

SEQUENCE LISTING

<110> ONCOTHERAPY SCIENCE, INC.
 TOKUSHIMA UNIVERSITY

<120> Peptide derivatives and pharmaceutical compositions comprising
 the same

<130> ONC-A1701P

<150> JP 2017-140101
 <151> 2017-07-19

<160> 21

<170> PatentIn version 3.5

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 <213> Artificial Sequence

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Ser Glu Ser Arg Lys Arg Ser Ile Ser Lys Arg Lys Ser His Leu Asp	
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Leu Leu Lys Leu Ile Met Asp Gly Met Thr Glu Ala Cys Ile Lys Gly	
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Gly Ile Glu Ala Cys Tyr Ala Ala Val Ser Cys Val Cys Thr Leu Leu	
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Phe Thr Ala Leu Gln Pro	Ala Val Phe Pro Cys	Ile Ser Gln Leu	
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<212> PRT
<213> Homo sapiens

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<400> 7

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Met Glu Glu Ile Leu Arg Lys Leu Gln Lys Glu Ala Ser Gly Ser Lys
1             5             10             15

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```

Tyr Lys Ala Ile Lys Glu Ser Cys Thr Trp Ala Leu Glu Thr Leu Gly
      20             25             30

```

```

Gly Leu Asp Thr Ile Val Lys Ile Pro Pro His Val Leu Arg Glu Lys
      35             40             45

```

```

Cys Leu Leu Pro Leu Gln Leu Ala Leu Glu Ser Lys Asn Val Lys Leu
      50             55             60

```

```

Ala Gln His Ala Leu Ala Gly Met Gln Lys Leu Leu Ser Glu Glu Arg
65             70             75             80

```

```

Phe Val Ser Met Glu Thr Asp Ser Asp Glu Lys Gln Leu Leu Asn Gln
      85             90             95

```

```

Ile Leu Asn Ala Val Lys Val Thr Pro Ser Leu Asn Glu Asp Leu Gln
      100            105            110

```

```

Val Glu Val Met Lys Val Leu Leu Cys Ile Thr Tyr Thr Pro Thr Phe

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115		120		125
Asp Leu Asn Gly Ser Ala Val Leu Lys Ile Ala Glu Val Cys Ile Glu				
130		135		140
Thr Tyr Ile Ser Ser Cys His Gln Arg Ser Ile Asn Thr Ala Val Arg				
145		150		155
				160
Ala Thr Leu Ser Gln Met Leu Ser Asp Leu Thr Leu Gln Leu Arg Gln				
		165		170
				175
Arg Gln Glu Asn Thr Ile Ile Glu Asn Pro Asp Val Pro Gln Asp Phe				
		180		185
				190
Gly Asn Gln Gly Ser Thr Val Glu Ser Leu Cys Asp Asp Val Val Ser				
		195		200
				205
Val Leu Thr Val Leu Cys Glu Lys Leu Gln Ala Ala Ile Asn Asp Ser				
		210		215
				220
Gln Gln Leu Gln Leu Leu Tyr Leu Glu Cys Ile Leu Ser Val Leu Ser				
225		230		235
				240
Ser Ser Ser Ser Ser Met His Leu His Arg Arg Phe Thr Asp Leu Ile				
		245		250
				255
Trp Lys Asn Leu Cys Pro Ala Leu Ile Val Ile Leu Gly Asn Pro Ile				
		260		265
				270
His Asp Lys Thr Ile Thr Ser Ala His Thr Ser Ser Thr Ser Thr Ser				
		275		280
				285
Leu Glu Ser Asp Ser Ala Ser Pro Gly Val Ser Asp His Gly Arg Gly				
		290		295
				300
Ser Gly Cys Ser Cys Thr Ala Pro Ala Leu Ser Gly Pro Val Ala Arg				
305		310		315
				320

Thr Ile Tyr Tyr Ile Ala Ala Glu Leu Val Arg Leu Val Gly Ser Val
 325 330 335

Asp Ser Met Lys Pro Val Leu Gln Ser Leu Tyr His Arg Val Leu Leu
 340 345 350

Tyr Pro Pro Pro Gln His Arg Val Glu Ala Ile Lys Ile Met Lys Glu
 355 360 365

Ile Leu Gly Ser Pro Gln Arg Leu Cys Asp Leu Ala Gly Pro Ser Ser
 370 375 380

Thr Glu Ser Glu Ser Arg Lys Arg Ser Ile Ser Lys Arg Lys Ser His
 385 390 395 400

Leu Asp Leu Leu Lys Leu Ile Met Asp Gly Met Thr Glu Ala Cys Ile
 405 410 415

Lys Gly Gly Ile Glu Ala Cys Tyr Ala Ala Val Ser Cys Val Cys Thr
 420 425 430

Leu Leu Gly Ala Leu Asp Glu Leu Ser Gln Gly Lys Gly Leu Ser Glu
 435 440 445

Gly Gln Val Gln Leu Leu Leu Leu Arg Leu Glu Glu Leu Lys Asp Gly
 450 455 460

Ala Glu Trp Ser Arg Asp Ser Met Glu Ile Asn Glu Ala Asp Phe Arg
 465 470 475 480

Trp Gln Arg Arg Val Leu Ser Ser Glu His Thr Pro Trp Glu Ser Gly
 485 490 495

Asn Glu Arg Ser Leu Asp Ile Ser Ile Ser Val Thr Thr Asp Thr Gly
 500 505 510

Gln Thr Thr Leu Glu Gly Glu Leu Gly Gln Thr Thr Pro Glu Asp His
 515 520 525

Ser Gly Asn His Lys Asn Ser Leu Lys Ser Pro Ala Ile Pro Glu Gly
 530 535 540

Lys Glu Thr Leu Ser Lys Val Leu Glu Thr Glu Ala Val Asp Gln Pro
 545 550 555 560

Asp Val Val Gln Arg Ser His Thr Val Pro Tyr Pro Asp Ile Thr Asn
 565 570 575

Phe Leu Ser Val Asp Cys Arg Thr Arg Ser Tyr Gly Ser Arg Tyr Ser
 580 585 590

Glu Ser Asn Phe Ser Val Asp Asp Gln Asp Leu Ser Arg Thr Glu Phe
 595 600 605

Asp Ser Cys Asp Gln Tyr Ser Met Ala Ala Glu Lys Asp Ser Gly Arg
 610 615 620

Ser Asp Val Ser Asp Ile Gly Ser Asp Asn Cys Ser Leu Ala Asp Glu
 625 630 635 640

Glu Gln Thr Pro Arg Asp Cys Leu Gly His Arg Ser Leu Arg Thr Ala
 645 650 655

Ala Leu Ser Leu Lys Leu Leu Lys Asn Gln Glu Ala Asp Gln His Ser
 660 665 670

Ala Arg Leu Phe Ile Gln Ser Leu Glu Gly Leu Leu Pro Arg Leu Leu
 675 680 685

Ser Leu Ser Asn Val Glu Glu Val Asp Thr Ala Leu Gln Asn Phe Ala
 690 695 700

Ser Thr Phe Cys Ser Gly Met Met His Ser Pro Gly Phe Asp Gly Asn
705 710 715 720

Ser Ser Leu Ser Phe Gln Met Leu Met Asn Ala Asp Ser Leu Tyr Thr
725 730 735

Ala Ala His Cys Ala Leu Leu Leu Asn Leu Lys Leu Ser His Gly Asp
740 745 750

Tyr Tyr Arg Lys Arg Pro Thr Leu Ala Pro Gly Val Met Lys Asp Phe
755 760 765

Met Lys Gln Val Gln Thr Ser Gly Val Leu Met Val Phe Ser Gln Ala
770 775 780

Trp Ile Glu Glu Leu Tyr His Gln Val Leu Asp Arg Asn Met Leu Gly
785 790 795 800

Glu Ala Gly Tyr Trp Gly Ser Pro Glu Asp Asn Ser Leu Pro Leu Ile
805 810 815

Thr Met Leu Thr Asp Ile Asp Gly Leu Glu Ser Ser Ala Ile Gly Gly
820 825 830

Gln Leu Met Ala Ser Ala Ala Thr Glu Ser Pro Phe Ala Gln Ser Arg
835 840 845

Arg Ile Asp Asp Ser Thr Val Ala Gly Val Ala Phe Ala Arg Tyr Ile
850 855 860

Leu Val Gly Cys Trp Lys Asn Leu Ile Asp Thr Leu Ser Thr Pro Leu
865 870 875 880

Thr Gly Arg Met Ala Gly Ser Ser Lys Gly Leu Ala Phe Ile Leu Gly
885 890 895

Ala Glu Gly Ile Lys Glu Gln Asn Gln Lys Glu Arg Asp Ala Ile Cys

	900		905		910
Met Ser	Leu Asp Gly Leu Arg Lys Ala Ala Arg Leu Ser Cys Ala Leu				
	915		920		925
Gly Val	Ala Ala Asn Cys Ala Ser Ala Leu Ala Gln Met Ala Ala Ala				
	930		935		940
Ser Cys Val	Gln Glu Glu Lys Glu Glu Arg Glu Ala Gln Glu Pro Ser				
945		950		955	960
Asp Ala Ile Thr	Gln Val Lys Leu Lys Val Glu Gln Lys Leu Glu Gln				
	965		970		975
Ile Gly Lys Val	Gln Gly Val Trp Leu His Thr Ala His Val Leu Cys				
	980		985		990
Met Glu Ala Ile	Leu Ser Val Gly Leu Glu Met Gly Ser His Asn Pro				
	995		1000		1005
Asp Cys Trp Pro	His Val Phe Arg Val Cys Glu Tyr Val Gly Thr				
	1010		1015		1020
Leu Glu His Asn	His Phe Ser Asp Gly Ala Ser Gln Pro Pro Leu				
	1025		1030		1035
Thr Ile Ser Gln	Pro Gln Lys Ala Thr Gly Ser Ala Gly Leu Leu				
	1040		1045		1050
Gly Asp Pro Glu	Cys Glu Gly Ser Pro Pro Glu His Ser Pro Glu				
	1055		1060		1065
Gln Gly Arg Ser	Leu Ser Thr Ala Pro Val Val Gln Pro Leu Ser				
	1070		1075		1080
Ile Gln Asp Leu	Val Arg Glu Gly Ser Arg Gly Arg Ala Ser Asp				
	1085		1090		1095

Phe Arg Gly Gly Ser Leu Met Ser Gly Ser Ser Ala Ala Lys Val
 1100 1105 1110

Val Leu Thr Leu Ser Thr Gln Ala Asp Arg Leu Phe Glu Asp Ala
 1115 1120 1125

Thr Asp Lys Leu Asn Leu Met Ala Leu Gly Gly Phe Leu Tyr Gln
 1130 1135 1140

Leu Lys Lys Ala Ser Gln Ser Gln Leu Phe His Ser Val Thr Asp
 1145 1150 1155

Thr Val Asp Tyr Ser Leu Ala Met Pro Gly Glu Val Lys Ser Thr
 1160 1165 1170

Gln Asp Arg Lys Ser Ala Leu His Leu Phe Arg Leu Gly Asn Ala
 1175 1180 1185

Met Leu Arg Ile Val Arg Ser Lys Ala Arg Pro Leu Leu His Val
 1190 1195 1200

Met Arg Cys Trp Ser Leu Val Ala Pro His Leu Val Glu Ala Ala
 1205 1210 1215

Cys His Lys Glu Arg His Val Ser Gln Lys Ala Val Ser Phe Ile
 1220 1225 1230

His Asp Ile Leu Thr Glu Val Leu Thr Asp Trp Asn Glu Pro Pro
 1235 1240 1245

His Phe His Phe Asn Glu Ala Leu Phe Arg Pro Phe Glu Arg Ile
 1250 1255 1260

Met Gln Leu Glu Leu Cys Asp Glu Asp Val Gln Asp Gln Val Val
 1265 1270 1275

Thr Ser Ile Gly Glu Leu Val Glu Val Cys Ser Thr Gln Ile Gln
1280 1285 1290

Ser Gly Trp Arg Pro Leu Phe Ser Ala Leu Glu Thr Val His Gly
1295 1300 1305

Gly Asn Lys Ser Glu Met Lys Glu Tyr Leu Val Gly Asp Tyr Ser
1310 1315 1320

Met Gly Lys Gly Gln Ala Pro Val Phe Asp Val Phe Glu Ala Phe
1325 1330 1335

Leu Asn Thr Asp Asn Ile Gln Val Phe Ala Asn Ala Ala Thr Ser
1340 1345 1350

Tyr Ile Met Cys Leu Met Lys Phe Val Lys Gly Leu Gly Glu Val
1355 1360 1365

Asp Cys Lys Glu Ile Gly Asp Cys Ala Pro Ala Pro Gly Ala Pro
1370 1375 1380

Ser Thr Asp Leu Cys Leu Pro Ala Leu Asp Tyr Leu Arg Arg Cys
1385 1390 1395

Ser Gln Leu Leu Ala Lys Ile Tyr Lys Met Pro Leu Lys Pro Ile
1400 1405 1410

Phe Leu Ser Gly Arg Leu Ala Gly Leu Pro Arg Arg Leu Gln Glu
1415 1420 1425

Gln Ser Ala Ser Ser Glu Asp Gly Ile Glu Ser Val Leu Ser Asp
1430 1435 1440

Phe Asp Asp Asp Thr Gly Leu Ile Glu Val Trp Ile Ile Leu Leu
1445 1450 1455

Glu Gln Leu Thr Ala Ala Val Ser Asn Cys Pro Arg Gln His Gln
1460 1465 1470

Pro Pro Thr Leu Asp Leu Leu Phe Glu Leu Leu Arg Asp Val Thr
1475 1480 1485

Lys Thr Pro Gly Pro Gly Phe Gly Ile Tyr Ala Val Val His Leu
1490 1495 1500

Leu Leu Pro Val Met Ser Val Trp Leu Arg Arg Ser His Lys Asp
1505 1510 1515

His Ser Tyr Trp Asp Met Ala Ser Ala Asn Phe Lys His Ala Ile
1520 1525 1530

Gly Leu Ser Cys Glu Leu Val Val Glu His Ile Gln Ser Phe Leu
1535 1540 1545

His Ser Asp Ile Arg Tyr Glu Ser Met Ile Asn Thr Met Leu Lys
1550 1555 1560

Asp Leu Phe Glu Leu Leu Val Ala Cys Val Ala Lys Pro Thr Glu
1565 1570 1575

Thr Ile Ser Arg Val Gly Cys Ser Cys Ile Arg Tyr Val Leu Val
1580 1585 1590

Thr Ala Gly Pro Val Phe Thr Glu Glu Met Trp Arg Leu Ala Cys
1595 1600 1605

Cys Ala Leu Gln Asp Ala Phe Ser Ala Thr Leu Lys Pro Val Lys
1610 1615 1620

Asp Leu Leu Gly Cys Phe His Ser Gly Thr Glu Ser Phe Ser Gly
1625 1630 1635

Glu Gly Cys Gln Val Arg Val Ala Ala Pro Ser Ser Ser Pro Ser

1640		1645		1650
Ala Glu	Ala Glu Tyr Trp	Arg Ile Arg Ala Met	Ala Gln Gln Val	
1655		1660	1665	
Phe Met	Leu Asp Thr Gln Cys	Ser Pro Lys Thr	Pro Asn Asn Phe	
1670		1675	1680	
Asp His	Ala Gln Ser Cys Gln	Leu Ile Ile Glu Leu	Pro Pro Asp	
1685		1690	1695	
Glu Lys	Pro Asn Gly His Thr	Lys Lys Ser Val	Ser Phe Arg Glu	
1700		1705	1710	
Ile Val	Val Ser Leu Leu Ser	His Gln Val Leu Leu	Gln Asn Leu	
1715		1720	1725	
Tyr Asp	Ile Leu Leu Glu Glu	Phe Val Lys Gly	Pro Ser Pro Gly	
1730		1735	1740	
Glu Glu	Lys Thr Ile Gln Val	Pro Glu Ala Lys Leu	Ala Gly Phe	
1745		1750	1755	
Leu Arg	Tyr Ile Ser Met Gln	Asn Leu Ala Val	Ile Phe Asp Leu	
1760		1765	1770	
Leu Leu	Asp Ser Tyr Arg Thr	Ala Arg Glu Phe Asp	Thr Ser Pro	
1775		1780	1785	
Gly Leu	Lys Cys Leu Leu Lys	Lys Val Ser Gly Ile	Gly Gly Ala	
1790		1795	1800	
Ala Asn	Leu Tyr Arg Gln Ser	Ala Met Ser Phe Asn	Ile Tyr Phe	
1805		1810	1815	
His Ala	Leu Val Cys Ala Val	Leu Thr Asn Gln Glu	Thr Ile Thr	
1820		1825	1830	

Ala Glu Gln Val Lys Lys Val Leu Phe Glu Asp Asp Glu Arg Ser
1835 1840 1845

Thr Asp Ser Ser Gln Gln Cys Ser Ser Glu Asp Glu Asp Ile Phe
1850 1855 1860

Glu Glu Thr Ala Gln Val Ser Pro Pro Arg Gly Lys Glu Lys Arg
1865 1870 1875

Gln Trp Arg Ala Arg Met Pro Leu Leu Ser Val Gln Pro Val Ser
1880 1885 1890

Asn Ala Asp Trp Val Trp Leu Val Lys Arg Leu His Lys Leu Cys
1895 1900 1905

Met Glu Leu Cys Asn Asn Tyr Ile Gln Met His Leu Asp Leu Glu
1910 1915 1920

Asn Cys Met Glu Glu Pro Pro Ile Phe Lys Gly Asp Pro Phe Phe
1925 1930 1935

Ile Leu Pro Ser Phe Gln Ser Glu Ser Ser Thr Pro Ser Thr Gly
1940 1945 1950

Gly Phe Ser Gly Lys Glu Thr Pro Ser Glu Asp Asp Arg Ser Gln
1955 1960 1965

Ser Arg Glu His Met Gly Glu Ser Leu Ser Leu Lys Ala Gly Gly
1970 1975 1980

Gly Asp Leu Leu Leu Pro Pro Ser Pro Lys Val Glu Lys Lys Asp
1985 1990 1995

Pro Ser Arg Lys Lys Glu Trp Trp Glu Asn Ala Gly Asn Lys Ile
2000 2005 2010

Tyr Thr Met Ala Ala Asp Lys Thr Ile Ser Lys Leu Met Thr Glu
2015 2020 2025

Tyr Lys Lys Arg Lys Gln Gln His Asn Leu Ser Ala Phe Pro Lys
2030 2035 2040

Glu Val Lys Val Glu Lys Lys Gly Glu Pro Leu Gly Pro Arg Gly
2045 2050 2055

Gln Asp Ser Pro Leu Leu Gln Arg Pro Gln His Leu Met Asp Gln
2060 2065 2070

Gly Gln Met Arg His Ser Phe Ser Ala Gly Pro Glu Leu Leu Arg
2075 2080 2085

Gln Asp Lys Arg Pro Arg Ser Gly Ser Thr Gly Ser Ser Leu Ser
2090 2095 2100

Val Ser Val Arg Asp Ala Glu Ala Gln Ile Gln Ala Trp Thr Asn
2105 2110 2115

Met Val Leu Thr Val Leu Asn Gln Ile Gln Ile Leu Pro Asp Gln
2120 2125 2130

Thr Phe Thr Ala Leu Gln Pro Ala Val Phe Pro Cys Ile Ser Gln
2135 2140 2145

Leu Thr Cys His Val Thr Asp Ile Arg Val Arg Gln Ala Val Arg
2150 2155 2160

Glu Trp Leu Gly Arg Val Gly Arg Val Tyr Asp Ile Ile Val
2165 2170 2175

<210> 8

<211> 1457

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (211)..(1110)

<400> 8

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tcaaagggag cgcacttcog ctgcccttcc tttgccagc cttacgggcc cgaaccctcg 120

tgtgaagggt gcagtaccta agccggagcg gggtagaggc gggccggcac ccccttctga 180

cctccagtgc cgccggcctc aagatcagac atg gcc cag aac ttg aag gac ttg 234
 Met Ala Gln Asn Leu Lys Asp Leu
 1 5

gcg gga cgg ctg ccc gcc ggg ccc cgg ggc atg ggc acg gcc ctg aag 282
 Ala Gly Arg Leu Pro Ala Gly Pro Arg Gly Met Gly Thr Ala Leu Lys
 10 15 20

ctg ttg ctg ggg gcc ggc gcc gtg gcc tac ggt gtg cgc gaa tct gtg 330
 Leu Leu Leu Gly Ala Gly Ala Val Ala Tyr Gly Val Arg Glu Ser Val
 25 30 35 40

ttc acc gtg gaa ggc ggg cac aga gcc atc ttc ttc aat cgg atc ggt 378
 Phe Thr Val Glu Gly Gly His Arg Ala Ile Phe Phe Asn Arg Ile Gly
 45 50 55

gga gtg cag cag gac act atc ctg gcc gag ggc ctt cac ttc agg atc 426
 Gly Val Gln Gln Asp Thr Ile Leu Ala Glu Gly Leu His Phe Arg Ile
 60 65 70

cct tgg ttc cag tac ccc att atc tat gac att cgg gcc aga cct cga 474
 Pro Trp Phe Gln Tyr Pro Ile Ile Tyr Asp Ile Arg Ala Arg Pro Arg
 75 80 85

aaa atc tcc tcc cct aca ggc tcc aaa gac cta cag atg gtg aat atc 522
 Lys Ile Ser Ser Pro Thr Gly Ser Lys Asp Leu Gln Met Val Asn Ile
 90 95 100

tcc ctg cga gtg ttg tct cga ccc aat gct cag gag ctt cct agc atg 570
 Ser Leu Arg Val Leu Ser Arg Pro Asn Ala Gln Glu Leu Pro Ser Met
 105 110 115 120

tac cag cgc cta ggg ctg gac tac gag gaa cga gtg ttg cgg tcc att 618
 Tyr Gln Arg Leu Gly Leu Asp Tyr Glu Glu Arg Val Leu Pro Ser Ile
 125 130 135

gtc aac gag gtg ctc aag agt gtg gtg gcc aag ttc aat gcc tca cag Val Asn Glu Val Leu Lys Ser Val Val Ala Lys Phe Asn Ala Ser Gln 140 145 150	666
ctg atc acc cag cgg gcc cag gta tcc ctg ttg atc cgc cgg gag ctg Leu Ile Thr Gln Arg Ala Gln Val Ser Leu Leu Ile Arg Arg Glu Leu 155 160 165	714
aca gag agg gcc aag gac ttc agc ctc atc ctg gat gat gtg gcc atc Thr Glu Arg Ala Lys Asp Phe Ser Leu Ile Leu Asp Asp Val Ala Ile 170 175 180	762
aca gag ctg agc ttt agc cga gag tac aca gct gct gta gaa gcc aaa Thr Glu Leu Ser Phe Ser Arg Glu Tyr Thr Ala Ala Val Glu Ala Lys 185 190 195 200	810
caa gtg gcc cag cag gag gcc cag cgg gcc caa ttc ttg gta gaa aaa Gln Val Ala Gln Gln Glu Ala Gln Arg Ala Gln Phe Leu Val Glu Lys 205 210 215	858
gca aag cag gaa cag cgg cag aaa att gtg cag gcc gag ggt gag gcc Ala Lys Gln Glu Gln Arg Gln Lys Ile Val Gln Ala Glu Gly Glu Ala 220 225 230	906
gag gct gcc aag atg ctt gga gaa gca ctg agc aag aac cct ggc tac Glu Ala Ala Lys Met Leu Gly Glu Ala Leu Ser Lys Asn Pro Gly Tyr 235 240 245	954
atc aaa ctt cgc aag att cga gca gcc cag aat atc tcc aag acg atc Ile Lys Leu Arg Lys Ile Arg Ala Ala Gln Asn Ile Ser Lys Thr Ile 250 255 260	1002
gcc aca tca cag aat cgt atc tat ctc aca gct gac aac ctt gtg ctg Ala Thr Ser Gln Asn Arg Ile Tyr Leu Thr Ala Asp Asn Leu Val Leu 265 270 275 280	1050
aac cta cag gat gaa agt ttc acc agg gga agt gac agc ctc atc aag Asn Leu Gln Asp Glu Ser Phe Thr Arg Gly Ser Asp Ser Leu Ile Lys 285 290 295	1098
ggt aag aaa tga gcctagtcac caagaactcc acccccagag gaagtggatc Gly Lys Lys	1150
tgcttctcca gtttttgagg agccagccag gggccagca cagccctacc ccgccccagt	1210
atcatgcat ggtccccac accggttccc tgaaccctc ttggattaag gaagactgaa	1270
gactagcccc ttttctgggg aattactttc ctccctcctg tgttaactgg ggctgttggg	1330

gacagtgcgt gatttctcag tgatttcta cagtgttggt ccctccctca aggctgggag 1390

gagataaaca ocaaccagg aattctcaat aaatttttat tacttaacct gaaaaaaaaa 1450

aaaaaaaa 1457

<210> 9

<211> 299

<212> PRT

<213> Homo sapiens

<400> 9

Met Ala Gln Asn Leu Lys Asp Leu Ala Gly Arg Leu Pro Ala Gly Pro
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Arg Gly Met Gly Thr Ala Leu Lys Leu Leu Leu Gly Ala Gly Ala Val
20 25 30

Ala Tyr Gly Val Arg Glu Ser Val Phe Thr Val Glu Gly Gly His Arg
35 40 45

Ala Ile Phe Phe Asn Arg Ile Gly Gly Val Gln Gln Asp Thr Ile Leu
50 55 60

Ala Glu Gly Leu His Phe Arg Ile Pro Trp Phe Gln Tyr Pro Ile Ile
65 70 75 80

Tyr Asp Ile Arg Ala Arg Pro Arg Lys Ile Ser Ser Pro Thr Gly Ser
85 90 95

Lys Asp Leu Gln Met Val Asn Ile Ser Leu Arg Val Leu Ser Arg Pro
100 105 110

Asn Ala Gln Glu Leu Pro Ser Met Tyr Gln Arg Leu Gly Leu Asp Tyr
115 120 125

Glu Glu Arg Val Leu Pro Ser Ile Val Asn Glu Val Leu Lys Ser Val
130 135 140

Val Ala Lys Phe Asn Ala Ser Gln Leu Ile Thr Gln Arg Ala Gln Val
 145 150 155 160

Ser Leu Leu Ile Arg Arg Glu Leu Thr Glu Arg Ala Lys Asp Phe Ser
 165 170 175

Leu Ile Leu Asp Asp Val Ala Ile Thr Glu Leu Ser Phe Ser Arg Glu
 180 185 190

Tyr Thr Ala Ala Val Glu Ala Lys Gln Val Ala Gln Gln Glu Ala Gln
 195 200 205

Arg Ala Gln Phe Leu Val Glu Lys Ala Lys Gln Glu Gln Arg Gln Lys
 210 215 220

Ile Val Gln Ala Glu Gly Glu Ala Glu Ala Ala Lys Met Leu Gly Glu
 225 230 235 240

Ala Leu Ser Lys Asn Pro Gly Tyr Ile Lys Leu Arg Lys Ile Arg Ala
 245 250 255

Ala Gln Asn Ile Ser Lys Thr Ile Ala Thr Ser Gln Asn Arg Ile Tyr
 260 265 270

Leu Thr Ala Asp Asn Leu Val Leu Asn Leu Gln Asp Glu Ser Phe Thr
 275 280 285

Arg Gly Ser Asp Ser Leu Ile Lys Gly Lys Lys
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<210> 10

<211> 1343

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (211)..(996)

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tgtgaagggt gcagtaccta agccggagcg gggtagaggc gggccggcac ccccttctga	180
cctccagtgc cgcgggcctc aagatcagac atg gcc cag aac ttg aag gac ttg	234
Met Ala Gln Asn Leu Lys Asp Leu	
1 5	
gcg gga cgg ctg ccc gcc ggg ccc cgg ggc atg ggc acg gcc ctg aag	282
Ala Gly Arg Leu Pro Ala Gly Pro Arg Gly Met Gly Thr Ala Leu Lys	
10 15 20	
ctg ttg ctg ggg gcc ggc gcc gtg gcc tac ggt gtg cgc gaa tct gtg	330
Leu Leu Leu Gly Ala Gly Ala Val Ala Tyr Gly Val Arg Glu Ser Val	
25 30 35 40	
ttc acc gtg gaa ggc ggg cac aga gcc atc ttc ttc aat cgg atc ggt	378
Phe Thr Val Glu Gly Gly His Arg Ala Ile Phe Phe Asn Arg Ile Gly	
45 50 55	
gga gtg cag cag gac act atc ctg gcc gag ggc ctt cac ttc agg atc	426
Gly Val Gln Gln Asp Thr Ile Leu Ala Glu Gly Leu His Phe Arg Ile	
60 65 70	
cct tgg ttc cag tac ccc att atc tat gac att cgg gcc aga cct cga	474
Pro Trp Phe Gln Tyr Pro Ile Ile Tyr Asp Ile Arg Ala Arg Pro Arg	
75 80 85	
aaa atc tcc tcc cct aca ggc tcc aaa gac cta cag atg gtg aat atc	522
Lys Ile Ser Ser Pro Thr Gly Ser Lys Asp Leu Gln Met Val Asn Ile	
90 95 100	
tcc ctg cga gtg ttg tct cga ccc aat gct cag gag ctt cct agc atg	570
Ser Leu Arg Val Leu Ser Arg Pro Asn Ala Gln Glu Leu Pro Ser Met	
105 110 115 120	
tac cag cgc cta ggg ctg gac tac gag gaa cga gtg ttg ccg tcc att	618
Tyr Gln Arg Leu Gly Leu Asp Tyr Glu Glu Arg Val Leu Pro Ser Ile	
125 130 135	
gtc aac gag gtg ctc aag agt gtg gtg gcc aag ttc aat gcc tca cag	666
Val Asn Glu Val Leu Lys Ser Val Val Ala Lys Phe Asn Ala Ser Gln	
140 145 150	

ctg atc acc cag cgg gcc cag gta tcc ctg ttg atc cgc cgg gag ctg Leu Ile Thr Gln Arg Ala Gln Val Ser Leu Leu Ile Arg Arg Glu Leu 155 160 165	714
aca gag agg gcc aag gac ttc agc ctc atc ctg gat gat gtg gcc atc Thr Glu Arg Ala Lys Asp Phe Ser Leu Ile Leu Asp Asp Val Ala Ile 170 175 180	762
aca gag ctg agc ttt agc cga gag tac aca gct gct gta gaa gcc aaa Thr Glu Leu Ser Phe Ser Arg Glu Tyr Thr Ala Ala Val Glu Ala Lys 185 190 195 200	810
caa gtg gca ctg agc aag aac cct ggc tac atc aaa ctt cgc aag att Gln Val Ala Leu Ser Lys Asn Pro Gly Tyr Ile Lys Leu Arg Lys Ile 205 210 215	858
cga gca gcc cag aat atc tcc aag acg atc gcc aca tca cag aat cgt Arg Ala Ala Gln Asn Ile Ser Lys Thr Ile Ala Thr Ser Gln Asn Arg 220 225 230	906
atc tat ctc aca gct gac aac ctt gtg ctg aac cta cag gat gaa agt Ile Tyr Leu Thr Ala Asp Asn Leu Val Leu Asn Leu Gln Asp Glu Ser 235 240 245	954
ttc acc agg gga agt gac agc ctc atc aag ggt aag aaa tga Phe Thr Arg Gly Ser Asp Ser Leu Ile Lys Gly Lys Lys 250 255 260	996
gcctagtcac caagaactcc acccccagag gaagtggatc tgcttctcca gtttttgagg	1056
agccagccag ggggtccagca cagccctacc ccgccccagt atcatgcgat ggtccccac	1116
accggttccc tgaaccctc ttggattaag gaagactgaa gactagcccc ttttctgggg	1176
aattactttc ctctccctg tgttaactgg ggctgttggg gacagtgcgt gatttctcag	1236
tgatttcta cagtgttggt ccctccctca aggotgggag gagataaaca ccaaccagg	1296
aattctcaat aaatttttat tacttaacct gaaaaaaaaa aaaaaaa	1343

<210> 11
 <211> 261
 <212> PRT
 <213> Homo sapiens

<400> 11

Met Ala Gln Asn Leu Lys Asp Leu Ala Gly Arg Leu Pro Ala Gly Pro
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Arg Gly Met Gly Thr Ala Leu Lys Leu Leu Leu Gly Ala Gly Ala Val
 20 25 30

Ala Tyr Gly Val Arg Glu Ser Val Phe Thr Val Glu Gly Gly His Arg
 35 40 45

Ala Ile Phe Phe Asn Arg Ile Gly Gly Val Gln Gln Asp Thr Ile Leu
 50 55 60

Ala Glu Gly Leu His Phe Arg Ile Pro Trp Phe Gln Tyr Pro Ile Ile
 65 70 75 80

Tyr Asp Ile Arg Ala Arg Pro Arg Lys Ile Ser Ser Pro Thr Gly Ser
 85 90 95

Lys Asp Leu Gln Met Val Asn Ile Ser Leu Arg Val Leu Ser Arg Pro
 100 105 110

Asn Ala Gln Glu Leu Pro Ser Met Tyr Gln Arg Leu Gly Leu Asp Tyr
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Glu Glu Arg Val Leu Pro Ser Ile Val Asn Glu Val Leu Lys Ser Val
 130 135 140

Val Ala Lys Phe Asn Ala Ser Gln Leu Ile Thr Gln Arg Ala Gln Val
 145 150 155 160

Ser Leu Leu Ile Arg Arg Glu Leu Thr Glu Arg Ala Lys Asp Phe Ser
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Leu Ile Leu Asp Asp Val Ala Ile Thr Glu Leu Ser Phe Ser Arg Glu
 180 185 190

Tyr Thr Ala Ala Val Glu Ala Lys Gln Val Ala Leu Ser Lys Asn Pro

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Thr Met Thr Leu His Thr Lys Ala Ser Gly Met Ala Leu Leu His Gln			
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Ile Gln Gly Asn Glu Leu Glu Pro Leu Asn Arg Pro Gln Leu Lys Ile			
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Ala	Val	Tyr	Asn	Tyr	Pro	Glu	Gly	Ala	Ala	Tyr	Glu	Phe	Asn	Ala	Ala	
50					55					60					65	
gcc	gcc	gcc	aac	gcg	cag	gtc	tac	ggc	cag	acc	ggc	ctc	ccc	tac	ggc	477
Ala	Ala	Ala	Asn	Ala	Gln	Val	Tyr	Gly	Gln	Thr	Gly	Leu	Pro	Tyr	Gly	
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ccc	ggg	tct	gag	gct	gcg	gcg	ttc	ggc	tcc	aac	ggc	ctg	ggg	ggc	ttc	525
Pro	Gly	Ser	Glu	Ala	Ala	Ala	Phe	Gly	Ser	Asn	Gly	Leu	Gly	Gly	Phe	
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Pro	Pro	Leu	Asn	Ser	Val	Ser	Pro	Ser	Pro	Leu	Met	Leu	Leu	His	Pro	
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Pro	Pro	Gln	Leu	Ser	Pro	Phe	Leu	Gln	Pro	His	Gly	Gln	Gln	Val	Pro	
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Arg	Glu	Arg	Leu	Ala	Ser	Thr	Asn	Asp	Lys	Gly	Ser	Met	Ala	Met	Glu	
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Ser	Ala	Lys	Glu	Thr	Arg	Tyr	Cys	Ala	Val	Cys	Asn	Asp	Tyr	Ala	Ser	
		180					185					190				
ggc	tac	cat	tat	gga	gtc	tgg	tcc	tgt	gag	ggc	tgc	aag	gcc	ttc	ttc	861
Gly	Tyr	His	Tyr	Gly	Val	Trp	Ser	Cys	Glu	Gly	Cys	Lys	Ala	Phe	Phe	
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Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro Gly

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ttc tgc gct gtc tgc agc gat tac gca tcg gga tat cac tat gga gtc Phe Cys Ala Val Cys Ser Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val 150 155 160			957
tgg tcg tgt gaa gga tgt aag gcc ttt ttt aaa aga agc att caa gga Trp Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly 165 170 175			1005
cat aat gat tat att tgt cca gct aca aat cag tgt aca atc gat aaa His Asn Asp Tyr Ile Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Lys 180 185 190 195			1053
aac cgg cgc aag agc tgc cag gcc tgc cga ctt cgg aag tgt tac gaa Asn Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu 200 205 210			1101
gtg gga atg gtg aag tgt ggc tcc cgg aga gag aga tgt ggg tac cgc Val Gly Met Val Lys Cys Gly Ser Arg Arg Glu Arg Cys Gly Tyr Arg 215 220 225			1149
ctt gtg cgg aga cag aga agt gcc gac gag cag ctg cac tgt gcc ggc Leu Val Arg Arg Gln Arg Ser Ala Asp Glu Gln Leu His Cys Ala Gly 230 235 240			1197
aag gcc aag aga agt ggc ggc cac gcg ccc cga gtg cgg gag ctg ctg Lys Ala Lys Arg Ser Gly Gly His Ala Pro Arg Val Arg Glu Leu Leu 245 250 255			1245

ctg gac gcc ctg agc ccc gag cag cta gtg ctc acc ctc ctg gag gct Leu Asp Ala Leu Ser Pro Glu Gln Leu Val Leu Thr Leu Leu Glu Ala 260 265 270 275	1293
gag ccg ccc cat gtg ctg atc agc cgc ccc agt gcg ccc ttc acc gag Glu Pro Pro His Val Leu Ile Ser Arg Pro Ser Ala Pro Phe Thr Glu 280 285 290	1341
gcc tcc atg atg atg tcc ctg acc aag ttg gcc gac aag gag ttg gta Ala Ser Met Met Met Ser Leu Thr Lys Leu Ala Asp Lys Glu Leu Val 295 300 305	1389
cac atg atc agc tgg gcc aag aag att ccc ggc ttt gtg gag ctc agc His Met Ile Ser Trp Ala Lys Lys Ile Pro Gly Phe Val Glu Leu Ser 310 315 320	1437
ctg ttc gac caa gtg cgg ctc ttg gag agc tgt tgg atg gag gtg tta Leu Phe Asp Gln Val Arg Leu Leu Glu Ser Cys Trp Met Glu Val Leu 325 330 335	1485
atg atg ggg ctg atg tgg cgc tca att gac cac ccc ggc aag ctc atc Met Met Gly Leu Met Trp Arg Ser Ile Asp His Pro Gly Lys Leu Ile 340 345 350 355	1533
ttt gct cca gat ctt gtt ctg gac agg gat gag ggg aaa tgc gta gaa Phe Ala Pro Asp Leu Val Leu Asp Arg Asp Glu Gly Lys Cys Val Glu 360 365 370	1581
gga att ctg gaa atc ttt gac atg ctc ctg gca act act tca agg ttt Gly Ile Leu Glu Ile Phe Asp Met Leu Leu Ala Thr Thr Ser Arg Phe 375 380 385	1629
cga gag tta aaa ctc caa cac aaa gaa tat ctc tgt gtc aag gcc atg Arg Glu Leu Lys Leu Gln His Lys Glu Tyr Leu Cys Val Lys Ala Met 390 395 400	1677
atc ctg ctc aat tcc agt atg tac cct ctg gtc aca gcg acc cag gat Ile Leu Leu Asn Ser Ser Met Tyr Pro Leu Val Thr Ala Thr Gln Asp 405 410 415	1725
gct gac agc agc cgg aag ctg gct cac ttg ctg aac gcc gtg acc gat Ala Asp Ser Ser Arg Lys Leu Ala His Leu Leu Asn Ala Val Thr Asp 420 425 430 435	1773
gct ttg gtt tgg gtg att gcc aag agc ggc atc tcc tcc cag cag caa Ala Leu Val Trp Val Ile Ala Lys Ser Gly Ile Ser Ser Gln Gln Gln 440 445 450	1821

tcc atg cgc ctg gct aac ctc ctg atg ctc ctg tcc cac gtc agg cat 1869
 Ser Met Arg Leu Ala Asn Leu Leu Met Leu Leu Ser His Val Arg His
 455 460 465

gcg agt aac aag ggc atg gaa cat ctg ctc aac atg aag tgc aaa aat 1917
 Ala Ser Asn Lys Gly Met Glu His Leu Leu Asn Met Lys Cys Lys Asn
 470 475 480

gtg gtc cca gtg tat gac ctg ctg ctg gag atg ctg aat gcc cac gtg 1965
 Val Val Pro Val Tyr Asp Leu Leu Leu Glu Met Leu Asn Ala His Val
 485 490 495

ctt cgc ggg tgc aag tcc tcc atc acg ggg tcc gag tgc agc ccg gca 2013
 Leu Arg Gly Cys Lys Ser Ser Ile Thr Gly Ser Glu Cys Ser Pro Ala
 500 505 510 515

gag gac agt aaa agc aaa gag ggc tcc cag aac cca cag tct cag tga 2061
 Glu Asp Ser Lys Ser Lys Glu Gly Ser Gln Asn Pro Gln Ser Gln
 520 525 530

cgcctggccc tgaggtgaac tggcccacag aggtcacagg ctgaagcgtg aactccagtg 2121

tgtcaggagc ctgggcttca tctttctgct gtgtggtccc tcatttgg 2169

<210> 15

<211> 530

<212> PRT

<213> Homo sapiens

<400> 15

Met Asp Ile Lys Asn Ser Pro Ser Ser Leu Asn Ser Pro Ser Ser Tyr
 1 5 10 15

Asn Cys Ser Gln Ser Ile Leu Pro Leu Glu His Gly Ser Ile Tyr Ile
 20 25 30

Pro Ser Ser Tyr Val Asp Ser His His Glu Tyr Pro Ala Met Thr Phe
 35 40 45

Tyr Ser Pro Ala Val Met Asn Tyr Ser Ile Pro Ser Asn Val Thr Asn
 50 55 60

Leu Glu Gly Gly Pro Gly Arg Gln Thr Thr Ser Pro Asn Val Leu Trp

65		70		75		80
Pro Thr Pro Gly	His Leu Ser Pro Leu Val Val His Arg Gln Leu Ser					
	85		90		95	
His Leu Tyr Ala Glu Pro Gln Lys Ser Pro Trp Cys Glu Ala Arg Ser						
	100		105		110	
Leu Glu His Thr Leu Pro Val Asn Arg Glu Thr Leu Lys Arg Lys Val						
	115		120		125	
Ser Gly Asn Arg Cys Ala Ser Pro Val Thr Gly Pro Gly Ser Lys Arg						
	130		135		140	
Asp Ala His Phe Cys Ala Val Cys Ser Asp Tyr Ala Ser Gly Tyr His						
	145		150		155	160
Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser						
		165		170		175
Ile Gln Gly His Asn Asp Tyr Ile Cys Pro Ala Thr Asn Gln Cys Thr						
	180		185		190	
Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys						
	195		200		205	
Cys Tyr Glu Val Gly Met Val Lys Cys Gly Ser Arg Arg Glu Arg Cys						
	210		215		220	
Gly Tyr Arg Leu Val Arg Arg Gln Arg Ser Ala Asp Glu Gln Leu His						
	225		230		235	240
Cys Ala Gly Lys Ala Lys Arg Ser Gly Gly His Ala Pro Arg Val Arg						
		245		250		255
Glu Leu Leu Leu Asp Ala Leu Ser Pro Glu Gln Leu Val Leu Thr Leu						
	260		265		270	

Leu Glu Ala Glu Pro Pro His Val Leu Ile Ser Arg Pro Ser Ala Pro
 275 280 285

Phe Thr Glu Ala Ser Met Met Met Ser Leu Thr Lys Leu Ala Asp Lys
 290 295 300

Glu Leu Val His Met Ile Ser Trp Ala Lys Lys Ile Pro Gly Phe Val
 305 310 315 320

Glu Leu Ser Leu Phe Asp Gln Val Arg Leu Leu Glu Ser Cys Trp Met
 325 330 335

Glu Val Leu Met Met Gly Leu Met Trp Arg Ser Ile Asp His Pro Gly
 340 345 350

Lys Leu Ile Phe Ala Pro Asp Leu Val Leu Asp Arg Asp Glu Gly Lys
 355 360 365

Cys Val Glu Gly Ile Leu Glu Ile Phe Asp Met Leu Leu Ala Thr Thr
 370 375 380

Ser Arg Phe Arg Glu Leu Lys Leu Gln His Lys Glu Tyr Leu Cys Val
 385 390 395 400

Lys Ala Met Ile Leu Leu Asn Ser Ser Met Tyr Pro Leu Val Thr Ala
 405 410 415

Thr Gln Asp Ala Asp Ser Ser Arg Lys Leu Ala His Leu Leu Asn Ala
 420 425 430

Val Thr Asp Ala Leu Val Trp Val Ile Ala Lys Ser Gly Ile Ser Ser
 435 440 445

Gln Gln Gln Ser Met Arg Leu Ala Asn Leu Leu Met Leu Leu Ser His
 450 455 460

Val Arg His Ala Ser Asn Lys Gly Met Glu His Leu Leu Asn Met Lys
 465 470 475 480

Cys Lys Asn Val Val Pro Val Tyr Asp Leu Leu Leu Glu Met Leu Asn
 485 490 495

Ala His Val Leu Arg Gly Cys Lys Ser Ser Ile Thr Gly Ser Glu Cys
 500 505 510

Ser Pro Ala Glu Asp Ser Lys Ser Lys Glu Gly Ser Gln Asn Pro Gln
 515 520 525

Ser Gln
 530

<210> 16
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> an HA-tag peptide

<400> 16

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
 1 5

<210> 17
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PHB2 peptide containing Ser39

<400> 17

Tyr Gly Val Arg Glu Ser Val Phe Thr Val Glu
 1 5 10

<210> 18
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> An artificially synthesized primer sequence for BIG3

<400> 18

cttgacaagg cctttggagt

20

<210> 19
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> An artificially synthesized primer sequence for BIG3

<400> 19

caatatgctt ttcccgcttt

20

<210> 20
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> An artificially synthesized primer sequence for beta 2-MG

<400> 20

aacttagagg tggggagcag

20

<210> 21
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>

<223> An artificially synthesized primer sequence for beta 2-MG

<400> 21

cacaaccatg ccttacttta tc

22