SEQUENCE LISTING

SEQ ID NO: 1 - Mouse IL-4C118 cDNA Forward primer

GGATCCACCATGGGTCTCAACCCCCAGCTA

SEQ ID NO: 2 - Mouse IL-4C118 cDNA Reverse primer

GAATTCTAATCCATTTGCATGATGCTC

SEQ ID NO: 3 - Mouse IL4C118 DNA sequence

```
  1  gga tcc acc atg ggt ctc aac ccc cag cta gtt gtc atc ctg ctc ttc ttt
ctc gaa tgt acc agg agc cat atc cac gga tgc gac
                 Met Gly Leu Asn Pro Gln Leu Val Val Ile Leu Leu Phe Phe
Leu Glu Cys Thr Arg Ser His Ile His Gly Cys Asp

 88  aaa aat cac ttg aga gag atc atc ggc att ttg aac gag gtc aca gga gaa
ggg acg cca tgc acg gag atg gat gtg cca aac gtc
     Lys Asn His Leu Arg Glu Ile Ile Gly Ile Leu Asn Glu Val Thr Gly Glu
Gly Thr Pro Cys Thr Glu Met Asp Val Pro Asn Val

175  ctc aca gca acg aag aac acc aca gag agt gag ctc gtc tgt agg gct tcc
aag gtg ctt cgc ata ttt tat tta aaa cat ggg aaa
     Leu Thr Ala Thr Lys Asn Thr Thr Glu Ser Glu Leu Val Cys Arg Ala Ser
Lys Val Leu Arg Ile Phe Tyr Leu Lys His Gly Lys

262  act cca tgc ttg aag aag aac tct agt gtt ctc atg gag ctg cag aga ctc
ttt cgg gct ttt cga tgc ctg gat tca tcg ata agc
     Thr Pro Cys Leu Lys Lys Asn Ser Ser Val Leu Met Glu Leu Gln Arg Leu
Phe Arg Ala Phe Arg Cys Leu Asp Ser Ser Ile Ser

349  tgc acc atg aat gag tc c aag tcc aca tca ctg aaa gac ttc ctg gaa
agc cta aag agc atc atg caa atg gat tag aat tc
     Cys Thr Met Asn Glu Ser Lys Ser Thr Ser Leu Lys Asp Phe Leu Glu Ser
Leu Lys Ser Ile Met Gln Met Asp ---
```

SEQ ID NO: 4 - Rhesus Macaque IL4C123 DNA sequence

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  1  gga tcc gcc acc atg ggt ctc acc tcc caa ctg ctt ccc cct ctg ttc ttc
ctg cta gca tgt gcc ggc aac ttt gcc cac gga cac
                    Met Gly Leu Thr Ser Gln Leu Leu Pro Pro Leu Phe Phe
Leu Leu Ala Cys Ala Gly Asn Phe Ala His Gly His

 88  aac tgc cat atc gcc tta cgg gag atc atc gaa act ctg aac agc ctc aca
gag cag aag act ctg tgc acc aag ttg acc ata acg
     Asn Cys His Ile Ala Leu Arg Glu Ile Ile Glu Thr Leu Asn Ser Leu Thr
Glu Gln Lys Thr Leu Cys Thr Lys Leu Thr Ile Thr

175  gac atc ctt gct gcc tcc aag aac aca act gag aag gaa acc ttc tgc agg
gct gcg act gtg ctc cgg cag ttc tac agc cac cat
     Asp Ile Leu Ala Ala Ser Lys Asn Thr Thr Glu Lys Glu Thr Phe Cys Arg
Ala Ala Thr Val Leu Arg Gln Phe Tyr Ser His His

262  gag aag gac act cgc tgc ctg ggt gcg act gca cag cag ttt cac agg cac
aag cag ctg atc cga ttc ctg aaa cgg ctc gac agg
     Glu Lys Asp Thr Arg Cys Leu Gly Ala Thr Ala Gln Gln Phe His Arg His
Lys Gln Leu Ile Arg Phe Leu Lys Arg Leu Asp Arg
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349  aac ctc tgg ggc ctg gcg ggc ttg aac tcc tgt cct gtg aag gaa gcc agc
cag agt acg ttg gaa gac ttc ttg gaa agg cta aag
     Asn Leu Trp Gly Leu Ala Gly Leu Asn Ser Cys Pro Val Lys Glu Ala Ser
Gln Ser Thr Leu Glu Asp Phe Leu Glu Arg Leu Lys

436  acg atc atg aaa gag aaa tga agc tt
     Thr Ile Met Lys Glu Lys ---
```

SEQ ID NO: 5 - Human IL4C123

```
1   ATGGGTCTCA CCTCCCAACT GCTTCCCCCT CTGTTCTTCC TGCTAGCATG TGCCGGCAAC
61  TTTGTCCACG GACACAAGTG CGATATCACC TTACAGGAGA TCATCAAAAC TTTGAACAGC
121 CTCACAGAGC AGAAGACTCT GTGCACCGAG TTGACCGTAA CAGACATCTT TGCTGCCTCC
181 AAGAACACAA CTGAGAAGGA AACCTTCTGC AGGGCTGCGA CTGTGCTCCG GCAGTTCTAC
241 AGCCACCATG AGAAGGACAC TCGCTGCCTG GGTGCGACTG CACAGCAGTT CCACAGGCAC
301 AAGCAGCTGA TCCGATTCCT GAAACGGCTC GACAGGAACC TCTGGGGCCT GGCGGGCTTG
361 AATTCCTGTC CTGTGAAGGA AGCCAACCAG AGTACGTTGG AAAACTTCTT GGAAAGGCTA
421 AAGACGATCA TGAGAGAGAA ATGA
```

SEQ ID NO: 6 - Human IL4C123 (optimised)

```
1   ATGGGCCTGA CCAGCCAGCT GCTGCCCCCC CTGTTCTTCC TGCTGGCCTG CGCCGGCAAC
61  TTCGTGCACG GCCACAAGTG CGACATCACC CTGCAGGAGA TCATCAAGAC CCTGAACAGC
121 CTGACCGAGC AGAAGACCCT GTGCACCGAG CTGACCGTGA CCGACATCTT CGCCGCCAGC
181 AAGAACACCA CCGAGAAGGA GACCTTCTGC AGAGCCGCCA CCGTGCTGAG ACAGTTCTAC
241 AGCCACCACG AGAAGGACAC CAGATGCCTG GGCGCCACCG CCCAGCAGTT CCACAGACAC
301 AAGCAGCTGA TCAGATTCCT GAAGAGACTG GACAGAAACC TGTGGGGCCT GGCCGGCCTG
361 AACAGCTGCC CCGTGAAGGA GGCCAACCAG AGCACCCTGG AGAACTTCCT GGAGAGACTG
421 AAGACCATCA TGAGAGAGAA GTGA
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SEQ ID NO: 7 - Human IL4C123 (optimised no FseI site)

```
1   ATGGGCCTGA CCAGCCAGCT GCTGCCCCCC CTGTTCTTCC TGCTGGCCTG CGCCGGCAAC
61  TTCGTGCACG GCCACAAGTG CGACATCACC CTGCAGGAGA TCATCAAGAC CCTGAACAGC
121 CTGACCGAGC AGAAGACCCT GTGCACCGAG CTGACCGTGA CCGACATCTT CGCCGCCAGC
181 AAGAACACCA CCGAGAAGGA GACCTTCTGC AGAGCCGCCA CCGTGCTGAG ACAGTTCTAC
241 AGCCACCACG AGAAGGACAC CAGATGCCTG GGCGCCACCG CCCAGCAGTT CCACAGACAC
301 AAGCAGCTGA TCAGATTCCT GAAGAGACTG GACAGAAACC TGTGGGGCTT AGCTGGTTTA
361 AACAGCTGCC CCGTGAAGGA GGCCAACCAG AGCACCCTGG AGAACTTCCT GGAGAGACTG
421 AAGACCATCA TGAGAGAGAA GTGA
```

SEQ ID NO: 8 - Macaca mulatta interleukin 4 (IL4), mRNA

```
  1 atgggtctca cctcccaact gcttcccctc ctgttcttcc tgctagcatg tgccggcaac
 61 tttgcccacg gacacaactg ccatatcgcc ttacgggaga tcatcgaaac tctgaacagc
121 ctcacagagc agaagactct gtgcaccaag ttgaccataa cggacatcct tgctgcctcc
181 aagaacacaa ctgagaagga aaccttctgc agggctgcga ctgtgctccg gcagttctac
241 agccaccatg agaaggacac tcgctgcctg ggtgcgactg cacagcagtt tcacaggcac
301 aagcagctga tccgattcct gaaacggctc gacaggaacc tctggggcct ggcgggcttg
361 aactcctgtc ctgtgaagga agccagccag agtacgttgg aagacttctt ggaaaggcta
421 aagacgatca tgaaagagaa atattcaaag tgtcggagct ga
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SEQ ID NO: 9 - Macaca mulatta interleukin 4 (IL4), peptide

```
MGLTSQLLPPLFFLLACAGNFAHGHNCHIALREIIETLNSLTEQKTLCTKLTITDILAASKNTTEKETFCRA
ATVLRQFYSHHEKDTRCLGATAQQFHRHKQLIRFLKRLDRNLWGLAGLNSCPVKEASQSTLEDFLERLKTIM
KEKYSKCRS
```

SEQ ID NO: 10 - MVA del-III synthetic vector sequence

gcggccgcgg cgcgccacct aaagatgcca ttcctgttat tatatccata ggaaaggata 60
gagatgtttg tgaactatta atctcatctg ataaagcgtg tgcgtgtata gagttaaatt 120
catataaagt agccattctt cccatggatg tttccttttt taccaaagga aatgcatcat 180
tgattattct cctgtttgat ttctctatcg atgcggcacc tctcttaaga agtgtaaccg 240
ataataatgt tattatatct agacaccagc gtctacatga cgagcttccg agttccaatt 300
ggttcaagtt ttacataagt ataaagtccg actattgttc tatattatat atggttgttg 360
atggatctgt gatgcatgca atagctgata atagaactta cgcaaatatt agcaaaaata 420
tattagacaa tactacaatt aacgatgagt gtagatgctg ttattttgaa ccacagatta 480
ggattcttga tagagatgag atgctcaatg gatcatcgtg tgatatgaac agacattgta 540
ttatgatgaa tttacctgat gtaggcgaat ttggatctag tatgttgggg aaatatgaac 600
ctgacatgat taagattgct ctttcggtgg ctggtatttg gaaagtttta taggccggcc 660
gcgatcgcat ttagtatcct aaaattgaat tgtaattatc gataataaat ggacggatcc 720
cgggtcgact gcagaagctt tagttgatag aacaaaatac ataattttgt aaaaataaat 780
cacttttat actaatatga cacgattacc aatacttttg ttactaatat cattagtata 840
cgctacacct tttcctcaga catctaaaaa aataggtgat gatgcaactt tatcatgtaa 900
tcgaaataat acaaatgact acgttgttat gagtgcttgg tataaggagc ccaattccat 960
tattctttta gctgctaaaa gcgacgtctt gtattttgat aattatacca aggataaaat 1020
atcttacgac tctccatacg atgatctagt tacaactatc acaattaaat cattgactgc 1080
tagagatgcc ggtacttatg tatgtgcatt ctttatgaca tcgcctacaa atgacactga 1140
taaagtagat tatgaagaat actccacaga gttgattgta aatacagata gtgaatcgac 1200
tatagacata atactatctg gatctacaca ttcaccggaa actagttctg agaaacctga 1260
ttatatagat aattctaatt gctcgtcggt attcgaaatc gcggccgc 1308

SEQ ID NO: 11 - MVA "HindIII F" insertion site

gcggccgcgg cgcgcccggt atccaagcta gaaaagaact gtaatgcgta tgcggaggtt 60
aataatatta tagatataca gaaattggat atcggagaat gttcggctcc gcccggtcaa 120
catatgcttt tacagatagt taatacagga tccgcggaag caaattgtgg tttacagaca 180
attgttaagt ccttaaataa aatatacgtt ccacctatta tcgaaaaccg attgccgtat 240
tacgatccgt ggtttctagt gggtgtagca attattctag ttatttttac tgtagctatt 300
tgttctatta gacgaaatct ggctcttaaa tacagatacg gaacgttttt atacgtttaa 360
ttaataaaaa aatttaatta caaggtataa aatagtactc catctacgca atcgcgataa 420
tggagggatc taaacgcaga cacgacagtc ggcgactaca acaagaacag gagcagcctc 480
gtccacgtac accgccatca tatgaagaaa ttgcaaaata tggacactca tttaacgtga 540
aaagatttac gaatgaagaa atgtgtctta agaatgatta tccacgaatt atatcatata 600
atcctccacc aaaatagttt tttttggccg gccgcgatcg caagcttagt atatatatat 660
catcatttca tgatgtatac tactgacata gtttcaatgt gaacttttca ctttcttgcc 720
ggttatgaag aatattttta ttttaatggt cattactaat cgtatattat aattgaaaat 780
ggattagttt aatatgacgc tcgtcatggg atcctgctgt ggtagattct gtgacgctaa 840
gaataagaat aagaaggaag atgtagaaga gggaagagaa ggatgttaca attataagaa 900
ccttaatgat ctggatgaat ccgaagcacg tgtagaattt ggaccattat atatgataaa 960
tgaagaaaaa tcagacataa atacattgga tataaaaaga agatatagac acacgataga 1020
gtctgtatat ttctaaaagt ttttataaaa aatgagtaaa atactcacgt ttgttaaaaa 1080
taagataatt gacttgatta ataatgacca aattaaatat tctagagtta taatgataga 1140
agagtccgat agtcttttac cggttgatga ggtgcatgct aaccacggat ttgactgtgt 1200
ggagatgata gatgaaaata taagcaatga gaatatcgaa cagtataagc ggccgc 1256

SEQ ID NO: 12 - synthetic SIV mac239 gag/pol sequence optimised for expression in macaque monkeys

1 GAATTCGGCC GGCCATTTAG TATCCTAAAA TTGAATTGTA ATTATCGATA ATAAATGGGC
61 GTGAGGAACT CCGTGCTGTC CGGCAAGAAG GCCGACGAGC TGGAGAAGAT CAGGCTGAGG
121 CCCAACGGCA AGAAGAAGTA CATGCTGAAG CACGTGGTGT GGGCCGCCAA CGAGCTGGAC
181 AGGTTCGGCC TGGCCGAGTC CCTGCTGGAG AACAAGGAGG GCTGCCAGAA GATCCTGTCC
241 GTGCTGGCCC CCCTGGTGCC CACCGGCTCC GAGAACCTGA AGTCCCTGTA CAACACCGTG
301 TGCGTGATCT GGTGCATCCA CGCCGAGGAG AAGGTGAAGC ACACCGAGGA GGCCAAGCAG

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361   ATCGTGCAGA GGCACCTGGT GGTGGAGACC GGCACCACCG AGACCATGCC CAAGACCTCC
421   AGGCCCACCG CCCCCTCCTC CGGCAGGGGC GGCAACTACC CCGTGCAGCA GATCGGCGGC
481   AACTACGTGC ACCTGCCCCT GTCCCCCAGG ACCCTGAACG CCTGGGTGAA GCTGATCGAG
541   GAGAAGAAGT TCGGCGCCGA GGTGGTGCCC GGCTTCCAGG CCCTGTCCGA GGGCTGCACC
601   CCCTACGACA TCAACCAGAT GCTGAACTGC GTGGGCGACC ACCAGGCCGC CATGCAGATC
661   ATCAGGGACA TCATCAACGA GGAGGCCGCC GACTGGGACC TCCAGCACCC CCAGCCCGCC
721   CCCCAGCAGG GCCAGCTGAG GGAGCCCTCC GGCTCCGACA TCGCCGGCAC CACCTCCTCC
781   GTGGACGAGC AGATCCAGTG GATGTACAGG CAGCAGAACC CCATCCCCGT GGGCAACATC
841   TACAGGAGGT GGATTCAGCT GGGCCTGCAA AAGTGCGTGA GGATGTACAA CCCCACCAAC
901   ATCCTGGACG TGAAGCAGGG CCCCAAGGAG CCCTTCCAGT CCTACGTGGA CAGGTTCTAC
961   AAGTCCCTGA GGGCCGAGCA GACCGACGCC GCCGTGAAGA ACTGGATGAC CCAGACCCTG
1021  CTGATCCAGA ACGCCAACCC CGACTGCAAG CTGGTGCTGA AGGGCCTGGG CGTGAACCCC
1081  ACCCTGGAGG AGATGCTGAC CGCCTGCCAG GGCGTGGGCG GCCCCGGCCA GAAGGCCAGG
1141  CTGATGGCCG AGGCCCTGAA GGAGGCCCTG GCCCCCGTGC CCATCCCCTT CGCCGCCGCC
1201  CAGCAGAGGG GCCCCAGGAA GCCCATCAAG TGCTGGAACT GCGGCAAGGA GGGCCACTCC
1261  GCCAGGCAAT GCAGAGCCCC AAGAAGACAG GGATGCTGGA AATGTGGAAA AATGGACCAT
1321  GTTATGGCCA AATGCCCAGA CAGACAGGCG GGTTTTTTAG GCCTTGGTCC ATGGGGAAAG
1381  AAGCCCCGCA ATTTCCCCAT GGCTCAAGTG CATCAGGGGC TGATGCCAAC TGCTCCCCCA
1441  GAGGACCCAG CTGTGGATCT GCTAAAGAAC TACATGCAGT TGGGCAAGCA GCAGAGAGAA
1501  AAGCAGAGAG AAAGCAGAGA GAAGCCTTAC AAGGAGGTGA CAGAGGATTT GCTGCACCTC
1561  AATTCTCTCT TTGGAGGAGA CCAGTAGTGA CCGCCCACAT CGAGGGCCAG CCCGTGGAGG
1621  TGCTGCTGGA CACCGGCGCC GACGACTCCA TCGTGACCGG CATCGAGCTG GGCCCCCACT
1681  ACACCCCCAA GATCGTGGGC GGCATCGGCG GCTTCATCAA CACCAAGGAG TACAAGAACG
1741  TGGAGATCGA GGTGCTGGGC AAGAGGATCA AGGGCACCAT CATGACCGGC GACACCCCCA
1801  TCAACATCTT CGGCAGGAAC CTGCTGACCG CCCTGGGCAT GTCCCTGAAC TTCCCCATCG
1861  CCAAGGTGGA GCCCGTGAAG GTGGCCCTGA AGCCCGGCAA GGACGGCCCC AAGCTGAAGC
1921  AGTGGCCCCT GTCCAAGGAG AAGATCGTGG CCCTGAGGGA GATCTGCGAG AAGATGGAGA
1981  AGGACGGCCA GCTGGAGGAG GCCCCCCCCA CCAACCCCTA CAACACCCCC ACCTTCGCCA
2041  TCAAGAAGAA GGACAAGAAC AAGTGGAGGA TGCTGATCGA CTTCAGGGAG CTGAACAGGG
2101  TGACCCAGGA CTTCACCGAG GTGCAGCTGG GCATCCCCCA CCCCGCCGGC CTGGCCAAGA
2161  GGAAGAGGAT CACCGTGCTG GACATCGGCG ACGCCTACTT CTCCATCCCC CTGGACGAGG
2221  AGTTCAGGCA GTACACCGCC TTCACCCTGC CCTCCGTGAA CAACGCCGAG CCCGGCAAGA
2281  GGTACATCTA CAAGGTGCTG CCCCAGGGCT GGAAGGGCTC CCCCGCCATC TTCCAGTACA
2341  CCATGAGGCA CGTGCTGGAG CCCTTCAGGA AGGCCAACCC CGACGTGACC CTGGTGCAGT
2401  ACATGGACGA CATCCTGATC GCCTCCGACA GGACCGACCT GGAGCACGAC AGGGTGGTGC
2461  TCCAGTCCAA GGAGCTGCTG AACTCCATCG GCTTCTCCAC CCCCGAGGAG AAGTTCCAGA
2521  AGGACCCCCC CTTCCAGTGG ATGGGCTACG AGCTGTGGCC CACCAAGTGG AAGCTGCAAA
2581  AGATCGAGCT GCCCCAGAGG GAGACCTGGA CCGTGAACGA CATCCAGAAG CTGGTGGGCG
2641  TGCTGAACTG GGCCGCCCAG ATCTACCCCG GCATCAAGAC CAAGCACCTG TGCAGGCTGA
2701  TCAGGGGCAA GATGACCCTG ACCGAGGAGG TGCAGTGGAC CGAGATGGCC GAGGCCGAGT
2761  ACGAGGAGAA CAAGATCATC CTGTCCCAGG AGCAGGAGGG CTGCTACTAC CAGGAGGGCA
2821  AGCCCCTGGA GGCCACCGTG ATCAAGTCCC AGGACAACCA GTGGTCCTAC AAGATCCACC
2881  AGGAGGACAA GATCCTGAAG GTGGGCAAGT TCGCCAAGAT CAAGAACACC CACACCAACG
2941  GCGTGAGGCT GCTGGCCCAC GTGATCCAGA AGATCGGCAA GGAGGCCATC GTGATCTGGG
3001  GCCAGGTGCC CAAGTTCCAC CTGCCCGTGG AGAAGGACGT GTGGGAGCAG TGGTGGACCG
3061  ACTACTGGCA GGTGACCTGG ATTCCCGAGT GGGACTTCAT CTCCACCCCC CCCCTGGTGA
3121  GGCTGGTGTT CAACCTGGTG AAGGACCCCA TCGAGGGCGA GGAGACCTAC TACACCGACG
3181  GCTCCTGCAA CAAGCAGTCC AAGGAGGGCA AGGCCGGCTA CATCACCGAC AGGGGCAAGG
3241  ACAAGGTGAA GGTGCTGGAG CAGACCACCA ACCAGCAGGC CGAGCTGGAG GCCTTCCTGA
3301  TGGCCCTGAC CGACTCCGGC CCCAAGGCCA ACATCATCGT GGACTCCCAG TACGTGATGG
3361  GCATCATCAC CGGCTGCCCC ACCGAGTCCG AGTCCAGGCT GGTGAACCAG ATCATCGAGG
3421  AGATGATCAA GAAGTCCGAG ATCTACGTGG CCTGGGTGCC CGCCCACAAG GGCATCGGCG
3481  GCAACCAGGA GATCGACCAC CTGGTGTCCC AGGGCATCAG GCAGGTGCTG TTCCTGGAGA
3541  AGATCGAGCC CGCCCAGGAG GAGCACGACA AGTACCACTC CAACGTGAAG GAGCTGGTGT
3601  TCAAGTTCGG CCTGCCCAGG ATCGTGGCCA GGCAGATCGT GGACACCTGC GACAAGTGCC
3661  ACCAGAAGGG CGAGGCCATC CACGGCCAGG CCAACTCCGA CCTGGGCACC TGGCAGATGG
3721  ACTGCACCCA CCTGGAGGGC AAGATCATCA TCGTGGCCGT GCACGTGGCC TCCGGCTTCA
3781  TCGAGGCCGA GGTGATCCCC CAGGAGACCG GCAGGCAGAC CGCCCTGTTC CTGCTGAAGC
3841  TGGCCGGCAG GTGGCCCATC ACCCACCTGC ACACCGACAA CGGCGCCAAC TTCGCCTCCC
3901  AGGAGGTGAA GATGGTGGCC TGGTGGGCCG GCATCGAGCA CACCTTCGGC GTGCCCTACA
3961  ACCCCCAGTC CCAGGGCGTG GTGGAGGCCA TGAACCACCA CCTGAAGAAC CAGATCGACA
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4021  GGATCAGGGA GCAGGCCAAC TCCGTGGAGA CCATCGTGCT GATGGCCGTG CACTGCATGA
4081  ACTTCAAGAG GAGGGGCGGC ATCGGCGACA TGACCCCCGC CGAGAGGCTG ATCAACATGA
4141  TCACCACCGA GCAGGAGATC CAGTTCCAGC AGTCCAAGAA CTCCAAGTTC AAGAACTTCA
4201  GGGTGTACTA CAGGGAGGGC AGGGACCAGC TGTGGAAGGG CCCCGGCGAG CTGCTGTGGA
4261  AGGGCGAGGG CGCCGTGATC CTGAAGGTGG GCACCGACAT CAAGGTGGTG CCCAGGAGGA
4321  AGGCCAAGAT CATCAAGGAC TACGGCGGCG GCAAGGAGGT GGACTCCTCC TCCCACATGG
4381  AGGACACCGG CGAGGCCAGG GAGGTGGCCT AGTTTTTTTT GCGATCGCAA GCTT
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SEQ ID NO: 13 - Natural human IL-4

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1   ATG GGT CTC ACC TCC CAA CTG CTT CCC CCT CTG TTC TTC CTG CTA GCA TGT
    Met Gly Leu Thr Ser Gln Leu Leu Pro Pro Leu Phe Phe Leu Leu Ala Cys

52  GCC GGC AAC TTT GTC CAC GGA CAC AAG TGC GAT ATC ACC TTA CAG GAG ATC
    Ala Gly Asn Phe Val His Gly His Lys Cys Asp Ile Thr Leu Gln Glu Ile

103 ATC AAA ACT TTG AAC AGC CTC ACA GAG CAG AAG ACT CTG TGC ACC GAG TTG
    Ile Lys Thr Leu Asn Ser Leu Thr Glu Gln Lys Thr Leu Cys Thr Glu Leu

154 ACC GTA ACA GAC ATC TTT GCT GCC TCC AAG AAC ACA ACT GAG AAG GAA ACC
    Thr Val Thr Asp Ile Phe Ala Ala Ser Lys Asn Thr Thr Glu Lys Glu Thr

205 TTC TGC AGG GCT GCG ACT GTG CTC CGG CAG TTC TAC AGC CAC CAT GAG AAG
    Phe Cys Arg Ala Ala Thr Val Leu Arg Gln Phe Tyr His Glu Lys Asp Thr

256 GAC ACT CGC TGC CTG GGT GCG ACT GCA CAG CAG TTC CAC AGG CAC AAG CAG
    Arg Ser His Cys Leu Gly Ala Thr Ala Gln Gln Phe His Arg His Lys Gln

307 CTG ATC CGA TTC CTG AAA CGG CTC GAC AGG AAC CTC TGG GGC CTG GCG GGC
    Leu Ile Arg Phe Leu Lys Arg Leu Asp Arg Asn Leu Trp Gly Leu Ala Gly

358 TTG AAT TCC TGT CCT GTG AAG GAA GCC AAC CAG AGT ACG TTG GAA AAC TTC
    Leu Asn Ser Cys Pro Val Lys Glu Ala Asn Gln Ser Thr Leu Glu Asn Phe

409 TTG GAA AGG CTA AAG ACG ATC ATG AGA GAG AAA TAT TCA AAG TGT TCG AGC
    Leu Glu Arg Leu Lys Thr Ile Met Arg Glu Lys Tyr Ser Lys Cys Ser Ser

460 TGA
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SEQ ID NO: 14 - H-2K^{d} immuno-dominant CD8+ T cell epitope, $Gag_{197-205}$

AMQMLKETI