SEQUENCE LISTING

<110> Novartis AG

<120> Expression system

<130> 50 858 K

<150> EP08163161.6
<151> 2008-08-28

<160> 7

<170> PatentIn version 3.5

<210> 1
<211> 219
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a human IgG1 transmembrane domain including stuffer

<220>
<221> misc_feature
<222> (1)..(7)
<223> Stuffer including stop codon

<220>
<221> misc_feature
<222> (1)..(3)
<223> Stop codon

<220>
<221> misc_feature
<222> (4)..(6)
<223> Additional codon to mediate leakyness of the upstream stop codon

<400> 1
tgactagagc tgcaactgga ggagagctgt gcggaggcgc aggacgggga gctggacggg 60

ctgtggacga ccatcaccat cttcatcaca ctcttcctgt taagcgtgtg ctacagtgcc 120

accgtcacct tcttcaaggt gaagtggatc ttctcctcgg tggtggacct gaagcagacc 180

atcatccccg actacaggaa catgatcgga caggggcc 219

<210> 2
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a putative transmembrane region derived from a human IgG1 transmembrane domain

<400> 2

Leu Trp Thr Thr Ile Thr Ile Phe Ile Thr Leu Phe Leu Leu Ser Val
1 5 10 15

Cys Tyr Ser Ala Thr Val Thr Phe Phe
20 25

<210> 3
<211> 73
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of an Ig transmembrane region derived from the human IgG1 transmembrane domain comprising the amino acids derived from the stop codon and the adjacent codon, a connecting region and a putative transmembrane region

<220>
<221> MISC_FEATURE
<222> (1)..(2)
<223> amino acids that are most likely used at the TGA stop codon and the downstream codon in case of read through

<220>
<221> MISC_FEATURE
<222> (3)..(20)
<223> Putative connecting region derived from the human IgG1 transmembrane domain

<220>
<221> MISC_FEATURE
<222> (21)..(45)
<223> Putative transmembrane region derived from the human IgG1 transmembrane domain - said region may also be deemed as comprising the next two amino acids

<220>
<221> MISC_FEATURE
<222> (46)..(73)
<223> Putative cytoplasmatic region derived from human IgG1 - the first two amino acids may also be deemed as belonging to the transmembrane domain

<400> 3

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Trp Leu Glu Leu Gln Leu Glu Glu Ser Cys Ala Glu Ala Gln Asp Gly
1               5                  10                  15

Glu Leu Asp Gly Leu Trp Thr Thr Ile Thr Ile Phe Ile Thr Leu Phe
            20                  25                  30

Leu Leu Ser Val Cys Tyr Ser Ala Thr Val Thr Phe Phe Lys Val Lys
        35                  40                  45

Trp Ile Phe Ser Ser Val Val Asp Leu Lys Gln Thr Ile Ile Pro Asp
    50                  55                  60

Tyr Arg Asn Met Ile Gly Gln Gly Ala
65                  70
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<210> 4
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Cytoplasmatic region derived from an human IgG1 transmembrane

domain

<400> 4

Lys Val Lys Trp Ile Phe Ser Ser Val Val Asp Leu Lys Gln Thr Ile
1 5 10 15

Ile Pro Asp Tyr Arg Asn Met Ile Gly Gln Gly Ala
20 25

<210> 5
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Connecting region derived from the human IgG1 transmembrane domain

<400> 5

Glu Leu Gln Leu Glu Glu Ser Cys Ala Glu Ala Gln Asp Gly Glu Leu
1 5 10 15

Asp Gly

<210> 6
<211> 26
<212> PRT
<213> Artificial sequence

<220>
<223> Cytoplasmatic region derived from an human IgG1 transmembrane domain

<400> 6

Lys Trp Ile Phe Ser Ser Val Val Asp Leu Lys Gln Thr Ile Ile Pro
1 5 10 15

Asp Tyr Arg Asn Met Ile Gly Gln Gly Ala
20 25

<210> 7
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a putative transmembrane region derived from a human IgG1 transmembrane domain

<400> 7

Leu Trp Thr Thr Ile Thr Ile Phe Ile Thr Leu Phe Leu Leu Ser Val
1 5 10 15

Cys Tyr Ser Ala Thr Val Thr Phe Phe Lys Val
20 25