SEQUENCE LISTING

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<120> Frizzled-Binding Agents and Uses Thereof

<130> 2293.051PC04

<140> PCT/US09/58635
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<150> 61/176,741
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<150> 61/144,248
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<150> 61/100,639
<151> 2008-09-26

<160> 97

<170> PatentIn version 3.3

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<400> 1

Gly Phe Thr Phe Ser His Tyr Thr Leu Ser
1 5 10

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<223> heavy chain CDR2

<400> 2

Val Ile Ser Gly Asp Gly Ser Tyr Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

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Asn Phe Ile Lys Tyr Val Phe Ala Asn
1 5

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Ser Gly Asp Lys Leu Gly Lys Lys Tyr Ala Ser
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Glu Lys Asp Asn Arg Pro Ser Gly
1 5

<210> 6
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<400> 6

Ser Ser Phe Ala Gly Asn Ser Leu Glu
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Ser Gly Asp Asn Ile Gly Ser Phe Tyr Val His
1 5 10

<210> 8

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<213> Artificial Sequence

<220>
<223> light chain CDR2

<400> 8

Asp Lys Ser Asn Arg Pro Ser Gly
1 5

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

<220>
<223> light chain CDR3

<400> 9

Gln Ser Tyr Ala Asn Thr Leu Ser Leu
1 5

<210> 10
<211> 118
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<213> Artificial Sequence

<220>
<223> 18R5/18R8 heavy chain

<400> 10

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr
20 25 30

Thr Leu Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Ser Gly Asp Gly Ser Tyr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ser Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asn Phe Ile Lys Tyr Val Phe Ala Asn Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 11
<211> 463
<212> PRT
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<220>
<223> 18R5/18R8 heavy chain (IgG2)

<400> 11

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
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Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
            20                  25                  30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
        35                  40                  45

Ser His Tyr Thr Leu Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60

Glu Trp Val Ser Val Ile Ser Gly Asp Gly Ser Tyr Thr Tyr Tyr Ala
65                  70                  75                  80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ser Asp Asn Ser Lys Asn
                85                  90                  95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Arg Asn Phe Ile Lys Tyr Val Phe Ala Asn Trp Gly
        115                 120                 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
145                 150                 155                 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
    210                 215                 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys
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225 230 235 240

Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
245 250 255

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
260 265 270

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
275 280 285

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
290 295 300

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser
305 310 315 320

Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
325 330 335

Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile
340 345 350

Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
355 360 365

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
370 375 380

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
385 390 395 400

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
405 410 415

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
420 425 430

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
435 440 445

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455 460

<210> 12
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> 18R8 light chain

<400> 12

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Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1               5                  10                  15

Thr Ala Arg Ile Ser Cys Ser Gly Asp Lys Leu Gly Lys Lys Tyr Ala
            20                  25                  30

Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
        35                  40                  45

Glu Lys Asp Asn Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
65                  70                  75                  80

Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Phe Ala Gly Asn Ser Leu Glu
                85                  90                  95

Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105
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<210> 13
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> 18R8 light chain (lambda)

<400> 13

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Met Ala Trp Ala Leu Leu Leu Leu Thr Leu Leu Thr Gln Gly Thr Gly
1               5                  10                  15

Ser Trp Ala Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala
            20                  25                  30

Pro Gly Gln Thr Ala Arg Ile Ser Cys Ser Gly Asp Lys Leu Gly Lys
        35                  40                  45

Lys Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu
    50                  55                  60

Val Ile Tyr Glu Lys Asp Asn Arg Pro Ser Gly Ile Pro Glu Arg Phe
65                  70                  75                  80

Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr
                85                  90                  95

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Phe Ala Gly Asn
            100                 105                 110

Ser Leu Glu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
```

115 120 125

Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
130 135 140

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
145 150 155 160

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
165 170 175

Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
180 185 190

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
195 200 205

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
210 215 220

Thr Val Ala Pro Thr Glu Cys Ser
225 230

<210> 14
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> 18R5 light chain

<400> 14

Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1 5 10 15

Thr Ala Arg Ile Ser Cys Ser Gly Asp Asn Ile Gly Ser Phe Tyr Val
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

Asp Lys Ser Asn Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Ala Asn Thr Leu Ser Leu
85 90 95

Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105

<210> 15
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> 18R5 light chain (lambda)

<400> 15

Met Ala Trp Ala Leu Leu Leu Leu Thr Leu Leu Thr Gln Gly Thr Gly
1 5 10 15

Ser Trp Ala Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala
20 25 30

Pro Gly Gln Thr Ala Arg Ile Ser Cys Ser Gly Asp Asn Ile Gly Ser
35 40 45

Phe Tyr Val His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu
50 55 60

Val Ile Tyr Asp Lys Ser Asn Arg Pro Ser Gly Ile Pro Glu Arg Phe
65 70 75 80

Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr
85 90 95

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Ala Asn Thr
100 105 110

Leu Ser Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
115 120 125

Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
130 135 140

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
145 150 155 160

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
165 170 175

Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
180 185 190

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
195 200 205

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
210 215 220

Thr Val Ala Pro Thr Glu Cys Ser

225 230

<210> 16
<211> 485
<212> PRT
<213> Artificial Sequence

<220>
<223> Fzd7 ECD Fc fusion protein

<400> 16

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

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

Gln Pro Tyr His Gly Glu Lys Gly Ile Ser Val Pro Asp His Gly Phe
35 40 45

Cys Gln Pro Ile Ser Ile Pro Leu Cys Thr Asp Ile Ala Tyr Asn Gln
50 55 60

Thr Ile Leu Pro Asn Leu Leu Gly His Thr Asn Gln Glu Asp Ala Gly
65 70 75 80

Leu Glu Val His Gln Phe Tyr Pro Leu Val Lys Val Gln Cys Ser Pro
85 90 95

Glu Leu Arg Phe Phe Leu Cys Ser Met Tyr Ala Pro Val Cys Thr Val
100 105 110

Leu Asp Gln Ala Ile Pro Pro Cys Arg Ser Leu Cys Glu Arg Ala Arg
115 120 125

Gln Gly Cys Glu Ala Leu Met Asn Lys Phe Gly Phe Gln Trp Pro Glu
130 135 140

Arg Leu Arg Cys Glu Asn Phe Pro Val His Gly Ala Gly Glu Ile Cys
145 150 155 160

Val Gly Gln Asn Thr Ser Asp Gly Ser Gly Gly Pro Gly Gly Gly Pro
165 170 175

Thr Ala Tyr Pro Thr Ala Pro Tyr Leu Pro Asp Leu Pro Phe Thr Ala
180 185 190

Leu Pro Pro Gly Ala Ser Asp Gly Arg Gly Arg Pro Ala Phe Pro Phe
195 200 205

Ser Cys Pro Arg Gln Leu Lys Val Pro Pro Tyr Leu Gly Tyr Arg Phe
210 215 220

```
Leu Gly Glu Arg Asp Cys Gly Ala Pro Cys Glu Pro Gly Arg Ala Asn
225                 230                 235                 240

Gly Leu Met Tyr Phe Lys Glu Glu Glu Arg Arg Phe Ala Arg Leu Gly
                245                 250                 255

Arg Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
            260                 265                 270

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

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
    290                 295                 300

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
305                 310                 315                 320

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
                325                 330                 335

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
            340                 345                 350

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
        355                 360                 365

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
    370                 375                 380

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
385                 390                 395                 400

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
                405                 410                 415

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
            420                 425                 430

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
        435                 440                 445

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
    450                 455                 460

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
465                 470                 475                 480

Leu Ser Pro Gly Lys
                485
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<210> 17
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> 18R5/18R8 heavy chain

<400> 17
gaagtgcaac tggtggaaag cggcggcggc ctggtgcaac ctggcggcag cctgagactg 60

agctgcgctg cctccggatt tacctttttct cattatactc tgtcttgggt gcgccaagcc 120

cctgggaagg gtctcgagtg ggtgagcgtt atctctggtg atggtagcta tacctattat 180

gctgatagcg tgaaaggcag atttaccatt tcaagtgata attccaaaaa caccctgtat 240

ctgcaaatga acagcctgag agctgaagat acagccgtgt attattgcgc tagaaatttt 300

attaagtatg tttttgctaa ttggggccaa ggcaccctgg tgacagttag ctca 354

<210> 18
<211> 1389
<212> DNA
<213> Artificial Sequence

<220>
<223> 18R5/18R8 heavy chain (IgG2)

<400> 18
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt cctgtccgaa 60

gtgcaactgg tggaaagcgg cggcggcctg gtgcaacctg gcggcagcct gagactgagc 120

tgcgctgcct ccggatttac cttttctcat tatactctgt cttgggtgcg ccaagcccct 180

gggaagggtc tcgagtgggt gagcgttatc tctggtgatg gtagctatac ctattatgct 240

gatagcgtga aaggcagatt taccatttca agtgataatt ccaaaaacac cctgtatctg 300

caaatgaaca gcctgagagc tgaagataca gccgtgtatt attgcgctag aaattttatt 360

aagtatgttt ttgctaattg gggccaaggc accctggtga cagttagctc agccagcaca 420

aagggcccta gcgtcttccc tctggctccc tgcagcagga gcaccagcga gagcacagcc 480

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 540

ggcgctctga ccagcggcgt gcacaccttc ccagctgtcc tacagtcctc aggactctac 600

tccctcagca gcgtggtgac cgtgccctcc agcaacttcg gcacccagac ctacacctgc 660

aacgtagatc acaagcccag caacaccaag gtggacaaga cagttgagcg caaatgttgt 720

gtcgagtgcc caccgtgccc agcaccacct gtggcaggac cgtcagtctt cctcttcccc 780

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacgtg cgtggtggtg 840

gacgtgagcc acgaagaccc cgaggtccag ttcaactggt acgtggacgg cgtggaggtg 900

cataatgcca agacaaagcc acgggaggag cagttcaaca gcacgttccg tgtggtcagc 960

gtcctcaccg ttgtgcacca ggactggctg aacggcaagg agtacaagtg caaggtctcc 1020

aacaaaggcc tcccagcccc catcgagaaa accatctcca aaaccaaagg gcagccccga 1080

gaaccacagg tgtacaccct gcccccatcc cgggaggaga tgaccaagaa ccaggtcagc 1140

ctgacctgcc tggtcaaagg cttctacccc agcgacatcg ccgtggagtg ggagagcaat 1200

gggcagccgg agaacaacta caagaccaca cctcccatgc tggactccga cggctccttc 1260

ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1320

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ccgggtaaa 1389

<210> 19
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 18R8 light chain

<400> 19
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tcttgtagcg gcgataagct gggtaagaag tatgcttctt ggtaccagca gaaacccggg 120

caggctccag ttctggtgat ttatgagaag gataatagac cctcaggcat ccctgaacgc 180

tttagcggat ccaacagcgg caacaccgct accctgacca ttagcggcac tcaggctgaa 240

gacgaagccg attattattg ctcttctttt gctggtaatt ctctggaggt gtttggcggc 300

ggcaccaagt taaccgtcct gggt 324

<210> 20
<211> 696
<212> DNA
<213> Artificial Sequence

<220>
<223> 18R8 light chain (lambda)

<400> 20
atggcctggg ctctgctgct cctcaccctc ctcactcagg gcacaggatc ctgggctgat 60

atcgaactga cccagcctcc ttcagtgagc gttgcaccag gtcagaccgc tagaatctct 120

tgtagcggcg ataagctggg taagaagtat gcttcttggt accagcagaa acccgggcag 180

gctccagttc tggtgattta tgagaaggat aatagaccct caggcatccc tgaacgcttt 240

agcggatcca acagcggcaa caccgctacc ctgaccatta gcggcactca ggctgaagac 300

gaagccgatt attattgctc ttcttttgct ggtaattctc tggaggtgtt tggcggcggc 360

accaagttaa ccgtcctggg tcagcccaag gctgccccca gcgtcactct gttccctccc 420

tcctctgagg agctgcaagc caacaaggcc acactggtgt gtctcataag tgacttctac 480

cctggagccg tgacagtggc ctggaaggca gatagcagcc ccgtcaaggc tggagtggag 540

accaccacac cctccaaaca aagcaacaac aagtacgctg ccagcagcta tctgagcctg 600

acacctgagc agtggaagtc ccacagaagc tacagctgcc aggtcacaca tgaagggagc 660

accgtggaga agacagtggc ccctacagaa tgttca 696

<210> 21
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 18R5 light chain

<400> 21
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agctgctccg gggacaatat cggatctttc tacgtgcact ggtatcagca gaagcctggt 120

caggctccag ttctcgttat ctatgataag agtaatcgcc cctctgggat tccagagcgc 180

ttcagcggaa gcaacagcgg aaatactgca actctcacaa tttccggtac tcaggctgag 240

gacgaagccg actattactg ccaaagctac gcaaacaccc tgtccctcgt cttcggaggc 300

ggaaccaagt taaccgtcct gggt 324

<210> 22
<211> 696
<212> DNA
<213> Artificial Sequence

<220>
<223> 18R5 light chain (lambda)

<400> 22
atggcatggg cactgctgct gctcactctg ctgacacaag gtactggctc ttgggccgat 60

atcgagctga ctcagcctcc atccgtgagt gtggcccctg gtcagacagc acgcatcagc 120

tgctccgggg acaatatcgg atctttctac gtgcactggt atcagcagaa gcctggtcag 180

gctccagttc tcgttatcta tgataagagt aatcgcccct ctgggattcc agagcgcttc 240

agcggaagca acagcggaaa tactgcaact ctcacaattt ccggtactca ggctgaggac 300

gaagccgact attactgcca aagctacgca aacaccctgt ccctcgtctt cggaggcgga 360

accaagttaa ccgtcctggg tcagcccaag gctgccccca gcgtcactct gttccctccc 420

tcctctgagg agctgcaagc caacaaggcc acactggtgt gtctcataag tgacttctac 480

cctggagccg tgacagtggc ctggaaggca gatagcagcc ccgtcaaggc tggagtggag 540

accaccacac cctccaaaca aagcaacaac aagtacgctg ccagcagcta tctgagcctg 600

acacctgagc agtggaagtc ccacagaagc tacagctgcc aggtcacaca tgaagggagc 660

accgtggaga agacagtggc ccctacagaa tgttca 696

<210> 23
<211> 1455
<212> DNA
<213> Artificial Sequence

<220>
<223> Fzd7 ECD Fc fusion protein

<400> 23
atgcgggacc ccggcgcggc cgctccgctt tcgtccctgg gcctctgtgc cctggtgctg 60

gcgctgctgg gcgcactgtc cgcgggcgcc ggggcgcagc cgtaccacgg agagaagggc 120

atctccgtgc cggaccacgg cttctgccag cccatctcca tcccgctgtg cacggacatc 180

gcctacaacc agaccatcct gcccaacctg ctgggccaca cgaaccaaga ggacgcgggc 240

ctcgaggtgc accagttcta cccgctggtg aaggtgcagt gttctcccga actccgcttt 300

ttcttatgct ccatgtatgc gcccgtgtgc accgtgctcg atcaggccat cccgccgtgt 360

cgttctctgt gcgagcgcgc ccgccagggc tgcgaggcgc tcatgaacaa gttcggcttc 420

cagtggcccg agcggctgcg ctgcgagaac ttcccggtgc acggtgcggg cgagatctgc 480

gtgggccaga acacgtcgga cggctccggg ggcccaggcg gcggccccac tgcctaccct 540

accgcgccct acctgccgga cctgcccttc accgcgctgc ccccgggggc ctcagatggc 600

aggggcgtc ccgccttccc cttctcatgc ccccgtcagc tcaaggtgcc cccgtacctg 660

ggctaccgct tcctgggtga gcgcgattgt ggcgccccgt gcgaaccggg ccgtgccaac 720

ggcctgatgt actttaagga ggaggagagg cgcttcgccc gcctcgggcg cgccgacaaa 780

actcacacat gcccaccgtg cccagcacct gaactcctgg ggggaccgtc agtcttcctc 840

ttcccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 900

gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 960

gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg 1020

gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 1080

gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaagggcag 1140

ccccgagaac cacaggtgta caccctgccc ccatcccggg atgagctgac caagaaccag 1200

gtcagcctga cctgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 1260

agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1320

tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1380

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacacagaa gagcctctcc 1440

ctgtctccgg gtaaa 1455

<210> 24
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> fragment of Human frizzled receptor

<400> 24

Gln Asp Glu Glu Asp Ala Gly Leu Glu Val His Gln Phe Tyr Trp Pro
1 5 10 15

Leu

<210> 25

<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> fragment of human frizzled receptor

<400> 25

Gly Leu Glu Val His Gln
1 5

<210> 26
<211> 647
<212> PRT
<213> Artificial Sequence

<220>
<223> Human frizzled receptor FZD1

<400> 26

Met Ala Glu Glu Glu Ala Pro Lys Lys Ser Arg Ala Ala Gly Gly Gly
1 5 10 15

Ala Ser Trp Glu Leu Cys Ala Gly Ala Leu Ser Ala Arg Leu Ala Glu
20 25 30

Glu Gly Ser Gly Asp Ala Gly Gly Arg Arg Arg Pro Pro Val Asp Pro
35 40 45

Arg Arg Leu Ala Arg Gln Leu Leu Leu Leu Leu Trp Leu Leu Glu Ala
50 55 60

Pro Leu Leu Leu Gly Val Arg Ala Gln Ala Ala Gly Gln Gly Pro Gly
65 70 75 80

Gln Gly Pro Gly Pro Gly Gln Gln Pro Pro Pro Pro Pro Gln Gln Gln
85 90 95

Gln Ser Gly Gln Gln Tyr Asn Gly Glu Arg Gly Ile Ser Val Pro Asp
100 105 110

His Gly Tyr Cys Gln Pro Ile Ser Ile Pro Leu Cys Thr Asp Ile Ala
115 120 125

Tyr Asn Gln Thr Ile Met Pro Asn Leu Leu Gly His Thr Asn Gln Glu
130 135 140

Asp Ala Gly Leu Glu Val His Gln Phe Tyr Pro Leu Val Lys Val Gln
145 150 155 160

Cys Ser Ala Glu Leu Lys Phe Phe Leu Cys Ser Met Tyr Ala Pro Val
165 170 175

Cys Thr Val Leu Glu Gln Ala Leu Pro Pro Cys Arg Ser Leu Cys Glu

180 185 190

Arg Ala Arg Gln Gly Cys Glu Ala Leu Met Asn Lys Phe Gly Phe Gln
195 200 205

Trp Pro Asp Thr Leu Lys Cys Glu Lys Phe Pro Val His Gly Ala Gly
210 215 220

Glu Leu Cys Val Gly Gln Asn Thr Ser Asp Lys Gly Thr Pro Thr Pro
225 230 235 240

Ser Leu Leu Pro Glu Phe Trp Thr Ser Asn Pro Gln His Gly Gly Gly
245 250 255

Gly His Arg Gly Gly Phe Pro Gly Gly Ala Gly Ala Ser Glu Arg Gly
260 265 270

Lys Phe Ser Cys Pro Arg Ala Leu Lys Val Pro Ser Tyr Leu Asn Tyr
275 280 285

His Phe Leu Gly Glu Lys Asp Cys Gly Ala Pro Cys Glu Pro Thr Lys
290 295 300

Val Tyr Gly Leu Met Tyr Phe Gly Pro Glu Glu Leu Arg Phe Ser Arg
305 310 315 320

Thr Trp Ile Gly Ile Trp Ser Val Leu Cys Cys Ala Ser Thr Leu Phe
325 330 335

Thr Val Leu Thr Tyr Leu Val Asp Met Arg Arg Phe Ser Tyr Pro Glu
340 345 350

Arg Pro Ile Ile Phe Leu Ser Gly Cys Tyr Thr Ala Val Ala Val Ala
355 360 365

Tyr Ile Ala Gly Phe Leu Leu Glu Asp Arg Val Val Cys Asn Asp Lys
370 375 380

Phe Ala Glu Asp Gly Ala Arg Thr Val Ala Gln Gly Thr Lys Lys Glu
385 390 395 400

Gly Cys Thr Ile Leu Phe Met Met Leu Tyr Phe Phe Ser Met Ala Ser
405 410 415

Ser Ile Trp Trp Val Ile Leu Ser Leu Thr Trp Phe Leu Ala Ala Gly
420 425 430

Met Lys Trp Gly His Glu Ala Ile Glu Ala Asn Ser Gln Tyr Phe His
435 440 445

Leu Ala Ala Trp Ala Val Pro Ala Ile Lys Thr Ile Thr Ile Leu Ala

450 455 460

Leu Gly Gln Val Asp Gly Asp Val Leu Ser Gly Val Cys Phe Val Gly
465 470 475 480

Leu Asn Asn Val Asp Ala Leu Arg Gly Phe Val Leu Ala Pro Leu Phe
485 490 495

Val Tyr Leu Phe Ile Gly Thr Ser Phe Leu Leu Ala Gly Phe Val Ser
500 505 510

Leu Phe Arg Ile Arg Thr Ile Met Lys His Asp Gly Thr Lys Thr Glu
515 520 525

Lys Leu Glu Lys Leu Met Val Arg Ile Gly Val Phe Ser Val Leu Tyr
530 535 540

Thr Val Pro Ala Thr Ile Val Ile Ala Cys Tyr Phe Tyr Glu Gln Ala
545 550 555 560

Phe Arg Asp Gln Trp Glu Arg Ser Trp Val Ala Gln Ser Cys Lys Ser
565 570 575

Tyr Ala Ile Pro Cys Pro His Leu Gln Ala Gly Gly Gly Ala Pro Pro
580 585 590

His Pro Pro Met Ser Pro Asp Phe Thr Val Phe Met Ile Lys Tyr Leu
595 600 605

Met Thr Leu Ile Val Gly Ile Thr Ser Gly Phe Trp Ile Trp Ser Gly
610 615 620

Lys Thr Leu Asn Ser Trp Arg Lys Phe Tyr Thr Arg Leu Thr Asn Ser
625 630 635 640

Lys Gln Gly Glu Thr Thr Val
645

<210> 27
<211> 321
<212> PRT
<213> Artificial Sequence

<220>
<223> extracellular domain (ECD) of FZD1

<400> 27

Met Ala Glu Glu Glu Ala Pro Lys Lys Ser Arg Ala Ala Gly Gly Gly
1 5 10 15

Ala Ser Trp Glu Leu Cys Ala Gly Ala Leu Ser Ala Arg Leu Ala Glu
20 25 30

Glu Gly Ser Gly Asp Ala Gly Gly Arg Arg Arg Pro Pro Val Asp Pro
35 40 45

Arg Arg Leu Ala Arg Gln Leu Leu Leu Leu Trp Leu Leu Glu Ala
50 55 60

Pro Leu Leu Leu Gly Val Arg Ala Gln Ala Ala Gly Gln Gly Pro Gly
65 70 75 80

Gln Gly Pro Gly Pro Gly Gln Gln Pro Pro Pro Pro Pro Gln Gln Gln
85 90 95

Gln Ser Gly Gln Gln Tyr Asn Gly Glu Arg Gly Ile Ser Val Pro Asp
100 105 110

His Gly Tyr Cys Gln Pro Ile Ser Ile Pro Leu Cys Thr Asp Ile Ala
115 120 125

Tyr Asn Gln Thr Ile Met Pro Asn Leu Leu Gly His Thr Asn Gln Glu
130 135 140

Asp Ala Gly Leu Glu Val His Gln Phe Tyr Pro Leu Val Lys Val Gln
145 150 155 160

Cys Ser Ala Glu Leu Lys Phe Phe Leu Cys Ser Met Tyr Ala Pro Val
165 170 175

Cys Thr Val Leu Glu Gln Ala Leu Pro Pro Cys Arg Ser Leu Cys Glu
180 185 190

Arg Ala Arg Gln Gly Cys Glu Ala Leu Met Asn Lys Phe Gly Phe Gln
195 200 205

Trp Pro Asp Thr Leu Lys Cys Glu Lys Phe Pro Val His Gly Ala Gly
210 215 220

Glu Leu Cys Val Gly Gln Asn Thr Ser Asp Lys Gly Thr Pro Thr Pro
225 230 235 240

Ser Leu Leu Pro Glu Phe Trp Thr Ser Asn Pro Gln His Gly Gly Gly
245 250 255

Gly His Arg Gly Gly Phe Pro Gly Gly Ala Gly Ala Ser Glu Arg Gly
260 265 270

Lys Phe Ser Cys Pro Arg Ala Leu Lys Val Pro Ser Tyr Leu Asn Tyr
275 280 285

His Phe Leu Gly Glu Lys Asp Cys Gly Ala Pro Cys Glu Pro Thr Lys
290 295 300

Val Tyr Gly Leu Met Tyr Phe Gly Pro Glu Glu Leu Arg Phe Ser Arg
305 310 315 320

Thr

<210> 28
<211> 151
<212> PRT
<213> Artificial Sequence

<220>
<223> Human FZD1 Fri domain

<400> 28

Gln Gln Pro Pro Pro Pro Pro Gln Gln Gln Gln Ser Gly Gln Gln Tyr
1 5 10 15

Asn Gly Glu Arg Gly Ile Ser Val Pro Asp His Gly Tyr Cys Gln Pro
20 25 30

Ile Ser Ile Pro Leu Cys Thr Asp Ile Ala Tyr Asn Gln Thr Ile Met
35 40 45

Pro Asn Leu Leu Gly His Thr Asn Gln Glu Asp Ala Gly Leu Glu Val
50 55 60

His Gln Phe Tyr Pro Leu Val Lys Val Gln Cys Ser Ala Glu Leu Lys
65 70 75 80

Phe Phe Leu Cys Ser Met Tyr Ala Pro Val Cys Thr Val Leu Glu Gln
85 90 95

Ala Leu Pro Pro Cys Arg Ser Leu Cys Glu Arg Ala Arg Gln Gly Cys
100 105 110

Glu Ala Leu Met Asn Lys Phe Gly Phe Gln Trp Pro Asp Thr Leu Lys
115 120 125

Cys Glu Lys Phe Pro Val His Gly Ala Gly Glu Leu Cys Val Gly Gln
130 135 140

Asn Thr Ser Asp Lys Gly Thr
145 150

<210> 29
<211> 1944
<212> DNA
<213> Artificial Sequence

<220>
<223> Human FZD1

<400> 29

atggctgagg aggaggcgcc taagaagtcc cgggccgccg gcggtggcgc gagctgggaa 60

ctttgtgccg gggcgctctc ggcccggctg gcggaggagg gcagcgggga cgccggtggc 120

cgccgccgcc cgccagttga cccccggcga ttggcgcgcc agctgctgct gctgctttgg 180

ctgctggagg ctccgctgct gctgggggtc cgggcccagg cggcgggcca ggggccaggc 240

caggggcccg ggccggggca gcaaccgccg ccgccgcctc agcagcaaca gagcgggcag 300

cagtacaacg gcgagcgggg catctccgtc ccggaccacg gctattgcca gcccatctcc 360

atcccgctgt gcacggacat cgcgtacaac cagaccatca tgcccaacct gctgggccac 420

acgaaccagg aggacgcggg cctggaggtg caccagttct accctctagt gaaagtgcag 480

tgttccgctg agctcaagtt cttcctgtgc tccatgtacg cgcccgtgtg caccgtgcta 540

gagcaggcgc tgccgccctg ccgctccctg tgcgagcgcg cgcgccaggg ctgcgaggcg 600

ctcatgaaca agttcggctt ccagtggcca gacacgctca agtgtgagaa gttcccggtg 660

cacggcgccg gcgagctgtg cgtgggccag aacacgtccg acaagggcac cccgacgccc 720

tcgctgcttc cagagttctg gaccagcaac cctcagcacg gcggcggagg gcaccgtggc 780

ggcttcccgg ggggcgccgg cgcgtcggag cgaggcaagt tctcctgccc gcgcgccctc 840

aaggtgccct cctacctcaa ctaccacttc ctgggggaga aggactgcgg cgcaccttgt 900

gagccgacca aggtgtatgg gctcatgtac ttcgggcccg aggagctgcg cttctcgcgc 960

acctggattg gcatttggtc agtgctgtgc tgcgcctcca cgctcttcac ggtgcttacg 1020

tacctggtgg acatgcggcg cttcagctac ccggagcggc ccatcatctt cttgtccggc 1080

tgttacacgg ccgtggccgt ggcctacatc gccggcttcc tcctggaaga ccgagtggtg 1140

tgtaatgaca agttcgccga ggacggggca cgcactgtgg cgcagggcac caagaaggag 1200

ggctgcacca tcctcttcat gatgctctac ttcttcagca tggccagctc catctggtgg 1260

gtgatcctgt cgctcacctg gttcctggcg gctggcatga agtggggcca cgaggccatc 1320

gaagccaact cacagtattt tcacctggcc gcctgggctg tgccggccat caagaccatc 1380

accatcctgg cgctgggcca ggtggacggc gatgtgctga gcggagtgtg cttcgtgggg 1440

cttaacaacg tggacgcgct gcgtggcttc gtgctggcgc ccctcttcgt gtacctgttt 1500

atcggcacgt cctttctgct ggccggcttt gtgtcgctct tccgcatccg caccatcatg 1560

aagcacgatg gcaccaagac cgagaagctg gagaagctca tggtgcgcat tggcgtcttc 1620

agcgtgctgt acactgtgcc agccaccatc gtcatcgcct gctacttcta cgagcaggcc 1680

ttccgggacc agtgggaacg cagctgggtg gcccagagct gcaagagcta cgctatcccc 1740

tgccctcacc tccaggcggg cggaggcgcc ccgccgcacc cgcccatgag cccggacttc 1800

acggtcttca tgattaagta ccttatgacg ctgatcgtgg gcatcacgtc gggcttctgg 1860

atctggtccg gcaagaccct caactcctgg aggaagttct acacgaggct caccaacagc 1920

aaacaagggg agactacagt ctga 1944

<210> 30

<211> 565
<212> PRT
<213> Artificial Sequence

<220>
<223> Human FZD2

<400> 30

Met Arg Pro Arg Ser Ala Leu Pro Arg Leu Leu Leu Pro Leu Leu Leu
1 5 10 15

Leu Pro Ala Ala Gly Pro Ala Gln Phe His Gly Glu Lys Gly Ile Ser
20 25 30

Ile Pro Asp His Gly Phe Cys Gln Pro Ile Ser Ile Pro Leu Cys Thr
35 40 45

Asp Ile Ala Tyr Asn Gln Thr Ile Met Pro Asn Leu Leu Gly His Thr
50 55 60

Asn Gln Glu Asp Ala Gly Leu Glu Val His Gln Phe Tyr Pro Leu Val
65 70 75 80

Lys Val Gln Cys Ser Pro Glu Leu Arg Phe Phe Leu Cys Ser Met Tyr
85 90 95

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

Ile Cys Glu Arg Ala Arg Gln Gly Cys Glu Ala Leu Met Asn Lys Phe
115 120 125

Gly Phe Gln Trp Pro Glu Arg Leu Arg Cys Glu His Phe Pro Arg His
130 135 140

Gly Ala Glu Gln Ile Cys Val Gly Gln Asn His Ser Glu Asp Gly Ala
145 150 155 160

Pro Ala Leu Leu Thr Thr Ala Pro Pro Pro Gly Leu Gln Pro Gly Ala
165 170 175

Gly Gly Thr Pro Gly Gly Pro Gly Gly Gly Gly Ala Pro Pro Arg Tyr
180 185 190

Ala Thr Leu Glu His Pro Phe His Cys Pro Arg Val Leu Lys Val Pro
195 200 205

Ser Tyr Leu Ser Tyr Lys Phe Leu Gly Glu Arg Asp Cys Ala Ala Pro
210 215 220

Cys Glu Pro Ala Arg Pro Asp Gly Ser Met Phe Phe Ser Gln Glu Glu
225 230 235 240

Thr Arg Phe Ala Arg Leu Trp Ile Leu Thr Trp Ser Val Leu Cys Cys
245 250 255

Ala Ser Thr Phe Phe Thr Val Thr Thr Tyr Leu Val Asp Met Gln Arg
260 265 270

Phe Arg Tyr Pro Glu Arg Pro Ile Ile Phe Leu Ser Gly Cys Tyr Thr
275 280 285

Met Val Ser Val Ala Tyr Ile Ala Gly Phe Val Leu Gln Glu Arg Val
290 295 300

Val Cys Asn Glu Arg Phe Ser Glu Asp Gly Tyr Arg Thr Val Val Gln
305 310 315 320

Gly Thr Lys Lys Glu Gly Cys Thr Ile Leu Phe Met Met Leu Tyr Phe
325 330 335

Phe Ser Met Ala Ser Ser Ile Trp Trp Val Ile Leu Ser Leu Thr Trp
340 345 350

Phe Leu Ala Ala Gly Met Lys Trp Gly His Glu Ala Ile Glu Ala Asn
355 360 365

Ser Gln Tyr Phe His Leu Ala Ala Trp Ala Val Pro Ala Val Lys Thr
370 375 380

Ile Thr Ile Leu Ala Met Gly Gln Ile Asp Gly Asp Leu Leu Ser Gly
385 390 395 400

Val Cys Phe Val Gly Leu Asn Ser Leu Asp Pro Leu Arg Gly Phe Val
405 410 415

Leu Ala Pro Leu Phe Val Tyr Leu Phe Ile Gly Thr Ser Phe Leu Leu
420 425 430

Ala Gly Phe Val Ser Leu Phe Arg Ile Arg Thr Ile Met Lys His Asp
435 440 445

Gly Thr Lys Thr Glu Lys Leu Glu Arg Leu Met Val Arg Ile Gly Val
450 455 460

Phe Ser Val Leu Tyr Thr Val Pro Ala Thr Ile Val Ile Ala Cys Tyr
465 470 475 480

Phe Tyr Glu Gln Ala Phe Arg Glu His Trp Glu Arg Ser Trp Val Ser
485 490 495

Gln His Cys Lys Ser Leu Ala Ile Pro Cys Pro Ala His Tyr Thr Pro
500 505 510

Arg Met Ser Pro Asp Phe Thr Val Tyr Met Ile Lys Tyr Leu Met Thr
515 520 525

Leu Ile Val Gly Ile Thr Ser Gly Phe Trp Ile Trp Ser Gly Lys Thr
530 535 540

Leu His Ser Trp Arg Lys Phe Tyr Thr Arg Leu Thr Asn Ser Arg His
545 550 555 560

Gly Glu Thr Thr Val
565

<210> 31
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> extracellular domain (ECD) of FZD2

<400> 31

Met Arg Pro Arg Ser Ala Leu Pro Arg Leu Leu Leu Pro Leu Leu Leu
1 5 10 15

Leu Pro Ala Ala Gly Pro Ala Gln Phe His Gly Glu Lys Gly Ile Ser
20 25 30

Ile Pro Asp His Gly Phe Cys Gln Pro Ile Ser Ile Pro Leu Cys Thr
35 40 45

Asp Ile Ala Tyr Asn Gln Thr Ile Met Pro Asn Leu Leu Gly His Thr
50 55 60

Asn Gln Glu Asp Ala Gly Leu Glu Val His Gln Phe Tyr Pro Leu Val
65 70 75 80

Lys Val Gln Cys Ser Pro Glu Leu Arg Phe Phe Leu Cys Ser Met Tyr
85 90 95

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

Ile Cys Glu Arg Ala Arg Gln Gly Cys Glu Ala Leu Met Asn Lys Phe
115 120 125

Gly Phe Gln Trp Pro Glu Arg Leu Arg Cys Glu His Phe Pro Arg His
130 135 140

Gly Ala Glu Gln Ile Cys Val Gly Gln Asn His Ser Glu Asp Gly Ala
145 150 155 160

Pro Ala Leu Leu Thr Thr Ala Pro Pro Pro Gly Leu Gln Pro Gly Ala

165 170 175

Gly Gly Thr Pro Gly Gly Pro Gly Gly Gly Gly Ala Pro Pro Arg Tyr
180 185 190

Ala Thr Leu Glu His Pro Phe His Cys Pro Arg Val Leu Lys Val Pro
195 200 205

Ser Tyr Leu Ser Tyr Lys Phe Leu Gly Glu Arg Asp Cys Ala Ala Pro
210 215 220

Cys Glu Pro Ala Arg Pro Asp Gly Ser Met Phe Phe Ser Gln Glu Glu
225 230 235 240

Thr Arg Phe Ala Arg Leu Trp Ile Leu Thr
245 250

<210> 32
<211> 136
<212> PRT
<213> Artificial Sequence

<220>
<223> Human FZD2 Fri domain

<400> 32

Gln Phe His Gly Glu Lys Gly Ile Ser Ile Pro Asp His Gly Phe Cys
1 5 10 15

Gln Pro Ile Ser Ile Pro Leu Cys Thr Asp Ile Ala Tyr Asn Gln Thr
20 25 30

Ile Met Pro Asn Leu Leu Gly His Thr Asn Gln Glu Asp Ala Gly Leu
35 40 45

Glu Val His Gln Phe Tyr Pro Leu Val Lys Val Gln Cys Ser Pro Glu
50 55 60

Leu Arg Phe Phe Leu Cys Ser Met Tyr Ala Pro Val Cys Thr Val Leu
65 70 75 80

Glu Gln Ala Ile Pro Pro Cys Arg Ser Ile Cys Glu Arg Ala Arg Gln
85 90 95

Gly Cys Glu Ala Leu Met Asn Lys Phe Gly Phe Gln Trp Pro Glu Arg
100 105 110

Leu Arg Cys Glu His Phe Pro Arg His Gly Ala Glu Gln Ile Cys Val
115 120 125

Gly Gln Asn His Ser Glu Asp Gly
130 135

<210> 33
<211> 1698
<212> DNA
<213> Artificial Sequence

<220>
<223> Human FZD2

<400> 33
atgcggcccc gcagcgccct gccccgcctg ctgctgccgc tgctgctgct gcccgccgcc 60

gggccggccc agttccacgg ggagaagggc atctccatcc cggaccacgg cttctgccag 120

cccatctcca tcccgctgtg cacggacatc gcctacaacc agaccatcat gcccaacctt 180

ctgggccaca cgaaccagga ggacgcaggc ctagaggtgc accagttcta tccgctggtg 240

aaggtgcagt gctcgcccga actgcgcttc ttcctgtgct ccatgtacgc acccgtgtgc 300

accgtgctgg aacaggccat cccgccgtgc cgctctatct gtgagcgcgc gcgccagggc 360

tgcgaagccc tcatgaacaa gttcggtttt cagtggcccg agcgcctgcg ctgcgagcac 420

ttcccgcgcc acggcgccga gcagatctgc gtcggccaga accactccga ggacggagct 480

cccgcgctac tcaccaccgc gccgccgccg ggactgcagc cgggtgccgg gggcaccccg 540

ggtggcccgg gcggcggcgg cgctcccccg cgctacgcca cgctggagca ccccttccac 600

tgcccgcgcg tcctcaaggt gccatcctat ctcagctaca agtttctggg cgagcgtgat 660

tgtgctgcgc cctgcgaacc tgcgcggccc gatggttcca tgttcttctc acaggaggag 720

acgcgtttcg cgcgcctctg gatcctcacc tggtcggtgc tgtgctgcgc ttccaccttc 780

ttcactgtca ccacgtactt ggtagacatg cagcgcttcc gctacccaga gcggcctatc 840

atttttctgt cgggctgcta caccatggtg tcggtggcct acatcgcggg cttcgtgctc 900

caggagcgcg tggtgtgcaa cgagcgcttc tccgaggacg gttaccgcac ggtggtgcag 960

ggcaccaaga aggagggctg caccatcctc ttcatgatgc tctacttctt cagcatggcc 1020

agctccatct ggtgggtcat cctgtcgctc acctggttcc tggcagccgg catgaagtgg 1080

ggccacgagg ccatcgaggc caactctcag tacttccacc tggccgcctg ggccgtgccg 1140

gccgtcaaga ccatcaccat cctggccatg ggccagatcg acggcgacct gctgagcggc 1200

gtgtgcttcg taggcctcaa cagcctggac ccgctgcggg gcttcgtgct agcgccgctc 1260

ttcgtgtacc tgttcatcgg cacgtccttc ctcctggccg gcttcgtgtc gctcttccgc 1320

atccgcacca tcatgaagca cgacggcacc aagaccgaaa agctggagcg gctcatggtg 1380

cgcatcggcg tcttctccgt gctctacaca gtgcccgcca ccatcgtcat cgcttgctac 1440

ttctacgagc aggccttccg cgagcactgg gagcgctcgt gggtgagcca gcactgcaag 1500

agcctggcca tcccgtgccc ggcgcactac acgccgcgca tgtcgcccga cttcacggtc 1560

tacatgatca aatacctcat gacgctcatc gtgggcatca cgtcgggctt ctggatctgg 1620

tcgggcaaga cgctgcactc gtggaggaag ttctacactc gcctcaccaa cagccgacac 1680

ggtgagacca ccgtgtga 1698

<210> 34
<211> 666
<212> PRT
<213> Artificial Sequence

<220>
<223> Human FZD3

<400> 34

Met Ala Met Thr Trp Ile Val Phe Ser Leu Trp Pro Leu Thr Val Phe
1 5 10 15

Met Gly His Ile Gly Gly His Ser Leu Phe Ser Cys Glu Pro Ile Thr
20 25 30

Leu Arg Met Cys Gln Asp Leu Pro Tyr Asn Thr Thr Phe Met Pro Asn
35 40 45

Leu Leu Asn His Tyr Asp Gln Gln Thr Ala Ala Leu Ala Met Glu Pro
50 55 60

Phe His Pro Met Val Asn Leu Asp Cys Ser Arg Asp Phe Arg Pro Phe
65 70 75 80

Leu Cys Ala Leu Tyr Ala Pro Ile Cys Met Glu Tyr Gly Arg Val Thr
85 90 95

Leu Pro Cys Arg Arg Leu Cys Gln Arg Ala Tyr Ser Glu Cys Ser Lys
100 105 110

Leu Met Glu Met Phe Gly Val Pro Trp Pro Glu Asp Met Glu Cys Ser
115 120 125

Arg Phe Pro Asp Cys Asp Glu Pro Tyr Pro Arg Leu Val Asp Leu Asn
130 135 140

Leu Ala Gly Glu Pro Thr Glu Gly Ala Pro Val Ala Val Gln Arg Asp
145 150 155 160

Tyr Gly Phe Trp Cys Pro Arg Glu Leu Lys Ile Asp Pro Asp Leu Gly
165 170 175

Tyr Ser Phe Leu His Val Arg Asp Cys Ser Pro Pro Cys Pro Asn Met
180 185 190

Tyr Phe Arg Arg Glu Glu Leu Ser Phe Ala Arg Tyr Phe Ile Gly Leu
195 200 205

Ile Ser Ile Ile Cys Leu Ser Ala Thr Leu Phe Thr Phe Leu Thr Phe
210 215 220

Leu Ile Asp Val Thr Arg Phe Arg Tyr Pro Glu Arg Pro Ile Ile Phe

225 230 235 240

Tyr Ala Val Cys Tyr Met Met Val Ser Leu Ile Phe Phe Ile Gly Phe
245 250 255

Leu Leu Glu Asp Arg Val Ala Cys Asn Ala Ser Ile Pro Ala Gln Tyr
260 265 270

Lys Ala Ser Thr Val Thr Gln Gly Ser His Asn Lys Ala Cys Thr Met
275 280 285

Leu Phe Met Ile Leu Tyr Phe Phe Thr Met Ala Gly Ser Val Trp Trp
290 295 300

Val Ile Leu Thr Ile Thr Trp Phe Leu Ala Ala Val Pro Lys Trp Gly
305 310 315 320

Ser Glu Ala Ile Glu Lys Lys Ala Leu Leu Phe His Ala Ser Ala Trp
325 330 335

Gly Ile Pro Gly Thr Leu Thr Ile Ile Leu Leu Ala Met Asn Lys Ile
340 345 350

Glu Gly Asp Asn Ile Ser Gly Val Cys Phe Val Gly Leu Tyr Asp Val
355 360 365

Asp Ala Leu Arg Tyr Phe Val Leu Ala Pro Leu Cys Leu Tyr Val Val
370 375 380

Val Gly Val Ser Leu Leu Leu Ala Gly Ile Ile Ser Leu Asn Arg Val
385 390 395 400

Arg Ile Glu Ile Pro Leu Glu Lys Glu Asn Gln Asp Lys Leu Val Lys
405 410 415

Phe Met Ile Arg Ile Gly Val Phe Ser Ile Leu Tyr Leu Val Pro Leu
420 425 430

Leu Val Val Ile Gly Cys Tyr Phe Tyr Glu Gln Ala Tyr Arg Gly Ile
435 440 445

Trp Glu Thr Thr Trp Ile Gln Glu Arg Cys Arg Glu Tyr His Ile Pro
450 455 460

Cys Pro Tyr Gln Val Thr Gln Met Ser Arg Pro Asp Leu Ile Leu Phe
465 470 475 480

Leu Met Lys Tyr Leu Met Ala Leu Ile Val Gly Ile Pro Ser Val Phe
485 490 495

Trp Val Gly Ser Lys Lys Thr Cys Phe Glu Trp Ala Ser Phe Phe His

500 505 510

Gly Arg Arg Lys Lys Glu Ile Val Asn Glu Ser Arg Gln Val Leu Gln
515 520 525

Glu Pro Asp Phe Ala Gln Ser Leu Leu Arg Asp Pro Asn Thr Pro Ile
530 535 540

Ile Arg Lys Ser Arg Gly Thr Ser Thr Gln Gly Thr Ser Thr His Ala
545 550 555 560

Ser Ser Thr Gln Leu Ala Met Val Asp Asp Gln Arg Ser Lys Ala Gly
565 570 575

Ser Ile His Ser Lys Val Ser Ser Tyr His Gly Ser Leu His Arg Ser
580 585 590

Arg Asp Gly Arg Tyr Thr Pro Cys Ser Tyr Arg Gly Met Glu Glu Arg
595 600 605

Leu Pro His Gly Ser Met Ser Arg Leu Thr Asp His Ser Arg His Ser
610 615 620

Ser Ser His Arg Leu Asn Glu Gln Ser Arg His Ser Ser Ile Arg Asp
625 630 635 640

Leu Ser Asn Asn Pro Met Thr His Ile Thr His Gly Thr Ser Met Asn
645 650 655

Arg Val Ile Glu Glu Asp Gly Thr Ser Ala
660 665

<210> 35
<211> 204
<212> PRT
<213> Artificial Sequence

<220>
<223> extracellular domain (ECD) of FZD3

<400> 35

Met Ala Met Thr Trp Ile Val Phe Ser Leu Trp Pro Leu Thr Val Phe
1 5 10 15

Met Gly His Ile Gly Gly His Ser Leu Phe Ser Cys Glu Pro Ile Thr
20 25 30

Leu Arg Met Cys Gln Asp Leu Pro Tyr Asn Thr Thr Phe Met Pro Asn
35 40 45

Leu Leu Asn His Tyr Asp Gln Gln Thr Ala Ala Leu Ala Met Glu Pro
50 55 60

```
Phe His Pro Met Val Asn Leu Asp Cys Ser Arg Asp Phe Arg Pro Phe
65                  70                  75                  80

Leu Cys Ala Leu Tyr Ala Pro Ile Cys Met Glu Tyr Gly Arg Val Thr
                85                  90                  95

Leu Pro Cys Arg Arg Leu Cys Gln Arg Ala Tyr Ser Glu Cys Ser Lys
            100                 105                 110

Leu Met Glu Met Phe Gly Val Pro Trp Pro Glu Asp Met Glu Cys Ser
        115                 120                 125

Arg Phe Pro Asp Cys Asp Glu Pro Tyr Pro Arg Leu Val Asp Leu Asn
    130                 135                 140

Leu Ala Gly Glu Pro Thr Glu Gly Ala Pro Val Ala Val Gln Arg Asp
145                 150                 155                 160

Tyr Gly Phe Trp Cys Pro Arg Glu Leu Lys Ile Asp Pro Asp Leu Gly
                165                 170                 175

Tyr Ser Phe Leu His Val Arg Asp Cys Ser Pro Pro Cys Pro Asn Met
            180                 185                 190

Tyr Phe Arg Arg Glu Glu Leu Ser Phe Ala Arg Tyr
        195                 200
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<210> 36
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> Human FZD3 Fri domain

<400> 36

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Gly His Ile Gly Gly His Ser Leu Phe Ser Cys Glu Pro Ile Thr Leu
1               5                   10                  15

Arg Met Cys Gln Asp Leu Pro Tyr Asn Thr Thr Phe Met Pro Asn Leu
            20                  25                  30

Leu Asn His Tyr Asp Gln Gln Thr Ala Ala Leu Ala Met Glu Pro Phe
        35                  40                  45

His Pro Met Val Asn Leu Asp Cys Ser Arg Asp Phe Arg Pro Phe Leu
    50                  55                  60

Cys Ala Leu Tyr Ala Pro Ile Cys Met Glu Tyr Gly Arg Val Thr Leu
65                  70                  75                  80

Pro Cys Arg Arg Leu Cys Gln Arg Ala Tyr Ser Glu Cys Ser Lys Leu
```

85 90 95

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

Phe Pro Asp Cys Asp Glu Pro Tyr Pro Arg Leu Val Asp Leu
115 120 125

<210> 37
<211> 2001
<212> DNA
<213> Artificial Sequence

<220>
<223> Human FZD3

<400> 37
atggctatga cttggattgt cttctctctt tggcccttga ctgtgttcat ggggcatata 60

ggtgggcaca gtttgttttc ttgtgaacct attaccttga ggatgtgcca agatttgcct 120

tataatacta ccttcatgcc taatcttctg aatcattatg accaacagac agcagctttg 180

gcaatggagc cattccaccc tatggtgaat ctggattgtt ctcgggattt ccggcctttt 240

ctttgtgcac tctacgctcc tatttgtatg gaatatggac gtgtcacact tccctgtcgt 300

aggctgtgtc agcgggctta cagtgagtgt tcgaagctca tggagatgtt tggtgttcct 360

tggcctgaag atatggaatg cagtaggttc ccagattgtg atgagccata tcctcgactt 420

gtggatctga atttagctgg agaaccaact gaaggagccc cagtggcagt gcagagagac 480

tatggttttt ggtgtccccg agagttaaaa attgatcctg atctgggtta ttcttttctg 540

catgtgcgtg attgttcacc tccttgtcca aatatgtact tcagaagaga agaactgtca 600

tttgctcgct atttcatagg attgatttca atcatttgcc tctcggccac attgtttact 660

tttttaactt ttttgattga tgtcacaaga ttccgttatc ctgaaaggcc tattatattt 720

tatgcagtct gctacatgat ggtatcctta attttcttca ttggattttt gcttgaagat 780

cgagtagcct gcaatgcatc catccctgca caatataagg cttccacagt gacacaagga 840

tctcataata aagcctgtac catgcttttt atgatactct atttttttac tatggctggc 900

agtgtatggt gggtaattct taccatcaca tggtttttag cagctgtgcc aaagtggggt 960

agtgaagcta ttgagaagaa agcattgctg tttcacgcca gtgcatgggg catccccgga 1020

actctaacca tcatcctttt agcgatgaat aaaattgaag gtgacaatat tagtggcgtg 1080

tgttttgttg gcctctacga tgttgatgca ttgagatatt ttgttcttgc tcccctctgc 1140

ctgtatgtgg tagttggggt ttctctcctc ttagctggca ttatatccct aaacagagtt 1200

cgaattgaga ttccattaga aaaggagaac caagataaat tagtgaagtt tatgatccgg 1260

atcggtgttt tcagcattct ttatctcgta ccactcttgg ttgtaattgg atgctacttt 1320

tatgagcaag cttaccgggg catctgggaa acaacgtgga tacaagaacg ctgcagagaa 1380

tatcacattc catgtccata tcaggttact caaatgagtc gtccagactt gattctcttt 1440

ctgatgaaat acctgatggc tctcatagtt ggcattccct ctgtattttg ggttggaagc 1500

aaaaagacat gctttgaatg ggccagtttt tttcatggtc gtaggaaaaa agagatagtg 1560

aatgagagcc gacaggtact ccaggaacct gattttgctc agtctctcct gagggatcca 1620

aatactccta tcataagaaa gtcaagggga acttccactc aaggaacatc cacccatgct 1680

tcttcaactc agctggctat ggtggatgat caaagaagca aagcaggaag catccacagc 1740

aaagtgagca gctaccacgg cagcctccac agatcacgtg atggcaggta cacgccctgc 1800

agttacagag gaatggagga gagactacct catggcagca tgtcacgact aacagatcac 1860

tccaggcata gtagttctca tcggctcaat gaacagtcac gacatagcag catcagagat 1920

ctcagtaata atcccatgac tcatatcaca catggcacca gcatgaatcg ggttattgaa 1980

gaagatggaa ccagtgctta a 2001

<210> 38
<211> 540
<212> PRT
<213> Artificial Sequence

<220>
<223> Human FZD4

<400> 38

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

Pro Gly Gly Val Gly Leu Ser Leu Gly Leu Leu Leu Gln Leu Leu Leu
20 25 30

Leu Leu Gly Pro Ala Arg Gly Phe Gly Asp Glu Glu Glu Arg Arg Cys
35 40 45

Asp Pro Ile Arg Ile Ser Met Cys Gln Asn Leu Gly Tyr Asn Val Thr
50 55 60

Lys Met Pro Asn Leu Val Gly His Glu Leu Gln Thr Asp Ala Glu Leu
65 70 75 80

Gln Leu Thr Thr Phe Thr Pro Leu Ile Gln Tyr Gly Cys Ser Ser Gln
85 90 95

Leu Gln Phe Phe Leu Cys Ser Val Tyr Val Pro Met Cys Thr Glu Lys
100 105 110

Ile Asn Ile Pro Ile Gly Pro Cys Gly Gly Met Cys Leu Ser Val Lys
115 120 125

Arg Arg Cys Glu Pro Val Leu Lys Glu Phe Gly Phe Ala Trp Pro Glu
130 135 140

Ser Leu Asn Cys Ser Lys Phe Pro Pro Gln Asn Asp His Asn His Met

145 150 155 160

Cys Met Glu Gly Pro Gly Asp Glu Glu Val Pro Leu Pro His Lys Thr
165 170 175

Pro Ile Gln Pro Gly Glu Glu Cys His Ser Val Gly Thr Asn Ser Asp
180 185 190

Gln Tyr Ile Trp Val Lys Arg Ser Leu Asn Cys Val Leu Lys Cys Gly
195 200 205

Tyr Asp Ala Gly Leu Tyr Ser Arg Ser Ala Lys Glu Phe Thr Asp Ile
210 215 220

Trp Met Ala Val Trp Ala Ser Leu Cys Phe Ile Ser Thr Ala Phe Thr
225 230 235 240

Val Leu Thr Phe Leu Ile Asp Ser Ser Arg Phe Ser Tyr Pro Glu Arg
245 250 255

Pro Ile Ile Phe Leu Ser Met Cys Tyr Asn Ile Tyr Ser Ile Ala Tyr
260 265 270

Ile Val Arg Leu Thr Val Gly Arg Glu Arg Ile Ser Cys Asp Phe Glu
275 280 285

Glu Ala Ala Glu Pro Val Leu Ile Gln Glu Gly Leu Lys Asn Thr Gly
290 295 300

Cys Ala Ile Ile Phe Leu Leu Met Tyr Phe Phe Gly Met Ala Ser Ser
305 310 315 320

Ile Trp Trp Val Ile Leu Thr Leu Thr Trp Phe Leu Ala Ala Gly Leu
325 330 335

Lys Trp Gly His Glu Ala Ile Glu Met His Ser Ser Tyr Phe His Ile
340 345 350

Ala Ala Trp Ala Ile Pro Ala Val Lys Thr Ile Val Ile Leu Ile Met
355 360 365

Arg Leu Val Asp Ala Asp Glu Leu Thr Gly Leu Cys Tyr Val Gly Asn
370 375 380

Gln Asn Leu Asp Ala Leu Thr Gly Phe Val Val Ala Pro Leu Phe Thr
385 390 395 400

Tyr Leu Val Ile Gly Thr Leu Phe Ile Ala Ala Gly Leu Val Ala Leu
405 410 415

Phe Lys Ile Arg Ser Asn Leu Gln Lys Asp Gly Thr Lys Thr Asp Lys

420 425 430

Leu Glu Arg Leu Met Val Lys Ile Gly Val Phe Ser Val Leu Tyr Thr
435 440 445

Val Pro Ala Thr Cys Val Ile Ala Cys Tyr Phe Tyr Glu Ile Ser Asn
450 455 460

Trp Ala Leu Phe Arg Tyr Ser Ala Asp Asp Ser Asn Met Ala Val Glu
465 470 475 480

Met Leu Lys Ile Phe Met Ser Leu Leu Val Gly Ile Thr Ser Gly Met
485 490 495

Trp Ile Trp Ser Ala Lys Thr Leu His Thr Trp Gln Lys Cys Ser Asn
500 505 510

Arg Leu Val Asn Ser Gly Lys Val Lys Arg Glu Lys Arg Gly Asn Gly
515 520 525

Trp Val Lys Pro Gly Lys Gly Ser Glu Thr Val Val
530 535 540

<210> 39
<211> 224
<212> PRT
<213> Artificial Sequence

<220>
<223> extracellular domain (ECD) of FZD4

<400> 39

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

Pro Gly Gly Val Gly Leu Ser Leu Gly Leu Leu Leu Gln Leu Leu Leu
20 25 30

Leu Leu Gly Pro Ala Arg Gly Phe Gly Asp Glu Glu Glu Arg Arg Cys
35 40 45

Asp Pro Ile Arg Ile Ser Met Cys Gln Asn Leu Gly Tyr Asn Val Thr
50 55 60

Lys Met Pro Asn Leu Val Gly His Glu Leu Gln Thr Asp Ala Glu Leu
65 70 75 80

Gln Leu Thr Thr Phe Thr Pro Leu Ile Gln Tyr Gly Cys Ser Ser Gln
85 90 95

Leu Gln Phe Phe Leu Cys Ser Val Tyr Val Pro Met Cys Thr Glu Lys
100 105 110

Ile Asn Ile Pro Ile Gly Pro Cys Gly Gly Met Cys Leu Ser Val Lys
115 120 125

Arg Arg Cys Glu Pro Val Leu Lys Glu Phe Gly Phe Ala Trp Pro Glu
130 135 140

Ser Leu Asn Cys Ser Lys Phe Pro Pro Gln Asn Asp His Asn His Met
145 150 155 160

Cys Met Glu Gly Pro Gly Asp Glu Glu Val Pro Leu Pro His Lys Thr
165 170 175

Pro Ile Gln Pro Gly Glu Glu Cys His Ser Val Gly Thr Asn Ser Asp
180 185 190

Gln Tyr Ile Trp Val Lys Arg Ser Leu Asn Cys Val Leu Lys Cys Gly
195 200 205

Tyr Asp Ala Gly Leu Tyr Ser Arg Ser Ala Lys Glu Phe Thr Asp Ile
210 215 220

<210> 40
<211> 131
<212> PRT
<213> Artificial Sequence

<220>
<223> Human FZD4 Fri domain

<400> 40

Phe Gly Asp Glu Glu Glu Arg Arg Cys Asp Pro Ile Arg Ile Ser Met
1 5 10 15

Cys Gln Asn Leu Gly Tyr Asn Val Thr Lys Met Pro Asn Leu Val Gly
20 25 30

His Glu Leu Gln Thr Asp Ala Glu Leu Gln Leu Thr Thr Phe Thr Pro
35 40 45

Leu Ile Gln Tyr Gly Cys Ser Ser Gln Leu Gln Phe Phe Leu Cys Ser
50 55 60

Val Tyr Val Pro Met Cys Thr Glu Lys Ile Asn Ile Pro Ile Gly Pro
65 70 75 80

Cys Gly Gly Met Cys Leu Ser Val Lys Arg Arg Cys Glu Pro Val Leu
85 90 95

Lys Glu Phe Gly Phe Ala Trp Pro Glu Ser Leu Asn Cys Ser Lys Phe
100 105 110

Pro Pro Gln Asn Asp His Asn His Met Cys Met Glu Gly Pro Gly Asp

115 120 125

Glu Glu Val
130

<210> 41
<211> 1623
<212> DNA
<213> Artificial Sequence

<220>
<223> Human FZD4

<400> 41
atgctggcca tggcctggcg gggcgcaggg ccgagcgtcc cgggggcgcc cgggggcgtc 60

ggtctcagtc tggggttgct cctgcagttg ctgctgctcc tggggccggc gcggggcttc 120

ggggacgagg aagagcggcg ctgcgacccc atccgcatct ccatgtgcca gaacctcggc 180

tacaacgtga ccaagatgcc caacctggtt gggcacgagc tgcagacgga cgccgagctg 240

cagctgacaa ctttcacacc gctcatccag tacggctgct ccagccagct gcagttcttc 300

ctttgttctg tttatgtgcc aatgtgcaca gagaagatca acatccccat tggcccatgc 360

ggcggcatgt gtctttcagt caagagacgc tgtgaacccg tcctgaagga atttggattt 420

gcctggccag agagtctgaa ctgcagcaaa ttcccaccac agaacgacca caaccacatg 480

tgcatggaag ggccaggtga tgaagaggtg cccttacctc acaaaacccc catccagcct 540

ggggaagagt gtcactctgt gggaaccaat tctgatcagt acatctgggt gaaaaggagc 600

ctgaactgtg tgctcaagtg tggctatgat gctggcttat acagccgctc agccaaggag 660

ttcactgata tctggatggc tgtgtgggcc agcctgtgtt tcatctccac tgccttcaca 720

gtactgacct tcctgatcga ttcttctagg ttttcctacc ctgagcgccc catcatattt 780

ctcagtatgt gctataatat ttatagcatt gcttatattg tcaggctgac tgtaggccgg 840

gaaaggatat cctgtgattt tgaagaggca gcagaacctg ttctcatcca agaaggactt 900

aagaacacag gatgtgcaat aattttcttg ctgatgtact tttttggaat ggccagctcc 960

atttggtggg ttattctgac actcacttgg tttttggcag caggactcaa atggggtcat 1020

gaagccattg aaatgcacag ctcttatttc cacattgcag cctgggccat ccccgcagtg 1080

aaaaccattg tcatcttgat tatgagactg gtggatgcag atgaactgac tggcttgtgc 1140

tatgttggaa accaaaatct cgatgccctc accgggttcg tggtggctcc cctctttact 1200

tatttggtca ttggaacttt gttcattgct gcaggtttgg tggccttgtt caaaattcgg 1260

tcaaatcttc aaaaggatgg gacaaagaca gacaagttag aaagactgat ggtcaagatt 1320

ggggtgttct cagtactgta cacagttcct gcaacgtgtg tgattgcctg ttatttttat 1380

gaaatctcca actgggcact ttttcggtat tctgcagatg attccaacat ggctgttgaa 1440

atgttgaaaa tttttatgtc tttgttggtg ggcatcactt caggcatgtg gatttggtct 1500

gccaaaactc ttcacacgtg gcagaagtgt tccaacagat tggtgaattc tggaaaggta 1560

aagagagaga agagaggaaa tggttgggtg aagcctggaa aaggcagtga gactgtggta 1620

taa 1623

<210> 42
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> human FZD5

<400> 42

Met Ala Arg Pro Asp Pro Ser Ala Pro Pro Ser Leu Leu Leu Leu Leu
1 5 10 15

Leu Ala Gln Leu Val Gly Arg Ala Ala Ala Ala Ser Lys Ala Pro Val
20 25 30

Cys Gln Glu Ile Thr Val Pro Met Cys Arg Gly Ile Gly Tyr Asn Leu
35 40 45

Thr His Met Pro Asn Gln Phe Asn His Asp Thr Gln Asp Glu Ala Gly
50 55 60

Leu Glu Val His Gln Phe Trp Pro Leu Val Glu Ile Gln Cys Ser Pro
65 70 75 80

Asp Leu Arg Phe Phe Leu Cys Ser Met Tyr Thr Pro Ile Cys Leu Pro
85 90 95

Asp Tyr His Lys Pro Leu Pro Pro Cys Arg Ser Val Cys Glu Arg Ala
100 105 110

Lys Ala Gly Cys Ser Pro Leu Met Arg Gln Tyr Gly Phe Ala Trp Pro
115 120 125

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

Val Leu Cys Met Asp Tyr Asn Arg Ser Glu Ala Thr Thr Ala Pro Pro
145 150 155 160

Arg Pro Phe Pro Ala Lys Pro Thr Leu Pro Gly Pro Pro Gly Ala Pro
165 170 175

Ala Ser Gly Gly Glu Cys Pro Ala Gly Gly Pro Phe Val Cys Lys Cys
180 185 190

Arg Glu Pro Phe Val Pro Ile Leu Lys Glu Ser His Pro Leu Tyr Asn
195 200 205

Lys Val Arg Thr Gly Gln Val Pro Asn Cys Ala Val Pro Cys Tyr Gln

210 215 220

Pro Ser Phe Ser Ala Asp Glu Arg Thr Phe Ala Thr Phe Trp Ile Gly
225 230 235 240

Leu Trp Ser Val Leu Cys Phe Ile Ser Thr Ser Thr Thr Val Ala Thr
245 250 255

Phe Leu Ile Asp Met Glu Arg Phe Arg Tyr Pro Glu Arg Pro Ile Ile
260 265 270

Phe Leu Ser Ala Cys Tyr Leu Cys Val Ser Leu Gly Phe Leu Val Arg
275 280 285

Leu Val Val Gly His Ala Ser Val Ala Cys Ser Arg Glu His Asn His
290 295 300

Ile His Tyr Glu Thr Thr Gly Pro Ala Leu Cys Thr Ile Val Phe Leu
305 310 315 320

Leu Val Tyr Phe Phe Gly Met Ala Ser Ser Ile Trp Trp Val Ile Leu
325 330 335

Ser Leu Thr Trp Phe Leu Ala Ala Gly Met Lys Trp Gly Asn Glu Ala
340 345 350

Ile Ala Gly Tyr Ala Gln Tyr Phe His Leu Ala Ala Trp Leu Ile Pro
355 360 365

Ser Val Lys Ser Ile Thr Ala Leu Ala Leu Ser Ser Val Asp Gly Asp
370 375 380

Pro Val Ala Gly Ile Cys Tyr Val Gly Asn Gln Asn Leu Asn Ser Leu
385 390 395 400

Arg Gly Phe Val Leu Gly Pro Leu Val Leu Tyr Leu Leu Val Gly Thr
405 410 415

Leu Phe Leu Leu Ala Gly Phe Val Ser Leu Phe Arg Ile Arg Ser Val
420 425 430

Ile Lys Gln Gly Gly Thr Lys Thr Asp Lys Leu Glu Lys Leu Met Ile
435 440 445

Arg Ile Gly Ile Phe Thr Leu Leu Tyr Thr Val Pro Ala Ser Ile Val
450 455 460

Val Ala Cys Tyr Leu Tyr Glu Gln His Tyr Arg Glu Ser Trp Glu Ala
465 470 475 480

Ala Leu Thr Cys Ala Cys Pro Gly His Asp Thr Gly Gln Pro Arg Ala

485 490 495

Lys Pro Glu Tyr Trp Val Leu Met Leu Lys Tyr Phe Met Cys Leu Val
500 505 510

Val Gly Ile Thr Ser Gly Val Trp Ile Trp Ser Gly Lys Thr Val Glu
515 520 525

Ser Trp Arg Arg Phe Thr Ser Arg Cys Cys Cys Arg Pro Arg Arg Gly
530 535 540

His Lys Ser Gly Gly Ala Met Ala Ala Gly Asp Tyr Pro Glu Ala Ser
545 550 555 560

Ala Ala Leu Thr Gly Arg Thr Gly Pro Pro Gly Pro Ala Ala Thr Tyr
565 570 575

His Lys Gln Val Ser Leu Ser His Val
580 585

<210> 43
<211> 233
<212> PRT
<213> Artificial Sequence

<220>
<223> extracellular domain (ECD) of FZD5

<400> 43

Met Ala Arg Pro Asp Pro Ser Ala Pro Pro Ser Leu Leu Leu Leu Leu
1 5 10 15

Leu Ala Gln Leu Val Gly Arg Ala Ala Ala Ala Ser Lys Ala Pro Val
20 25 30

Cys Gln Glu Ile Thr Val Pro Met Cys Arg Gly Ile Gly Tyr Asn Leu
35 40 45

Thr His Met Pro Asn Gln Phe Asn His Asp Thr Gln Asp Glu Ala Gly
50 55 60

Leu Glu Val His Gln Phe Trp Pro Leu Val Glu Ile Gln Cys Ser Pro
65 70 75 80

Asp Leu Arg Phe Phe Leu Cys Ser Met Tyr Thr Pro Ile Cys Leu Pro
85 90 95

Asp Tyr His Lys Pro Leu Pro Pro Cys Arg Ser Val Cys Glu Arg Ala
100 105 110

Lys Ala Gly Cys Ser Pro Leu Met Arg Gln Tyr Gly Phe Ala Trp Pro
115 120 125

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

Val Leu Cys Met Asp Tyr Asn Arg Ser Glu Ala Thr Thr Ala Pro Pro
145 150 155 160

Arg Pro Phe Pro Ala Lys Pro Thr Leu Pro Gly Pro Pro Gly Ala Pro
165 170 175

Ala Ser Gly Gly Glu Cys Pro Ala Gly Gly Pro Phe Val Cys Lys Cys
180 185 190

Arg Glu Pro Phe Val Pro Ile Leu Lys Glu Ser His Pro Leu Tyr Asn
195 200 205

Lys Val Arg Thr Gly Gln Val Pro Asn Cys Ala Val Pro Cys Tyr Gln
210 215 220

Pro Ser Phe Ser Ala Asp Glu Arg Thr
225 230

<210> 44
<211> 131
<212> PRT
<213> Artificial Sequence

<220>
<223> Human FZD5 Fri domain

<400> 44

Ala Ser Lys Ala Pro Val Cys Gln Glu Ile Thr Val Pro Met Cys Arg
1 5 10 15

Gly Ile Gly Tyr Asn Leu Thr His Met Pro Asn Gln Phe Asn His Asp
20 25 30

Thr Gln Asp Glu Ala Gly Leu Glu Val His Gln Phe Trp Pro Leu Val
35 40 45

Glu Ile Gln Cys Ser Pro Asp Leu Arg Phe Phe Leu Cys Ser Met Tyr
50 55 60

Thr Pro Ile Cys Leu Pro Asp Tyr His Lys Pro Leu Pro Pro Cys Arg
65 70 75 80

Ser Val Cys Glu Arg Ala Lys Ala Gly Cys Ser Pro Leu Met Arg Gln
85 90 95

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

Leu Gly Arg Asp Ala Glu Val Leu Cys Met Asp Tyr Asn Arg Ser Glu

115 120 125

Ala Thr Thr
130

<210> 45
<211> 1758
<212> DNA
<213> Artificial Sequence

<220>
<223> Human FZD5

<400> 45
atggctcggc ctgacccatc cgcgccgccc tcgctgttgc tgctgctcct ggcgcagctg 60

gtgggccggg cggccgccgc gtccaaggcc ccggtgtgcc aggaaatcac ggtgcccatg 120

tgccgcggca tcggctacaa cctgacgcac atgcccaacc agttcaacca cgacacgcag 180

gacgaggcgg gcctggaggt gcaccagttc tggccgctgg tggagatcca atgctcgccg 240

gacctgcgct tcttcctatg ctctatgtac acgcccatct gtctgcccga ctaccacaag 300

ccgctgccgc cctgccgctc ggtgtgcgag cgcgccaagg ccggctgctc gccgctgatg 360

cgccagtacg gcttcgcctg gcccgagcgc atgagctgcg accgcctccc ggtgctgggc 420

cgcgacgccg aggtcctctg catggattac aaccgcagcg aggccaccac ggcgcccccc 480

aggcctttcc cagccaagcc cacccttcca ggcccgccag gggcgccggc ctcgggggc 540

gaatgccccg ctgggggccc gttcgtgtgc aagtgtcgcg agcccttcgt gcccattctg 600

aaggagtcac acccgctcta caacaaggtg cggacgggcc aggtgcccaa ctgcgcggta 660

ccctgctacc agccgtcctt cagtgccgac gagcgcacgt tcgccacctt ctggataggc 720

ctgtggtcgg tgctgtgctt catctccacg tccaccacag tggccacctt cctcatcgac 780

atggaacgct tccgctatcc tgagcgcccc atcatcttcc tgtcagcctg ctacctgtgc 840

gtgtcgctgg gcttcctggt gcgtctggtc gtgggccatg ccagcgtggc ctgcagccgc 900

gagcacaacc acatccacta cgagaccacg ggccctgcac tgtgcaccat cgtcttcctc 960

ctggtctact tcttcggcat ggccagctcc atctggtggg tcatcctgtc gctcacctgg 1020

ttcctggccg ccggcatgaa gtggggcaac gaggccatcg cgggctacgc gcagtacttc 1080

cacctggctg cgtggctcat ccccagcgtc aagtccatca cggcactggc gctgagctcc 1140

gtggacgggg acccagtggc cggcatctgc tacgtgggca accagaacct gaactcgctg 1200

cgcggcttcg tgctgggccc gctggtgctc tacctgctgg tgggcacgct cttcctgctg 1260

gcgggcttcg tgtcgctctt ccgcatccgc agcgtcatca agcagggcgg caccaagacg 1320

gacaagctgg agaagctcat gatccgcatc ggcatcttca cgctgctcta cacggtcccc 1380

gccagcattg tggtggcctg ctacctgtac gagcagcact accgcgagag ctgggaggcg 1440

gcgctcacct gcgcctgccc gggccacgac accggccagc cgcgcgccaa gcccgagtac 1500

tgggtgctca tgctcaagta cttcatgtgc ctggtggtgg gcatcacgtc gggcgtctgg 1560

atctggtcgg gcaagacggt ggagtcgtgg cggcgtttca ccagccgctg ctgctgccgc 1620

ccgcggcgcg gccacaagag cgggggcgcc atggccgcag gggactaccc cgaggcgagc 1680

gccgcgctca caggcaggac cgggccgccg ggccccgccg ccacctacca caagcaggtg 1740

tccctgtcgc acgtgtag 1758

<210> 46
<211> 706
<212> PRT
<213> Artificial Sequence

<220>
<223> Human FZD6

<400> 46

Met Glu Met Phe Thr Phe Leu Leu Thr Cys Ile Phe Leu Pro Leu Leu
1 5 10 15

Arg Gly His Ser Leu Phe Thr Cys Glu Pro Ile Thr Val Pro Arg Cys
20 25 30

Met Lys Met Ala Tyr Asn Met Thr Phe Phe Pro Asn Leu Met Gly His
35 40 45

Tyr Asp Gln Ser Ile Ala Ala Val Glu Met Glu His Phe Leu Pro Leu
50 55 60

Ala Asn Leu Glu Cys Ser Pro Asn Ile Glu Thr Phe Leu Cys Lys Ala
65 70 75 80

Phe Val Pro Thr Cys Ile Glu Gln Ile His Val Val Pro Pro Cys Arg
85 90 95

Lys Leu Cys Glu Lys Val Tyr Ser Asp Cys Lys Lys Leu Ile Asp Thr
100 105 110

Phe Gly Ile Arg Trp Pro Glu Glu Leu Glu Cys Asp Arg Leu Gln Tyr
115 120 125

Cys Asp Glu Thr Val Pro Val Thr Phe Asp Pro His Thr Glu Phe Leu
130 135 140

Gly Pro Gln Lys Lys Thr Glu Gln Val Gln Arg Asp Ile Gly Phe Trp
145 150 155 160

Cys Pro Arg His Leu Lys Thr Ser Gly Gly Gln Gly Tyr Lys Phe Leu
165 170 175

Gly Ile Asp Gln Cys Ala Pro Pro Cys Pro Asn Met Tyr Phe Lys Ser
180 185 190

Asp Glu Leu Glu Phe Ala Lys Ser Phe Ile Gly Thr Val Ser Ile Phe

195 200 205

Cys Leu Cys Ala Thr Leu Phe Thr Phe Leu Thr Phe Leu Ile Asp Val
210 215 220

Arg Arg Phe Arg Tyr Pro Glu Arg Pro Ile Ile Tyr Tyr Ser Val Cys
225 230 235 240

Tyr Ser Ile Val Ser Leu Met Tyr Phe Ile Gly Phe Leu Leu Gly Asp
245 250 255

Ser Thr Ala Cys Asn Lys Ala Asp Glu Lys Leu Glu Leu Gly Asp Thr
260 265 270

Val Val Leu Gly Ser Gln Asn Lys Ala Cys Thr Val Leu Phe Met Leu
275 280 285

Leu Tyr Phe Phe Thr Met Ala Gly Thr Val Trp Trp Val Ile Leu Thr
290 295 300

Ile Thr Trp Phe Leu Ala Ala Gly Arg Lys Trp Ser Cys Glu Ala Ile
305 310 315 320

Glu Gln Lys Ala Val Trp Phe His Ala Val Ala Trp Gly Thr Pro Gly
325 330 335

Phe Leu Thr Val Met Leu Leu Ala Met Asn Lys Val Glu Gly Asp Asn
340 345 350

Ile Ser Gly Val Cys Phe Val Gly Leu Tyr Asp Leu Asp Ala Ser Arg
355 360 365

Tyr Phe Val Leu Leu Pro Leu Cys Leu Cys Val Phe Val Gly Leu Ser
370 375 380

Leu Leu Leu Ala Gly Ile Ile Ser Leu Asn His Val Arg Gln Val Ile
385 390 395 400

Gln His Asp Gly Arg Asn Gln Glu Lys Leu Lys Lys Phe Met Ile Arg
405 410 415

Ile Gly Val Phe Ser Gly Leu Tyr Leu Val Pro Leu Val Thr Leu Leu
420 425 430

Gly Cys Tyr Val Tyr Glu Gln Val Asn Arg Ile Thr Trp Glu Ile Thr
435 440 445

Trp Val Ser Asp His Cys Arg Gln Tyr His Ile Pro Cys Pro Tyr Gln
450 455 460

Ala Lys Ala Lys Ala Arg Pro Glu Leu Ala Leu Phe Met Ile Lys Tyr

465 470 475 480

Leu Met Thr Leu Ile Val Gly Ile Ser Ala Val Phe Trp Val Gly Ser
485 490 495

Lys Lys Thr Cys Thr Glu Trp Ala Gly Phe Phe Lys Arg Asn Arg Lys
500 505 510

Arg Asp Pro Ile Ser Glu Ser Arg Arg Val Leu Gln Glu Ser Cys Glu
515 520 525

Phe Phe Leu Lys His Asn Ser Lys Val Lys His Lys Lys Lys His Tyr
530 535 540

Lys Pro Ser Ser His Lys Leu Lys Val Ile Ser Lys Ser Met Gly Thr
545 550 555 560

Ser Thr Gly Ala Thr Ala Asn His Gly Thr Ser Ala Val Ala Ile Thr
565 570 575

Ser His Asp Tyr Leu Gly Gln Glu Thr Leu Thr Glu Ile Gln Thr Ser
580 585 590

Pro Glu Thr Ser Met Arg Glu Val Lys Ala Asp Gly Ala Ser Thr Pro
595 600 605

Arg Leu Arg Glu Gln Asp Cys Gly Glu Pro Ala Ser Pro Ala Ala Ser
610 615 620

Ile Ser Arg Leu Ser Gly Glu Gln Val Asp Gly Lys Gly Gln Ala Gly
625 630 635 640

Ser Val Ser Glu Ser Ala Arg Ser Glu Gly Arg Ile Ser Pro Lys Ser
645 650 655

Asp Ile Thr Asp Thr Gly Leu Ala Gln Ser Asn Asn Leu Gln Val Pro
660 665 670

Ser Ser Ser Glu Pro Ser Ser Leu Lys Gly Ser Thr Ser Leu Leu Val
675 680 685

His Pro Val Ser Gly Val Arg Lys Glu Gln Gly Gly Gly Cys His Ser
690 695 700

Asp Thr
705

<210> 47
<211> 207
<212> PRT
<213> Artificial Sequence

<220>
<223> extracellular domain (ECD) of FZD6

<400> 47

Met Glu Met Phe Thr Phe Leu Leu Thr Cys Ile Phe Leu Pro Leu Leu
1 5 10 15

Arg Gly His Ser Leu Phe Thr Cys Glu Pro Ile Thr Val Pro Arg Cys
20 25 30

Met Lys Met Ala Tyr Asn Met Thr Phe Phe Pro Asn Leu Met Gly His
35 40 45

Tyr Asp Gln Ser Ile Ala Ala Val Glu Met Glu His Phe Leu Pro Leu
50 55 60

Ala Asn Leu Glu Cys Ser Pro Asn Ile Glu Thr Phe Leu Cys Lys Ala
65 70 75 80

Phe Val Pro Thr Cys Ile Glu Gln Ile His Val Val Pro Pro Cys Arg
85 90 95

Lys Leu Cys Glu Lys Val Tyr Ser Asp Cys Lys Lys Leu Ile Asp Thr
100 105 110

Phe Gly Ile Arg Trp Pro Glu Glu Leu Glu Cys Asp Arg Leu Gln Tyr
115 120 125

Cys Asp Glu Thr Val Pro Val Thr Phe Asp Pro His Thr Glu Phe Leu
130 135 140

Gly Pro Gln Lys Lys Thr Glu Gln Val Gln Arg Asp Ile Gly Phe Trp
145 150 155 160

Cys Pro Arg His Leu Lys Thr Ser Gly Gly Gln Gly Tyr Lys Phe Leu
165 170 175

Gly Ile Asp Gln Cys Ala Pro Pro Cys Pro Asn Met Tyr Phe Lys Ser
180 185 190

Asp Glu Leu Glu Phe Ala Lys Ser Phe Ile Gly Thr Val Ser Ile
195 200 205

<210> 48
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> Human FZD6 Fri domain

<400> 48

His Ser Leu Phe Thr Cys Glu Pro Ile Thr Val Pro Arg Cys Met Lys

1 5 10 15

Met Ala Tyr Asn Met Thr Phe Phe Pro Asn Leu Met Gly His Tyr Asp
20 25 30

Gln Ser Ile Ala Ala Val Glu Met Glu His Phe Leu Pro Leu Ala Asn
35 40 45

Leu Glu Cys Ser Pro Asn Ile Glu Thr Phe Leu Cys Lys Ala Phe Val
50 55 60

Pro Thr Cys Ile Glu Gln Ile His Val Val Pro Pro Cys Arg Lys Leu
65 70 75 80

Cys Glu Lys Val Tyr Ser Asp Cys Lys Lys Leu Ile Asp Thr Phe Gly
85 90 95

Ile Arg Trp Pro Glu Glu Leu Glu Cys Asp Arg Leu Gln Tyr Cys Asp
100 105 110

Glu Thr Val Pro Val Thr Phe Asp Pro His Thr Glu Phe Leu Gly
115 120 125

<210> 49
<211> 2121
<212> DNA
<213> Artificial Sequence

<220>
<223> Human FZD6

<400> 49
atggaaatgt ttacattttt gttgacgtgt atttttctac ccctcctaag agggcacagt 60

ctcttcacct gtgaaccaat tactgttccc agatgtatga aaatggccta caacatgacg 120

tttttcccta atctgatggg tcattatgac cagagtattg ccgcggtgga aatggagcat 180

tttcttcctc tcgcaaatct ggaatgttca ccaaacattg aaactttcct ctgcaaagca 240

tttgtaccaa cctgcataga acaaattcat gtggttccac cttgtcgtaa actttgtgag 300

aaagtatatt ctgattgcaa aaaattaatt gacacttttg ggatccgatg gcctgaggag 360

cttgaatgtg acagattaca atactgtgat gagactgttc ctgtaacttt tgatccacac 420

acagaatttc ttggtcctca gaagaaaaca gaacaagtcc aaagagacat tggattttgg 480

tgtccaaggc atcttaagac ttctggggga caaggatata agtttctggg aattgaccag 540

tgtgcgcctc catgccccaa catgtatttt aaaagtgatg agctagagtt tgcaaaaagt 600

tttattggaa cagtttcaat attttgtctt tgtgcaactc tgttcacatt ccttactttt 660

ttaattgatg ttagaagatt cagataccca gagagaccaa ttatatatta ctctgtctgt 720

tacagcattg tatctcttat gtacttcatt ggatttttgc taggcgatag cacagcctgc 780

aataaggcag atgagaagct agaacttggt gacactgttg tcctaggctc tcaaaataag 840

gcttgcaccg ttttgttcat gcttttgtat tttttcacaa tggctggcac tgtgtggtgg 900

gtgattctta ccattacttg gttcttagct gcaggaagaa aatggagttg tgaagccatc 960

gagcaaaaag cagtgtggtt tcatgctgtt gcatggggaa caccaggttt cctgactgtt 1020

atgcttcttg ctatgaacaa agttgaagga gacaacatta gtggagtttg ctttgttggc 1080

ctttatgacc tggatgcttc tcgctacttt gtactcttgc cactgtgcct ttgtgtgttt 1140

gttgggctct ctcttctttt agctggcatt atttccttaa atcatgttcg acaagtcata 1200

caacatgatg gccggaacca agaaaaacta aagaaattta tgattcgaat tggagtcttc 1260

agcggcttgt atcttgtgcc attagtgaca cttctcggat gttacgtcta tgagcaagtg 1320

aacaggatta cctgggagat aacttgggtc tctgatcatt gtcgtcagta ccatatccca 1380

tgtccttatc aggcaaaagc aaaagctcga ccagaattgg ctttatttat gataaaatac 1440

ctgatgacat taattgttgg catctctgct gtcttctggg ttggaagcaa aaagacatgc 1500

acagaatggg ctgggttttt taaacgaaat cgcaagagag atccaatcag tgaaagtcga 1560

agagtactac aggaatcatg tgagtttttc ttaaagcaca attctaaagt taaacacaaa 1620

aagaagcact ataaaccaag ttcacacaag ctgaaggtca tttccaaatc catgggaacc 1680

agcacaggag ctacagcaaa tcatggcact tctgcagtag caattactag ccatgattac 1740

ctaggacaag aaactttgac agaaatccaa acctcaccag aaacatcaat gagagaggtg 1800

aaagcggacg gagctagcac ccccaggtta agagaacagg actgtggtga acctgcctcg 1860

ccagcagcat ccatctccag actctctggg gaacaggtcg acgggaaggg ccaggcaggc 1920

agtgtatctg aaagtgcgcg gagtgaagga aggattagtc caaagagtga tattactgac 1980

actggcctgg cacagagcaa caatttgcag gtccccagtt cttcagaacc aagcagcctc 2040

aaaggttcca catctctgct tgttcacccg gtttcaggag tgagaaaaga gcagggaggt 2100

ggttgtcatt cagatacttg a 2121

<210> 50
<211> 574
<212> PRT
<213> Artificial Sequence

<220>
<223> Human FZD7

<400> 50

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

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

Gln Pro Tyr His Gly Glu Lys Gly Ile Ser Val Pro Asp His Gly Phe
35 40 45

Cys Gln Pro Ile Ser Ile Pro Leu Cys Thr Asp Ile Ala Tyr Asn Gln

50 55 60

Thr Ile Leu Pro Asn Leu Leu Gly His Thr Asn Gln Glu Asp Ala Gly
65 70 75 80

Leu Glu Val His Gln Phe Tyr Pro Leu Val Lys Val Gln Cys Ser Pro
85 90 95

Glu Leu Arg Phe Phe Leu Cys Ser Met Tyr Ala Pro Val Cys Thr Val
100 105 110

Leu Asp Gln Ala Ile Pro Pro Cys Arg Ser Leu Cys Glu Arg Ala Arg
115 120 125

Gln Gly Cys Glu Ala Leu Met Asn Lys Phe Gly Phe Gln Trp Pro Glu
130 135 140

Arg Leu Arg Cys Glu Asn Phe Pro Val His Gly Ala Gly Glu Ile Cys
145 150 155 160

Val Gly Gln Asn Thr Ser Asp Gly Ser Gly Gly Pro Gly Gly Gly Pro
165 170 175

Thr Ala Tyr Pro Thr Ala Pro Tyr Leu Pro Asp Leu Pro Phe Thr Ala
180 185 190

Leu Pro Pro Gly Ala Ser Asp Gly Arg Gly Arg Pro Ala Phe Pro Phe
195 200 205

Ser Cys Pro Arg Gln Leu Lys Val Pro Pro Tyr Leu Gly Tyr Arg Phe
210 215 220

Leu Gly Glu Arg Asp Cys Gly Ala Pro Cys Glu Pro Gly Arg Ala Asn
225 230 235 240

Gly Leu Met Tyr Phe Lys Glu Glu Glu Arg Arg Phe Ala Arg Leu Trp
245 250 255

Val Gly Val Trp Ser Val Leu Cys Cys Ala Ser Thr Leu Phe Thr Val
260 265 270

Leu Thr Tyr Leu Val Asp Met Arg Arg Phe Ser Tyr Pro Glu Arg Pro
275 280 285

Ile Ile Phe Leu Ser Gly Cys Tyr Phe Met Val Ala Val Ala His Val
290 295 300

Ala Gly Phe Leu Leu Glu Asp Arg Ala Val Cys Val Glu Arg Phe Ser
305 310 315 320

Asp Asp Gly Tyr Arg Thr Val Ala Gln Gly Thr Lys Lys Glu Gly Cys

325 330 335

Thr Ile Leu Phe Met Val Leu Tyr Phe Phe Gly Met Ala Ser Ser Ile
340 345 350

Trp Trp Val Ile Leu Ser Leu Thr Trp Phe Leu Ala Ala Gly Met Lys
355 360 365

Trp Gly His Glu Ala Ile Glu Ala Asn Ser Gln Tyr Phe His Leu Ala
370 375 380

Ala Trp Ala Val Pro Ala Val Lys Thr Ile Thr Ile Leu Ala Met Gly
385 390 395 400

Gln Val Asp Gly Asp Leu Leu Ser Gly Val Cys Tyr Val Gly Leu Ser
405 410 415

Ser Val Asp Ala Leu Arg Gly Phe Val Leu Ala Pro Leu Phe Val Tyr
420 425 430

Leu Phe Ile Gly Thr Ser Phe Leu Leu Ala Gly Phe Val Ser Leu Phe
435 440 445

Arg Ile Arg Thr Ile Met Lys His Asp Gly Thr Lys Thr Glu Lys Leu
450 455 460

Glu Lys Leu Met Val Arg Ile Gly Val Phe Ser Val Leu Tyr Thr Val
465 470 475 480

Pro Ala Thr Ile Val Leu Ala Cys Tyr Phe Tyr Glu Gln Ala Phe Arg
485 490 495

Glu His Trp Glu Arg Thr Trp Leu Leu Gln Thr Cys Lys Ser Tyr Ala
500 505 510

Val Pro Cys Pro Pro Gly His Phe Pro Pro Met Ser Pro Asp Phe Thr
515 520 525

Val Phe Met Ile Lys Tyr Leu Met Thr Met Ile Val Gly Ile Thr Thr
530 535 540

Gly Phe Trp Ile Trp Ser Gly Lys Thr Leu Gln Ser Trp Arg Arg Phe
545 550 555 560

Tyr His Arg Leu Ser His Ser Ser Lys Gly Glu Thr Ala Val
565 570

<210> 51
<211> 255
<212> PRT
<213> Artificial Sequence

<220>
<223> extracellular domain (ECD) of FZD7

<400> 51

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

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

Gln Pro Tyr His Gly Glu Lys Gly Ile Ser Val Pro Asp His Gly Phe
35 40 45

Cys Gln Pro Ile Ser Ile Pro Leu Cys Thr Asp Ile Ala Tyr Asn Gln
50 55 60

Thr Ile Leu Pro Asn Leu Leu Gly His Thr Asn Gln Glu Asp Ala Gly
65 70 75 80

Leu Glu Val His Gln Phe Tyr Pro Leu Val Lys Val Gln Cys Ser Pro
85 90 95

Glu Leu Arg Phe Phe Leu Cys Ser Met Tyr Ala Pro Val Cys Thr Val
100 105 110

Leu Asp Gln Ala Ile Pro Pro Cys Arg Ser Leu Cys Glu Arg Ala Arg
115 120 125

Gln Gly Cys Glu Ala Leu Met Asn Lys Phe Gly Phe Gln Trp Pro Glu
130 135 140

Arg Leu Arg Cys Glu Asn Phe Pro Val His Gly Ala Gly Glu Ile Cys
145 150 155 160

Val Gly Gln Asn Thr Ser Asp Gly Ser Gly Gly Pro Gly Gly Gly Pro
165 170 175

Thr Ala Tyr Pro Thr Ala Pro Tyr Leu Pro Asp Leu Pro Phe Thr Ala
180 185 190

Leu Pro Pro Gly Ala Ser Asp Gly Arg Gly Arg Pro Ala Phe Pro Phe
195 200 205

Ser Cys Pro Arg Gln Leu Lys Val Pro Pro Tyr Leu Gly Tyr Arg Phe
210 215 220

Leu Gly Glu Arg Asp Cys Gly Ala Pro Cys Glu Pro Gly Arg Ala Asn
225 230 235 240

Gly Leu Met Tyr Phe Lys Glu Glu Glu Arg Arg Phe Ala Arg Leu
245 250 255

<210> 52
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
<223> Human FZD7 Fri domain

<400> 52

Ala Gln Pro Tyr His Gly Glu Lys Gly Ile Ser Val Pro Asp His Gly
1 5 10 15

Phe Cys Gln Pro Ile Ser Ile Pro Leu Cys Thr Asp Ile Ala Tyr Asn
20 25 30

Gln Thr Ile Leu Pro Asn Leu Leu Gly His Thr Asn Gln Glu Asp Ala
35 40 45

Gly Leu Glu Val His Gln Phe Tyr Pro Leu Val Lys Val Gln Cys Ser
50 55 60

Pro Glu Leu Arg Phe Phe Leu Cys Ser Met Tyr Ala Pro Val Cys Thr
65 70 75 80

Val Leu Asp Gln Ala Ile Pro Pro Cys Arg Ser Leu Cys Glu Arg Ala
85 90 95

Arg Gln Gly Cys Glu Ala Leu Met Asn Lys Phe Gly Phe Gln Trp Pro
100 105 110

Glu Arg Leu Arg Cys Glu Asn Phe Pro Val His Gly Ala Gly Glu Ile
115 120 125

Cys Val Gly Gln Asn Thr Ser Asp Gly Ser Gly
130 135

<210> 53
<211> 1725
<212> DNA
<213> Artificial Sequence

<220>
<223> Human FZD7

<400> 53
atgcgggacc ccggcgcggc cgctccgctt tcgtccctgg gcctctgtgc cctggtgctg 60

gcgctgctgg gcgcactgtc cgcgggcgcc ggggcgcagc cgtaccacgg agagaagggc 120

atctccgtgc cggaccacgg cttctgccag cccatctcca tcccgctgtg cacggacatc 180

gcctacaacc agaccatcct gcccaacctg ctgggccaca cgaaccaaga ggacgcgggc 240

ctcgaggtgc accagttcta cccgctggtg aaggtgcagt gttctcccga actccgcttt 300

ttcttatgct ccatgtatgc gcccgtgtgc accgtgctcg atcaggccat cccgccgtgt 360

cgttctctgt gcgagcgcgc ccgccagggc tgcgaggcgc tcatgaacaa gttcggcttc 420

cagtggcccg agcggctgcg ctgcgagaac ttcccggtgc acggtgcggg cgagatctgc 480

gtgggccaga acacgtcgga cggctccggg ggcccaggcg gcggccccac tgcctaccct 540

accgcgccct acctgccgga cctgcccttc accgcgctgc ccccgggggc ctcagatggc 600

aggggcgtc ccgccttccc cttctcatgc ccccgtcagc tcaaggtgcc cccgtacctg 660

ggctaccgct tcctgggtga gcgcgattgt ggcgccccgt gcgaaccggg ccgtgccaac 720

ggcctgatgt actttaagga ggaggagagg cgcttcgccc gcctctgggt gggcgtgtgg 780

tccgtgctgt gctgcgcctc gacgctcttt accgttctca cctacctggt ggacatgcgg 840

cgcttcagct acccagagcg gcccatcatc ttcctgtcgg gctgctactt catggtggcc 900

gtggcgcacg tggccggctt ccttctagag gaccgcgccg tgtgcgtgga gcgcttctcg 960

gacgatggct accgcacggt ggcgcagggc accaagaagg agggctgcac catcctcttc 1020

atggtgctct acttcttcgg catggccagc tccatctggt gggtcattct gtctctcact 1080

tggttcctgg cggccggcat gaagtggggc cacgaggcca tcgaggccaa ctcgcagtac 1140

ttccacctgg ccgcgtgggc cgtgcccgcc gtcaagacca tcactatcct ggccatgggc 1200

caggtagacg gggacctgct gagcggggtg tgctacgttg gcctctccag tgtggacgcg 1260

ctgcggggct tcgtgctggc gcctctgttc gtctacctct tcataggcac gtccttcttg 1320

ctggccggct tcgtgtccct cttccgtatc cgcaccatca tgaaacacga cggcaccaag 1380

accgagaagc tggagaagct catggtgcgc atcggcgtct tcagcgtgct ctacacagtg 1440

cccgccacca tcgtcctggc ctgctacttc tacgagcagg ccttccgcga gcactgggag 1500

cgcacctggc tcctgcagac gtgcaagagc tatgccgtgc cctgcccgcc cggccacttc 1560

ccgcccatga gccccgactt caccgtcttc atgatcaagt acctgatgac catgatcgtc 1620

ggcatcacca ctggcttctg gatctggtcg ggcaagaccc tgcagtcgtg gcgccgcttc 1680

taccacagac ttagccacag cagcaagggg gagactgcgg tatga 1725

<210> 54
<211> 694
<212> PRT
<213> Artificial Sequence

<220>
<223> Human FZD8

<400> 54

Met Glu Trp Gly Tyr Leu Leu Glu Val Thr Ser Leu Leu Ala Ala Leu
1 5 10 15

Ala Leu Leu Gln Arg Ser Ser Gly Ala Ala Ala Ala Ser Ala Lys Glu
20 25 30

Leu Ala Cys Gln Glu Ile Thr Val Pro Leu Cys Lys Gly Ile Gly Tyr
35 40 45

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Asn Tyr Thr Tyr Met Pro Asn Gln Phe Asn His Asp Thr Gln Asp Glu
    50                  55                  60

Ala Gly Leu Glu Val His Gln Phe Trp Pro Leu Val Glu Ile Gln Cys
65                  70                  75                  80

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

Leu Glu Asp Tyr Lys Lys Pro Leu Pro Pro Cys Arg Ser Val Cys Glu
            100                 105                 110

Arg Ala Lys Ala Gly Cys Ala Pro Leu Met Arg Gln Tyr Gly Phe Ala
        115                 120                 125

Trp Pro Asp Arg Met Arg Cys Asp Arg Leu Pro Glu Gln Gly Asn Pro
    130                 135                 140

Asp Thr Leu Cys Met Asp Tyr Asn Arg Thr Asp Leu Thr Thr Ala Ala
145                 150                 155                 160

Pro Ser Pro Pro Arg Arg Leu Pro Pro Pro Pro Pro Gly Glu Gln Pro
                165                 170                 175

Pro Ser Gly Ser Gly His Gly Arg Pro Pro Gly Ala Arg Pro Pro His
            180                 185                 190

Arg Gly Gly Gly Arg Gly Gly Gly Gly Gly Asp Ala Ala Ala Pro Pro
        195                 200                 205

Ala Arg Gly Gly Gly Gly Gly Gly Lys Ala Arg Pro Pro Gly Gly Gly
    210                 215                 220

Ala Ala Pro Cys Glu Pro Gly Cys Gln Cys Arg Ala Pro Met Val Ser
225                 230                 235                 240

Val Ser Ser Glu Arg His Pro Leu Tyr Asn Arg Val Lys Thr Gly Gln
                245                 250                 255

Ile Ala Asn Cys Ala Leu Pro Cys His Asn Pro Phe Phe Ser Gln Asp
            260                 265                 270

Glu Arg Ala Phe Thr Val Phe Trp Ile Gly Leu Trp Ser Val Leu Cys
        275                 280                 285

Phe Val Ser Thr Phe Ala Thr Val Ser Thr Phe Leu Ile Asp Met Glu
    290                 295                 300

Arg Phe Lys Tyr Pro Glu Arg Pro Ile Ile Phe Leu Ser Ala Cys Tyr
305                 310                 315                 320
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Leu Phe Val Ser Val Gly Tyr Leu Val Arg Leu Val Ala Gly His Glu
325 330 335

Lys Val Ala Cys Ser Gly Gly Ala Pro Gly Ala Gly Gly Ala Gly Gly
340 345 350

Ala Gly Gly Ala Ala Ala Gly Ala Gly Ala Ala Gly Ala Gly Ala Gly
355 360 365

Gly Pro Gly Gly Arg Gly Glu Tyr Glu Glu Leu Gly Ala Val Glu Gln
370 375 380

His Val Arg Tyr Glu Thr Thr Gly Pro Ala Leu Cys Thr Val Val Phe
385 390 395 400

Leu Leu Val Tyr Phe Phe Gly Met Ala Ser Ser Ile Trp Trp Val Ile
405 410 415

Leu Ser Leu Thr Trp Phe Leu Ala Ala Gly Met Lys Trp Gly Asn Glu
420 425 430

Ala Ile Ala Gly Tyr Ser Gln Tyr Phe His Leu Ala Ala Trp Leu Val
435 440 445

Pro Ser Val Lys Ser Ile Ala Val Leu Ala Leu Ser Ser Val Asp Gly
450 455 460

Asp Pro Val Ala Gly Ile Cys Tyr Val Gly Asn Gln Ser Leu Asp Asn
465 470 475 480

Leu Arg Gly Phe Val Leu Ala Pro Leu Val Ile Tyr Leu Phe Ile Gly
485 490 495

Thr Met Phe Leu Leu Ala Gly Phe Val Ser Leu Phe Arg Ile Arg Ser
500 505 510

Val Ile Lys Gln Gln Asp Gly Pro Thr Lys Thr His Lys Leu Glu Lys
515 520 525

Leu Met Ile Arg Leu Gly Leu Phe Thr Val Leu Tyr Thr Val Pro Ala
530 535 540

Ala Val Val Val Ala Cys Leu Phe Tyr Glu Gln His Asn Arg Pro Arg
545 550 555 560

Trp Glu Ala Thr His Asn Cys Pro Cys Leu Arg Asp Leu Gln Pro Asp
565 570 575

Gln Ala Arg Arg Pro Asp Tyr Ala Val Phe Met Leu Lys Tyr Phe Met
580 585 590

Cys Leu Val Val Gly Ile Thr Ser Gly Val Trp Val Trp Ser Gly Lys
595 600 605

Thr Leu Glu Ser Trp Arg Ser Leu Cys Thr Arg Cys Cys Trp Ala Ser
610 615 620

Lys Gly Ala Ala Val Gly Gly Gly Ala Gly Ala Thr Ala Ala Gly Gly
625 630 635 640

Gly Gly Gly Pro Gly Gly Gly Gly Gly Gly Gly Pro Gly Gly Gly Gly
645 650 655

Gly Pro Gly Gly Gly Gly Gly Ser Leu Tyr Ser Asp Val Ser Thr Gly
660 665 670

Leu Thr Trp Arg Ser Gly Thr Ala Ser Ser Val Ser Tyr Pro Lys Gln
675 680 685

Met Pro Leu Ser Gln Val
690

<210> 55
<211> 277
<212> PRT
<213> Artificial Sequence

<220>
<223> extracellular domain (ECD) of FZD8

<400> 55

Met Glu Trp Gly Tyr Leu Leu Glu Val Thr Ser Leu Leu Ala Ala Leu
1 5 10 15

Ala Leu Leu Gln Arg Ser Ser Gly Ala Ala Ala Ala Ser Ala Lys Glu
20 25 30

Leu Ala Cys Gln Glu Ile Thr Val Pro Leu Cys Lys Gly Ile Gly Tyr
35 40 45

Asn Tyr Thr Tyr Met Pro Asn Gln Phe Asn His Asp Thr Gln Asp Glu
50 55 60

Ala Gly Leu Glu Val His Gln Phe Trp Pro Leu Val Glu Ile Gln Cys
65 70 75 80

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

Leu Glu Asp Tyr Lys Lys Pro Leu Pro Pro Cys Arg Ser Val Cys Glu
100 105 110

Arg Ala Lys Ala Gly Cys Ala Pro Leu Met Arg Gln Tyr Gly Phe Ala

115 120 125

Trp Pro Asp Arg Met Arg Cys Asp Arg Leu Pro Glu Gln Gly Asn Pro
130 135 140

Asp Thr Leu Cys Met Asp Tyr Asn Arg Thr Asp Leu Thr Thr Ala Ala
145 150 155 160

Pro Ser Pro Pro Arg Arg Leu Pro Pro Pro Pro Pro Gly Glu Gln Pro
165 170 175

Pro Ser Gly Ser Gly His Gly Arg Pro Pro Gly Ala Arg Pro Pro His
180 185 190

Arg Gly Gly Gly Arg Gly Gly Gly Gly Gly Asp Ala Ala Ala Pro Pro
195 200 205

Ala Arg Gly Gly Gly Gly Gly Gly Lys Ala Arg Pro Pro Gly Gly Gly
210 215 220

Ala Ala Pro Cys Glu Pro Gly Cys Gln Cys Arg Ala Pro Met Val Ser
225 230 235 240

Val Ser Ser Glu Arg His Pro Leu Tyr Asn Arg Val Lys Thr Gly Gln
245 250 255

Ile Ala Asn Cys Ala Leu Pro Cys His Asn Pro Phe Phe Ser Gln Asp
260 265 270

Glu Arg Ala Phe Thr
275

<210> 56
<211> 131
<212> PRT
<213> Artificial Sequence

<220>
<223> Human FZD8 Fri domain

<400> 56

Ala Ser Ala Lys Glu Leu Ala Cys Gln Glu Ile Thr Val Pro Leu Cys
1 5 10 15

Lys Gly Ile Gly Tyr Asn Tyr Thr Tyr Met Pro Asn Gln Phe Asn His
20 25 30

Asp Thr Gln Asp Glu Ala Gly Leu Glu Val His Gln Phe Trp Pro Leu
35 40 45

Val Glu Ile Gln Cys Ser Pro Asp Leu Lys Phe Phe Leu Cys Ser Met
50 55 60

Tyr Thr Pro Ile Cys Leu Glu Asp Tyr Lys Lys Pro Leu Pro Pro Cys
65 70 75 80

Arg Ser Val Cys Glu Arg Ala Lys Ala Gly Cys Ala Pro Leu Met Arg
85 90 95

Gln Tyr Gly Phe Ala Trp Pro Asp Arg Met Arg Cys Asp Arg Leu Pro
100 105 110

Glu Gln Gly Asn Pro Asp Thr Leu Cys Met Asp Tyr Asn Arg Thr Asp
115 120 125

Leu Thr Thr
130

<210> 57
<211> 2085
<212> DNA
<213> Artificial Sequence

<220>
<223> Human FZD8

<400> 57
atggagtggg gttacctgtt ggaagtgacc tcgctgctgg ccgccttggc gctgctgcag 60

cgctctagcg gcgctgcggc cgcctcggcc aaggagctgg catgccaaga gatcaccgtg 120

ccgctgtgta agggcatcgg ctacaactac acctacatgc ccaatcagtt caaccacgac 180

acgcaagacg aggcgggcct ggaggtgcac cagttctggc cgctggtgga gatccagtgc 240

tcgcccgatc tcaagttctt cctgtgcagc atgtacacgc ccatctgcct agaggactac 300

aagaagccgc tgccgccctg ccgctcggtg tgcgagcgcg ccaaggccgg ctgcgcgccg 360

ctcatgcgcc agtacggctt cgcctggccc gaccgcatgc gctgcgaccg gctgcccgag 420

caaggcaacc ctgacacgct gtgcatggac tacaaccgca ccgacctaac caccgccgcg 480

cccagcccgc cgcgccgcct gccgccgccg ccgcccggcg agcagccgcc ttcgggcagc 540

ggccacggcc gcccgccggg ggccaggccc ccgcaccgcg gaggcggcag gggcggtggc 600

ggcggggacg cggcggcgcc cccagctcgc ggcggcggcg gtggcgggaa ggcgcggccc 660

cctggcggcg gcgcggctcc ctgcgagccc gggtgccagt gccgcgcgcc tatggtgagc 720

gtgtccagcg agcgccaccc gctctacaac cgcgtcaaga caggccagat cgctaactgc 780

gcgctgccct gccacaaccc ctttttcagc caggacgagc gcgccttcac cgtcttctgg 840

atcggcctgt ggtcggtgct ctgcttcgtg tccaccttcg ccaccgtctc caccttcctt 900

atcgacatgg agcgcttcaa gtacccggag cggcccatta tcttcctctc ggcctgctac 960

ctcttcgtgt cggtgggcta cctagtgcgc ctggtggcgg gccacgagaa ggtggcgtgc 1020

agcggtggcg cgccgggcgc gggggcgcgt gggggcgcgg gcggcgcggc ggcgggcgcg 1080

ggcgcggcgg gcgcgggcgc gggcggcccg ggcgggcgcg gcgagtacga ggagctgggc 1140

gcggtggagc agcacgtgcg ctacgagacc accggccccg cgctgtgcac cgtggtcttc 1200

ttgctggtct acttcttcgg catggccagc tccatctggt gggtgatctt gtcgctcaca 1260

tggttcctgg cggccggtat gaagtggggc aacgaagcca tcgccggcta ctcgcagtac 1320

ttccacctgg ccgcgtggct tgtgcccagc gtcaagtcca tcgcggtgct ggcgctcagc 1380

tcggtggacg gcgacccggt ggcgggcatc tgctacgtgg gcaaccagag cctggacaac 1440

ctgcgcggct tcgtgctggc gccgctggtc atctacctct tcatcggcac catgttcctg 1500

ctggccggct tcgtgtccct gttccgcatc cgctcggtca tcaagcaaca ggacggcccc 1560

accaagacgc acaagctgga gaagctgatg atccgcctgg gcctgttcac cgtgctctac 1620

accgtgcccg ccgcggtggt ggtcgcctgc ctcttctacg agcagcacaa ccgcccgcgc 1680

tgggaggcca cgcacaactg cccgtgcctg cgggacctgc agcccgacca ggcacgcagg 1740

cccgactacg ccgtcttcat gctcaagtac ttcatgtgcc tagtggtggg catcacctcg 1800

ggcgtgtggg tctggtccgg caagacgctg gagtcctggc gctccctgtg cacccgctgc 1860

tgctgggcca gcaagggcgc cgcggtgggc gggggcgcgg gcgccacggc cgcgggggggt 1920

ggcggcgggc cgggggggcgg cggcggcggg ggacccggcg gcggcggggg gccgggcggc 1980

ggcgggggct ccctctacag cgacgtcagc actggcctga cgtggcggtc gggcacggcg 2040

agctccgtgt cttatccaaa gcagatgcca ttgtcccagg tctga 2085

<210> 58
<211> 591
<212> PRT
<213> Artificial Sequence

<220>
<223> Human FZD9

<400> 58

Met Ala Val Ala Pro Leu Arg Gly Ala Leu Leu Leu Trp Gln Leu Leu
1 5 10 15

Ala Ala Gly Gly Ala Ala Leu Glu Ile Gly Arg Phe Asp Pro Glu Arg
20 25 30

Gly Arg Gly Ala Ala Pro Cys Gln Ala Val Glu Ile Pro Met Cys Arg
35 40 45

Gly Ile Gly Tyr Asn Leu Thr Arg Met Pro Asn Leu Leu Gly His Thr
50 55 60

Ser Gln Gly Glu Ala Ala Ala Glu Leu Ala Glu Phe Ala Pro Leu Val
65 70 75 80

Gln Tyr Gly Cys His Ser His Leu Arg Phe Phe Leu Cys Ser Leu Tyr
85 90 95

Ala Pro Met Cys Thr Asp Gln Val Ser Thr Pro Ile Pro Ala Cys Arg

100 105 110

Pro Met Cys Glu Gln Ala Arg Leu Arg Cys Ala Pro Ile Met Glu Gln
115 120 125

Phe Asn Phe Gly Trp Pro Asp Ser Leu Asp Cys Ala Arg Leu Pro Thr
130 135 140

Arg Asn Asp Pro His Ala Leu Cys Met Glu Ala Pro Glu Asn Ala Thr
145 150 155 160

Ala Gly Pro Ala Glu Pro His Lys Gly Leu Gly Met Leu Pro Val Ala
165 170 175

Pro Arg Pro Ala Arg Pro Pro Gly Asp Leu Gly Pro Gly Ala Gly Gly
180 185 190

Ser Gly Thr Cys Glu Asn Pro Glu Lys Phe Gln Tyr Val Glu Lys Ser
195 200 205

Arg Ser Cys Ala Pro Arg Cys Gly Pro Gly Val Glu Val Phe Trp Ser
210 215 220

Arg Arg Asp Lys Asp Phe Ala Leu Val Trp Met Ala Val Trp Ser Ala
225 230 235 240

Leu Cys Phe Phe Ser Thr Ala Phe Thr Val Leu Thr Phe Leu Leu Glu
245 250 255

Pro His Arg Phe Gln Tyr Pro Glu Arg Pro Ile Ile Phe Leu Ser Met
260 265 270

Cys Tyr Asn Val Tyr Ser Leu Ala Phe Leu Ile Arg Ala Val Ala Gly
275 280 285

Ala Gln Ser Val Ala Cys Asp Gln Glu Ala Gly Ala Leu Tyr Val Ile
290 295 300

Gln Glu Gly Leu Glu Asn Thr Gly Cys Thr Leu Val Phe Leu Leu Leu
305 310 315 320

Tyr Tyr Phe Gly Met Ala Ser Ser Leu Trp Trp Val Val Leu Thr Leu
325 330 335

Thr Trp Phe Leu Ala Ala Gly Lys Lys Trp Gly His Glu Ala Ile Glu
340 345 350

Ala His Gly Ser Tyr Phe His Met Ala Ala Trp Gly Leu Pro Ala Leu
355 360 365

Lys Thr Ile Val Ile Leu Thr Leu Arg Lys Val Ala Gly Asp Glu Leu

370 375 380

Thr Gly Leu Cys Tyr Val Ala Ser Thr Asp Ala Ala Ala Leu Thr Gly
385 390 395 400

Phe Val Leu Val Pro Leu Ser Gly Tyr Leu Val Leu Gly Ser Ser Phe
405 410 415

Leu Leu Thr Gly Phe Val Ala Leu Phe His Ile Arg Lys Ile Met Lys
420 425 430

Thr Gly Gly Thr Asn Thr Glu Lys Leu Glu Lys Leu Met Val Lys Ile
435 440 445

Gly Val Phe Ser Ile Leu Tyr Thr Val Pro Ala Thr Cys Val Ile Val
450 455 460

Cys Tyr Val Tyr Glu Arg Leu Asn Met Asp Phe Trp Arg Leu Arg Ala
465 470 475 480

Thr Glu Gln Pro Cys Ala Ala Ala Ala Gly Pro Gly Gly Arg Arg Asp
485 490 495

Cys Ser Leu Pro Gly Gly Ser Val Pro Thr Val Ala Val Phe Met Leu
500 505 510

Lys Ile Phe Met Ser Leu Val Val Gly Ile Thr Ser Gly Val Trp Val
515 520 525

Trp Ser Ser Lys Thr Phe Gln Thr Trp Gln Ser Leu Cys Tyr Arg Lys
530 535 540

Ile Ala Ala Gly Arg Ala Arg Ala Lys Ala Cys Arg Ala Pro Gly Ser
545 550 555 560

Tyr Gly Arg Gly Thr His Cys His Tyr Lys Ala Pro Thr Val Val Leu
565 570 575

His Met Thr Lys Thr Asp Pro Ser Leu Glu Asn Pro Thr His Leu
580 585 590

<210> 59
<211> 230
<212> PRT
<213> Artificial Sequence

<220>
<223> extracellular domain (ECD) of FZD9

<400> 59

Met Ala Val Ala Pro Leu Arg Gly Ala Leu Leu Leu Trp Gln Leu Leu
1 5 10 15

Ala Ala Gly Gly Ala Ala Leu Glu Ile Gly Arg Phe Asp Pro Glu Arg
20 25 30

Gly Arg Gly Ala Ala Pro Cys Gln Ala Val Glu Ile Pro Met Cys Arg
35 40 45

Gly Ile Gly Tyr Asn Leu Thr Arg Met Pro Asn Leu Leu Gly His Thr
50 55 60

Ser Gln Gly Glu Ala Ala Ala Glu Leu Ala Glu Phe Ala Pro Leu Val
65 70 75 80

Gln Tyr Gly Cys His Ser His Leu Arg Phe Phe Leu Cys Ser Leu Tyr
85 90 95

Ala Pro Met Cys Thr Asp Gln Val Ser Thr Pro Ile Pro Ala Cys Arg
100 105 110

Pro Met Cys Glu Gln Ala Arg Leu Arg Cys Ala Pro Ile Met Glu Gln
115 120 125

Phe Asn Phe Gly Trp Pro Asp Ser Leu Asp Cys Ala Arg Leu Pro Thr
130 135 140

Arg Asn Asp Pro His Ala Leu Cys Met Glu Ala Pro Glu Asn Ala Thr
145 150 155 160

Ala Gly Pro Ala Glu Pro His Lys Gly Leu Gly Met Leu Pro Val Ala
165 170 175

Pro Arg Pro Ala Arg Pro Pro Gly Asp Leu Gly Pro Gly Ala Gly Gly
180 185 190

Ser Gly Thr Cys Glu Asn Pro Glu Lys Phe Gln Tyr Val Glu Lys Ser
195 200 205

Arg Ser Cys Ala Pro Arg Cys Gly Pro Gly Val Glu Val Phe Trp Ser
210 215 220

Arg Arg Asp Lys Asp Phe
225 230

<210> 60
<211> 137
<212> PRT
<213> Artificial Sequence

<220>
<223> Human FZD9 fri domain

<400> 60

Leu Glu Ile Gly Arg Phe Asp Pro Glu Arg Gly Arg Gly Ala Ala Pro

1 5 10 15

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

Thr Arg Met Pro Asn Leu Leu Gly His Thr Ser Gln Gly Glu Ala Ala
35 40 45

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

His Leu Arg Phe Phe Leu Cys Ser Leu Tyr Ala Pro Met Cys Thr Asp
65 70 75 80

Gln Val Ser Thr Pro Ile Pro Ala Cys Arg Pro Met Cys Glu Gln Ala
85 90 95

Arg Leu Arg Cys Ala Pro Ile Met Glu Gln Phe Asn Phe Gly Trp Pro
100 105 110

Asp Ser Leu Asp Cys Ala Arg Leu Pro Thr Arg Asn Asp Pro His Ala
115 120 125

Leu Cys Met Glu Ala Pro Glu Asn Ala
130 135

<210> 61
<211> 1776
<212> DNA
<213> Artificial Sequence

<220>
<223> Human FZD9

<400> 61
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gcggcactgg agatcggccg cttcgacccg gagcgcgggc gcggggctgc gccgtgccag 120

gcggtggaga tccccatgtg ccgcggcatc ggctacaacc tgacccgcat gcccaacctg 180

ctgggccaca cgtcgcaggg cgaggcggct gccgagctag cggagttcgc gccgctggtg 240

cagtacggct gccacagcca cctgcgcttc ttcctgtgct cgctctacgc gcccatgtgc 300

accgaccagg tctcgacgcc cattcccgcc tgccggccca tgtgcgagca ggcgcgcctg 360

cgctgcgcgc ccatcatgga gcagttcaac ttcggctggc cggactcgct cgactgcgcc 420

cggctgccca cgcgcaacga cccgcacgcg ctgtgcatgg aggcgcccga gaacgccacg 480

gccggccccg cggagcccca caagggcctg ggcatgctgc ccgtggcgcc gcggcccgcg 540

cgccctcccg gagacctggg cccgggcgcg ggcggcagtg gcacctgcga gaaccccgag 600

aagttccagt acgtggagaa gagccgctcg tgcgcaccgc gctgcgggcc cggcgtcgag 660

gtgttctggt cccggcgcga caaggacttc gcgctggtct ggatggccgt gtggtcggcg 720

ctgtgcttct tctccaccgc cttcactgtg ctcaccttct tgctggagcc ccaccgcttc 780

cagtaccccg agcgccccat catcttcctc tccatgtgct acaacgtcta ctcgctggcc 840

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ctctacgtga tccaggaggg cctggagaac acgggctgca cgctggtctt cctactgctc 960

tactacttcg gcatggccag ctcgctctgg tgggtggtcc tgacgctcac ctggttcctg 1020

gctgccggga agaaatgggg ccacgaggcc atcgaggccc acggcagcta tttccacatg 1080

gctgcctggg gcctgcccgc gctcaagacc atcgtcatcc tgaccctgcg caaggtggcg 1140

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ttcgtggccc tcttccacat ccgcaagatc atgaagacgg gcggcaccaa cacagagaag 1320

ctggagaagc tcatggtcaa gatcggggtc ttctccatcc tctacacggt gcccgccacc 1380

tgcgtcatcg tttgctatgt ctacgaacgc ctcaacatgg acttctggcg ccttcgggcc 1440

acagagcagc catgcgcagc ggccgcgggg cccggaggcc ggagggactg ctcgctgcca 1500

gggggctcgg tgcccaccgt ggcggtcttc atgctcaaaa ttttcatgtc actggtggtg 1560

gggatcacca gcggcgtctg ggtgtggagc tccaagactt tccagacctg gcagagcctg 1620

tgctaccgca agatagcagc tggccgggcc cgggccaagg cctgccgcgc ccccgggagc 1680

tacggacgtg gcacgcactg ccactataag gctcccaccg tggtcttgca catgactaag 1740

acggacccct ctttggagaa ccccacacac ctctag 1776

<210> 62
<211> 581
<212> PRT
<213> Artificial Sequence

<220>
<223> Human FZD10

<400> 62

Met Gln Arg Pro Gly Pro Arg Leu Trp Leu Val Leu Gln Val Met Gly
1 5 10 15

Ser Cys Ala Ala Ile Ser Ser Met Asp Met Glu Arg Pro Gly Asp Gly
20 25 30

Lys Cys Gln Pro Ile Glu Ile Pro Met Cys Lys Asp Ile Gly Tyr Asn
35 40 45

Met Thr Arg Met Pro Asn Leu Met Gly His Glu Asn Gln Arg Glu Ala
50 55 60

Ala Ile Gln Leu His Glu Phe Ala Pro Leu Val Glu Tyr Gly Cys His
65 70 75 80

Gly His Leu Arg Phe Phe Leu Cys Ser Leu Tyr Ala Pro Met Cys Thr

```
                85                  90                  95

Glu Gln Val Ser Thr Pro Ile Pro Ala Cys Arg Val Met Cys Glu Gln
            100                 105                 110

Ala Arg Leu Lys Cys Ser Pro Ile Met Glu Gln Phe Asn Phe Lys Trp
        115                 120                 125

Pro Asp Ser Leu Asp Cys Arg Lys Leu Pro Asn Lys Asn Asp Pro Asn
    130                 135                 140

Tyr Leu Cys Met Glu Ala Pro Asn Asn Gly Ser Asp Glu Pro Thr Arg
145                 150                 155                 160

Gly Ser Gly Leu Phe Pro Pro Leu Phe Arg Pro Gln Arg Pro His Ser
                165                 170                 175

Ala Gln Glu His Pro Leu Lys Asp Gly Gly Pro Gly Arg Gly Gly Cys
            180                 185                 190

Asp Asn Pro Gly Lys Phe His His Val Glu Lys Ser Ala Ser Cys Ala
        195                 200                 205

Pro Leu Cys Thr Pro Gly Val Asp Val Tyr Trp Ser Arg Glu Asp Lys
    210                 215                 220

Arg Phe Ala Val Val Trp Leu Ala Ile Trp Ala Val Leu Cys Phe Phe
225                 230                 235                 240

Ser Ser Ala Phe Thr Val Leu Thr Phe Leu Ile Asp Pro Ala Arg Phe
                245                 250                 255

Arg Tyr Pro Glu Arg Pro Ile Ile Phe Leu Ser Met Cys Tyr Cys Val
            260                 265                 270

Tyr Ser Val Gly Tyr Leu Ile Arg Leu Phe Ala Gly Ala Glu Ser Ile
        275                 280                 285

Ala Cys Asp Arg Asp Ser Gly Gln Leu Tyr Val Ile Gln Glu Gly Leu
    290                 295                 300

Glu Ser Thr Gly Cys Thr Leu Val Phe Leu Val Leu Tyr Tyr Phe Gly
305                 310                 315                 320

Met Ala Ser Ser Leu Trp Trp Val Val Leu Thr Leu Thr Trp Phe Leu
                325                 330                 335

Ala Ala Gly Lys Lys Trp Gly His Glu Ala Ile Glu Ala Asn Ser Ser
            340                 345                 350

Tyr Phe His Leu Ala Ala Trp Ala Ile Pro Ala Val Lys Thr Ile Leu
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355 360 365

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

Tyr Val Gly Ser Met Asp Val Asn Ala Leu Thr Gly Phe Val Leu Ile
385 390 395 400

Pro Leu Ala Cys Tyr Leu Val Ile Gly Thr Ser Phe Ile Leu Ser Gly
405 410 415

Phe Val Ala Leu Phe His Ile Arg Arg Val Met Lys Thr Gly Gly Glu
420 425 430

Asn Thr Asp Lys Leu Glu Lys Leu Met Val Arg Ile Gly Leu Phe Ser
435 440 445

Val Leu Tyr Thr Val Pro Ala Thr Cys Val Ile Ala Cys Tyr Phe Tyr
450 455 460

Glu Arg Leu Asn Met Asp Tyr Trp Lys Ile Leu Ala Ala Gln His Lys
465 470 475 480

Cys Lys Met Asn Asn Gln Thr Lys Thr Leu Asp Cys Leu Met Ala Ala
485 490 495

Ser Ile Pro Ala Val Glu Ile Phe Met Val Lys Ile Phe Met Leu Leu
500 505 510

Val Val Gly Ile Thr Ser Gly Met Trp Ile Trp Thr Ser Lys Thr Leu
515 520 525

Gln Ser Trp Gln Gln Val Cys Ser Arg Arg Leu Lys Lys Lys Ser Arg
530 535 540

Arg Lys Pro Ala Ser Val Ile Thr Ser Gly Gly Ile Tyr Lys Lys Ala
545 550 555 560

Gln His Pro Gln Lys Thr His His Gly Lys Tyr Glu Ile Pro Ala Gln
565 570 575

Ser Pro Thr Cys Val
580

<210> 63
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> extracellular domain (ECD) of FZD10

<400> 63

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Met Gln Arg Pro Gly Pro Arg Leu Trp Leu Val Leu Gln Val Met Gly
1               5                  10                  15

Ser Cys Ala Ala Ile Ser Ser Met Asp Met Glu Arg Pro Gly Asp Gly
            20                  25                  30

Lys Cys Gln Pro Ile Glu Ile Pro Met Cys Lys Asp Ile Gly Tyr Asn
        35                  40                  45

Met Thr Arg Met Pro Asn Leu Met Gly His Glu Asn Gln Arg Glu Ala
    50                  55                  60

Ala Ile Gln Leu His Glu Phe Ala Pro Leu Val Glu Tyr Gly Cys His
65                  70                  75                  80

Gly His Leu Arg Phe Phe Leu Cys Ser Leu Tyr Ala Pro Met Cys Thr
                85                  90                  95

Glu Gln Val Ser Thr Pro Ile Pro Ala Cys Arg Val Met Cys Glu Gln
            100                 105                 110

Ala Arg Leu Lys Cys Ser Pro Ile Met Glu Gln Phe Asn Phe Lys Trp
        115                 120                 125

Pro Asp Ser Leu Asp Cys Arg Lys Leu Pro Asn Lys Asn Asp Pro Asn
    130                 135                 140

Tyr Leu Cys Met Glu Ala Pro Asn Asn Gly Ser Asp Glu Pro Thr Arg
145                 150                 155                 160

Gly Ser Gly Leu Phe Pro Pro Leu Phe Arg Pro Gln Arg Pro His Ser
                165                 170                 175

Ala Gln Glu His Pro Leu Lys Asp Gly Gly Pro Gly Arg Gly Gly Cys
            180                 185                 190

Asp Asn Pro Gly Lys Phe His His Val Glu Lys Ser Ala Ser Cys Ala
        195                 200                 205

Pro Leu Cys Thr Pro Gly Val Asp Val Tyr Trp Ser Arg Glu Asp Lys
    210                 215                 220

Arg Phe Ala
225
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<210> 64
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Human FZD10 fri domain

<400> 64

Ile Ser Ser Met Asp Met Glu Arg Pro Gly Asp Gly Lys Cys Gln Pro
1 5 10 15

Ile Glu Ile Pro Met Cys Lys Asp Ile Gly Tyr Asn Met Thr Arg Met
20 25 30

Pro Asn Leu Met Gly His Glu Asn Gln Arg Glu Ala Ala Ile Gln Leu
35 40 45

His Glu Phe Ala Pro Leu Val Glu Tyr Gly Cys His Gly His Leu Arg
50 55 60

Phe Phe Leu Cys Ser Leu Tyr Ala Pro Met Cys Thr Glu Gln Val Ser
65 70 75 80

Thr Pro Ile Pro Ala Cys Arg Val Met Cys Glu Gln Ala Arg Leu Lys
85 90 95

Cys Ser Pro Ile Met Glu Gln Phe Asn Phe Lys Trp Pro Asp Ser Leu
100 105 110

Asp Cys Arg Lys Leu Pro Asn Lys Asn Asp Pro Asn Tyr Leu Cys Met
115 120 125

Glu Ala Pro Asn Asn Gly
130

<210> 65
<211> 1746
<212> DNA
<213> Artificial Sequence

<220>
<223> Human FZD10

<400> 65
atgcagcgcc cgggcccccg cctgtggctg gtcctgcagg tgatgggctc gtgcgccgcc 60

atcagctcca tggacatgga gcgcccgggc gacggcaaat gccagcccat cgagatcccg 120

atgtgcaagg acatcggcta caacatgact cgtatgccca acctgatggg ccacgagaac 180

cagcgcgagg cagccatcca gttgcacgag ttcgcgccgc tggtggagta cggctgccac 240

ggccacctcc gcttcttcct gtgctcgctg tacgcgccga tgtgcaccga gcaggtctct 300

acccccatcc ccgcctgccg ggtcatgtgc gagcaggccc ggctcaagtg ctccccgatt 360

atggagcagt tcaacttcaa gtggcccgac tccctggact gccggaaact ccccaacaag 420

aacgacccca actacctgtg catggaggcg cccaacaacg gctcggacga gcccacccgg 480

ggctcgggcc tgttcccgcc gctgttccgg ccgcagcggc cccacagcgc gcaggagcac 540

ccgctgaagg acgggggccc cgggcgcggc ggctgcgaca acccgggcaa gttccaccac 600

gtggagaaga gcgcgtcgtg cgcgccgctc tgcacgcccg gcgtggacgt gtactggagc 660

cgcgaggaca agcgcttcgc agtggtctgg ctggccatct gggcggtgct gtgcttcttc 720

tccagcgcct tcaccgtgct caccttcctc atcgacccgg cccgcttccg ctaccccgag 780

cgccccatca tcttcctctc catgtgctac tgcgtctact ccgtgggcta cctcatccgc 840

ctcttcgccg gcgccgagag catcgcctgc gaccgggaca gcggccagct ctatgtcatc 900

caggagggac tggagagcac cggctgcacg ctggtcttcc tggtcctcta ctacttcggc 960

atggccagct cgctgtggtg ggtggtcctc acgctcacct ggttcctggc cgccggcaag 1020

aagtggggcc acgaggccat cgaagccaac agcagctact tccacctggc agcctgggcc 1080

atcccggcgg tgaagaccat cctgatcctg gtcatgcgca gggtggcggg ggacgagctc 1140

accggggtct gctacgtggg cagcatggac gtcaacgcgc tcaccggctt cgtgctcatt 1200

cccctggcct gctacctggt catcggcacg tccttcatcc tctcgggctt cgtggccctg 1260

ttccacatcc ggagggtgat gaagacgggc ggcgagaaca cggacaagct ggagaagctc 1320

atggtgcgta tcgggctctt ctctgtgctg tacaccgtgc cggccacctg tgtgatcgcc 1380

tgctactttt acgaacgcct caacatggat tactggaaga tcctggcggc gcagcacaag 1440

tgcaaaatga acaaccagac taaaacgctg gactgcctga tggccgcctc catccccgcc 1500

gtggagatct tcatggtgaa gatctttatg ctgctggtgg tggggatcac cagcgggatg 1560

tggatttgga cctccaagac tctgcagtcc tggcagcagg tgtgcagccg taggttaaag 1620

aagaagagcc ggagaaaacc ggccagcgtg atcaccagcg gtgggattta caaaaaagcc 1680

cagcatcccc agaaaactca ccacgggaaa tatgagatcc ctgcccagtc gcccacctgc 1740

gtgtga 1746

<210> 66
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic fragment of human frizzled receptor

<400> 66

Gln Tyr Gly Phe Ala
1 5

<210> 67
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic fragment of human frizzled receptor

<400> 67

Gln Asp Glu Ala Gly Leu Glu Val His Gln Phe Trp Pro Leu
1 5 10

<210> 68
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic fragment of human frizzled receptor

<400> 68

Ala Gly Leu Glu Val His Gln Phe
1 5

<210> 69
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic fragment of human frizzled receptor

<400> 69

Lys Gln Phe Tyr Gly Phe Gln Ala
1 5

<210> 70
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> conformational epitope of FZD8

<400> 70

Phe Pro Leu Ile Tyr Leu Met Trp Pro Asp Arg
1 5 10

<210> 71
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> light chain CDR1

<400> 71

Ser Gly Asp Lys Asn Leu Ile Gly Lys Ser Lys Phe Tyr Ala Val Ser
1 5 10 15

His

<210> 72
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> a light chain CDR2

<400> 72

Glu Asp Lys Asp Ser Asn Arg Pro Ser Gly
1 5 10

<210> 73
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> light chain CDR3

<400> 73

Ser Gln Ser Phe Tyr Ala Gly Asn Asn Thr Leu Ser Leu Glu
1 5 10

<210> 74
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> fragment of FZD8

<400> 74

Tyr Gly Phe Ala
1

<210> 75
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic primer

<400> 75
cgctctccaa ggcgccaagg agagg 25

<210> 76
<211> 696
<212> DNA
<213> Artificial Sequence

<220>
<223> 18R5 light chain of anti-FZD IgG antibodies

<400> 76
atggcctggg ccctgctgct gctgaccctg ctgacacagg gcaccggctc ttgggccgac 60

atcgagctga cccagcctcc ctccgtgtcc gtggcccctg gccagaccgc ccggatctcc 120

tgctccggcg acaacatcgg cagcttctac gtgcactggt atcagcagaa acctggacag 180

gcccctgtgc tggtgatcta cgacaagtcc aaccggcctt ccggcatccc tgagcggttc 240

tccggctcca actccggcaa caccgccacc ctgaccatct ccggcaccca ggccgaggac 300

gaggccgact actactgcca gtcctacgcc aacaccctgt ccctggtgtt tggcggcgga 360

acaaagctga ccgtgctggg ccagcctaag gccgctcctt ccgtgaccct gttccctcct 420

tcctccgagg agctgcaggc caacaaggcc accctggtgt gcctgatctc cgacttctac 480

cctggcgctg tgactgtggc ttggaaggcc gactcctccc ctgtgaaggc cggcgtggag 540

acaaccaccc cttccaagca gtccaacaac aagtacgccg cctcctccta cctgtccctg 600

acccctgagc agtggaagtc ccaccggtcc tactcttgcc aggtgaccca cgagggctcc 660

accgtggaaa agacagtggc acccaccgag tgctcc 696

<210> 77
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain CDR1

<400> 77

Gly Phe Thr Phe Ser Ser Tyr Tyr Ile Thr
1 5 10

<210> 78
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain CDR2

<400> 78

Thr Ile Ser Tyr Ser Ser Ser Asn Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 79
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain CDR3

<400> 79

Ser Ile Val Phe Asp Tyr
1 5

<210> 80
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> light chain CDR1

<400> 80

Ser Gly Asp Ala Leu Gly Asn Arg Tyr Val Tyr
1 5 10

<210> 81
<211> 2
<212> PRT
<213> Artificial Sequence

<220>
<223> light chain CDR2

<400> 81

Ser Gly
1

<210> 82
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> light chain CDR3

<400> 82

Gly Ser Trp Asp Thr Arg Pro Tyr Pro Lys Tyr
1 5 10

<210> 83
<211> 696
<212> DNA
<213> Artificial Sequence

<220>
<223> 18R4605 light chain of anti-FZD antibodies

<400> 83
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atagaactaa ctcagccacc ctctgttagc gttgcaccgg gacagacggc acgtatatcg 120

tgctcgggag acaatatagg aagtttctat gtacattggt atcaacagaa acctggtcaa 180

gcacctgtat tagtaatcta tgacaaaagt aaccgacctt ccggaatacc tgagcgtttc 240

agtggttcga actccggcaa cactgcaact ttaactatat ctggaactca ggcggaggat 300

gaggctgact actactgcca gagttacgca aacactctgt ccctggtgtt tggcggcgga 360

acaaagttaa ccgtgctggg ccagcctaag gccgcacctt cggtgaccct attccctcct 420

tcatccgagg agctacaggc caacaaggcc accttagtgt gcctaatctc cgacttctat 480

cctggtgctg taacggtagc gtggaaggcc gactcatcgc cggtgaaggc cggtgtggag 540

acaacgactc cttccaagca gtccaacaac aaatacgccg cgtcctccta cctgtcccta 600

acccctgagc agtggaagtc ccaccgttca tactcgtgcc aggtgacgca cgagggttca 660

acggtcgaaa agacagtagc acctactgaa tgctca 696

<210> 84

<211> 696
<212> DNA
<213> Artificial Sequence

<220>
<223> 18R4805 light chain of anti-FZD antibodies

<400> 84
atggcatggg cattattact acttactcta cttacgcaag gaacgggttc atgggcagac 60

atagaactaa ctcagccgcc gtctgttagc gttgcaccgg gacagacggc acgtatatcg 120

tgctcgggag acaatattgg ttctttctat gtacattggt atcaacagaa acctggtcaa 180

gcacctgtat tagtaatata tgacaaaagt aaccgtcctt cgggaatacc tgagcgtttc 240

agtggttcga actcgggcaa cactgcaact ttaactatat ctggaacgca ggcggaggat 300

gaggcggact actattgcca aagttacgca aacactctat ccttagtgtt tggtggagga 360

acaaagttaa ccgtgctagg ccagcctaag gccgcacctt cggtgaccct attccctcct 420

tcatccgagg agctacaggc gaacaaagcc accttagtgt gcctaatctc agacttttat 480

cctggtgctg taacggtagc gtggaaggcg gactcatcgc cggtgaaggc cggtgtggag 540

acaacgactc cttccaagca gtccaacaac aaatacgcag cgagtagtta cctgtcccta 600

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acggtcgaaa agacagtagc acctacggaa tgctca 696

<210> 85
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> 44R24 heavy chain of anti-FZD antibodies

<400> 85

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Tyr Ile Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Thr Ile Ser Tyr Ser Ser Ser Asn Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Ile Val Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr

100 105 110

Val Ser Ser
115

<210> 86
<211> 104
<212> PRT
<213> Artificial Sequence

<220>
<223> 44R24 light chain of anti-FZD antibodies

<400> 86

Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1 5 10 15

Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Asn Arg Tyr Val
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Pro
35 40 45

Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala
50 55 60

Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu Asp Glu Ala Asp Tyr Tyr
65 70 75 80

Cys Gly Ser Trp Asp Thr Arg Pro Tyr Pro Lys Tyr Val Phe Gly Gly
85 90 95

Gly Thr Lys Leu Thr Val Leu Gly
100

<210> 87
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> 18R5/18R8 heavy chain of anti-FZD antibodies

<400> 87
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tcctgcgccg cctccggctt caccttctcc cactacaccc tgtcctgggt gcgccaggca 120

ccagggaagg gactggagtg ggtctccgtg atctccggcg acggctccta cacctactac 180

gccgactccg tgaagggccg gttcaccatc tcctccgaca actccaagaa caccctgtac 240

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atcaagtacg tgttcgccaa ctggggccag ggcaccctgg tgaccgtgtc ctcc 354

<210> 88

<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 18R8 light chain of anti-FZD antibodies

<400> 88
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tcctgctccg gcgacaagct gggcaagaag tacgcctcct ggtatcagca gaagcctgga 120

caggcccctg tgctggtcat ctacgagaag gacaaccggc ctagcggcat ccctgagcgg 180

ttctccggct ccaactccgg caacaccgcc accctgacca tctccggcac ccaggccgag 240

gacgaggccg actactactg ctcctccttc gccggcaact ccctggaagt gttcggcgga 300

ggcaccaagc tgaccgtgct gggc 324

<210> 89
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 18R5 light chain of anti-FZD antibodies

<400> 89
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caggcccctg tgctggtgat ctacgacaag tccaaccggc cttccggcat ccctgagcgg 180

ttctccggct ccaactccgg caacaccgcc accctgacca tctccggcac ccaggccgag 240

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ggaacaaagc tgaccgtgct gggc 324

<210> 90
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 18R4605 anti-FZD antibodies

<400> 90
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tcgtgctcgg gagacaatat aggaagtttc tatgtacatt ggtatcaaca gaaacctggt 120

caagcacctg tattagtaat ctatgacaaa agtaaccgac cttccggaat acctgagcgt 180

ttcagtggtt cgaactccgg caacactgca actttaacta tatctggaac tcaggcggag 240

gatgaggctg actactactg ccagagttac gcaaacactc tgtccctggt gtttggcggc 300

ggaacaaagt taaccgtgct gggc 324

<210> 91
<211> 1365
<212> DNA

<213> Artificial Sequence

<220>
<223> 44R24 heavy chain of anti-FZD antibodies

<400> 91
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gtgcagctgg tggagtctgg cggaggactg gtgcagcctg gcggctccct gagactgtct 120

tgcgccgcct ccggcttcac cttctcctct tactacatca cctgggtgcg ccaggctcct 180

ggcaagggac tggaatgggt gtccaccatc tcctactcct ccagcaacac ctactacgcc 240

gactccgtga agggccggtt caccatctcc cgggacaact ccaagaacac cctgtacctg 300

cagatgaact ccctgagggc cgaggacacc gccgtgtact actgcgcccg gtccatcgtg 360

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ccttgctccc ggtccacctc tgagtctacc gccgctctgg gctgcctggt gaaggactac 480

ttccctgagc ctgtgaccgt gtcctggaac tctggcgccc tgacctctgg cgtgcacacc 540

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aaggtggaca agaccgtgga gcggaagtgc tgcgtggagt gccctccttg tcctgctcct 720

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gaacagttca actccacctt ccgggtggtg tctgtgctga ccgtggtgca ccaggactgg 960

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acccctccta tgctggactc cgacggctcc ttcttcctgt actccaagct gacagtggac 1260

aagtcccggt ggcagcaggg caacgtgttc tcctgctccg tgatgcacga ggccctgcac 1320

aaccactaca cccagaagtc cctgtccctg tctcctggca agtga 1365

<210> 92
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 18R4805 anti-FZD antibodies

<400> 92
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tcgtgctcgg gagacaatat tggttctttc tatgtacatt ggtatcaaca gaaacctggt 120

caagcacctg tattagtaat atatgacaaa agtaaccgtc cttcgggaat acctgagcgt 180

ttcagtggtt cgaactcggg caacactgca actttaacta tatctggaac gcaggcggag 240

gatgaggcgg actactattg ccaaagttac gcaaacactc tatccttagt gtttggtgga 300

ggaacaaagt taaccgtgct aggc 324

<210> 93
<211> 672
<212> DNA
<213> Artificial Sequence

<220>
<223> 44R24 light chain of anti-FZD antibodies

<400> 93
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tgctctggcg acgccctggg caacagatac gtgtactggt atcagcagaa gccaggccag 180

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aacaccgcca ccctgaccat ctctggcacc caggccgagg acgaggccga ctactactgc 300

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gccaccctgg tgtgcctgat ctccgacttc taccctggcg ccgtgaccgt ggcttggaag 480

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aacaagtacg ccgcctcctc ctacctgtcc ctgaccctg agcagtggaa gtcccaccgg 600

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gagtgctcct ag 672

<210> 94
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> 44R24 heavy chain of anti-FZD antibodies

<400> 94
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tcttgcgccg cctccggctt caccttctcc tcttactaca tcacctgggt gcgccaggct 120

cctggcaagg gactggaatg ggtgtccacc atctcctact cctccagcaa cacctactac 180

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gtgttcgact actggggcca gggcaccctg gtgaccgtgt cctct 345

<210> 95
<211> 312
<212> DNA
<213> Artificial Sequence

<220>
<223> 44R24 light chain of anti-FZD antibodies

<400> 95
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caggcccctg tgctggtgat cccttccggc atccctgagc ggttctccgg ctccaactcc 180

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<210> 96
<211> 1389
<212> DNA
<213> Artificial Sequence

<220>
<223> 18R5/18R8/18R4605/18R4805 IgG2 heavy chain of anti-FZD antibodies

<400> 96
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cctggcaag 1389

<210> 97
<211> 696
<212> DNA
<213> Artificial Sequence

<220>
<223> 1848 lambda high chain of anti-FZD antibodies

<400> 97
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gcccctgtgc tggtcatcta cgagaaggac aaccggccta gcggcatccc tgagcggttc 240

tccggctcca actccggcaa caccgccacc ctgaccatct ccggcaccca ggccgaggac 300

gaggccgact actactgctc ctccttcgcc ggcaactccc tggaagtgtt cggcggaggc 360

accaagctga ccgtgctggg ccagcctaag gccgctcctt ccgtgaccct gttccctcct 420

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cctggcgccg tgaccgtggc ctggaaggcc gactcctccc ctgtgaaggc cggcgtggag 540

acaaccaccc cttccaagca gtccaacaac aagtacgccg cctcctccta cctgtccctg 600

acccctgagc agtggaagtc ccaccggtcc tactcttgcc aggtcaccca cgagggctcc 660

accgtggaaa agacagtggc ccccaccgag tgctcc 696