

1168 WO\_PCT Seq List AS FILED.txt  
SEQUENCE LISTING

<110> Laboratoires Serono SA

<120> SARP-1 FUSION PROTEINS AND USES THEREOF

<130> 1168 WO/PCT

<150> EP07123115.3  
<151> 2007-12-13

<150> US61/008,329  
<151> 2007-12-17

<160> 32

<170> PatentIn version 3.3

<210> 1  
<211> 295  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> (1)..(24)

<220>  
<221> mat\_peptide  
<222> (25)..(295)  
<223> SARP-1

<220>  
<221> DOMAIN  
<222> (35)..(155)  
<223> Frizzled domain

<220>  
<221> DOMAIN  
<222> (169)..(295)  
<223> Netrin domain

<300>  
<308> Swissprot / Q96HF1  
<309> 2005-03-15  
<313> (1)..(295)

<400> 1

Met Leu Gln Gly Pro Gly Ser Leu Leu Leu Phe Leu Ala Ser His  
                    -20                    -15                    -10

Cys Cys Leu Gly Ser Ala Arg Gly Leu Phe Leu Phe Gly Gln Pro Asp  
          -5                    -1  1                    5

Phe Ser Tyr Lys Arg Ser Asn Cys Lys Pro Ile Pro Ala Asn Leu Gln  
  10                    15                    20

Leu Cys His Gly Ile Glu Tyr Gln Asn Met Arg Leu Pro Asn Leu Leu  
25                    30                    35                    40

Gly His Glu Thr Met Lys Glu Val Leu Glu Gln Ala Gly Ala Trp Ile  
          45                    50                    55

1168 WO\_PCT Seq List AS FILED.txt

Pro Leu Val Met Lys Gln Cys His Pro Asp Thr Lys Lys Phe Leu Cys  
60 65 70

Ser Leu Phe Ala Pro Val Cys Leu Asp Asp Leu Asp Glu Thr Ile Gln  
75 80 85

Pro Cys His Ser Leu Cys Val Gln Val Lys Asp Arg Cys Ala Pro Val  
90 95 100

Met Ser Ala Phe Gly Phe Pro Trp Pro Asp Met Leu Glu Cys Asp Arg  
105 110 115 120

Phe Pro Gln Asp Asn Asp Leu Cys Ile Pro Leu Ala Ser Ser Asp His  
125 130 135

Leu Leu Pro Ala Thr Glu Glu Ala Pro Lys Val Cys Glu Ala Cys Lys  
140 145 150

Asn Lys Asn Asp Asp Asp Asn Asp Ile Met Glu Thr Leu Cys Lys Asn  
155 160 165

Asp Phe Ala Leu Lys Ile Lys Val Lys Glu Ile Thr Tyr Ile Asn Arg  
170 175 180

Asp Thr Lys Ile Ile Leu Glu Thr Lys Ser Lys Thr Ile Tyr Lys Leu  
185 190 195 200

Asn Gly Val Ser Glu Arg Asp Leu Lys Lys Ser Val Leu Trp Leu Lys  
205 210 215

Asp Ser Leu Gln Cys Thr Cys Glu Glu Met Asn Asp Ile Asn Ala Pro  
220 225 230

Tyr Leu Val Met Gly Gln Lys Gln Gly Gly Glu Leu Val Ile Thr Ser  
235 240 245

Val Lys Arg Trp Gln Lys Gly Gln Arg Glu Phe Lys Arg Ile Ser Arg  
250 255 260

Ser Ile Arg Lys Leu Gln Cys  
265 270

<210> 2  
<211> 271  
<212> PRT  
<213> Homo sapiens

<220>  
<221> mat\_peptide  
<222> (1)..(271)  
<223> Q96HF1 without the signal peptide

<400> 2

1168 WO\_PCT Seq List AS FILED.txt

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

1168 WO\_PCT Seq List AS FILED.txt

<210> 3  
<211> 882  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (265)..(882)  
<223> SARP-1

<220>  
<221> misc\_feature  
<222> (615)..(615)  
<223> n is a, c, g, or t

<300>  
<308> GenBank / AF017986  
<309> 1999-07-29  
<313> (1)..(882)

<400> 3  
gaattcgttc agcctgggta agtccaagct ggctcattct gtccccccg gtcggagccc 60  
cccggagctg cgcgcgggct tgcagcgcct cgcccgcgct gtcctcccgg tgtcccgctt 120  
ctccgcgccc cagccgccgg ctgccagctt ttcggggccc cgagtcgcac ccagcgaaga 180  
gagcgggccc gggacaagct cgaactccgg ccgcctcgcc cttaaccagc tccgtccctc 240  
tacccttag gggtcgcgcc cacg atg ctg cag ggc cct ggc tcg ctg ctg 291  
Met Leu Gln Gly Pro Gly Ser Leu Leu  
1 5  
ctg ctg ttc ctc gcc tcg cac tgc tgc ctg ggc tcg gcg cgc ggg ctc 339  
Leu Leu Phe Leu Ala Ser His Cys Cys Leu Gly Ser Ala Arg Gly Leu  
10 15 20 25  
ttc ctc ttt ggc cag ccc gac ttc tcc tac aag cgc agc aat tgc aag 387  
Phe Leu Phe Gly Gln Pro Asp Phe Ser Tyr Lys Arg Ser Asn Cys Lys  
30 35 40  
ccc atc ccg gcc aac ctg cag ctg tgc cac ggc atc gaa tac cag aac 435  
Pro Ile Pro Ala Asn Leu Gln Leu Cys His Gly Ile Glu Tyr Gln Asn  
45 50 55  
atg cgg ctg ccc aac ctg ctg ggc cac gag acc atg aag gag gtg ctg 483  
Met Arg Leu Pro Asn Leu Leu Gly His Glu Thr Met Lys Glu Val Leu  
60 65 70  
gag cag gcc ggc gct tgg atc ccg ctg gtc atg aag cag tgc cac ccg 531  
Glu Gln Ala Gly Ala Trp Ile Pro Leu Val Met Lys Gln Cys His Pro  
75 80 85  
gac acc aag aag ttc ctg tgc tcg ctc ttc gcc ccc gtc tgc ctc gat 579  
Asp Thr Lys Lys Phe Leu Cys Ser Leu Phe Ala Pro Val Cys Leu Asp  
90 95 100 105  
gac cta gac gag acc atc cag cca tgc cac tct cgn tgc gtg cag gtg 627  
Asp Leu Asp Glu Thr Ile Gln Pro Cys His Ser Arg Cys Val Gln Val  
110 115 120  
aag gat cgc tgc gcc ccg gtc atg tcc gcc ttc ccc tgg ccc gac atg 675  
Lys Asp Arg Cys Ala Pro Val Met Ser Ala Phe Pro Trp Pro Asp Met  
125 130 135  
ctt gag tgc gac cgt ttc ccc cag gac aac gac ctt tgc atc ccc ctc 723  
Leu Glu Cys Asp Arg Phe Pro Gln Asp Asn Asp Leu Cys Ile Pro Leu  
140 145 150

1168 WO\_PCT Seq List AS FILED.txt

gct agc agc gac cac ctc ctg cca gcc acc gag gaa gct cca aag gta 771  
Ala Ser Ser Asp His Leu Leu Pro Ala Thr Glu Glu Ala Pro Lys Val  
155 160 165

tgt gaa gcc tgc aaa aat aaa aat gat gat gac aac gac ata atg gaa 819  
Cys Glu Ala Cys Lys Asn Lys Asn Asp Asp Asp Asn Asp Ile Met Glu  
170 175 180 185

acg ctt tgt aaa aat gat ttt gca ctg aaa ata aaa gtg aag gag ata 867  
Thr Leu Cys Lys Asn Asp Phe Ala Leu Lys Ile Lys Val Lys Glu Ile  
190 195 200

acc tac atc aac cgt 882  
Thr Tyr Ile Asn Arg  
205

<210> 4  
<211> 206  
<212> PRT  
<213> Homo sapiens

<400> 4

Met Leu Gln Gly Pro Gly Ser Leu Leu Leu Leu Phe Leu Ala Ser His  
1 5 10 15

Cys Cys Leu Gly Ser Ala Arg Gly Leu Phe Leu Phe Gly Gln Pro Asp  
20 25 30

Phe Ser Tyr Lys Arg Ser Asn Cys Lys Pro Ile Pro Ala Asn Leu Gln  
35 40 45

Leu Cys His Gly Ile Glu Tyr Gln Asn Met Arg Leu Pro Asn Leu Leu  
50 55 60

Gly His Glu Thr Met Lys Glu Val Leu Glu Gln Ala Gly Ala Trp Ile  
65 70 75 80

Pro Leu Val Met Lys Gln Cys His Pro Asp Thr Lys Lys Phe Leu Cys  
85 90 95

Ser Leu Phe Ala Pro Val Cys Leu Asp Asp Leu Asp Glu Thr Ile Gln  
100 105 110

Pro Cys His Ser Arg Cys Val Gln Val Lys Asp Arg Cys Ala Pro Val  
115 120 125

Met Ser Ala Phe Pro Trp Pro Asp Met Leu Glu Cys Asp Arg Phe Pro  
130 135 140

Gln Asp Asn Asp Leu Cys Ile Pro Leu Ala Ser Ser Asp His Leu Leu  
145 150 155 160

Pro Ala Thr Glu Glu Ala Pro Lys Val Cys Glu Ala Cys Lys Asn Lys  
165 170 175

1168 WO\_PCT Seq List AS FILED.txt

Asn Asp Asp Asp Asn Asp Ile Met Glu Thr Leu Cys Lys Asn Asp Phe  
180 185 190

Ala Leu Lys Ile Lys Val Lys Glu Ile Thr Tyr Ile Asn Arg  
195 200 205

<210> 5  
<211> 1988  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (238)..(1125)  
<223> SARP-1

<300>  
<308> GenBank / AF311912  
<309> 2001-07-13  
<313> (1)..(1988)

<400> 5  
ggctcattct gctcccccg gtcggagccc cccggagctg cgcgcgggct tgcagcgctt 60  
cgccccgcgt gtcctcccg tgtcccgtt ctccgcgccc cagccgccgg ctgccagctt 120  
ttcggggccc cgagtcgcac ccagcgaaga gagcggggccc gggacaagct cgaactccgg 180  
ccgcctcgcc cttccccggc tccgctccct ctgccccctc ggggtcgcgc gccacg 237  
atg ctg cag ggc cct ggc tcg ctg ctg ctg ctc ttc ctc gcc tcg cac 285  
Met Leu Gln Gly Pro Gly Ser Leu Leu Leu Phe Leu Ala Ser His  
1 5 10 15  
tgc tgc ctg ggc tcg ggc cgc ggg ctc ttc ctc ttt ggc cag ccc gac 333  
Cys Cys Leu Gly Ser Ala Arg Gly Leu Phe Leu Phe Gly Gln Pro Asp  
20 25 30  
ttc tcc tac aag cgc agc aat tgc aag ccc atc ccg gcc aac ctg cag 381  
Phe Ser Tyr Lys Arg Ser Asn Cys Lys Pro Ile Pro Ala Asn Leu Gln  
35 40 45  
ctg tgc cac ggc atc gaa tac cag aac atg cgg ctg ccc aac ctg ctg 429  
Leu Cys His Gly Ile Glu Tyr Gln Asn Met Arg Leu Pro Asn Leu Leu  
50 55 60  
ggc cac gag acc atg aag gag gtg ctg gag cag gcc gcc gct tgg atc 477  
Gly His Glu Thr Met Lys Glu Val Leu Glu Gln Ala Gly Ala Trp Ile  
65 70 75 80  
ccg ctg gtc atg aag cag tgc cac ccg gac acc aag aag ttc ctg tgc 525  
Pro Leu Val Met Lys Gln Cys His Pro Asp Thr Lys Lys Phe Leu Cys  
85 90 95  
tcg ctc ttc gcc ccc gtc tgc ctc gat gac cta gac gag acc atc cag 573  
Ser Leu Phe Ala Pro Val Cys Leu Asp Asp Leu Asp Glu Thr Ile Gln  
100 105 110  
cca tgc cac tcg ctc tgc gtg cag gtg aag gac cgc tgc gcc ccg gtc 621  
Pro Cys His Ser Leu Cys Val Gln Val Lys Asp Arg Cys Ala Pro Val  
115 120 125  
atg tcc gcc ttc ggc ttc ccc tgg ccc gac atg ctt gag tgc gac cgt 669  
Met Ser Ala Phe Gly Phe Pro Trp Pro Asp Met Leu Glu Cys Asp Arg  
130 135 140

1168 WO\_PCT Seq List AS FILED.txt

ttc	ccc	cag	gac	aac	gac	ctt	tgc	atc	ccc	ctc	gct	agc	agc	gac	cac	717
Phe	Pro	Gln	Asp	Asn	Asp	Leu	Cys	Ile	Pro	Leu	Ala	Ser	Ser	Asp	His	
145					150					155					160	
ctc	ctg	cca	gcc	acc	gag	gaa	gct	cca	aag	gta	tgt	gaa	gcc	tgc	aaa	765
Leu	Leu	Pro	Ala	Thr	Glu	Glu	Ala	Pro	Lys	Val	Cys	Glu	Ala	Cys	Lys	
				165					170					175		
aat	aaa	aat	gat	gat	gac	aac	gac	ata	atg	gaa	acg	ctt	tgt	aaa	aat	813
Asn	Lys	Asn	Asp	Asp	Asp	Asn	Asp	Ile	Met	Glu	Thr	Leu	Cys	Lys	Asn	
			180					185					190			
gat	ttt	gca	ctg	aaa	ata	aaa	gtg	aag	gag	ata	acc	tac	atc	aac	cga	861
Asp	Phe	Ala	Leu	Lys	Ile	Lys	Val	Lys	Glu	Ile	Thr	Tyr	Ile	Asn	Arg	
		195					200					205				
gat	acc	aaa	atc	atc	ctg	gag	acc	aag	agc	aag	acc	att	tac	aag	ctg	909
Asp	Thr	Lys	Ile	Ile	Leu	Glu	Thr	Lys	Ser	Lys	Thr	Ile	Tyr	Lys	Leu	
	210					215					220					
aac	ggt	gtg	tcc	gaa	agg	gac	ctg	aag	aaa	tgc	gtg	ctg	tgg	ctc	aaa	957
Asn	Gly	Val	Ser	Glu	Arg	Asp	Leu	Lys	Lys	Ser	Val	Leu	Trp	Leu	Lys	
225					230					235					240	
gac	agc	tgg	cag	tgc	acc	tgt	gag	gag	atg	aac	gac	atc	aac	gcg	ccc	1005
Asp	Ser	Leu	Gln	Cys	Thr	Cys	Glu	Glu	Met	Asn	Asp	Ile	Asn	Ala	Pro	
				245					250					255		
tat	ctg	gtc	atg	gga	cag	aaa	cag	ggt	ggg	gag	ctg	gtg	atc	acc	tgc	1053
Tyr	Leu	Val	Met	Gly	Gln	Lys	Gln	Gly	Gly	Glu	Leu	Val	Ile	Thr	Ser	
			260					265					270			
gtg	aag	cgg	tgg	cag	aag	ggg	cag	aga	gag	ttc	aag	cgc	atc	tcc	cgc	1101
Val	Lys	Arg	Trp	Gln	Lys	Gly	Gln	Arg	Glu	Phe	Lys	Arg	Ile	Ser	Arg	
		275					280					285				
agc	atc	cgc	aag	ctg	cag	tgc	tag	tcccggc	atc	ctgatgg	ctc	cgacagg	cct			1155
Ser	Ile	Arg	Lys	Leu	Gln	Cys										
	290					295										
gctccagagc	acggctgacc	atttctgctc	cgggatctca	gctcccgttc	cccaagcaca											1215
ctcctagctg	ctccagtctc	agcctgggca	gcttccccct	gccttttgca	cgtttgcac											1275
cccagcattt	cctgagttat	aaggccacag	gagtggatag	ctgtttttcac	ctaaaggaaa											1335
agcccacccg	aatcttgtag	aaatattcaa	actaataaaa	tcatgaatat	ttttatgaag											1395
tttaaaaata	gctcacttta	aagctagttt	tgaataggtg	caactgtgac	ttgggtctgg											1455
ttggttgttg	tttgttgttt	tgagtcagct	gatttttact	tcccactgag	gttgtcataa											1515
catgcaaatt	gcttcaattt	tctctgtggc	ccaaacttgt	gggtcacaaa	ccctgttgag											1575
ataaagctgg	ctgttatctc	aacatcttca	tcagctccag	actgagactc	agtgctctaag											1635
tcttacaaca	attcatcatt	ttataccttc	aatgggaact	taaactgtta	catgtatcac											1695
attccagcta	caatacttcc	atttattaga	agcacattaa	ccattttctat	agcatgattt											1755
cttcaagtaa	aaggcaaaag	atataaattt	tataattgac	ttgagtactt	taagccttgt											1815
ttaaaacatt	tcttacttaa	cttttgcaaa	ttaaaccat	tgtagcttac	ctgtaataata											1875
catagtagtt	tacctttaaa	agttgtaaaa	atattgcttt	aaccaacact	gtaaatatatt											1935
cagataaaca	ttatattcct	gtatataaac	tttacatcct	gttttaccta	taa											1988

1168 WO\_PCT Seq List AS FILED.txt

<210> 6  
 <211> 295  
 <212> PRT  
 <213> Homo sapiens

<400> 6

```

Met Leu Gln Gly Pro Gly Ser Leu Leu Leu Leu Phe Leu Ala Ser His
1      5      10      15

Cys Cys Leu Gly Ser Ala Arg Gly Leu Phe Leu Phe Gly Gln Pro Asp
20      25      30

Phe Ser Tyr Lys Arg Ser Asn Cys Lys Pro Ile Pro Ala Asn Leu Gln
35      40      45

Leu Cys His Gly Ile Glu Tyr Gln Asn Met Arg Leu Pro Asn Leu Leu
50      55      60

Gly His Glu Thr Met Lys Glu Val Leu Glu Gln Ala Gly Ala Trp Ile
65      70      75      80

Pro Leu Val Met Lys Gln Cys His Pro Asp Thr Lys Lys Phe Leu Cys
85      90      95

Ser Leu Phe Ala Pro Val Cys Leu Asp Asp Leu Asp Glu Thr Ile Gln
100     105     110

Pro Cys His Ser Leu Cys Val Gln Val Lys Asp Arg Cys Ala Pro Val
115     120     125

Met Ser Ala Phe Gly Phe Pro Trp Pro Asp Met Leu Glu Cys Asp Arg
130     135     140

Phe Pro Gln Asp Asn Asp Leu Cys Ile Pro Leu Ala Ser Ser Asp His
145     150     155     160

Leu Leu Pro Ala Thr Glu Glu Ala Pro Lys Val Cys Glu Ala Cys Lys
165     170     175

Asn Lys Asn Asp Asp Asp Asn Asp Ile Met Glu Thr Leu Cys Lys Asn
180     185     190

Asp Phe Ala Leu Lys Ile Lys Val Lys Glu Ile Thr Tyr Ile Asn Arg
195     200     205

Asp Thr Lys Ile Ile Leu Glu Thr Lys Ser Lys Thr Ile Tyr Lys Leu
210     215     220

Asn Gly Val Ser Glu Arg Asp Leu Lys Lys Ser Val Leu Trp Leu Lys
225     230     235     240

Asp Ser Leu Gln Cys Thr Cys Glu Glu Met Asn Asp Ile Asn Ala Pro
245     250     255
    
```



1168 WO\_PCT Seq List AS FILED.txt

Tyr Leu Val Met Gly Gln Lys Gln Gly Gly Glu Leu Val Ile Thr Ser  
260 265 270

Val Lys Arg Trp Gln Lys Gly Gln Arg Glu Phe Lys Arg Ile Ser Arg  
275 280 285

Ser Ile Arg Lys Leu Gln Cys  
290 295

<210> 7  
<211> 1196  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (44)..(931)  
<223> SARP-1

<300>  
<308> GenBank / AY359001  
<309> 2003-10-03  
<313> (1)..(1196)

<400> 7  
cccggctccg ctccctctgc cccctcgggg tcgctgcgcc acg atg ctg cag ggc 55  
Met Leu Gln Gly  
1

cct ggc tcg ctg ctg ctg ctc ttc ctc gcc tcg cac tgc tgc ctg ggc 103  
Pro Gly Ser Leu Leu Leu Leu Phe Leu Ala Ser His Cys Cys Leu Gly  
5 10 15 20

tcg gcg cgc ggc ctc ttc ctc ttt ggc cag ccc gac ttc tcc tac aag 151  
Ser Ala Arg Gly Leu Phe Leu Phe Gly Gln Pro Asp Phe Ser Tyr Lys  
25 30 35

cgc agc aat tgc aag ccc atc ccg gtc aac ctg cag ctg tgc cac ggc 199  
Arg Ser Asn Cys Lys Pro Ile Pro Val Asn Leu Gln Leu Cys His Gly  
40 45 50

atc gaa tac cag aac atg cgg ctg ccc aac ctg ctg ggc cac gag acc 247  
Ile Glu Tyr Gln Asn Met Arg Leu Pro Asn Leu Leu Gly His Glu Thr  
55 60 65

atg aag gag gtg ctg gag cag gcc ggc gct tgg atc ccg ctg gtc atg 295  
Met Lys Glu Val Leu Glu Gln Ala Gly Ala Trp Ile Pro Leu Val Met  
70 75 80

aag cag tgc cac ccg gac acc aag aag ttc ctg tgc tcg ctc ttc gcc 343  
Lys Gln Cys His Pro Asp Thr Lys Lys Phe Leu Cys Ser Leu Phe Ala  
85 90 100

ccc gtc tgc ctc gat gac cta gac gag acc atc cag cca tgc cac tcg 391  
Pro Val Cys Leu Asp Asp Leu Asp Glu Thr Ile Gln Pro Cys His Ser  
105 110 115

ctc tgc gtg cag gtg aag gac cgc tgc gcc ccg gtc atg tcc gcc ttc 439  
Leu Cys Val Gln Val Lys Asp Arg Cys Ala Pro Val Met Ser Ala Phe  
120 125 130

ggc ttc ccc tgg ccc gac atg ctt gag tgc gac cgt ttc ccc cag gac 487  
Gly Phe Pro Trp Pro Asp Met Leu Glu Cys Asp Arg Phe Pro Gln Asp

1168 WO\_PCT Seq List AS FILED.txt  
140 145

135

aac	gac	ctt	tgc	atc	ccc	ctc	gct	agc	agc	gac	cac	ctc	ctg	cca	gcc	535
Asn	Asp	Leu	Cys	Ile	Pro	Leu	Ala	Ser	Ser	Asp	His	Leu	Leu	Pro	Ala	
	150					155					160					
acc	gag	gaa	gct	cca	aag	gta	tgt	gaa	gcc	tgc	aaa	aat	aaa	aat	gat	583
Thr	Glu	Glu	Ala	Pro	Lys	Val	Cys	Glu	Ala	Cys	Lys	Asn	Lys	Asn	Asp	
165					170					175					180	
gat	gac	aac	gac	ata	atg	gaa	acg	ctt	tgt	aaa	aat	gat	ttt	gca	ctg	631
Asp	Asp	Asn	Asp	Ile	Met	Glu	Thr	Leu	Cys	Lys	Asn	Asp	Phe	Ala	Leu	
				185					190					195		
aaa	ata	aaa	gtg	aag	gag	ata	acc	tac	atc	aac	cga	gat	acc	aaa	atc	679
Lys	Ile	Lys	Val	Lys	Glu	Ile	Thr	Tyr	Ile	Asn	Arg	Asp	Thr	Lys	Ile	
			200					205					210			
atc	ctg	gag	acc	aag	agc	aag	acc	att	tac	aag	ctg	aac	ggg	gtg	tcc	727
Ile	Leu	Glu	Thr	Lys	Ser	Lys	Thr	Ile	Tyr	Lys	Leu	Asn	Gly	Val	Ser	
		215					220					225				
gaa	agg	gac	ctg	aag	aaa	tcg	gtg	ctg	tgg	ctc	aaa	gac	agc	ttg	cag	775
Glu	Arg	Asp	Leu	Lys	Lys	Ser	Val	Leu	Trp	Leu	Lys	Asp	Ser	Leu	Gln	
	230					235					240					
tgc	acc	tgt	gag	gag	atg	aac	gac	atc	aac	gcg	ccc	tat	ctg	gtc	atg	823
Cys	Thr	Cys	Glu	Glu	Met	Asn	Asp	Ile	Asn	Ala	Pro	Tyr	Leu	Val	Met	
245					250					255					260	
gga	cag	aaa	cag	ggg	ggg	gag	ctg	gtg	atc	acc	tcg	gtg	aag	cgg	tgg	871
Gly	Gln	Lys	Gln	Gly	Gly	Glu	Leu	Val	Ile	Thr	Ser	Val	Lys	Arg	Trp	
				265					270					275		
cag	aag	ggg	cag	aga	gag	ttc	aag	cgc	atc	tcc	cgc	agc	atc	cgc	aag	919
Gln	Lys	Gly	Gln	Arg	Glu	Phe	Lys	Arg	Ile	Ser	Arg	Ser	Ile	Arg	Lys	
			280					285					290			
ctg	cag	tgc	tag	tcccggcatc	ctgatggctc	cgacaggcct	gctccagagc									971
Leu	Gln	Cys														
		295														
acggctgacc	atttctgctc	cgggatctca	gctcccgttc	cccaagcaca	ctcctagctg											1031
ctccagtctc	agcctgggca	gcttccccct	gccttttgca	cgtttgcatc	cccagcattt											1091
cctgagttat	aaggccacag	gagtggatag	ctgttttcac	ctaaaggaaa	agcccacccg											1151
aatctttag	aaatattcaa	actaataaaa	tcatgaatat	tttaa												1196

<210> 8  
<211> 295  
<212> PRT  
<213> Homo sapiens

<400> 8

Met	Leu	Gln	Gly	Pro	Gly	Ser	Leu	Leu	Leu	Leu	Phe	Leu	Ala	Ser	His
1				5					10					15	
Cys	Cys	Leu	Gly	Ser	Ala	Arg	Gly	Leu	Phe	Leu	Phe	Gly	Gln	Pro	Asp
			20					25					30		
Phe	Ser	Tyr	Lys	Arg	Ser	Asn	Cys	Lys	Pro	Ile	Pro	Val	Asn	Leu	Gln
		35					40					45			

1168 WO\_PCT Seq List AS FILED.txt

Leu Cys His Gly Ile Glu Tyr Gln Asn Met Arg Leu Pro Asn Leu Leu  
50 55 60

Gly His Glu Thr Met Lys Glu Val Leu Glu Gln Ala Gly Ala Trp Ile  
65 70 75 80

Pro Leu Val Met Lys Gln Cys His Pro Asp Thr Lys Lys Phe Leu Cys  
85 90 95

Ser Leu Phe Ala Pro Val Cys Leu Asp Asp Leu Asp Glu Thr Ile Gln  
100 105 110

Pro Cys His Ser Leu Cys Val Gln Val Lys Asp Arg Cys Ala Pro Val  
115 120 125

Met Ser Ala Phe Gly Phe Pro Trp Pro Asp Met Leu Glu Cys Asp Arg  
130 135 140

Phe Pro Gln Asp Asn Asp Leu Cys Ile Pro Leu Ala Ser Ser Asp His  
145 150 155 160

Leu Leu Pro Ala Thr Glu Glu Ala Pro Lys Val Cys Glu Ala Cys Lys  
165 170 175

Asn Lys Asn Asp Asp Asp Asn Asp Ile Met Glu Thr Leu Cys Lys Asn  
180 185 190

Asp Phe Ala Leu Lys Ile Lys Val Lys Glu Ile Thr Tyr Ile Asn Arg  
195 200 205

Asp Thr Lys Ile Ile Leu Glu Thr Lys Ser Lys Thr Ile Tyr Lys Leu  
210 215 220

Asn Gly Val Ser Glu Arg Asp Leu Lys Lys Ser Val Leu Trp Leu Lys  
225 230 235 240

Asp Ser Leu Gln Cys Thr Cys Glu Glu Met Asn Asp Ile Asn Ala Pro  
245 250 255

Tyr Leu Val Met Gly Gln Lys Gln Gly Gly Glu Leu Val Ile Thr Ser  
260 265 270

Val Lys Arg Trp Gln Lys Gly Gln Arg Glu Phe Lys Arg Ile Ser Arg  
275 280 285

Ser Ile Arg Lys Leu Gln Cys  
290 295

<210> 9  
<211> 1394  
<212> DNA  
<213> Homo sapiens

1168 WO\_PCT Seq List AS FILED.txt

```
<220>
<221> CDS
<222> (222)..(1109)
<223> SARP-1
```

```
<300>
<308> GenBank / BC008666
<309> 2006-07-15
<313> (1)..(1394)
```

<400>	9																
ccgggtc	gga	gcccccgga	gctgcgcgcgcg	ggcttgcagc	gcctcgcgccg	cgctgtcctc											60
ccggtgtccc	gcttctccgc	gccccagccg	ccggctgccca	gcttttcggg	gccccgagtc												120
gcacccagcg	aagagagcgg	gcccggggaca	agctcgaact	ccggccgcct	cgcccttccc												180
cggctccgct	ccctctgccc	cctcgggggtc	gcgcgccccac	g	atg	ctg	cag	ggc	cct								236
										Met	Leu	Gln	Gly	Pro			
										1							
ggc	tgc	ctg	ctg	ctg	ctc	ttc	ctc	gcc	tgc	cac	tgc	tgc	ctg	ggc	tgc		284
Gly	Ser	Leu	Leu	Leu	Leu	Phe	Leu	Ala	Ser	His	Cys	Cys	Leu	Gly	Ser		
				10					15					20			
gcg	cgc	ggg	ctc	ttc	ctc	ttt	ggc	cag	ccc	gac	ttc	tcc	tac	aag	cgc		332
Ala	Arg	Gly	Leu	Phe	Leu	Phe	Gly	Gln	Pro	Asp	Phe	Ser	Tyr	Lys	Arg		
			25					30					35				
agc	aat	tgc	aag	ccc	atc	ccg	gtc	aac	ctg	cag	ctg	tgc	cac	ggc	atc		380
Ser	Asn	Cys	Lys	Pro	Ile	Pro	Val	Asn	Leu	Gln	Leu	Cys	His	Gly	Ile		
		40					45					50					
gaa	tac	cag	aac	atg	cgg	ctg	ccc	aac	ctg	ctg	ggc	cac	gag	acc	atg		428
Glu	Tyr	Gln	Asn	Met	Arg	Leu	Pro	Asn	Leu	Leu	Gly	His	Glu	Thr	Met		
	55					60					65						
aag	gag	gtg	ctg	gag	cag	gcc	ggc	gct	tgg	atc	ccg	ctg	gtc	atg	aag		476
Lys	Glu	Val	Leu	Glu	Gln	Ala	Gly	Ala	Trp	Ile	Pro	Leu	Val	Met	Lys		
	70				75				80						85		
cag	tgc	cac	ccg	gac	acc	aag	aag	ttc	ctg	tgc	tgc	ctc	ttc	gcc	ccc		524
Gln	Cys	His	Pro	Asp	Thr	Lys	Lys	Phe	Leu	Cys	Ser	Leu	Phe	Ala	Pro		
				90					95					100			
gtc	tgc	ctc	gat	gac	cta	gac	gag	acc	atc	cag	cca	tgc	cac	tgc	ctc		572
Val	Cys	Leu	Asp	Asp	Leu	Asp	Glu	Thr	Ile	Gln	Pro	Cys	His	Ser	Leu		
			105					110					115				
tgc	gtg	cag	gtg	aag	gac	cgc	tgc	gcc	ccg	gtc	atg	tcc	gcc	ttc	ggc		620
Cys	Val	Gln	Val	Lys	Asp	Arg	Cys	Ala	Pro	Val	Met	Ser	Ala	Phe	Gly		
		120					125					130					
ttc	ccc	tgg	ccc	gac	atg	ctt	gag	tgc	gac	cgt	ttc	ccc	cag	gac	aac		668
Phe	Pro	Trp	Pro	Asp	Met	Leu	Glu	Cys	Asp	Arg	Phe	Pro	Gln	Asp	Asn		
	135					140					145						
gac	ctt	tgc	atc	ccc	ctc	gct	agc	agc	gac	cac	ctc	ctg	cca	gcc	acc		716
Asp	Leu	Cys	Ile	Pro	Leu	Ala	Ser	Ser	Asp	His	Leu	Leu	Pro	Ala	Thr		
					155					160					165		
gag	gaa	gct	cca	aag	gta	tgt	gaa	gcc	tgc	aaa	aat	aaa	aat	gat	gat		764
Glu																	

1168 WO\_PCT Seq List AS FILED.txt

185

190

195

ata	aaa	gtg	aag	gag	ata	acc	tac	atc	aac	cga	gat	acc	aaa	atc	atc	860
Ile	Lys	Val	Lys	Glu	Ile	Thr	Tyr	Ile	Asn	Arg	Asp	Thr	Lys	Ile	Ile	
		200					205					210				
ctg	gag	acc	aag	agc	aag	acc	att	tac	aag	ctg	aac	ggg	gtg	tcc	gaa	908
Leu	Glu	Thr	Lys	Ser	Lys	Thr	Ile	Tyr	Lys	Leu	Asn	Gly	Val	Ser	Glu	
		215					220					225				
agg	gac	ctg	aag	aaa	tcg	gtg	ctg	tgg	ctc	aaa	gac	agc	ttg	cag	tgc	956
Arg	Asp	Leu	Lys	Lys	Ser	Val	Leu	Trp	Leu	Lys	Asp	Ser	Leu	Gln	Cys	
		230				235					240				245	
acc	tgt	gag	gag	atg	aac	gac	atc	aac	gcg	ccc	tat	ctg	gtc	atg	gga	1004
Thr	Cys	Glu	Glu	Met	Asn	Asp	Ile	Asn	Ala	Pro	Tyr	Leu	Val	Met	Gly	
				250					255					260		
cag	aaa	cag	ggg	ggg	gag	ctg	gtg	atc	acc	tcg	gtg	aag	cgg	tgg	cag	1052
Gln	Lys	Gln	Gly	Gly	Glu	Leu	Val	Ile	Thr	Ser	Val	Lys	Arg	Trp	Gln	
			265					270					275			
aag	ggg	cag	aga	gag	ttc	aag	cgc	atc	tcc	cgc	agc	atc	cgc	aag	ctg	1100
Lys	Gly	Gln	Arg	Glu	Phe	Lys	Arg	Ile	Ser	Arg	Ser	Ile	Arg	Lys	Leu	
		280					285					290				
cag	tgc	tag	tcccggcatc	ctgatggctc	cgacaggcct	gctccagagc										1149
Gln	Cys															
	295															
acggctgacc	atttctgctc	cgggatctca	gctcccgttc	cccaagcaca	ctcctagctg											1209
ctccagtctc	agcctgggca	gcttccccct	gccttttgca	cgtttgcatc	cccagcattt											1269
cctgagttat	aaggccacag	gagtggatag	ctgttttcac	ctaaaggaaa	agcccacccg											1329
aatcttgtag	aaatattcaa	actaataaaa	tcatgaatat	ttttatgaag	tttaaaaaaa											1389
aaaaa																1394

<210> 10  
 <211> 295  
 <212> PRT  
 <213> Homo sapiens  
 <400> 10

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

Ser Leu Phe Ala Pro Val Cys Leu Asp Asp Leu Asp Glu Thr Ile Gln  
100 105 110

Pro Cys His Ser Leu Cys Val Gln Val Lys Asp Arg Cys Ala Pro Val  
115 120 125

Met Ser Ala Phe Gly Phe Pro Trp Pro Asp Met Leu Glu Cys Asp Arg  
130 135 140

Phe Pro Gln Asp Asn Asp Leu Cys Ile Pro Leu Ala Ser Ser Asp His  
145 150 155 160

Leu Leu Pro Ala Thr Glu Glu Ala Pro Lys Val Cys Glu Ala Cys Lys  
165 170 175

Asn Lys Asn Asp Asp Asp Asn Asp Ile Met Glu Thr Leu Cys Lys Asn  
180 185 190

Asp Phe Ala Leu Lys Ile Lys Val Lys Glu Ile Thr Tyr Ile Asn Arg  
195 200 205

Asp Thr Lys Ile Ile Leu Glu Thr Lys Ser Lys Thr Ile Tyr Lys Leu  
210 215 220

Asn Gly Val Ser Glu Arg Asp Leu Lys Lys Ser Val Leu Trp Leu Lys  
225 230 235 240

Asp Ser Leu Gln Cys Thr Cys Glu Glu Met Asn Asp Ile Asn Ala Pro  
245 250 255

Tyr Leu Val Met Gly Gln Lys Gln Gly Gly Glu Leu Val Ile Thr Ser  
260 265 270

Val Lys Arg Trp Gln Lys Gly Gln Arg Glu Phe Lys Arg Ile Ser Arg  
275 280 285

Ser Ile Arg Lys Leu Gln Cys  
290 295

<210> 11  
<211> 1155  
<212> DNA  
<213> Artificial

<220>  
<223> Homo sapiens SARP-1(Fz)-Fc

<220>  
<221> CDS  
<222> (1)..(1155)

<220>

<221> sig\_peptide  
<222> (1)..(72)

<220>  
<221> misc\_feature  
<222> (73)..(453)  
<223> Frizzled domain

<220>  
<221> mat\_peptide  
<222> (73)..(1155)

<220>  
<221> misc\_feature  
<222> (460)..(1155)  
<223> Fc region

<400> 11  
atg ctg cag ggc cct ggc tcg ctg ctg ctg ctc ttc ctc gcc tcg cac 48  
Met Leu Gln Gly Pro Gly Ser Leu Leu Leu Leu Phe Leu Ala Ser His  
-20 -15 -10

tgc tgc ctg ggc tcg gcg cgc ggg ctc ttc ctc ttt ggc cag ccc gac 96  
Cys Cys Leu Gly Ser Ala Arg Gly Leu Phe Leu Phe Gly Gln Pro Asp  
-5 -1 1 5

ttc tcc tac aag cgc agc aat tgc aag ccc atc ccg gcc aac ctg cag 144  
Phe Ser Tyr Lys Arg Ser Asn Cys Lys Pro Ile Pro Ala Asn Leu Gln  
10 15 20

ctg tgc cac ggc atc gaa tac cag aac atg cgg ctg ccc aac ctg ctg 192  
Leu Cys His Gly Ile Glu Tyr Gln Asn Met Arg Leu Pro Asn Leu Leu  
25 30 35 40

ggc cac gag acc atg aag gag gtg ctg gag cag gcc ggc gct tgg atc 240  
Gly His Glu Thr Met Lys Glu Val Leu Glu Gln Ala Gly Ala Trp Ile  
45 50 55

ccg ctg gtc atg aag cag tgc cac ccg gac acc aag aag ttc ctg tgc 288  
Pro Leu Val Met Lys Gln Cys His Pro Asp Thr Lys Lys Phe Leu Cys  
60 65 70

tcg ctc ttc gcc ccc gtc tgc ctc gat gac cta gac gag acc atc cag 336  
Ser Leu Phe Ala Pro Val Cys Leu Asp Asp Leu Asp Glu Thr Ile Gln  
75 80 85

cca tgc cac tcg ctc tgc gtg cag gtg aag gac cgc tgc gcc ccg gtc 384  
Pro Cys His Ser Leu Cys Val Gln Val Lys Asp Arg Cys Ala Pro Val  
90 95 100

atg tcc gcc ttc ggc ttc ccc tgg ccc gac atg ctt gag tgc gac cgt 432  
Met Ser Ala Phe Gly Phe Pro Trp Pro Asp Met Leu Glu Cys Asp Arg  
105 110 115 120

ttc ccc cag gac aac gac ctt tgc atc gag ccc aaa tct tgt gac aaa 480  
Phe Pro Gln Asp Asn Asp Leu Cys Ile Glu Pro Lys Ser Cys Asp Lys  
125 130 135

act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg 528  
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro  
140 145 150

tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc 576  
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser  
155 160 165

cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac 624  
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp  
170 175 180

1168 WO\_PCT Seq List AS FILED.txt

cct Pro 185	gag Glu	gtc Val	aag Lys	ttc Phe	aac Asn 190	tgg Trp	tac Tyr	gtg Val	gac Asp	ggc Gly 195	gtg Val	gag Glu	gtg Val	cat His	aat Asn 200	672
gcc Ala	aag Lys	aca Thr	aag Lys	ccg Pro 205	cgg Arg	gag Glu	gag Glu	cag Gln	tac Tyr 210	aac Asn	agc Ser	acg Thr	tac Tyr	cgt Arg 215	gtg Val	720
gtc Val	agc Ser	gtc Val	ctc Leu 220	acc Thr	gtc Val	ctg Leu	cac His	cag Gln 225	gac Asp	tgg Trp	ctg Leu	aat Asn	ggc Gly 230	aag Lys	gag Glu	768
tac Tyr	aag Lys	tgc Cys 235	aag Lys	gtc Val	tcc Ser	aac Asn	aaa Lys 240	gcc Ala	ctc Leu	cca Pro	gcc Ala	ccc Pro 245	atc Ile	gag Glu	aaa Lys	816
acc Thr	atc Ile 250	tcc Ser	aaa Lys	gcc Ala	aaa Lys	ggg Gly 255	cag Gln	ccc Pro	cga Arg	gaa Glu	cca Pro 260	cag Gln	gtg Val	tac Tyr	acc Thr	864
ctg Leu 265	ccc Pro	cca Pro	tcc Ser	cgg Arg	gag Glu 270	gag Glu	atg Met	acc Thr	aag Lys	aac Asn 275	cag Gln	gtc Val	agc Ser	ctg Leu 280	acc Thr	912
tgc Cys	ctg Leu	gtc Val	aaa Lys	ggc Gly 285	ttc Phe	tat Tyr	ccc Pro	agc Ser	gac Asp 290	atc Ile	gcc Ala	gtg Val	gag Glu	tgg Trp 295	gag Glu	960
agc Ser	aat Asn	ggg Gly	cag Gln 300	ccg Pro	gag Glu	aac Asn	aac Asn	tac Tyr 305	aag Lys	acc Thr	acg Thr	cct Pro	ccc Pro 310	gtg Val	ctg Leu	1008
gac Asp	tcc Ser	gac Asp 315	ggc Gly	tcc Ser	ttc Phe	ttc Phe	ctc Leu 320	tac Tyr	agc Ser	aag Lys	ctc Leu	acc Thr 325	gtg Val	gac Asp	aag Lys	1056
agc Ser	agg Arg 330	tgg Trp	cag Gln	cag Gln	ggg Gly	aac Asn 335	gtc Val	ttc Phe	tca Ser	tgc Cys	tcc Ser 340	gtg Val	atg Met	cat His	gag Glu	1104
gct Ala 345	ctg Leu	cac His	aac Asn	cac His	tac Tyr 350	acg Thr	cag Gln	aag Lys	agc Ser	ctc Leu 355	tcc Ser	ctg Leu	tct Ser	ccg Pro	ggt Gly 360	1152
aaa Lys																1155

<210> 12  
 <211> 385  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 12

Met Leu Gln Gly Pro Gly Ser Leu Leu Leu Leu Phe Leu Ala Ser His  
 -20 -15 -10

Cys Cys Leu Gly Ser Ala Arg Gly Leu Phe Leu Phe Gly Gln Pro Asp  
 -5 -1 1 5

Phe Ser Tyr Lys Arg Ser Asn Cys Lys Pro Ile Pro Ala Asn Leu Gln



10

Leu Cys His Gly Ile Glu Tyr Gln Asn Met Arg Leu Pro Asn Leu Leu  
25 30 35 40

Gly His Glu Thr Met Lys Glu Val Leu Glu Gln Ala Gly Ala Trp Ile  
45 50 55

Pro Leu Val Met Lys Gln Cys His Pro Asp Thr Lys Lys Phe Leu Cys  
60 65 70

Ser Leu Phe Ala Pro Val Cys Leu Asp Asp Leu Asp Glu Thr Ile Gln  
75 80 85

Pro Cys His Ser Leu Cys Val Gln Val Lys Asp Arg Cys Ala Pro Val  
90 95 100

Met Ser Ala Phe Gly Phe Pro Trp Pro Asp Met Leu Glu Cys Asp Arg  
105 110 115 120

Phe Pro Gln Asp Asn Asp Leu Cys Ile Glu Pro Lys Ser Cys Asp Lys  
125 130 135

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro  
140 145 150

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser  
155 160 165

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp  
170 175 180

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn  
185 190 195 200

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val  
205 210 215

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu  
220 225 230

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys  
235 240 245

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr  
250 255 260

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr  
265 270 275 280

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu  
285 290 295

1168 WO\_PCT Seq List AS FILED.txt

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu  
300 305 310

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys  
315 320 325

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu  
330 335 340

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly  
345 350 355 360

Lys

<210> 13  
<211> 1062  
<212> DNA  
<213> Artificial

<220>  
<223> SARP-1(Fz)delta7-Fc

<220>  
<221> CDS  
<222> (1)..(1062)

<220>  
<221> misc\_feature  
<222> (1)..(366)  
<223> Frizzled domain delta7

<220>  
<221> mat\_peptide  
<222> (1)..(1062)

<220>  
<221> misc\_feature  
<222> (367)..(1062)  
<223> Fc region

<400> 13  
gac ttc tcc tac aag cgc agc aat tgc aag ccc atc ccg gcc aac ctg 48  
Asp Phe Ser Tyr Lys Arg Ser Asn Cys Lys Pro Ile Pro Ala Asn Leu  
1 5 10 15

cag ctg tgc cac ggc atc gaa tac cag aac atg cgg ctg ccc aac ctg 96  
Gln Leu Cys His Gly Ile Glu Tyr Gln Asn Met Arg Leu Pro Asn Leu  
20 25 30

ctg ggc cac gag acc atg aag gag gtg ctg gag cag gcc ggc gct tgg 144  
Leu Gly His Glu Thr Met Lys Glu Val Leu Glu Gln Ala Gly Ala Trp  
35 40 45

atc ccg ctg gtc atg aag cag tgc cac ccg gac acc aag aag ttc ctg 192  
Ile Pro Leu Val Met Lys Gln Cys His Pro Asp Thr Lys Lys Phe Leu  
50 55 60

tgc tcg ctc ttc gcc ccc gtc tgc ctc gat gac cta gac gag acc atc 240  
Cys Ser Leu Phe Ala Pro Val Cys Leu Asp Asp Leu Asp Glu Thr Ile  
65 70 75 80

1168 WO\_PCT Seq List AS FILED.txt

cag	cca	tgc	cac	tcg	ctc	tgc	gtg	cag	gtg	aag	gac	cgc	tgc	gcc	ccg	288
Gln	Pro	Cys	His	Ser 85	Leu	Cys	Val	Gln	Val 90	Lys	Asp	Arg	Cys	Ala 95	Pro	
gtc	atg	tcc	gcc	ttc	ggc	ttc	ccc	tgg	ccc	gac	atg	ctt	gag	tgc	gac	336
Val	Met	Ser	Ala 100	Phe	Gly	Phe	Pro	Trp 105	Pro	Asp	Met	Leu	Glu 110	Cys	Asp	
cgt	ttc	ccc	cag	gac	aac	gac	ctt	tgc	atc	gag	ccc	aaa	tct	tgt	gac	384
Arg	Phe	Pro 115	Gln	Asp	Asn	Asp	Leu 120	Cys	Ile	Glu	Pro	Lys 125	Ser	Cys	Asp	
aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	gca	cct	gaa	ctc	ctg	ggg	gga	432
Lys	Thr 130	His	Thr	Cys	Pro	Pro 135	Cys	Pro	Ala	Pro	Glu 140	Leu	Leu	Gly	Gly	
ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	atc	480
Pro	Ser	Val	Phe	Leu	Phe 150	Pro	Pro	Lys	Pro	Lys 155	Asp	Thr	Leu	Met	Ile 160	
tcc	cgg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	gac	gtg	agc	cac	gaa	528
Ser	Arg	Thr	Pro	Glu 165	Val	Thr	Cys	Val	Val 170	Val	Asp	Val	Ser	His 175	Glu	
gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	cat	576
Asp	Pro	Glu	Val 180	Lys	Phe	Asn	Trp	Tyr 185	Val	Asp	Gly	Val	Glu 190	Val	His	
aat	gcc	aag	aca	aag	ccg	cgg	gag	gag	cag	tac	aac	agc	acg	tac	cgt	624
Asn	Ala	Lys 195	Thr	Lys	Pro	Arg	Glu 200	Glu	Gln	Tyr	Asn	Ser 205	Thr	Tyr	Arg	
gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg	ctg	aat	ggc	aag	672
Val	Val 210	Ser	Val	Leu	Thr	Val 215	Leu	His	Gln	Asp	Trp 220	Leu	Asn	Gly	Lys	
gag	tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	ctc	cca	gcc	ccc	atc	gag	720
Glu	Tyr	Lys	Cys	Lys	Val 230	Ser	Asn	Lys	Ala	Leu 235	Pro	Ala	Pro	Ile	Glu 240	
aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	tac	768
Lys	Thr	Ile	Ser	Lys 245	Ala	Lys	Gly	Gln	Pro 250	Arg	Glu	Pro	Gln	Val 255	Tyr	
acc	ctg	ccc	cca	tcc	cgg	gag	gag	atg	acc	aag	aac	cag	gtc	agc	ctg	816
Thr	Leu	Pro	Pro 260	Ser	Arg	Glu	Glu	Met 265	Thr	Lys	Asn	Gln	Val 270	Ser	Leu	
acc	tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc	agc	gac	atc	gcc	gtg	gag	tgg	864
Thr	Cys	Leu 275	Val	Lys	Gly	Phe	Tyr 280	Pro	Ser	Asp	Ile	Ala 285	Val	Glu	Trp	
gag	agc	aat	ggg	cag	ccg	gag	aac	aac	tac	aag	acc	acg	cct	ccc	gtg	912
Glu	Ser 290	Asn	Gly	Gln	Pro	Glu 295	Asn	Asn	Tyr	Lys	Thr 300	Thr	Pro	Pro	Val	
ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	gac	960
Leu	Asp	Ser	Asp	Gly	Ser 310	Phe	Phe	Leu	Tyr	Ser 315	Lys	Leu	Thr	Val	Asp 320	
aag	agc	agg	tgg	cag	cag	ggg	aac	gtc	ttc	tca	tgc	tcc	gtg	atg	cat	1008
Lys	Ser	Arg	Trp	Gln 325	Gln	Gly	Asn	Val	Phe 330	Ser	Cys	Ser	Val	Met 335	His	
gag	gct	ctg	cac	aac	cac	tac	acg	cag	aag	agc	ctc	tcc	ctg	tct	ccg	1056
Glu	Ala	Leu	His 340	Asn	His	Tyr	Thr	Gln 345	Lys	Ser	Leu	Ser	Leu 350	Ser	Pro	

ggt aaa  
Gly Lys

<210> 14  
<211> 354  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 14

Asp Phe Ser Tyr Lys Arg Ser Asn Cys Lys Pro Ile Pro Ala Asn Leu  
1 5 10 15

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

Leu Gly His Glu Thr Met Lys Glu Val Leu Glu Gln Ala Gly Ala Trp  
35 40 45

Ile Pro Leu Val Met Lys Gln Cys His Pro Asp Thr Lys Lys Phe Leu  
50 55 60

Cys Ser Leu Phe Ala Pro Val Cys Leu Asp Asp Leu Asp Glu Thr Ile  
65 70 75 80

Gln Pro Cys His Ser Leu Cys Val Gln Val Lys Asp Arg Cys Ala Pro  
85 90 95

Val Met Ser Ala Phe Gly Phe Pro Trp Pro Asp Met Leu Glu Cys Asp  
100 105 110

Arg Phe Pro Gln Asp Asn Asp Leu Cys Ile Glu Pro Lys Ser Cys Asp  
115 120 125

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
130 135 140

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
145 150 155 160

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
165 170 175

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
180 185 190

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg  
195 200 205

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
210 215 220

1168 WO\_PCT Seq List AS FILED.txt

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
225 230 235 240

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
245 250 255

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu  
260 265 270

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
275 280 285

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
290 295 300

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
305 310 315 320

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
325 330 335

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
340 345 350

Gly Lys

<210> 15  
<211> 330  
<212> PRT  
<213> Homo sapiens

<220>  
<221> DOMAIN  
<222> (1)..(98)  
<223> IgG1 CH1 domain

<220>  
<221> DOMAIN  
<222> (99)..(110)  
<223> IgG1 hinge region

<220>  
<221> DOMAIN  
<222> (111)..(223)  
<223> IgG1 CH2 domain

<220>  
<221> DOMAIN  
<222> (224)..(330)  
<223> IgG1 CH3 domain

<300>  
<308> GenBank / P01857  
<309> 1986-07-21  
<313> (1)..(330)

&lt;400&gt; 15

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

1168 WO\_PCT Seq List AS FILED.txt

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe  
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn  
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr  
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
325 330

<210> 16  
<211> 326  
<212> PRT  
<213> Homo sapiens

<220>  
<221> DOMAIN  
<222> (1)..(98)  
<223> IgG2 CH1 domain

<220>  
<221> DOMAIN  
<222> (99)..(110)  
<223> IgG2 hinge region

<220>  
<221> DOMAIN  
<222> (111)..(219)  
<223> IgG2 CH2 domain

<220>  
<221> DOMAIN  
<222> (220)..(326)  
<223> IgG2 CH3 domain

<300>  
<308> GenBank / P01859  
<309> 1986-07-21  
<313> (1)..(326)

<400> 16

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg  
1 5 10 15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr  
65 70 75 80

1168 WO\_PCT Seq List AS FILED.txt

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys  
 85 90 95  
 Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro  
 100 105 110  
 Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
 115 120 125  
 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
 130 135 140  
 Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly  
 145 150 155 160  
 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn  
 165 170 175  
 Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp  
 180 185 190  
 Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro  
 195 200 205  
 Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu  
 210 215 220  
 Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
 225 230 235 240  
 Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
 245 250 255  
 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
 260 265 270  
 Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
 275 280 285  
 Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
 290 295 300  
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
 305 310 315 320  
 Ser Leu Ser Pro Gly Lys  
 325

<210> 17  
 <211> 290  
 <212> PRT  
 <213> Homo sapiens



<220>  
 <221> DOMAIN  
 <222> (12)..(73)  
 <223> IgG3 hinge region

<220>  
 <221> DOMAIN  
 <222> (74)..(183)  
 <223> IgG3 CH2 domain

<220>  
 <221> DOMAIN  
 <222> (184)..(289)  
 <223> IgG3 CH3 domain

<300>  
 <308> GenBank / P01860  
 <309> 1986-07-21  
 <313> (1)..(290)

<400> 17

Gln Met Gln Gly Val Asn Cys Thr Val Ser Ser Glu Leu Lys Thr Pro  
 1 5 10 15

Leu Gly Asp Thr Thr His Thr Cys Pro Arg Cys Pro Glu Pro Lys Ser  
 20 25 30

Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys  
 35 40 45

Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp  
 50 55 60

Thr Pro Pro Pro Cys Pro Arg Cys Pro Ala Pro Glu Leu Leu Gly Gly  
 65 70 75 80

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
 85 90 95

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
 100 105 110

Asp Pro Glu Val Gln Phe Lys Trp Tyr Val Asp Gly Val Gln Val His  
 115 120 125

Asn Ala Lys Thr Lys Pro Arg Glu Gln Gln Phe Asn Ser Thr Phe Arg  
 130 135 140

Val Val Ser Val Leu Thr Val Leu His Gln Asn Trp Leu Asp Gly Lys  
 145 150 155 160

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
 165 170 175

Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
 Page 25

180

185

190

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu  
 195 200 205

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
 210 215 220

Glu Ser Ser Gly Gln Pro Glu Asn Asn Tyr Asn Thr Thr Pro Pro Met  
 225 230 235 240

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
 245 250 255

Lys Ser Arg Trp Gln Gln Gly Asn Ile Phe Ser Cys Ser Val Met His  
 260 265 270

Glu Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu Ser Leu Ser Pro  
 275 280 285

Gly Lys  
 290

<210> 18  
 <211> 327  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> DOMAIN  
 <222> (1)..(98)  
 <223> IgG4 CH1 domain

<220>  
 <221> DOMAIN  
 <222> (99)..(110)  
 <223> IgG4 hinge region

<220>  
 <221> DOMAIN  
 <222> (111)..(220)  
 <223> IgG4 CH2 domain

<220>  
 <221> DOMAIN  
 <222> (221)..(327)  
 <223> IgG4 CH3 domain

<300>  
 <308> GenBank / P01861  
 <309> 1986-07-21  
 <313> (1)..(327)

<400> 18

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg  
 1 5 10 15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
 Page 26

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
 35 40 45  
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
 50 55 60  
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr  
 65 70 75 80  
 Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys  
 85 90 95  
 Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro  
 100 105 110  
 Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
 115 120 125  
 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
 130 135 140  
 Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp  
 145 150 155 160  
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe  
 165 170 175  
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp  
 180 185 190  
 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu  
 195 200 205  
 Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
 210 215 220  
 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys  
 225 230 235 240  
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
 245 250 255  
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
 260 265 270  
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
 275 280 285  
 Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser  
 290 295 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
305 310 315 320

Leu Ser Leu Ser Leu Gly Lys  
325

<210> 19  
<211> 31  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> (1)..(31)  
<223> sFRP-1 signal peptide

<400> 19

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

Val Leu Leu Ala Leu Gly Ala Ala Leu Leu Ala Val Gly Ser Ala  
20 25 30

<210> 20  
<211> 24  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> (1)..(24)  
<223> sFRP-2 (SARP-1) signal peptide

<400> 20

Met Leu Gln Gly Pro Gly Ser Leu Leu Leu Leu Phe Leu Ala Ser His  
1 5 10 15

Cys Cys Leu Gly Ser Ala Arg Gly  
20

<210> 21  
<211> 32  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> (1)..(32)  
<223> sFRP-3 signal peptide

<400> 21

Met Val Cys Gly Ser Pro Gly Gly Met Leu Leu Leu Arg Ala Gly Leu  
1 5 10 15

Leu Ala Leu Ala Ala Leu Cys Leu Leu Arg Val Pro Gly Ala Arg Ala  
                   20                                  25                                  30

<210> 22  
 <211> 18  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> (1)..(18)  
 <223> sFRP-4 signal peptide

<400> 22

Met Phe Leu Ser Ile Leu Val Ala Leu Cys Leu Trp Leu His Leu Ala  
 1                  5                                  10                                  15

Leu Gly

<210> 23  
 <211> 29  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> (1)..(28)  
 <223> sFRP-5 signal peptide

<400> 23

Met Arg Ala Ala Ala Ala Ala Gly Gly Val Arg Thr Ala Ala Leu Ala  
 1                  5                                  10                                  15

Leu Leu Leu Gly Ala Leu His Trp Ala Pro Ala Arg Cys  
                   20                                  25

<210> 24  
 <211> 87  
 <212> DNA  
 <213> Artificial

<220>  
 <223> mIgSP-tPA-pro signal peptide comprising the mouse immunoglobuline  
 signal peptide (mIgSP) and the tissue plasminogen activator  
 signal pro peptide (tPApro)

<220>  
 <221> misc\_signal  
 <222> (1)..(87)

<400> 24  
 atgaagtgc gctgggtgat cttcttcctg atggccgtgg tgaccggcgt gaattccagc 60  
 caggagatcc acgccagggt cgcgaga 87

<210> 25  
 <211> 30

<212> DNA  
 <213> Artificial  
  
 <220>  
 <223> hSARP-1 forward primer  
  
 <400> 25  
 gccaaagcttc ccacgatgct gcagggccct 30  
  
 <210> 26  
 <211> 30  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> hSARP-1 reverse primer  
  
 <400> 26  
 gcgctcgagc tagcactgca gcttgcggtat 30  
  
 <210> 27  
 <211> 22  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> Sarp1-B1p-121 forward primer  
  
 <400> 27  
 gcaggcttcg ccaccatgct gc 22  
  
 <210> 28  
 <211> 34  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> Sarp1-hFC-1036-R reverse primer  
  
 <400> 28  
 cacaagattt gggctcgac tgcagcttgc ggat 34  
  
 <210> 29  
 <211> 37  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> attB1-K forward primer  
  
 <400> 29  
 ggggacaagt ttgtacaaa aagcaggctt cgccacc 37  
  
 <210> 30  
 <211> 30  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> attB2 reverse primer  
  
 <400> 30  
 ggggaccact ttgtacaaga aagctgggtt 30

1168 WO\_PCT Seq List AS FILED.txt

<210> 31  
 <211> 70  
 <212> DNA  
 <213> Artificial

<220>  
 <223> 5'-tPA-SARP primer

<400> 31  
 cggaattcca gccaggagat ccacgccagg ttccgcagag acttctccta caagcgcagc 60  
 aattgcaagc 70

<210> 32  
 <211> 30  
 <212> DNA  
 <213> Artificial

<220>  
 <223> 3'FcSARPwt primer

<400> 32  
 ctagctagct ttacccggag acagggagag 30