

## SEQUENCE LISTING

## SEQ ID NO:1 HBc

MDIDPYKEFG	ATVELLSFLP	SDFFPSVRDL	LDTASALYRE	ALESPEHCSP	HHTALRQAIL	60
CWGELMTLAT	WVGNNLEDPA	SRDLVVNYVN	TNMGKLKIRQL	LWFHISCLTF	GRETVLEYLV	120
SFGVWIRTPP	AYRPPNAPIL	STLPETTIVR	RRDRGRSPRR	RTPSPRRRRS	QSPRRRRSQS	180
RESQC						185

## SEQ ID NO:2 HBc mutant

MDIDPYKEFG	ATVELLSFLP	SDFFPSVRDL	LDTAAALYRD	ALESPEHCSP	HHTALRQAIL	60
CWGDLMTLAT	WVGTLNLEDG	KGGSRDVVVS	YVNTNVGLKF	RQLLWFHISC	LTFGRETVLE	120
YLVSGVWIR	TPPAYRPPNA	PILSTLPETT	VVRRDRGRS	PRRRTSPRR	RRSQSPRRR	180
SQSRESQC						188

## SEQ ID NO:3 Qbeta CP

AKLETVTTLGN	IGKDGKQTLV	LNPRGVNPTN	GVASLSQAGA	VPALRKRVT	SVSQPSRNRK	60
NYKVQVKIQN	PTACTANGSC	DPSVTRQAYA	DVTFSFTQYS	TDEERAFVRT	ELAALLASPL	120
LIDAIDQLNP	AY					132

## SEQ ID NO:4 Qbeta A1

MAKLETVTTLG	NIGKDGKQTL	VLNPRGVNPT	NGVASLSQAG	AVPALEKRVT	VSVSQPSRNR	60
KNYKVQVKIQ	NPTACTANGS	CDPSVTRQAY	ADVTFSTQY	STDEERAFVR	TELAALLASP	120
LLIDAIDQLN	PAYWTLIIAG	GGSGSKPDPV	IPDPIDPPP	GTGKYTCPFA	IWSLEEVYEP	180
PTKNRPWPIY	NAVELQPREF	DVALKDLLGN	TKWRDWD SRL	SYTTFRGCRG	NGYIDL DATY	240
LATDQAMRDQ	KYDIREGKKP	GAFGNIERFI	YLKSINAYCS	LSDIAAYHAD	GVIVGFWRDP	300
SSGGAIPDFD	TKFDKTKCPI	QAVIVVPRA				329

## SEQ ID NO:5 R17

ASNFTQFVLV	NDGGTGNVTV	APSNFANGVA	EWISSNSRSQ	AYKVTCSVRQ	SSAQNRKYTI	60
KVEVPKVAT	TVGGVELPVA	AWRSYLNME	TIPFATNSD	CELIVKAMQG	LLKDGNPIS	120
AIAANSIY						129

## SEQ ID NO:6 fr

MASNFEEFVL	VDNGGTGDVK	VAPSNFANGV	AEWISSNSRS	QAYKVTCSVR	QSSANNRKYT	60
VKVEVPKVAT	QVQGGVELPV	AAWRSYMNME	LTIPVFATND	DCALIVKALQ	GTFTGNPIA	120
TAIAANSIY						130

## SEQ ID NO:7 GA

MATLRSFVLV	DNGGTGNVTV	VPVSNANGVA	EWLSNNSRSQ	AYRVTASYRA	SGADKRKYAI	60
KLEVPKIVTQ	VVNGVELPGS	AWKAYASIDL	TIPFAATDD	VTVISKSLAG	LKVGNPPIAE	120
AISSQSGFYA						130

## SEQ ID NO:8 SP

MAKLNQVTLS	KIGKNGDQTL	TLTPRGVNPT	NGVASLSEAG	AVPALEKRVT	VSVQPSRNR	60
KNFKVQIKLQ	NPTACTRDAC	DPSVTRSAFA	DVTLSFTSYS	TDEERALIRT	ELAALLADPL	120
IVDAIDNLNP	AY					132

## SEQ ID NO:9 SP A1

AKLNQVTLSK	IGKNGDQTLT	LTPRGVNPTN	GVASLSEAGA	VPALRKRVT	SVAQPSRNRK	60
NFKVQIKLQN	PTACTRDACD	PSVTRSAFAD	VTLSTSYST	DEERALIRTE	LAALLADPLI	120
VDAIDNLNPA	YWAALLVASS	GGGDNPSPDP	VPVVPDVKPP	DGTGRYKCPF	ACYRLGSIYE	180
VGKEGSPDIY	ERGDEVSFTF	DYALEDFLGN	TNWRNWDQRL	SDYDIANRRR	CRGNGYIDL	240
ATAMQSDDFV	LSGRYGVKRV	KFPGAFGSIK	YLLNIQGDW	LDLSEVTAYR	SYGMVIGFWT	300
DSKSPQLPTD	FTQFNSANCP	VQTVIIIPS				329

## SEQ ID NO:10 MS2

MASNFTQFVL	VDNGGTGDVLT	VAPSNFANGV	AEWISSNSRS	QAYKVTCSVR	QSSAQNRKYT	60
IKVEVPKVAT	QTVGGVELPV	AAWRSYLNME	LTIPFATNS	DCALIVKAMQ	GLKDGNPPI	120
SAIAANSIY						130

## SEQ ID NO:11 M11

MAKLQAITLS	GIGKNGDVTL	DLNPRGVNPT	NGVAALSEAG	AVPALEKRVT	ISVSQPSRNR	60
KNYKVQVKIQ	NPTSCTASGT	CDPSVTRSAY	SDVTFSTQY	STVEERALVR	TELQALLADP	120
MLVNAIDNLN	PAY					133

## SEQ ID NO:12 MX1

MAKLQAITLS	GIGKNGDVTL	NLNPRGVNPT	NGVAALSEAG	AVPALEKRVT	ISVSQPSRNR	60
KNYKVQVKIQ	NPTSCTASGT	CDPSVTRSAY	ADVTFSTQY	STDEERALVR	TELKALLADP	120
MLIDAIDNLN	PAY					133

## SEQ ID NO:13 NL95

MAKLNKVTLT	GIGKAGNQTL	TLTPRGVNPT	NGVASLSEAG	AVPALEKRVT	VSVAPQSRNR	60
KNYKVQIKLQ	NPTACTKDAC	DPSVTRSGSR	DVTLSFTSYS	TERERALIRT	ELAALLKDDL	120
IVDAIDNLNP	AYWAALLAAS	PGGGNNPYPG	VPDSPNVKPP	GGTGTYRCPF	ACYRRGELIT	180
EAKDGACALY	ACGSEALVEF	EYALEDFLGN	EFWRNWDGRL	SKYDIETHRR	CRGNGYVDLD	240
ASVMQSDEYV	LSGAYDVVKM	QPPGTFDSPR	YYLHLMGDIY	VDLAEVTAYR	SYGMVIGFWT	300
DSKSPQLPTD	FTRFNRHNCP	VQTVIVIPSL				330

## SEQ ID NO:14 f2

ASNFTQFVLV	NDGGTGNVTV	APSNFANGVA	EWISSNSRSQ	AYKVTCSVRQ	SSAQNRKYTI	60
KVEVPKVATQ	TVGGVELPVA	AWRSYLNLEL	TIPIFATNSD	CELIVKAMQG	LLKDGNPIS	120
AIAANSIGIY						129

## SEQ ID NO:15 PP7

MSKTIVLSVG	EATRILTETI	Q	STADRQIFEE	KVGPLVGRRL	LTASLRQNGA	KTAYRVNLKL	60
DQADVVDCT	SVCGELPKVR	YTQVWSDVT	IVANSTEASR	KSPLYDLTKSL	VATSQVEDLV		120
VNLVPLGR							128

## SEQ ID NO:16 Qbeta-240

AKLETVTTLGN	IGRDGKQTLV	LNPRGVNPTN	GVASLSQAGA	VPALAKRVTV	SVSQPSNRK	60
NYKVQVKIQN	PTACTANGSC	DPSVTRQKYA	DVTFSFTQYS	TDEERAFVRT	ELAALLASPL	120
LIDAIDQLNP	AY					132

## SEQ ID NO:17 Qbeta-243

AKLETVTTLGK	IGKDGKQTLV	LNPRGVNPTN	GVASLSQAGA	VPALAKRVTV	SVSQPSNRK	60
NYKVQVKIQN	PTACTANGSC	DPSVTRQKYA	DVTFSFTQYS	TDEERAFVRT	ELAALLASPL	120
LIDAIDQLNP	AY					132

## SEQ ID NO:18 Qbeta-250

ARLETVTTLGN	IGRDGKQTLV	LNPRGVNPTN	GVASLSQAGA	VPALAKRVTV	SVSQPSNRK	60
NYKVQVKIQN	PTACTANGSC	DPSVTRQKYA	DVTFSFTQYS	TDEERAFVRT	ELAALLASPL	120
LIDAIDQLNP	AY					132

## SEQ ID NO:19 Qbeta-251

ARLETVTTLGN	IGRDGKQTLV	LNPRGVNPTN	GVASLSQAGA	VPALAKRVTV	SVSQPSNRK	60
NYKVQVKIQN	PTACTANGSC	DPSVTRQKYA	DVTFSFTQYS	TDEERAFVRT	ELAALLASPL	120
LIDAIDQLNP	AY					132

## SEQ ID NO:20 Qbeta-259

ARLETVTTLGN	IGKDGKQTLV	LNPRGVNPTN	GVASLSQAGA	VPALAKRVTV	SVSQPSNRK	60
NYKVQVKIQN	PTACTANGSC	DPSVTRQKYA	DVTFSFTQYS	TDEERAFVRT	ELAALLASPL	120
LIDAIDQLNP	AY					132

## SEQ ID NO:21 AP205

MANKPMQPIT	STANKIVWSD	PTLSTTFSA	SLLRQRVKVG	IAELNNVSGQ	YVSVYKRPAP	60	
KPEGCADACV	IMPENQSI	R	TVISGSAENL	ATLKAEWETH	KRNVDTLFAS	GNAGLGFLDP	120
TAAIVSSDTT	A						131

## SEQ ID NO:22 AP205 P5T

MANKTMQPIT	STANKIVWSD	PTLSTTFSA	SLLRQRVKVG	IAELNNVSGQ	YVSVYKRPAP	60	
KPEGCADACV	IMPENQSI	R	TVISGSAENL	ATLKAEWETH	KRNVDTLFAS	GNAGLGFLDP	120
TAAIVSSDTT	A						131

## SEQ ID NO:23 AP205 N14D

MANKPMQPIT	STADKIVWSD	PTLSTTFSA	SLLRQRVKVG	IAELNNVSGQ	YVSVYKRPAP	60	
KPEGCADACV	IMPENQSI	R	TVISGSAENL	ATLKAEWETH	KRNVDTLFAS	GNAGLGFLDP	120
TAAIVSSDTT	A						131

## SEQ ID NO:24 IL1alpha1

atatatgcta	gcccccttaca	cctaccagag	tgatttg			37
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## SEQ ID NO:25 IL1alpha2

atatatctcg	agtgatatct	ggaagtctgt	catagag			37
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## SEQ ID NO:26 ILbeta1

atatatgcta	gccccatta	gacagctgca	ctacagg			37
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## SEQ ID NO:27 ILbeta2

atatatctcg	agggaagaca	cagattccat	ggtgaag			37
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## SEQ ID NO:28 cystein containing linker

GGGGGCG

7

## SEQ ID NO:29 pModEC1

acatcgatata	acgtttactgg	tttcacattc	accaccctga	attgactctc	ttccggggcg	60
tatcatgccca	taccgcgaaa	ggtttttgcg	cattcgatgg	tgccgggat	ctcgacgctc	120
tcccttatgc	gactcctgca	ttaggaagca	gccagtagt	aggttgaggc	cggtgagcac	180
cgccgcccga	aggaatggtg	catgcaagga	gatggcgccc	aacagtcccc	cgccacgggg	240
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## SEQ ID NO:30 primerMCS-1F

```
tatggatcgg gctagcgctc gaggggttaa acggcgggccg cat 43
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## SEQ ID NO:31 primerMCS-1R

```
tcgaatgcgg ccgccgttta aaccctcgag cgctagccgg atcca 45
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## SEQ ID NO:32 Bamhis6-EK-Nhe-F

```
gatccacacc accaccacca ccacggttct ggtgacgacg atgacaaagc gctagccc 58
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## SEQ ID NO:33 Bamhis6-EK-Nhe-R

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tcgagggcta gcgctttgtc atcgctcgta ccagaaccgt ggtgggtgtg gtgggtgtg 58
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## SEQ ID NO:34 oligo1F-C-glycine-linker

```
tcgaggggtg tggtgggtgg tgccgttaat aagtttaaac gc 42
```

## SEQ ID NO:35 oligo1R-C-glycine-linker

```
ggccgcgttt aaacttatta accgcaacca ccaccaccac cc 42
```

## SEQ ID NO:36 HIL-1 alpha

```

MAKVPDMFED LKNCYSENEE DSSSIDHLSL NQKSFYHVSY GPLHEGCMQ SVLSISSETS 60
KTSKLTFFKES MVVVATNGKV LKKRRLSLSQ SITDDLEAI ANDSEEEI IK PRSSPFSFSL 120
NVKYNFMRII KYEFILNDAL NQSIIRANDQ YLTAAALHNL DEAVKFDMDGA YKSSKDDAKI 180
TVILRISKQ LYVTAQDEDQ PVLLKEMPEI PKTITGSETN LFFFWETHGT KNYFTSVAHP 240
NLFIATKQDY WVCLAGGPPS ITDFQILENQ A 271

```

## SEQ ID NO:37 IL-1 alpha Macaca

```

MAKVPDMFED LKNCYSENEE DSSSIDHLSL NQKSFYDVSY GPLHEGCMQ SVLSISEIS 60
KTSKLTFFKES MVVVSTNGKV LKKRRLSLSQ SITDNLEAI ANDSEEEI IK PRSAPFSFSL 120
NMTYHFIRII KHEFILNDTL NQTIIRANDQ HLTAALHNL DEAVKFDMDGA YTSSKDDTKV 180
PVILRISKQ LYVSAQDEDQ PVLLKEMPEI NKTITGSETN FLFFWETHGT KNYFISVAHP 240
NLFIATKHND WVCLAKGLPS ITDFQILENQ A 271

```

## SEQ ID NO:38 IL-1 alpha Equus

```

MAKVPDLFED LKNCYSENEE YSSEIDHLSL TQKSFYDASY DPLPEDCMDT FMSLTSETS 60
KTSKLNFKES VVLVAANGKT LKKRRLSLNQ FITDDLEAI ANDPEEGIR PRSVHYNFQS 120
NTKYNFMRII NHQCTLNDAL NQSVIRDTSG QYLATAALNN LDDAVKFDMDG AYTSEEDSQL 180
PVTLRISKTR LFVSAQNEDE PVLLKEMPDT PKTIKDETNL LFFWERHGSK NYFKSVAHPK 240
LFIATKQGKL VHMARGQPSI TDFQILDNQF 270

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## SEQ ID NO:39 IL-1 alpha Ovis

```

MAKVPDLFED LKNCYSENEE YSSEIDHLSL NQKSFYDASY EPLREDHMK FMSLDTSETS 60
KTSRLSFKEN VMMMTANGKI LKKRRLSLNQ FITDDLEAI ANDTEEEI IK PRSAHYSFQS 120
NVKYNFMRII HQECILNDAL NQSIIRDMSG PYLTAATLNN LEEAVKFDMDV AYVSEEDSQL 180
PVTLRISKQ LFVSAQNEDE PVLLKEMPET PKIIKDETNL LFFWEKHGSM DYFKSVAHPK 240
LFIATKQEK VHMASGPPSI TDFQILEK 268

```

## SEQ ID NO:40 IL-1 alpha Felis

```
MAKVPDLFED LKNCYSENEE YSSEIDHLSL NQKSFYDASY DPLHEDCTDK FMSPSTSETS 60
```

KTPQLTLKKS	VVMVAANGKI	LKKRRLSLNQ	FLTADDLEAI	ANEVEEEEIMK	PRSVAPNFYS	120
SEKYNYQKII	KSQFILNDNL	SQSVIRKAGG	KYLAAAALQN	LDDAVKFDMG	AYTSKEDSKL	180
PVTLRISKTR	LFVSAQNEDE	PVLLKEMPET	PKTIRDETNL	LFFWERHGSK	NYFKSVAHPK	240
LFIATQEEQL	VHMARGLPSV	TDFQILETQS				270

## SEQ ID NO:41 IL-1 alpha Bos

MAKVPDLFED	LKNCSYSENEE	YSSEIDHLSL	NQKSFYDASY	EPLREDQMKN	FMSLDTSETS	60
KTSKLSFKEN	VVMVAASGKI	LKKRRLSLNQ	FITDDDLLEAI	ANNTEEEIHK	PRSAHYSFQS	120
NVKYNFMRV	HQECILNDAL	NQSIIRDMSG	PYLTTATLNN	LEEAVKFDMV	AYVSEEDSQL	180
PVTLRISKTR	LFVSAQNEDE	PVLLKEMPET	PKTIKDETSL	LFFWEKHGSM	DYFKSVAHPK	240
LFIATKQEK	VHMASGPPSI	TDFQILEK				268

## SEQ ID NO:42 IL-1 alpha Sus

MAKVPDLFED	LKNCSYSENEE	YSSDIDHLSL	NQKSFYDASY	EPLPGDGMDK	FMPLSTSKTS	60
KTSRLNFKDS	VVMAAANGKI	LKKRRLSLNQ	FITDDDLLEAI	ANDTEEEIHK	PRSATYSFQS	120
NMKYNFMRV	NHQCILNDAL	NQSLVRDPSG	QYLMAAVLNN	LDEAVKFDMA	AYTSNDDSQL	180
PVTLRISETR	LFVSAQNEDE	PVLLKELPET	PKTIKDETSL	LFFWEKHGSM	DYFKSAAHPK	240
LFIATRQEK	VHMAPGLPSV	TDFQILENQS				270

## SEQ ID NO:43 IL-1 alpha Oryctolagus

MAKVPDLFED	LKNCSYSENEE	YSSAIDHLSL	NQKSFYDASY	EPLHEDCMNK	VVSLSTSETS	60
VSPNLTFQEN	VVAVTASGKI	LKKRRLSLNQ	PITDDDLLEAI	VSDPEEGIIK	PRSVPYTFQR	120
NMRYKYLRII	KQEFFLNDAL	NQSLVRDPSG	QYLRAAPLQN	LGDVAVKFDMG	VYMTSKEDSI	180
LPVTLRISQT	PLFVSAQNEDE	EPVLLKEMPE	TPRIITDSES	DILFFWETQG	NKNYFKSAAN	240
PQLFIATKPE	HLVHMARGLP	SMTDFQIS				268

## SEQ ID NO:44 IL-1 alpha Canis

MAKVPDLFED	LKNCSYSENEE	YSSEIDHLSL	NQKSFYDMSC	DPLHEDCMSL	STSEISKTSQ	60
LTFKENVVVV	AANGKILKKR	RLSLSQFITD	DDLEGIANDT	EEVIMKPRSV	AYNFHNNEKY	120
NYIRIIKSQF	ILNDNLNQSI	VRQTGGNYLM	TAALQNLDDA	VKFDMGAYTS	EDSKLPVTLR	180
ISKTRLFVSA	QNEDEPVLLK	EMPETPKTIR	DETNLFFWE	RHGSKHYFYS	VAQPKLFIAT	240
QERKLVMAR	GQPSITDFRL	LETQP				265

## SEQ ID NO:45 IL-1 alpha Mus

MAKVPDLFED	LKNCSYSENEE	YSSAIDHLSL	NQKSFYDASY	GSLHETCTDQ	FVSLRTSETS	60
KMSNFTFKES	RVTVSATSSN	GKILKKRRLS	FSETFTEDDL	QSITHDLEET	IQPRSAPTY	120
QSDLRYLKLM	LVRQKFVMND	SLNQTIYQDV	DKHYLSTTWL	NDLQEVKFD	MYAYSSGGDD	180
SKYPVTLKIS	DSQLFVSAQG	EDQPVLLKEL	PETPKLITGS	ETDLIFFWKS	INSKNYFTSA	240
AYPELFIATK	EQSRVHLARG	LPSMTDFQIS				270

## SEQ ID NO:46 IL-1 alpha Rattus

MAKVPDLFED	LKNCSYSENEE	YSSAIDHLSL	NQKSFYDASY	GSLHENCTDK	FVSLRTSETS	60
KMSTFTFKES	RVVVSATSNK	GKILKKRRLS	FNQPTFTEDDL	EAIAHDLEET	IQPRSAHPSF	120
QNNLRYKLIR	IVKQEFIMND	SLNQNIYVDM	DRIHLKAASL	NDLQEVKFD	MYAYSSGGDD	180
SKYPVTLKVS	NTQLFVSAQG	EDKPVLLKEI	PETPKLITGS	ETDLIFFWEK	INSKNYFTSA	240
AFPELLIATK	EQSQVHLARG	LPSMIDFQIS				270

## SEQ ID NO:47 IL-1 alpha Gorilla

KNCYSENEED	SSSIDHLSLN	QKSFYHVTYG	PLHEGCMQDS	VSLSISETSK	TSKLTFKESM	60
VVVATNGKVL	KRRRLSLSQS	ITDDDLLEAIA	NDSEEEIHKP	RSAPFSFLSN	VKYNFMRIIK	120
NEFILNDALN	QSIIRANDQY	LTAAALHNLD	EA			152

## SEQ ID NO:48 hIL-1 alpha Cavia

FEDLKNCSYSE	NEEYASAIH	LSLNQKSFYD	TNYDPLHENR	VDEPVSPNPY	ENSEESNFTL	60
EDSSDSSAVV	LTSAGGEVLK	KRRRLSLNQTM	SNEDLEAIA	DSEEEIIEPW	SVPSYFQSNL	120
KFKYQRSIKK	GAVITDAMHQ	SLIRESNGQH	LKAMHVVDK	HEVKFDIDGY	VSTATRIRPV	180
TLKISKTQLY	VCAQEEGQPV	LLKE				204

## SEQ ID NO:49 hIL-1 beta

MAEVPDLASE	MMAYYSGNED	DLFFEADGPK	QMKCSFQDLD	LCPLDGGIQL	RISDHHYSKG	60
FRQAASVVVA	MDKLRMLVP	CPQTFQENDL	STFFPFIFEE	EPIFFDTWDN	EAYVHDAPVR	120
SLNCTLRDSQ	QKSLVMSGPY	ELKALHLQGQ	DMEQQVVFMS	SFVQGEESND	KIPVALGLKE	180
KNLYLSCVLK	DDKPTLQLES	VDPKNYPKKK	MEKRFVFNKI	EINNKLFEFS	AQFPNWIIST	240
SQAENMPVFL	GGTKGGQDIT	DFTMQFVSS				269

## SEQ ID NO:50 IL-1 beta Pan

MLVPCPQTFQ	ENDLSTFFPF	IFEEPIFFD	TWENEAYVHD	APVRSNLCTL	RDSQQKSLVM	60
SGPYELKALH	LQGQDMEQQV	VFSMSFVQGE	ESNDKIPVAL	GLKEKNLYLS	CVLKDDKPTL	120
QLESVDPKNY	PKKKMEKRFV	FNKIEINNKL	EFESAQFPNW	YISTSQAENM	PVFLGGTKGG	180
QDITDFTMQF	VSS					193

## SEQ ID NO:51 IL-1 beta Macaca

MAEVPPELASE	MMAYYSGNED	DLFFDVGDPK	QMKCSFQDLD	LCPLGGGIQL	QISHEHYNEG	60
FRQAVSVVVA	MEKLRKMLVP	CPQIFQDNDL	STLIPFIFEE	EPVFLDTRNN	DACVHDAPVR	120
SLHCTLRDAQ	LKSLVMSGPY	ELKALHLQGG	DLEQQVVFMS	SFVQGEESND	KIPVALGLKA	180
KNLYLSCVLK	DDKPTLQLES	VDPKNYPKKK	MEKRFVFNKI	EINNKFES	AQFPNWIIST	240
SQAENMPVFL	GGTRGGQDIT	DFTMQFVSS				269

## SEQ ID NO:52 IL-1 beta Oryctolagus

MATVPELTSE	MMAYHSGNEN	DLFFEADGPN	YMKSCFQDLD	LCCPDEGIQL	RISCQPYNKS	60
FRQVLSVVVA	LEKLRQKAVP	CPQAFQDDGL	RTFFSLIFEE	EPVLCNTWDD	YSLECDAVRS	120
LHCRLQDAQQ	KSLVLSGTY	LKALHLNAEN	LNQQVVFMS	FVQGEESNDK	IPVALGLRGK	180
NLYLSCVMKD	DKPTLQLESV	DPNRYPKKKM	EKRFEVFNKIE	IKDKLEFESA	QFPNWIISTS	240
QTEYMPVFLG	NNSGGQDLID	FSMEFVSS				268

## SEQ ID NO:53 IL-1 beta Mus

MATVPELNCE	MPPFDSDEND	LFFEVDGPKQ	MKGCFQTFDL	GCPDESIQLQ	ISQQHINKSF	60
RQAVSLIVAV	EKLWQLPVSF	PWTFQDEDM	TFFSFIFEEE	PILCDSWDDD	DNLLVCDVPI	120
RQLHYRLRDE	QKSLVLSDP	YELKALHLNG	QNINQQVIFS	MSFVQGEPSN	DKIPVALGLK	180
GKNLYLSCVM	KDGTPTLQLE	SVDPKQYPKK	KMEKRFVFNK	IEVKSKEFEF	SAEFPNWIIS	240
TSQAEHKPVF	LGNNSGQDII	DFTMESVSS				269

## SEQ ID NO:54 IL-1 beta Rattus

MATVPELNCE	IAAFDSEEND	LFFEADRPQK	IKDCFQALDL	GCPDESIQLQ	ISQQHLDKSF	60
RKAVSLIVAV	EKLWQLPMSC	PWSFQDEDP	TFFSFIFEEE	PVLCDSWDDD	DLVCDVPIR	120
QLHCRRLRDE	QKCLVLSDP	ELKALHLNGQ	NISQQVVFMS	SFVQGETSND	KIPVALGLKG	180
LNLYLSCVMK	DGTPTLQLES	VDPKQYPKKK	MEKRFVFNKI	EVKTKVEFES	AQFPNWIIST	240
SQAEHRPVFL	GNSNGRDIIV	FTMEPVSS				268

## SEQ ID NO:55 IL-1 beta Equus

MAAVPDTSDM	MTYCSGNEND	LFFEEDGPKQ	MKGSFQDLDL	SSMGNGGIQL	QFSHQLYNKT	60
FKHVSVIIVA	MEKLRKIPVP	CSQAFQDDDL	RSLSFVIFEE	EPIICDNWDD	DYVCDAAVHS	120
VNCRRLDIYH	KSLVLSGACE	LQAVHLNGEN	TNQQVVFMS	FVQGEETDK	IPVALGLKEK	180
NLYLSCGMKD	GKPTLQLETV	DPNTYPKRKM	EKRFEVFNKME	IKGNVEFESA	MYPNWIISTS	240
QAEKKPVFLG	NTRGGRDITD	FIMEITSA				268

## SEQ ID NO:56 IL-1 beta Felis

MAPVPELTSE	MMAYSDEND	LFFEADGPEK	MKGSLLQNL	SFLGDEGIQL	QISHQPDNKS	60
LRHAVSVIVA	MEKLRKISFA	CSQPLQDEDL	KSLFCCIFEE	EPIICDTWDD	GFVCDAAIIS	120
QDYTFRDISQ	KSLVLSGSYE	LRLHLNGQN	MNQQVVFMS	FVHGEENSCK	IPVVLICIKK	180
NLYLSCVMKD	GKPTLQLEML	DPKVYPKKKM	EKRFEVFNKTE	IKGNVEFESS	QFPNWIISTS	240
QAEEMPVFLG	NTKGGQDITD	FIMESAS				267

## SEQ ID NO:57 IL-1 beta Sus

MATVPEPAKE	VMANNGDNNN	DLFFEADGPK	EMKCRQNL	LSPLGDGSIQ	LQISHQLCNE	60
SSRPMVSIV	AKEEPMNPSS	QVVCDDDPKS	IFSSVFEEEP	IVLEKHANGF	LCDATPVQSV	120
DCKLQDKDEK	ALVLAGPHEL	KALHLKGD	KREVFVCMF	VQGDSDDKI	PVTLGKGN	180
LYLSCVMKDD	TPTLQLEDVD	PKSYPKRME	KRFVFKTEI	KNRVEFESAL	YPNWIISTSQ	240
AEQKPVFLGN	SKGRQDITDF	TMEVLSP				267

## SEQ ID NO:58 IL-1 beta Cavia

MAAVPELSSE	VTAYHSDENE	LFFEVDGPNK	MQYCFQDRDL	CSLDEGIKLQ	ISHQHFNKSF	60
RQTVSLIVAV	EKLRLKAPC	TWAFQDDDL	PLLPFIFEEE	PIVCDTWDEE	YESDTPVPSR	120
NCTLHDIQHK	KLVLSDPCEL	KALHLNGDNL	NRQVVFMSF	VQGERSDNKM	PVALGLKGN	180
LYLSCVMKDG	KPVQLLESVD	GKQYPKKME	KRFVFNKITS	KSTVEFESAQ	FPNWIISTSQ	240
AEHKPVFLGN	NNGQDIIDFK	LELVSS				266

## SEQ ID NO:59 IL-1 beta Bos

MATVPEPINE	MMAYSDENE	LLFEADDPKQ	MKSCIQHLDL	GSMGDGNIQL	QISHQFYNKS	60
FRQVSVVIVA	MEKLRNSAY	HVFHDDDLRS	ILSFIFEEEP	VIFETSSDEF	LCDAVPVQSIK	120
CKLQDREQKS	LVLASPCVLK	ALHLLSQEMN	REVVFVCMF	QGEERDNKIP	VALGIKDKNL	180
YLSCVKKGDT	PTLQLEEDVD	KVYPKRMEK	RFVFKTEIK	NTVEFESVLY	PNWIISTSQI	240
EERPVLGHF	RGQDITDFR	METLSP				266

## SEQ ID NO:60 IL-1 beta Ovis

MATVPEPINE	VMAYSDENE	LLFEVDGPKQ	MKSCQHLDL	GSMGDGNIQL	QISHQLYNKS	60
FRQVSVVIVA	MEKLRNSAY	HVFRDDDLRS	ILSFIFEEEP	VIFETSSDEL	LCDAAVQSVK	120
CKLQDREQKS	LVLDSPCVLK	ALHLLSQEMS	REVVFVCMF	QGEERDNKIP	VALGIRDKNL	180
YLSCVKKGDT	PTLQLEEDVD	KVYPKRMEK	RFVFKTEIK	NTVEFESVLY	PNWIISTSQI	240
EELPVFLGRF	RGQDITDFR	METLSP				266

## SEQ ID NO:61 IL-1 beta Gallus

MAFVPDLVDVL	ESSSLSEETF	YGPSCLCCLQK	KPRLDSEHTT	VDVQVTVRKG	RGARSFERRAA	60
VLVVAMTKLL	RRPRSDFAD	SDLSALLEEV	FEPVTFQRLE	SSYAGAPAFR	YTRSQSFDIF	120
DINQKCFVLE	SPTQLVALHL	QGPSSSQKVR	LNIALYRPRG	PRGSAGTGQM	PVALGIKGYK	180
LYMSCVMSGT	EPTLQLEEAD	VMRDIDSVEL	TRFIFYRLDS	PTEGTTTFES	AAFPGWFICT	240
SLQPRQPVGI	TNQPDQVNIA	TYKLSGR				267

## SEQ ID NO:62 IL-1 beta Canis

GPGGSNVKCC	CQDLNHSSLV	DEGIQLQVSH	QLCNKSLRHF	VSVIVALEKL	KKPCPQVLQE	60
DDLKSIFCYI	FEETPIICKT	DADNFMSDAA	MQSVDCKLQD	ISHKYLVLNS	SYELRALHLN	120
GENVNKA						127

## SEQ ID NO:63 hIL-1 alpha 119-271

LSNVKYNFMR	IIKYEFILND	ALNQSIIRAN	DQYLTAALH	NLDEAVKFDM	GAYKSSKDDA	60
KITVILRISK	TQLYVTAQDE	DQPVLLKEMP	EIPKTITGSE	TNLLFFWETH	GTKNYFTSVA	120
HPNLFIAATKQ	DYWVCLAGGP	PSITDFQILE	NQA			153

## SEQ ID NO:64 hIL-1 beta 117-269

APVRSLNCTL	RDSQQKSLVM	SGPYELKALH	LQQQDMEQQV	VFSMSFVQGE	ESNDKIPVAL	60
GLKEKNLYLS	CVLKDDKPTL	QLESVDPKNY	PKKKMEKRFV	FNKIEINNKL	EFESAQFPNW	120
YISTSQAENM	PVFLGGTKGG	QDITDFTMQF	VSS			153

## SEQ ID NO:65 mIL-1alpha117-270

MDPHHHHHHG	SGDDDDKALA	PITYQSDLRV	KLMKLVRQKF	VMNDSLNTI	YQDVKHYLS	60
TTWLNDLQQE	VKFDYAYSS	GGDDSKYPVT	LKISDSQLFV	SAQGEDQPVL	LKELPETPKL	120
ITGSETDLIF	FWKSINSKNY	FTSAAYPELF	IATKEQSRVH	LARGLPSMTD	FQISLEGGGG	180
GCG						183

## SEQ ID NO:66 mIL-1beta119-269

MDPHHHHHHG	SGDDDDKALA	PIRQLHYRLR	DEQQKSLVLS	DPYELKALHL	NGQNINQQVI	60
FMSFVQGE	SNDKIPVALG	LKGNLYLSC	VMKDGTPTLQ	LESVDPKQYP	KKKMEKRFVF	120
NKIEVKSKVE	FESAEPFNWY	ISTSQAEHKP	VFLGNNSQD	IIDFTMESVS	SLEGGGGGCG	180

## SEQ ID NO:67 hIL-1 alpha 009-020

MRIIKYEFIL	ND					12
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## SEQ ID NO:68 hIL-1 alpha 010-015

RIIKYE						6
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## SEQ ID NO:69 hIL-1 alpha 014-023

YEFILNDALN						10
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## SEQ ID NO:70 hIL-1 alpha 019-030

NDALNQSIIR	AN					12
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## SEQ ID NO:71 hIL-1 alpha 035-044

TAAALHNLDE						10
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## SEQ ID NO:72 hIL-1 alpha 035-046

TAAALHNLDE	AV					12
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## SEQ ID NO:73 hIL-1 alpha 045-054

AVKFDMGAYK						10
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## SEQ ID NO:74 hIL-1 alpha 052-062

AYKSSKDDAK	I					11
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## SEQ ID NO:75 hIL-1 alpha 055-084

SSKDDAKITV	ILRISKTYLY	VTAQDEDQPV	L			31
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## SEQ ID NO:76 hIL-1 alpha 063-075

VILRISKTYL	YVT					13
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## SEQ ID NO:77 hIL-1 alpha 063-084

VILRISKTYL	YVTAQDEDQPV	VL				22
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## SEQ ID NO:78 hIL-1 alpha 069-089

TQLYVTAQDE	DQPVLLKEMP					20
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## SEQ ID NO:79 hIL-1 alpha 082-102

PVLLKEMPEI PKTITGSETN L	21
SEQ ID NO:80 hIL-1 alpha 087-100 EMPEIPKTIT GSET	14
SEQ ID NO:81 hIL-1 alpha 093-104 KTITGSETNL LF	12
SEQ ID NO:82 hIL-1 alpha 093-113 PKTITGSETN LLFFWETHGT K	21
SEQ ID NO:83 hIL-1 alpha 097-106 GSETNLLFFW	10
SEQ ID NO:84 hIL-1 alpha 123-134 LFIATKQDYW VC	12
SEQ ID NO:85 hIL-1 alpha 124-136 FIATKQDYWV CLA	13
SEQ ID NO:86 hIL-1 alpha 125-142 IATKQDYWVC LAGGPPSI	18
SEQ ID NO:87 hIL-1 alpha 129-133 KQDYW	5
SEQ ID NO:88 hIL-1 alpha 147-153 QILENQA	7
SEQ ID NO:89 hIL-1 beta 001-006 APVRSL	6
SEQ ID NO:90 hIL-1 beta 001-012 APVRSLNCTL RD	12
SEQ ID NO:91 hIL-1 beta 006-015 LNCTLRDSQQ	10
SEQ ID NO:92 hIL-1 beta 011-022 RDSQQKSLVM SG	12
SEQ ID NO:93 hIL-1 beta 027-038 KALHLQGQDM EQ	12
SEQ ID NO:94 hIL-1 beta 027-040 KALHLQGQDM EQQV	14
SEQ ID NO:95 hIL-1 beta 039-048 QVVFMSFVQ	10
SEQ ID NO:96 hIL-1 beta 046-056 FVQGEESNDK I	11
SEQ ID NO:97 hIL-1 beta 049-080 GEESNDKIPV ALGLKEKNLY LSCVLKDDKP TL	32
SEQ ID NO:98 hIL-1 beta 058-070 VALGLKEKNL YLS	13
SEQ ID NO:99 hIL-1 beta 058-080 VALGLKEKNL YLSCVLKDDK PTL	23
SEQ ID NO:100 hIL-1 beta 066-085 KNLYLSCVLK DDKPTLQLES V	21
SEQ ID NO:101 hIL-1 beta 078-097 PTLQLESVDP KNYPKKKMEK	20



SEQ ID NO:102 hIL-1 beta 083-095 ESVDPKNYPK KKM	13
SEQ ID NO:103 hIL-1 beta 088-099 KNYPKKKMEK RF	12
SEQ ID NO:104 hIL-1 beta 092-101 KKKMEKRFFV	10
SEQ ID NO:105 hIL-1 beta 092-109 KKKMEKRFFV NKIEINN	18
SEQ ID NO:106 hIL-1 beta 120-133 WYISTSQAEN MPVF	14
SEQ ID NO:107 hIL-1 beta 121-135 YISTSQAENM PVFLG	15
SEQ ID NO:108 hIL-1 beta 122-143 ISTSQAENMP VFLGGTKGGQ DI	22
SEQ ID NO:109 hIL-1 beta 126-131 QAENMP	6
SEQ ID NO:110 hIL-1 beta 147-152 TMQFVSS	7
SEQ ID NO:111 mIL-1 beta 001-012 VPIRQLHYRL RD	12
SEQ ID NO:112 mIL-1 beta 027-040 KALHLNGQNI NQQV	14
SEQ ID NO:113 mIL-1 beta 121-135 YISTSQAENM PVFLG	15
SEQ ID NO:114 rIL-1 beta 066-085 NLYLSCVMKD GTPTLQLESV	20
SEQ ID NO:115 rIL-1 beta 078-097 PTLQLESVDP KQYPKKKMEK	20
SEQ ID NO:116 rIL-1 beta 122-143 ISTSQAENMP VFLGNSNGRD IV	22
SEQ ID NO:117 AP590 atggcaaaata agccaatgca accgatcaca tctacagcaa ataaaattgt gtggtcggat ccaactcgtt tatcaactac attttcagca agtctgttac gccaacgtgt taaagttggt atagccgaac tgaataatgt ttcaggtcaa tatgtatctg tttataagcg tcctgcacct aaaccggaag gttgtgcaga tgccgtgtgc attatgccga atgaaaacca atccattcgc acagtgattt cagggtcagc cgaaaacttg gctaccttaa aagcagaatg ggaaactcac aaacgtaacg ttgacacact cttcgcgagc ggcaacgccg gtttgggttt ccttgaccct actgcccgtc tcgtatcgtc tgatactact gcttagggat ccggataatg catctaagct t	60 120 180 240 300 360 420 421
SEQ ID NO:118 AP592 atggcaaaata agccaatgca accgatcaca tctacagcaa ataaaattgt gtggtcggat ccaactcgtt tatcaactac attttcagca agtctgttac gccaacgtgt taaagttggt atagccgaac tgaataatgt ttcaggtcaa tatgtatctg tttataagcg tcctgcacct aaaccggaag gttgtgcaga tgccgtgtgc attatgccga atgaaaacca atccattcgc acagtgattt cagggtcagc cgaaaacttg gctaccttaa aagcagaatg ggaaactcac aaacgtaacg ttgacacact cttcgcgagc ggcaacgccg gtttgggttt ccttgaccct actgcccgtc tcgtatcgtc tgatactact gcttagggat ccggataatg catctaagct t	60 120 180 240 300 360 420 421
SEQ ID NO:119 p1.44 nnccatggca aataagccaa tgcaaccg	28

SEQ ID NO:120 pINC-36	
gtaagcttag atgcattatc cggatcccta agcagtagta tcagacgata cg	52
SEQ ID NO:121 pINC-40	
gtaagcttag atgcattatc cggatcccta agcagtagta tcagacgata cg	52
SEQ ID NO:122 pINC-34	
ggcccgagc gctagccct tacac	25
SEQ ID NO:123 pINC-35	
gtaagcttat gcattatgat atctggaagt ctgtcataga	40
SEQ ID NO:124 HIL-1	
atatatgata tccctgtacg atcactgaac tgcacg	36
SEQ ID NO:125 HIL-2	
atatatctcg aggggaagaca caaattgcat ggtgaag	37
SEQ ID NO:126 42-1	
tatggatata gaattcaagc ttctgcagct gctcgagtaa ttgattac	48
SEQ ID NO:127 42-2	
ctaggtaatc aattactoga gcagctgcag aagcttgaat tcgatatcca	50
SEQ ID NO:128 42T-1	
tcgagcacca ccaccaccac cacggtggtt gctaataata attgattaat ac	52
SEQ ID NO:129 42T-2	
ctaggтата atcaattatt attagcaacc accgtggtgg tgggtggtgg gc	52
SEQ ID NO:130 hIL-1 beta 116-269	
MDIPVRS LNC TLRDSQQKSL VMSGPYELKA LHLQGQDMEQ QVVFMSMFVQ GEESNDKIPV	60
ALGLKEKNLY LSCVLKDDKP TLQLESVDPK NYPKKKMEKR FVFNKIEINN KLEFESAQFP	120
NWYISTSQAE NMPVFLGGTK GGQDITDFTM QFVSSLEHHH HHHGGC	166
SEQ ID NO:131 hIL-1 beta 116-269(R4D)	
MDIPVDSLNC TLRDSQQKSL VMSGPYELKA LHLQGQDMEQ QVVFMSMFVQ GEESNDKIPV	60
ALGLKEKNLY LSCVLKDDKP TLQLESVDPK NYPKKKMEKR FVFNKIEINN KLEFESAQFP	120
NWYISTSQAE NMPVFLGGTK GGQDITDFTM QFVSS	155
SEQ ID NO:132 hIL-1 beta 116-269(L6A)	
MDIPVRSANC TLRDSQQKSL VMSGPYELKA LHLQGQDMEQ QVVFMSMFVQ GEESNDKIPV	60
ALGLKEKNLY LSCVLKDDKP TLQLESVDPK NYPKKKMEKR FVFNKIEINN KLEFESAQFP	120
NWYISTSQAE NMPVFLGGTK GGQDITDFTM QFVSS	155
SEQ ID NO:133 hIL-1 beta 116-269(T9G)	
MDIPVRS LNC GLRDSQQKSL VMSGPYELKA LHLQGQDMEQ QVVFMSMFVQ GEESNDKIPV	60
ALGLKEKNLY LSCVLKDDKP TLQLESVDPK NYPKKKMEKR FVFNKIEINN KLEFESAQFP	120
NWYISTSQAE NMPVFLGGTK GGQDITDFTM QFVSS	155
SEQ ID NO:134 hIL-1 beta 116-269(R11G)	
MDIPVRS LNC TLGDSQQKSL VMSGPYELKA LHLQGQDMEQ QVVFMSMFVQ GEESNDKIPV	60
ALGLKEKNLY LSCVLKDDKP TLQLESVDPK NYPKKKMEKR FVFNKIEINN KLEFESAQFP	120
NWYISTSQAE NMPVFLGGTK GGQDITDFTM QFVSS	155
SEQ ID NO:135 hIL-1 beta 116-269(D54R)	
MDIPVRS LNC TLRDSQQKSL VMSGPYELKA LHLQGQDMEQ QVVFMSMFVQ GEESNRKIPV	60
ALGLKEKNLY LSCVLKDDKP TLQLESVDPK NYPKKKMEKR FVFNKIEINN KLEFESAQFP	120
NWYISTSQAE NMPVFLGGTK GGQDITDFTM QFVSS	155
SEQ ID NO:136 hIL-1 beta 116-269(D145K)	
MDIPVRS LNC TLRDSQQKSL VMSGPYELKA LHLQGQDMEQ QVVFMSMFVQ GEESNDKIPV	60
ALGLKEKNLY LSCVLKDDKP TLQLESVDPK NYPKKKMEKR FVFNKIEINN KLEFESAQFP	120
NWYISTSQAE NMPVFLGGTK GGQDITKFTM QFVSS	155
SEQ ID NO:137 hIL-1 beta 116-269(DEE50,51)	
MDIPVRS LNC TLRDSQQKSL VMSGPYELKA LHLQGQDMEQ QVVFMSMFVQ GSNDKIPVAL	60
GLKEKNLYLS CVLKDDKPTL QLESVDPKNY PKKKMEKRFV FNKIEINNKL EFESAQFPNW	120

YISTSQAENM PVFLGGTKGG QDITDFTMQF VSS	153
SEQ ID NO:138 hIL-1 beta 116-269(DSND52-54)	
MDIPVRSLNC TLRDSQQKSL VMSGPYELKA LHLQGQDMEQ QVVFMSMFVQ GEEKIPVALG	60
LKEKNLYLSC VLKDDKPTLQ LESVDPKNYP KKKMEKRFEV NKIEINNKL FESAQFPNWy	120
ISTSQAENMP VFLGGTKGGQ DITDFTMQFV SS	152
SEQ ID NO:139 hIL-1 beta 116-269(K63S/K65S)	
MDIPVRSLNC TLRDSQQKSL VMSGPYELKA LHLQGQDMEQ QVVFMSMFVQ GEESNDKIPV	60
ALGLSESPLY LSCVLKDDKP TLQLESVDPK NYPKKKMEKR FVFNKIEINN KLEFESAQFP	120
NWYISTSQAE NMPVFLGGTK GGQDITDFTM QFVSS	155
SEQ ID NO:140 hIL-1 beta 116-269(Q126A/E128A)	
MDIPVRSLNC TLRDSQQKSL VMSGPYELKA LHLQGQDMEQ QVVFMSMFVQ GEESNDKIPV	60
ALGLKEKNLY LSCVLKDDKP TLQLESVDPK NYPKKKMEKR FVFNKIEINN KLEFESAQFP	120
NWYISTSAAA NMPVFLGGTK GGQDITDFTM QFVSS	155
SEQ ID NO:141 HIL-3	
atatatcata tgctgagcaa tgtgaaatac aactttatg	39
SEQ ID NO:142 HIL-4	
atatatctcg agcgccctgg tttccagtat ctgaaaag	37
SEQ ID NO:143 R4D-1	
catatggata tccctgtaga ctcactgaac tgcacgctc	39
SEQ ID NO:144 R4D-2	
gagcgtgcag ttcagtgagt ctacagggat atccatatg	39
SEQ ID NO:145 L6A-1	
gatataccctg tacgatcagc taactgcacg ctccgggac	39
SEQ ID NO:146 L6A-2	
gtcccgagc gtgcagttag ctgatcgta caggatatac	39
SEQ ID NO:147 T9G-1	
gtacgatcac tgaactgcgg tctccgggac tcacagc	37
SEQ ID NO:148 T9G-2	
gctgtgagtc ccggagaccg cagttcagtg atcgta c	37
SEQ ID NO:149 R11G-1	
gaactgcacg ctccgggact cacagc	26
SEQ ID NO:150 R11G-2	
gctgtgagtc ccgagcgtg cagttc	26
SEQ ID NO:151 D54R-1	
caaggagaag aaagtaatcg caaaatacct gtggccttg	39
SEQ ID NO:152 D54R-2	
caaggccaca ggtattttgc gattactttc ttctccttg	39
SEQ ID NO:153 EE-1	
catgtccttt gtacaaggaa gtaatgacaa aatacctgtg	40
SEQ ID NO:154 EE-2	
cacaggtatt ttgtcattac ttccttgta c aaaggacatg	40
SEQ ID NO:155 SND-1	
ctttgtacaa ggagaagaaa aaatacctgt ggccttg	37
SEQ ID NO:156 SND-2	
caaggccaca ggtatttttt cttctccttg tacaaag	37
SEQ ID NO:157 K6365S-1	
gtggccttg gctcagcga aagcaatctg tacctgtcct g	41

SEQ ID NO:158 K6365S-2	
caggacaggt acagattgct ttcgctgagg cccaaggcca c	41
SEQ ID NO:159 QE-1	
gtacatcagc acctctgcag cagcaaacat gcccgctcttc	40
SEQ ID NO:160 QE-2	
gaagacgggc atgtttgctg ctgcagaggt gctgatgtac	40
SEQ ID NO:161 D145K-1	
gcggccagga tataactaaa ttcaccatgc aatttgtgtc	40
SEQ ID NO:162 D145K-2	
gacacaaatt gcatggtgaa tttagttata tcctggccgc	40
SEQ ID NO:163 mL-1 alpha 117-270 without tag	
PYTYQSDLR Y KLMKLVQRKF VMNDSLNTI YQDVDKHYLS TTWLNLIQQE VKFDMYAYSS	60
GGDDSKYPVT LKISDSQLFV SAQGEDQPV LKELPETPKL ITGSETDLIF FWKSINSKNY	120
FTSAAYPELF IATKEQSRVH LARGLPSTMD FQIS	154
SEQ ID NO:164 mL-1 beta 119-269 without tag	
PIRQLHYRLR DEQQKSLVLS DPYELKALHL NGQNINQQVI FMSFVQGEF SNDKIPVALG	60
LKGNLYLSC VMKDGTPTLQ LESVDPKQYP KKKMEKRFVF NKIEVKSKVE FESAEPNWW	120
ISTSQAEHKP VFLGNNSGQD IIDFTMESVS S	151
SEQ ID NO:165 hIL-1 beta 116-269 without tag	
MDIPVRSNLC TLRDSQQKSL VMSGPYELKA LHLQGQDMEQ QVVFMSFVQ GEESNDKIPV	60
ALGLKEKNLY LSCVLKDDKP TLQLESVDPK NYPKKKMEKR FVFNKIEINN KLEFESAQFP	120
NWYISTSQAE NMPVFLGGTK GGQDITDFTM QFVSS	155
SEQ ID NO:166 interleukin 1 receptor, type I	
MKVLLRLICF IALLISLEA DKCKEREKI ILVSSANEID VRPCPLNPNE HKGTITWYKD	60
DSKTPVSTEQ ASRIHQHKEK LWFVPAKVED SGHYVCVVRN SSYCLRIKIS AKFVENEPNL	120
CYNAQAIFKQ NLPVAGDGGL VCPYMEFFKN ENNELPKLQW YKDCPLLLD NIHFSGVKDR	180
LIVMNVAEKH RGNVTHASY TYLGKQYPIT RVIEFITLEE NKPTRPVIIV PANETMEVDL	240
GSQIQLICNV TGLSDIAYW KWNGSVIEDV DPVLGEDYYS VENPANKRRS TLITVLNISE	300
IESRFYKHPF TCFAKNTHGI DAAIYQLIYP VTNFQKHMIG ICVTLTVIIV CSVFIYKIFK	360
IDIVLWYRDS CYDFLPIKAS DGKTYDAYIL YPKTVGEGST SDCDIFVFKV LPEVLEKQCG	420
YKLFYIGRDD YVGEDIVEVI NENVKKSRL IILVRETSS FSWLGGSSSE QIAMYNALVQ	480
DGIKVVLEL EKIQDYKMP ESIKFIQKH GAIRWSGDFT QGPQSAKTRF WKNVRYHMPV	540
QRRSPSSKHQ LLSPATKEKL QREAHVPLG	569
SEQ ID NO:167 interleukin 1 receptor, type II	
MLRLYVLVMG VSAFTLQPAH HTGAARSCRF RGRHYKREFR LEGEPVALRC PQVPYWLWAS	60
VSPRINLTWH KNDSARTVPG EEETRMWAQD GALWLLPALQ EDSGTYYCTT RNASYCDKMS	120
IELRVFENTD AFLPFISYPQ ILLTSTSGVL VCPDLSEFTR DKTDVQIYQY KDSLLLDKDN	180
EKFLSVRGTT HLLVHDVALE DAGYYRCVLT FAHEGQQYNI TRSIELRIKK KKEETIPVII	240
SPLKTISASL GSRLTIPCKV FLGTGTPLTT MLWWTANDTH IESAYPGGRV TEGPRQEYSE	300
NNENYIEVPL IFDPVTREDL HMDFKCVVHN TLSFQTLRRT VKEASSTFSW GIVLAPLSLA	360
FLVLGGIWMH RRCKHRTGKA DGLTVLWPHH QDFQSYPK	398
SEQ ID NO:168 interleukin 1 receptor, type I (mouse)	
MENMKVLLGL ICLMVPLLSL EIDVCTEYPN QIVLFLSVNE IDIRKCLTP NKMHGDTIIV	60
YKNSDKTPIS ADRDSRIHQQ NEHLWFPVAK VEDSGYYICI VRNSTYCLKT KVTVTVLEND	120
PGLCYSTQAT FPQRLHIAGD GSLVCPYVSY FKDENNELPE VQWYKNCKPL LLDNVSFSGV	180
KDKLLVRNVA EEHRGDYICR MSYTFRGKQY PVTRVIQFIT IDENKRDRPV ILSRNETIE	240
ADPGSMIQLI CNVTGQFSDL VYWKWNGSEI EWNDPFLAED YQFVEHPSTK RKYTLITTLN	300
ISEVKSQFYR YPFICVVKNT NIFESAHVQL IYPVPDFKNY LIGGFILTA TIVCCVCYK	360
VFKVDIVLWY RDSCSGFLPS KASDGKTYDA YILYPKTLGE GSFSDLDTFV FKLLPEVLEG	420
QFGYKLFYIY RDDYVGEDTI EVTNENVKKS RRLIILVRD MGGFSWLGQS SEEQIAIYNA	480
LIQEGIKIVL LELEKIQDYE KMPDSIQFIK QKHGVICWSG DFQERPQSAK TRFWKNLRYQ	540
MPAQRRSPLS KHRLLTLDPV RDTKEKLPAH THLPLG	576
SEQ ID NO:169 interleukin 1 receptor, type II (mouse)	
MFILLVLVLTG VSAFTTPTVV HTGKVSSEPI TSEKFTVHGD NCQFRGREFK SELRLEGEPV	60
VLRCPLAPHS DISSSSHSFL TWSKLDSSQL IPRDEPRMWV KGNILWILPA VQQDSGTYIC	120
TFRNASHCEQ MSVELKVFKN TEASLPHVSY LQISALSTTG LLVCPDLKEF ISSNADGKIY	180
WYKGAILLDK GNKEFLSAGD PTRLLISNTS MDDAGYYRCV MTFTYNGQEY NITRNIELRV	240
KGTTTEPIPV IISPLETIPA SLGSRLIVPC KVFLGTGTSS NTIVWWLANS TFISAAYPRG	300
RVTGLLHHQY SENDENYVEV SLIFDPVTRE DLHTDFKCVV SNPRSSQSLH TTVKEVSSTF	360
SWSIALAPLS LIILVVGAIW MRRRCKRRAG KTYGLTKLRT DNQDFPSSPN	410

SEQ ID NO:170 peptide GGKGG	5
SEQ ID NO:171 linker CGG CGG	3
SEQ ID NO:172 linker CGDKTHTSPP CGDKTHTSPP	10
SEQ ID NO:173 linker CGGPKPSTPPGSSGGAP CGGPKPSTPP GSSGGAP	17
SEQ ID NO:174 linker GCGGGG GCGGGG	6
SEQ ID NO:175 linker GCG GCG	3
SEQ ID NO:176 linker GGGGS GGGS	5
SEQ ID NO:177 linker GCGSGGGGS GCGSGGGGS	9
SEQ ID NO:178 linker GGC GGC	3
SEQ ID NO:179 linker GGC-NH2 GGC	3
SEQ ID NO:180 linker DKTHTSPPCG	10
SEQ ID NO:181 linker PKPSTPPGSSGGAPGGCG PKPSTPPGSS GGAPGGCG	18
SEQ ID NO:182 linker GGGGCG GGGGCG	6
SEQ ID NO:183 linker GCG (2) GCG	3
SEQ ID NO:184 linker SGGGG SGGGG	5
SEQ ID NO:185 linker GSGGGSGCG	10
SEQ ID NO:186 linker GGKKGC GGKKGC	6
SEQ ID NO:187 linker CGKKGG CGKKGG	6
SEQ ID NO:188 linker GGCG GGCG	4
SEQ ID NO:189 linker GSG GSG	3
SEQ ID NO:190 His-Tag with Linker LEHHHHHHGG C	11
SEQ ID NO:191 MOG peptide MEVGWYRSPF SRVVHLYRNG K	21

SEQ ID NO:192 pINC-75 gatccggagg tgggtgtcccc attagacagc t	31
SEQ ID NO:193 pINC-77 gtaagcttag gaagacacag attccat	27
SEQ ID NO:194 pINC-74 gatccggagg tgggtgcccct gtacgatcac tgaactg	37
SEQ ID NO:195 pINC-76 gtagtcatta ggaagacaca aattgcatgg tgaagtc	37
SEQ ID NO:196 IL1a1C atatatcata tgtctgcccc ttacacctac cagagtg	37
SEQ ID NO:197 alphaD145K-1 ggactgccct ctatgacaaa attccagata tcactcgag	39
SEQ ID NO:198 alphaD145K-2 ctcgagtgat atctggaatt ttgtcataga gggcagtcc	39
SEQ ID NO:199 halphaD145K-1 gggccaccct ctactactaa atttcagata ctggaaaacc	40
SEQ ID NO:200 halphaD145K-2 ggttttccag tatctgaaat ttagtgatag aggggtggccc	40
SEQ ID NO:201 Histag-GGC LEHHHHHHGG C	11
SEQ ID NO:202 mIL-1 alpha 115-270 without tag MSAPYTYQSD LRYKLMKLV R QKFVMNDSL N QTIYQDV D K H YLSTTWLNDL QQEVKFDMYA YSSGGDDSKY PVT L K I S D S Q L F V S A Q G E D Q P V L L K E L P E T P K L I T G S E T D L I F F W K S I N S KNYFTSAAYP ELFIATKEQS RVHLARGLPS MTD F Q I S	60 120 157
SEQ ID NO:203 hIL-1 alpha 119-271 without tag MLSNVKNFM R I I K Y E F I L N D A L N Q S I I R A N D Q Y L T A A A L H N L D E A V K F D M G A Y K S S K D D AKITVILRIS K T Q L Y V T A Q D E D Q P V L L K E M P E I P K T I T G S E T N L L F F W E T H G T K N Y F T S V AHPNLFIA TK Q D Y W V C L A G G P P S I T D F Q I L E N Q A	60 120 154
SEQ ID NO:204 mIL-1 alpha 115-270 (D145K) DSAPYTYQSD LRYKLMKLV R QKFVMNDSL N QTIYQDV D K H YLSTTWLNDL QQEVKFDMYA YSSGGDDSKY PVT L K I S D S Q L F V S A Q G E D Q P V L L K E L P E T P K L I T G S E T D L I F F W K S I N S KNYFTSAAYP ELFIATKEQS RVHLARGLPS M T K F Q I S	60 120 157
SEQ ID NO:205 hIL-1 beta 116-269 (K88N) MDIPVRSLNC TLRDSQQKSL VMSGPYELKA LHLQGQDMEQ QVVFMSMFVQ GEESNDKIPV ALGLKEKNLY LSCVLKDDKP TLQLESVDPN NYPKKKMEKR FVFNKIEINN KLEFESAQFP NWIYISTSQAE NMPVFLGGTK GGQDITDFTM QFVSS	60 120 155
SEQ ID NO:206 hIL-1 beta 116-269 (R98Q) MDIPVRSLNC TLRDSQQKSL VMSGPYELKA LHLQGQDMEQ QVVFMSMFVQ GEESNDKIPV ALGLKEKNLY LSCVLKDDKP TLQLESVDPK NYPKKKMEKR FVFNKIEINN KLEFESAQFP NWIYISTSQAE NMPVFLGGTK GGQDITDFTM QFVSS	60 120 155
SEQ ID NO:207 hIL-1 beta 116-269 (K103L) MDIPVRSLNC TLRDSQQKSL VMSGPYELKA LHLQGQDMEQ QVVFMSMFVQ GEESNDKIPV ALGLKEKNLY LSCVLKDDKP TLQLESVDPK NYPKKKMEKR FVFNLIEINN KLEFESAQFP NWIYISTSQAE NMPVFLGGTK GGQDITDFTM QFVSS	60 120 155
SEQ ID NO:208 hIL-1 beta 116-269 (Rkkk92-94) MDIPVRSLNC TLRDSQQKSL VMSGPYELKA LHLQGQDMEQ QVVFMSMFVQ GEESNDKIPV ALGLKEKNLY LSCVLKDDKP TLQLESVDPK NYPMEKRFVF NKIEINN KLE FESAQFP N W Y ISTSQAENMP VFLGGTKGGQ DITDFTMQFV S S	60 120 152
SEQ ID NO:209 hIL-1 beta 116-269 (L10N) MDIPVRSLNC TNRDSQQKSL VMSGPYELKA LHLQGQDMEQ QVVFMSMFVQ GEESNDKIPV ALGLKEKNLY LSCVLKDDKP TLQLESVDPK NYPKKKMEKR FVFNKIEINN KLEFESAQFP NWIYISTSQAE NMPVFLGGTK GGQDITDFTM QFVSS	60 120 155

## SEQ ID NO:210 hIL-1 alpha 119-271(D145K)

MLSNVKYNFM	RIIKYEFILN	DALNQSIIRA	NDQYLTAAL	HNLDEAVKFD	MGAYKSSKDD	60
AKITVILRIS	KTQLYVTAQD	EDQPVLLKEM	PEIPKTITGS	ETNLLFFWET	HGTKNYFTSV	120
AHPNLFIAATK	QDYWVCLAGG	PPSITKFQIL	ENQA			154

## SEQ ID NO:211 hIL-1 alpha 119-271(L18K)

MLSNVKYNFM	RIIKYEFIKN	DALNQSIIRA	NDQYLTAAL	HNLDEAVKFD	MGAYKSSKDD	60
AKITVILRIS	KTQLYVTAQD	EDQPVLLKEM	PEIPKTITGS	ETNLLFFWET	HGTKNYFTSV	120
AHPNLFIAATK	QDYWVCLAGG	PPSITDFQIL	ENQA			154

## SEQ ID NO:212 hIL-1 alpha 119-271(F146N)

MLSNVKYNFM	RIIKYEFILN	DALNQSIIRA	NDQYLTAAL	HNLDEAVKFD	MGAYKSSKDD	60
AKITVILRIS	KTQLYVTAQD	EDQPVLLKEM	PEIPKTITGS	ETNLLFFWET	HGTKNYFTSV	120
AHPNLFIAATK	QDYWVCLAGG	PPSITDNQIL	ENQA			154

## SEQ ID NO:213 hIL-1 alpha 119-271(R10A)

MLSNVKYNFM	AIIKYEFILN	DALNQSIIRA	NDQYLTAAL	HNLDEAVKFD	MGAYKSSKDD	60
AKITVILRIS	KTQLYVTAQD	EDQPVLLKEM	PEIPKTITGS	ETNLLFFWET	HGTKNYFTSV	120
AHPNLFIAATK	QDYWVCLAGG	PPSITDFQIL	ENQA			154

## SEQ ID NO:214 hIL-1 alpha 119-271(I62A)

MLSNVKYNFM	RIIKYEFILN	DALNQSIIRA	NDQYLTAAL	HNLDEAVKFD	MGAYKSSKDD	60
AKATVILRIS	KTQLYVTAQD	EDQPVLLKEM	PEIPKTITGS	ETNLLFFWET	HGTKNYFTSV	120
AHPNLFIAATK	QDYWVCLAGG	PPSITDFQIL	ENQA			154

## SEQ ID NO:215 hIL-1 alpha 119-271(W107F)

MLSNVKYNFM	RIIKYEFILN	DALNQSIIRA	NDQYLTAAL	HNLDEAVKFD	MGAYKSSKDD	60
AKITVILRIS	KTQLYVTAQD	EDQPVLLKEM	PEIPKTITGS	ETNLLFFFET	HGTKNYFTSV	120
AHPNLFIAATK	QDYWVCLAGG	PPSITDFQIL	ENQA			154

## SEQ ID NO:216 hIL-1 alpha 119-271(D20V)

MLSNVKYNFM	RIIKYEFILN	VALNQSIIRA	NDQYLTAAL	HNLDEAVKFD	MGAYKSSKDD	60
AKITVILRIS	KTQLYVTAQD	EDQPVLLKEM	PEIPKTITGS	ETNLLFFWET	HGTKNYFTSV	120
AHPNLFIAATK	QDYWVCLAGG	PPSITDFQIL	ENQA			154

## SEQ ID NO:217 hIL-1 alpha 119-271(rFIL16-18)

RRSNVKYNFM	RIIKYENDAL	NQSIIRANDQ	YLTAAALHNL	DEAVKFDMGA	YKSSKDDAKI	60
TVILRISKTD	LYVTAQDEDQ	PVLLKEMPEI	PKTITGSETN	LLFFWETHGT	KNYFTSVAHP	120
NLFIAATKQDY	WVCLAGGPPS	ITDFQILENQ	A			151

## SEQ ID NO:218 hIL-1 alpha 119-271(rITGS96-99)

MLSNVKYNFM	RIIKYEFILN	DALNQSIIRA	NDQYLTAAL	HNLDEAVKFD	MGAYKSSKDD	60
AKITVILRIS	KTQLYVTAQD	EDQPVLLKEM	PEIPKTETNL	LEFFWETHGT	NYFTSVAHPN	120
LFIATKQDYW	VCLAGGPPSI	TDFQILENQA				150

## SEQ ID NO:219 Histag-GGC

LEHHHHHHGG	CG	12
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## SEQ ID NO:220 hIL-1 beta 116-269(D145K) with LEHHHHHHGGCG-tag

MDIPVRSLNC	TLRDSQQKSL	VMSGPYELKA	LHLQGQDMEQ	QVVFMSFVQ	GEESNDKIPV	60
ALGLKEKNLY	LSCVLKDDKP	TLQLESVDPK	NYPKKMEKR	FVFNKIEINN	KLEFESAQFP	120
NWYISTSQAE	NMPVFLGGTK	GGQDITKFTM	QFVSSLEHHH	HHHGGCG		167

## SEQ ID NO:221 hIL-1 beta 116-269(D145K) with GGCG-tag

MDIPVRSLNC	TLRDSQQKSL	VMSGPYELKA	LHLQGQDMEQ	QVVFMSFVQ	GEESNDKIPV	60
ALGLKEKNLY	LSCVLKDDKP	TLQLESVDPK	NYPKKMEKR	FVFNKIEINN	KLEFESAQFP	120
NWYISTSQAE	NMPVFLGGTK	GGQDITKFTM	QFVSSGGCG			159

## SEQ ID NO:222 hIL-1 beta 116-269(D145K) with GGC-tag

MDIPVRSLNC	TLRDSQQKSL	VMSGPYELKA	LHLQGQDMEQ	QVVFMSFVQ	GEESNDKIPV	60
ALGLKEKNLY	LSCVLKDDKP	TLQLESVDPK	NYPKKMEKR	FVFNKIEINN	KLEFESAQFP	120
NWYISTSQAE	NMPVFLGGTK	GGQDITKFTM	QFVSSGGC			158

## SEQ ID NO:223 hIL-1 beta 116-269 with GGCG-tag

MDIPVRSLNC	TLRDSQQKSL	VMSGPYELKA	LHLQGQDMEQ	QVVFMSFVQ	GEESNDKIPV	60
ALGLKEKNLY	LSCVLKDDKP	TLQLESVDPK	NYPKKMEKR	FVFNKIEINN	KLEFESAQFP	120
NWYISTSQAE	NMPVFLGGTK	GGQDITDFTM	QFVSSGGCG			159

## SEQ ID NO:224 hIL-1 alpha 119-271 (SEQ ID NO:203) with GGCG-tag

MLSNVKYNFM	RIIKYEFILN	DALNQSIIRA	NDQYLTAAL	HNLDEAVKFD	MGAYKSSKDD	60
AKITVILRIS	KTQLYVTAQD	EDQPVLLKEM	PEIPKTITGS	ETNLLFFWET	HGTKNYFTSV	120
AHPNLFIAATK	QDYWVCLAGG	PPSITDFQIL	ENQAGGCG			158

SEQ ID NO:225 hIL-1 alpha 119-271 (D145K) (SEQ ID NO:204) with GGCG-tag

MLSNVKYNFM	RIIKYEFILN	DALNQSIIRA	NDQYLTAAL	HNLDEAVKFD	MGAYKSSKDD	60
AKITVILRIS	KTQLYVTAQD	EDQPVLLKEM	PEIPKTITGS	ETNLLFFWET	HGTKNYFTSV	120
AHPNLFIAATK	QDYWVCLAGG	PPSITKFQIL	ENQAGGCG			158

SEQ ID NO:226 IL1BETA-3

atatatgata	tccccattag	acagctgcac	tacagg	36
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SEQ ID NO:227 IL1BETA-2

atatatctcg	aggggaagaca	cagattccat	ggtgaag	37
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SEQ ID NO:228 mIL-1 beta 116-269 (D145K)

MDIPIRQLHY	RLRDEQQKSL	VLSDPYELKA	LHLNGQNINQ	QVIFSMSFVQ	GEPSNDKIPV	60
ALGLKGKNLY	LSCVMKDGTP	TLQLESVDPK	QYPKKKMEKR	FVFNKIEVKS	KVEFESAEP	120
NWYISTSQAE	HKPVFLGNS	GQDIKFTME	SVSSLEHHHH	HHGGC		165

SEQ ID NO:229 D143K-1

cagtggctcag	gacataatta	aattcaccat	ggaatctgtg	tc	42
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SEQ ID NO:230 D143K-2

gacacagatt	ccatggtgaa	tttaattatg	tcctgaccac	tg	42
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