SEQUENCE LISTING

<110> ST. JUDE CHILDREN'S RESEARCH HOSPITAL, INC.
NATIONAL UNIVERSITY OF SINGAPORE

<120> A CHIMERIC RECEPTOR WITH NKG2D SPECIFICITY
FOR USE IN CELL THERAPY AGAINST CANCER AND
INFECTIOUS DISEASE

<130> 243734.51

<150> 61/757,481
<151> 2013-01-28

<160> 26

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer for the cloning of
the cytoplasmic domain of human CD3 zeta

<400> 1
atatatgaat tcgccgccac catgagagtg aagttcagca g 41

<210> 2
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer for the cloning of
the cytoplasmic domain of human CD3 zeta

<400> 2
ccgaccacga atccacccgc gaggggggcag ggcctgcatg 40

<210> 3
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer for the cloning of
human NKG2D

<400> 3
catgcaggcc ctgccccctc gcgggtggat tcgtggtcgg 40

<210> 4
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer for the cloning of
human NKG2D

<400> 4

tatatagaat tcttacacag tcctttgcat gc 32

<210> 5
<211> 110
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer for the cloning of
human DAP10 and the FLAG-tag

<400> 5
atatatccat ggatgatcca tctgggtcac atcctcttcc tgcttttgct cccagtggct 60
gcagctgact acaaagacga tgacgacaag cagacgactc caggagagag 110

<210> 6
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer for the cloning of
human DAP10 and the FLAG-tag

<400> 6
tatatagcgg ccgctcagcc cctgcctggc atg 33

<210> 7
<400> 7
000

<210> 8
<400> 8
000

<210> 9
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<223> cDNA encoding the cytoplasmic domain of human CD3 zeta
of the chimeric receptor

<400> 9
atgagagtga agttcagcag gagcgcagac gcccccgcgt accagcaggg ccagaaccag 60
ctctataacg agctcaatct aggacgaaga gaggagtacg atgttttgga caagagacgt 120
ggccgggacc ctgagatggg gggaaagccg cagagaagga agaaccctca ggaaggcctg 180
tacaatgaac tgcagaaaga taagatggcg gaggcctaca gtgagattgg gatgaaaggc 240
gagcgccgga ggggcaaggg gcacgatggc ctttaccagg gtctcagtac agccaccaag 300
gacacctacg acgcccttca catgcaggcc ctgccccctc gc 342

<210> 10
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid sequence of the cytoplasmic domain of human
CD3 zeta of the chimeric receptor

<400> 10
Met Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
1 5 10 15

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
            20   25   30
Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
        35   40   45
Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
    50   55   60
Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
65   70   75   80
Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
                85   90   95
Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
            100   105   110
Pro Arg

<210> 11
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> cDNA encoding human NKG2D of the chimeric receptor

<400> 11
gggtggattc gtggtcggag gtctcgacac agctgggaga tgagtgaatt tcataattat 60
aacttggatc tgaagaagag tgatttttca acacgatggc aaaagcaaag atgtccagta 120
gtcaaaagca aatgtagaga aaatgcatct ccatttttt tctgctgctt catcgctgta 180
gccatgggaa tccgtttcat tattatggta acaatatgga gtgctgtatt cctaaactca 240
ttattcaacc aagaagttca aattcccttg accgaaagtt actgtggccc atgtcctaaa 300
aactggatat gttacaaaaa taactgctac caatttttg atgagagtaa aaactggtat 360
gagagccagg cttcttgtat gtctcaaaat gccagccttc tgaaagtata cagcaaagag 420
gaccaggatt tacttaaact ggtgaagtca tatcattgga tgggactagt acacattcca 480
acaaatggat cttggcagtg ggaagatggc tccattctct cacccaacct actaacaata 540
attgaaatgc agaagggaga ctgtgcactc tatgcctcga gctttaaagg ctatatagaa 600
aactgttcaa ctccaaatac gtacatctgc atgcaaagga ctgtgtaa   648

<210> 12
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid sequence of human NKG2D of the chiremic receptor

<400> 12
Gly Trp Ile Arg Gly Arg Arg Ser Arg His Ser Trp Glu Met Ser Glu
 1   5   10   15
Phe His Asn Tyr Asn Leu Asp Leu Lys Lys Ser Asp Phe Ser Thr Arg
            20   25   30
Trp Gln Lys Gln Arg Cys Pro Val Val Lys Ser Lys Cys Arg Glu Asn
        35   40   45
Ala Ser Pro Phe Phe Phe Cys Cys Phe Ile Ala Val Ala Met Gly Ile
    50   55   60
Arg Phe Ile Ile Met Val Thr Ile Trp Ser Ala Val Phe Leu Asn Ser
65   70   75   80
Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Cys Gly
                85   90   95
Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn Cys Tyr Gln Phe
            100   105   110
Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala Ser Cys Met Ser
        115   120   125
Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu Asp Gln Asp Leu
    130   135   140
Leu Lys Leu Val Lys Ser Tyr His Trp Met Gly Leu Val His Ile Pro
145   150   155   160
Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile Leu Ser Pro Asn

```
                165                 170                 175
Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys Ala Leu Tyr Ala
            180                 185                 190
Ser Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser Thr Pro Asn Thr Tyr
        195                 200                 205
Ile Cys Met Gln Arg Thr Val
    210                 215
```

<210> 13
<211> 279
<212> DNA
<213> Artificial Sequence

<220>
<223> human DAP10 cDNA

<400> 13
atgatccatc tgggtcacat cctcttcctg cttttgctcc cagtggctgc agctcagacg 60
actccaggag agagatcatc actccctgcc ttttaccctg gcacttcagg ctcttgttcc 120
ggatgtgggt ccctctctct gccgctcctg gcaggcctcg tggctgctga tgcggtggca 180
tcgctgctca tcgtgggggc ggtgttcctg tgcgcacgcc cacgccgcag ccccgcccaa 240
gatggcaaag tctacatcaa catgccaggc aggggctga 279

<210> 14
<211> 92
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid sequence of human DAP10

<400> 14
```
Met Ile His Leu Gly His Ile Leu Phe Leu Leu Leu Leu Pro Val Ala
 1               5                  10                  15
Ala Ala Gln Thr Thr Pro Gly Glu Arg Ser Ser Leu Pro Ala Phe Tyr
            20                  25                  30
Pro Gly Thr Ser Gly Ser Cys Ser Gly Cys Gly Ser Leu Ser Leu Pro
        35                  40                  45
Leu Leu Ala Gly Leu Val Ala Ala Asp Ala Val Ala Ser Leu Leu Ile
    50                  55                  60
Val Gly Ala Val Phe Leu Cys Ala Arg Pro Arg Arg Ser Pro Ala Gln
65                  70                  75                  80
Asp Gly Lys Val Tyr Ile Asn Met Pro Gly Arg Gly
                85                  90
```

<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> FLAG-tag

<400> 15
gactacaaag acgatgacga caag 24

<210> 16
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid sequence of FLAG-tag

<400> 16
Asp Tyr Lys Asp Asp Asp Asp Lys
 1   5

<210> 17
<211> 303
<212> DNA
<213> Artificial Sequence

<220>
<223> DAP10-FLAG-tag

<400> 17
atgatccatc tgggtcacat cctcttcctg cttttgctcc cagtggctgc agctgactac 60
aaagacgatg acgacaagca gacgactcca ggagagagat catcactccc tgccttttac 120
cctggcactt caggctcttg ttccggatgt gggtccctct ctctgccgct cctggcaggc 180
ctcgtggctg ctgatgcggt ggcatcgctg ctcatcgtgg gggcggtgtt cctgtgcgca 240
cgcccacgcc gcagccccgc ccaagatggc aaagtctaca tcaacatgcc aggcaggggc 300
tga   303

<210> 18
<211> 100
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid sequence of DAP10-FLAG-tag

<400> 18
Met Ile His Leu Gly His Ile Leu Phe Leu Leu Leu Leu Pro Val Ala
 1   5   10   15
Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Gln Thr Thr Pro Gly Glu
            20   25   30
Arg Ser Ser Leu Pro Ala Phe Tyr Pro Gly Thr Ser Gly Ser Cys Ser
        35   40   45
Gly Cys Gly Ser Leu Ser Leu Pro Leu Leu Ala Gly Leu Val Ala Ala
    50   55   60
Asp Ala Val Ala Ser Leu Leu Ile Val Gly Ala Val Phe Leu Cys Ala
65   70   75   80
Arg Pro Arg Arg Ser Pro Ala Gln Asp Gly Lys Val Tyr Ile Asn Met
                85   90   95
Pro Gly Arg Gly
            100

<210> 19
<211> 1891
<212> DNA
<213> Artificial Sequence

<220>
<223> CD3zeta-NKG2D-IRES-DAP10-FLAG-tag

<400> 19
atgagagtga agttcagcag gagcgcagac gcccccgcgt accagcaggg ccagaaccag 60
ctctataacg agctcaatct aggacgaaga gaggagtacg atgttttgga caagagacgt 120
ggccgggacc ctgagatggg gggaaagccg cagagaagga agaaccctca ggaaggcctg 180
tacaatgaac tgcagaaaga taagatggcg gaggcctaca gtgagattgg gatgaaaggc 240
gagcgccgga ggggcaaggg gcacgatggc ctttaccagg gtctcagtac agccaccaag 300
gacacctacg acgcccttca catgcaggcc ctgcccccctc gcgggtggat tcgtggtcgg 360
aggtctcgac acagctggga gatgagtgaa tttcataatt ataacttgga tctgaagaag 420
agtgattttt caacacgatg gcaaaagcaa agatgtccag tagtcaaaag caaatgtaga 480
gaaaatgcat ctccattttt tttctgctgc ttcatcgctg tagccatggg aatccgtttc 540
attattatgg taacaatatg gagtgctgta ttcctaaact cattattcaa ccaagaagtt 600
caaattccct tgaccgaaag ttactgtggc ccatgtccta aaaactggat atgttacaaa 660
aataactgct accaattttt tgatgagagt aaaaactggt atgagagcca ggcttcttgt 720

atgtctcaaa atgccagcct tctgaaagta tacagcaaag aggaccagga tttacttaaa 780
ctggtgaagt catatcattg gatgggacta gtacacattc caacaaatgg atcttggcag 840
tgggaagatg gctccattct ctcacccaac ctactaacaa taattgaaat gcagaaggga 900
gactgtgcac tctatgcctc gagctttaaa ggctatatag aaaactgttc aactccaaat 960
acgtacatct gcatgcaaag gactgtgtaa gaattcgtta acctcgagcg ggatcaattc 1020
cgccccccc ctaacgttac tggccgaagc cgcttggaat aaggccggtg tgcgtttgtc 1080
tatatgttat tttccaccat attgccgtct tttggcaatg tgagggcccg gaaacctggc 1140
cctgtcttct tgacgagcat tcctaggggt ctttcccctc tcgccaaagg aatgcaaggt 1200
ctgttgaatg tcgtgaagga agcagttcct ctggaagctt cttgaagaca aacaacgtct 1260
gtagcgaccc tttgcaggca gcggaacccc ccacctggcg acaggtgcct ctgcggccaa 1320
aagccacgtg tataagatac acctgcaaag gcggcacaac cccagtgcca cgttgtgagt 1380
tggatagttg tggaaagagt caaatggctc tcctcaagcg tattcaacaa ggggctgaag 1440
gatgcccaga aggtacccca ttgtatggga tctgatctgg ggcctcggtg cacatgcttt 1500
acatgtgttt agtcgaggtt aaaaaaacgt ctaggccccc cgaaccacgg ggacgtggtt 1560
ttcctttgaa aaacacgata ataccatgat gatccatctg ggtcacatcc tcttcctgct 1620
tttgctccca gtggctgcag ctgactacaa agacgatgac gacaagcaga cgactccagg 1680
agagagatca tcactccctg ccttttaccc tggcacttca ggctcttgtt ccggatgtgg 1740
gtccctctct ctgccgctcc tggcaggcct cgtggctgct gatgcggtgg catcgctgct 1800
catcgtgggg gcggtgttcc tgtgcgcacg cccacgccgc agccccgccc aagatggcaa 1860
agtctacatc aacatgccag gcaggggctg a 1891

<210> 20
<211> 1867
<212> DNA
<213> Artificial Sequence

<220>
<223> CD3zeta-NKG2D-IRES-DAP10

<400> 20
atgagagtga agttcagcag gagcgcagac gcccccgcgt accagcaggg ccagaaccag 60
ctctataacg agctcaatct aggacgaaga gaggagtacg atgttttgga caagagacgt 120
ggccgggacc ctgagatggg gggaaagccg cagagaagga agaaccctca ggaaggcctg 180
tacaatgaac tgcagaaaga taagatggcg gaggcctaca gtgagattgg gatgaaaggc 240
gagcgccgga ggggcaaggg gcacgatggc ctttaccagg gtctcagtac agccaccaag 300
gacacctacg acgcccttca catgcaggcc ctgccccctc gcgggtggat tcgtggtcgg 360
aggtctcgac acagctggga gatgagtgaa tttcataatt ataacttgga tctgaagaag 420
agtgattttt caacacgatg gcaaaagcaa agatgtccag tagtcaaaag caaatgtaga 480
gaaaatgcat ctccattttt tttctgctgc ttcatcgctg tagccatggg aatccgtttc 540
attattatgg taacaatatg gagtgctgta ttcctaaact cattattcaa ccaagaagtt 600
caaattccct tgaccgaaag ttactgtggc ccatgtccta aaaactggat atgttacaaa 660
aataactgct accaattttt tgatgagagt aaaaactggt atgagagcca ggcttcttgt 720
atgtctcaaa atgccagcct tctgaaagta tacagcaaag aggaccagga tttacttaaa 780
ctggtgaagt catatcattg gatgggacta gtacacattc caacaaatgg atcttggcag 840
tgggaagatg gctccattct ctcacccaac ctactaacaa taattgaaat gcagaaggga 900
gactgtgcac tctatgcctc gagctttaaa ggctatatag aaaactgttc aactccaaat 960
acgtacatct gcatgcaaag gactgtgtaa gaattcgtta acctcgagcg ggatcaattc 1020
cgccccccc ctaacgttac tggccgaagc cgcttggaat aaggccggtg tgcgtttgtc 1080
tatatgttat tttccaccat attgccgtct tttggcaatg tgagggcccg gaaacctggc 1140
cctgtcttct tgacgagcat tcctaggggt ctttcccctc tcgccaaagg aatgcaaggt 1200
ctgttgaatg tcgtgaagga agcagttcct ctggaagctt cttgaagaca aacaacgtct 1260
gtagcgaccc tttgcaggca gcggaacccc ccacctggcg acaggtgcct ctgcggccaa 1320
aagccacgtg tataagatac acctgcaaag gcggcacaac cccagtgcca cgttgtgagt 1380
tggatagttg tggaaagagt caaatggctc tcctcaagcg tattcaacaa ggggctgaag 1440
gatgcccaga aggtacccca ttgtatggga tctgatctgg ggcctcggtg cacatgcttt 1500
acatgtgttt agtcgaggtt aaaaaaacgt ctaggccccc cgaaccacgg ggacgtggtt 1560
ttcctttgaa aaacacgata ataccatgat gatccatctg ggtcacatcc tcttcctgct 1620
tttgctccca gtggctgcag ctcagacgac tccaggagag agatcatcac tccctgcctt 1680
ttaccctggc acttcaggct cttgttccgg atgtgggtcc ctctctctgc cgctcctggc 1740
aggcctcgtg gctgctgatg cggtggcatc gctgctcatc gtgggggcgg tgttcctgtg 1800
cgcacgccca cgccgcagcc ccgcccaaga tggcaaagtc tacatcaaca tgccaggcag 1860
gggctga 1867

<210> 21
<211> 651
<212> DNA

<213> Artificial Sequence

<220>
<223> human NKG2D cDNA

<400> 21
atggggtgga ttcgtggtcg gaggtctcga cacagctggg agatgagtga atttcataat 60
tataacttgg atctgaagaa gagtgatttt tcaacacgat ggcaaaagca aagatgtcca 120
gtagtcaaaa gcaaatgtag agaaaatgca tctccatttt ttttctgctg cttcatcgct 180
gtagccatgg gaatccgttt cattattatg gtaacaatat ggagtgctgt attcctaaac 240
tcattattca accaagaagt tcaaattccc ttgaccgaaa gttactgtgg cccatgtcct 300
aaaaactgga tatgttacaa aaataactgc taccaatttt ttgatgagag taaaaactgg 360
tatgagagcc aggcttcttg tatgtctcaa aatgccagcc ttctgaaagt atacagcaaa 420
gaggaccagg atttacttaa actggtgaag tcatatcatt ggatgggact agtacacatt 480
ccaacaaatg gatcttggca gtgggaagat ggctccattc tctcacccaa cctactaaca 540
ataattgaaa tgcagaaggg agactgtgca ctctatgcct cgagctttaa aggctatata 600
gaaaactgtt caactccaaa tacgtacatc tgcatgcaaa ggactgtgta a 651

<210> 22
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid sequence of human NKG2D

<400> 22
Met Gly Trp Ile Arg Gly Arg Arg Ser Arg His Ser Trp Glu Met Ser
 1   5   10   15
Glu Phe His Asn Tyr Asn Leu Asp Leu Lys Lys Ser Asp Phe Ser Thr
            20   25   30
Arg Trp Gln Lys Gln Arg Cys Pro Val Val Lys Ser Lys Cys Arg Glu
        35   40   45
Asn Ala Ser Pro Phe Phe Phe Cys Cys Phe Ile Ala Val Ala Met Gly
    50   55   60
Ile Arg Phe Ile Ile Met Val Thr Ile Trp Ser Ala Val Phe Leu Asn
65   70   75   80
Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Cys
                85   90   95
Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn Cys Tyr Gln
            100   105   110
Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala Ser Cys Met
        115   120   125
Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu Asp Gln Asp
    130   135   140
Leu Leu Lys Leu Val Lys Ser Tyr His Trp Met Gly Leu Val His Ile
145   150   155   160
Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile Leu Ser Pro
                165   170   175
Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys Ala Leu Tyr
            180   185   190
Ala Ser Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser Thr Pro Asn Thr
        195   200   205
Tyr Ile Cys Met Gln Arg Thr Val
    210   215

<210> 23
<211> 5448
<212> DNA
<213> Artificial Sequence

<220>
<223> pCMV6-XL5-CD3zeta-NKG2D

<220>
<221> CDS

<222> (994)...(1983)

<400> 23

```
aacaaaatat taacgcttac aatttccatt cgccattcag gctgcgcaac tgttgggaag 60
ggcgatcggt gcgggcctct tcgctattac gccagctggc gaaaggggga tgtgctgcaa 120
ggcgattaag ttgggtaacg ccagggtttt cccagtcacg acgttgtaaa acgacggcca 180
gtgccaagct gatctataca ttgaatcaat attggcaatt agccatatta gtcattggtt 240
atatagcata aatcaatatt ggctattggc cattgcatac gttgtatcta tatcataata 300
tgtacattta tattggctca tgtccaatat gaccgccatg ttgacattga ttattgacta 360
gttattaata gtaatcaatt acggggtcat tagttcatag cccatatatg gagttccgcg 420
ttacataact tacggtaaat ggcccgcctg gctgaccgcc caacgacccc cgcccattga 480
cgtcaataat gacgtatgtt cccatagtaa cgccaatagg gactttccat tgacgtcaat 540
gggtggagta tttacggtaa actgcccact tggcagtaca tcaagtgtat catatgccaa 600
gtccgccccc tattgacgtc aatgacggta aatggcccgc ctggcattat gcccagtaca 660
tgaccttacg ggactttcct acttggcagt acatctacgt attagtcatc gctattacca 720
tggtgatgcg gttttggcag tacaccaatg ggcgtggata gcggtttgac tcacggggat 780
ttccaagtct ccaccccatt gacgtcaatg ggagtttgtt ttggcaccaa aatcaacggg 840
actttccaaa atgtcgtaat aaccccgccc cgttgacgca aatgggcggt aggcgtgtac 900
ggtgggaggt ctatataagc agagctcgtt tagtgaaccg tcagaatttt gtaatacgac 960
tcactatagg gcggccgcga attcgccgcc acc atg aga gtg aag ttc agc agg  1014
                                       Met Arg Val Lys Phe Ser Arg
                                        1               5

agc gca gac gcc ccc gcg tac cag cag ggc cag aac cag ctc tat aac   1062
Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
         10                  15                  20

gag ctc aat cta gga cga aga gag gag tac gat gtt ttg gac aag aga   1110
Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
     25                  30                  35

cgt ggc cgg gac cct gag atg ggg gga aag ccg cag aga agg aag aac   1158
Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn
 40                  45                  50                  55

cct cag gaa ggc ctg tac aat gaa ctg cag aaa gat aag atg gcg gag   1206
Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
                 60                  65                  70

gcc tac agt gag att ggg atg aaa ggc gag cgc cgg agg ggc aag ggg   1254
Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
             75                  80                  85

cac gat ggc ctt tac cag ggt ctc agt aca gcc acc aag gac acc tac   1302
His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
         90                  95                 100

gac gcc ctt cac atg cag gcc ctg ccc cct cgc ggg tgg att cgt ggt   1350
Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Trp Ile Arg Gly
    105                 110                 115

cgg agg tct cga cac agc tgg gag atg agt gaa ttt cat aat tat aac   1398
Arg Arg Ser Arg His Ser Trp Glu Met Ser Glu Phe His Asn Tyr Asn
120                 125                 130                 135

ttg gat ctg aag aag agt gat ttt tca aca cga tgg caa aag caa aga   1446
Leu Asp Leu Lys Lys Ser Asp Phe Ser Thr Arg Trp Gln Lys Gln Arg
                140                 145                 150

tgt cca gta gtc aaa agc aaa tgt aga gaa aat gca tct cca ttt ttt   1494
Cys Pro Val Val Lys Ser Lys Cys Arg Glu Asn Ala Ser Pro Phe Phe
            155                 160                 165

ttc tgc tgc ttc atc gct gta gcc atg gga atc cgt ttc att att atg   1542
Phe Cys Cys Phe Ile Ala Val Ala Met Gly Ile Arg Phe Ile Ile Met
        170                 175                 180

gta aca ata tgg agt gct gta ttc cta aac tca tta ttc aac caa gaa   1590
```

```
Val Thr Ile Trp Ser Ala Val Phe Leu Asn Ser Leu Phe Asn Gln Glu
    185                 190                 195

gtt caa att ccc ttg acc gaa agt tac tgt ggc cca tgt cct aaa aac   1638
Val Gln Ile Pro Leu Thr Glu Ser Tyr Cys Gly Pro Cys Pro Lys Asn
200                 205                 210                 215

tgg ata tgt tac aaa aat aac tgc tac caa ttt ttt gat gag agt aaa   1686
Trp Ile Cys Tyr Lys Asn Asn Cys Tyr Gln Phe Phe Asp Glu Ser Lys
                220                 225                 230

aac tgg tat gag agc cag gct tct tgt atg tct caa aat gcc agc ctt   1734
Asn Trp Tyr Glu Ser Gln Ala Ser Cys Met Ser Gln Asn Ala Ser Leu
            235                 240                 245

ctg aaa gta tac agc aaa gag gac cag gat tta ctt aaa ctg gtg aag   1782
Leu Lys Val Tyr Ser Lys Glu Asp Gln Asp Leu Leu Lys Leu Val Lys
        250                 255                 260

tca tat cat tgg atg gga cta gta cac att cca aca aat gga tct tgg   1830
Ser Tyr His Trp Met Gly Leu Val His Ile Pro Thr Asn Gly Ser Trp
    265                 270                 275

cag tgg gaa gat ggc tcc att ctc tca ccc aac cta cta aca ata att   1878
Gln Trp Glu Asp Gly Ser Ile Leu Ser Pro Asn Leu Leu Thr Ile Ile
280                 285                 290                 295

gaa atg cag aag gga gac tgt gca ctc tat gcc tcg agc ttt aaa ggc   1926
Glu Met Gln Lys Gly Asp Cys Ala Leu Tyr Ala Ser Ser Phe Lys Gly
                300                 305                 310

tat ata gaa aac tgt tca act cca aat acg tac atc tgc atg caa agg   1974
Tyr Ile Glu Asn Cys Ser Thr Pro Asn Thr Tyr Ile Cys Met Gln Arg
            315                 320                 325

act gtg taa tctagattgc ggccgcggtc atagctgttt cctgaacaga           2023
Thr Val  *


tcccgggtgg catccctgtg acccctcccc agtgcctctc ctggccctgg aagttgccac 2083
tccagtgccc accagccttg tcctaataaa attaagttgc atcattttgt ctgactaggt 2143
gtccttctat aatattatgg ggtggagggg ggtggtatgg agcaaggggc aagttgggaa 2203
gacaacctgt agggcctgcg gggtctattg ggaaccaagc tggagtgcag tggcacaatc 2263
ttggctcact gcaatctccg cctcctgggt tcaagcgatt ctcctgcctc agcctcccga 2323
gttgttggga ttccaggcat gcatgaccag gctcagctaa tttttgtttt tttggtagag 2383
acggggtttc accatattgg ccaggctggt ctccaactcc taatctcagg tgatctaccc 2443
accttggcct cccaaattgc tgggattaca ggcgtgaacc actgctccct tccctgtcct 2503
tctgatttta aaataactat accagcagga ggacgtccag acacagcata ggctacctgg 2563
ccatgcccaa ccggtgggac atttgagttg cttgcttggc actgtcctct catgcgttgg 2623
gtccactcag tagatgcctg ttgaattggg tacgcggcca gcttggctgt ggaatgtgtg 2683
tcagttaggg tgtggaaagt ccccaggctc cccagcaggc agaagtatgc aaagcatgca 2743
tctcaattag tcagcaacca ggtgtggaaa gtccccaggc tccccagcag gcagaagtat 2803
gcaaagcatg catctcaatt agtcagcaac catagtcccg cccctaactc cgcccatccc 2863
gcccctaact ccgcccagtt ccgcccattc tccgccccat ggctgactaa ttttttttat 2923
ttatgcagag gccgaggccg cctcggcctc tgagctattc cagaagtagt gaggaggctt 2983
ttttggaggc ctaggctttt gcaaaaagct cctcgactgc attaatgaat cggccaacgc 3043
gcggggagag gcggtttgcg tattgggcgc tcttccgctt cctcgctcac tgactcgctg 3103
cgctcggtcg ttcggctgcg gcgagcggta tcagctcact caaaggcggt aatacggtta 3163
tccacagaat caggggataa cgcaggaaag aacatgtgag caaaaggcca gcaaaaggcc 3223
aggaaccgta aaaaggccgc gttgctggcg tttttccata ggctccgccc ccctgacgag 3283
catcacaaaa atcgacgctc aagtcagagg tggcgaaacc cgacaggact ataaagatac 3343
caggcgtttc cccctggaag ctccctcgtg cgctctcctg ttccgaccct gccgcttacc 3403
ggatacctgt ccgcctttct cccttcggga agcgtggcgc tttctcatag ctcacgctgt 3463
aggtatctca gttcggtgta ggtcgttcgc tccaagctgg gctgtgtgca cgaacccccc 3523
gttcagcccg accgctgcgc cttatccggt aactatcgtc ttgagtccaa cccggtaaga 3583
cacgacttat cgccactggc agcagccact ggtaacagga ttagcagagc gaggtatgta 3643
ggcggtgcta cagagttctt gaagtggtgg cctaactacg gctacactag aagaacagta 3703
tttggtatct gcgctctgct gaagccagtt accttcggaa aaagagttgg tagctcttga 3763
```

tccggcaaac aaaccaccgc tggtagcggt ggtttttttg tttgcaagca gcagattacg 3823
cgcagaaaaa aaggatctca agaagatcct ttgatctttt ctacggggtc tgacgctcag 3883
tggaacgaaa actcacgtta agggattttg gtcatgagat tatcaaaaag gatcttcacc 3943
tagatccttt taaattaaaa atgaagtttt aaatcaatct aaagtatata tgagtaaact 4003
tggtctgaca gttaccaatg cttaatcagt gaggcaccta tctcagcgat ctgtctattt 4063
cgttcatcca tagttgcctg actccccgtc gtgtagataa ctacgatacg ggagggctta 4123
ccatctggcc ccagtgctgc aatgataccg cgagacccac gctcaccggc tccagattta 4183
tcagcaataa accagccagc cggaagggcc gagcgcagaa gtggtcctgc aactttatcc 4243
gcctccatcc agtctattaa ttgttgccgg gaagctagag taagtagttc gccagttaat 4303
agtttgcgca acgttgttgc cattgctaca ggcatcgtgg tgtcacgctc gtcgtttggt 4363
atggcttcat tcagctccgg ttcccaacga tcaaggcgag ttacatgatc ccccatgttg 4423
tgcaaaaaag cggttagctc cttcggtcct ccgatcgttg tcagaagtaa gttggccgca 4483
gtgttatcac tcatggttat ggcagcactg cataattctc ttactgtcat gccatccgta 4543
agatgctttt ctgtgactgg tgagtactca accaagtcat tctgagaata gtgtatgcgg 4603
cgaccgagtt gctcttgccc ggcgtcaata cgggataata ccgcgccaca tagcagaact 4663
ttaaaagtgc tcatcattgg aaaacgttct tcggggcgaa aactctcaag gatcttaccg 4723
ctgttgagat ccagttcgat gtaacccact cgtgcaccca actgatcttc agcatctttt 4783
actttcacca gcgtttctgg gtgagcaaaa acaggaaggc aaaatgccgc aaaaaaggga 4843
ataagggcga cacggaaatg ttgaatactc atactcttcc tttttcaata ttattgaagc 4903
atttatcagg gttattgtct catgagcgga tacatatttg aatgtattta gaaaaataaa 4963
caaatagggg ttccgcgcac atttccccga aaagtgccac ctgacgcgcc ctgtagcggc 5023
gcattaagcg cggcgggtgt ggtggttacg cgcagcgtga ccgctacact tgccagcgcc 5083
ctagcgcccg ctcctttcgc tttcttccct tcctttctcg ccacgttcgc cggctttccc 5143
cgtcaagctc taaatcgggg gctcccttta gggttccgat ttagtgcttt acggcacctc 5203
gaccccaaaa aacttgatta gggtgatggt tcacgtagtg ggccatcgcc ctgatagacg 5263
gtttttcgcc ctttgacgtt ggagtccacg ttctttaata gtggactctt gttccaaact 5323
ggaacaacac tcaaccctat ctcggtctat tcttttgatt tataagggat tttgccgatt 5383
tcggcctatt ggttaaaaaa tgagctgatt taacaaaaat ttaacgcgaa ttttaacaaa 5443
atatt 5448

<210> 24
<211> 4745
<212> DNA
<213> Artificial Sequence

<220>
<223> pCMV6-XL5-DAP10

<220>
<221> CDS
<222> (994)...(1272)

<400> 24
aacaaaatat taacgcttac aatttccatt cgccattcag gctgcgcaac tgttgggaag 60
ggcgatcggt gcgggcctct tcgctattac gccagctggc gaaaggggga tgtgctgcaa 120
ggcgattaag ttgggtaacg ccagggtttt cccagtcacg acgttgtaaa acgacggcca 180
gtgccaagct gatctataca ttgaatcaat attggcaatt agccatatta gtcattggtt 240
atatagcata aatcaatatt ggctattggc cattgcatac gttgtatcta tatcataata 300
tgtacattta tattggctca tgtccaatat gaccgccatg ttgacattga ttattgacta 360
gttattaata gtaatcaatt acggggtcat tagttcatag cccatatatg gagttccgcg 420
ttacataact tacggtaaat ggcccgcctg gctgaccgcc caacgacccc cgcccattga 480
cgtcaataat gacgtatgtt cccatagtaa cgccaatagg gactttccat tgacgtcaat 540
gggtggagta tttacggtaa actgcccact tggcagtaca tcaagtgtat catatgccaa 600
gtccgccccc tattgacgtc aatgacggta aatggcccgc ctggcattat gcccagtaca 660
tgaccttacg ggactttcct acttggcagt acatctacgt attagtcatc gctattacca 720
tggtgatgcg gttttggcag tacaccaatg ggcgtggata gcggtttgac tcacggggat 780
ttccaagtct ccaccccatt gacgtcaatg ggagtttgtt ttggcaccaa aatcaacggg 840
actttccaaa atgtcgtaat aaccccgccc cgttgacgca aatgggcggt aggcgtgtac 900
ggtgggaggt ctatataagc agagctcgtt tagtgaaccg tcagaatttt gtaatacgac 960
tcactatagg gcggccgcga attcgccgcc acc atg atc cat ctg ggt cac atc 1014
                                    Met Ile His Leu Gly His Ile
                                     1   5

ctc ttc ctg ctt ttg ctc cca gtg gct gca gct cag acg act cca gga   1062
Leu Phe Leu Leu Leu Leu Pro Val Ala Ala Ala Gln Thr Thr Pro Gly
         10   15   20

```
gag aga tca tca ctc cct gcc ttt tac cct ggc act tca ggc tct tgt   1110
Glu Arg Ser Ser Leu Pro Ala Phe Tyr Pro Gly Thr Ser Gly Ser Cys
     25                  30                  35

tcc gga tgt ggg tcc ctc tct ctg ccg ctc ctg gca ggc ctc gtg gct   1158
Ser Gly Cys Gly Ser Leu Ser Leu Pro Leu Leu Ala Gly Leu Val Ala
 40                  45                  50                  55

gct gat gcg gtg gca tcg ctg ctc atc gtg ggg gcg gtg ttc ctg tgc   1206
Ala Asp Ala Val Ala Ser Leu Leu Ile Val Gly Ala Val Phe Leu Cys
                 60                  65                  70

gca cgc cca cgc cgc agc ccc gcc caa gat ggc aaa gtc tac atc aac   1254
Ala Arg Pro Arg Arg Ser Pro Ala Gln Asp Gly Lys Val Tyr Ile Asn
             75                  80                  85

atg cca ggc agg ggc tga tctatatatc tagattgcgg ccgcggtcat          1302
Met Pro Gly Arg Gly  *
         90

agctgtttcc tgaacagatc ccgggtggca tccctgtgac ccctccccag tgcctctcct 1362
ggccctggaa gttgccactc cagtgcccac cagccttgtc ctaataaaat taagttgcat 1422
cattttgtct gactaggtgt ccttctataa tattatgggg tggaggggag tggtatggag 1482
caaggggcaa gttgggaaga caacctgtag ggcctgcggg gtctattggg aaccaagctg 1542
gagtgcagtg gcacaatctt ggctcactgc aatctccgcc tcctgggttc aagcgattct 1602
cctgcctcag cctcccgagt tgttgggatt ccaggcatgc atgaccaggc tcagctaatt 1662
tttgtttttt tggtagagac ggggtttcac catattggcc aggctggtct ccaactccta 1722
atctcaggtg atctacccac cttggcctcc caaattgctg ggattacagg cgtgaaccac 1782
tgctcccttc cctgtccttc tgattttaaa ataactatac cagcaggagg acgtccagac 1842
acagcatagg ctacctggcc atgcccaacc ggtgggacat ttgagttgct tgcttggcac 1902
tgtcctctca tgcgttgggt ccactcagta gatgcctgtt gaattgggta cgcggccagc 1962
ttggctgtgg aatgtgtgtc agttagggtg tggaaagtcc ccaggctccc cagcaggcag 2022
aagtatgcaa agcatgcatc tcaattagtc agcaaccagg tgtggaaagt ccccaggctc 2082
cccagcaggc agaagtatgc aaagcatgca tctcaattag tcagcaacca tagtcccgcc 2142
cctaactccg cccatcccgc ccctaactcc gcccagttcc gcccattctc cgccccatgg 2202
ctgactaatt ttttttattt atgcagaggc cgaggccgcc tcggcctctg agctattcca 2262
gaagtagtga ggaggctttt ttggaggcct aggcttttgc aaaaagctcc tcgactgcat 2322
taatgaatcg gccaacgcgc ggggagaggc ggtttgcgta ttgggcgctc ttccgcttcc 2382
tcgctcactg actcgctgcg ctcggtcgtt cggctgcggc gagcggtatc agctcactca 2442
aaggcggtaa tacggttatc cacagaatca ggggataacg caggaaagaa catgtgagca 2502
aaaggccagc aaaaggccag gaaccgtaaa aaggccgcgt tgctggcgtt tttccatagg 2562
ctccgccccc ctgacgagca tcacaaaaat cgacgctcaa gtcagaggtg gcgaaacccg 2622
acaggactat aaagatacca ggcgtttccc cctggaagct ccctcgtgcg ctctcctgtt 2682
ccgaccctgc cgcttaccgg atacctgtcc gcctttctcc cttcgggaag cgtggcgctt 2742
tctcatagct cacgctgtag gtatctcagt tcggtgtagg tcgttcgctc caagctgggc 2802
tgtgtgcacg aacccccccgt tcagcccgac cgctgcgcct tatccggtaa ctatcgtctt 2862
gagtccaacc cggtaagaca cgacttatcg ccactggcag cagccactgg taacaggatt 2922
agcagagcga ggtatgtagg cggtgctaca gagttcttga agtggtggcc taactacggc 2982
tacactagaa gaacagtatt tggtatctgc gctctgctga agccagttac cttcggaaaa 3042
agagttggta gctcttgatc cggcaaacaa accaccgctg gtagcggtgg ttttttgtt 3102
tgcaagcagc agattacgcg cagaaaaaaa ggatctcaag aagatccttt gatcttttct 3162
acggggtctg acgctcagtg gaacgaaaac tcacgttaag ggattttggt catgagatta 3222
tcaaaaagga tcttcaccta gatcctttta aattaaaaat gaagttttaa atcaatctaa 3282
agtatatatg agtaaacttg gtctgacagt taccaatgct taatcagtga ggcacctatc 3342
tcagcgatct gtctatttcg ttcatccata gttgcctgac tccccgtcgt gtagataact 3402
acgatacggg agggcttacc atctggcccc agtgctgcaa tgataccgcg agacccacgc 3462
tcaccggctc cagatttatc agcaataaac cagccagccg gaagggccga gcgcagaagt 3522
ggtcctgcaa ctttatccgc ctccatccag tctattaatt gttgccggga agctagagta 3582
agtagttcgc cagttaatag tttgcgcaac gttgttgcca ttgctacagg catcgtggtg 3642
tcacgctcgt cgtttggtat ggcttcattc agctccggtt cccaacgatc aaggcgagtt 3702
acatgatccc ccatgttgtg caaaaaagcg gttagctcct tcggtcctcc gatcgttgtc 3762
agaagtaagt tggccgcagt gttatcactc atggttatgg cagcactgca taattctctt 3822
actgtcatgc catccgtaag atgcttttct gtgactggtg agtactcaac caagtcattc 3882
tgagaatagt gtatgcggcg accgagttgc tcttgcccgg cgtcaatacg ggataatacc 3942
gcgccacata gcagaacttt aaaagtgctc atcattggaa aacgttcttc ggggcgaaaa 4002
ctctcaagga tcttaccgct gttgagatcc agttcgatgt aacccactcg tgcacccaac 4062
tgatcttcag catcttttac tttcaccagc gtttctgggt gagcaaaaac aggaaggcaa 4122
aatgccgcaa aaaagggaat aagggcgaca cggaaatgtt gaatactcat actcttcctt 4182
```

tttcaatatt attgaagcat ttatcagggt tattgtctca tgagcggata catatttgaa 4242
tgtatttaga aaaataaaca aataggggtt ccgcgcacat ttccccgaaa agtgccacct 4302
gacgcgccct gtagcggcgc attaagcgcg gcgggtgtgg tggttacgcg cagcgtgacc 4362
gctacacttg ccagcgccct agcgcccgct cctttcgctt tcttcccttc ctttctcgcc 4422
acgttcgccg gctttccccg tcaagctcta aatcgggggc tcccttttagg gttccgattt 4482
agtgctttac ggcacctcga ccccaaaaaa cttgattagg gtgatggttc acgtagtggg 4542
ccatcgccct gatagacggt ttttcgccct ttgacgttgg agtccacgtt ctttaatagt 4602
ggactcttgt tccaaactgg aacaacactc aaccctatct cggtctattc ttttgattta 4662
taagggattt tgccgatttc ggcctattgg ttaaaaaatg agctgattta acaaaaattt 4722
aacgcgaatt ttaacaaaat att 4745

<210> 25
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> CD3zeta-NKG2D

<400> 25
atgagagtga agttcagcag gagcgcagac gcccccgcgt accagcaggg ccagaaccag 60
ctctataacg agctcaatct aggacgaaga gaggagtacg atgttttgga caagagacgt 120
ggccgggacc ctgagatggg gggaaagccg cagagaagga agaaccctca ggaaggcctg 180
tacaatgaac tgcagaaaga taagatggcg gaggcctaca gtgagattgg gatgaaaggc 240
gagcgccgga ggggcaaggg gcacgatggc ctttaccagg gtctcagtac agccaccaag 300
gacacctacg acgcccttca catgcaggcc ctgcccccctc gcgggtggat tcgtggtcgg 360
aggtctcgac acagctggga gatgagtgaa tttcataatt ataacttgga tctgaagaag 420
agtgattttt caacacgatg gcaaaagcaa agatgtccag tagtcaaaag caaatgtaga 480
gaaaatgcat ctccattttt tttctgctgc ttcatcgctg tagccatggg aatccgtttc 540
attattatgg taacaatatg gagtgctgta ttcctaaact cattattcaa ccaagaagtt 600
caaattccct tgaccgaaag ttactgtggc ccatgtccta aaaactggat atgttacaaa 660
aataactgct accaattttt tgatgagagt aaaaactggt atgagagcca ggcttcttgt 720
atgtctcaaa atgccagcct tctgaaagta tacagcaaag aggaccagga tttacttaaa 780
ctggtgaagt catatcattg gatgggacta gtacacattc caacaaatgg atcttggcag 840
tgggaagatg gctccattct ctcacccaac ctactaacaa taattgaaat gcagaaggga 900
gactgtgcac tctatgcctc gagctttaaa ggctatatag aaaactgttc aactccaaat 960
acgtacatct gcatgcaaag gactgtgtaa 990

<210> 26
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid sequence of CD3zeta-NKG2D

<400> 26
Met Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
 1   5   10   15
Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
            20   25   30
Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
        35   40   45
Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
    50   55   60
Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
65   70   75   80
Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
                85   90   95
Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
            100   105   110
Pro Arg Gly Trp Ile Arg Gly Arg Arg Ser Arg His Ser Trp Glu Met
        115   120   125
Ser Glu Phe His Asn Tyr Asn Leu Asp Leu Lys Lys Ser Asp Phe Ser
    130   135   140
Thr Arg Trp Gln Lys Gln Arg Cys Pro Val Val Lys Ser Lys Cys Arg

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