

# SEQUENCE LISTING

<110> Firmenich SA

<120> METHOD FOR IDENTIFYING POSITIVE ALLOSTERIC MODULATORS FOR ODORANT RECEPTORS

<130> 10590/WO

<160> 17

<170> PatentIn version 3.5

<210> 1

<211> 937

<212> DNA

<213> Homo sapiens

<400> 1

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| gcctggaacc tctccctcat tgttttaata aggatggatt cccacctcca tacacccatg   | 180 |
| tatttcttcc tcagtaacct gtccttcata gatgtctgct atatcagctc cacagtcccc   | 240 |
| aagatgctct ccaacctctt acaggaacag caaactatca cttttgttgg ttgtattatt   | 300 |
| cagtacttta tcttttcaac gatgggactg agtgagtctt gtctcatgac agccatggct   | 360 |
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<213> Homo sapiens

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Gly Phe Ser Asp Phe Pro Arg Ile Ile Lys Val Leu Phe Thr Ile Phe  
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Leu Val Ile Tyr Ile Thr Ser Leu Ala Trp Asn Leu Ser Leu Ile Val  
35 40 45

Leu Ile Arg Met Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu  
50 55 60

Ser Asn Leu Ser Phe Ile Asp Val Cys Tyr Ile Ser Ser Thr Val Pro  
65 70 75 80

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

Gly Cys Ile Ile Gln Tyr Phe Ile Phe Ser Thr Met Gly Leu Ser Glu  
100 105 110

Ser Cys Leu Met Thr Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys  
115 120 125

Asn Pro Leu Leu Tyr Ser Ser Ile Met Ser Pro Thr Leu Cys Val Trp  
130 135 140

Met Val Leu Gly Ala Tyr Met Thr Gly Leu Thr Ala Ser Leu Phe Gln  
145 150 155 160

Ile Gly Ala Leu Leu Gln Leu His Phe Cys Gly Ser Asn Val Ile Arg

165

170

175

His Phe Phe Cys Asp Met Pro Gln Leu Leu Ile Leu Ser Cys Thr Asp  
 180 185 190

Thr Phe Phe Val Gln Val Met Thr Ala Ile Leu Thr Met Phe Phe Gly  
 195 200 205

Ile Ala Ser Ala Leu Val Ile Met Ile Ser Tyr Gly Tyr Ile Gly Ile  
 210 215 220

Ser Ile Met Lys Ile Thr Ser Ala Lys Gly Arg Ser Lys Ala Phe Asn  
 225 230 235 240

Thr Cys Ala Ser His Leu Thr Ala Val Ser Leu Phe Tyr Thr Ser Gly  
 245 250 255

Ile Phe Val Tyr Leu Ser Ser Ser Ser Gly Gly Ser Ser Ser Phe Asp  
 260 265 270

Arg Phe Ala Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro  
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Leu Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Asp Ala Leu Lys Arg  
 290 295 300

Leu Gln Lys Arg Lys Cys Cys  
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&lt;210&gt; 3

&lt;211&gt; 930

&lt;212&gt; DNA

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&lt;400&gt; 3

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gctaacatca tcattgtgac tatcatctgc attgaccatc atctccacac tcccatgtat 180

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| atgttctttt ttgttatctt ggccactaat aattgcttcc tgcttactgc aatgggggtat  | 360 |
| gaccgctatg tggccatctg cagaccctg agatacactg tcatcatgag caagggacta    | 420 |
| tgtgcccagc tgggtgtgtgg gtcctttggc attgggtctga ctatggcagt tctccatgtg | 480 |
| acagccatgt tcaatttgcc gttctgtggc acagtggtag accacttctt ttgtgacatt   | 540 |
| taccagtc tgaactttt ttgcattgat accactatca atgagataat aaattatggt      | 600 |
| gtaagttcat ttgtgatttt tgtgcccata ggctgatata ttatctccta tgtccttgtc   | 660 |
| atctcttcca tccttcaa tgcctcagct gagggtgga agaagacctt tgccacctgt      | 720 |
| gtctcccacc tctgtgtgtg tattgtccac tgtggctgtg cctccattgc ctacctcaag   | 780 |
| ccgaagtcag aaagttcaat agaaaaagac cttgttctct cagtgcgta caccatcatc    | 840 |
| actcccttgc tgaaccctgt tgtttacagt ctgagaaaca aggaggtaaa ggatgcccta   | 900 |
| tgcagagttg tgggcagaaa tatttcttaa                                    | 930 |

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<400> 4

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Arg | Lys | Asn | Phe | Thr | Glu | Val | Ser | Glu | Phe | Ile | Phe | Leu | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Ser | Ser | Phe | Gly | Lys | His | Gln | Ile | Thr | Leu | Phe | Val | Val | Phe | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Val | Tyr | Ile | Leu | Thr | Leu | Val | Ala | Asn | Ile | Ile | Ile | Val | Thr | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Cys | Ile | Asp | His | His | Leu | His | Thr | Pro | Met | Tyr | Phe | Phe | Leu | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

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

Met Leu Leu Ser Leu Ile Phe His Asn Gln Pro Ile Ser Leu Ala Gly  
85 90 95

Cys Ala Thr Gln Met Phe Phe Phe Val Ile Leu Ala Thr Asn Asn Cys  
100 105 110

Phe Leu Leu Thr Ala Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys Arg  
115 120 125

Pro Leu Arg Tyr Thr Val Ile Met Ser Lys Gly Leu Cys Ala Gln Leu  
130 135 140

Val Cys Gly Ser Phe Gly Ile Gly Leu Thr Met Ala Val Leu His Val  
145 150 155 160

Thr Ala Met Phe Asn Leu Pro Phe Cys Gly Thr Val Val Asp His Phe  
165 170 175

Phe Cys Asp Ile Tyr Pro Val Met Lys Leu Ser Cys Ile Asp Thr Thr  
180 185 190

Ile Asn Glu Ile Ile Asn Tyr Gly Val Ser Ser Phe Val Ile Phe Val  
195 200 205

Pro Ile Gly Leu Ile Phe Ile Ser Tyr Val Leu Val Ile Ser Ser Ile  
210 215 220

Leu Gln Ile Ala Ser Ala Glu Gly Trp Lys Lys Thr Phe Ala Thr Cys  
225 230 235 240

Val Ser His Leu Thr Val Val Ile Val His Cys Gly Cys Ala Ser Ile  
245 250 255

Ala Tyr Leu Lys Pro Lys Ser Glu Ser Ser Ile Glu Lys Asp Leu Val

260

265

270

Leu Ser Val Thr Tyr Thr Ile Ile Thr Pro Leu Leu Asn Pro Val Val  
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Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala Leu Cys Arg Val Val  
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Gly Arg Asn Ile Ser  
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| gtgtggaact tgggcctcat catcttgatt aggattgacc cttacctaca cacacctatg  | 180 |
| tacttcttcc tcagcaatth gtcattttta gatttctgtt acatttcac tacaaccct    | 240 |
| aaaatgctct cgggattctt ccagaagtct aaatctatct cttttgttgg gtgcaccatg  | 300 |
| cagtacttca tcttctcaag cctgggtctg tccgaatgct gccttctggc agccatggct  | 360 |
| tatgaccggg atgctgccat ttgtaatcct cttctctaca cagccatcat gtccccgtca  | 420 |
| ctctgtgtgc acatgggtgg tggagcctat agtactggc tcttgggttc attgattcaa   | 480 |
| ctgtgtgcta tacttcagct ccatttctgt gggccaaata ttataaacca tttcttttgt  | 540 |
| gacctgcctc agctattagt tctttcctgc tctgaaacct ttcccctgca agtcttgaaa  | 600 |
| tttgtaatag cagtgattht tgggggtggc tctgtcattg ttatcctgat atcctatggg  | 660 |
| tatatcattg gcacaatcct gaatatcagc tcagtagaag gtaggtccaa ggcattcaat  | 720 |
| acctgtgcct ctccactgac agcagtcacc ctcttttttg gatcaggact ctttgtctat  | 780 |
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Gly Phe Ser Asp Phe Pro Lys Leu Lys Leu Val Leu Phe Val Ile Phe  
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Leu Gly Ser Tyr Leu Ser Thr Val Val Trp Asn Leu Gly Leu Ile Ile  
35 40 45

Leu Ile Arg Ile Asp Pro Tyr Leu His Thr Pro Met Tyr Phe Phe Leu  
50 55 60

Ser Asn Leu Ser Phe Leu Asp Phe Cys Tyr Ile Ser Ser Thr Thr Pro  
65 70 75 80

Lys Met Leu Ser Gly Phe Phe Gln Lys Ser Lys Ser Ile Ser Phe Val  
85 90 95

Gly Cys Thr Met Gln Tyr Phe Ile Phe Ser Ser Leu Gly Leu Ser Glu  
100 105 110

Cys Cys Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys  
115 120 125

Asn Pro Leu Leu Tyr Thr Ala Ile Met Ser Pro Ser Leu Cys Val His  
130 135 140

Met Val Val Gly Ala Tyr Ser Thr Gly Leu Leu Gly Ser Leu Ile Gln  
145 150 155 160

Leu Cys Ala Ile Leu Gln Leu His Phe Cys Gly Pro Asn Ile Ile Asn  
165 170 175

His Phe Phe Cys Asp Leu Pro Gln Leu Leu Val Leu Ser Cys Ser Glu  
180 185 190

Thr Phe Pro Leu Gln Val Leu Lys Phe Val Ile Ala Val Ile Phe Gly  
195 200 205

Val Ala Ser Val Ile Val Ile Leu Ile Ser Tyr Gly Tyr Ile Ile Gly  
210 215 220

Thr Ile Leu Asn Ile Ser Ser Val Glu Gly Arg Ser Lys Ala Phe Asn  
225 230 235 240

Thr Cys Ala Ser His Leu Thr Ala Val Thr Leu Phe Phe Gly Ser Gly  
245 250 255

Leu Phe Val Tyr Met Arg Pro Ser Ser Asn Ser Ser Gln Gly Tyr Asp  
260 265 270

Lys Met Ala Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro  
275 280 285

Leu Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Asp Ala Leu Gln Arg  
290 295 300

Cys Lys Asn Lys Cys Phe Ser Gln Cys His Cys  
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 gatcgttatg tggctatttg taatcctctg agatatacaa tcatcatgag caagggaatg 420  
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 gtaagttcat ttgtaattct tgtgcccata gggctgatat ttatctccta tgtgctcatt 660  
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 gcctctcatc tcaactgtggc cattgtccac tatggctgtg cctccattgc ctacctcaaa 780  
 cccaaatcag aaagttcagt agaaaaagac cttcttctct ctgtgaccta cactatcatc 840  
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 tgcagagctg tgggcagaaa cacttcttaa 930

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 <211> 309  
 <212> PRT  
 <213> Mus musculus

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Phe Ser Ser Phe Gly Lys His Gln Ile Thr Leu Phe Val Val Phe Leu  
 20 25 30

Thr Ile Tyr Ile Leu Thr Leu Ala Gly Asn Ile Ile Ile Val Thr Ile  
 35 40 45

Thr His Ile Asp His His Leu His Thr Pro Met Tyr Phe Phe Leu Ser

50

55

60

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

Met Leu Ser Ser Leu Ile Phe Tyr Asn Leu Pro Ile Ser Leu Ala Gly  
 85 90 95

Cys Ala Thr Gln Met Phe Phe Phe Val Thr Leu Ala Thr Asn Asn Cys  
 100 105 110

Phe Leu Leu Thr Ala Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys Asn  
 115 120 125

Pro Leu Arg Tyr Thr Ile Ile Met Ser Lys Gly Met Cys Ala Leu Leu  
 130 135 140

Val Cys Gly Ser Leu Gly Thr Gly Leu Val Met Ala Val Leu His Val  
 145 150 155 160

Pro Ala Met Phe His Leu Pro Phe Cys Gly Thr Val Val Glu His Phe  
 165 170 175

Phe Cys Asp Ile Tyr Pro Val Met Lys Leu Ser Cys Val Asp Thr Thr  
 180 185 190

Val Asn Glu Ile Ile Asn Tyr Gly Val Ser Ser Phe Val Ile Leu Val  
 195 200 205

Pro Ile Gly Leu Ile Phe Ile Ser Tyr Val Leu Ile Val Ser Ser Ile  
 210 215 220

Leu Lys Ile Val Ser Thr Glu Gly Gln Lys Lys Ala Phe Ala Thr Cys  
 225 230 235 240

Ala Ser His Leu Thr Val Val Ile Val His Tyr Gly Cys Ala Ser Ile  
 245 250 255

Ala Tyr Leu Lys Pro Lys Ser Glu Ser Ser Val Glu Lys Asp Leu Leu  
260 265 270

Leu Ser Val Thr Tyr Thr Ile Ile Thr Pro Leu Leu Asn Pro Val Val  
275 280 285

Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala Leu Cys Arg Ala Val  
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Gly Arg Asn Thr Ser  
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Asp Tyr Lys Asp Asp Asp Asp Lys  
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<400> 12

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Thr Gly Val Val  
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Ala

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<220>  
<223> Motif

<400> 17

Pro Met Leu Asn Pro Phe Ile Tyr  
1 5