

## SEQUENCE LISTING

SEQ ID NO:1 (human IL-1 receptor, type I)				
MKVLLRLICF	IALLISSLEA	DKCKEREEKI	ILVSSANEID	VRPCPLNPNE HKGTITWYKD 60
DSKTPVSTEQ	ASRIHQHKEK	LWFVPAKVED	SGHYVCVVRN	SSYCLRIKIS AKFVENEPNL 120
CYNAQAIFKQ	NLPVAGDGGL	VCPYMEFFKN	ENNELPKLQW	YKCKPLLLLD NIHFSGVKDR 180
LIVMNVAEKH	RGNYTCHASY	TYLGKQYPIT	RVIEFITLEE	NKPTRPVIVS PANETMEVDL 240
GSQIQLICNV	TGQLSDIAYW	KWNGSVIDED	DPVLGEDYYS	VENPANKRRS TLITVLNISE 300
IESRFYKHPF	TCFAKNTHGI	DAAYIQLIYP	VTNFQKHMIG	ICVTLTVIIV CSVFIYKIFK 360
IDIVLWYRDS	CYDFLPIKAS	DGKTYDAYIL	YPKTVGEGST	SDCDIFVFKV LPEVLEKQCG 420
YKLFYIGRDD	YVGEDIVEVI	NENVKKSRR	IIILVRETSS	FSWLGGSSSE QIAMYNALVQ 480
DGIKVVLELE	EKIQDYEKMP	ESIKFIKQKH	GAIRWSGDFT	QGPQSAKTRF WKNVRYHMPV 540
QRRSPSSKHQ	LLSPATKEKL	QREAHVPLG		569
SEQ ID NO:2 (human IL-1 receptor, type II)				
MLRLYLVMG	VSAFTLQPA	HTGAARSCR	RGRHYKREFR	LEGEVALRC PQVPYWLWAS 60
VSPRINTLWH	KNDSARTVPG	EEETRMWAQD	GALWLLPALQ	EDSGTYVCTT RNASYCDKMS 120
IELRVFENTD	AFLPFISYPQ	ILTLSTSGVL	VCPDLSEFTR	DKTDVKIQWY KDSLLLDKDN 180
EKFLSVRGTT	HLLVHDVALE	DAGYYRCVLT	FAHEGQQYNI	TRSIELRIKK KKEETIPVII 240
SPLKTISASL	GSRLTIPCKV	FLGTGTPLTT	MLWWTANDTH	IESAYPGGRV TEGPRQEYSE 300
NNENYIEVPL	IFDPVTREDL	HMDFKCVVHN	TLSFQTLRTT	VKEASSTFSW GIVLAPLSLA 360
FLVLGGIWMH	RRCKHRTGKA	DGLTVLWPHH	QDFQSYPK	398
SEQ ID NO:3 (Q $\beta$ CP)				
AKLETVTLGN	IGKDGKQTLV	LNPRGVNPTN	GVASLSQAGA	VPALVKRVTV SVSQPSRNRK 60
NYKVQVKIQN	PTACTANGSC	DPSVTRQAYA	DVTFSFTQYS	TDEERAFVRT ELAALLASPL 120
LIDAIDQLNP	AY			132
SEQ ID NO:4 (human IL-1 $\beta$ 116-269)				
APVRSNLCTL	RDSQQKSLVM	SGPYELKALH	LQGQDMEQQV	VFSMSFVQGE ESNDKIPVAL 60
GLKEKNLYLS	CVLKDDKPTL	QLESVDPKNY	PKKKMEKRFB	FNKIEINNKL EFESAQFPNW 120
YISTSQAENM	PVFLGGTKGG	QDITDFTMQF	VSS	153
SEQ ID NO:5 (N-terminal sequence)				
MDI				3
SEQ ID NO:6 (human IL-1 $\beta$ 116-269 MDI D145K)				
MDIPVRSNLNC	TLRDSQQKSL	VMSGPYELKA	LHLQGQDMEQ	QVVFMSFVQ GEESNDKIPV 60
ALGLKEKNLY	LSCVLKDDKP	TLQLESVDPK	NYPKKKMEKR	FVFNKIEINN KLEFESAQFP 120
NWYISTSQAE	NMPVFLGGTK	GGQDITKFTM	QFVSS	155
SEQ ID NO:7 (GGCG linker)				
GGCG				4
SEQ ID NO:8 (GGC linker)				
GGC				3
SEQ ID NO:9 (His-GGCG linker)				
LEHHHHHHGG	CG			12
SEQ ID NO:10 (His-GGC linker)				
LEHHHHHHGG	C			11
SEQ ID NO:11 (human IL1 $\beta$ MDI D145K His6 GGCG)				
MDIPVRSNLNC	TLRDSQQKSL	VMSGPYELKA	LHLQGQDMEQ	QVVFMSFVQ GEESNDKIPV 60
ALGLKEKNLY	LSCVLKDDKP	TLQLESVDPK	NYPKKKMEKR	FVFNKIEINN KLEFESAQFP 120
NWYISTSQAE	NMPVFLGGTK	GGQDITKFTM	QFVSSLEHHH	HHHGGCG 167
SEQ ID NO:12 (human IL1 $\beta$ MDI D145K His6 GGC)				
MDIPVRSNLNC	TLRDSQQKSL	VMSGPYELKA	LHLQGQDMEQ	QVVFMSFVQ GEESNDKIPV 60
ALGLKEKNLY	LSCVLKDDKP	TLQLESVDPK	NYPKKKMEKR	FVFNKIEINN KLEFESAQFP 120
NWYISTSQAE	NMPVFLGGTK	GGQDITKFTM	QFVSSLEHHH	HHHGGC 166

SEQ ID NO:13 (human IL1 $\beta$  MDI D145K GGCG)  
MDIPVRSLNC TLRDSQQKSL VMSGPYELKA LHLQGQDMEQ QVVFMSFSVQ GEESNDKIPV 60  
ALGLKEKNLY LSCVLKDDKP TLQLESVDPK NYPKKKMEKR FVFNKIEINN KLEFESAQFP 120  
NWIISTSQAE NMPVFLGGTK GGQDITKFTM QFVSSGGCG 159

SEQ ID NO:14 (human IL1 $\beta$  MDI D145K GGC)  
MDIPVRSLNC TLRDSQQKSL VMSGPYELKA LHLQGQDMEQ QVVFMSFSVQ GEESNDKIPV 60  
ALGLKEKNLY LSCVLKDDKP TLQLESVDPK NYPKKKMEKR FVFNKIEINN KLEFESAQFP 120  
NWIISTSQAE NMPVFLGGTK GGQDITKFTM QFVSSGGC 158

SEQ ID NO:15 (Primer IL1BETA-3)  
atatatgata tccccattag acagctgcac tacagg 36

SEQ ID NO:16 (Primer IL1BETA-2)  
atatatctcg aggggaagaca cagattccat ggtgaag 37

SEQ ID NO:17 (mIL-1 $\beta$  116-269 D145K)  
MDIPIRQLHY RLRDEQQKSL VLSDPYELKA LHLNGQNINQ QVIFMSFSVQ GEPSNDKIPV 60  
ALGLKGKNLY LSCVMKDGTG TLQLESVDPK QYPKKKMEKR FVFNKIEVKS KVEFESAEFP 120  
NWIISTSQAE HKPVFLGNS GQDIKFTME SVSSLEHHHH HHGGC 165

SEQ ID NO:18 (Primer D143K-1)  
cagtggtcag gacataatta aattcaccat ggaatctgtg tc 42

SEQ ID NO:19 (Primer D143K-2)  
gacacagatt ccatggtgaa ttttaattatg tcctgaccac tg 42

SEQ ID NO:20 (human IL-1 $\beta$  116-269)  
MAPVRSLNCT LRDSQQKSLV MSGPYELKAL HLQGQDMEQQ VVFMSFSVQG EESNDKIPVA 60  
LGLKEKNLYL SCVLKDDKPT LQLESVDPKN YPKKKMEKRF VFNKIEINNK LEFESAQFPN 120  
WYISTSQAEN MPVFLGGTKG GQDITDFTMQ FVSS 154

SEQ ID NO:21 (rhesus IL-1 $\beta$  MDI D145K His6 GGCG)  
MDIPVRSLHC TLRDAQLKSL VMSGPYELKA LHLQGQDLEQ QVVFMSFSVQ GEESNDKIPV 60  
ALGLKAKNLY LSCVLKDDKP TLQLESVDPK NYPKKKMEKR FVFNKIEINN KLEFESAQFP 120  
NWIISTSQAE NMPVFLGGTR GGQDITKFTM QFVSSLEHHH HHHGGCG 167