating the secondary biological effects of TIE-2 ligand/TIE-2 receptor binding, including, but not limited to, cell growth and/or differentiation or immediate early gene expression or phosphorylation of TIE-2. For example, the ability of the test molecule to induce differentiation can be tested in cells that lack tie-2 and in comparable cells that express tie-2; differentiation in tie-2-expressing cells but not in comparable cells that lack tie-2 would be indicative of a specific test molecule/TIE-2 interaction. A similar analysis could be performed by detecting immediate early gene (e.g. fos and jun) induction in tie-2-minus and tie-2-plus cells, or by detecting phosphorylation of TIE-2 using standard phosphorylation assays known in the art. Such analysis might be useful in identifying agonists or antagonists that do not competitively bind to TIE-2.

[0058] Similarly, the present invention provides for a method of identifying an molecule that has the biological activity of a TIE-2 ligand comprising (i) exposing a cell that expresses tie-2 to a test molecule and (ii) detecting the specific binding of the test molecule to TIE-2 receptor, in which specific binding to TIE-2 positively correlates with TIE-2 like activity. Specific binding may be detected by either assaying for direct binding or the secondary biological effects of binding, as discussed supra. Such a method may be particularly useful in identifying new members of the TIE ligand family or, in the pharmaceutical industry, in screening a large array of peptide and non-peptide molecules (e.g., peptidomimetics) for TIE associated biological activity. In a preferred, specific, nonlimiting embodiment of the invention, a large grid of culture wells may be prepared that contain, in alternate rows, PC12 (or fibroblasts, see infra) cells that are either tie-2-minus or engineered to be tie-2-plus. A variety of test molecules may then be added such that each column of the grid, or a portion thereof, contains a different test molecule. Each well could then be scored for the presence or absence of growth and/or differentiation. An extremely large number of test molecules could be screened for such activity in this manner.

[0059] In additional embodiments, the invention provides for methods of detecting or measuring TIE-like activity or

identifying a molecule as having such activity comprising (i) exposing a test molecule to a TIE-2 receptor protein in vitro under conditions that permit binding to occur and (ii) detecting binding of the test molecule to the TIE-2 protein, in which binding of test molecule to TIE-2 correlates with TIE-like activity. According to such methods, the TIE-2 may or may not be substantially purified, may be affixed to a solid support (e.g. as an affinity column or as an ELISA assay), or may be incorporated into an artificial membrane. Binding of test molecule to TIE-2 may be evaluated by any method known in the art. In preferred embodiments, the binding of test molecule may be detected or measured by evaluating its ability to compete with detectably labeled known TIE-2 ligands for TIE-2 receptor binding.

[0060] The present invention also provides for a method of detecting the ability of a test molecule to function as an antagonist of TIE-like activity comprising detecting the ability of the molecule to inhibit an effect of TIE ligand binding to TIE-2 on a cell that expresses tie-2. Such an antagonist may or may not interfere with TIE-2 ligand/TIE-2 receptor binding. Effects of TIE-2 ligand binding to TIE-2 receptor are preferably biological or biochemical effects, including, but not limited to, cell survival or proliferation, cell transformation, immediate early gene induction, or TIE-2 phosphorylation.

[0061] The invention further provides for both a method of identifying antibodies or other molecules capable of neutralizing the ligand or blocking binding to the receptor, as well as the molecules identified by the method. By way of nonlimiting example, the method may be performed via an assay which is conceptually similar to an ELISA assay. For example, TIE receptorbody may be bound to a solid support, such as a plastic multiwell plate. As a control, a known amount of TIE ligand which has been Myc-tagged may then be introduced to the well and any tagged TIE ligand which binds the receptorbody may then be identified by means of a reporter antibody directed against the Myc-tag. This assay system may then be used to screen test samples for molecules which are capable of i) binding to the tagged ligand or ii) binding to the receptorbody and thereby blocking binding to the receptorbody by the tagged ligand. For example, a test sample containing a putative molecule of interest together with a known amount of tagged ligand may be introduced to the well and the amount of tagged ligand which binds to the receptorbody may be measured. By comparing the amount of bound tagged ligand in the test sample to the amount in the control, samples containing molecules which are capable of blocking ligand binding to the receptor may be identified. The molecules of interest thus identified may be isolated using methods well known to one of skill in the art.

[0062] Once a blocker of ligand binding is found, one of skill in the art would know to perform secondary assays to determine whether the blocker is binding to the receptor or to the ligand, as well as assays to determine if the blocker molecule can neutralize the biological activity of the ligand. For example, by using a binding assay which employs BIAcore biosensor technology (or the equivalent), in which either TIE receptorbody or TIE ligand is covalently attached to a solid support (e.g. carboxymethyl dextran on a gold surface), one of skill in the art would be able to determine if the blocker molecule is binding specifically to the ligand or to the receptorbody. To determine if the blocker molecule

can neutralize the biological activity of the ligand, one of skill in the art could perform a phosphorylation assay (see Example 5) or alternatively, a functional bioassay, such as a survival assay, by using primary cultures of, for example, endothelial cells. Alternatively, a blocker molecule which binds to the receptorbody could be an agonist and one of skill in the art would know to how to determine this by performing an appropriate assay for identifying additional agonists of the TIE-2 receptor.

[0063] Because TIE-2 receptor has been identified in association with endothelial cells and, as demonstrated herein, blocking of the ligand appears to prevent vascularization, applicants have demonstrated that the TIE-2 ligand will be useful for the induction of vascularization in diseases or disorders where such vascularization is indicated. Such diseases or disorders would include wound healing, ischaemia and diabetes. On the other hand, antagonists of the TIE-2 receptor, such as receptorbodies as described herein in Examples 2 and 3, and TIE-2 ligand 2 as described in Example 9, would be useful to prevent or attenuate vascularization, thus preventing or attenuating, for example, tumor growth.

[0064] The present invention also provides for pharmaceutical compositions comprising the TIE-2 ligands described herein, peptide fragments thereof, or derivatives in a pharmacologically acceptable vehicle. The TIE-2 ligand proteins, peptide fragments, or derivatives may be administered systemically or locally. Any appropriate mode of administration known in the art may be used, including, but not limited to, intravenous, intrathecal, intraarterial, intranasal, oral, subcutaneous, intraperitoneal, or by local injection or surgical implant. Sustained release formulations are also provided for.

[0065] The present invention further provides for an isolated and purified nucleic acid molecule comprising a nucleic acid sequence encoding a human TIE-2 ligand, wherein the nucleic acid sequence is selected from the group consisting of:

[0066] (a) the nucleic acid sequence comprising the coding region of the human TIE-2 ligand as set forth in **FIG. 6**;

[0067] (b) a nucleic acid sequence that hybridizes under moderately stringent conditions to the nucleic acid sequence of (a) and which encodes a TIE-2 ligand that binds TIE-2 receptor; and

[0068] (c) a nucleic acid sequence that is degenerate as a result of the genetic code to a nucleic acid sequence of (a) or (b), and which encodes a TIE-2 ligand that binds TIE-2 receptor.

[0069] The present invention further provides for an isolated and purified human TIE-2 ligand encoded by an isolated nucleic acid molecule of the invention. The invention also provides a vector which comprises an isolated nucleic acid molecule comprising a nucleic acid sequence encoding a human TIE-2 ligand. In one embodiment, the vector is designated as pBluescript KS encoding human TIE 2 ligand 2.

[0070] The invention further provides for an expression vector comprising a DNA molecule encoding a human TIE-2 ligand, wherein the DNA molecule is operatively

linked to an expression control sequence. The invention also provides a host-vector system for the production of a polypeptide having the biological activity of a human TIE-2 ligand which comprises the expression vector of the invention in a suitable host cell. In one embodiment, the suitable host cell may be a bacterial cell, yeast cell, insect cell, or mammalian cell. The invention further provides for a method of producing a polypeptide having the activity of a biologically active TIE-2 ligand which comprises growing cells of the host-vector system of the invention, under conditions permitting production of the polypeptide and recovering the polypeptide so produced.

[0071] The invention herein described of an isolated nucleic acid molecule encoding a TIE-2 ligand further provides for the development of the ligand, a fragment or derivative thereof, or another molecule which is a receptor agonist or antagonist, as a therapeutic for the treatment of patients suffering from disorders involving cells, tissues or organs which express the TIE receptor. The present invention also provides for an antibody which specifically binds such a therapeutic molecule. The antibody may be monoclonal or polyclonal. The invention also provides for a method of using such a monoclonal or polyclonal antibody to measure the amount of the therapeutic molecule in a sample taken from a patient for purposes of monitoring the course of therapy.

[0072] The invention further provides for a therapeutic composition comprising a human TIE-2 ligand and a cytotoxic agent conjugated thereto. In one embodiment, the cytotoxic agent may be a radioisotope or toxin.

[0073] The invention also provides for an antibody which specifically binds a human TIE-2 ligand. The antibody may be monoclonal or polyclonal. The invention further provides for a method of purifying a human TIE-2 ligand comprising:

- [0074]** a) coupling at least one TIE-2 binding substrate to a solid matrix;
- [0075]** b) incubating the substrate of a) with a cell lysate so that the substrate forms a complex with any human TIE-2 ligand in the cell lysate;
- [0076]** c) washing the solid matrix; and
- [0077]** d) eluting the human TIE-2 ligand from the coupled substrate.

[0078] The substrate may be any substance that specifically binds the human TIE-2 ligand. In one embodiment, the substrate is selected from the group consisting of anti-TIE-2 ligand antibody, TIE-2 receptor and TIE-2 receptorbody. The invention further provides for a receptorbody which specifically binds a human TIE-2 ligand, as well as a therapeutic composition comprising the receptorbody in a pharmaceutically acceptable vehicle, and a method of blocking blood vessel growth in a human comprising administering an effective amount of the therapeutic composition.

[0079] The invention also provides for a therapeutic composition comprising a human TIE-2 ligand in a pharmaceutically acceptable vehicle, as well as a method of promoting neovascularization in a patient comprising administering to the patient an effective amount of the therapeutic composition.

[0080] In addition, the present invention provides for a method for identifying a cell which expresses TIE-2 receptor

which comprises contacting a cell with a detectably labeled TIE-2 ligand, under conditions permitting binding of the detectably labeled ligand to the TIE-2 receptor and determining whether the detectably labeled ligand is bound to the TIE-2 receptor, thereby identifying the cell as one which expresses TIE-2 receptor. The present invention also provides for a therapeutic composition comprising a TIE-2 ligand and a cytotoxic agent conjugated thereto. The cytotoxic agent may be a radioisotope or toxin.

[0081] The invention also provides a method of detecting expression of TIE-2 ligand by a cell which comprises obtaining mRNA from the cell, contacting the mRNA so obtained with a labelled nucleic acid molecule encoding a TIE-2 ligand, under hybridizing conditions, determining the presence of mRNA hybridized to the labelled molecule, and thereby detecting the expression of the TIE-2 ligand in the cell.

[0082] The invention further provides a method of detecting expression of a TIE-2 ligand in tissue sections which comprises contacting the tissue sections with a labelled nucleic acid molecule encoding a TIE-2 ligand, under hybridizing conditions, determining the presence of mRNA hybridized to the labelled molecule, and thereby detecting the expression of the TIE-2 ligand in tissue sections.

EXAMPLE 1

Identification of the ABAE Cell Line as Reporter Cells for the TIE-2 Receptor

[0083] Adult BAE cells are registered in the European Cell Culture Repository, under ECACC#92010601. (See PNAS 75:2621 (1978)). Northern (RNA) analyses revealed moderate levels of tie-2 transcripts in the ABAE (Adult Bovine Arterial Endothelial) cell line, consistent with in situ hybridization results that demonstrated almost exclusive localization of tie-2 RNAs to vascular endothelial cells. We therefore examined ABAE cell lysates for the presence of TIE-2 protein, as well as the extent to which this TIE-2 protein is tyrosine-phosphorylated under normal versus serum-deprived growth conditions. ABAE cell lysates were harvested and subjected to immunoprecipitation, followed by Western blot analyses of immunoprecipitated proteins with TIE-2 specific and phosphotyrosine-specific antisera. Omission or inclusion of TIE-2 peptides as specific blocking molecules during TIE-2 immunoprecipitation allowed unambiguous identification of TIE-2 as a moderately detectable protein of ~150 kD whose steady-state phosphotyrosine levels diminish to near undetectable levels by prior serum-starvation of the cells.

[0084] Culture of ABAE cells and harvest of cell lysates was done as follows. Low-passage-number ABAE cells were plated as a monolayer at a density of 2×10^6 cells/150 mm plastic petri plate (Falcon) and cultured in Dulbecco's modified Eagle's medium (DMEM) containing 10% bovine calf serum (10% BCS), 2 mM L-glutamine (Q) and 1% each of penicillin and streptomycin (P-S) in an atmosphere of 5% CO₂. Prior to harvest of cell lysates, cells were serum-starved for 24 hours in DMEM/Q/P-S, followed by aspiration of the medium and rinsing of the plates with ice-cold phosphate buffered saline (PBS) supplemented with sodium orthovanadate, sodium fluoride and sodium benzamide. Cells were lysed in a small volume of this rinse buffer that

had been supplemented with 1% NP40 detergent and the protease inhibitors, PMSF and aprotinin. Insoluble debris was removed from the cell lysates by centrifugation at 14,000×G for 10 minutes, at 4° C. and the supernatants were subjected to immune-precipitation with antisera specific for TIE-2 receptor, with or without the presence of blocking peptides added to ~20 µg/ml lysate. Immunoprecipitated proteins were resolved by PAGE (7.5% Laemmli gel), and then electro-transferred to PVDF membrane and incubated either with various TIE-2- or phosphotyrosine-specific antisera. TIE-2-protein was visualized by incubation of the membrane with HRP-linked secondary antisera followed by treatment with ECL reagent (Amersham).

EXAMPLE 2

Cloning and Expression of TIE-2 Receptorbody for Affinity-based Study of TIE-2 Ligand Interactions

[0085] An expression construct was created that would yield a secreted protein consisting of the entire extracellular portion of the rat TIE-2 receptor fused to the human immunoglobulin gamma-1 constant region (IgG1 Fc). This fusion protein is called a TIE-2 “receptorbody” (RB), and would be normally expected to exist as a dimer in solution based on formation of disulfide linkages between individual IgG1 Fc tails. The Fc portion of the TIE-2 RB was prepared as follows. A DNA fragment encoding the Fc portion of human IgG1 that spans from the hinge region to the carboxy-terminus of the protein, was amplified from human placental cDNA by PCR with oligonucleotides corresponding to the published sequence of human IgG1; the resulting DNA fragment was cloned in a plasmid vector. Appropriate DNA restriction fragments from a plasmid encoding the full-length TIE-2 receptor and from the human IgG1 Fc plasmid were ligated on either side of a short PCR-derived fragment that was designed so as to fuse, in-frame, the TIE-2 and human IgG1 Fc protein-coding sequences. Thus, the resulting TIE-2 ectodomain-Fc fusion protein precisely substituted the IgG1 Fc in place of the region spanning the TIE-2 transmembrane and cytoplasmic domains. An alternative method of preparing RBs is described in Goodwin, et. al. Cell 73:447-456 (1993).

[0086] Milligram quantities of TIE-2 RB were obtained by cloning the TIE-2 RB DNA fragment into the pVL1393 baculovirus vector and subsequently infecting the *Spodoptera frugiperda* SF-21AE insect cell line. Alternatively, the cell line SF-9 (ATCC Accession No. CRL-1711) or the cell line BTI-TN-5b1-4 may be used. DNA encoding the TIE-2 RB was cloned as an Eco RI-NotI fragment into the baculovirus transfer plasmid pVL1393. Plasmid DNA purified by cesium chloride density gradient centrifugation was recombined into viral DNA by mixing 3 µg of plasmid DNA with 0.5 µg of Baculo-Gold DNA (Pharminigen), followed by introduction into liposomes using 30 µg Lipofectin (GIBCO-BRL). DNA-liposome mixtures were added to SF-21AE cells (2×10⁶ cells/60 mm dish) in TMN-FH medium (Modified Grace's Insect Cell Medium (GIBCO-BRL) for 5 hours at 27° C., followed by incubation at 27° C. for 5 days in TMN-FH medium supplemented with 5% fetal calf serum. Tissue culture medium was harvested for plaque purification of recombinant viruses, which was carried out using methods previously described (O'Reilly, D. R., L. K. Miller, and V. A. Luckow, *Baculovirus Expression*

Vectors—A Laboratory Manual. 1992, New York: W. H. Freeman) except that the agarose overlay contained 125 µg/mL X-gal (5-bromo-4-chloro-3-indolyl-β-D-galactopyranoside; GIBCO-BRL). After 5 days of incubation at 27° C., non-recombinant plaques were scored by positive chromogenic reaction to the X-gal substrate, and their positions marked. Recombinant plaques were then visualized by addition of a second overlay containing 100 µg/mL MTT (3-[4, 5-dimethylthiazol-2-yl]2,5-diphenyltetrazolium bromide; Sigma). Putative recombinant virus plaques were picked by plug aspiration, and purified by multiple rounds of plaque isolation to assure homogeneity. Virus stocks were generated by serial, low-multiplicity passage of plaque-purified virus. Low passage stocks of one virus clone (vTIE-2 receptor body) were produced.

[0087] SF-21AE cells were cultured in serum free medium (SF-900 II, Gibco BRL) containing 1×antibiotic/antimycotic solution (Gibco BRL) and 25 mg/L Gentamycin (Gibco BRL). Pluronic F-68 was added as a surfactant to a final concentration of 1 g/L. Cultures (4 L) were raised in a bioreactor (Artisan Cell Station System) for at least three days prior to infection. Cells were grown at 27° C., with gassing to 50% dissolved oxygen, at a gas flow rate of 80 mL/min (aeration at a sparge ring). Agitation was by means of a marine impeller at a rate of 100 rpm. Cells were harvested in mid-logarithmic growth phase (~2×10⁶ cells per mL), concentrated by centrifugation, and infected with 5 plaque forming units of vTIE-2 Receptor Body per cell. Cells and inoculum were brought to 400 mL with fresh medium, and virus was adsorbed for 2 hours at 27° C. in a spinner flask. The culture was then resuspended in a final volume of 8 L with fresh serum-free medium, and the cells incubated in the bioreactor using the previously described conditions. Culture medium from vTIE-2 Receptor Body-infected SF21AE cells were collected by centrifugation (500×g, 10 minutes) at 72 hours post-infection. Cell supernatants were brought to pH 8 with NaOH. EDTA was added to a final concentration of 10 mM and the supernatant pH was readjusted to 8. Supernatants were filtered (0.45 µm, Millipore) and loaded on a protein A column (protein A sepharose 4 fast flow or HiTrap protein A, both from Pharmacia). The column was washed with PBS containing 0.5 M NaCl until the absorbance at 280 nm decreased to baseline. The column was washed in PBS and eluted with 0.5 M acetic acid. Column fractions were immediately neutralized by eluting into tubes containing 1 M Tris pH 9. The peak fractions containing the TIE-2 RB were pooled and dialyzed versus PBS.

EXAMPLE 3

Demonstration that TIE-2 has a Critical Role in Development of the Vasculature

[0088] Given the absence of a known ligand for TIE-2 receptor, it was reasoned that it might be possible to gain insight into the function of TIE-2 by introduction of “excess” soluble TIE-2 receptor body (TIE-2 RB) into a developing system. The potential ability of TIE-2 RB to bind, and thereby neutralize, available TIE-2 ligand could result in an observable disruption of normal vascular development and characterization of the ligand. To examine whether TIE-2 RB could be used to disrupt vascular development in early chick embryos, small pieces of a biologi-

cally resorbable foam were soaked with TIE-2 RB and inserted immediately beneath the chorioallantoic membrane at positions just lateral to the primitive embryo.

[0089] Early chicken embryos develop atop the yolk from a small disk of cells that is covered by the chorioallantoic membrane (CAM). The endothelial cells that will come to line the vasculature in the embryo arise from both extra- and intra-embryonic cell sources. Extraembryonically-derived endothelial cells, which provide the major source for endothelial cells in the embryo, originate from accretions of mesenchyme that are situated laterally around the embryo-proper, just underneath the CAM. As these mesenchyme cells mature, they give rise to a common progenitor of both the endothelial and hematopoietic cell lineages, termed the hemangioblast. In turn, the hemangioblast gives rise to a mixed population of angioblasts (the endothelial cell progenitor) and hematoblasts (the pluripotent hematopoietic precursor). Formation of rudiments of the circulatory system begins when endothelial cell progeny segregate to form a one-cell-thick vesicle that surrounds the primitive blood cells. Proliferation and migration of these cellular components eventually produces a vast network of blood-filled microvessels under the CAM that will ultimately invade the embryo to join with limited, intraembryonically-derived vascular elements.

[0090] Newly fertilized chicken eggs obtained from Spafas, Inc. (Boston, Mass.) were incubated at 99.5° F., 55% RH. At about 24 hrs. of development, the egg shell was wiped down with 70% ethanol and a dentist's drill was used to make a 1.5 cm. hole in the blunt apex of each egg. The shell membrane was removed to reveal an air space directly above the embryo. Small rectangular pieces of sterile Gelfoam (Upjohn) were cut with a scalpel and soaked in equal concentrations of either TIE-2- or EHK-1 receptorbody. EHK-1 receptorbody was made as set forth in Example 2 using the EHK-1 extracellular domain instead of the TIE-2 extracellular domain (Maisonpierre et al., *Oncogene* 8:3277-3288 (1993). Each Gelfoam piece absorbed approximately 6 μ g of protein in 30 μ l. Sterile watchmakers forceps were used to make a small tear in the CAM at a position several millimeters lateral to the primitive embryo. The majority of the piece of RB-soaked Gelfoam was inserted under the CAM and the egg shell was sealed over with a piece of adhesive tape. Other similarly-staged eggs were treated in parallel with RB of the unrelated, neuronally expressed receptor tyrosine kinase, EHK-1 (Maisonpierre et al., *Oncogene* 8:3277-3288 (1993). Development was allowed to proceed for 4 days and then the embryos were examined by visual inspection. Embryos were removed by carefully breaking the shells in dishes of warmed PBS and carefully cutting away the embryo with surrounding CAM. Of 12 eggs treated with each RB, 6 TIE-2 RB and 5 EHK-1 RB treated embryos had developed beyond the stage observed at the start of the experiment. A dramatic difference was seen between these developed embryos, as shown in **FIGS. 1A and 1B**. Those treated with EHK-1 RB appeared to have developed relatively normally. Four out of five EHK-1 embryos were viable as judged by the presence of a beating heart. Furthermore, the extra-embryonic vasculature, which is visually obvious due to the presence of red blood cells, was profuse and extended several centimeters laterally under the CAM. By contrast, those treated with TIE-2 RB were severely stunted, ranging from 2-5 mm. in diameter, as compared with more than 10 mm. in diameter for the EHK-1

RB embryos. All of the TIE-2 RB treated embryos were dead and their CAMs were devoid of blood vessels. The ability of TIE-2 RB to block vascular development in the chicken demonstrates that TIE-2 ligand is necessary for development of the vasculature.

EXAMPLE 4

Identification of a TIE-2-Specific Binding Activity in Conditioned Medium from the ras Oncogene-Transformed C2C12 Mouse Myoblast Cell Line

[0091] Screening of ten-fold-concentrated cell-conditioned media (10 \times CCM) from various cell lines for the presence of soluble, TIE-2-specific binding activity (BIAcore; Pharmacia Biosensor, Piscataway, N.J.) revealed binding activity in serum-free medium from oncogenic-ras-transformed C2C12 cells (C2C12-ras), RAT 2-ras (which is a ras transformed fibroblast cell line), human glioblastoma T98G and the human neuroblastoma cell line known as SHEP-1.

[0092] The C2C12-ras 10 \times CCM originated from a stably-transfected line of C2C12 myoblasts that was oncogenically transformed by transfection with the T-24 mutant of H-ras by standard calcium phosphate-based methods. An SV40 based neomycin-resistance expression plasmid was physically linked with the ras expression plasmid in order to permit selection of transfected clones. Resulting G418-resistant ras-C2C12 cells were routinely maintained as a monolayer on plastic dishes in DMEM/glutamine/penicillin-streptomycin supplemented with 10% fetal calf serum (FCS). Serum-free C2C12-ras 10 \times CCM was made by plating the cells at 60% confluence in a serum free defined media for 12 hours. (Zhan and Goldfarb, *Mol. Cell. Biol.* 6: 3541-3544 (1986)); Zhan, et al. *Oncogene* 1: 369-376 (1987)). The medium was discarded and replaced with fresh DMEM/Q/P-S for 24 hours. This medium was harvested and cells were refed fresh DMEM/Q/P-S, which was also harvested after a further 24 hours. These CCM were supplemented with the protease inhibitors PMSF (1 mM) and aprotinin (10 μ g/ml), and ten-fold concentrated on sterile size-exclusion membranes (Amicon). TIE-2-binding activity could be neutralized by incubation of the medium with an excess of TIE-2 RB, but not by incubation with EHK-1 RB, prior to BIAcore analysis.

[0093] Binding activity of the 10 \times CCM was measured using biosensor technology (BIAcore; Pharmacia Biosensor, Piscataway, N.J.) which monitors biomolecular interactions in real-time via surface plasmon resonance. Purified TIE-2 RB was covalently coupled through primary amines to the carboxymethyl dextran layer of a CM5 research grade sensor chip (Pharmacia Biosensor; Piscataway, N.J.). The sensor chip surface was activated using a mixture of N-hydroxysuccinimide (NHS) and N-ethyl-N'-(3-dimethylaminopropyl)carbodiimide (EDC), followed by immobilization of TIE-2 RB (25 μ g/mL, pH 4.5) and deactivation of unreacted sites with 1.0 M ethanolamine (pH 8.5). A negative control surface of the EHK-1 receptorbody was prepared in a similar manner. The running buffer used in the system was HBS (10 mM Hepes, 3.4 mM edta, 150 mM NaCl, 0.005% P20 surfactant, pH 7.4). The 10 \times CCM samples were centrifuged for 15 min at 4 C. and further clarified using a sterile, low protein-binding 0.45 μ m filter

(Millipore; Bedford, Mass.). Dextran (2 mg/ml) and P20 surfactant (0.005%) were added to each CCM sample. Aliquots of 40 μ L were injected across the immobilized surface (either TIE-2 or EHK-1) at a flow rate of 5 μ L/min and the receptor binding was monitored for 8 min. The binding activity (resonance units, RU) was measured as the difference between a baseline value determined 30 s prior to the sample injection and a measurement taken at 30 s post-injection. Regeneration of the surface was accomplished with one 12- μ L pulse of 3 M $MgCl_2$. The instrument noise level is 20 RU; therefore, any binding activity with a signal above 20 RU may be interpreted as a real interaction with the receptor. For C2C12-ras conditioned media, the binding activities were in the range 60-90 RU for the TIE-2 RB immobilized surface. For the same samples assayed on a EHK-1 RB immobilized surface, the measured activities were less than 35 RU. Specific binding to the TIE-2 receptorbody was evaluated by incubating the samples with an excess of either soluble TIE-2 or EHK-1 RB prior to assaying the binding activity. The addition of soluble EHK-1 RB had no effect on the TIE-2 binding activity of any of the samples, while in the presence of soluble TIE-2 binding to the surface is two-thirds less than that measured in the absence of TIE-2. A repeat assay using >50 \times concentrated C2C12-ras CCM resulted in a four-fold enhancement over background of the TIE-2 specific binding signal.

EXAMPLE 5

C2C12-ras CCM Contains an Activity that Induces Tyrosine Phosphorylation of TIE-2 Receptor

[0094] C2C12-ras 10 \times CCM was examined for its ability to induce tyrosine phosphorylation of TIE-2 in ABAE cells. Serum-starved ABAE cells were briefly incubated with C2C12-ras CCM, lysed and subjected to immunoprecipitation and Western analyses as described above. Stimulation of serum-starved ABAE cells with serum-free C2C12-ras 10 \times CCM was done as follows. The medium of ABAE cells starved as described above was removed and replaced with either defined medium or 10 \times CCM that had been pre-warmed to 37 $^{\circ}$ C. After 10 minutes, the media were removed and the cells were twice rinsed on ice with an excess of chilled PBS supplemented with orthovanadate/NaF/benzamidine. Cell lysis and TIE-2-specific immunoprecipitation was done as described above.

[0095] ABAE cells incubated for 10 minutes with defined medium showed no induction of TIE-2 tyrosine phosphorylation, whereas incubation with C2C12-ras CCM stimulated at least a 100 \times increase in TIE-2 phosphorylation. This activity was almost totally depleted by pre-incubation of the C2C12-ras 10 \times CCM for 90 minutes at room temperature with 13 μ g of TIE-2 RB coupled to protein G-Sepharose beads. Medium incubated with protein G Sepharose alone was not depleted of this phosphorylating activity.

EXAMPLE 6

Expression Cloning of TIE-2 Ligand

[0096] COS-7 cells were cultured in Dulbecco's modified Eagle's medium (DMEM) containing 10% fetal bovine serum (FBS), 1% each of penicillin and streptomycin (P/S) and 2 mM glutamine in an atmosphere of 5% CO_2 . The mouse myoblast C2C12 ras cell line was cultured in Eagle's

minimal essential medium (EMEM) with 10% FBS, (P/S) and 2 mM glutamine. Full length mouse TIE-2 ligand cDNA clones were obtained by screening a C2C12 ras cDNA library in the pJFE14 vector expressed in COS cells. This vector, as shown in FIG. 2, is a modified version of the vector pSR $_{\alpha}$ (Takebe, et al. 1988, Mol. Cell. Biol. 8:466-472). The library was created using the two BSTX1 restriction sites in the pJFE14 vector.

[0097] COS-7 cells were transiently transfected with either the pJFE14 library or control vector by the DEAE-dextran transfection protocol. Briefly, COS-7 cells were plated at a density of 1.0×10^6 cells per 100 mm plate 24 hours prior to transfection. For transfection, the cells were cultured in serum-free DMEM containing 400 μ g/ml of DEAE-dextran, 1 μ M chloroquine, and 2 mM glutamine, and 1 μ g of the appropriate DNA for 3-4 hours at 37 $^{\circ}$ C. in an atmosphere of 5% CO_2 . The transfection media was aspirated and replaced with phosphate-buffered saline with 10% DMSO for 2-3 min. Following this DMSO "shock", the COS-7 cells were placed into DMEM with 10% FBS, 1% each of penicillin and streptomycin, and 2 mM glutamine for 48 hours. Because the TIE-2 ligand is secreted it was necessary to permeabilize the cells to detect binding of the receptorbody probe to the ligand. Two days after transfection the cells were rinsed with PBS and then incubated with PBS containing 1.8% formaldehyde for 15-30 min. at room temperature. Cells were then washed with PBS and incubated for 15 min. with PBS containing 0.1% Triton X-100 and 10% Bovine Calf Serum to permeabilize the cells and block non-specific binding sites. The screening was conducted by direct localization of staining using a TIE-2 receptorbody, which consisted of the extracellular domain of TIE-2 fused to the IgG1 constant region. This receptorbody was prepared as set forth in Example 2. A 100 mm dish of transfected, fixed and permeabilized COS cells was probed by incubating them for 30 min with TIE-2-RB. The cells were then washed twice with PBS and incubated for an additional 30 min with PBS/10% Bovine Calf Serum/anti-human IgG-alkaline phosphatase conjugate. After three PBS washes, cells were incubated in alkaline-phosphatase substrate for 30-60 min. The dish was then inspected microscopically for the presence of stained cells. For each stained cell, a small area of cells including the stained cell was scraped from the dish using a plastic pipette tip and plasmid DNA was then rescued and used to electroporate bacterial cells. Single bacterial colonies resulting from the electroporation were picked and plasmid DNA prepared from these colonies was used to transfect COS-7 cells which were probed for TIE-2 ligand expression as evidenced by binding to TIE-2 receptorbodies. This allowed identification of single clones coding for TIE-2 ligand. Confirmation of TIE-2 ligand expression was obtained by phosphorylation of the TIE-2 receptor using the method set forth in Example 5. A plasmid clone encoding the TIE-2 ligand was deposited with the ATCC on Oct. 7, 1994 and designated as "pJFE14 encoding TIE-2 ligand" under ATCC Accession No. 75910.

EXAMPLE 7

Isolation and Sequencing of Full Length cDNA Clone Encoding Human TIE-2 Ligand

[0098] A human fetal lung cDNA library in lambda gt-10 (see FIG. 3) was obtained from Clontech Laboratories, Inc.

(Palo Alto, Calif.). Plaques were plated at a density of $1.25 \times 10^6/20 \times 20$ cm plate, and replica filters taken following standard procedures (Sambrook, et al., *Molecular Cloning: A Laboratory Manual*, 2nd Ed., page 8.46, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.).

[0099] Isolation of human tie-2 ligand clones was carried out as follows. A 2.2 kb XhoI fragment from the deposited tie-2 ligand clone (ATCC NO. 75910—see Example 6 above) was labeled by random priming to a specific activity of approximately 5×10^8 cpm/ng. Hybridization was carried out at 65° C. in hybridization solution containing 0.5 mg/ml salmon sperm DNA. The filters were washed at 65° C. in 2×SSC, 0.1% SDS and exposed to Kodak XAR-5 film overnight at -70° C. Positive phage were plaque purified. High titre phage lysates of pure phage were used for isolation of DNA via a Qiagen column using standard techniques (Qiagen, Inc., Chatsworth, Calif., 1995 catalog, page 36). Phage DNA was digested with EcoRI to release the cloned cDNA fragment for subsequent subcloning. A lambda phage vector containing human tie-2 ligand DNA was deposited with the ATCC on Oct. 26, 1994 under the designation λ gt10 encoding htie-2 ligand 1 (ATCC Accession No. 75928). Phage DNA may be subjected directly to DNA sequence analysis by the dideoxy chain termination method (Sanger, et al., 1977, *Proc. Natl. Acad. Sci. U.S.A.* 74: 5463-5467).

[0100] Subcloning Human TIE-2 Ligand into a Mammalian Expression Vector

[0101] The clone λ gt10 encoding htie-2 ligand 1 contains an EcoRI site located 490 base pairs downstream from the start of the coding sequence for the human tie-2 ligand. The coding region may be excised using unique restriction sites upstream and downstream of the initiator and stop codons respectively. For example, an SpeI site, located 70 bp 5' to the initiator codon, and a Bpu1102i (also known as B1pI) site, located 265 bp 3' to the stop codon, may be used to excise the complete coding region. This may then be subcloned into the pJFE14 cloning vector, using the XbaI (compatible to the SpeI overhang) and the PstI sites (the PstI and Bpu1102i sites are both made blunt ended).

[0102] Sequencing of Human TIE-2 Ligand

[0103] The coding region from the clone λ gt10 encoding htie-2 ligand 1 was sequenced using the ABI 373A DNA sequencer and Taq Dyedexy Terminator Cycle Sequencing Kit (Applied Biosystems, Inc., Foster City, Calif.). The nucleotide and deduced amino acid sequence of human TIE-2 ligand from the clone λ gt10 encoding htie-2 ligand 1 is shown in **FIG. 4**.

[0104] In addition, full length human TIE-2 ligand cDNA clones were obtained by screening a human glioblastoma T98G cDNA library in the pJFE14 vector. Clones encoding human tie-2 ligand were identified by DNA hybridization using a 2.2 kb XhoI fragment from the deposited tie-2 ligand clone (ATCC NO. 75910) as a probe (see Example 6 above). The coding region was sequenced using the ABI 373A DNA sequencer and Taq Dyedexy Terminator Cycle Sequencing Kit (Applied Biosystems, Inc., Foster City, Calif.). This sequence was nearly identical to that of clone λ gt10 encoding htie-2 ligand 1. As shown in **FIG. 4**, the clone λ gt10 encoding htie-2 ligand 1 contains an additional glycine residue which is encoded by nucleotides 1114-1116. The

coding sequence of the T98G clone does not contain this glycine residue but otherwise is identical to the coding sequence of the clone λ gt10 encoding htie-2 ligand 1. **FIG. 5** sets forth the nucleotide and deduced amino acid sequence of human TIE-2 ligand from the T98G clone.

EXAMPLE 8

Isolation and Sequencing of Second Full Length cDNA Clone a Encoding Human TIE-2 Ligand

[0105] A human fetal lung cDNA library in lambda gt-10 (see **FIG. 3**) was obtained from Clontech Laboratories, Inc. (Palo Alto, Calif.). Plaques were plated at a density of $1.25 \times 10^6/20 \times 20$ cm plate, and replica filters taken following standard procedures (Sambrook, et al., *Molecular Cloning: A Laboratory Manual*, 2nd Ed., page 8.46, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.). Duplicate filters were screened at low stringency (2×SSC, 55° C.) with probes made to the human tie 2L-1 sequence. One of the duplicate filters was probed with a 5' probe, encoding amino acids 25-265 of human tie 2 L-1 as set forth in **FIG. 4**. The second duplicate filter was probed with a 3' probe, encoding amino acids 282-498 of human tie 2 L-1 sequence (see **FIG. 4**). Both probes were hybridized at 55 C. in hybridization solution containing 0.5 mg/ml salmon sperm DNA. Filters were washed in 2×SSC at 55° C. and exposed overnight to X-ray film. In addition, duplicate filters were also hybridized at normal stringency (2×SSC, 65° C.) to the full length coding probe of mouse tie2L (F3-15, XhoI insert). Three positive clones were picked that fulfilled the following criteria: i. hybridization had not been seen to the full length (mouse) probe at normal stringency, and ii. hybridization was seen at low stringency to both 5' and 3' probes. EcoRI digestion of phage DNA obtained from these clones indicated two independent clones with insert sizes of approximately 2.2 kb and approximately 1.8 kb. The 2.2 kb EcoRI insert was subcloned into the EcoRI sites of both pBluescript KS (Stratagene) and a mammalian expression vector suitable for use in COS cells. Two orientations were identified for the mammalian expression vector. The 2.2 kb insert in pBluescript KS was deposited with the ATCC on Dec. 9, 1994 and designated as pBluescript KS encoding human TIE 2 ligand 2. The start site of the TIE-2 ligand 2 coding sequence is approximately 355 base pairs downstream of the pBluescript EcoRI site.

[0106] COS-7 cells were transiently transfected with either the expression vector or control vector by the DEAE-dextran transfection protocol. Briefly, COS-7 cells were plated at a density of 1.0×10^6 cells per 100 mm plate 24 hours prior to transfection. For transfection, the cells were cultured in serum-free DMEM containing 400 μ g/ml of DEAE-dextran, 1 μ M chloroquine, and 2 mM glutamine, and 1 μ g of the appropriate DNA for 3-4 hours at 37° C. in an atmosphere of 5% CO₂. The transfection media was aspirated and replaced with phosphate-buffered saline with 10% DMSO for 2-3 min. Following this DMSO "shock", the COS-7 cells were placed into DMEM with 10% FBS, 1% each of penicillin and streptomycin, and 2 mM glutamine for 48 hours.

[0107] Because the TIE-2 ligand is secreted it was necessary to permeabilize the cells to detect binding of the receptorbody probe to the ligand. Transfected COS-7 cells were plated at a density of 1.0×10^6 cells per 100 mm plate.

The cells were rinsed with PBS and then incubated with PBS containing 1.8% formaldehyde for 15-30 min. at room temperature. Cells were then washed with PBS and incubated for 15 min. with PBS containing 0.1% Triton X-100 and 10% Bovine Calf Serum to permeabilize the cells and block non-specific binding sites. The screening was conducted by direct localization of staining using a TIE-2 receptorbody, which consisted of the extracellular domain of TIE-2 fused to the IgG1 constant region. This receptorbody was prepared as set forth in Example 2. Transfected COS cells were probed by incubating them for 30 min with TIE-2-RB. The cells were then washed twice with PBS, fixed with methanol, and then incubated for an additional 30 min with PBS/10% Bovine Calf Serum/anti-human IgG-alkaline phosphatase conjugate. After three PBS washes, cells were incubated in alkaline-phosphatase substrate for 30-60 min. The dish was then inspected microscopically for the presence of stained cells. Cells expressing one orientation of the clone, but not the other orientation, were seen to bind the TIE-2 receptor body.

[0108] One of skill in the art will readily see that the described methods may be used to further identify other related members of the TIE ligand family.

[0109] Sequencing of Second Human TIE-2 Ligand

[0110] The coding region from the clone pBluescript KS encoding human TIE-2 ligand 2 was sequenced using the ABI 373A DNA sequencer and Taq Dyedexy Terminator Cycle Sequencing Kit (Applied Biosystems, Inc., Foster City, Calif.). The nucleotide and deduced amino acid sequence of human TIE-2 ligand from the clone pBluescript KS encoding human TIE-2 ligand 2 is shown in **FIG. 6**.

EXAMPLE 9

TIE-2 Ligand 2 is a Receptor Antagonist

[0111] Conditioned media from COS cells expressing either TIE-2 ligand 2 (TL2) or TIE-2 ligand 1 (TL1) were compared for their ability to activate TIE-2 receptors naturally present in a human endothelial cell line.

[0112] Lipofectamine reagent (GIBCO-BRL, Inc.) and recommended protocols were used to transfect COS-7 cells with either the pJFE14 expression vector alone, pJFE14 vector containing the human TIE-2 ligand 1 cDNA, or with a pMT21 expression vector (Kaufman, R. J., 1985, Proc. Natl. Acad. Sci. USA 82: 689-693) containing the human TIE-2 ligand 2 cDNA. COS media containing secreted ligands were harvested after three days and concentrated 20-fold by diafiltration (DIAFLO ultrafiltration membranes, Amicon, Inc.). The quantity of active TIE-2 ligand 1 and TIE-2 ligand 2 present in these media was determined and expressed as the amount (in resonance units, R.U.) of TIE-2 receptor specific binding activity measured by a BIAcore binding assay.

[0113] Northern (RNA) analyses revealed significant levels of TIE-2 transcripts in HAEC (Human Aortic Endothelial Cell) human primary endothelial cells (Clonetics, Inc.). Therefore, these cells were used to examine whether TIE-2 receptor is tyrosine-phosphorylated when exposed to COS media containing the TIE-2 ligands. HAEC cells were maintained in a complete endothelial cell growth medium (Clonetics, Inc.) that contained 5% fetal bovine serum,

soluble bovine brain extract, 10 ng/ml human EGF, 1 mg/ml hydrocortisone, 50 mg/ml gentamicin and 50 ng/ml amphotericin-B. Assessment of whether TL1 and TL2 could activate TIE-2 receptor in the HAEC cells was done as follows. Semi-confluent HAEC cells were serum-starved for two hours in high-glucose Dulbecco's MEM with added L-glutamine and penicillin-streptomycin at 37° C. followed by replacement of the starvation medium with ligand-containing conditioned COS media for 7 minutes at 37° C. in a 5% CO₂ incubator. The cells were subsequently lysed and TIE-2 receptor protein was recovered by immunoprecipitation of the lysates with TIE-2 peptide antiserum, followed by Western blotting with antiphosphotyrosine antiserum, exactly as described in example 1. The results are shown in **FIG. 7**. Phosphotyrosine levels on the TIE-2 receptor (TIE2-R) were induced by treatment of HEAC cells with TIE-2 ligand 1 (Lane L1) but not by TIE-2 ligand 2 (Lane L2) conditioned COS media. MOCK is conditioned media from COS transfected with JFE14 empty vector.

[0114] Evidence that both TL1 and TL2 specifically bind to the TIE-2 receptor was demonstrated by using a BIAcore to assay the TIE-2 receptor specific binding activities in transfected COS media and by immunostaining of TL1- and TL2-expressing COS cells with TIE-2 receptorbodies.

[0115] Because TL2 did not activate the TIE-2 receptor, applicants set out to determine whether TL2 might be capable of serving as an antagonist of TL1 activity. HAEC phosphorylation assays were performed in which cells were first incubated with an "excess" of TL2, followed by addition of dilute TL1. It was reasoned that prior occupancy of TIE-2 receptor due to high levels of TL2 might prevent subsequent stimulation of the receptor following exposure to TL1 present at a limiting concentration.

[0116] Semi-confluent HAEC cells were serum-starved as described above and then incubated for 3 min., at 37° C. with 1-2 ml. of 20×COS/JFE14-TL2 conditioned medium. Control plates were treated with 20×COS/JFE14-only medium (MOCK). The plates were removed from the incubator and various dilutions of COS/JFE14-TL1 medium were then added, followed by further incubation of the plates for 5-7 min. at 37° C. Cells were subsequently rinsed, lysed and TIE-2-specific tyrosine phosphorylation in the lysates was examined by receptor immunoprecipitation and Western blotting, as described above. TL1 dilutions were made using 20×COS/JFE14-TL1 medium diluted to 2×, 0.5×, 0.1×, or 0.02× by addition of 20×COS/JFE14-alone medium. An assay of the initial 20×TL1 and 20×TL2 COS media using BIAcore biosensor technology indicated that they contained similar amounts of TIE-2-specific binding activities, i.e., 445 R.U. and 511 R.U. for TL1 and TL2, respectively. The results of the antiphosphotyrosine Western blot, shown in **FIG. 8**, indicate that when compared to prior treatment of HAEC cells with MOCK medium (lane 1), prior treatment of HAEC cells with excess TIE-2 ligand 2 (lane 2) antagonizes the subsequent ability of dilute TIE-2 ligand 1 to activate the TIE-2 receptor (TIE2-R).

[0117] These data indicate that, unlike TL1, TL2 was not able to stimulate TIE-2 receptor kinase activity in HAEC cells. Furthermore, pre-incubation of the endothelial cells with high concentrations of TL2 followed by addition of TL1 blocked the ability of TL1 to stimulate the TIE-2 receptor, indicating that TL2 is a TIE-2 receptor antagonist.

DEPOSITS

[0118] The following have been deposited with the American Type Culture Collection, 12301 Parklawn Drive, Rockville, Md. 20852 in accordance with the Budapest Treaty. A plasmid clone encoding a TIE-2 ligand was deposited with the ATCC on Oct. 7, 1994 and designated as "pJFE14 encoding TIE-2 ligand" under ATCC Accession No. 75910. Recombinant *Autographa californica* baculovirus encoding TIE-2 receptor body was deposited with the ATCC on Oct. 7, 1994 and designated as "vTIE-2 receptor body" under ATCC Accession No. VR2484. A lambda phage vector containing human tie-2 ligand DNA was deposited with the ATCC on Oct. 26, 1994 and designated as λ gt10 encoding

htie-2 ligand 1 under ATCC Accession No. 75928. A plasmid clone encoding a second TIE-2 ligand was deposited with the ATCC on Dec. 9, 1994 and designated as "pBluescript KS encoding human TIE 2 ligand 2" under ATCC Accession No. 75963.

[0119] The present invention is not to be limited in scope by the specific embodiments described herein. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(iii) NUMBER OF SEQUENCES: 6

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2149 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 310..1806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CAGCTGACTC AGGCAGGCTC CATGCTGAAC GGTCACACAG AGAGGAAACA ATAAATCTCA	60
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AAAATTTTAA AATTTTAGAA CAAAGCTAAC AAATGGCTAG TTTTCTATGA TTCTTCTTCA	180
AACGCTTTCT TTGAGGGGGA AAGAGTCAAA CAAACAAGCA GTTTTACCTG AAATAAAGAA	240
CTAGTTTITAG AGGTCAGAAG AAAGGAGCAA GTTTTGCGAG AGGCACGGAA GGAGTGTGCT	300
GGCAGTACA ATG ACA GTT TTC CTT TCC TTT GCT TTC CTC GCT GCC ATT	348
Met Thr Val Phe Leu Ser Phe Ala Phe Leu Ala Ala Ile	
1 5 10	
CTG ACT CAC ATA GGG TGC AGC AAT CAG CGC CGA AGT CCA GAA AAC AGT	396
Leu Thr His Ile Gly Cys Ser Asn Gln Arg Arg Ser Pro Glu Asn Ser	
15 20 25	
GGG AGA AGA TAT AAC CGG ATT CAA CAT GGG CAA TGT GCC TAC ACT TTC	444
Gly Arg Arg Tyr Asn Arg Ile Gln His Gly Gln Cys Ala Tyr Thr Phe	
30 35 40 45	
ATT CTT CCA GAA CAC GAT GGC AAC TGT CGT GAG AGT ACG ACA GAC CAG	492
Ile Leu Pro Glu His Asp Gly Asn Cys Arg Glu Ser Thr Thr Asp Gln	
50 55 60	
TAC AAC ACA AAC GCT CTG CAG AGA GAT GCT CCA CAC GTG GAA CCG GAT	540
Tyr Asn Thr Asn Ala Leu Gln Arg Asp Ala Pro His Val Glu Pro Asp	
65 70 75	
TTC TCT TCC CAG AAA CTT CAA CAT CTG GAA CAT GTG ATG GAA AAT TAT	588
Phe Ser Ser Gln Lys Leu Gln His Leu Glu His Val Met Glu Asn Tyr	
80 85 90	

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ACT	CAG	TGG	CTG	CAA	AAA	CTT	GAG	AAT	TAC	ATT	GTG	GAA	AAC	ATG	AAG	636
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95						100					105					
TCG	GAG	ATG	GCC	CAG	ATA	CAG	CAG	AAT	GCA	GTT	CAG	AAC	CAC	ACG	GCT	684
Ser	Glu	Met	Ala	Gln	Ile	Gln	Gln	Asn	Ala	Val	Gln	Asn	His	Thr	Ala	
110					115					120					125	
ACC	ATG	CTG	GAG	ATA	GGA	ACC	AGC	CTC	CTC	TCT	CAG	ACT	GCA	GAG	CAG	732
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					130					135					140	
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Arg	Leu	Glu	Ile	Gln	Leu	Leu	Glu	Asn	Ser	Leu	Ser	Thr	Tyr	Lys	Leu	
			160				165					170				
GAG	AAG	CAA	CTT	CTT	CAA	CAG	ACA	AAT	GAA	ATC	TTG	AAG	ATC	CAT	GAA	876
Glu	Lys	Gln	Leu	Leu	Gln	Gln	Thr	Asn	Glu	Ile	Leu	Lys	Ile	His	Glu	
	175					180					185					
AAA	AAC	AGT	TTA	TTA	GAA	CAT	AAA	ATC	TTA	GAA	ATG	GAA	GGA	AAA	CAC	924
Lys	Asn	Ser	Leu	Leu	Glu	His	Lys	Ile	Leu	Glu	Met	Glu	Gly	Lys	His	
190					195				200						205	
AAG	GAA	GAG	TTG	GAC	ACC	TTA	AAG	GAA	GAG	AAA	GAG	AAC	CTT	CAA	GGC	972
Lys	Glu	Glu	Leu	Asp	Thr	Leu	Lys	Glu	Glu	Lys	Glu	Asn	Leu	Gln	Gly	
			210					215						220		
TTG	GTT	ACT	CGT	CAA	ACA	TAT	ATA	ATC	CAG	GAG	CTG	GAA	AAG	CAA	TTA	1020
Leu	Val	Thr	Arg	Gln	Thr	Tyr	Ile	Ile	Gln	Glu	Leu	Glu	Lys	Gln	Leu	
			225					230					235			
AAC	AGA	GCT	ACC	ACC	AAC	AAC	AGT	GTC	CTT	CAG	AAG	CAG	CAA	CTG	GAG	1068
Asn	Arg	Ala	Thr	Thr	Asn	Asn	Ser	Val	Leu	Gln	Lys	Gln	Gln	Leu	Glu	
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CTG	ATG	GAC	ACA	GTC	CAC	AAC	CTT	GTC	AAT	CTT	TGC	ACT	AAA	GAA	GGT	1116
Leu	Met	Asp	Thr	Val	His	Asn	Leu	Val	Asn	Leu	Cys	Thr	Lys	Glu	Gly	
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GTT	TTA	CTA	AAG	GGA	GGA	AAA	AGA	GAG	GAA	GAG	AAA	CCA	TTT	AGA	GAC	1164
Val	Leu	Leu	Lys	Gly	Gly	Lys	Arg	Glu	Glu	Glu	Lys	Pro	Phe	Arg	Asp	
270					275					280					285	
TGT	GCA	GAT	GTA	TAT	CAA	GCT	GGT	TTT	AAT	AAA	AGT	GGA	ATC	TAC	ACT	1212
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Asp	Val	Asn	Gly	Gly	Gly	Trp	Thr	Val	Ile	Gln	His	Arg	Glu	Asp	Ala	
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AGT	CTA	GAT	TTC	CAA	AGA	GGC	TGG	AAG	GAA	TAT	AAA	ATG	GGT	TTT	GGA	1356
Ser	Leu	Asp	Phe	Gln	Arg	Gly	Trp	Lys	Glu	Tyr	Lys	Met	Gly	Phe	Gly	
			335			340					345					
AAT	CCC	TCC	GGT	GAA	TAT	TGG	CTG	GGG	AAT	GAG	TTT	ATT	TTT	GCC	ATT	1404
Asn	Pro	Ser	Gly	Glu	Tyr	Trp	Leu	Gly	Asn	Glu	Phe	Ile	Phe	Ala	Ile	
			350			355				360					365	
ACC	AGT	CAG	AGG	CAG	TAC	ATG	CTA	AGA	ATT	GAG	TTA	ATG	GAC	TGG	GAA	1452
Thr	Ser	Gln	Arg	Gln	Tyr	Met	Leu	Arg	Ile	Glu	Leu	Met	Asp	Trp	Glu	
					370				375					380		
GGG	AAC	CGA	GCC	TAT	TCA	CAG	TAT	GAC	AGA	TTC	CAC	ATA	GGA	AAT	GAA	1500
Gly	Asn	Arg	Ala	Tyr	Ser	Gln	Tyr	Asp	Arg	Phe	His	Ile	Gly	Asn	Glu	
			385					390					395			

-continued

AAG CAA AAC TAT AGG TTG TAT TTA AAA GGT CAC ACT GGG ACA GCA GGA Lys Gln Asn Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly	1548
400 405 410	
AAA CAG AGC AGC CTG ATC TTA CAC GGT GCT GAT TTC AGC ACT AAA GAT Lys Gln Ser Ser Leu Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp	1596
415 420 425	
GCT GAT AAT GAC AAC TGT ATG TGC AAA TGT GCC CTC ATG TTA ACA GGA Ala Asp Asn Asp Asn Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly	1644
430 435 440 445	
GGA TGG TGG TTT GAT GCT TGT GGC CCC TCC AAT CTA AAT GGA ATG TTC Gly Trp Trp Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe	1692
450 455 460	
TAT ACT GCG GGA CAA AAC CAT GGA AAA CTG AAT GGG ATA AAG TGG CAC Tyr Thr Ala Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys Trp His	1740
465 470 475	
TAC TTC AAA GGG CCC AGT TAC TCC TTA CGT TCC ACA ACT ATG ATG ATT Tyr Phe Lys Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr Met Met Ile	1788
480 485 490	
CGA CCT TTA GAT TTT TGA AAGCGCAATG TCAGAAGCGA TTATGAAAGC Arg Pro Leu Asp Phe *	1836
495	
AACAAAGAAA TCCGGAGAAG CTGCCAGGTG AGAAACTGTT TGAAACTTC AGAAGCAAAC	1896
AATATTGTCT CCCTTCCAGC AATAAGTGGT AGTTATGTGA AGTCACCAAG GTTCTTGACC	1956
GTGAATCTGG AGCCGTTTGA GTTCACAAGA GTCTCTACTT GGGGTGACAG TGCTCACGTG	2016
GCTCGACTAT AGAAAACTCC ACTGACTGTC GGGCTTTAAA AAGGGAAGAA ACTGCTGAGC	2076
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TATGGTTAAT TTC	2149

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Thr Val Phe Leu Ser Phe Ala Phe Leu Ala Ala Ile Leu Thr His 1 5 10 15	
Ile Gly Cys Ser Asn Gln Arg Arg Ser Pro Glu Asn Ser Gly Arg Arg 20 25 30	
Tyr Asn Arg Ile Gln His Gly Gln Cys Ala Tyr Thr Phe Ile Leu Pro 35 40 45	
Glu His Asp Gly Asn Cys Arg Glu Ser Thr Thr Asp Gln Tyr Asn Thr 50 55 60	
Asn Ala Leu Gln Arg Asp Ala Pro His Val Glu Pro Asp Phe Ser Ser 65 70 75 80	
Gln Lys Leu Gln His Leu Glu His Val Met Glu Asn Tyr Thr Gln Trp 85 90 95	
Leu Gln Lys Leu Glu Asn Tyr Ile Val Glu Asn Met Lys Ser Glu Met 100 105 110	
Ala Gln Ile Gln Gln Asn Ala Val Gln Asn His Thr Ala Thr Met Leu 115 120 125	

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Glu	Ile	Gly	Thr	Ser	Leu	Leu	Ser	Gln	Thr	Ala	Glu	Gln	Thr	Arg	Lys
130						135					140				
Leu	Thr	Asp	Val	Glu	Thr	Gln	Val	Leu	Asn	Gln	Thr	Ser	Arg	Leu	Glu
145					150					155					160
Ile	Gln	Leu	Leu	Glu	Asn	Ser	Leu	Ser	Thr	Tyr	Lys	Leu	Glu	Lys	Gln
				165					170					175	
Leu	Leu	Gln	Gln	Thr	Asn	Glu	Ile	Leu	Lys	Ile	His	Glu	Lys	Asn	Ser
				180				185					190		
Leu	Leu	Glu	His	Lys	Ile	Leu	Glu	Met	Glu	Gly	Lys	His	Lys	Glu	Glu
		195					200					205			
Leu	Asp	Thr	Leu	Lys	Glu	Glu	Lys	Glu	Asn	Leu	Gln	Gly	Leu	Val	Thr
	210					215					220				
Arg	Gln	Thr	Tyr	Ile	Ile	Gln	Glu	Leu	Glu	Lys	Gln	Leu	Asn	Arg	Ala
225					230					235					240
Thr	Thr	Asn	Asn	Ser	Val	Leu	Gln	Lys	Gln	Gln	Leu	Glu	Leu	Met	Asp
				245					250					255	
Thr	Val	His	Asn	Leu	Val	Asn	Leu	Cys	Thr	Lys	Glu	Gly	Val	Leu	Leu
			260					265					270		
Lys	Gly	Gly	Lys	Arg	Glu	Glu	Glu	Lys	Pro	Phe	Arg	Asp	Cys	Ala	Asp
		275					280					285			
Val	Tyr	Gln	Ala	Gly	Phe	Asn	Lys	Ser	Gly	Ile	Tyr	Thr	Ile	Tyr	Ile
	290					295					300				
Asn	Asn	Met	Pro	Glu	Pro	Lys	Lys	Val	Phe	Cys	Asn	Met	Asp	Val	Asn
305					310					315					320
Gly	Gly	Gly	Trp	Thr	Val	Ile	Gln	His	Arg	Glu	Asp	Ala	Ser	Leu	Asp
				325					330					335	
Phe	Gln	Arg	Gly	Trp	Lys	Glu	Tyr	Lys	Met	Gly	Phe	Gly	Asn	Pro	Ser
			340					345					350		
Gly	Glu	Tyr	Trp	Leu	Gly	Asn	Glu	Phe	Ile	Phe	Ala	Ile	Thr	Ser	Gln
		355					360					365			
Arg	Gln	Tyr	Met	Leu	Arg	Ile	Glu	Leu	Met	Asp	Trp	Glu	Gly	Asn	Arg
	370					375					380				
Ala	Tyr	Ser	Gln	Tyr	Asp	Arg	Phe	His	Ile	Gly	Asn	Glu	Lys	Gln	Asn
385					390					395					400
Tyr	Arg	Leu	Tyr	Leu	Lys	Gly	His	Thr	Gly	Thr	Ala	Gly	Lys	Gln	Ser
				405					410					415	
Ser	Leu	Ile	Leu	His	Gly	Ala	Asp	Phe	Ser	Thr	Lys	Asp	Ala	Asp	Asn
			420					425					430		
Asp	Asn	Cys	Met	Cys	Lys	Cys	Ala	Leu	Met	Leu	Thr	Gly	Gly	Trp	Trp
		435					440					445			
Phe	Asp	Ala	Cys	Gly	Pro	Ser	Asn	Leu	Asn	Gly	Met	Phe	Tyr	Thr	Ala
	450					455					460				
Gly	Gln	Asn	His	Gly	Lys	Leu	Asn	Gly	Ile	Lys	Trp	His	Tyr	Phe	Lys
465					470					475					480
Gly	Pro	Ser	Tyr	Ser	Leu	Arg	Ser	Thr	Thr	Met	Met	Ile	Arg	Pro	Leu
				485					490					495	

Asp Phe

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2146 base pairs

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(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 310..1803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CAGCTGACTC AGGCAGGCTC CATGCTGAAC GGTACACAG AGAGGAAACA ATAAATCTCA	60
GCTACTATGC AATAAATATC TCAAGTTTTC ACGAAGAAAA ACATCATTGC AGTGAAATAA	120
AAAATTTTAA AATTTTAGAA CAAAGCTAAC AAATGGCTAG TTTTCTATGA TTCTTCTTCA	180
AACGCTTTCT TTAGAGGGGA AAGAGTCAAA CAAACAAGCA GTTTTACCTG AAATAAAGAA	240
CTAGTTTTCAG AGGTCAGAAG AAAGGAGCAA GTTTTGCGAG AGGCACGGAA GGAGTGTGCT	300
GGCAGTACA ATG ACA GTT TTC CTT TCC TTT GCT TTC CTC GCT GCC ATT	348
Met Thr Val Phe Leu Ser Phe Ala Phe Leu Ala Ala Ile	
1 5 10	
CTG ACT CAC ATA GGG TGC AGC AAT CAG CGC CGA AGT CCA GAA AAC AGT	396
Leu Thr His Ile Gly Cys Ser Asn Gln Arg Arg Ser Pro Glu Asn Ser	
15 20 25	
GGG AGA AGA TAT AAC CGG ATT CAA CAT GGG CAA TGT GCC TAC ACT TTC	444
Gly Arg Arg Tyr Asn Arg Ile Gln His Gly Gln Cys Ala Tyr Thr Phe	
30 35 40 45	
ATT CTT CCA GAA CAC GAT GGC AAC TGT CGT GAG AGT ACG ACA GAC CAG	492
Ile Leu Pro Glu His Asp Gly Asn Cys Arg Glu Ser Thr Thr Asp Gln	
50 55 60	
TAC AAC ACA AAC GCT CTG CAG AGA GAT GCT CCA CAC GTG GAA CCG GAT	540
Tyr Asn Thr Asn Ala Leu Gln Arg Asp Ala Pro His Val Glu Pro Asp	
65 70 75	
TTC TCT TCC CAG AAA CTT CAA CAT CTG GAA CAT GTG ATG GAA AAT TAT	588
Phe Ser Ser Gln Lys Leu Gln His Leu Glu His Val Met Glu Asn Tyr	
80 85 90	
ACT CAG TGG CTG CAA AAA CTT GAG AAT TAC ATT GTG GAA AAC ATG AAG	636
Thr Gln Trp Leu Gln Lys Leu Glu Asn Tyr Ile Val Glu Asn Met Lys	
95 100 105	
TCG GAG ATG GCC CAG ATA CAG CAG AAT GCA GTT CAG AAC CAC ACG GCT	684
Ser Glu Met Ala Gln Ile Gln Gln Asn Ala Val Gln Asn His Thr Ala	
110 115 120 125	
ACC ATG CTG GAG ATA GGA ACC AGC CTC CTC TCT CAG ACT GCA GAG CAG	732
Thr Met Leu Glu Ile Gly Thr Ser Leu Leu Ser Gln Thr Ala Glu Gln	
130 135 140	
ACC AGA AAG CTG ACA GAT GTT GAG ACC CAG GTA CTA AAT CAA ACT TCT	780
Thr Arg Lys Leu Thr Asp Val Glu Thr Gln Val Leu Asn Gln Thr Ser	
145 150 155	
CGA CTT GAG ATA CAG CTG CTG GAG AAT TCA TTA TCC ACC TAC AAG CTA	828
Arg Leu Glu Ile Gln Leu Leu Glu Asn Ser Leu Ser Thr Tyr Lys Leu	
160 165 170	
GAG AAG CAA CTT CTT CAA CAG ACA AAT GAA ATC TTG AAG ATC CAT GAA	876
Glu Lys Gln Leu Leu Gln Gln Thr Asn Glu Ile Leu Lys Ile His Glu	
175 180 185	
AAA AAC AGT TTA TTA GAA CAT AAA ATC TTA GAA ATG GAA GGA AAA CAC	924
Lys Asn Ser Leu Leu Glu His Lys Ile Leu Glu Met Glu Gly Lys His	
190 195 200 205	
AAG GAA GAG TTG GAC ACC TTA AAG GAA GAG AAA GAG AAC CTT CAA GGC	972
Lys Glu Glu Leu Asp Thr Leu Lys Glu Glu Lys Glu Asn Leu Gln Gly	

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															210		215					220						
TTG	GTT	ACT	CGT	CAA	ACA	TAT	ATA	ATC	CAG	GAG	CTG	GAA	AAG	CAA	TTA	1020												
Leu	Val	Thr	Arg	Gln	Thr	Tyr	Ile	Ile	Gln	Glu	Leu	Glu	Lys	Gln	Leu													
			225					230					235															
AAC	AGA	GCT	ACC	ACC	AAC	AAC	AGT	GTC	CTT	CAG	AAG	CAG	CAA	CTG	GAG	1068												
Asn	Arg	Ala	Thr	Thr	Asn	Asn	Ser	Val	Leu	Gln	Lys	Gln	Gln	Leu	Glu													
			240					245					250															
CTG	ATG	GAC	ACA	GTC	CAC	AAC	CTT	GTC	AAT	CTT	TGC	ACT	AAA	GAA	GTT	1116												
Leu	Met	Asp	Thr	Val	His	Asn	Leu	Val	Asn	Leu	Cys	Thr	Lys	Glu	Val													
			255					260					265															
TTA	CTA	AAG	GGA	GGA	AAA	AGA	GAG	GAA	GAC	AAA	CCA	TTT	AGA	GAC	TGT	1164												
Leu	Leu	Lys	Gly	Gly	Lys	Arg	Glu	Glu	Asp	Lys	Pro	Phe	Arg	Asp	Cys													
270			275			280			285																			
GCA	GAT	GTA	TAT	CAA	GCT	GGT	TTT	AAT	AAA	AGT	GGA	ATC	TAC	ACT	ATT	1212												
Ala	Asp	Val	Tyr	Gln	Ala	Gly	Phe	Asn	Lys	Ser	Gly	Ile	Tyr	Thr	Ile													
			290					295					300															
TAT	ATT	AAT	AAT	ATG	CCA	GAA	CCC	AAA	AAG	GTG	TTT	TGC	AAT	ATG	GAT	1260												
Tyr	Ile	Asn	Asn	Met	Pro	Glu	Pro	Lys	Lys	Val	Phe	Cys	Asn	Met	Asp													
			305					310					315															
GTC	AAT	GGG	GGA	GGT	TGG	ACT	GTA	ATA	CAA	CAT	CGT	GAA	GAT	GGA	AGT	1308												
Val	Asn	Gly	Gly	Gly	Trp	Thr	Val	Ile	Gln	His	Arg	Glu	Asp	Gly	Ser													
			320					325					330															
CTA	GAT	TTC	CAA	AGA	GGC	TGG	AAG	GAA	TAT	AAA	ATG	GGT	TTT	GGA	AAT	1356												
Leu	Asp	Phe	Gln	Arg	Gly	Trp	Lys	Glu	Tyr	Lys	Met	Gly	Phe	Gly	Asn													
			335					340					345															
CCC	TCC	GGT	GAA	TAT	TGG	CTG	GGG	AAT	GAG	TTT	ATT	TTT	GCC	ATT	ACC	1404												
Pro	Ser	Gly	Glu	Tyr	Trp	Leu	Gly	Asn	Glu	Phe	Ile	Phe	Ala	Ile	Thr													
350			355			360			365																			
AGT	CAG	AGG	CAG	TAC	ATG	CTA	AGA	ATT	GAG	TTA	ATG	GAC	TGG	GAA	GGG	1452												
Ser	Gln	Arg	Gln	Tyr	Met	Leu	Arg	Ile	Glu	Leu	Met	Asp	Trp	Glu	Gly													
			370					375					380															
AAC	CGA	GCC	TAT	TCA	CAG	TAT	GAC	AGA	TTC	CAC	ATA	GGA	AAT	GAA	AAG	1500												
Asn	Arg	Ala	Tyr	Ser	Gln	Tyr	Asp	Arg	Phe	His	Ile	Gly	Asn	Glu	Lys													
			385					390					395															
CAA	AAC	TAT	AGG	TTG	TAT	TTA	AAA	GGT	CAC	ACT	GGG	ACA	GCA	GGA	AAA	1548												
Gln	Asn	Tyr	Arg	Leu	Tyr	Leu	Lys	Gly	His	Thr	Gly	Thr	Ala	Gly	Lys													
			400					405					410															
CAG	AGC	AGC	CTG	ATC	TTA	CAC	GGT	GCT	GAT	TTC	AGC	ACT	AAA	GAT	GCT	1596												
Gln	Ser	Ser	Leu	Ile	Leu	His	Gly	Ala	Asp	Phe	Ser	Thr	Lys	Asp	Ala													
			415					420					425															
GAT	AAT	GAC	AAC	TGT	ATG	TGC	AAA	TGT	GCC	CTC	ATG	TTA	ACA	GGA	GGA	1644												
Asp	Asn	Asp	Asn	Cys	Met	Cys	Lys	Cys	Ala	Leu	Met	Leu	Thr	Gly	Gly													
430			435			440			445																			
TGG	TGG	TTT	GAT	GCT	TGT	GGC	CCC	TCC	AAT	CTA	AAT	GGA	ATG	TTC	TAT	1692												
Trp	Trp	Phe	Asp	Ala	Cys	Gly	Pro	Ser	Asn	Leu	Asn	Gly	Met	Phe	Tyr													
			450					455					460															
ACT	GCG	GGA	CAA	AAC	CAT	GGA	AAA	CTG	AAT	GGG	ATA	AAG	TGG	CAC	TAC	1740												
Thr	Ala	Gly	Gln	Asn	His	Gly	Lys	Leu	Asn	Gly	Ile	Lys	Trp	His	Tyr													
			465					470					475															
TTC	AAA	GGG	CCC	AGT	TAC	TCC	TTA	CGT	TCC	ACA	ACT	ATG	ATG	ATT	CGA	1788												
Phe	Lys	Gly	Pro	Ser	Tyr	Ser	Leu	Arg	Ser	Thr	Thr	Met	Met	Ile	Arg													
			480					485					490															
CCT	TTA	GAT	TTT	TGA	AAGCGCAATG	TCAGAAGCGA	TTATGAAAGC	AACAAAGAAA								1843												
Pro	Leu	Asp	Phe	*												495												
TCCGGAGAAG CTGCCAGGTG AGAAACTGTT TGAAAACCTC AGAAGCAAAC AATATTGTCT																1903												

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CCCTTCCAGC AATAAGTGGT AGTTATGTGA AGTCACCAAG GTTCTTGACC GTGAATCTGG	1963
AGCCGTTTGA GTTCACAAGA GTCTCTACTT GGGGTGACAG TGCTCACGTG GCTCGACTAT	2023
AGAAAACTCC ACTGACTGTC GGGCTTTAAA AAGGAAGAA ACTGCTGAGC TTGCTGTGCT	2083
TCAAACACT ACTGGACCTT ATTTTGAAC TATGGTAGCC AGATGATAAA TATGGTTAAT	2143
TTC	2146

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Thr	Val	Phe	Leu	Ser	Phe	Ala	Phe	Leu	Ala	Ala	Ile	Leu	Thr	His	
1				5					10				15			
Ile	Gly	Cys	Ser	Asn	Gln	Arg	Arg	Ser	Pro	Glu	Asn	Ser	Gly	Arg	Arg	
			20					25					30			
Tyr	Asn	Arg	Ile	Gln	His	Gly	Gln	Cys	Ala	Tyr	Thr	Phe	Ile	Leu	Pro	
			35				40					45				
Glu	His	Asp	Gly	Asn	Cys	Arg	Glu	Ser	Thr	Thr	Asp	Gln	Tyr	Asn	Thr	
	50					55					60					
Asn	Ala	Leu	Gln	Arg	Asp	Ala	Pro	His	Val	Glu	Pro	Asp	Phe	Ser	Ser	
	65				70					75					80	
Gln	Lys	Leu	Gln	His	Leu	Glu	His	Val	Met	Glu	Asn	Tyr	Thr	Gln	Trp	
			85					90						95		
Leu	Gln	Lys	Leu	Glu	Asn	Tyr	Ile	Val	Glu	Asn	Met	Lys	Ser	Glu	Met	
			100					105					110			
Ala	Gln	Ile	Gln	Gln	Asn	Ala	Val	Gln	Asn	His	Thr	Ala	Thr	Met	Leu	
			115				120						125			
Glu	Ile	Gly	Thr	Ser	Leu	Leu	Ser	Gln	Thr	Ala	Glu	Gln	Thr	Arg	Lys	
			130				135				140					
Leu	Thr	Asp	Val	Glu	Thr	Gln	Val	Leu	Asn	Gln	Thr	Ser	Arg	Leu	Glu	
	145				150					155					160	
Ile	Gln	Leu	Leu	Glu	Asn	Ser	Leu	Ser	Thr	Tyr	Lys	Leu	Glu	Lys	Gln	
			165					170						175		
Leu	Leu	Gln	Gln	Thr	Asn	Glu	Ile	Leu	Lys	Ile	His	Glu	Lys	Asn	Ser	
			180					185					190			
Leu	Leu	Glu	His	Lys	Ile	Leu	Glu	Met	Glu	Gly	Lys	His	Lys	Glu	Glu	
		195					200				205					
Leu	Asp	Thr	Leu	Lys	Glu	Glu	Lys	Glu	Asn	Leu	Gln	Gly	Leu	Val	Thr	
	210					215					220					
Arg	Gln	Thr	Tyr	Ile	Ile	Gln	Glu	Leu	Glu	Lys	Gln	Leu	Asn	Arg	Ala	
	225				230					235					240	
Thr	Thr	Asn	Asn	Ser	Val	Leu	Gln	Lys	Gln	Gln	Leu	Glu	Leu	Met	Asp	
			245					250						255		
Thr	Val	His	Asn	Leu	Val	Asn	Leu	Cys	Thr	Lys	Glu	Val	Leu	Leu	Lys	
			260					265					270			
Gly	Gly	Lys	Arg	Glu	Glu	Asp	Lys	Pro	Phe	Arg	Asp	Cys	Ala	Asp	Val	
		275					280					285				

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Tyr	Gln	Ala	Gly	Phe	Asn	Lys	Ser	Gly	Ile	Tyr	Thr	Ile	Tyr	Ile	Asn
290					295					300					
Asn	Met	Pro	Glu	Pro	Lys	Lys	Val	Phe	Cys	Asn	Met	Asp	Val	Asn	Gly
305					310				315					320	
Gly	Gly	Trp	Thr	Val	Ile	Gln	His	Arg	Glu	Asp	Gly	Ser	Leu	Asp	Phe
				325					330					335	
Gln	Arg	Gly	Trp	Lys	Glu	Tyr	Lys	Met	Gly	Phe	Gly	Asn	Pro	Ser	Gly
				340				345					350		
Glu	Tyr	Trp	Leu	Gly	Asn	Glu	Phe	Ile	Phe	Ala	Ile	Thr	Ser	Gln	Arg
				355			360					365			
Gln	Tyr	Met	Leu	Arg	Ile	Glu	Leu	Met	Asp	Trp	Glu	Gly	Asn	Arg	Ala
				370		375					380				
Tyr	Ser	Gln	Tyr	Asp	Arg	Phe	His	Ile	Gly	Asn	Glu	Lys	Gln	Asn	Tyr
385				390					395					400	
Arg	Leu	Tyr	Leu	Lys	Gly	His	Thr	Gly	Thr	Ala	Gly	Lys	Gln	Ser	Ser
				405					410					415	
Leu	Ile	Leu	His	Gly	Ala	Asp	Phe	Ser	Thr	Lys	Asp	Ala	Asp	Asn	Asp
				420				425					430		
Asn	Cys	Met	Cys	Lys	Cys	Ala	Leu	Met	Leu	Thr	Gly	Gly	Trp	Trp	Phe
		435					440					445			
Asp	Ala	Cys	Gly	Pro	Ser	Asn	Leu	Asn	Gly	Met	Phe	Tyr	Thr	Ala	Gly
		450				455					460				
Gln	Asn	His	Gly	Lys	Leu	Asn	Gly	Ile	Lys	Trp	His	Tyr	Phe	Lys	Gly
465					470				475					480	
Pro	Ser	Tyr	Ser	Leu	Arg	Ser	Thr	Thr	Met	Met	Ile	Arg	Pro	Leu	Asp
				485					490					495	
Phe															

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 357..1847

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GAATTCCTGG	GTTGGTGT	TTT	ATCTCCTCCC	AGCCTTGAGG	GAGGGAACAA	CACTGTAGGA	60
TCTGGGGAGA	GAGGAACAAA	GGACCGTGAA	AGCTGCTCTG	TAAAAGCTGA	CACAGCCCTC		120
CCAAGTGAGC	AGGACTGTTT	TTCCCACTGC	AATCTGACAG	TTTACTGCAT	GCCTGGAGAG		180
AACACAGCAG	TAAAAACCAG	GTTTGCTACT	GGAAAAAGAG	GAAAGAGAAG	ACTTTCATTG		240
ACGGACCCAG	CCATGGCAGC	GTAGCAGCCC	TGCGTTTCAG	ACGGCAGCAG	CTCGGGACTC		300
TGGACGTGTG	TTTGCCCTCA	AGTTTGCTAA	GCTGCTGGTT	TATTACTGAA	GAAAGA		356
ATG	TGG	CAG	ATT	GTT	TTC	TTT	ACT
Met	Trp	Gln	Ile	Val	Phe	Phe	Thr
1				5			10
							15
GCA	GCC	TAT	AAC	AAC	TTT	CGG	AAG
Ala	Ala	Tyr	Asn	Asn	Phe	Arg	Lys
							452

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20					25					30						
CAA	TAT	CAG	GTC	CAG	CAT	GGG	TCC	TGC	AGC	TAC	ACT	TTC	CTC	CTG	CCA	500
Gln	Tyr	Gln	Val	Gln	His	Gly	Ser	Cys	Ser	Tyr	Thr	Phe	Leu	Leu	Pro	
		35					40					45				
GAG	ATG	GAC	AAC	TGC	CGC	TCT	TCC	TCC	AGC	CCC	TAC	GTG	TCC	AAT	GCT	548
Glu	Met	Asp	Asn	Cys	Arg	Ser	Ser	Ser	Ser	Pro	Tyr	Val	Ser	Asn	Ala	
	50					55					60					
GTG	CAG	AGG	GAC	GCG	CCG	CTC	GAA	TAC	GAT	GAC	TCG	GTG	CAG	AGG	CTG	596
Val	Gln	Arg	Asp	Ala	Pro	Leu	Glu	Tyr	Asp	Asp	Ser	Val	Gln	Arg	Leu	
	65				70					75					80	
CAA	GTG	CTG	GAG	AAC	ATC	ATG	GAA	AAC	AAC	ACT	CAG	TGG	CTA	ATG	AAG	644
Gln	Val	Leu	Glu	Asn	Ile	Met	Glu	Asn	Asn	Thr	Gln	Trp	Leu	Met	Lys	
				85					90					95		
CTT	GAG	AAT	TAT	ATC	CAG	GAC	AAC	ATG	AAG	AAA	GAA	ATG	GTA	GAG	ATA	692
Leu	Glu	Asn	Tyr	Ile	Gln	Asp	Asn	Met	Lys	Lys	Glu	Met	Val	Glu	Ile	
			100					105					110			
CAG	CAG	AAT	GCA	GTA	CAG	AAC	CAG	ACG	GCT	GTG	ATG	ATA	GAA	ATA	GGG	740
Gln	Gln	Asn	Ala	Val	Gln	Asn	Gln	Thr	Ala	Val	Met	Ile	Glu	Ile	Gly	
		115					120					125				
ACA	AAC	CTG	TTG	AAC	CAA	ACA	GCT	GAG	CAA	ACG	CGG	AAG	TTA	ACT	GAT	788
Thr	Asn	Leu	Leu	Asn	Gln	Thr	Ala	Glu	Gln	Thr	Arg	Lys	Leu	Thr	Asp	
	130					135				140						
GTG	GAA	GCC	CAA	GTA	TTA	AAT	CAG	ACC	ACG	AGA	CTT	GAA	CTT	CAG	CTC	836
Val	Glu	Ala	Gln	Val	Leu	Asn	Gln	Thr	Thr	Arg	Leu	Glu	Leu	Gln	Leu	
	145				150					155					160	
TTG	GAA	CAC	TCC	CTC	TCG	ACA	AAC	AAA	TTG	GAA	AAA	CAG	ATT	TTG	GAC	884
Leu	Glu	His	Ser	Leu	Ser	Thr	Asn	Lys	Leu	Glu	Lys	Gln	Ile	Leu	Asp	
			165					170					175			
CAG	ACC	AGT	GAA	ATA	AAC	AAA	TTG	CAA	GAT	AAG	AAC	AGT	TTC	CTA	GAA	932
Gln	Thr	Ser	Glu	Ile	Asn	Lys	Leu	Gln	Asp	Lys	Asn	Ser	Phe	Leu	Glu	
		180						185					190			
AAG	AAG	GTG	CTA	GCT	ATG	GAA	GAC	AAG	CAC	ATC	ATC	CAA	CTA	CAG	TCA	980
Lys	Lys	Val	Leu	Ala	Met	Glu	Asp	Lys	His	Ile	Ile	Gln	Leu	Gln	Ser	
		195					200					205				
ATA	AAA	GAA	GAG	AAA	GAT	CAG	CTA	CAG	GTG	TTA	GTA	TCC	AAG	CAA	AAT	1028
Ile	Lys	Glu	Glu	Lys	Asp	Gln	Leu	Gln	Val	Leu	Val	Ser	Lys	Gln	Asn	
	210					215					220					
TCC	ATC	ATT	GAA	GAA	CTA	GAA	AAA	AAA	ATA	GTG	ACT	GCC	ACG	GTG	AAT	1076
Ser	Ile	Ile	Glu	Glu	Leu	Glu	Lys	Lys	Ile	Val	Thr	Ala	Thr	Val	Asn	
	225				230					235					240	
AAT	TCA	GTT	CTT	CAA	AAG	CAG	CAA	CAT	GAT	CTC	ATG	GAG	ACA	GTT	AAT	1124
Asn	Ser	Val	Leu	Gln	Lys	Gln	Gln	His	Asp	Leu	Met	Glu	Thr	Val	Asn	
			245					250					255			
AAC	TTA	CTG	ACT	ATG	ATG	TCC	ACA	TCA	AAC	TCA	GCT	AAG	GAC	CCC	ACT	1172
Asn	Leu	Leu	Thr	Met	Met	Ser	Thr	Ser	Asn	Ser	Ala	Lys	Asp	Pro	Thr	
			260					265					270			
GTT	GCT	AAA	GAA	GAA	CAA	ATC	AGC	TTC	AGA	GAC	TGT	GCT	GAA	GTA	TTC	1220
Val	Ala	Lys	Glu	Glu	Gln	Ile	Ser	Phe	Arg	Asp	Cys	Ala	Glu	Val	Phe	
	275					280						285				
AAA	TCA	GGA	CAC	ACC	ACA	AAT	GGC	ATC	TAC	ACG	TTA	ACA	TTC	CCT	AAT	1268
Lys	Ser	Gly	His	Thr	Thr	Asn	Gly	Ile	Tyr	Thr	Leu	Thr	Phe	Pro	Asn	
	290					295					300					
TCT	ACA	GAA	GAG	ATC	AAG	GCC	TAC	TGT	GAC	ATG	GAA	GCT	GGA	GGA	GGC	1316
Ser	Thr	Glu	Glu	Ile	Lys	Ala	Tyr	Cys	Asp	Met	Glu	Ala	Gly	Gly	Gly	
	305				310					315					320	
GGG	TGG	ACA	ATT	ATT	CAG	CGA	CGT	GAG	GAT	GGC	AGC	GTT	GAT	TTT	CAG	1364
Gly	Trp	Thr	Ile	Ile	Gln	Arg	Arg	Glu	Asp	Gly	Ser	Val	Asp	Phe	Gln	

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325	330	335	
AGG ACT TGG AAA GAA TAT AAA GTG GGA TTT GGT AAC CCT TCA GGA GAA			1412
Arg Thr Trp Lys Glu Tyr Lys Val Gly Phe Gly Asn Pro Ser Gly Glu			
340	345	350	
TAT TGG CTG GGA AAT GAG TTT GTT TCG CAA CTG ACT AAT CAG CAA CGC			1460
Tyr Trp Leu Gly Asn Glu Phe Val Ser Gln Leu Thr Asn Gln Gln Arg			
355	360	365	
TAT GTG CTT AAA ATA CAC CTT AAA GAC TGG GAA GGG AAT GAG GCT TAC			1508
Tyr Val Leu Lys Ile His Leu Lys Asp Trp Glu Gly Asn Glu Ala Tyr			
370	375	380	
TCA TTG TAT GAA CAT TTC TAT CTC TCA AGT GAA GAA CTC AAT TAT AGG			1556
Ser Leu Tyr Glu His Phe Tyr Leu Ser Ser Glu Glu Leu Asn Tyr Arg			
385	390	395	400
ATT CAC CTT AAA GGA CTT ACA GGG ACA GCC GGC AAA ATA AGC AGC ATC			1604
Ile His Leu Lys Gly Leu Thr Gly Thr Ala Gly Lys Ile Ser Ser Ile			
405	410	415	
AGC CAA CCA GGA AAT GAT TTT AGC ACA AAG GAT GGA GAC AAC GAC AAA			1652
Ser Gln Pro Gly Asn Asp Phe Ser Thr Lys Asp Gly Asp Asn Asp Lys			
420	425	430	
TGT ATT TGC AAA TGT TCA CAA ATG CTA ACA GGA GGC TGG TGG TTT GAT			1700
Cys Ile Cys Lys Cys Ser Gln Met Leu Thr Gly Gly Trp Trp Phe Asp			
435	440	445	
GCA TGT GGT CCT TCC AAC TTG AAC GGA ATG TAC TAT CCA CAG AGG CAG			1748
Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Tyr Tyr Pro Gln Arg Gln			
450	455	460	
AAC ACA AAT AAG TTC AAC GGC ATT AAA TGG TAC TAC TGG AAA GGC TCA			1796
Asn Thr Asn Lys Phe Asn Gly Ile Lys Trp Tyr Tyr Trp Lys Gly Ser			
465	470	475	480
GGC TAT TCG CTC AAG GCC ACA ACC ATG ATG ATC CGA CCA GCA GAT TTC			1844
Gly Tyr Ser Leu Lys Ala Thr Thr Met Met Ile Arg Pro Ala Asp Phe			
485	490	495	
TAA ACATCCCACT CCACCTGAGG AACTGTCTCG AACTATTTTC AAAGACTTAA			1897
*			
GCCCACTGCA CTGAAAGTCA CGGCTGCGCA CTGTGTCCTC TTCCACCACA GAGGGCGTGT			1957
GCTCGGTGCT GACGGGACCC ACATGCTCCA GATTAGAGCC TGTAAACTTT ATCACTTAAA			2017
CTTGCACTCAC TTAACGGACC AAAGCAAGAC CCTAAACATC CATAATTGTG ATTAGACAGA			2077
ACACCTATGC AAAGATGAAC CCGAGGCTGA GAATCAGACT GACAGTTTAC AGACGCTGCT			2137
GTCACAACCA AGAATGTTAT GTGCAAGTTT ATCAGTAAAT AACTGGAAAA CAGAACACTT			2197
ATGTTATACA ATACAGATCA TCTTGAACT GCATTCTTCT GAGCACTGTT TATACACTGT			2257
GTAAATACCC ATATGTCCTG AATTC			2282

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 496 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met	Trp	Gln	Ile	Val	Phe	Phe	Thr	Leu	Ser	Cys	Asp	Leu	Val	Leu	Ala
1				5				10						15	
Ala	Ala	Tyr	Asn	Asn	Phe	Arg	Lys	Ser	Met	Asp	Ser	Ile	Gly	Lys	Lys
			20					25					30		

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Gln Tyr	Gln Val	Gln His	Gly	Ser Cys	Ser Tyr	Thr	Phe	Leu	Leu	Pro	
35				40			45				
Glu Met	Asp Asn	Cys Arg	Ser Ser	Ser Ser	Pro Tyr	Val	Ser	Asn	Ala		
50			55		60						
Val Gln	Arg Asp	Ala Pro	Leu Glu	Tyr Asp	Asp Ser	Val	Gln	Arg	Leu		
65		70		75					80		
Gln Val	Leu Glu	Asn Ile	Met Glu	Asn Asn	Thr Gln	Trp	Leu	Met	Lys		
		85		90				95			
Leu Glu	Asn Tyr	Ile Gln	Asp Asn	Met Lys	Lys Glu	Met	Val	Glu	Ile		
	100			105			110				
Gln Gln	Asn Ala	Val Gln	Asn Gln	Thr Ala	Val Met	Ile	Glu	Ile	Gly		
	115		120			125					
Thr Asn	Leu Leu	Asn Gln	Thr Ala	Glu Gln	Thr Arg	Lys	Leu	Thr	Asp		
130			135		140						
Val Glu	Ala Gln	Val Leu	Asn Gln	Thr Thr	Arg Leu	Glu	Leu	Gln	Leu		
145		150			155				160		
Leu Glu	His Ser	Leu Ser	Thr Asn	Lys Leu	Glu Lys	Gln	Ile	Leu	Asp		
	165			170			175				
Gln Thr	Ser Glu	Ile Asn	Lys Leu	Gln Asp	Lys Asn	Ser Phe	Leu	Glu			
	180			185		190					
Lys Lys	Val Leu	Ala Met	Glu Asp	Lys His	Ile Ile	Gln	Leu	Gln	Ser		
	195		200			205					
Ile Lys	Glu Glu	Lys Asp	Gln Leu	Gln Val	Leu Val	Ser Lys	Gln	Asn			
	210		215			220					
Ser Ile	Ile Glu	Glu Leu	Glu Lys	Lys Ile	Val Thr	Ala Thr	Val	Asn			
225		230			235			240			
Asn Ser	Val Leu	Gln Lys	Gln Gln	His Asp	Leu Met	Glu Thr	Val	Asn			
	245			250			255				
Asn Leu	Leu Thr	Met Met	Ser Thr	Ser Asn	Ser Ala	Lys Asp	Pro	Thr			
	260			265		270					
Val Ala	Lys Glu	Glu Gln	Ile Ser	Phe Arg	Asp Cys	Ala Glu	Val	Phe			
	275		280			285					
Lys Ser	Gly His	Thr Thr	Asn Gly	Ile Tyr	Thr Leu	Thr Phe	Pro	Asn			
	290		295		300						
Ser Thr	Glu Glu	Ile Lys	Ala Tyr	Cys Asp	Met Glu	Ala Gly	Gly	Gly			
305		310			315			320			
Gly Trp	Thr Ile	Ile Gln	Arg Arg	Glu Asp	Gly Ser	Val Asp	Phe	Gln			
	325			330			335				
Arg Thr	Trp Lys	Glu Tyr	Lys Val	Gly Phe	Gly Asn	Pro Ser	Gly	Glu			
	340			345		350					
Tyr Trp	Leu Gly	Asn Glu	Phe Val	Ser Gln	Leu Thr	Asn Gln	Gln	Arg			
	355		360			365					
Tyr Val	Leu Lys	Ile His	Leu Lys	Asp Trp	Glu Gly	Asn Glu	Ala	Tyr			
	370		375		380						
Ser Leu	Tyr Glu	His Phe	Tyr Leu	Ser Ser	Glu Glu	Leu Asn	Tyr	Arg			
385		390			395			400			
Ile His	Leu Lys	Gly Leu	Thr Gly	Thr Ala	Gly Lys	Ile Ser	Ser	Ile			
	405			410			415				
Ser Gln	Pro Gly	Asn Asp	Phe Ser	Thr Lys	Asp Gly	Asp Asn	Asp	Lys			
	420			425			430				

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Cys	Ile	Cys	Lys	Cys	Ser	Gln	Met	Leu	Thr	Gly	Gly	Trp	Trp	Phe	Asp
	435						440					445			
Ala	Cys	Gly	Pro	Ser	Asn	Leu	Asn	Gly	Met	Tyr	Tyr	Pro	Gln	Arg	Gln
	450					455				460					
Asn	Thr	Asn	Lys	Phe	Asn	Gly	Ile	Lys	Trp	Tyr	Tyr	Trp	Lys	Gly	Ser
465					470					475				480	
Gly	Tyr	Ser	Leu	Lys	Ala	Thr	Thr	Met	Met	Ile	Arg	Pro	Ala	Asp	Phe
			485					490						495	

What is claimed is:

1. An isolated and purified nucleic acid molecule comprising a nucleic acid sequence encoding a human TIE-2 ligand, wherein the nucleic acid sequence is selected from the group consisting of:

(a) the nucleic acid sequence comprising the coding region of the human TIE-2 ligand as set forth in **FIG. 6**;

(b) a nucleic acid sequence that hybridizes under moderately stringent conditions to the nucleic acid sequence of (a) and which encodes a TIE-2 ligand that binds TIE-2 receptor; and

(c) a nucleic acid sequence that is degenerate as a result of the genetic code to a nucleic acid sequence of (a) or (b), and which encodes a TIE-2 ligand that binds TIE-2 receptor.

2. Isolated and purified human TIE-2 ligand encoded by the nucleic acid molecule of claim 1.

3. A vector which comprises the isolated nucleic acid molecule of claim 1.

4. An expression vector comprising a DNA molecule of claim 1, wherein the DNA molecule is operatively linked to an expression control sequence.

5. A host-vector system for the production of a human TIE-2 ligand which comprises the vector of claim 4, in a suitable host cell.

6. The host-vector system of claim 5, wherein the suitable host cell is a bacterial cell, yeast cell, insect cell, or mammalian cell.

7. A method of producing a TIE-2 ligand which comprises growing cells of the host-vector system of claim 5, under conditions permitting production of the polypeptide and recovering the polypeptide so produced.

8. A therapeutic composition comprising a ligand of claim 2, and a pharmaceutically acceptable carrier.

9. A method of blocking blood vessel growth in a human comprising administering an effective amount of the therapeutic composition of claim 8.

10. An antibody which specifically binds the ligand of claim 2.

11. A monoclonal antibody of claim 10.

12. A method of purifying human TIE-2 ligand comprising:

a) coupling at least one TIE-2 ligand binding substrate to a solid matrix;

b) incubating the substrate of a) with a cell lysate so that the substrate forms a complex with any human TIE-2 ligand in the cell lysate;

c) washing the solid matrix; and

d) eluting the human TIE-2 ligand from the coupled substrate.

13. The method of claim 12, wherein the substrate is selected from the group consisting of anti-TIE-2 ligand antibody, TIE-2 receptor and TIE-2 receptorbody.

14. A receptorbody which specifically binds the ligand of claim 2.

15. A therapeutic composition comprising a receptorbody of claim 14, in a pharmaceutically acceptable vehicle.

16. A method of blocking blood vessel growth in a human comprising administering an effective amount of the composition of claim 15.

17. A method of inhibiting TIE-2 ligand activity in a mammal comprising administering to the mammal an effective amount of a TIE-2 antagonist.

18. The method of claim 17, wherein the antagonist is an antibody capable of specifically binding TIE-2 ligand.

19. The method of claim 17, wherein the antagonist is an antibody capable of specifically binding TIE-2 receptor.

20. The method of claim 17, wherein the antagonist is a TIE-2 receptorbody.

21. A method of inhibiting TIE-2 ligand activity in a mammal comprising administering to the mammal an effective amount of the ligand of claim 2.

22. The method of claim 17, wherein the mammal is a human.

23. The method of claim 17, used to attenuate or prevent tumor growth in a human.

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