

PhoenixTemp48751.tmp.txt  
SEQUENCE LISTING

<110> Laboratoires Serono SA  
<120> Method for purifying an Fc-containing protein  
<130> 1159 WO/PCT  
<150> EP07118983.1  
<151> 2007-10-22  
<150> US61/007,223  
<151> 2007-12-11  
<160> 5  
<170> PatentIn version 3.5  
<210> 1  
<211> 40  
<212> PRT  
<213> Artificial sequence  
<220>  
<223> consensus sequence, in which the specific amino acids at  
positions 3, 12, 14, 15, 18, 21, 25, 34 and 38 are spaced by any  
amino acid  
  
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<222> (1)..(2)  
<223> can be any amino acid  
  
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<222> (4)..(11)  
<223> can be any amino acid  
  
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<222> (13)..(13)  
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<222> (16)..(17)  
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<222> (19)..(20)  
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<222> (35)..(37)  
<223> can be any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (39)..(40)  
 <223> can be any amino acid  
  
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 1 5 10 15  
  
 Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 20 25 30  
  
 Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa  
 35 40  
  
 <210> 2  
 <211> 348  
 <212> PRT  
 <213> Artificial sequence  
  
 <220>  
 <223> this is a fusion protein sequence containing a portion of a human  
 TACI receptor and a portion of a human immunoglobulin heavy chain  
 sequence.  
  
 <220>  
 <221> source  
 <222> (1)..(121)  
 <223> Portion of human TACI receptor  
  
 <220>  
 <221> source  
 <222> (122)..(348)  
 <223> portion of a human immunoglobulin heavy chain sequence  
  
 <400> 2  
 Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly  
 1 5 10 15  
  
 Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg  
 20 25 30  
  
 Phe Arg Arg Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro  
 35 40 45  
  
 Leu Leu Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser  
 50 55 60  
  
 Gln Arg Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu  
 65 70 75 80  
  
 Gln Gly Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala  
 85 90 95  
  
 Ser Ile Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn  
 100 105 110

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Lys Leu Arg Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro  
 115 120 125  
 Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe  
 130 135 140  
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val  
 145 150 155 160  
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe  
 165 170 175  
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro  
 180 185 190  
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr  
 195 200 205  
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val  
 210 215 220  
 Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala  
 225 230 235 240  
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg  
 245 250 255  
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly  
 260 265 270  
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro  
 275 280 285  
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser  
 290 295 300  
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln  
 305 310 315 320  
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His  
 325 330 335  
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 340 345

<210> 3

<211> 1044

<212> DNA

<213> Artificial sequence

<220>

<223> DNA encoding SEQ ID NO: 2

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<220>
<221> source
<222> (1)..(1044)
<223> DNA encoding SEQ ID NO: 2

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tcgctcagcc aggaaatcca tgccgagttg agacgcttcc gtagagctat gagatcctgc      120
cccgaagagc agtactggga tcctctgctg ggtacctgca tgtcctgcaa aaccatttgc      180
aaccatcaga gccagcgcac ctgtgcagcc ttctgcaggt cactcagctg ccgcaaggag      240
caaggcaagt tctatgacca tctcctgagg gactgcatca gctgtgcctc catctgtgga      300
cagcacccta agcaatgtgc atacttctgt gagaacaagc tcaggagcga gcccaaattc      360
tcagacaaaa ctacacatg cccaccgtgc ccagcacctg aagccgaggg ggcaccgtca      420
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc      480
acatgctggt tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg      540
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg      600
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac      660
aagtgcaagg tctccaacaa agccctccca tcctccatcg agaaaaccat ctccaagacc      720
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc      780
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg      840
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac      900
tccgacggct ctttcttctt ctacagcaag ctaccctggt acaagagcag gtggcagcag      960
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag     1020
agcctctccc tgtctccggg taaa                                           1044

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```

<210> 4
<211> 393
<212> PRT
<213> Artificial sequence

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<220>
<223> This is a fusion protein sequence containing Interferon-beta and
a portion of human immunoglobulin heavy chain sequence

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<220>
<221> Source
<222> (1)..(166)
<223> Mature interferon beta

```

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<220>
<221> Source
<222> (167)..(393)
<223> Portion of a human immunoglobulin heavy chain sequence

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<400> 4
Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln
1           5           10          15

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

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met  
 290 295 300

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro  
 305 310 315 320

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn  
 325 330 335

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu  
 340 345 350

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val  
 355 360 365

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
 370 375 380

Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 385 390

<210> 5  
 <211> 1179  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> DNA encoding SEQ ID NO: 1

<220>  
 <221> source  
 <222> (1)..(1179)  
 <223> DNA encoding SEQ ID NO: 1

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 cctgaggaga ttaagcagct gcagcagttc cagaaggagg acgccgcatt gaccatctat 180  
 gagatgctcc agaacatctt tgctattttc agacaagatt catctagcac tggctggaat 240  
 gagactattg ttgagaacct cctggctaatt gtctatcatc agataaacca tctgaagaca 300  
 gtcctggaag aaaaactgga gaaagaagat ttcaccaggg gaaaactcat gagcagtctg 360  
 cacctgaaaa gatattatgg gaggattctg cttacactga agccaagga gtacagtcac 420  
 tgtgcctgga ccatagtcag agtggaatc ctaaggaact ttacttcat taacagactt 480  
 acaggttacc tccgaaacga caaaactcac acatgccac cgtagccagc acctgaagcc 540  
 gagggggcac cgtcagtctt cctcttcccc caaaaccca aggacaccct catgatctcc 600  
 cggacccctg aggtcacatg cgtgggtggtg gacgtgagcc acgaagacc tgaggtcaag 660  
 ttcaactggt acgtggacgg cgtggagggtg cataatgcca agacaaagcc gcgggaggag 720  
 cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 780

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aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccatcctc catcgagaaa	840
accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc	900
cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tggtaaagg cttctatccc	960
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg	1020
cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag	1080
agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcattgggc tctgcacaac	1140
cactacacgc agaagagcct ctccctgtct ccgggtaaa	1179