

1XG2	$\alpha 1$			$\alpha 2$			$\eta 2$	
	000000000			000000000			000	00
	1	10	20	20	30	30		
1XG2	ENHL	SEI	PKT	RNPSL	LQA	E	S	DPRSASKDLK
A1G02550	LHVSPA	VGSV	CSNT	DYAAE	CIVS	ILP	LLRDRFRK	FEP
A1G09360	GPTAL	INSI	CIENE	DYGF	CNKI	HEK	LKTP	TATIK
A1G09370	EKTQOR	VNGI	CKQTM	TRF	CSSL	LK	NLNTFP	PASNK
A1G10770	QVAESR	MINI	CSHT	AYPSL	CRPL	VKR	VTSR	PKATHR
A1G11362	EVTKSE	INSI	CTHTDV	DASL	CFEF	LNS	SPQIAAL	
A1G14890	TDDLDF	IRTS	CNTT	LYPDV	YTS	LAG	YASAVQ	DNPA
A1G23205	DDSDFI	RTS	CNTT	LYPDL	CFSS	LSF	SSSVHNDPA	
A1G23350	ATSSQALS	SISL	ADPCTVS	DFPAL	CRST	IKG	QTNVNA	ATDV
A1G47960	VSEGS	IIEPT	CKETP	DFNL	CVSL	LNS	DPGRSSA	
A1G48010	KKASTV	VRSE	HK	TMM	MEFS	ALD	PKIGK	LDPG
A1G48020	SEM	STI	CDKTL	NPSF	CLKF	LNTK	FASP	NLQ
A1G50325	KVTTDE	ICGM	ARRAV	NASF	YEF	MKS	STQVATL	
A1G50340			MAV	NTSF	YEF	MKS	IPQIATL	
A1G54620	RVENSL	VQKY	CNQSS	KYAERY	FYKF	CIAS	EENAES	SQKARNS
A1G54980	LTSTKY	IKL	CEMQS	VE	DKTF	CLQT	SANPLA	AASATGLLP
A1G55770	NANSGM	ISDL	CKHS	DDPNL	CLSS	ITS	RPE	SGEFAGT
A1G56100	CAEKDL	MKEE	CHNAQ	VPTI	CMQC	LES	DPTS	VHADRVG
A1G56620	APTML	IDS	CVNTK	NMYE	EQS	ISK	LGNPHA	EI
A1G60760	QATEAR	FISL	CAQT	AYPTL	CRPL	VKG	PNRRS	
A1G62760	QTNLDY	IKTS	CNIT	LYKTI	CYNS	LS	PYASTI	RSNPQ
A1G70540	AMAQRVM	GGRDP	CSVS	DFKVL	CRSV	VKG	QKNVNA	ATEV
A1G70720	NGSDF	IRLA	CNTT	LYPDL	CFST	LSF	FANSI	QNSDN
A2G01610	TNDLDF	IRTS	CNAT	LYPDV	CFTS	LSG	YASAVQ	DSPA
A2G10970		SLL	ISKA	CKGTAS	FSS	LEEE	IKS	LTDHRTKSAS
A2G15345								MQ
A2G31425	AMPISD	VHNF	CKETF	EVEF	CMKY	IGS	DQRLV	AARDF
A2G31430	AIPARD	IKL	CKETT	DVPF	CLKY	LGT	DPRI	PAARDL
A2G31432	MPTKD	VYSL	CKESS	EVD	CMKN	IGS	DKRIV	AARDF
A2G47050	PHHQKA	VGDI	CSVQ	DKRL	CSIT	LRN	VSPDD	PAVLVRY
A2G47340	MKIDTT	AKDL	CNT	DYNNE	IAA	L	PDQKQAE	EGGGIAPKDVMRMEAE
A2G47670	TQYSTY	VRNA	CNVT	RYNRL	CVRT	W	PF	AIVARNNTS
A3G05741	IVTKEL	INNF	CSNLEMF	DRQF	CAKW	F	NADQ	TKTSISVQG
A3G12880	RANEEL	MMQQ	CHNSD	NPTL	CLRC	LS	DPGS	HEADKVG
A3G17130	QSSDDL	IKI	QATP	FCDL	CEAS	LR	FSPSP	SDPKS
A3G17150	ATEPKP	IQEL	CKFNI	NPSL	CVST	L	NLDR	PSKNS
A3G17152	PPGSSL	VQRL	CKRNR	YQAL	LIST	L	NVDR	SKTS
A3G17220	NAQVAD	IKAI	CGKAK	NQSF	CTS	MKS	NPKT	SGA
A3G17225	KVTKTF	LSRL	CTEPHI	DNF	CITW	L	SDPT	TYTL
A3G17230_1	DKITKDL	LQQL	CASPHI	DHPF	CITW	L	ADPT	TFTL
A3G17230_2	ITPFSSSL	SPSDKVTNET	LNLQ	CSKPN	YNH	CI	AW	TS
A3G27999	LVTKDQ	HTI	CTKQEI	NSSF	FQV	L	NTN	PEIAKL
A3G36659	PLLSPE	IKTI	CGKTD	NPPL	CESS	V	SP	LLTPQLKPT
A3G47380	KRAINF	IQAS	CKAT	TYPTV	CVNS	L	GYANSI	QTSR
A3G47670	PISSAS	LKSL	CSVTR	YPET	CFNS	LS	SLNES	DSKLN
A3G49330	PPTQNL	INRI	CKQTI	DPKF	CNQT	IT	SQ	LVRRTSI
A3G55680	AMSIKD	MYAF	CKDTD	DVNF	CLKY	IG	TDIR	ILAAARDL
A3G62180	TPHAKA	VAGI	CTVIPT	DTSL	CKT	L	KH	VPTNDPIELIRA
A3G62820	SKRESY	VQNA	CSVT	RYQDL	AKT	L	PFAS	VAKNSPS
A4G00080	YDTKAY	VHSW	CR TTL	YPKL	CVRS	M	SR	VRSRAVQNP
A4G02250				VYVTV	IAA	A	T	APKLG
A4G03945		QI	HTI	CTKQDI	NSSY	FQV	L	NANPEIARL
A4G12390	SSSINF	VSS	CRVT	RYQTL	CVKC	L	A	FADKIRRNEN
A4G15750	RADEEL	IKTE	CNHTE	YQNV	LFLC	L	E	ADPISFNIDRAG
A4G24640	SPHMKY	DAI	CDR	SH	DQAF	VKT	L	TNPPTA
A4G25250	QNHTTY	VKTA	CNST	TYPTM	CYNC	LS	S	SSTIKSDPI
A4G25260	SGDTEF	IKAS	CETT	SYPR	CFQS	LS	S	YASEIKQPR
A5G20740	NGAEDI	VHSS	CEHA	SYPSL	CVRT	LS	S	YSGPTITNRR
A5G24370	KPTKSI	DR	CNQT	NFNE	CELI	V	T	SQ
A5G38610	KSTSDM	IDQT	CKSCAAKSTIFDYNF	CVSS	LNS	S	P	IALPSP
A5G46930	ATAQSL	IRDS	CKKATTKDPKLYDF	CVKS	L	E	N	PQSKTAKSL
A5G46940	ANGQTL	IRNS	CKKATATSPKFKYNL	CVTS	L	E	T	NPQAKTAKDL
A5G46950	ATAQTL	IQDS	CKKAFKDPQSSYDF	CVQS	L	T	Q	DPQSKAATL
A5G46960	ATAQTL	IQDS	CKKAFKDPQLSYDF	CVNS	L	T	Q	DPQSKAATL
A5G46970	TIAQSL	IQDF	CKKAADKPKIHYNF	CVKS	L	E	N	PQSKTARSL
A5G46980	RVADSL	IQKS	CKENTRYAEPYIYKF	CITS	L	K	E	NPESQKVRNI
A5G46990	RVANSL	IRDS	CKKASKMSEPHYIYKF	CIAS	L	S	E	NPESQKVRNI
A5G50030	LVNREY	IDSN	QR	VK	NKAF	C	I	Q
A5G50040	ASATTY	DAI	CQS	VT	DKAF	CA	K	T
A5G50050	ASATKY	DAI	CHL	VS	DKAF	CT	K	T
A5G50060	LTSTKY	DAL	QH	VE	NGTF	C	M	H
A5G50070	LTSTKY	INKL	QMSFVD	NKPF	CLQT	L	S	A
A5G51520	QNHKTF	VKTA	CNST	TYPDK	CYKS	LS	S	S
A5G62340	TKALNF	IQSS	CKSTT	YQSL	CVET	L	S	V
A5G62350	KKAINF	IQSS	CKTT	TYPAL	CVHS	L	S	V
A5G62360	TTNTEF	VKSS	CTFT	TYPRL	CFSS	L	S	T
A5G64620	SNTTTI	EST	CKTTN	YKPF	CVSA	L	K	S
O49909		NSNNI	INTT	CRAT	TNYPL	L	H	S
1RJ1		GAMGNNL	VETT	CKNT	PNYQL	L	L	S
1X91		SEM	STI	CDK	TLNPSF	CLKF	L	N

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	000000000000000000000000	000000000000000000000000	000000000000000000000000	
	40 ★ 50 ★ 60 70 ★ 80 ★ 90 ★			
1XG2	GIGQPSIDIAQASAKQTSKIIASLT.....NQATDPKLGKRYET	CSENYAD	AIDSLGQ	AKQFLTSG.
A1G02550	ALYEKANATLIDLAKRLIVDKSTP.....RDVADVLDL	CVDNYES	LDDLDK	ASVAVDDGD
A1G09360	SLIIYTTMAHASDITYIFIDNLRK.....WPGPKETSGLKT	CHAVYKR	ETNSFLE	IRFLFSKGE
A1G09370	NVTVSEAEERFAANTYFFIISTLLRN.....AGDERPDLQA	CAEAYAI	VNSAFTK	AVTFFKQAY
A1G10770	LEAKTKLALAEATARFKNGNQ.....VST	CYETLGD	AVYNLAS	ARKSIRKRD
A1G11362	GLTKYLITYESRKFSDMLKQFO.....SLVNSTTDP	SAKGSYHV	CVGTFDK	GTGCFDD
A1G14890	AIGVLSRAKYTAAYLSKLSR.....RAASA	AAVHD	CVSNVGD	AVDQMRG
A1G23205	AISVTLTKTLDLASYLANITTL.....QPESNEDGA	HPTAAAVFHD	CFDNLKD	AVEEMKG
A1G23350	ELMKRTRQAKKIAEKELKRDGG.....VAT	CLSNFNS	AFDNLEK	ALNTIKEND
A1G47960	GLALILLDKIKGLATKTLNEN.....GLYKKRPE	.LKRALDE	CSRRYKT	ILNADVPE
A1G48010	AKCLIHYAQQNALDTHNQLQLLAN.....STTDNRT	KESYIS	CSKYDYK	ALYSFDE
A1G48020	LAKTTLTLDSTQARATQTLKKLQ.....SIIDGVD	PRSKLAYRS	CVDEYES	AIGNLEESG
A1G50325	DLAKFLINYDFQNTFDLIKHFQ.....SLTNSTT	DPSSKGSYEL	CLHLFNL	INPLETAL
A1G50340	DLTKFLINYDFQITLDTLTKHFQ.....SLTNNTT	DRSSKDSYKL	CLDLFSL	IDPLETAL
A1G54620	GTTNNALSNLNTNVRKIVEKIFNE.....RKYKGR	LKLLQK	CLKLYSE	GYDALTS
A1G54980	EVVIRIGIDLPAKLLVKASDRAIE.....KIPALKE	QKFKE	QDSFLR	IVMSLKS
A1G55770	AISAASANASATSSYIKQKLSN.....EDLEPA	IEDTLED	CQKDYQD	AVEQLDD
A1G56100	EIIHCLDSRLDIITKQKGLQIG.....EVVEKK	TRKRKSK	SDNKIRK	KPSVETPT
A1G56620	IADIAAFNAVYLITSAGNYIRD.....KFIPIA	ENPLVKNQLV	CLATYRAV	QKLLG
A1G60760	ALEAKTKLAVITDSARFKSGNPT.....VAIT	VAI	CYATLVD	ASFNLR
A1G62760	ALNLTLSAKSASKFVKKNIS.....HGGGL	TRLEVVAVAD	CVVEIGD	SVTSLQD
A1G70540	ELMKRTIKAKEAKISRKSGGG.....LKT	CYSNYDS	ALENLQK	ALKNKQND
A1G70720	AISLTLHNTLHLLSYLQONAYNRD.....HPTPV	LRD	CFENLKD	AVDGMRG
A2G01610	AIGVLSQAKSTAFLSKLSRS.....AAKYS	GDG	HQTASAVIR	CVSNVED
A2G10970	VLELAKAALSAMEKAHTQFLIG.....SPKKP	CFKS	CMENYKD	SVVEGLM
A2G15345	GLVNMVYQQTERLGYKNLEMK.....GLDR	TENYSK	LKYYRS	CVKEYEL
A2G31425	MLLIPISETQIQVTNAITQIN.....NIRQ	RFDNTL	GGKRIAL	CEKEYES
A2G31430	LFLLIATQSKMQVDDATTHID.....RVRK	FNGPHGRR	RIEV	CKTNYGI
A2G31432	IFLIAVRSRTQIIVDTGLLVISGE.....DTRKN	YNEPFE	KNVAV	CEEKYKI
A2G47050	TAAEA.....SVKKG	FLSGIKPKYKGNAF	FATTCTITG
A2G47340	SLLKANATLDYAKRVVEDRKT.....MPVKE	AMSV	CVENYDS	LISGLED
A2G47670	SVAVITDTRKRVLRLLKTKQRS.....AVGES	ERIALSD	CRELFVD	SLDNLK
A3G05741	SLRVKTRTFEGLQTQALMSKLAKS.....SGKD	QQLKGS	YES	CVASYGQ
A3G12880	RIILKICINSHLLVLTKNASTLGSQ.....HYQNP	NTAAALKQ	CGLGFST	AKHVGGE
A3G17130	AAMASVLDGNMDDTLGYIQSLIKH.....AHP	PAERALAQ	CAELYRP	VVKFNI
A3G17150	EAWISIVDATSNKVNKMLNLYI.....SVSKN	IKDREDL	KYK	CIIDYGT
A3G17152	GLASISLDTATTKFNVTLTYI.....SVLKN	VGRVDF	ERYGT	CIEEYGA
A3G17220	TLANITFGSAQTSASEGFRKIQ.....SLVK	TATNPT	MKAYTS	CVQHYKS
A3G17225	GLLDLVFQKTQLLGNKNLAAMK.....GSVNT	TDP	TLKIPFET	CVRDYEG
A3G17230_1	GLLDLVFQKTQLLGYKSLAAMK.....GAVR	TDP	TLRSTYET	CVRDYEG
A3G17230_2	GLLDSVVFQKTQLLGYKSLAAMK.....GSVNT	TDP	PAKIPFET	CVTDYEV
A3G27999	SLFKFVLNYQAQNI	SDTLKQFKLSG	GYMPDVESQ
A3G36659	SSVLILAIQASITATKAAMAVEK.....VDAS	D	CQELYDD	AVVNLDE
A3G47380	ALNVTVTQAQSTKVFVWRLG.....RFTSL	KKREIQ	AVKD	CIEEIH
A3G47670	EISELISLRVAAKEISNLSISFRS.....INDM	PEDAAVGD	CVKLYTD	ALSQ
A3G49330	IAKLTAAKAWINAIQTLDNIED.....SLLPK	AKDKRDKAE	FDA	CRKAYKL
A3G55680	VLAIVAI	SQCQIQLTKATKQINKVR	KQFSGPIGRRLYF
A3G62180	AAET.....SVKQ	SVTFLSG	IKPKHMSDAT
A3G62820	GVSVAITDNKDVLRHLLKTRLS.....TIGK	RDRIALSD	CRELLQD	S
A4G00080	RFALKASLYRAKYTKAFLLKEVKN.....LETT	LRPQYASVHD	CLDQIRD	SVNQ
A4G02250	ALSIASSNASDTSFYIKAKLKQ.....KNLE	PALED	TLDD	CSKNYLD
A4G03945	SLFKFVLNYQAQNI	SDKLLKQFKLSG	GYTPGVE
A4G12390	ALAVTILRVQSTTIYVGKLT.....KARR	IKRREY	LAVKD	CVENLGD
A4G15750	NIHCLGSQQLDVLINTVTSLKLKMK.....GEGE	ANENVLKD	CVTGFAI	AQLR
A4G24640	EAVIN.LAISHAEKTAIFVDEKAK.....KDPT	VKVA	FTE	CHKAYL
A4G25250	SLNLNVKSAKNATLVVSNLQKAKA.....AKS	.HEVSI	LKD	CVDEMKD
A4G25260	ALAVS IARAKSAKTYVSEMT.....DYK	GITKRQ	HEAVAD	CLEEMGD
A5G20740	AIKISLSHAQSAAKKLA	VVRD	SVGKKKQ
A5G24370	ITEVMTKRALTFATETVSIQID.....YLLP	NATD	TQDKAV	FSA
A5G38610	LVPMLQALDNATATASTIQQLLIS.....DDG	SFRS	ACL	RD
A5G46930	STKNAVSKTTSKGMVDKILKE.....DKY	EV	ERPLD	CLELYTE
A5G46940	STKNAVTKATTLKGTVDKIIKQ.....KKV	NKM	TAMPLD	CLQLYTD
A5G46950	STKNVAAKITNLKGIVAQDLKQ.....RYQ	DIV	DLKL	CLGFYKD
A5G46960	STKTAATAKITNLKGIVAQDLKQ.....QRY	QD	IVEDLKL	CLGFYND
A5G46970	STKNVSKTTSKMGIVDKILKE.....NRF	EMY	SEKPLRD	CLELYSD
A5G46980	CTNSAISNLT	KVKG	TVENILNERKY
A5G46990	GVKNAISNMTNVKGI	VERILKDRKY	TSKMSEKMLRV
A5G50030	EAVVG.LAISHCEKTAGFAAETAK.....KDAT	LKTQ	FNE	CHDAYVG
A5G50040	TATLN.LAISYADKSAGFTGNAAK.....ENPT	LKTQ	FAA	QDAFVT
A5G50050	VATLH.LGVSYANNAAGFAGEAAK.....ENP	QLK	EFDA	CQLELAL
A5G50060	NAVIN.LGISYANNTGAFAGEAAK.....KEPT	LKVQ	FKS	FQHEYD
A5G50070	SAVIRGIVLPQAKKSASFANGAAK.....KEP	SLKTQ	FQT	CQEA
A5G51520	ALNLNVKSAKEATSVVSKLLK.....MSQ	KSTAGR	KGMLPEAL	LKD
A5G62340	LDAAITVSLNQLSTKLFISHLRKS.....QF	QLQD	CAPSTDT	FSTDCE
A5G62350	AIAVTILSRAQSTKLFVSRLT.....RMK	GLKRE	VEAIKD	CVVEEMND
A5G62360	ALNITLASAKVTSAMMVRLS.....NSRL	KPKEV	SAMRD	CVVEELGD
A5G64620	SIMVGGMTNATSTANYIAGNLSA.....TVK	D	TVLKKVLQD	CSEK
O49909	LTTGLVMDVAVKLSIEIMKSIKKLEKSNP.....ELR	LPLSQ	CYIVVYA	VLHADVT
1R1	LALIMVDAIKAKANQA	AVTISKLRH	SNPPAAWKGPLKN
1X91	LAKTTLTLDSTQARATQTLKKLQSI.....IDG	VDRS	KLAYRS	CVDEYES

	05			06																																													
1XG2	00000000000000000000	00000000000000000000	00000000000000000000	00000000000000000000	00000000000000000000	00000000000000000000																																											
	100	110	120	130																																													
1XG2DYN	SLNIYASA	AFD	GAGT	EDSFEGPPNIPTQLHQADLKLED	LC																																										
A1G02550FERLES	SVVSA	AIAD	VVT	CSDAFAESSELESPMANVDDF	LK																																										
A1G09360YELMDEA	ILST	AKILEE	CRGD	FLIPPYKEPLLEKRVMLRI	LI																																										
A1G09370YKIVNIE	KV	SMAVD	CKTDF	NVLGYQINPLIEKNRQTK	LL																																										
A1G10770VPAMNTY	LTA	AVSDY	GAC	VDFGTQQVN	AIQNAVVD	LR																																									
A1G11362YITLEW	SVECT	FDMA	AG	EDELSTFKPNPQLFKDIS	I	VKN	LS																																								
A1G14890	HRRPGDPAFRFQMS	NVQ	TWMSA	AL	TDEET	CTD	GVTEEMEDGETKTAICDRVAD	VK																																							
A1G23205	STGSLESFRFQMS	NVQ	TWLSA	AL	TDEET	CTD	GFIHDEPRKDDICARVDD	VK																																							
A1G23350GFSLN	NINLSA	AL	TDY	DT	CS	DSMKETKEVN	VIYK	SAGV	LY																																						
A1G47960	V.....PKFG	EDG	VID	AG	VEASVCQGG	FNGSSP	LSLTKS	MQK	IS																																						
A1G48010PDYLN	IEITA	ARQ	NAND	CKT	LDL	DKDVF	KPDPK	LIMK	IDF	LEN	VC																																				
A1G48020GMGM	NMKVSA	AL	DGADT	LD	DDV	KRLRS	VDSS	VVNN	SK	T	IKN	LC																																			
A1G50325YDTL	NRN	VDA	MSQ	FAME	CE	SELSSVIK	PIPK	LLK	RVS	I	VEN	VS																																			
A1G50340YDTL	N	TVG	MSQ	YAE	CG	SELSSI	KPI	SK	L	SGV	I	VEN	VS																																		
A1G54620L	FKV	SVHL	QAK	EAPS	CE	M	GFNGDNK	QI	SP	M	K	END	VF																																		
A1G54980SEL	KV	SPD	TA	NYDAM	CF	DE	TKRVKE	VIG	KN	ED	VT	SK	LI	EM	TL	R	ME	K	EL	I																											
A1G55770HTD	V	VWLSA	AI	SAIES	CG	SALGSRAG	NDEL	S	R	N	E	V	F	L																																
A1G56100	DN.....LLA	ELN	Q	T	DDA	EKE	GI	I	D	V	N	AT	SE	A	I	E	N	E	T	E	V	D	L	K	E	K	D	G	D	E	E	A	K	S	E	K	P	K	K	K	K	E	Q						
A1G56620YSD	MR	HY	Q	SSV	LG	M	L	D	N	CT	D	F	D	YM	V	R	T	N	W	G	V	R	L	M	I																						
A1G60760V	M	L	K	M	F	L	T	A	V	S	D	Y	G	VC	V	N	G	F	I	DS	H	Q	V	NT	L	Q	N	D	V	E	L	R													
A1G62760	YKDSAKF	E	M	V	M	S	D	V	E	T	W	V	S	A	A	L	T	N	D	D	TC	M	D	G	F	S	LV	K	T	A	V	K	D	L	V	R	R	H	V	V	E	V	A			
A1G70540G	F	S	L	N	I	N	L	S	A	A	L	T	D	F	D	TC	N	D	A	M	G	GG	T	A	S	N	V	F	K	S	T	L	H													
A1G70720	SASGSIESFRFQMS	NVK	TWLSA	AL	T	D	E	Y	T	CTD	G	F	K	DV	H	E	D	D	SI	K	D	D	V	K	R	S	V	E	D	D	V	K														
A2G01610	GRGGTAARRSVETFRFQMSNVQ	TWMSA	AL	T	D	E	E	TC	T	D	G	F	E	DM	D	E	G	L	K	T	T	V	C	D	R	L	E	V	E	V	K																
A2G10970	D.....V	D	E	T	D	D	L	S	L	A	R	D	A	A	D	YC	N	M	I	L	S	VD	P	D	D	T	R	S	L	V	F	A	A	N	V	D	V	N	H	I							
A2G15345Y	R	S	A	S	E	A	A	A	R	A	F	D	S	I	S	MC	E	A	Y	L	E	GS	K	T	P	G	Y	T	T	R	NW	F	E	R	M	C									
A2G31425	NS.....S	T	D	H	M	E	I	T	R	N	T	Q	A	G	F	D	A	V	CC	E	D	E	W	A	KH	G	P	K	Q	E	S	P	L	T	F	Y	H	N	V	L	K	L	C				
A2G31430F	W	D	V	E	K	L	A	R	I	G	T	N	A	V	I	DC	E	N	V	W	RD	G	P	I	Q	T	S	P	L	T	F	Y	N	M	N	V	K	L	S							
A2G31432	KS.....L	T	D	R	M	E	M	S	Q	L	T	E	A	G	F	E	A	V	L	DC	Q	D	E	W	T	KL	E	H	E	Q	A	C	P	F	S	Y	W	H	K	R	V	K	L	V			
A2G47050T	S	M	A	E	N	Y	F	T	C	K	K	M	T	S	I	F	T	Y	H	S	TL	C	D	D	I	Y	DK	T	L	H	K	V	V	E	G	G	I	G	L							
A2G47340Y	G	R	L	D	S	V	L	S	A	A	I	S	D	V	SC	S	D	N	F	V	DI	P	D	V	D	SP	T	A	S	L	D	D	L	M	K										
A2G47670	ADE.....F	Q	R	Q	I	S	D	L	A	T	W	L	S	A	A	L	T	D	D	D	TC	L	D	G	F	E	ET	S	S	R	T	R	V	M	R	R	K	A	T	C	M						
A3G05741F	T	Q	A	L	V	A	I	S	D	A	F	Y	K	A	G	DC	K	D	A	F	E	GP	S	N	E	P	P	L	V	F	N	R	V	E	N	F	A									
A3G12880Y	D	K	A	A	Y	D	V	S	V	V	N	N	P	P	V	SC	R	N	S	L	E	AL	N	I	Q	V	P	S	F	R	Y	H	M	D	V	Y	L									
A3G17130	K.....F	G	F	A	I	Y	V	L	G	A	E	K	Q	T	D	SC	Q	K	G	I	T	NA	G	A	D	D	E	S	S	V	A	T	A	R	N	K	L	V	K								
A3G17150	F.....F	S	L	A	K	S	D	M	E	S	V	S	I	P	D	M	SC	E	A	Q	F	GS	S	P	L	T	G	R	N	K	DI	A														
A3G17152	K.....Y	P	E	A	M	S	E	M	K	D	V	V	A	K	P	G	YC	E	D	Q	F	AE	S	P	V	T	A	R	N	K	AV	H	D	I	A											
A3G17220G	K	G	L	N	I	K	V	S	A	A	M	E	G	P	TC	E	Q	D	M	AF	K	V	D	P	S	A	V	K	NS	G	D	F	N	I	C										
A3G17225Y	P	L	A	S	Q	G	A	A	R	A	F	I	S	I	S	VC	E	A	Q	F	A	GN	V	P	A	Y	A	K	L	N	LF	F	K	R	M	C									
A3G17230_1Y	Q	L	A	S	Q	G	A	A	R	A	F	I	S	I	S	VC	E	A	Q	F	E	GR	D	D	V	P	P	K	T	A	Y	PK	V	R	N	V	S								
A3G17230_2Y	D	L	A	S	L	G	A	A	R	A	F	I	S	I	S	VC	E	T	Q	F	E	GR	D	N	V	P	V	Y	T	K	L	NP	F	K	R	M	C								
A3G27999Y	N	S	V	N	T	R	V	S	G	T	L	E	D	I	F	TC	T	D	D	L	SM	K	P	I	P	Q	F	M	T	E	S	N	L	I	K	E	L	S								
A3G36659I	A	T	V	N	T	N	L	S	A	A	M	T	D	Y	S	TC	N	D	G	F	ES	G	E	P	N	P	L	A	V	A	D	K	L	T												
A3G47380	SAKGRDQF	W	F	H	M	S	N	A	Q	T	W	T	S	A	A	L	T	N	A	N	TC	S	D	G	F	A	GR	V	M	D	G	R	V	K	N	S	R	A	R	I	L	N	L	G		
A3G47670	KKGGNNWLT	E	E	V	G	D	V	K	T	W	I	S	A	A	L	T	D	E	TC	S	D	G	I	E	EM	G	T	I	V	GN	E	I	K	K	M	E	M	A	N						
A3G49330Y	R	F	M	R	A	Y	Q	A	L	A	M	N	I	S	MC	R	T	S	F	F	HP	T	M	V	Y	A	N	W	N	K	M	L	T													
A3G55680L	E	S	I	A	Q	L	S	A	V	D	G	S	H	Y	M	FC	E	D	E	W	K	NN	G	P	I	Q	K	S	P	F	T	F	Y	T	N	V	E	L	L							
A3G62180T	T	L	A	H	N	Y	F	T	C	K	K	E	L	M	S	I	M	G	H	S	TL	D	D	I	E	DK	I	L	L	K	E	V	G	I	G	I	V									
A3G62820	ASE.....F	Q	Q	M	S	D	L	A	T	W	L	S	S	L	T	D	K	D	TC	L	D	G	F	E	KT	S	T	R	S	S	T	V	R	M	I	R	K	R	V	T	S	M					
A4G00080	RRQKSGGD	L	H	W	H	I	N	L	Q	T	W	T	S	A	L	T	D	A	E	TC	V	S	Q	F	P	GR	R	M	S	K	L	K	A	T	I	K	G	K	V	N	E					
A4G02250F	I	D	V	D	I	W	L	N	T	A	I	S	D	G	E	AC	E	N	A	L	N	DR	A	G	N	D	AE	L	A	R	R	N	T	N	L	L									
A4G03945Y	G	S	V	N	T	M	V	G	T	A	I	N	D	E	TC	A	D	D	L	SM	K	P	V	P	Q	F	F	V	T	E	S	N	L	I	K	E	L	S								
A4G12390	RSGRDRDEF	L	W	R	L	S	N	V	E	T	W	V	S	A	A	L	T	D	E	TC	L	D	G	F	DK	V	M	D	G	V	K	S	A	I	R	R	V	V	A							
A4G15750Y	D	K	A	Y	E	L	V	K	T	A	L	N	Y	P	R	TC	E	E	N	L	QL	K	F	K	D	SD	V	Y	D	D	I	L	A	Y	S										
A4G24640V	K	L	K	A	S	P	D	T	A	N	Y	D	V	R	A	SC	S	D	S	M	RV	N	E	L	V	G	K	N	T	D	K	A	S	T	L	K	E	M	T	V	Q	M	E	K	L	L
A4G25250	GGGKTT	E	E	H	L	K	N	V	K	T	W	V	S	A	L	T	D	E	G	TC	T	D	G	F	E	EG	R	V	N	V	ET	K	K	K	V	K	A	I	S	E	L	S			
A4G25260	EGDSGEDF	W	F	C	L	S	N	V	R	T	W	T	S	A	A	L	T	D	E	TC	M	D	G	F	GK	A	M	A	G	E	L	K	S	L	I	R	T	H	I	V	S	V	A			
A5G20740	VSGGSKEF	R	F	Q	M	S	N	A	Q	T	W	A	S	A	A	L	T	D	D	D	TC	L	D	G	F	QM	D	D	G	EI	K	T	E	V	K	Q	M	T	K	V	A				
A5G24370Y	V	A	M	K	A	Q	Q	N	A	L	G	Y	I	D	VC	V	E	R	T	N	FF	R	R	T	P	M	V	A	A	N	Y	V	R	L	T	A										
A5G38610E	L	G	T	V	N	V	M	V	S	A	A	M	E	S	A	V	TC	E	N	G	F	RR	D	D	G	D	G	G	G	G	V	T	T	S	P	I	G	N	E	H	L	F				
A5G46930Y	K	T	A	T	M	L	M	S	A	A	M	D	A	P	G	SC	E	T	K	F	T	KR	K	K	A	V	K	S	P	F	T	K	E	N	D	V	L	F								
A5G46940Y	P	T	V	K	T	V	L	S	A	A	M	D	T	P	S	TC	E	T	G	F	K	ER	K	A	P	S	P	V	T	K	E															

1XG2	000000000
	140 150
1XG2	DIVLVISNLLPGS.....
A1G02550	KLCSNVLAI.....
A1G09360	TMSAVS.....
A1G09370	SMEQIV.....
A1G10770	KISSNCLAL.....
A1G11362	IMGLVI.....
A1G14890	RFTSNALAL.....
A1G23205	KMTSNALALV.....
A1G23350	RMADNCLAL.....
A1G47960	NVTRAI.....
A1G48010	GILLSI.....
A1G48020	GIALVIS.....
A1G50325	DIIFVI.....
A1G50340	DIVLVI.....
A1G54620	DVINIPYSF.....
A1G54980	FLALGA.....
A1G55770	KLCKNALMI.....
A1G56100	RKSRFKKM.....
A1G56620	NISLLA.....
A1G60760	KMGTNCLLLATL.....
A1G62760	RLTSNALAL.....
A1G70540	EMADNCLAL.....
A1G70720	KLTSNALAL.....
A2G01610	RLTSNALAL.....
A2G10970	TFVMSVADLL.....
A2G15345	DIDKIFDILLISAKF.....
A2G31425	QITRLI.....
A2G31430	GIILLI.....
A2G31432	KITRVI.....
A2G47050	GKRMSGESVDV.....
A2G47340	KLCSNVLAM.....
A2G47670	RLCSNALAL.....
A3G05741	NMCYVT.....
A3G12880	AL.....
A3G17130	NLCDVAISV.....
A3G17150	NMTADIIRY.....
A3G17152	DMTADI.....
A3G17220	GIVLVI.....
A3G17225	NIDRVF.....
A3G17230_1	SLPLLVLLSITPFSSSLSPSD
A3G17230_2	NIDRVF.....
A3G27999	KILLVI.....
A3G36659	KMVSNC LAI.....
A3G47380	RGTSNALAL.....
A3G47670	QMMSISLAI.....
A3G49330	DAIAYA.....
A3G55680	SIIQVI.....
A3G62180	GKNLTSDFSFDV.....
A3G62820	YLSSNSLAL.....
A4G00080	ETTSNALAF.....
A4G02250	KLCKDALLI.....
A4G03945	KILLVI.....
A4G12390	RVTSNALAL.....
A4G15750	QLTSVAKTL.....
A4G24640	DLAAGA.....
A4G25250	KTTSNTLAL.....
A4G25260	EETSNALAL.....
A5G20740	RVTSNALYM.....
A5G24370	KIASIAGQILAP.....
A5G38610	EFGQIALCI.....
A5G46930	YMVLIPIAF.....
A5G46940	QMILIPLAF.....
A5G46950	KTIVIPLAF.....
A5G46960	KTILIPLAF.....
A5G46970
A5G46980	DMINIPYYF.....
A5G46990	DTV DIAQSF.....
A5G50030	DLAAGA.....
A5G50040	TIAVGA.....
A5G50050	FLAIGA.....
A5G50060	DVALGA.....
A5G50070	PLALAS.....
A5G51520	TTTSNTLAL.....
A5G62340	QEINNAKML.....
A5G62350	HETSNALSL.....
A5G62360	HLTSNALAL.....
A5G64620	RICGVVSGI.....
O49909	SVAKSI.....
1RJ1	DVGRAIVRNLL.....
1X91	GIALVISN.....