Data Supplement - Murphy SC et al.
1,988 component*P. yoelii* liver-stage minigene library design

Minigene number	protein	Predicted allele	Core 9-mer peptide	Predicted affinity (nM)	Full peptide	Minigene coding sequence
P1-1	PY00024	H2-Kd	SFNKTTSFI	31.1	LKDSSFNKTTSFINSKY*	CTGAAGGATAGTAGCTTTAATAAGACCACTAGCTTCATAAATAGTAAGTACTGA
P1-2	PY00030	H2-Kd	FYNNNINII	4.56	QELSFYNNNINIIMDSQ*	CAGGAGTTATCGTTCTATAATAATAACATAAACATAATAATGGACTCCCAGTGA
P1-3	PY00030	H2-Kd	CYYNVSSKI	7.38	RQVSCYYNVSSKIVHCS*	CGGCAAGTATCTTGCTACTATAACGTGAGTAGTAAGATAGTTCATTGCTCTTGA
P1-4	PY00030	H2-Kd	SYDSEHSTI	22.63	LSSHSYDSEHSTIGLRF*	CTGAGTAGCCATAGCTATGATAGTGAGCATAGCACCATAGGCCTGAGGTTTTGA
P1-5	PY00030	H2-Kd	SYICNICSF	39.06	RVLDSYICNICSFNKGK*	AGAGTGCTAGATAGCTACATCTGTAACATCTGTAGCTTTAATAAGGGTAAATGA
P1-6	PY00033	H2-Kd	SYLEMDVKI	13.23	EDRLSYLEMDVKIVGKI*	GAGGATAGACTGAGCTACCTAGAGATGGACGTGAAGATAGTAGGTAAAATATGA
P1-7	PY00033	H2-Kd	CYVAAGSYL	16.33	MTVNCYVAAGSYLSKFK*	ATGACAGTGAATTGCTACGTAGCCGCCGGTAGCTACCTGAGTAAATTTAAGTGA
P1-8	PY00033	H2-Kd	RYNVYDNEI	16.85	ETPPRYNVYDNEIQDKL*	GAAACCCCACCTAGATATAACGTGTATGATAATGAGATCCAGGATAAGCTCTGA
P1-9	PY00033	H2-Kd	TYNKYFDEL	45.12	SHSLTYNKYFDELVGGL*	TCGCATAGCCTAACCTATAATAAGTACTTTGATGAGCTAGTAGGTGGGCTTTGA
P1-10	PY00040	H2-Kd	IYMPSTDTI	2.67	GVNDIYMPSTDTIYFYG*	GGTGTGAATGATATCTACATGCCTAGCACTGACACCATCTACTTTTACGGCTGA
P2-1	PY00040	H2-Kd	KYIDIIQSL	4.69	RKKSKYIDIIQSLPTLT*	CGTAAAAAGTCTAAGTACATAGACATAATCCAGAGCCTGCCTACCTTAACCTGA
P2-2	PY00040	H2-Kd	RYINPFKTI	6.23	LLLRRYINPFKTIISGL*	CTCCTCTTACGTAGATACATAAACCCTTTTAAGACCATAATTTCCGGCTTGTGA
P2-3	PY00040	H2-Kd	KYIEDRLNI	6.87	PETMKYIEDRLNIVFGI*	CCTGAAACGATGAAGTACATAGAGGATAGACTGAACATAGTCTTCGGGATATGA
P2-4	PY00040	H2-Kd	IYNDLHSEI	7.44	IGASIYNDLHSEIFEFY*	ATAGGAGCTTCCATCTATAATGACCTGCATAGTGAGATCTTTGAATTCTATTGA
P2-5	PY00040	H2-Kd	LYLKNVSTL	7.99	KRMCLYLKNVSTLFSVS*	AAAAGAATGTGCCTGTACCTGAAGAACGTGAGCACCCTGTTCTCCGTGAGCTGA
P2-6	PY00040	H2-Kd	YYEDGFTSL	12.34	LTALYYEDGFTSLTSEI*	CTGACCGCACTGTACTATGAGGACGGCTTCACTAGCCTGACCTCTGAAATTTGA
P2-7	PY00040	H2-Kd	HYHRNYLQI	13.5	LQYSHYHRNYLQISLSS*	CTGCAATATAGCCACTACCATAGAAACTACCTGCAGATCTCACTTTCTAGCTGA
P2-8	PY00040	H2-Kd	YYNEDSSEI	15.8	CGVFYYNEDSSEIIIFG*	TGCGGCGTGTTTTACTATAATGAGGATAGTAGTGAGATAATAATCTTCGGCTGA
P2-9	PY00040	H2-Kd	FYSKYKTVL	16.18	SALLFYSKYKTVLFRSK*	AGCGCTCTGCTCTTCTATAGTAAGTATAAGACCGTGCTGTTTAGAAGTAAGTGA
P2-10	PY00040	H2-Kd	LYSNNSNNI	17.9	NHISLYSNNSNNIRENT*	AATCACATTTCCCTGTATAGTAATAATAGTAATAACATCCGTGAAAACACCTGA
P3-1	PY00040	H2-Kd	YFTEMISSI	19.36	LIPLYFTEMISSIRCKD*	CTAATTCCCCTTTACTTCACTGAGATGATAAGTAGCATAAGATGTAAGGATTGA
P3-2	PY00040	H2-Kd	SYNRFNENI	20.44	KVQPSYNRFNENIEFRL*	AAAGTCCAGCCTAGCTATAATAGATTTAATGAGAACATAGAGTTTAGGCTGTGA
P3-3	PY00040	H2-Kd	KYLKRKNEI	21.67	GETRKYLKRKNEIGDPQ*	GGTGAGACTAGAAAGTACCTGAAGAGAAAGAATGAGATAGGTGACCCCCAGTGA
P3-4	PY00040	H2-Kd	KYNNEYNML	24.78	VVDVKYNNEYNMLEPSP*	GTAGTAGATGTGAAGTATAATAATGAGTATAACATGCTAGAGCCTAGCCCATGA
P3-5	PY00040	H2-Kd	KYTWKLNII	25.08	SPSGKYTWKLNIIKEVP*	TCGCCTAGCGGTAAGTACACCTGGAAGCTGAACATAATAAAGGAGGTGCCGTGA
P3-6	PY00040	H2-Kd	FYKNYLAFI	25.73	PTREFYKNYLAFIFINI*	CCTACACGTGAGTTCTATAAGAACTACCTAGCCTTCATCTTCATAAACATCTGA
P3-7	PY00040	H2-Kd	MYKENLYYL	28.94	HSVVMYKENLYYLLRVG*	CATAGCGTAGTGATGTATAAGGAGAACCTGTACTACCTGCTGAGAGTAGGATGA
P3-8	PY00040	H2-Kd	IYYNEMQNI	31.05	ALVRIYYNEMQNILKQE*	GCCTTAGTGAGGATCTACTATAATGAGATGCAGAACATCCTGAAACAGGAGTGA
P3-9	PY00040	H2-Kd	RYSSLPFSL	31.94	EWDNRYSSLPFSLAVEA*	GAATGGGATAATAGATATAGTAGCCTGCCTTTTAGCCTAGCCGTAGAGGCCTGA
P3-10	PY00040	H2-Kd	KQAPIYQSI	32.36	WCLLKQAPIYQSIAIVD*	TGGTGTTTGCTGAAGCAGGCCCCTATCTACCAGAGCATAGCTATAGTAGACTGA
P4-1	PY00040	H2-Kd	FYMAKKVKL	33.88	WPLSFYMAKKVKLSIVL*	TGGCCGCTGTCATTCTACATGGCTAAGAAGGTGAAGCTGTCCATAGTACTCTGA
P4-2	PY00040	H2-Kd	KYNKFPYYL	33.94	AQINKYNKFPYYLVSIL*	GCTCAAATAAATAAGTATAATAAGTTCCCTTACTACCTAGTGAGTATCCTGTGA
P4-3	PY00040	H2-Kd	SYNKLQELI	35.28	AEKASYNKLQELIYPLT*	GCTGAGAAGGCTAGCTATAATAAGCTGCAGGAGCTGATCTATCCTCTGACATGA
P4-4	PY00040	H2-Kd	VYISDLIEI	36.95	TGSIVYISDLIEICSRK*	ACTGGCTCGATAGTGTACATAAGTGACCTGATAGAGATCTGCTCTAGGAAGTGA
P4-5	PY00040	H2-Kd	KHINLKMSI	43.03	LHDGKHINLKMSIYRMF*	CTGCATGATGGTAAGCACATAAACCTGAAGATGAGCATCTATAGAATGTTCTGA
P4-6	PY00040	H2-Kd	IYNNQLYII	46.33	QNWCIYNNQLYIISMVY*	CAGAATTGGTGCATCTATAATAACCAGCTGTACATAATCTCAATGGTCTACTGA
P4-7	PY00040	H2-Kd	KYSLNNNNL	48.73	GPNDKYSLNNNNLPTET*	GGCCCTAATGATAAGTATAGCCTGAATAATAACCTGCCAACTGAAACATGA
P4-8	PY00066	H2-Kd	SYFYSLFLL	6.53	SGTDSYFYSLFLLGFND*	TCCGGCACTGATAGCTACTTCTATAGCCTGTTCCTGCTAGGATTTAATGACTGA
P4-9	PY00066	H2-Kd	SFINGHYFI	7.83	VLSSSFINGHYFIRFST*	GTTCTGTCGTCTAGCTTCATAAACGGCCACTACTTCATAAGATTTAGTACCTGA
P4-10	PY00066	H2-Kd	SYICSNIGI	8.33	LKFESYICSNIGIPGVM*	CTGAAATTTGAGAGCTACATCTGTAGTAACATAGGCATCCCCGGAGTAATGTGA
P5-1	PY00066	H2-Kd	LYFDTAALL	23.35	YQKLLYFDTAALLEYGQ*	TACCAGAAGCTGCTGTACTTTGACACCGCCGCCCTGCTAGAGTACGGGCAGTGA
P5-2	PY00066	H2-Kd	NYISNNENI	28.29	EASINYISNNENIALWN*	GAGGCCTCAATAAACTACATAAGTAATAATGAGAACATAGCACTTTGGAATTGA
P5-3	PY00066	H2-Kd	MYISKILGI	36.87	LMQTMYISKILGIRQLS*	CTAATGCAGACTATGTACATAAGTAAGATCCTAGGCATAAGGCAGCTGAGCTGA
P5-4	PY00066	H2-Ld	SPFHFTFLM	36.68	GDEGSPFHFTFLMALPE*	GGTGATGAAGGTAGCCCTTTCCACTTCACCTTCCTGATGGCCCTGCCTGAATGA
P5-5	PY00067	H2-Kd	FYNYTFNFL	8.27	TRNEFYNYTFNFLREAG*	ACTAGGAATGAATTCTATAACTACACCTTTAACTTCCTGAGGGAGGCTGGTTGA
P5-6	PY00067	H2-Kd	IYIFTNISI	9.34	NIGWIYIFTNISIETTW*	AACATAGGCTGGATCTACATCTTCACTAACATAAGCATAGAAACGACATGGTGA
P5-7	PY00070	H2-Kd	FYINIFNFL	6.71	ILARFYINIFNFLNLEE*	ATACTAGCACGGTTCTACATAAACATCTTTAACTTCCTGAATCTAGAGGAATGA
P5-8	PY00070	H2-Kd	KMNNNISNI	24.56	ELYMKMNNNISNIMMYS*	GAGCTCTATATGAAGATGAATAATAACATAAGTAACATAATGATGTATAGCTGA
P5-9	PY00070	H2-Kd	YQHNNINNI	34	CLVAYQHNNINNITSPA*	TGCCTAGTAGCATACCAGCATAATAACATAAATAACATAACTAGCCCCGCCTGA
P5-10	PY00072	H2-Kd	YYYNYISRL	3.33	PLMLYYYNYISRLKIWN*	CCTCTGATGTTGTACTACTATAACTACATAAGTAGCTGAAAATCTGGAATTGA
P6-1	PY00072	H2-Kd	KYVSVYNTL	5.25	EKLQKYVSVYNTLYPIV*	GAGAAGCTACAGAAGTACGTGAGCGTGTATAACACCCTGTACCCTATAGTTTGA
P6-2	PY00072	H2-Kd	NYYKSQYHI	8.74	SNQVNYYKSQYHISCLI*	TCTAACCAAGTGAACTACTATAAGAGCCAGTACCACATCTCTTGCCTGATCTGA
P6-3	PY00072	H2-Kd	NYYCWYVNI	20.07	VELINYYCWYVNITLNI*	GTAGAACTGATAAACTACTACTGCTGGTACGTGAACATAACCCTGAACATTTGA
P6-4	PY00072	H2-Kd	KYLDYAKTL	23.11	VGGKKYLDYAKTLEGLN*	GTAGGGGGTAAAAAGTACCTAGACTACGCTAAGACCCTAGAAGGACTGAATTGA
P6-5	PY00072	H2-Kd	QYIPLYRTL	32.71	SGQSQYIPLYRTLTKLC*	TCAGGACAGTCTCAGTACATCCCTCTGTATAGAACCCTGACTAAGTTGTGTTGA
P6-6	PY00072	H2-Kd	RYYDTKYFV	48.42	LVRSRYYDTKYFVHLLK*	CTAGTGAGGTCTAGATACTATGACACTAAGTACTTCGTGCATCTTCTGAAGTGA
P6-7	PY00095	H2-Kd	LYIENSSTI	3.47	LTALLYIENSSTIMPVD*	CTGACAGCCTTGCTGTACATAGAGAATAGTAGCACCATAATGCCCGTAGATTGA
P6-8	PY00095	H2-Kd	FYMINTCKI	7.75	ERDDFYMINTCKISVAL*	GAACGTGATGATTTCTACATGATAAACACCTGTAAGATCTCCGTAGCCTTGTGA
P6-9	PY00095	H2-Kd	FYLKGHLII	16.09	NSAAFYLKGHLIIKQEF*	AATTCCGCCGCCTTCTACCTGAAGGGCCACCTGATAATAAAACAAGAGTTTTGA
P6-10	PY00095	H2-Kd	KYIGGLDYV	21.31	SPSGKYIGGLDYVFDKK*	AGTCCTAGCGGTAAGTACATAGGCGGCCTAGACTACGTGTTTGATAAAAAGTGA
P7-1	PY00095	H2-Kd	FYIPSNYFF	34.88	QSYIFYIPSNYFFKTRV*	CAGTCTTACATCTTCTACATCCCTAGTAACTACTTCTTTAAGACCCGCGTCTGA
P7-2	PY00095	H2-Kd	KYPFDISNI	37.29	VATNKYPFDISNIDAAV*	GTAGCCACTAATAAGTACCCTTTTGACATAAGTAACATAGATGCCGCTGTCTGA
P7-3	PY00095	H2-Kd	KQYSNSCSL	47.31	NHVDKQYSNSCSLKPDA*	AACCACGTAGATAAGCAGTATAGTAATAGCTGTAGCCTGAAGCCTGACGCCTGA
P7-4	PY00109	H2-Kd	VYFKNQTNV	39.11	TSYIVYFKNQTNVQVPR*	ACTAGTTATATAGTGTACTTTAAGAACCAGACTAACGTGCAGGTCCCGCGCTGA
P7-5	PY00109	H2-Kd	NYFKKLLPI	44.49	VFGGNYFKKLLPIATPC*	GTTTTCGGGGGTAACTACTTTAAGAAGCTGCTGCCTATAGCAACCCCTTGTTGA
P7-6	PY00109	H2-Ld	HPFLSFLYF	29.56	EHASHPFLSFLYFCAAI*	GAACATGCTAGTCACCCTTTCCTGAGCTTCCTGTACTTCTGTGCCGCAATTTGA
P7-7	PY00110	H2-Kd	LYSSIRTFI	8.29	ETTFLYSSIRTFISPQC*	GAGACCACATTTCTGTATAGTAGCATAAGAACCTTCATCTCGCCTCAGTGCTGA
P7-8	PY00110	H2-Kd	KYKRHFLEI	39.33	HIAPKYKRHFLEIPKSV*	CACATAGCACCTAAGTATAAGAGACACTTCCTAGAGATCCCTAAGTCAGTCTGA
P7-9	PY00115	H2-Kd	LYFENRSKL	10.07	GLWQLYFENRSKLEGSK*	GGTCTGTGGCAGCTGTACTTTGAGAATAGAAGTAAGCTAGAAGGTAGTAAATGA
P7-10	PY00115	H2-Kd	LYLRIATEL	20.4	FLVYLYLRIATELLVQT*	TTTTTAGTGTACCTGTACCTGAGAATAGCCACTGAGCTGCTAGTCCAAACCTGA
P8-1	PY00115	H2-Kd	IYQNQPFFI	25.3	ARVSIYQNQPFFIAGLL*	GCTAGAGTGAGTATCTACCAGAACCAGCCTTTCTTCATAGCTGGTCTCCTGTGA
P8-2	PY00121	H2-Kd	SYNNYYYNI	6.79	IMAASYNNYYYNINVLI*	ATAATGGCTGCTAGCTATAATAACTACTACTATAACATAAACGTCCTGATATGA
P8-3	PY00121	H2-Kd	YYYNIYKQL	17.41	HLPTYYYNIYKQLTNDQ*	CATCTTCCAACATACTACTATAACATCTATAAGCAGCTGACTAATGACCAGTGA
P8-4	PY00130	H2-Kd	IYYITGESI	25.29	VKRCIYYITGESIFETF*	GTGAAGAGGTGCATCTACTACATAACCGGTGAGAGCATCTTTGAGACATTCTGA
P8-5	PY00150	H2-Kd	SYVGTFHYI	2.49	RQKISYVGTFHYIKHKH*	CGACAGAAGATAAGCTACGTAGGCACCTTCCACTACATAAAGCATAAGCACTGA
P8-6	PY00150	H2-Kd	KYNNDHTLI	6.54	HTHPKYNNDHTLITQNP*	CATACCCACCCTAAGTATAATAATGACCACACCCTGATAACTCAGAACCCCTGA
P8-7	PY00150	H2-Kd	SYFNGQENL	6.92	VRTTSYFNGQENLSGIA*	GTTCGCACTACTAGCTACTTTAACGGCCAGGAGAACCTGAGTGGCATAGCATGA
P8-8	PY00150	H2-Kd	VYYKNSQSI	7.36	IVFTVYYKNSQSINKPA*	ATAGTCTTCACCGTGTACTATAAGAATAGCCAGAGCATAAATAAGCCTGCATGA
P8-9	PY00150	H2-Kd	YYMTKAIKI	12.21	GLTKYYMTKAIKISYKA*	GGGTTGACTAAATACTACATGACTAAGGCCATAAAGATCTCTTATAAGGCTTGA
P8-10	PY00150	H2-Kd	QYAKNNNSI	14.41	PEEPQYAKNNNSIKLYE*	CCTGAGGAGCCTCAGTACGCTAAGAATAATAATAGCATAAAGCTCTATGAGTGA
P9-1	PY00150	H2-Kd	IYHEILSII	15.18	SFIAIYHEILSIIGWIQ*	TCCTTCATAGCAATCTACCATGAGATCCTGAGCATAATAGGTTGGATTCAATGA
P9-2	PY00150	H2-Kd	WYIQKYLNI	15.44	EVECWYIQKYLNIWGQI*	GAGGTAGAGTGTTGGTACATCCAGAAGTACCTGAACATCTGGGGGCAGATTTGA
P9-3	PY00150	H2-Kd	NYMASHKNI	15.51	GKDNNYMASHKNIALLG*	GGTAAAGATAATAACTACATGGCTAGCCATAAGAACATAGCCCTTCTAGGCTGA
P9-4	PY00150	H2-Kd	YYTYTNIYI	16.27	NLDLYYTYTNIYISAKI*	AACCTAGACCTGTACTACACCTACACTAACATCTACATAAGCGCTAAAATCTGA
P9-5	PY00150	H2-Kd	TYFQYKINI	18.02	REMATYFQYKINIACNC*	CGTGAAATGGCCACCTACTTCCAGTATAAGATAAACATAGCCTGTAATTGCTGA
P9-6	PY00150	H2-Kd	NYANYINFI	18.16	NLCANYANYINFIPGSF*	AACTTGTGTGCTAACTACGCTAACTACATAAACTTCATCCCTGGCTCTTTTTGA
P9-7	PY00150	H2-Kd	FYYKIMNKI	19.18	LFLVFYYKIMNKIVLFL*	CTGTTCCTAGTGTTCTACTATAAGATAATGAATAAGATAGTCTTGTTTCTCTGA
P9-8	PY00150	H2-Kd	IYIENDFFL	22.99	LVPKIYIENDFFLSSNK*	TTAGTGCCTAAAATCTACATAGAGAATGACTTCTTCCTGTCTAGTAATAAGTGA
P9-9	PY00150	H2-Kd	YHFYMVHNI	23.04	LLQEYHFYMVHNIYFTA*	CTCCTCCAAGAATACCACTTCTACATGGTGCATAACATCTATTTACTGCTTGA
P9-10	PY00150	H2-Kd	RYWYVYKEI	29.11	SVKSRYWYVYKEISRTT*	AGCGTGAAGTCTAGATACTGGTACGTGTATAAGGAGATCTCTCGGACGACTTGA
P10-1	PY00150	H2-Kd	IYYYSSPNL	33.9	MREMIYYYSSPNLNVDP*	ATGCGTGAAATGATCTACTACTATAGTAGCCCTAACCTGAACGTAGACCCCTGA
P10-2	PY00150	H2-Kd	FYLNYERNI	34.76	GPLPFYLNYERNISSSA*	GGACCTCTCCCTTTCTACCTGAACTATGAGAGAAACATAAGCTCTAGTGCCTGA
P10-3	PY00150	H2-Kd	KYIKKEHTM	37.68	RVEKKYIKKEHTMRETM*	CGGGTAGAAAAAAAGTACATAAAGAAGGAGCACACCATGAGGGAGACCATGTGA
P10-4	PY00150	H2-Kd	GYKKNTSTL	39.1	LVGLGYKKNTSTLHQKL*	TTAGTAGGACTAGGCTATAAGAAGAACACTAGCACCCTGCATCAGAAGCTGTGA
P10-5	PY00150	H2-Kd	WFNCSFNFI	42.22	AHGSWFNCSFNFIAWMI*	GCCCACGGTAGCTGGTTTAACTGTAGCTTTAACTTCATAGCCTGGATGATCTGA
P10-6	PY00150	H2-Kd	KMILIVSSI	45.61	LNLSKMILIVSSIDTHH*	CTGAATCTGAGTAAGATGATCCTGATAGTGAGTAGCATAGATACACACCATTGA
P10-7	PY00150	H2-Kd	YYYIVVITL	47.18	LMLPYYYIVVITLRPVD*	CTAATGCTGCCTTACTACTACATAGTAGTGATAACCCTGAGGCCAGTAGATTGA

P10-8	PY00150	H2-Kd	NQYNTISFI	48.6	NFLSNQYNTISFIPFHT*	AATTTTCTGAGTAACCAGTATAACACCATAAGCTTCATCCCATTCCATACGTGA
P10-9	PY00150	H2-Ld	MPERNFDQM	24.06	SRKCMPERNFDQMHRPV	TCTAGAAAGTGCATGCCTGAGAGAAACTTTGACCAGATGCATAGGCCCTGGTGA
P10-10	PY00150	H2-Ld	TPHHYHYYF	40.93	RPQDTPHHYHYYFKEQR'	CGGCCGCAGGACACCCCTCACCACTACCACTACTACTTTAAGGAGCAGAGGTGA
P11-1	PY00154	H2-Kd	QYSPSRETI	14.89	EVGGQYSPSRETIQGLN*	GAAGTAGGAGGCCAGTATAGCCCTAGTAGAGAGACCCTCAAGGCTTAAATTGA
P11-2	PY00155	H2-Kd	KYISNLCDI	5.25	ISELKYISNLCDIQYAY*	ATCTCTGAACTGAAGTACATAAGTAACCTGTGTGACATCCAGTACGCATATTGA
P11-3	PY00155	H2-Kd	KYYPTVVPL	5.34	TRPPKYYPTVVPLHISE*	ACCCGCCCACCTAAGTACTACCCTACCGTAGTGCCTCTGCATATAAGTGAATGA
P11-4	PY00155	H2-Kd	LYNKVSEYL	46.28	SENVLYNKVSEYLFASS*	TCTGAGAACGTGCTGTATAATAAGGTGAGTGAGTACCTGTTTGCTAGCTCCTGA
P11-5	PY00183	H2-Kd	NYASSTTPI	10.51	EASLNYASSTTPIIFLI*	GAGGCTAGTCTGAACTACGCTAGTAGCACCACCCCTATAATCTTCCTGATTTGA
P11-6	PY00183	H2-Kd	KYSENINDI	18.61	KMTGKYSENINDIRRPL*	AAAATGACAGGTAAGTATAGTGAGAACATAAATGACATAAGACGCCCTTTATGA
P11-7	PY00183	H2-Kd	YYKNYLNGI	22.97	GASFYYKNYLNGILYWS*	GGCGCTTCGTTCTACTATAAGAACTACCTGAACGGCATCCTGTATTGGTCATGA
P11-8	PY00183	H2-Kd	NYNKNHNPL	42.66	TLELNYNKNHNPLFPTR*	ACGTTAGAGTTGAACTATAATAAGAACCATAACCCTCTGTTCCCCACTAGATGA
P11-9	PY00183	H2-Ld	IPNINFANI	26.47	SLHSIPNINFANIYFGE*	AGCCTACACTCCATCCCTAACATAAACTTCGCTAACATCTATTTCGGTGAATGA
P11-10	PY00188	H2-Kd	GYYLGEFSI	14.42	DVASGYYLGEFSISEIG*	GACGTAGCGTCCGGCTACTACCTAGGTGAGTTTAGCATCTCTGAAATAGGATGA
P12-1	PY00194	H2-Kd	NYINNIHQI	4.39	QTLKNYINNIHQIYVKP*	CAAACCCTGAAGAACTACATAAATAACATCCACCAGATCTATGTGAAACCTTGA
P12-2	PY00194	H2-Kd	FYDPNYSTL	5.78	SDFDFYDPNYSTLGRQK*	AGTGACTTTGACTTCTATGACCCTAACTATAGCACCCTAGGGCGACAGAAATGA
P12-3	PY00194	H2-Kd	SYIQEAGNI	25.93	YTFNSYIQEAGNIVVNA*	TACACATTTAATAGCTACATCCAGGAGGCCGGTAACATAGTAGTGAATGCTTGA
P12-4	PY00194	H2-Ld	IPYMNLTNL	14.34	ICPSIPYMNLTNLKTGF*	ATCTGTCCTAGCATCCCTTACATGAACCTGACTAACCTGAAGACCGGCTTCTGA
P12-5	PY00230	H2-Kd	VYIKNLVNI	8.47	SQGDVYIKNLVNIDGVN*	AGTCAAGGTGACGTGTACATAAAGAACCTAGTGAACATAGACGGCGTGAACTGA
P12-6	PY00230	H2-Kd	KYILGFFVI	8.87	RISVKYILGFFVIYEMG*	AGGATTTCGGTGAAGTACATCCTAGGCTTCTTCGTGATCTATGAAATGGGTTGA
P12-7	PY00230	H2-Kd	YYILNRVKI	9.08	SLPPYYILNRVKIGNRA*	TCACTGCCACCTTACTACATCCTGAATAGAGTGAAGATAGGTAATAGAGCTTGA
P12-8	PY00230	H2-Kd	SYADTVLNI	18.98	FGKKSYADTVLNIKRAQ*	TTTGGTAAGAAAAGCTACGCTGACACCGTGCTGAACATAAAGCGCGCCCAGTGA
P12-9	PY00230	H2-Kd	SYPYSLSKL	37.09	QWGESYPYSLSKLAISH*	CAGTGGGGTGAAAGCTACCCTTATAGCCTGAGTAAGCTAGCCATCTCACACTGA
P12-10	PY00230	H2-Kd	KYPDNFFHI	48.04	SLSLKYPDNFFHIKSAL*	TCCCTATCCCTGAAGTACCCTGATAACTTCTTCCACATAAAGTCCGCTCTCTGA
P13-1	PY00232	H2-Kd	GYLAIVCVI	24.87	LLGRGYLAIVCVILFQV*	TTACTAGGACGCGGCTACCTAGCCATAGTGTGCGTGATCTTGTTCCAGGTATGA
P13-2	PY00232	H2-Kd	RYFKDPELI	31.68	CRAIRYFKDPELILSPE*	TGTAGAGCCATAAGATACTTTAAGGACCCTGAGCTGATCCTGAGCCCTGAGTGA
P13-3	PY00238	H2-Kd	YYNVTYYFL	8.02	PLEAYYNVTYYFLSALI*	CCTCTAGAAGCTTACTATAACGTGACCTACTACTTCCTGTCTGCTCTAATCTGA
P13-4	PY00238	H2-Kd	YYLFEKNII	22.46	ANIFYYLFEKNIITDCT*	GCTAACATTTTTTACTACCTGTTTGAGAAGAACATAATAACTGATTGCACCTGA
P13-5	PY00238	H2-Kd	IYLFYINLI	39.46	KQQAIYLFYINLIAISY*	AAGCAGCAAGCTATCTACCTGTTCTACATAAACCTGATAGCTATCTCCTATTGA
P13-6	PY00248	H2-Kd	YWFPLIHMI	12.79	EQDPYWFPLIHMIVRCY*	GAGCAAGACCCTTACTGGTTCCCTCTGATCCACATGATAGTGAGGTGCTACTGA
P13-7	PY00248	H2-Kd	NYHLMVYQI	46.09	YVEPNYHLMVYQIYALK*	TACGTAGAACCTAACTACCACCTGATGGTGTACCAGATCTATGCACTGAAGTGA
P13-8	PY00252	H2-Kd	KYFSTLMNL	4.67	KVIPKYFSTLMNLTLNP*	AAAGTAATTCCTAAGTACTTTAGCACCCTGATGAACCTGACCTTAAACCCCTGA
P13-9	PY00252	H2-Kd	YMFDGFSFI	9.73	NQAVYMFDGFSFITYRD*	AATCAGGCTGTGTACATGTTTGACGGCTTTAGCTTCATAACGTATAGAGATTGA
P13-10	PY00286	H2-Kd	FYLSYSFHL	16.32	YKGTFYLSYSFHLSPTS*	TATAAGGGCACATTCTACCTGAGCTATAGCTTCCACCTGTCTCCCACTAGCTGA
P14-1	PY00286	H2-Kd	SYSFHLIPI	19.75	IAYQSYSFHLIPIWSDI*	ATAGCCTACCAGAGCTATAGCTTCCACCTGATCCCTATCTGGTCTGATATCTGA
P14-2	PY00290	H2-Kd	LYFKSYSLI	5.06	VKTPLYFKSYSLIELGH*	GTGAAGACTCCACTGTACTTTAAGAGCTATAGCCTGATAGAATTAGGGCATTGA
P14-3	PY00290	H2-Kd	FYISLIHRL	8.61	WRFEFYISLIHRLFKPA*	TGGCGTTTTGAGTTCTACATAAGCCTGATCCATAGACTGTTTAAGCCCGCCTGA
P14-4	PY00290	H2-Kd	TYFNNCALL	10.22	KTTTTYFNNCALLNFTS*	AAAACTACTACGACCTACTTTAATAACTGCGCCCTGCTGAACTTCACCTCCTGA
P14-5	PY00290	H2-Kd	KYIKADNIL	14.73	ERFIKYIKADNILFERW*	GAACGTTTTATAAAGTACATAAAGGCTGATAACATCCTGTTTGAGCGGTGGTGA
P14-6	PY00290	H2-Kd	NYYFYISLI	16.82	LQLRNYYFYISLIQLDH*	CTGCAACTCCGTAACTACTACTTCTACATAAGCCTGATCCAGTTAGATCACTGA
P14-7	PY00290	H2-Kd	NYINTKNYL	22.01	AKNKNYINTKNYLDARV*	GCTAAGAATAAGAACTACATAAACACTAAGAACTACCTAGACGCCCGAGTTTGA
P14-8	PY00290	H2-Kd	KEMSVIYFI	41.59	QLKNKEMSVIYFIAHQR*	CAGTTGAAGAATAAGGAGATGAGCGTGATCTACTTCATAGCTCATCAGCGGTGA
P14-9	PY00293	H2-Kd	AYIKTQGVI	28.72	FWAPAYIKTQGVILFYA*	TTCTGGGCCCCAGCCTACATAAAGACCCAGGGCGTGATCCTCTTTTACGCATGA
P14-10	PY00293	H2-Kd	KAFAFISYI	44.29	IEYPKAFAFISYIVGRG*	ATAGAGTATCCTAAGGCCTTCGCCTTCATAAGCTACATAGTAGGCCGCGGTTGA
P15-1	PY00331	H2-Kd	IYFHNFHTL	3.59	RKIQIYFHNFHTLMGLT*	CGTAAGATCCAGATCTACTTCCATAACTTCCACACCCTGATGGGACTGACATGA
P15-2	PY00331	H2-Kd	KYINIESLI	4.5	FIQCKYINIESLIALAV*	TTTATCCAGTGTAAGTACATAAACATAGAGAGCCTGATAGCTCTAGCAGTGTGA
P15-3	PY00331	H2-Kd	SYSSYLNNI	5.98	MYTDSYSSYLNNIPVLR*	ATGTACACTGATAGCTATAGTAGCTACCTGAATAACATCCCAGTGCTGAGGTGA
P15-4	PY00331	H2-Kd	KYVHLESEI	7.59	VGGAKYVHLESEINGLL*	GTAGGCGGAGCTAAGTACGTGCACCTAGAGAGTGAGATAAACGGGCTGCTTTGA
P15-5	PY00331	H2-Kd	HYISFPPFI	8	QCYSHYISFPPFIPKKF*	CAGTGCTATTCTCACTACATAAGCTTCCCTCCTTTCATCCCTAAGAAGTTTTGA
P15-6	PY00331	H2-Kd	FYFDKSFYI	10.7	NDLGFYFDKSFYIHGFV*	AATGATCTAGGTTTCTACTTTGATAAGAGCTTCTACATCCACGGCTTCGTGTGA
P15-7	PY00331	H2-Kd	IYFSISLSI	11.41	KTGGIYFSISLSIDYLY*	AAAACTGGTGGAATCTACTTTAGCATAAGCCTGAGCATAGACTACCTATATTGA
P15-8	PY00331	H2-Kd	KYSSTFLKI	11.68	QVIAKYSSTFLKIALHA*	CAGGTGATAGCTAAGTATAGTAGCACCTTCCTGAAGATAGCCCTGCACGCTTGA
P15-9	PY00331	H2-Kd	KYNSSGFYL	15.86	VGVDKYNSSGFYLKCTL*	GTAGGTGTAGATAAGTATAATAGTAGCGGCTTCTACCTGAAGTGCACGTTATGA
P15-10	PY00331	H2-Kd	LYIDYYVSL	16.19	ASCMLYIDYYVSLLTTL*	GCTAGTTGCATGCTGTACATAGACTACTACGTGAGCCTGCTGACCACTCTTTGA
P16-1	PY00331	H2-Kd	KYIFLEIYI	22.04	FQAGKYIFLEIYISTFL*	TTCCAGGCTGGTAAGTACATCTTCCTAGAGATCTACATCTCAACATTCTTGTGA
P16-2	PY00331	H2-Kd	IYQNAKNKI	24.03	VPLPIYQNAKNKISQVR*	GTTCCCCTGCCTATCTACCAGAACGCTAAGAATAAGATCTCACAAGTTCGTTGA
P16-3	PY00331	H2-Kd	FYQNKKYYL	24.76	RASEFYQNKKYYLSLSY*	CGGGCGTCTGAGTTCTACCAGAATAAGAAGTACTACCTGTCACTGAGCTATTGA
P16-4	PY00331	H2-Kd	NYFNSYSGV	36.92	IAYGNYFNSYSGVAISA*	ATAGCATACGGTAACTACTTTAATAGCTATAGCGGCGTAGCTATATCTGCCTGA
P16-5	PY00331	H2-Kd	KYYLAFFFL	45.89	KGTFKYYLAFFFLIFSP*	AAGGGCACGTTTAAGTACTACCTAGCCTTCTTCTTCCTGATCTTTAGTCCTTGA
P16-6	PY00331	H2-Kd	IYIRYYIEL	48.22	SQFKIYIRYYIELEDHR*	TCACAGTTTAAGATCTACATAAGATACTACATAGAGCTAGAGGACCACCGCTGA
P16-7	PY00333	H2-Ld	SPKLNFITL	26.97	SPASSPKLNFITLGALP*	AGTCCTGCGTCTAGCCCTAAGCTGAACTTCATAACCCTAGGGGCTCTCCCCTGA
P16-8	PY00361	H2-Kd	KYAWVLDKL	18.36	KKKDKYAWVLDKLQFMS'	AAAAAGAAGGATAAGTACGCCTGGGTGCTAGATAAGCTGCAGTTCATGAGTTGA
P16-9	PY00398	H2-Kd	KYKNIFENL	43.68	NRDRKYKNIFENLFGAT*	AATAGGGATAGAAAGTATAAGAACATCTTTGAGAACCTGTTCGGCGCAACCTGA
P16-10	PY00433	H2-Kd	SYQNNYNRI	3.57	DSRYSYQNNYNRILKTN*	GATTCTAGGTATAGCTACCAGAATAACTATAATAGAATCCTGAAAACTAACTGA
P17-1	PY00433	H2-Kd	IYITYCTNI	4.69	FLLEIYITYCTNIPCEK*	TTCTTGTTAGAGATCTACATAACCTACTGCACTAACATCCCCTGTGAGAAATGA
P17-2	PY00433	H2-Kd	NYFPMCLSI	4.75	FADLNYFPMCLSIEPFS*	TTCGCTGACCTGAACTACTTCCCTATGTGCCTGAGCATAGAACCCTTTAGTTGA
P17-3	PY00433	H2-Kd	KYFKHILNL	8.94	RNITKYFKHILNLIKGI*	CGTAACATAACTAAGTACTTTAAGCACATCCTGAACCTGATAAAGGGCATATGA
P17-4	PY00433	H2-Kd	YYSIDQNTI	17.05	ERVGYYSIDQNTISGWE*	GAAAGAGTAGGCTACTATAGCATAGACCAGAACACCATAAGCGGCTGGGAATGA
P17-5	PY00433	H2-Kd	KYNRIILSL	18.67	QKPQKYNRIILSLKDPM*	CAGAAGCCTCAGAAGTATAATAGAATAATCCTGAGCCTGAAGGATCCTATGTGA
P17-6	PY00433	H2-Kd	LYFMCNHII	22.02	LSHRLYFMCNHIILDPL*	CTGTCACACCGGCTGTACTTCATGTGTAACCACATAATCCTAGATCCACTGTGA
P17-7	PY00433	H2-Kd	TYINKLMKI	24.43	GKYGTYINKLMKIYPDT*	GGTAAGTATGGTACCTACATAAATAAGCTGATGAAGATCTACCCTGATACCTGA
P17-8	PY00433	H2-Kd	YFLWNPHTL	29.04	FERDYFLWNPHTLWVND	TTTGAACGTGACTACTTCCTGTGGAACCCTCACACCCTGTGGGTGAATGATTGA
P17-9	PY00433	H2-Kd	YYSQFYISL	42.53	QDWAYYSQFYISLSESV*	CAGGATTGGGCCTACTATAGCCAGTTCTACATAAGCCTGAGTGAATCCGTATGA
P17-10	PY00444	H2-Kd	KYFSNLDIL	7.42	WSTLKYFSNLDILFQER*	TGGAGTACACTGAAGTACTTTAGTAACCTAGACATCCTGTTTCAGGAACGTTGA
P18-1	PY00444	H2-Kd	SYTQVFWKI	10.77	ANYVSYTQVFWKIEDVE*	GCTAATTACGTGAGCTACACCCAGGTGTTCTGGAAGATAGAGGACGTAGAATGA
P18-2	PY00444	H2-Kd	RYLSILGAI	14.45	FLSHRYLSILGAIPTHQ*	TTTCTTTCTCATAGATACCTGAGCATCCTAGGCGCCATCCCAACACACCAGTGA
P18-3	PY00444	H2-Kd	FYGKITYSI	15.05	PDRHFYGKITYSISSTV*	CCTGATCGGCACTTCTACGGTAAGATAACCTATAGCATCTCCTCTACCGTCTGA
P18-4	PY00444	H2-Kd	SWIYVLTLI	20.32	DEPQSWIYVLTLIEGGP*	GATGAGCCACAGAGCTGGATCTACGTGCTGACCCTGATAGAAGGAGGCCCTTGA
P18-5	PY00444	H2-Kd	YYINKYNYM	49.52	GSFVYYINKYNYMGQSQ*	GGTTCCTTTGTGTACTACATAAATAAGTATAACTACATGGGACAGTCTCAGTGA
P18-6	PY00444	H2-Ld	FPSITAHIF	37.88	TGYGFPSITAHIFGVCC*	ACCGGGTACGGGTTCCCTAGCATAACCGCCCACATCTTCGGTGTATGTTGTTGA
P18-7	PY00454	H2-Kd	AYMNAVDIL	26.74	SSTDAYMNAVDILPAFT*	AGTAGCACTGACGCCTACATGAACGCCGTAGACATCCTGCCAGCTTTCACCTGA
P18-8	PY00463	H2-Kd	KYKGATWLL	47.74	GHMQKYKGATWLLHFYS	GGTCATATGCAGAAGTATAAGGGCGCCACCTGGCTGCTGCACTTCTATTCGTGA
P18-9	PY00479	H2-Kd	KYFFHNNFI	2.66	HLNLKYFFHNNFIAATE*	CATCTGAATCTGAAGTACTTCTTCCATAATAACTTCATAGCCGCCACTGAATGA
P18-10	PY00479	H2-Kd	SYINATQSI	2.73	YLDESYINATQSICELG*	TACCTAGATGAAAGCTACATAAACGCCACCCAGAGCATCTGTGAGCTAGGGTGA
P19-1	PY00479	H2-Kd	YYLNIYFTI	3.79	AEISYYLNIYFTISEEF*	GCTGAAATATCCTACTACCTGAACATCTACTTCACCATAAGTGAAGAATTCTGA
P19-2	PY00479	H2-Kd	SYIRYLYLI	6.43	LVSTSYIRYLYLILIQN*	CTAGTGAGTACTAGCTACATAAGATACCTGTACCTGATCCTAATTCAAAATTGA
P19-3	PY00479	H2-Kd	YYHNILENL	11.05	KNARYYHNILENLIQDR*	AAAAATGCCCGCTACTACCATAACATCCTAGAGAACCTGATCCAAGATAGATGA
P19-4	PY00479	H2-Kd	YYIKNNKNI	15.68	YDLSYYIKNNKNITTIA*	TATGATCTATCCTACTACATAAAGAATAATAAGAACATAACCACAATAGCATGA
P19-5	PY00479	H2-Kd	KYMEKLKHL	22.55	ECVEKYMEKLKHLGCQA*	GAGTGCGTAGAGAAGTACATGGAGAAGCTGAAGCACCTAGGATGTCAGGCATGA
P19-6	PY00479	H2-Kd	QYRNMFNVI	42.39	APAAQYRNMFNVIPQTT*	GCCCCCGCCGCTCAGTATAGAAACATGTTTAACGTGATCCCACAGACAACCTGA
P19-7	PY00479	H2-Ld	RPLINLSTL	18.6	LLETRPLINLSTLSTVD*	CTCCTAGAGACTAGACCTCTGATAAACCTGAGCACCCTGTCAACTGTAGATTGA
P19-8	PY00487	H2-Kd	SYYKKHENI	13.13	TKRRSYYKKHENIDVVR*	ACTAAGCGCCGTAGCTACTATAAGAAGCATGAGAACATAGACGTAGTGCGCTGA
P19-9	PY00487	H2-Kd	FYNPNKDKL	25.19	YLPEFYNPNKDKLDAPE*	TACCTGCCTGAGTTCTATAACCCTAATAAGGATAAGCTAGACGCTCCTGAATGA
P19-10	PY00487	H2-Kd	FYNNSGEYL	26.28	TVSDFYNNSGEYLGLDQ*	ACAGTGTCTGATTTCTATAATAATAGCGGTGAGTACCTAGGTCTAGACCAATGA
P20-1	PY00487	H2-Kd	KYLDLQNDI	49.21	LAFQKYLDLQNDICNHT*	CTAGCATTCCAGAAGTACCTAGACCTGCAGAATGACATCTGTAACCACACCTGA
P20-2	PY00487	H2-Ld	YPVSNANSF	19.91	IQREYPVSNANSFDLLV*	ATCCAGCGTGAGTACCCTGTGAGTAACGCTAATAGCTTTGATCTGCTAGTCTGA
P20-3	PY00538	H2-Kd	IYNNFLESL	40.99	DADNIYNNFLESLYQAP*	GACGCTGATAATATCTATAATAACTTCCTAGAGAGCCTGTACCAGGCACCATGA
P20-4	PY00543	H2-Kd	KYFPNAKLI	7.68	PGILKYFPNAKLIERTG*	CCAGGAATACTGAAGTACTTCCCTAACGCTAAGCTGATAGAAAGGACCGGCTGA
P20-5	PY00543	H2-Kd	SYNCGITWL	8.09	SQMTSYNCGITWLEGIN*	TCACAAATGACTAGCTATAACTGCGGCATAACCTGGCTAGAAGGCATAAATTGA
P20-6	PY00543	H2-Kd	IYLYNTMVI	15.09	RDYLIYLYNTMVIETGI*	CGTGACTATCTAATCTACCTGTATAACACCATGGTGATAGAAACAGGCATCTGA
P20-7	PY00544	H2-Kd	YYVRILSTL	3.21	ETEPYYVRILSTLAGQY*	GAAACTGAACCCTACTACGTGAGAATCCTGAGCACCCTAGCCGGCCAATACTGA
P20-8	PY00544	H2-Kd	KYYSQISEL	5.1	FKPTKYYSQISELFHEP*	TTTAAGCCGACTAAGTACTATAGCCAGATAAGTGAGCTGTTTCATGAACCTTGA

P20-9	PY00576	H2-Kd	TFIRSYQYI	31.85	GTRATFIRSYQYIGQTH*	GGAACCCGAGCCACCTTCATAAGAAGCTACCAGTACATAGGTCAGACACACTGA
P20-10	PY00598	H2-Ld	YPLYSYFIF	12.84	RDRGYPLYSYFIFLHKL*	CGTGACCGAGGATACCCTCTGTATAGCTACTTCATCTTCCTGCATAAGCTGTGA
P21-1	PY00619	H2-Kd	SYNNYLDYI	6.07	RVDQSYNNYLDYIKLLL*	AGAGTAGATCAGAGCTATAATAACTACCTAGACTACATAAAACTCCTCCTTTGA
P21-2	PY00619	H2-Kd	KYTPNFMIL	12.17	LHDNKYTPNFMILPPNY*	TTGCATGATAATAAGTACACCCCTAACTTCATGATCCTGCCTCCTAACTACTGA
P21-3	PY00619	H2-Kd	RYNKLNLPI	15.95	GHKVRYNKLNLPICYYI*	GGGCATAAGGTGAGATATAATAAGCTGAACCTGCCTATCTGCTACTATATCTGA
P21-4	PY00619	H2-Kd	KYFDPVLNI	16.31	KLAQKYFDPVLNINCSI*	AAACTAGCGCAAAAGTACTTTGACCCTGTGCTGAACATAAATTGTTCCATATGA
P21-5	PY00619	H2-Kd	HYNSYNNYL	18.8	RKEFHYNSYNNYLLARL*	AGAAAGGAGTTCCACTATAATAGCTATAATAACTACCTGCTAGCTAGGCTTTGA
P21-6	PY00619	H2-Kd	RYYSFLALI	18.86	AHFPRYYSFLALITSGF*	GCCCATTTCCCTAGATACTATAGCTTCCTAGCCCTGATAACATCAGGCTTCTGA
P21-7	PY00619	H2-Kd	HYMYMNYNV	21.9	PFLQHYMYMNYNVVKHA	CCCTTTCTCCAACACTACATGTACATGAACTATAACGTAGTGAAACATGCTTGA
P21-8	PY00619	H2-Kd	RYFVIIGHI	26.47	PLDRRYFVIIGHIGQNS*	CCACTAGATAGGAGATACTTCGTGATAATAGGCCACATAGGGCAAAATTCTTGA
P21-9	PY00619	H2-Kd	MYMNYNVFV	34.74	SSLIMYMNYNVFVAKTG*	TCTAGCCTGATAATGTACATGAACTATAACGTGTTCGTAGCTAAAACAGGCTGA
P21-10	PY00619	H2-Kd	CYIQKSPLI	37.41	PTQYCYIQKSPLIQPVP*	CCTACCCAGTATTGCTACATCCAGAAGAGCCCTCTGATCCAGCCCGTCCCCTGA
P22-1	PY00619	H2-Kd	NYFRRNDPL	47.99	REIKNYFRRNDPLSHPK*	CGTGAAATAAAGAACTACTTTAGAAGAAATGACCCTCTGAGCCACCCTAAATGA
P22-2	PY00620	H2-Kd	KYSNFSQQI	12.98	AVKTKYSNFSQQIEGHD*	GCGGTGAAAACTAAGTATAGTAACTTTAGCCAGCAGATAGAGGGGCATGATTGA
P22-3	PY00620	H2-Kd	SYNANIQIL	13.12	SIDSSYNANIQILLRVG*	AGCATAGACTCTAGCTATAACGCTAACATCCAGATCCTGTTGAGAGTAGGCTGA
P22-4	PY00620	H2-Kd	KYSDSKYNI	18.82	NVRIKYSDSKYNIGNEL*	AACGTGAGAATAAAGTATAGTGATAGTAAGTATAACATAGGTAATGAGCTGTGA
P22-5	PY00620	H2-Kd	QYFINNLYI	20.97	VQVVQYFINNLYILLHM*	GTCCAGGTAGTGCAGTACTTCATAAATAACCTGTACATCCTCCTTCATATGTGA
P22-6	PY00624	H2-Kd	TYLSIISAL	15.16	PTRTTYLSIISALAAPD*	CCAACTAGAACAACCTACCTGAGCATAATAAGCGCCCTAGCAGCACCTGACTGA
P22-7	PY00624	H2-Kd	KYDNAWNTL	25.14	PEELKYDNAWNTLIGMR*	CCTGAAGAGCTGAAGTATGATAACGCCTGGAACACCCTGATAGGAATGAGATGA
P22-8	PY00628	H2-Kd	LYLTSSSNI	8.62	VQRALYLTSSSNILPLP*	GTACAGCGCGCACTGTACCTGACTAGTAGTAGTAACATCCTGCCATTGCCCTGA
P22-9	PY00628	H2-Kd	LYGQNINLI	45	DARLLYGQNINLISVLS*	GACGCACGCCTTCTGTACGGCCAGAACATAAACCTGATCTCTGTCCTGAGCTGA
P22-10	PY00638	H2-Kd	KYISFLLFL	24.54	YSGPKYISFLLFLGIHT*	TATAGCGGGCCTAAGTACATAAGCTTCCTGCTGTTCCTAGGAATTCACACTTGA
P23-1	PY00643	H2-Kd	SFIKSFQYI	19.18	RRMQSFIKSFQYIVPLS*	CGCCGAATGCAAAGCTTCATAAAGAGCTTCCAGTACATAGTTCCACTCTCGTGA
P23-2	PY00659	H2-Kd	IYMDKLSSL	8.74	GGQAIYMDKLSSLSAEP*	GGAGGTCAGGCAATCTACATGGATAAGCTGAGTAGCCTGTCCGCTGAGCCCTGA
P23-3	PY00659	H2-Ld	YPHVFVEAF	23.48	VFIDYPHVFVEAFLDRV*	GTATTTATAGACTACCCTCACGTGTTCGTAGAGGCCTTCTTAGACCGCGTGTGA
P23-4	PY00665	H2-Kd	KYAKSLDSI	4.87	SQIVKYAKSLDSITNHI*	TCACAGATAGTGAAGTACGCTAAGAGCCTAGATAGCATAACTAACCACATCTGA
P23-5	PY00665	H2-Kd	KYVKYAKSL	21.6	HLQLKYVKYAKSLRVLT*	CATTTGCAGCTGAAGTACGTGAAGTACGCTAAGAGCCTGAGAGTTCTAACCTGA
P23-6	PY00665	H2-Kd	IFLNMLTNI	30.07	FPRAIFLNMLTNILAQR*	TTTCCCCGTGCTATCTTCCTGAACATGCTGACTAACATCCTAGCCCAGCGTTGA
P23-7	PY00688	H2-Kd	RQFNITHAI	19.34	PTETRQFNITHAIVSKK*	CCAACTGAAACTAGACAGTTTAACATAACCCACGCCATAGTCTCTAAGAAGTGA
P23-8	PY00688	H2-Ld	YPLINGMKL	32.13	TYLVYPLINGMKLGIHP*	ACATACTTAGTGTACCCTCTGATAAACGGCATGAAGCTAGGTATTCACCCTTGA
P23-9	PY00694	H2-Kd	YYVIPKSQI	16.75	EFFVYYVIPKSQIQGIL*	GAGTTCTTTGTATACTACGTGATCCCTAAGAGCCAGATCCAGGGAATCCTCTGA
P23-10	PY00694	H2-Kd	NYYITIPFI	29.37	ARYFNYYITIPFIVIVL*	GCTAGGTATTTTAACTACTACATAACCATCCCTTTCATAGTAATAGTGTTGTGA
P24-1	PY00694	H2-Kd	KYIYIDNLL	31.85	QDGVKYIYIDNLLKKAE*	CAGGATGGCGTGAAGTACATCTACATAGATAACCTGCTGAAGAAAGCTGAATGA
P24-2	PY00694	H2-Kd	IYTGRRSFI	42.03	DVFYIYTGRRSFIEKKQ*	GATGTGTTCTACATCTACACCGGTAGAAGAAGCTTCATAGAGAAGAAGCAGTGA
P24-3	PY00694	H2-Kd	IYSKVDNLI	42.76	LLRPIYSKVDNLIMEHS*	CTCCTACGTCCCATCTATAGTAAGGTAGATAACCTGATAATGGAACACTCGTGA
P24-4	PY00704	H2-Kd	NYNNNVNNI	19.88	LVCRNYNNNVNNIPAKL*	TTAGTGTGTCGTAACTATAATAATAACGTGAATAACATCCCAGCTAAGCTATGA
P24-5	PY00704	H2-Kd	RYEGILYTI	22.66	RTVIRYEGILYTIPKSV*	CGCACTGTAATAAGATATGAGGGCATCCTGTACACCATCCCTAAATCGGTGTGA
P24-6	PY00718	H2-Kd	RYIYNRLIL	17.91	PTNQRYIYNRLILDFGK*	CCAACTAACCAGAGATACATCTATAATAGACTGATCCTAGACTTTGGTAAGTGA
P24-7	PY00718	H2-Kd	NYMVLVFTI	21.82	ESKINYMVLVFTIDAGA*	GAAAGTAAAATAAACTACATGGTGCTAGTGTTCACCATAGATGCCGGAGCTTGA
P24-8	PY00718	H2-Kd	AYIENVSPF	30.49	FSRHAYIENVSPFGFAR*	TTCTCCCGGCATGCCTACATAGAGAACGTGAGCCCTTTCGGGTTCGCGCGGTGA
P24-9	PY00718	H2-Kd	SYSKRSSNL	32.29	MYRHSYSKRSSNLTIPE*	ATGTATAGGCATAGCTATAGTAAGAGAAGTAGTAACCTGACGATACCTGAGTGA
P24-10	PY00718	H2-Kd	NYNNVTQNI	34.98	RAIPNYNNVTQNIHKTL*	CGAGCTATTCCTAACTATAATAACGTGACCCAGAACATCCATAAGACCTTGTGA
P25-1	PY00718	H2-Ld	HPMIQFHAL	29.85	SLNDHPMIQFHALFLIV*	TCCCTGAATGATCACCCTATGATCCAGTCCACGCCCTGTTCCTGATAGTTTGA
P25-2	PY00718	H2-Ld	YPHIYVRIF	40.1	NELCYPHIYVRIFTYMS*	AATGAGCTGTGTTACCCTCACATCTACGTGAGAATCTTCACCTACATGAGTTGA
P25-3	PY00718	H2-Ld	SPFIEKYNM	48.09	TGSKSPFIEKYNMPDNP*	ACTGGATCTAAAAGCCCTTTCATAGAGAAGTATAACATGCCTGATAATCCGTGA
P25-4	PY00738	H2-Kd	SYFPSYIYM	19.63	IQKNSYFPSYIYMAQWD*	ATCCAAAAAAATAGCTACTTCCCTAGCTACATCTACATGGCACAATGGGACTGA
P25-5	PY00738	H2-Kd	SYIYMEHVM	19.88	KLSKSYIYMEHVMVSLT*	AAGCTGAGTAAGAGCTACATCTACATGGAGCACGTGATGGTGAGTCTAACCTGA
P25-6	PY00738	H2-Kd	NYFKGFIII	22.05	GLSQNYFKGFIIILTHY*	GGTCTCTCCCAGAACTACTTTAAGGGCTTCATAATAATCCTAACACATTATTGA
P25-7	PY00738	H2-Ld	IPLSSQYSL	31.25	FLPPIPLSSQYSLTETA*	TTCTTGCCACCCATCCCTCTGAGTAGCCAGTATAGCCTGACTGAGACAGCATGA
P25-8	PY00764	H2-Kd	NYSKNFSFI	6.11	LSLDNYSKNFSFIPDWL*	CTGAGTCTAGATAACTATAGTAAGAACTTTAGCTTCATCCCTGACTGGCTATGA
P25-9	PY00764	H2-Kd	KYNSNILNI	6.44	DVECKYNSNILNIEVQG*	GACGTAGAATGTAAGTATAATAGTAACATCCTGAACATAGAGGTGCAAGGGTGA
P25-10	PY00764	H2-Kd	KYKNIFNTI	8.07	LKASKYKNIFNTIISPP*	CTGAAAGCTAGTAAGTATAAGAACATCTTTAACACCATAATAAGTCCTCCATGA
P26-1	PY00764	H2-Kd	QYIGNVDHI	15.71	VQQYQYIGNVDHITSTN*	GTGCAGCAGTACCAGTACATAGGTAACGTAGACCACATAACATCGACTAACTGA
P26-2	PY00764	H2-Kd	HWICCKYSI	31.8	KSRPHWICCKYSIKYPT*	AAAAGCCGGCCTCACTGGATCTGCTGTAAGTATAGCATAAAATACCCTACGTGA
P26-3	PY00764	H2-Kd	SYCRIKHGI	31.98	LVLWSYCRIKHGIPSVQ*	CTAGTGCTTTGGAGCTACTGTAGAATAAAGCACGGCATCCCTAGCGTTCAGTGA
P26-4	PY00764	H2-Kd	NYYKLKYQI	34.1	VPTVNYYKLKYQIVESQ*	GTCCCAACTGTGAACTACTATAAGCTGAAGTACCAGATAGTAGAGTCTCAGTGA
P26-5	PY00764	H2-Ld	YPHFNDYQL	16.12	DLLPYPHFNDYQLNEFR*	GACTTGCTGCCATACCCTCACTTTAATGACTACCAGCTGAATGAGTTTCGCTGA
P26-6	PY00764	H2-Ld	FPFNHLYNF	19.42	AFVLFPFNHLYNFLWTS*	GCCTTTGTGTTATTCCCTTTTAACCACCTGTATAACTTCTTATGGACTTCTTGA
P26-7	PY00764	H2-Ld	MPMAGNNLL	33.36	SAISMPMAGNNLLYDFK*	TCAGCTATCTCCATGCCTATGGCCGGTAATAACCTGCTGTATGACTTTAAATGA
P26-8	PY00768	H2-Kd	YYVNILSFV	20.98	TYRLYYVNILSFVFRLY*	ACTTATAGGCTGTACTACGTGAACATCCTGAGCTTCGTGTTTAGGCTCTATTGA
P26-9	PY00769	H2-Kd	KYDNNGNPI	22.59	TKVRKYDNNGNPISTTQ*	ACTAAAGTGCGTAAGTATGATAATAACGGTAACCCTATAAGCACAACCCAGTGA
P26-10	PY00769	H2-Kd	KMFNLNTII	25.82	MVEYKMFNLNTIISCHE*	ATGGTAGAGTATAAGATGTTTAACCTGAACACCATAATAAGCTGCCATGAATGA
P27-1	PY00769	H2-Kd	NYNQSSSFL	26.89	PSLANYNQSSSFLTFEP*	CCTTCGTTAGCTAACTATAACCAGAGTAGTAGCTTCCTGACTTTTGAGCCTTGA
P27-2	PY00769	H2-Kd	IYIKIKEGI	38.8	NRIQIYIKIKEGITIDI*	AATAGAATCCAGATCTACATAAAGATAAAGGAGGGCATAACGATAGACATCTGA
P27-3	PY00769	H2-Kd	KYRISINNI	44.78	YHSAKYRISINNINLSV*	TATCACTCTGCTAAGTATAGAATAAGCATAAATAACATAAACCTGAGCGTCTGA
P27-4	PY00769	H2-Kd	KYYFQEEGI	46.64	NKECKYYFQEEGIFLFA*	AATAAGGAGTGTAAGTACTACTTCCAGGAGGAGGGCATCTTTCTGTTCGCATGA
P27-5	PY00775	H2-Kd	TYMSSNFGI	5.83	ASLKTYMSSNFGIEGVD*	GCATCCCTGAAGACCTACATGAGTAGTAACTTCGGCATAGAAGGAGTAGACTGA
P27-6	PY00775	H2-Kd	TYGFLLSVI	25.85	GFKMTYGFLLSVITKFK*	GGCTTTAAGATGACCTACGGCTTCCTGCTGAGCGTGATAACTAAGTTTAAGTGA
P27-7	PY00775	H2-Kd	LYYLWFSFL	48.5	QMVPLYYLWFSFLEDCS*	CAGATGGTCCCTCTGTACTACCTGTGGTTTAGCTTCCTAGAGGACTGTTCTTGA
P27-8	PY00775	H2-Ld	YPRINSISL	30.92	RQDSYPRINSISLSGQL*	CGCCAGGATTCTTACCCTAGAATAAATAGCATAAGCCTGAGCGGTCAACTGTGA
P27-9	PY00796	H2-Kd	IYMVSKNNI	5.35	SLRVIYMVSKNNICAQP*	AGTTTGAGGGTGATCTACATGGTGAGTAAGAATAACATCTGCGCCCAGCCATGA
P27-10	PY00796	H2-Kd	YYNLNYMPI	6.92	AGAIYYNLNYMPIASLG*	GCGGGCGCCATCTACTATAACCTGAACTACATGCCTATAGCTAGCCTAGGCTGA
P28-1	PY00796	H2-Kd	SYINNKSYV	7.66	RILHSYINNKSYVFMRK*	AGGATTCTCCATAGCTACATAAATAATAAGAGCTACGTGTTTATGAGGAAGTGA
P28-2	PY00796	H2-Kd	FYNNHSIFI	19.44	KRFMFYNNHSIFIIEQP*	AAAAGGTTCATGTTCTATAATAACCATAGCATCTTCATAATAGAGCAACCCTGA
P28-3	PY00796	H2-Kd	SYSKSNNEL	22.86	YHLRSYSKSNNELVDDE*	TATCACCTGAGGAGCTATAGTAAGAGTAATAATGAGCTAGTAGATGATGAATGA
P28-4	PY00796	H2-Kd	RYIFLYYVL	30.68	MNPLRYIFLYYVLLSLI*	ATGAACCCTCTGAGATACATCTTCCTGTACTACGTGCTGCTGTCCTTGATTTGA
P28-5	PY00796	H2-Kd	IYMTLLECI	37.06	IHYDIYMTLLECINDED*	ATTCACTATGACATCTACATGACCCTGCTAGAGTGCATAAATGATGAGGATTGA
P28-6	PY00801	H2-Kd	YYNNMGSVI	2.89	TVFAYYNNMGSVILFAQ*	ACAGTCTTCGCATACTATAATAACATGGGTAGCGTGATCTTGTTTGCTCAGTGA
P28-7	PY00801	H2-Kd	SYISNFINL	6.55	MEVESYISNFINLRRDQ*	ATGGAGGTAGAAAGCTACATAAGTAACTTCATAAACCTGAGACGTGACCAGTGA
P28-8	PY00801	H2-Kd	KYVVNFYLI	7.39	LSYEKYVVNFYLIEAEA*	CTTTCCTATGAGAAGTACGTAGTGAACTTCTACCTGATAGAGGCTGAAGCCTGA
P28-9	PY00801	H2-Kd	YYLAIAFFI	8.93	GSLYYYLAIAFFILYEH*	GGTAGCCTGTATTACTACCTAGCCATAGCCTTCTTCATCTTATATGAGCATTGA
P28-10	PY00801	H2-Kd	YYMHNKEML	9.62	IAATYYMHNKEMLVSGQ*	ATAGCAGCTACCTACTACATGCATAATAAGGAGATGCTAGTGAGCGGACAGTGA
P29-1	PY00801	H2-Kd	KYYNNMGSV	18.44	PKGEKYYNNMGSVLLQK*	CCTAAGGGTGAGAAGTACTATAATAACATGGGTAGCGTGCTGCTTCAAAAATGA
P29-2	PY00801	H2-Kd	VYFIVASFL	19.53	TAPSVYFIVASFLHLRS*	ACGGCCCCTAGCGTGTACTTCATAGTAGCTAGCTTCCTGCACTTGCGTAGTTGA
P29-3	PY00801	H2-Kd	FQIQNITNI	25.48	ILYKFQIQNITNITLDK*	ATTTTGTATAAGTTCCAGATCCAGAACATAACTAACATAACACTAGATAAGTGA
P29-4	PY00801	H2-Kd	SYTNKYFFL	33.16	KFDSSYTNKYFFLGYEL*	AAATTTGACTCTAGCTACACTAATAAGTACTTCTTCCTAGGCTATGAGCTGTGA
P29-5	PY00801	H2-Kd	KYYILKYKI	36.06	TVNGKYYILKYKIQADE*	ACAGTGAATGGTAAGTACTACATCCTGAAGTATAAGATCCAGGCTGATGAATGA
P29-6	PY00801	H2-Kd	LYINCYFLL	37.89	QLKSLYINCYFLLDPPY*	CAGCTGAAATCACTGTACATAAACTGCTACTTCCTGCTAGACCCGCCCTATTGA
P29-7	PY00801	H2-Ld	SPINANFLF	40.39	CGHTSPINANFLFISEP*	TGTGGGCATACTAGCCCTATAAACGCTAACTTCCTGTTCATAAGTGAGCCTTGA
P29-8	PY00802	H2-Kd	SYNKLYSHL	8.46	IGLQSYNKLYSHLTKTK*	ATAGGCCTGCAGAGCTATAATAAGCTGTATAGCCACCTGACTAAGACTAAGTGA
P29-9	PY00802	H2-Kd	RYHHYNFFI	12.22	ECGHRYHHYNFFIAPEE*	GAATGCGGTCATAGATACCACCACTATAACTTCTTCATAGCCCCTGAGGAATGA
P29-10	PY00802	H2-Kd	NYHKTGTPI	21.82	NSTMNYHKTGTPIPKAF*	AATAGTACCATGAACTACCATAAGACCGGCACCCCTATCCCTAAAGCATTCTGA
P30-1	PY00802	H2-Kd	LYNNLQQYI	29.48	HSPPLYNNLQQYIDSSK*	CACTCTCCACCACTGTATAATAACCTGCAGCAGTACATAGATAGTAGTAAGTGA
P30-2	PY00818	H2-Kd	KYNNNSDQI	10.44	RLVPKYNNNSDQIESEG*	CGGTTAGTACCTAAGTATAATAATAATAGTGACCAGATAGAATCTGAGGGATGA
P30-3	PY00818	H2-Kd	LYGPKTSEI	34.08	VSTWLYGPKTSEIQGRI*	GTCTCCACCTGGCTGTACGGCCCTAAGACTAGTGAGATCCAGGGTAGGATCTGA
P30-4	PY00834	H2-Kd	SYSSGYSEL	6.26	DSHMSYSSGYSELEPGE*	GACTCACACATGAGCTATAGTAGCGGCTATAGTGAGCTAGAACCCGGTGAATGA
P30-5	PY00834	H2-Kd	NYYDNIHNI	6.82	LVPLNYYDNIHNIADEC*	CTAGTCCCACTGAACTACTATGATAACATCCATAACATAGCTGATGAATGCTGA
P30-6	PY00834	H2-Kd	KYLFITNII	11.83	RIKLKYLFITNIISYAG*	CGGATAAAGCTGAAGTACCTGTTCATAACTAACATAATCTCCTATGCCGGATGA
P30-7	PY00834	H2-Kd	NYFISIDTI	13.18	SSTRNYFISIDTILAAF*	AGTTCTACTAGGAACTACTTCATAAGCATAGACACCATCCTAGCCGCATTTTGA
P30-8	PY00834	H2-Kd	AYNNIGTNI	16.53	PLILAYNNIGTNIEQKL*	CCACTAATACTAGCCTATAATAACATAGGCACTAACATAGAGCAGAAACTGTGA
P30-9	PY00834	H2-Kd	RYGDNNSTL	16.98	TRLLRYGDNNSTLLWGQ*	ACACGCCTCCTGAGATACGGTGATAATAATAGCACCCTGCTGTGGGGACAATGA

P30-10	PY00834	H2-Kd	FYLKTILLI	27.59	MSLKFYLKTILLIGSVP*	ATGTCGTTAAAGTTCTACCTGAAGACCATCCTGCTGATAGGTTCTGTGCCATGA
P31-1	PY00834	H2-Kd	KYILVFIKI	34.22	FKRDKYILVFIKISTML*	TTTAAGAGAGATAAGTACATCCTAGTGTTCATAAAGATAAGTACAATGTTATGA
P31-2	PY00834	H2-Kd	IYTFIISKI	41.66	RATAIYTFIISKIPEDL*	AGAGCAACAGCAATCTACACCTTCATAATAAGTAAGATCCCTGAGGACCTCTGA
P31-3	PY00834	H2-Kd	LYNNSRDNL	48.24	CDISLYNNSRDNLKFNA*	TGTGACATCTCACTGTATAATAATAGTAGAGATAACCTGAAATTTAACGCTTGA
P31-4	PY00851	H2-Kd	KWNKYTSFI	13.08	LARGKWNKYTSFIPQLR*	CTAGCCCGAGGTAAGTGGAATAAGTACACTAGCTTCATCCCACAACTGAGGTGA
P31-5	PY00851	H2-Kd	SFIQNRDTI	19.77	FRSMSFIQNRDTITSPT*	TTTAGGTCCATGAGCTTCATCCAGAATAGAGACACCATAACTTCACCCACATGA
P31-6	PY00851	H2-Ld	YPFNMPISL	21.82	EISIYPFNMPISLNRMG*	GAAATAAGCATCTACCCTTTTAACATGCCTATAAGCCTGAATAGAATGGGGTGA
P31-7	PY00851	H2-Ld	FPPCMRRIF	46.1	YYEDFPPCMRRIFTHVN*	TACTATGAGGATTTCCCTCCTTGCATGAGAAGAATCTTCACTCATGTGAACTGA
P31-8	PY00855	H2-Kd	IYVVSINYI	13.03	LQLPIYVVSINYIDAEA*	CTACAGTTGCCCATCTACGTAGTGAGCATAAACTACATAGATGCTGAGGCATGA
P31-9	PY00855	H2-Kd	YYWADHFGI	13.36	QGFNYYWADHFGIRPIV*	CAGGGTTTTAATTACTACTGGGCTGACCACTTCGGCATAAGACCCATAGTTTGA
P31-10	PY00855	H2-Kd	VYVNSLYEL	18.92	VFKQVYVNSLYELLNRK*	GTCTTTAAGCAGGTGTACGTGAATAGCCTGTATGAGCTGTTAAACCGTAAATGA
P32-1	PY00855	H2-Kd	AYINSFHYF	36.17	EYSSAYINSFHYFQEIL*	GAGTATAGTTCCGCCTACATAAATAGCTTCCACTACTTCCAAGAAATACTGTGA
P32-2	PY00896	H2-Kd	KYMNIKNGL	7.42	LDYAKYMNIKNGLEAGC*	TTAGACTACGCTAAGTACATGAACATAAAGAACGGCCTAGAGGCCGGCTGTTGA
P32-3	PY00896	H2-Kd	NYFYSIINL	43.15	YCDKNYFYSIINLLNGT*	TATTGTGATAAGAACTACTTCTATAGCATAATAAACCTGCTGAACGGAACATGA
P32-4	PY00896	H2-Kd	SYENKMSNI	46.6	KTNCSYENKMSNIERFE*	AAGACTAATTGTAGCTATGAGAATAAGATGAGTAACATAGAGCGGTTTGAGTGA
P32-5	PY00915	H2-Kd	GYLAILWKI	33.52	EDQAGYLAILWKIVMIG*	GAAGATCAAGCAGGCTACCTAGCCATCCTGTGGAAGATAGTGATGATAGGCTGA
P32-6	PY00916	H2-Kd	SYIEVLEHL	5.41	KEKDSYIEVLEHLSLAH*	AAAGAGAAAGATAGCTACATAGAGGTGCTAGAGCACCTGAGTCTAGCGCACTGA
P32-7	PY00916	H2-Kd	VYTYMSFNI	20.97	RYHSVYTYMSFNIFVRE*	AGGTACCATAGCGTGTACACCTACATGAGCTTTAACATCTTTGTGCGTGAATGA
P32-8	PY00916	H2-Kd	LYNRNLIQL	36.45	QIANLYNRNLIQLEIYM*	CAAATAGCTAATCTGTATAATAGAAACCTGATCCAGCTAGAGATATATATGTGA
P32-9	PY00916	H2-Kd	KYVKYTKNL	37.13	SIFPKYVKYTKNLQIQT*	TCCATTTTCCCTAAGTACGTGAAGTACACTAAGAACCTGCAGATCCAGACTTGA
P32-10	PY00916	H2-Kd	KQEAMRTYI	39.02	GVGIKQEAMRTYIGPAT*	GGAGTAGGGATAAAGCAGGAGGCCATGAGAACCTACATAGGACCTGCCACTTGA
P33-1	PY00928	H2-Kd	YMYTNSSEI	30.69	TNPIYMYTNSSEILEEV*	ACTAACCCTATTTACATGTACACTAATAGTAGTGAGATCTTAGAGGAGGTGTGA
P33-2	PY00959	H2-Kd	YYLQNYMQL	8.42	SAFSYYLQNYMQLGIIV*	AGCGCATTTTCATACTACCTGCAGAACTACATGCAGCTAGGGATAATAGTGTGA
P33-3	PY00959	H2-Kd	IYINFNNNI	9.76	KALYIYINFNNNIGRKP*	AAAGCCTTGTACATCTACATAAACTTTAATAATAACATAGGCCGTAAGCCTTGA
P33-4	PY00959	H2-Kd	FYSDFTSYI	10.03	DWMSFYSDFTSYIRVEM*	GACTGGATGAGCTTCTATAGTGACTTCACTAGCTACATAAGGGTAGAGATGTGA
P33-5	PY00959	H2-Kd	KYLKYKEFI	11.21	GADVKYLKYKEFILESE*	GGTGCTGATGTGAAGTACCTGAAGTATAAGGAGTTCATCCTAGAATCTGAATGA
P33-6	PY00959	H2-Kd	IYAENLQYI	14.36	TVSFIYAENLQYIAGAQ*	ACGGTGAGTTTCATCTACGCTGAGAACCTGCAGTACATAGCAGGCGCACAGTGA
P33-7	PY00959	H2-Kd	TYNDNNNPI	16.07	PNTFTYNDNNNPICVLF*	CCTAACACTTTCACCTATAATGATAATAATAACCCTATCTGTGTGCTCTTCTGA
P33-8	PY00959	H2-Kd	LYFTLFNII	16.45	WGEILYFTLFNIIEPLG*	TGGGGTGAAATTCTGTACTTCACCCTGTTTAACATAATAGAACCGCTAGGGTGA
P33-9	PY00959	H2-Kd	NYINNNEII	19.99	DLLSNYINNNEIISLNQ*	GATCTCCTGAGTAACTACATAAATAATAATGAGATAATCTCACTGAATCAGTGA
P33-10	PY00959	H2-Kd	KYIKGDIDI	21.61	IGCQKYIKGDIDILMPA*	ATAGGATGCCAAAAGTACATAAAGGGTGACATAGACATCCTGATGCCAGCCTGA
P34-1	PY00959	H2-Kd	SYHFCLYML	25.75	RKLSSYHFCLYMLQSAD*	AGAAAACTGAGTAGCTACCACTTCTGCCTGTACATGCTGCAGTCTGCTGATTGA
P34-2	PY00959	H2-Kd	NYITLSNII	26.07	NRVYNYITLSNIIAHGE*	AATAGAGTCTATAACTACATAACCCTGAGTAACATAATAGCCCATGGTGAATGA
P34-3	PY00959	H2-Kd	QYYLNCLPI	26.85	TAREQYYLNCLPICVVA*	ACCGCTAGGGAGCAGTACTACCTGAACTGCCTGCCTATCTGTGTAGTAGCGTGA
P34-4	PY00959	H2-Kd	KYLILKQYI	27.43	NPALKYLILKQYIFNER*	AACCCCGCCCTGAAGTACCTGATCCTGAAGCAGTACATCTTTAATGAGCGGTGA
P34-5	PY00959	H2-Kd	FYHCNHLFM	35.91	KGGVFYHCNHLFMELPW	AAGGGAGGAGTGTTCTACCACTGTAACCACCTGTTCATGGAGCTGCCGTGGTGA
P34-6	PY00959	H2-Kd	SFIDNIQSL	39.08	LASFSFIDNIQSLERLF*	CTAGCTAGCTTTAGCTTCATAGATAACATCCAGAGCCTAGAAAGACTGTTTTGA
P34-7	PY00959	H2-Kd	KYSIAKNII	40.09	ISNCKYSIAKNIIIPSR*	ATAAGTAACTGTAAGTATAGCATAGCTAAGAATAATAATCCCTAGTAGGTGA
P34-8	PY00959	H2-Kd	TYNNVVFLL	40.86	DREVTYNNVVFLLGPLP*	GATCGTGAGGTGACCTATAATAACGTAGTGTTCCTGCTAGGTCCTCTGCCCTGA
P34-9	PY00959	H2-Kd	SYFYFLDLL	44.39	EDGNSYFYFLDLLVPSK*	GAAGACGGTAATAGCTACTTCTACTTCCTAGACCTGCTAGTGCCTAGTAAGTGA
P34-10	PY00959	H2-Ld	YPYQSKYVM	15.97	NAFLYPYQSKYVMHAWD	AACGCTTTCCTCTACCCTTACCAGAGTAAGTACGTGATGACGACGCCTGGGATTGA
P35-1	PY00959	H2-Ld	LPNMNRNNF	33.54	TGGNLPNMNRNNFLSIF*	ACAGGGGGTAACCTGCCTAACATGAATAGAAATAACTTCTTAAGTATCTTCTGA
P35-2	PY00959	H2-Ld	SPIASTNIL	39.9	HSVLSPIASTNILLHTE*	CATTCCGTGCTGAGCCCTATAGCTAGCACTAACATCCTGCTCCATACTGAGTGA
P35-3	PY00967	H2-Kd	SYNSDRNSI	6.93	SCQASYNSDRNSIRAAL*	AGCTGTCAGGCTAGCTATAATAGTGATAGAAATAGCATCCGTGCCGCGCTTTGA
P35-4	PY00967	H2-Kd	KYFQDNDYI	10.15	ETLWKYFQDNDYISNEL*	GAAACTCTGTGGAAGTACTTCCAGGATAATGACTACATAAGTAATGAGCTGTGA
P35-5	PY00967	H2-Kd	LYIDMEYKL	28.57	FNSTLYIDMEYKLPQFC*	TTTAATTCTACCCTGTACATAGACATGGAGTATAAGCTGCCTCAGTTTTGCTGA
P35-6	PY00967	H2-Kd	LYMDKINYL	45.04	KSVYLYMDKINYLKRHN*	AAGTCCGTCTATCTGTACATGGATAAGATAAACTACCTGAAACGGCATAATTGA
P35-7	PY00972	H2-Kd	FYHTSKPLI	12.92	EDSLFYHTSKPLIYIAN*	GAGGATAGTCTATTCTACCACACTAGTAAGCCTCTGATCTATATAGCTAATTGA
P35-8	PY00972	H2-Kd	CYQKKDNTI	36.92	ARHCCYQKKDNTITLTT*	GCTAGGCATTGCTGCTACCAGAAGAAGGATAACACCATAACCCTAACCACATGA
P35-9	PY01008	H2-Kd	KMIEVISPI	13.95	SGTPKMIEVISPILLIH*	TCAGGTACACCTAAGATGATAGAGGTGATAAGCCCTATCCTCCTGATTCATTGA
P35-10	PY01008	H2-Kd	AYRNNWNSI	17.38	ASKLAYRNNWNSITLGP*	GCTTCTAAGCTAGCCTATAGAAATAACTGGAATAGCATAACACTAGGACCATGA
P36-1	PY01008	H2-Kd	LYNSDNNHI	40.31	RGVALYNSDNNHINETD*	AGAGGGGTAGCTCTGTATAATAGTGATAATAACCACATAAATGAAACTGATTGA
P36-2	PY01027	H2-Kd	KYIDYIKYI	9.12	KVRMKYIDYIKYIIAES*	AAGGTACGCATGAAGTACATAGACTACATAAAGTACATAATAGCTGAGTCCTGA
P36-3	PY01027	H2-Kd	KFLFNYSML	43.25	MLQAKFLFNYSMLYRPA*	ATGCTGCAAGCTAAGTTCCTGTTTAACTATAGCATGCTGTATAGGCCGGCCTGA
P36-4	PY01029	H2-Kd	GYIHTCACI	12.59	QRLLGYIHTCACIQEAC*	CAGCGCCTTCTAGGCTACATCCACACCTGCGCCTGCATCCAGGAAGCGTGCTGA
P36-5	PY01034	H2-Kd	LYINYLSFI	5.85	TFRQLYINYLSFIVLAV*	ACTTTTAGGCAACTGTACATAAACTACCTGAGCTTCATAGTGTTAGCAGTGTGA
P36-6	PY01034	H2-Kd	KYFVYLLYI	13.28	IIKGKYFVYLLYIQDHA*	ATAATAAAGGGTAAGTACTTCGTGTACCTGCTGTACATCCAAGACCACGCTTGA
P36-7	PY01034	H2-Kd	HYMKTELYL	14.12	ITKSHYMKTELYLGPFQ*	ATAACTAAAAGCCACTACATGAAGACTGAGCTGTACCTAGGTCCTTTCCAGTGA
P36-8	PY01034	H2-Kd	SYINKNNIL	15.88	DQVLSYINKNNILAAAY*	GATCAGGTGTTAAGCTACATAAATAAGAATAACATCCTAGCAGCCGCCTACTGA
P36-9	PY01034	H2-Kd	SFIFTNTKI	38.42	TSLLSFIFTNTKIYFIA*	ACTTCTTTATTAAGCTTCATCTTCACTAACACTAAGATCTACTTTATAGCGTGA
P36-10	PY01034	H2-Kd	TYLYLCFRI	45.21	DLQSTYLYLCFRIAGNL*	GATCTGCAGTCCACCTACCTGTACCTGTGCTTTAGAATAGCAGGTAATCTATGA
P37-1	PY01046	H2-Kd	AYNTGFQSI	5.49	TAKIAYNTGFQSIAPAQ*	ACGGCTAAAATAGCCTATAACACCGGCTTCCAGAGCATAGCCCCCGCGCAGTGA
P37-2	PY01046	H2-Kd	SYNNKRVSI	17.99	GFCVSYNNKRVSIKIEL*	GGCTTCTGCGTGAGCTATAATAATAAGAGAGTGAGCATAAAGATAGAACTTTGA
P37-3	PY01046	H2-Kd	IYNTVYDEL	30.15	VVETIYNTVYDELVLST*	GTAGTAGAGACAATCTATAACACCGTGTATGATGAGCTAGTGCTGAGTACCTGA
P37-4	PY01046	H2-Kd	NYYSLIWKI	41.52	YHELNYYSLIWKIDNFG*	TATCATGAGCTGAACTACTATAGCCTGATCTGGAAGATAGATAACTTTGGCTGA
P37-5	PY01063	H2-Kd	RYISDNNVI	6.55	QNPRRYISDNNVIKSHF*	CAGAACCCGCGTAGATACATAAGTGATAATAACGTGATAAAGTCACATTTCTGA
P37-6	PY01063	H2-Kd	TYLTNQTHL	11.82	PWAPTYLTNQTHLISPL*	CCTTGGGCTCCCACCTACCTGACTAACCAGACCCACCTGATAAGCCCCCTGTGA
P37-7	PY01063	H2-Kd	KYVKTNFYL	12.42	LISTKYVKTNFYLRQAI*	CTGATATCAACTAAGTACGTGAAGACTAACTTCTACCTGAGGCAGGCTATTTGA
P37-8	PY01063	H2-Kd	IYSKYGSNI	16.86	SGRAIYSKYGSNITSLE*	TCTGGTCGGGCTATCTATAGTAAGTACGGTAGTAACATAACATCGCTAGAGTGA
P37-9	PY01063	H2-Kd	KYSQLNLAI	23.64	ILLVKYSQLNLAIRKGV*	ATTTTGCTAGTGAAGTATAGCCAGCTGAACCTAGCCATAAGAAAGGGGGTTTGA
P37-10	PY01063	H2-Kd	QYFDNNIII	34.22	VSQPQYFDNNIIIAESP*	GTGAGCCAGCCTCAGTACTTTGATAATAACATAATAATAGCTGAGAGCCCATGA
P38-1	PY01063	H2-Kd	PYISTILSI	34.82	SNHTPYISTILSIRRMR*	TCTAATCATACTCCTTACATAAGCACCATCCTGAGCATAAGAAGGATGAGATGA
P38-2	PY01063	H2-Kd	KQFSKRNEI	43.75	SDFTKQFSKRNEIRHQE*	AGTGATTTTACTAAGCAGTTTAGTAAGAGAAATGAGATAAGGCACCAGGAATGA
P38-3	PY01063	H2-Kd	tYIVLCEKI	49.81	QLGITYIVLCEKIQLRE*	CAGCTAGGCATAACCTACATAGTGCTGTGTGAGAAGATCCAGCTGCGTGAATGA
P38-4	PY01063	H2-Kd	iYIVLCEKI	49.81	SGLSIYIVLCEKIIKHS*	AGCGGTCTGTCAATCTACATAGTGCTGTGTGAGAAGATAATAAAACATTCTTGA
P38-5	PY01065	H2-Kd	YYINEVNNI	7.11	TKVIYYINEVNNIAETN*	ACTAAAGTGATTTACTACATAAATGAGGTGAATAACATAGCTGAAACTAATTGA
P38-6	PY01065	H2-Kd	KYISRSINL	12.46	SFNPKYISRSINLRPDA*	AGTTTTAATCCTAAGTACATAAGTAGAAGCATAAACCTGCGCCCTGACGCATGA
P38-7	PY01065	H2-Kd	YYVLSKNGI	17.93	SPSQYYVLSKNGIWGDR*	TCCCCTAGCCAGTACTACGTGCTGAGTAAGAACGGCATCTGGGGTGATCGCTGA
P38-8	PY01065	H2-Kd	FFISYINTI	19.3	SLSAFFISYINTIQKYP*	TCCCTCTCCGCATTCTTCATAAGCTACATAAACACCATCCAAAAATACCCATGA
P38-9	PY01065	H2-Kd	IYSYSCSIL	21.43	NIHHIYSYSCSILRSKS*	AATATACACCACATCTATAGCTATAGCTGTAGCATCCTGCGTAGTAAGTCCTGA
P38-10	PY01065	H2-Kd	KYYKKNDYL	21.54	GAGAKYYKKNDYLEQEV*	GGCGCAGGTGCTAAGTACTATAAGAAGAATGACTACCTAGAACAAGAGGTGTGA
P39-1	PY01065	H2-Kd	SFIKMSSIL	42.23	SQVVSFIKMSSILGSPQ*	TCTCAGGTAGTGAGCTTCATAAAGATGAGTAGCATCCTAGGATCACCTCAATGA
P39-2	PY01065	H2-Ld	YPLNNIELF	42.54	LQAFYPLNNIELFNESG*	CTCCAGGCTTTTTACCCTCTGAATAACATAGAGCTGTTTAATGAATCTGGATGA
P39-3	PY01071	H2-Kd	YYNGVFGSI	4.02	VDSNYYNGVFGSIRSDQ*	GTAGATAGTAATTACTATAACGGCGTGTTCGGTAGCATCCGTAGTGACCAGTGA
P39-4	PY01071	H2-Kd	KYILTEHEI	6.75	LGRKKYILTEHEIEILV*	CTAGGCCGTAAAAAGTACATCCTGACTGAGCATGAGATAGAAATACTAGTGTGA
P39-5	PY01071	H2-Kd	FYTYHLTSI	7.57	PPILFYTYHLTSIAWTP*	CCCCCAATCCTGTTCTACACCTACCACCTGACTAGCATAGCCTGGACTCCTTGA
P39-6	PY01071	H2-Kd	NYYTPDTSI	20.26	DSALNYYTPDTSILLRE*	GATTCTGCTCTGAACTACTACACCCCTGACACTAGCATCTTGCTGCGTGAGTGA
P39-7	PY01071	H2-Kd	KYIRTLSNF	22.49	SAEPKYIRTLSNFHFMD*	AGTGCTGAGCCTAAGTACATAAGAACCCTGAGTAACTTCCATTTTATGGATTGA
P39-8	PY01071	H2-Kd	KYPFNASGI	28.03	DGPAKYPFNASGIHFAT*	GACGGGCCGGCTAAGTACCCTTTTAACGCTAGCGGCATCCATTTTGCAACCTGA
P39-9	PY01071	H2-Kd	FYLNCSDNL	49.56	TLFSFYLNCSDNLACFV*	ACACTGTTTAGTTTCTACCTGAACTGTAGTGATAACCTAGCATGCTTTGTATGA
P39-10	PY01089	H2-Kd	IYYANSKRI	35.74	IVYVIYYANSKRIGTLT*	ATAGTGTACGTAATCTACTACGCTAATAGTAAGAGAATAGGAACCCTGACATGA
P40-1	PY01089	H2-Ld	IPFWSRTRL	42.16	PQIHIPFWSRTRLMSAV*	CCACAGATACACATCCCTTTCTGGAGTAGAACTAGACTGATGAGTGCGGTGTGA
P40-2	PY01098	H2-Kd	YYINNLNRI	2.81	PLRSYYINNLNRIMVSE*	CCTCTGAGATCCTACTACATAAATAACCTGAATAGAATAATGGTGTCTGAATGA
P40-3	PY01098	H2-Kd	KYMENIENL	6.22	VMALKYMENIENLDRPF*	GTGATGGCACTGAAGTACATGGAGAACATAGAGAACCTAGACCGCCCATTTTGA
P40-4	PY01098	H2-Kd	FYFYLYENI	8.13	ALPEFYFYLYENIQEDA*	GCGCTGCCTGAGTTCTACTTCTACCTGTATGAGAACATCCAAGAGGACGCTTGA
P40-5	PY01098	H2-Kd	KYFYYEHML	8.96	ECSYKYFYYEHMLNFHW	GAGTGTTCCTATAAGTACTTCTACTATGAGCACATGCTGAATTTCCACTGGTGA
P40-6	PY01098	H2-Kd	KYVDMLLII	9.9	VQMLKYVDMLLIIALWS*	GTGCAGATGTTAAAGTACGTAGACATGCTGCTGATAATAGCCCTGTGGTCATGA
P40-7	PY01098	H2-Kd	SYIKEFCKI	12.22	HLTFSYIKEFCKIAELV*	CATCTAACTTTTAGCTACATAAAGGAGTTCTGTAAGATAGCTGAGCTAGTCTGA
P40-8	PY01098	H2-Kd	SYQKDLYFI	12.65	ILIHSYQKDLYFIESVK*	ATTCTGATTCATAGCTACCAGAAGGAACCTGTACTTCATAGAGTCTGTGAAATGA
P40-9	PY01098	H2-Kd	IYINYLNIL	14.21	SVIVIYINYLNILDEVV*	AGTGTAATAGTAATCTACATAAACTACCTGAACATCCTAGATGAGGTAGTGTGA
P40-10	PY01098	H2-Kd	KYIYELNIL	16.59	AFKVKYIYELNILIPSE*	GCCTTTAAAGTGAAGTACATCTATGAGCTGAACATCCTGATCCCTTCTGAGTGA

P41-1	PY01098	H2-Kd	NYNSGLNNI	16.85	SDKKNYNSGLNNINILL*	TCTGATAAGAAGAACTATAATAGCGGCCTGAATAACATAAATATCTTACTGTGA
P41-2	PY01098	H2-Kd	FYLEFENSI	17.53	HSHAFYLEFENSIMRKN*	CATAGCCACGCCTTCTACCTAGAGTTTGAGAATAGCATAATGCGGTAAGAACTGA
P41-3	PY01098	H2-Kd	YYNCMYVHM	23.54	KQRHYYNCMYVHMQIFL*	AAGCAGCGGCATTACTATAACTGCATGTACGTGCACATGCAGATCTTCCTGTGA
P41-4	PY01098	H2-Kd	KYIEEKLYL	27.18	ATQMKYIEEKLYLVGQA*	GCCACACAGATGAAGTACATAGAGGAGAAGCTGTACCTAGTAGGGCAGGCCTGA
P41-5	PY01098	H2-Kd	KYYEMNNAF	37.5	QLPPKYYEMNNAFRAAS*	CAACTGCCTCCTAAGTACTATGAGATGAATAACGCCTTTAGAGCCGCTAGCTGA
P41-6	PY01098	H2-Kd	LYSFLNDFI	41.5	DLMALYSFLNDFISRFL*	GACCTAATGGCTCTGTATAGCTTCCTGAATGACTTCATAAGTAGGTTCCTGTGA
P41-7	PY01098	H2-Kd	KMFNSLYSF	46.44	DPDKKMFNSLYSFTASA*	GATCCTGATAAAAAGATGTTTAATAGCCTGTATAGCTTCACAGCTAGTGCATGA
P41-8	PY01098	H2-Kd	KFITNLNKL	49.33	GRHQKFITNLNKLECPV*	GGGCGGCATCAGAAGTTCATAACTAACCTGAATAAGCTAGAATGTCCTGTCTGA
P41-9	PY01098	H2-Ld	YPMNNYEQF	12.62	LVPKYPMNNYEQFSSAK*	CTAGTGCCTAAGTACCCTATGAATAACTATGAGCAGTTCTCTAGTGCTAAGTGA
P41-10	PY01108	H2-Kd	KYFPLLHTL	2.58	GELKKYFPLLHTLVVLG*	GGTGAGCTGAAGAAGTACTTCCCTCTGCTGCACACCCTAGTAGTGCTAGGCTGA
P42-1	PY01108	H2-Kd	FYSKLNSSI	5.3	SHWRFYSKLNSSICGCN*	TCTCACTGGCGATTCTATAGTAAGCTGAATAGTAGCATCTGTGGCTGTAATTGA
P42-2	PY01108	H2-Kd	SYNFIKSQI	5.83	VLETSYNFIKSQITTSL*	GTTTTAGAAACTAGCTATAACTTCATAAAGAGCCAGATAACTACTAGTCTGTGA
P42-3	PY01108	H2-Kd	SYLNIYNLI	6.95	SQGTSYLNIYNLIVAGS*	TCCCAAGGCACTAGCTACCTGAACATCTATAACCTGATAGTAGCCGGTAGCTGA
P42-4	PY01108	H2-Kd	WYNDNNYNI	8.8	KSACWYNDNNYNIMIAM*	AAGTCAGCTTGCTGGTATAATGATAATAACTATAACATAATGATAGCCATGTGA
P42-5	PY01108	H2-Kd	FYSKIKETI	9.95	IPLKFYSKIKETIRFIV*	ATACCCCTGAAGTTCTATAGTAAGATAAAGGAGACCATAAGGTTCATAGTGTGA
P42-6	PY01108	H2-Kd	NYIKMFEVL	12.82	RLMINYIKMFEVLPDCV*	AGATTGATGATAAACTACATAAAGATGTTTGAGGTGCTGCCTGACTGCGTGTGA
P42-7	PY01108	H2-Kd	TYCVNFTNI	13.73	PSDLTYCVNFTNIELNK*	CCTTCTGACCTGACCTACTGCGTGAACTTCACTAACATAGAACTGAATAAGTGA
P42-8	PY01108	H2-Kd	YYIYNIDKL	15.06	QLIVYYIYNIDKLFWDT*	CAGCTGATAGTCTACTACATCTATAACATAGATAAGCTGTTCTGGGATACCTGA
P42-9	PY01108	H2-Kd	VYHNYVFEI	18.45	VYQEVYHNYVFEIIPWG*	GTGTACCAGGAAGTGTACCATAACTACGTGTTTGAGATAATCCCTTGGGGCTGA
P42-10	PY01108	H2-Kd	SYSNSEVSL	18.64	RKLRSYSNSEVSLSFSH*	AGGAAACTGAGGAGCTATAGTAATAGTGAGGTGAGCCTGTCTTTTTCCCACTGA
P43-1	PY01108	H2-Kd	KFISRIEYI	22.62	QESPKFISRIEYIIIFG*	CAGGAGTCCCCTAAGTTCATAAGTAGAATAGAGTACATAATAATTTTTGGATGA
P43-2	PY01108	H2-Kd	FYFLLINNI	25.8	MTSGFYFLLINNIWLGD*	ATGACCTCTGGATTCTACTTCCTGCTGATAAATAACATCTGGCTAGGTGATTGA
P43-3	PY01108	H2-Kd	MYCDILQNI	38.01	LRSGMYCDILQNIELRA*	CTGCGTTCGGGAATGTACTGTGACATCCTGCAGAACATAGAGCTGAGAGCCTGA
P43-4	PY01108	H2-Kd	FYFKYTRCI	40.51	ELAPFYFKYTRCIKELG*	GAGCTAGCTCCTTTCTACTTTAAGTACACTAGATGCATAAAGGAGCTAGGGTGA
P43-5	PY01108	H2-Ld	LPYTQLYIF	49.41	YPTVLPYTQLYIFAKAH*	TATCCAACTGTCCTGCCTTACACCCAGCTGTACATCTTCGCTAAAGCCCATTGA
P43-6	PY01122	H2-Kd	YYLNKATNI	6.64	LVRMYYLNKATNITVGY*	TTAGTGAGAATGTACTACCTGAATAAGGCCACTAACATAACCGTAGGGTACTGA
P43-7	PY01122	H2-Kd	VYYVNNEEI	34.15	MRDYVYYVNNEEILHSP*	ATGCGTGATTACGTGTACTACGTGAATAATGAGGAGATCCTCCACTCACCCTGA
P43-8	PY01123	H2-Kd	KYHYLLYHL	26.55	LETEKYHYLLYHLVPWL*	TTAGAAACTGAGAAGTACCACTACCTGCTGTACCACCTAGTGCCCTGGCTATGA
P43-9	PY01123	H2-Kd	QYVKAGSLI	29.41	NEEFQYVKAGSLIGYSL*	AATGAGGAGTTCCAGTACGTGAAGGCCGGTAGCCTGATAGGATATAGCCTGTGA
P43-10	PY01123	H2-Ld	YPHLNLNEI	38.06	TECLYPHLNLNEIKVNP*	ACTGAATGTTTATACCCTCACCTGAACCTGAATGAGATAAAAGTGAATCCTTGA
P44-1	PY01200	H2-Kd	SYFEKCKTI	16.44	VPEGSYFEKCKTIIVDR*	GTCCCTGAAGGTAGCTACTTTGAGAAGTGTAAGACCATAATAGTAGATAGGTGA
P44-2	PY01200	H2-Kd	NYIDVYINI	22.5	RPPANYIDVYINIIKVS*	CGGCCACCAGCTAACTACATAGACGTGTACATAAACATAATAAAGGTGAGCTGA
P44-3	PY01200	H2-Kd	IYCNTISNL	26.48	LSGSIYCNTISNLGRLT*	TTGAGCGGCTCTATCTACTGTAACACCATAAGTAACCTAGGGCGGCTGACCTGA
P44-4	PY01205	H2-Kd	KMIFSAYKI	30.71	KKRSKMIFSAYKIPADV*	AAGAAGCGGTCTAAGATGATCTTTAGCGCCTATAAGATCCCCGCTGACGTGTGA
P44-5	PY01205	H2-Kd	IYLHYFFTL	35.57	RSSGIYLHYFFTLGMEM*	CGTAGTAGCGGCATCTACCTGCACTACTTCTTCACCCTAGGTATGGAAATGTGA
P44-6	PY01206	H2-Kd	SFFRTFSQI	7.84	IAIQSFFRTFSQILVTS*	ATAGCTATCCAGAGCTTCTTTAGAACCTTTAGCCAGATCCTAGTGACCTCGTGA
P44-7	PY01220	H2-Kd	VYIKRGSGI	15.5	HRGFVYIKRGSGILLPS*	CATAGAGGTTTCGTGTACATAAAGAGAGGTAGCGGCATCTTATTACCATCCTGA
P44-8	PY01228	H2-Kd	SYIESIPEI	3.35	LTQHSYIESIPEIFVGA*	CTAACCCAGCATAGCTACATAGAGAGCATCCCTGAGATCTTCGTAGGAGCATGA
P44-9	PY01228	H2-Kd	KYNNLNAYI	6.93	YVTPKYNNLNAYIKKSE*	TATGTAACACCTAAGTATAATAACCTGAACGCCTACATAAAGAAGAGTGAATGA
P44-10	PY01228	H2-Kd	SYVDDINNI	12.97	DEERSYVDDINNISKYL*	GATGAAGAAAGAAGCTACGTAGATGACATAAATAACATCTCTAAATATCTCTGA
P45-1	PY01228	H2-Kd	YYRAVILQI	24.52	DAYDYYRAVILQIETCD*	GATGCCTATGACTACTATAGAGCCGTGATCCTGCAGATAGAAACATGTGACTGA
P45-2	PY01231	H2-Kd	KYLTNSEEI	9.66	TMPRKYLTNSEEINADK*	ACCATGCCACGTAAGTACCTGACTAATAGTGAGGAGATAAACGCTGATAAGTGA
P45-3	PY01231	H2-Kd	KYFCGPNAV	15.19	LCYAKYFCGPNAVLASE*	CTGTGCTACGCTAAGTACTTCTGCGGCCCTAACGCCGTGTTAGCCTCTGAGTGA
P45-4	PY01231	H2-Kd	LYLPSTLVI	16.82	TGAVLYLPSTLVIMGVL*	ACGGGCGCCGTGCTGTACCTGCCTAGCACCCTAGTGATAATGGGTGTTTTGTGA
P45-5	PY01231	H2-Kd	GYISCWVHL	19.61	GLPSGYISCWVHLPGDD*	GGCCTGCCTTCTGGCTACATAAGCTGCTGGGTGCACCTGCCAGGTGATGACTGA
P45-6	PY01234	H2-Kd	YYNDKYSYI	5.83	ISAIYYNDKYSYILVME*	ATAAGCGCGATATACTATAATGATAAGTATAGCTACATCCTAGTAATGGAGTGA
P45-7	PY01234	H2-Kd	SYIKELISI	9.01	PSEASYIKELISIRQSW*	CCATCTGAGGCTAGCTACATAAAGGAGCTGATAAGCATAAGGCAGTCCTGGTGA
P45-8	PY01234	H2-Kd	SYYMYKETL	9.21	LTSTSYYMYKETLGRRF*	TTAACCTCAACTAGCTACTACATGTATAAGGAGACCCTAGGTAGACGGTTCTGA
P45-9	PY01234	H2-Kd	KYYQDTNLL	10	MAQWKYYQDTNLLARNA	ATGGCTCAATGGAAGTACTACCAGGACACTAACCTGCTAGCTAGAAACGCTTGA
P45-10	PY01234	H2-Kd	SWMCMIFPI	10.34	KSPVSWMCMIFPISPED*	AAGTCTCCGGTGAGCTGGATGTGCATGATCTTCCCTATAAGTCCTGAAGACTGA
P46-1	PY01234	H2-Kd	YYIKSLRLL	15.56	LLQEYYIKSLRLLFDRP*	CTGCTTCAGGAATACTACATAAAGAGCCTGAGACTGCTGTTTGACCGACCCTGA
P46-2	PY01234	H2-Kd	SFFDNINQI	17.04	HTAWSFFDNINQIDNEE*	CACACCGCTTGGAGCTTCTTTGATAACATAAACCAGATAGATAATGAGGAGTGA
P46-3	PY01234	H2-Kd	KYASQLHKL	17.93	RKGGKYASQLHKLNGTA*	AGAAAAGGCGGTAAGTACGCTAGCCAGCTGCATAAGCTGAACGGCACTGCATGA
P46-4	PY01234	H2-Kd	FYVNAFLNL	21.76	ARATFYVNAFLNLMPGA*	GCTAGAGCTACTTTCTACGTGAACGCCTTCCTGAACCTGATGCCAGGGGCCTGA
P46-5	PY01234	H2-Kd	YFFSPSSYI	23.77	IVSQYFFSPSSYITVLQ*	ATAGTTTCACAGTACTTCTTTAGCCCTAGTAGCTACATAACGGTGCTACAATGA
P46-6	PY01234	H2-Kd	YYMYKETLL	24.85	GLSWYYMYKETLLTSGQ*	GGGCTGAGTTGGTACTACATGTATAAGGAGACCCTGCTGACCTCAGGACAGTGA
P46-7	PY01234	H2-Kd	SYILKNNTL	26.66	PNDESYILKNNTLFQRK*	CCTAATGATGAGAGCTACATCCTGAAGAATAACACCCTGTTTCAGCGTAAATGA
P46-8	PY01234	H2-Kd	NYFKNCINL	35.05	DQQGNYFKNCINLTFSK*	GATCAGCAAGGTAACTACTTTAAGAACTGCATAAACCTGACGTTTTCTAAGTGA
P46-9	PY01234	H2-Kd	HYTNTFINL	37.36	LHINHYTNTFINLHTED*	CTGCACATAAACCACTACACTAACACCTTCATAAACCTGCATACTGAGGATTGA
P46-10	PY01234	H2-Kd	IFQQNYSNI	37.85	RIFHIFQQNYSNITESL*	CGGATCTTTCATATCTTCCAGCAGAACTATAGTAACATAACTGAATCTCTGTGA
P47-1	PY01234	H2-Kd	KYNIPESNI	41.5	FLKPKYNIPESNISMAR*	TTTCTGAAGCCTAAGTATAACATCCCTGAGAGTAACATCTCCATGGCACGGTGA
P47-2	PY01234	H2-Kd	KYIEENKQI	45.03	RDEMKYIEENKQIVSHP*	CGTGATGAGATGAAGTACATAGAGGAGAATAAGCAGATAGTGTCCCATCCCTGA
P47-3	PY01234	H2-Kd	QYIKRGTLL	49.67	DSVGQYIKRGTLLNTKA*	GACTCTGTAGGCCAGTACATAAAGAAGGCACCCTGCTGAACACTAAAGCTTGA
P47-4	PY01234	H2-Ld	IPLTMPNMF	43.36	IITIIPLTMPNMFLESD*	ATAATAACCATAATCCCTCTGACCATGCCTAACATGTTCCTAGAGAGTGATTGA
P47-5	PY01234	H2-Ld	SPFEKLYTM	46.92	YNQESPFEKLYTMVSIT*	TATAACCAAGAGAGCCCTTTTGAGAAGCTGTACACCATGGTGAGCATAACGTGA
P47-6	PY01242	H2-Kd	NYIRNHNNI	4.94	SAKENYIRNHNNIEKIF*	AGCGCTAAGGAAAACTACATAAGAAACCATAATAACATAGAGAAGATATTCTGA
P47-7	PY01242	H2-Kd	FYYFINHKI	9.56	GLGFFYYFINHKIKPRG*	GGCCTAGGTTTTTTCTACTACTTCATAAACCATAAGATAAAACCTCGTGGATGA
P47-8	PY01242	H2-Kd	SYICENSSV	19.52	VSGWSYICENSSVSNDL*	GTATCAGGCTGGAGCTACATCTGTGAGAATAGTAGCGTGTCTAATGACTTGTGA
P47-9	PY01242	H2-Kd	WYQMDDSVI	21.26	WLDFWYQMDDSVIRVAA	TGGTTAGACTTCTGGTACCAGATGGATGATAGCGTGATCCGCGTAGCCGCTTGA
P47-10	PY01242	H2-Kd	KYNKNITKV	25.06	LSGPKYNKNITKVLLVK*	CTCTCCGGCCCTAAGTATAATAAGAACATAACTAAGGTGCTTCTAGTGAAGTGA
P48-1	PY01242	H2-Kd	KYYFLWKFI	25.06	PAMDKYYFLWKFIYSLL*	CCGGCCATGGATAAGTACTACTTCCTGTGGAAGTTCATCTATAGTCTCTTGTGA
P48-2	PY01242	H2-Kd	KYISPDNIL	25.18	SPQTKYISPDNILCHLG*	TCCCCCCAAACTAAGTACATAAGCCCTGATAACATCCTGTGTCATTTAGGCTGA
P48-3	PY01242	H2-Kd	GYSNGYFEL	27.49	LFSEGYSNGYFELASYK*	TTGTTTAGTGAAGGCTATAGTAACGGCTACTTTGAGCTAGCCTCCTATAAGTGA
P48-4	PY01242	H2-Kd	PYIRSNTSL	45.27	VDKIPYIRSNTSLGEKN*	GTAGATAAAATCCCTTACATAAGAAGTAACACTAGCTCAGGTGAAGAAGAACTGA
P48-5	PY01244	H2-Kd	KYWRNHVSI	3.21	LEWQKYWRNHVSIWASH	CTAGAATGGCAGAAGTACTGGAGAAACCACGTGAGCATCTGGGCTAGTCATTGA
P48-6	PY01246	H2-Kd	NYIKIDTPI	14.6	PGFTNYIKIDTPIVAEY*	CCTGGGTTTACTAACTACATAAAGATAGACACCCCTATAGTAGCTGAGTATTGA
P48-7	PY01264	H2-Kd	KYISNLNEL	3.7	RRFRKYISNLNELVGDL*	CGTAGGTTTCGTAAGTACATAAGTAACCTGAATGAGCTAGTAGGTGATCTATGA
P48-8	PY01264	H2-Kd	KYQIDKSAI	10.74	IFLSKYQIDKSAIDQDL*	ATATTCCTCTCTAAGTACCAGATAGATAAGAGCGCCATAGACCAAGATCTGTGA
P48-9	PY01264	H2-Kd	FQFKIISYI	17.27	CIERFQFKIISYIVEND*	TGCATAGAACGCTTCCAGTTTAAGATAATAAGCTACATAGTAGAGAATGATTGA
P48-10	PY01264	H2-Kd	RYIGPNTDI	20.06	EQRGRYIGPNTDIRPLQ*	GAGCAACGGGGTAGATACATAGGCCCTAACACTGACATCCGTCCACTCCAGTGA
P49-1	PY01264	H2-Kd	IYLGVLENI	22.75	SVSRIYLGVLENIAVTC*	AGTGTGAGTAGGATCTACCTAGGCGTGCTAGAGAACATAGCAGTAACTTGCTGA
P49-2	PY01264	H2-Kd	YYGISLNKI	38.89	YDPKYYGISLNKIFVNG*	TATGACCCTAAATACTACGGCATAAGCCTGAAGTAAGATCTTCGTGAACGGATGA
P49-3	PY01264	H2-Kd	KYEFKHCTI	42.14	ERSEKYEFKHCTIDIQA*	GAACGTTCTGAAAAGTATGAGTTTAAGCACTGCACCATAGACATTCAAGCCTGA
P49-4	PY01292	H2-Kd	FYYSVEPKI	12.77	NSSHFYYSVEPKIKGGK*	AATTCCTCCCACTTCTACTATAGCGTAGAGCCTAAGATAAAAGGAGGTAAGTGA
P49-5	PY01292	H2-Kd	KYLYVVEKI	13.65	LLLAKYLYVVEKIFKKG*	CTTCTCCTAGCTAAGTACCTGTACGTAGTAGAGAAGATCTTTAAAAAAGGATGA
P49-6	PY01292	H2-Kd	SYHDKKTNI	48.43	GPFHSYHDKKTNIHTFF*	GGGCCGTTCCATAGCTACCATGATAAGAAGACTAACATCCACACCTTTTTTTGA
P49-7	PY01292	H2-Kd	NYSITYTEI	49.73	FLHNNYSITYTEISFAE*	TTCCTGCATAATAACTATAGCATAACCTACACTGAGATAAGCTTCGCTGAATGA
P49-8	PY01292	H2-Kd	SMHSNNTNI	49.73	NSPPSMHSNNTNIIEQR*	AATAGCCCCCCTAGCATGCATAGTAATAACACTAACATAATAGAGCAGCGCTGA
P49-9	PY01306	H2-Kd	YYNVINNFI	5.49	KSQLYYNVINNFIAITK*	AAGAGTCAGTTATACTATAACGTGATAAATAACTTCATAGCCATAACTAAGTGA
P49-10	PY01306	H2-Kd	KYFYEKEQI	14.89	GVVAKYFYEKEQIRLSS*	GGAGTAGTAGCTAAGTACTTCTATGAGAAGGAGCAGATCCGCCTCTCTAGTTGA
P50-1	PY01306	H2-Kd	YYIREIEKI	25.28	QYKDYYIREIEKIGILM*	CAGTATAAAGATTACTACATAAGAGAGATAGAGAAGATAGGCATTCTGATGTGA
P50-2	PY01306	H2-Kd	VYTSPVHPI	38.16	SSLLVYTSPVHPIKRTN*	AGTTCTCTCCTAGTGTACACTAGCCCTGTGCACCCTATAAAACGCACTAATTGA
P50-3	PY01321	H2-Kd	RYVECYANI	9.11	LEIGRYVECYANISLGI*	CTAGAGATAGGTAGATACGTAGAGTGCTACGCTAACATAAGCCTAGGAATATGA
P50-4	PY01321	H2-Kd	LYSKNYVTI	10.87	HCGALYSKNYVTIVAAL*	CACTGCGGGGCCCTGTATAGTAAGAACTACGTGACCATAGTAGCTGCACTCTGA
P50-5	PY01321	H2-Kd	KYSGVFMGL	27.9	VEPSKYSGVFMGLHARL*	GTAGAGCCTTCTAAGTATAGCGGCGTGTTCATGGGCCTGCACGCCCGGCTTTGA
P50-6	PY01321	H2-Kd	KQVRSLWSL	40.26	QLELKQVRSLWSLNTFR*	CAACTAGAATTGAAGCAGGTGAGAAGCCTGTGGAGCCTGAACACCTTCCGGTGA
P50-7	PY01329	H2-Kd	GYFNSLNSI	2.71	SRPRGYFNSLNSIPVSG*	TCTCGACCTAGGGGCTACTTTAATAGCCTGAATAGCATCCCTGTTTCCGGCTGA
P50-8	PY01329	H2-Kd	AYYTDNSSI	5.11	CILLAYYTDNSSIIHIR*	TGTATTCTGCTAGCCTACTACACTGATAATAGTAGCATAATCCACATCCGTTGA
P50-9	PY01329	H2-Kd	KYSTNSSEI	5.48	VYPGKYSTNSSEITVSQ*	GTCTATCCTGGTAAGTATAGCACTAATAGTAGTGAGATAACTGTATCACAGTGA
P50-10	PY01329	H2-Kd	YYISNGANI	6.22	HVDTYYISNGANILQKC*	CATGTAGACACATACTACATAAGTAACGGCGCTAACATCCTGCAGAAATGCTGA
P51-1	PY01329	H2-Kd	YYTDNSSII	6.43	SGDLYYTDNSSIIHDEF*	TCCGGTGACCTGTACTACACTGATAATAGTAGCATAATCCATGATGAATTCTGA

P51-2	PY01329	H2-Kd	KYYPIINGI	6.59	FQKVKYYPIINGIVSNQ*	TTTCAGAAAGTGAAGTACTACCCTATAATAAACGGCATAGTCTCTAATCAGTGA
P51-3	PY01329	H2-Kd	KYDCGRTTI	6.99	HLGMKYDCGRTTIGDYA*	CATCTAGGGATGAAGTATGACTGCGGTAGAACCACCATAGGTGACTACGCGTGA
P51-4	PY01329	H2-Kd	FYIHICGPI	9.92	CESQFYIHICGPIPKLK*	TGTGAAAGTCAGTTCTACATCCACATCTGCGGCCCTATCCCTAAGCTGAAGTGA
P51-5	PY01329	H2-Kd	KYFLFQFTI	9.97	ESSIKYFLFQFTILSRR*	GAGAGTAGCATAAAGTACTTCCTGTTCCAGTTCACCATCCTGAGTCGGCGCTGA
P51-6	PY01329	H2-Kd	YYNNKNSNI	10.15	TGAFYYNNKNSNILVYP*	ACCGGAGCTTTTTACTATAATAATAAGAATAGTAACATCCTAGTGTACCCATGA
P51-7	PY01329	H2-Kd	YYYFNKKNI	12.04	LIEGYYYFNKKNIYFTS*	CTAATAGAGGGCTACTACTACTTTAATAAGAAGAACATCTACTTTACTTCTTGA
P51-8	PY01329	H2-Kd	AYICCFFVI	13.69	ELSDAYICCFFVIHDIW*	GAACTCTCTGACGCCTACATCTGCTGCTTCTTCGTGATCCATGATATTTGGTGA
P51-9	PY01329	H2-Kd	IYANLYANI	17.34	DISKIYANLYANIIYLP*	GACATTTCTAAAATCTACGCTAACCTGTACGCTAACATAATCTACCTTCCATGA
P51-10	PY01329	H2-Kd	TYHINYFNI	17.88	TDDRTYHINYFNIPSST*	ACTGATGATAGAACCTACCACATAAACTACTTTAACATCCCCTCATCTACCTGA
P52-1	PY01329	H2-Kd	IYISRNIQI	18.22	MDANIYISRNIQIFGPS*	ATGGACGCTAACATCTACATAAGTAGAAACATCCAGATCTTCGGACCTAGTTGA
P52-2	PY01329	H2-Kd	YQNPIYHSL	19.13	NLWRYQNPIYHSLFQSV*	AATCTATGGCGTTACCAGAACCCTATCTACCATAGCCTGTTTCAGAGCGTTTGA
P52-3	PY01329	H2-Kd	FYTDECSYI	19.48	ARAEFYTDECSYIDLVD*	GCTCGCGCTGAGTTCTACACTGATGAGTGTAGCTACATAGACCTAGTAGACTGA
P52-4	PY01329	H2-Kd	NYFNITFII	23.02	AVGLNYFNITFIICPVG*	GCTGTAGGACTGAACTACTTTAACATAACCTTCATAATCTGCCCTGTAGGCTGA
P52-5	PY01329	H2-Kd	SYLYFLVKI	30.35	NESSSYLYFLVKIGPNG*	AATGAGAGTTCTAGCTACCTGTACTTCCTAGTGAAGATAGGGCCTAACGGATGA
P52-6	PY01329	H2-Kd	FYSNRKESI	31.92	QKTCFYSNRKESIGEPA*	CAAAAAACCTGTTTCTATAGTAATAGAAAGGAGAGCATAGGTGAGCCCGCCTGA
P52-7	PY01329	H2-Kd	TYNNSIDGI	43.03	AFPDTYNNSIDGISEWE*	GCTTTTCCTGATACCTATAATAATAGCATAGACGGCATAAGTGAATGGGAGTGA
P52-8	PY01329	H2-Kd	FYYIYFFNL	45.73	RNMSFYYIYFFNLPCEL*	AGGAACATGAGTTTCTACTACATCTACTTCTTTAACCTGCCCTGTGAACTCTGA
P52-9	PY01329	H2-Kd	MQINKFTLI	48.94	KEQMMQINKFTLIIEVK*	AAAGAACAGATGATGCAGATAAATAAGTTCACCCTGATAATAGAAGTGAAGTGA
P52-10	PY01329	H2-Ld	YPIINGITL	14.94	WTEVYPIINGITLLLRV*	TGGACTGAGGTATACCCTATAATAAACGGCATAACCCTGCTGCTGAGGGTCTGA
P53-1	PY01329	H2-Ld	MPFRSANNF	29.79	RNSRMPFRSANNFTPVL*	CGTAATTCGCGAATGCCTTTTAGAAGCGCTAATAACTTCACCCCTGTGCTATGA
P53-2	PY01329	H2-Ld	SPMPNYKIL	37.35	PGGKSPMPNYKILFTIS*	CCAGGGGGTAAGAGCCCTATGCCTAACTATAAGATCCTGTTTACGATCCTCCTGA
P53-3	PY01338	H2-Kd	KYICTITVI	2.44	RVNRKYICTITVIVTEE*	AGAGTGAATCGTAAGTACATCTGCACCATAACCGTGATAGTGACTGAGGAATGA
P53-4	PY01338	H2-Kd	YYINTNNQI	2.97	SRDLYYINTNNQIAAMQ*	TCTCGTGACCTGTACTACATAAACACTAATAACCAGATAGCAGCCATGCAATGA
P53-5	PY01338	H2-Kd	KYFVYLNNL	6.42	KPHNKYFVYLNNLLQVL*	AAACCACATAATAAGTACTTCGTGTACCTGAATAACCTGCTGCAAGTGCTGTGA
P53-6	PY01338	H2-Kd	FYNENSDFI	9.59	TKHVFYNENSDFIRFPA*	ACTAAGCACGTATTCTATAATGAGAATAGTGACTTCATCCGCTTCCCGGCCTGA
P53-7	PY01338	H2-Kd	SFINTFNEI	10.83	MNHISFINTFNEISPLD*	ATGAACCACATAAGCTTCATAAACACCTTTAATGAGATCTCTCCTCTAGACTGA
P53-8	PY01338	H2-Kd	SYIEYIYIL	10.86	YDYLSYIEYIYILNEGV*	TATGATTATCTGAGCTACATAGAGTACATCTACATCCTGAATGAGGGTGTGTGA
P53-9	PY01338	H2-Kd	IYNFLCTNI	12.02	DYSVIYNFLCTNILEHE*	GACTATAGCGTGATCTATAACTTCCTGTGCACTAACATCCTAGAGCATGAGTGA
P53-10	PY01338	H2-Kd	IYINNWDKI	14.03	LTENIYINNWDKIKGKK*	CTGACTGAAAACATCTACATAAATAACTGGGATAAGATAAAAGGTAAAAAGTGA
P54-1	PY01338	H2-Kd	SYFDELENI	16.71	LEVESYFDELENITEVN*	CTAGAGGTAGAAAGCTACTTTGATGAGCTAGAGAACATAACTGAGGTGAACTGA
P54-2	PY01338	H2-Kd	YYIYIYIII	21.74	VLVHYYIYIYIIINAPL*	GTATTAGTGCACTACTACATCTACATCTACATAATAATAAACGCCCCACTGTGA
P54-3	PY01338	H2-Kd	KYKNLLMKI	35.99	VLTEKYKNLLMKIEQEQ*	GTCCTGACTGAGAAGTATAAGAACCTGCTGATGAAGATAGAGCAAGAGCAGTGA
P54-4	PY01338	H2-Kd	SYNYINQNL	38.96	QVKASYNYINQNLQVDE*	CAGGTGAAGGCTAGCTATAACTACATAAACCAGAACCTGCAAGTAGATGAGTGA
P54-5	PY01338	H2-Kd	KWNNNSNMI	39.4	AQKAKWNNNSNMIEQWL	GCCCAGAAAGCTAAGTGGAATAATAATAGTAACATGATAGAGCAGTGGTTATGA
P54-6	PY01338	H2-Kd	FYFNEIKHI	40.2	YYQMFYFNEIKHIISLT*	TATTATCAGATGTTCTACTTTAATGAGATAAAGCACATAATAAGTCTGACCTGA
P54-7	PY01338	H2-Kd	TLIKMFSHI	42.25	KYVETLIKMFSHIDARL*	AAGTATGTAGAGACCCTGATAAAGATGTTTAGCCACATAGATGCACGGCTTTGA
P54-8	PY01338	H2-Kd	IYIYIIIHI	47.53	FYTKIYIYIIIHIIHPE*	TTCTACACTAAAATCTACATCTACATAATAATCCACATAATTCACCCTGAGTGA
P54-9	PY01338	H2-Kd	TYYSNFPKM	49.46	GSAKTYYSNFPKMLISG*	GGCTCAGCTAAAACCTACTATAGTAACTTCCCTAAGATGCTAATAAGCGGTTGA
P54-10	PY01353	H2-Kd	LYLNVNNSI	7.32	STIPLYLNVNNSIRVRL*	TCTACTATACCACTGTACCTGAACGTGAATAATAGCATAAGAGTGAGATTGTGA
P55-1	PY01353	H2-Kd	WYKYNANKI	33.1	REVWWYKYNANKIASEF*	AGAGAGGTGTGGTGGTATAAGTATAACGCTAATAAGATAGCCTCTGAATTCTGA
P55-2	PY01353	H2-Kd	IYSGDSSII	46.73	KKRLIYSGDSSIISRWT*	AAGAAGAGGCTGATCTATAGCGGTGATAGTAGCATAATAAGCCGATGGACATGA
P55-3	PY01362	H2-Kd	KFINTFSKI	6.31	SVAKKFINTFSKINKAR*	TCTGTAGCTAAGAAGTTCATAAACACCTTTAGTAAGATAAATAAGGCTAGATGA
P55-4	PY01362	H2-Kd	KYNQVPAFI	7.47	IEGDKYNQVPAFILRAL*	ATAGAAGGTGATAAGTATAACCAGGTGCCTGCCTTCATCCTGAGAGCCCGTGTGA
P55-5	PY01362	H2-Kd	IYTNIYNYI	10.81	PLKIIYTNIYNYICPER*	CCTCTGAAGATAATCTACACTAACATCTATAACTACATCTGCCCTGAGCGATGA
P55-6	PY01362	H2-Kd	YYKNMFYKI	10.91	WSDHYYKNMFYKIILTR*	TGGTCTGACCACTACTATAAGAACATGTTCTATAAGATAATCCTAACCCGATGA
P55-7	PY01362	H2-Kd	KYIMIIFFI	16.9	TYTAKYIMIIFFIVVHK*	ACCTACACCGCTAAGTACATAATGATAATCTTCTTCATAGTAGTCCATAAATGA
P55-8	PY01362	H2-Kd	QYLYHFQNI	30.22	AVLPQYLYHFQNIGAAI*	GCCGTTTTGCCACAGTACCTGTACCACTTCCAGAACATAGGGGCTGCCATCTGA
P55-9	PY01362	H2-Ld	IPYTIGVSM	36.18	TSQKIPYTIGVSMDHSR*	ACTTCACAGAAGATCCCTTACACCATAGGCGTGAGCATGGACCACTCCCGGTGA
P55-10	PY01370	H2-Kd	FYLNNLEYI	5.8	RLSSFYLNNLEYIKGPF*	AGACTTTCATCTTTCTACCTGAATAACCTAGAGTACATAAAAGGACCGTTCTGA
P56-1	PY01370	H2-Kd	LYWISKSWI	21.69	MSELLYWISKSWIYTNA*	ATGTCTGAACTGCTGTACTGGATAAGTAAGAGCTGGATCTACACTAACGCCTGA
P56-2	PY01370	H2-Kd	SWIQFTESI	25.08	KIHNSWIQFTESIHVSV*	AAAATCCATAATAGCTGGATCCAGTTCACTGAGAGCATCCATGTCTCAGTGTGA
P56-3	PY01370	H2-Kd	SWMNLFNEL	28.02	PTLASWMNLFNELWEGS	CCTACCCTAGCTAGCTGGATGAACCTGTTTAATGAGCTGTGGGAGGGCTCATGA
P56-4	PY01375	H2-Kd	KYMSSSSTI	1.69	AVYLKYMSSSSTIVDSF*	GCCGTTTACCTGAAGTACATGAGTAGTAGTAGCACCATAGTAGATAGCTTCTGA
P56-5	PY01375	H2-Kd	IYNQIKTNI	13.96	MLVVIYNQIKTNITKLL*	ATGCTAGTAGTGATCTATAACCAGATAAAGACTAACATAACTAAACTGCTGTGA
P56-6	PY01375	H2-Kd	VYMDNEHIL	30.69	FLEIVYMDNEHILDRPP*	TTCCTAGAGATAGTGTACATGGATAATGAGCACATCCTAGACCGCCCACCATGA
P56-7	PY01396	H2-Kd	LYYVNERTI	48.81	SENDLYYVNERTILILR*	TCTGAGAATGATCTGTACTACGTGAATGAGAGAACCATCCTGATTCTGAGGTGA
P56-8	PY01409	H2-Kd	SYINKFEAI	4.82	HMPVSYINKFEAIWSTV*	CACATGCCTGTGAGCTACATAAATAAGTTGAGGCCATCTGGTCGACCGTATGA
P56-9	PY01409	H2-Kd	FYFYNNKLI	23.13	ADTFFYFYNNKLIVSEA*	GCTGATACCTTCTTCTACTTCTATAATAATAAGCTGATAGTTTCTGAAGCATGA
P56-10	PY01409	H2-Kd	SYQGCESDI	31.76	RKALSYQGCESDIFAAK*	CGTAAGGCACTGAGCTACCAGGGCTGTGAGAGTGACATCTTTGCGGCTAAATGA
P57-1	PY01409	H2-Kd	HYLFTQYRL	36.92	PDEKHYLFTQYRLALKA*	CCTGATGAGAAGCACTACCTGTTCACCCAGTATAGACTAGCGCTGAAGGCTTGA
P57-2	PY01412	H2-Kd	YYFRDTHSI	2.89	NLSGYYFRDTHSILAAY*	AACCTTTCGGGGTACTACTTTAGAGACACCCATAGCATCCTAGCCGCCTATTGA
P57-3	PY01412	H2-Kd	FYNDISNSI	7.32	EHQTFYNDISNSIYRRS*	GAGCACCAGACATTCTATAATGACATAAGTAATAGCATCTATAGGCGTAGCTGA
P57-4	PY01412	H2-Kd	SYNNNMLNI	8.91	TNNASYNNNMLNILRQD*	ACTAATAACGCTAGCTATAATAATAACATGCTGAACATCCTGCGCCAGGACTGA
P57-5	PY01412	H2-Kd	KYNNNYNNV	23.83	WLPAKYNNNYNNVDTAK*	TGGCTCCCAGCTAAGTATAATAATAACTATAATAACGTAGACACCGCTAAGTGA
P57-6	PY01412	H2-Kd	KYLSYENTV	28.98	GSITKYLSYENTVVFLA*	GGTTCAATAACTAAGTACCTGAGCTATGAGAACACCGTAGTCTTTCTAGCATGA
P57-7	PY01412	H2-Kd	NYNNVRHNL	35.78	PVKENYNNVRHNLLFTK*	CCTGTGAAGGAGAACTATAATAACGTGAGACATAACCTGTTGTTTACTAAGTGA
P57-8	PY01412	H2-Kd	LYLRRSTNI	36.84	HACRLYLRRSTNIQYDN*	CATGCCTGTAGACTGTACCTGAGAAGAAGCACTAACATCCAGTATGATAACTGA
P57-9	PY01412	H2-Kd	IYYNDIYIL	37.36	SCKQIYYNDIYILRPGP*	AGCTGTAAACAGATCTACTATAATGACATCTACATCCTGCGCCCCGGGCCTTGA
P57-10	PY01412	H2-Kd	GYRPTLFNL	44.26	LWTTGYRPTLFNLVLEK*	CTGTGGACCACCGGCTATAGACCTACCCTGTTTAACCTAGTTCTAGAAAAGTGA
P58-1	PY01412	H2-Kd	AYLYGHSIV	48.28	ARSQAYLYGHSIVEKET*	GCTAGAAGCCAGGCCTACCTGTACGGCCATAGCATAGTAGAAAAGGAGACTTGA
P58-2	PY01435	H2-Kd	TYFSNQPFI	4.47	FRFLTYFSNQPFIRLIQ*	TTTCGGTTCCTAACCTACTTTAGTAACCAGCCTTTCATAAGGTTGATTCAGTGA
P58-3	PY01435	H2-Kd	YYVASVVII	7.65	FTILYYVASVVIIHTGV*	TTTACAATACTCTACTACGTAGCTAGCGTAGTGATAATCCATACCGGAGTGTGA
P58-4	PY01435	H2-Kd	WFNKVTSTI	20.46	IPKLWFNKVTSTIAYKN*	ATCCCTAAGCTCTGGTTTAATAAGGTGACTAGCACCATAGCATATAAGAATTGA
P58-5	PY01452	H2-Kd	IYHPESNYI	19.23	APVSIYHPESNYISAEV*	GCACCCGTGAGCATCTACCACCCTGAGAGTAACTACATCTCAGCTGAGGTGTGA
P58-6	PY01452	H2-Kd	RYLQTIASV	21.43	STLLRYLQTIASVGETS*	TCGACTCTGCTGAGATACCTGCAGACCATAGCTAGCGTAGGTGAGACTTCTTGA
P58-7	PY01452	H2-Kd	YYTRHLQIL	23.26	KLMTYYTRHLQILLEMH*	AAATTGATGACATACTACACTAGACACCTGCAGATCCTGCTAGAAATGCATTGA
P58-8	PY01452	H2-Kd	NYYTRHLQI	33.05	ASSSNYYTRHLQITAEW*	GCCTCTTCCTCTAACTACTACACTAGACACCTGCAGATAACGGCTGAGTGGTGA
P58-9	PY01520	H2-Kd	NYMNNLNKI	5.65	RMLLNYMNNLNKIAVEL*	CGTATGTTGCTGAACTACATGAATAACCTGAATAAGATAGCTGTAGAACTGTGA
P58-10	PY01533	H2-Kd	SYYEVSDKL	26.35	SKRRSYYEVSDKLALLM*	AGTAAAAGACGTAGCTACTATGAGGTGAGTGATAAGCTAGCCCTGTTAATGTGA
P59-1	PY01533	H2-Kd	AYSRTEASI	29.77	DSRMAYSRTEASILTSV*	GATAGTCGCATGGCCTATAGTAGAACTGAGGCTAGCATCTTGACTAGTGTGTGA
P59-2	PY01533	H2-Kd	IYYSPNDLI	38.38	CNASIYYSPNDLIYVTP*	TGTAACGCATCTATCTACTATAGCCCTAATGACCTGATCTATGTAACCCCATGA
P59-3	PY01583	H2-Kd	NYFENTCNI	9.62	NADCNYFENTCNIVFVT*	AATGCTGACTGTAACTACTTTGAGAACACCTGTAACATAGTCTTTGTAACCTGA
P59-4	PY01583	H2-Kd	KYHKHYFPI	10.24	DVPRKYHKHYFPIHLFV*	GACGTGCCCCGTAAGTACCATAAGCACTACTTCCCTATCCACCTGTTCGTGTGA
P59-5	PY01583	H2-Kd	KYESFLSFL	26.57	EHELKYESFLSFLLSVS*	GAACATGAACTGAAGTATGAGAGCTTCCTGAGCTTCCTGCTGAGTGTGAGCTGA
P59-6	PY01583	H2-Kd	RFNAYLCTI	32.3	LVTARFNAYLCTIIMNP*	CTAGTAACAGCTAGATTTAACGCCTACCTGTGCACCATAATAATGAACCCCTGA
P59-7	PY01583	H2-Kd	GYNNMNTYV	34.99	YLLSGYNNMNTYVRCGM	TACCTCCTGTCTGGCTATAATAACATGAACACCTACGTGAGGTGCGGTATGTGA
P59-8	PY01583	H2-Ld	IPNYLFFFL	47.11	FLASIPNYLFFFLGPHR*	TTTCTAGCATCCATCCCTAACTACCTGTTCTTCTTCCTAGGGCCACACCGCTGA
P59-9	PY01602	H2-Kd	LFIPYTFSI	44.55	NKMQLFIPYTFSIKFWQ*	AATAAGATGCAGCTGTTCATCCCTTACACCTTTAGCATAAAATTCTGGCAATGA
P59-10	PY01615	H2-Kd	AYNNIYSNL	14.92	RMSLAYNNIYSNLLTNA*	AGAATGAGTCTAGCCTATAATAACATCTATAGTAACCTGCTAACTAACGCATGA
P60-1	PY01615	H2-Kd	EYMHTNFVI	35.49	IPTVEYMHTNFVIRRDS*	ATACCTACCGTAGAGTACATGCACACTAACTTCGTGATCCGTCGTGATTCCTGA
P60-2	PY01617	H2-Kd	FWIAGNAKI	43.43	ACCAFWIAGNAKINSGS*	GCGTGTTGCGCATTCTGGATAGCCGGTAACGCTAAGATAAACTCTGGTAGCTGA
P60-3	PY01620	H2-Ld	SPQGTFFIL	42.91	TKLLSPQGTFFILSIEH*	ACTAAATTGCTGAGCCCTCAGGGCACCTTCTTCATCCTGTCTATAGAACATTGA
P60-4	PY01622	H2-Kd	VYISDASGL	24.22	QPAPVYISDASGLHVEH*	CAACCGGCACCCGTGTACATAAGTGACGCTAGCGGCCTGCATGTAGAACGTTGA
P60-5	PY01622	H2-Kd	HQYAPFYSI	27.87	DLSLHQYAPFYSIAEKG*	GATTTGAGTCTCCACCAGTACGCCCCTTTCTATAGCATAGCTGAGAAAGGCTGA
P60-6	PY01639	H2-Kd	NYYQVPISL	40.58	VYEGNYYQVPISLMDQY*	GTGTATGAGGGTAACTACTACCAGGTGCCTATAAGCCTGATGGACCAGTACTGA
P60-7	PY01639	H2-Kd	YYNASLVPF	46.06	ALLAYYNASLVPFVLRP*	GCACTTCTAGCCTACTATAACGCTAGCCTAGTGCCTTTCGTCCTCCGCCCCTGA
P60-8	PY01643	H2-Kd	KYNVNNATI	6.94	ILMGKYNVNNATIYAGP*	ATTCTAATGGGTAAGTATAACGTGAATAACGCCACCATCTACGCCGGTCCATGA
P60-9	PY01672	H2-Kd	FYYHIMYTL	12.74	ALSRFYYHIMYTLLDSV*	GCACTGAGTAGATTCTACTACCACATAATGTACACCCTGCTAGATTCAGTGTGA
P60-10	PY01672	H2-Kd	FFFNVLTNI	15.46	GFNGFFFNVLTNIKVTL*	GGGTTTAACGGGTTCTTCTTTAACGTGCTGACTAACATAAAAGTGACACTCTGA
P61-1	PY01672	H2-Kd	NYINSHIFL	16.49	YAFPNYINSHIFLYALY*	TACGCTTTCCCTAACTACATAAATAGCCACATCTTCCTGTACGCTCTATACTGA
P61-2	PY01672	H2-Kd	FYLYSGKSI	33.02	EECLFYLYSGKSIIIGQ*	GAAGAATGTCTGTTCTACCTGTATAGCGGTAAGAGCATAATAATAGGTCAGTGA

P61-3	PY01672	H2-Kd	SYSVVLIAI	40.89	LHCVSYSVVLIAIGQRA*	CTGCACTGTGTGAGCTATAGCGTAGTGCTGATAGCCATAGGACAGAGGGCATGA
P61-4	PY01672	H2-Kd	KLFRYITEI	41.54	FMPTKLFRYITEIWLPA*	TTCATGCCAACTAAGCTGTTTAGATACATAACTGAGATCTGGCTGCCCGCATGA
P61-5	PY01680	H2-Kd	FYINNLIYI	5	RAKQFYINNLIYIRLQT*	CGAGCTAAGCAATTCTACATAAATAACCTGATCTACATCCGCTTGCAGACCTGA
P61-6	PY01680	H2-Kd	KYISYIKKI	8.55	LHYIKYISYIKKIEPVE*	TTACATTATATAAAGTACATAAGCTACATAAAGAAGATAGAACCGGTAGAGTGA
P61-7	PY01680	H2-Kd	FYIKSNNML	8.56	NHHYFYIKSNNMLKTAV*	AATCACCATTATTTCTACATAAAGAGTAATAACATGCTGAAGACAGCTGTCTGA
P61-8	PY01680	H2-Kd	SYIKHCYLL	8.72	DATVSYIKHCYLLQLLR*	GATGCTACAGTGAGCTACATAAAGCACTGCTACCTGCTGCAGTTACTGAGATGA
P61-9	PY01680	H2-Kd	WYNSDNSLI	11.89	NTTVWYNSDNSLIERNG*	AACACCACCGTGTGGTATAATAGTGATAATAGCCTGATAGAGAGGAACGGCTGA
P61-10	PY01680	H2-Kd	KYSFIYNVI	13.66	PPISKYSFIYNVIGESV*	CCACCTATTTCTAAGTATAGCTTCATCTATAACGTGATAGGTGAGAGTGTATGA
P62-1	PY01680	H2-Kd	YYLDLTLNI	15.16	SSILYYLDLTLNIYRRT*	TCTAGTATCCTTTACTACCTAGACCTGACCCTGAACATCTATAGGCGGACCTGA
P62-2	PY01680	H2-Kd	CYLLAFSFI	17.09	AAKLCYLLAFSFIRDKI*	GCCGCTAAGCTGTGCTACCTGCTAGCCTTTAGCTTCATCCGTGATAAAATATGA
P62-3	PY01680	H2-Kd	HMYNNIYFI	24.81	HTDMHMYNNIYFISVYD*	CACACTGATATGCACATGTATAATAACATCTACTTCATAAGCGTGTATGACTGA
P62-4	PY01680	H2-Kd	LYLKTIIEI	35.12	EHIELYLKTIIEIASPH*	GAACATATAGAGCTGTACCTGAAGACCATAATAGAGATAGCGTCACCCCACTGA
P62-5	PY01680	H2-Kd	LYQNCNINI	45.88	QDPVLYQNCNINIYQLC*	CAGGATCCTGTGCTGTACCAGAACTGTAACATAAACATCTACCAGCTCTGCTGA
P62-6	PY01681	H2-Kd	KYLSRQIQI	11.21	AATQKYLSRQIQIPYVI*	GCCGCTACCCAGAAGTACCTGAGTAGACAGATCCAGATCCCCTATGTGATATGA
P62-7	PY01681	H2-Kd	RYFLAVPYI	12.79	VGNYRYFLAVPYIYKAT*	GTAGGTAACTATAGATACTTCCTAGCCGTGCCTTACATCTATAAAGCCACTTGA
P62-8	PY01681	H2-Kd	NYHFWFTPI	13.1	MVCGNYHFWFTPIQIKA*	ATGGTCTGTGGTAACTACCACTTCTGGTTCACCCCTATCCAGATAAAGGCTTGA
P62-9	PY01681	H2-Kd	RYFDFILSL	14.04	EAELRYFDFILSLAEAF*	GAAGCTGAACTGAGATACTTTGACTTCATCCTGAGCCTAGCTGAGGCCTTTTGA
P62-10	PY01681	H2-Kd	KYSYDLSKL	19.41	GSPKKYSYDLSKLNVGD*	GGTAGCCCTAAGAAGTATAGCTATGACCTGAGTAAGCTGAATGTAGGTGATTGA
P63-1	PY01681	H2-Kd	SYLCMPLCI	20.87	PRSESYLCMPLCITRQY*	CCTAGGAGTGAAAGCTACCTGTGCATGCCTCTGTGCATAACTAGGCAGTATTGA
P63-2	PY01681	H2-Kd	KYEKSMSNL	21.27	TEFGKYEKSMSNLVAQL*	ACTGAGTTCGGTAAGTATGAGAAGAGCATGAGTAACCTAGTAGCCCAGCTGTGA
P63-3	PY01681	H2-Kd	LYVNLCSAL	22.92	VNSQLYVNLCSALSRAA*	GTGAACTCACAGCTGTACGTGAACCTGTGTAGCGCCCTGAGTAGAGCAGCATGA
P63-4	PY01681	H2-Kd	YYFLLSYKI	32.28	SYNIYYFLLSYKIIKRT*	TCATATAACATTTACTACTTCCTGCTGAGCTATAAGATAATAAAAAGGACTTGA
P63-5	PY01681	H2-Kd	RYNNITTDL	37.25	ETGDRYNNITTDLTVEL*	GAAACTGGTGATAGATATAATAACATAACCACTGACCTGACTGTAGAACTCTGA
P63-6	PY01681	H2-Kd	KQYVNANSL	39.38	PSFFKQYVNANSLFNLT*	CCGTCGTTTTTTAAGCAGTACGTGAACGCTAATAGCCTGTTTAATCTAACCTGA
P63-7	PY01681	H2-Kd	SYAHDRDNI	42.43	KLLESYAHDRDNIVDKQ*	AAACTCCTAGAGAGCTACGCCCATGATAGAGATAACATAGTAGATAAACAATGA
P63-8	PY01681	H2-Kd	FMIDCYNSI	45.94	SIQSFMIDCYNSIRHVC*	TCCATCCAGTCCTTCATGATAGACTGCTATAATAGCATAAGACATGTCTGCTGA
P63-9	PY01681	H2-Kd	EYVNIFVSI	46.74	HKYSEYVNIFVSIESEL*	CATAAATACTCTGAGTACGTGAACATCTTCGTGAGCATAGAATCTGAGTTGTGA
P63-10	PY01681	H2-Kd	SYKNANNQL	48.03	RAYKSYKNANNQLTQLG*	AGAGCCTATAAGAGCTATAAGAACGCTAATAACCAGCTGACCCAGCTAGGGTGA
P64-1	PY01681	H2-Kd	SYAHIDLSL	49.93	SSQGSYAHIDLSLSTRE*	TCTAGCCAGGGTAGCTACGCCCACATAGACCTGAGCCTGTCCACCCGTGAGTGA
P64-2	PY01681	H2-Ld	YPFKIKNNL	46.68	WLRLYPFKIKNNLKREG*	TGGCTGAGGCTTTACCCTTTTAAGATAAAGAATAACCTGAAGCGTGAGGGCTGA
P64-3	PY01681	H2-Ld	IPHFHIINF	49.99	LLTPIPHFHIINFAKAT*	CTGCTAACCCCAATCCCTCACTTCCACATAATAAACTTCGCTAAAGCAACATGA
P64-4	PY01682	H2-Kd	VYNASNNEL	40.79	SYPGVYNASNNELLYKS*	TCCTATCCCGGTGTGTATAACGCTAGTAATAATGAGCTGCTGTATAAGAGCTGA
P64-5	PY01695	H2-Kd	YYMHMYNNV	5.45	IYGEYYMHMYNNVANWG	ATATATGGTGAGTACTACATGCACATGTATAATAACGTAGCTAACTGGGGCTGA
P64-6	PY01695	H2-Kd	IYYNAFHII	6.4	VAEDIYYNAFHIISSPC*	GTAGCTGAAGATATCTACTATAACGCCTTCCACATAATCTCCTCACCTTGCTGA
P64-7	PY01695	H2-Kd	AYTYNYLSI	17	MYLQAYTYNYLSIQSDA*	ATGTATCTGCAAGCCTACACCTATAACTACCTGAGCATCCAGTCTGATGCCTGA
P64-8	PY01695	H2-Kd	SYNYANVSL	17.87	YLSPSYNYANVSLSKQF*	TATCTGTCTCCTAGCTATAACTACGCTAACGTGAGCCTGTCTAAGCAGTTCTGA
P64-9	PY01695	H2-Kd	YYNAFHIII	19.99	DARPYYNAFHIIIVLSE*	GATGCTAGACCTTACTATAACGCCTTCCACATAATAATAGTTCTGTCTGAATGA
P64-10	PY01695	H2-Kd	LYLSNSLEI	22.08	VYELLYLSNSLEIYACD*	GTGTATGAACTACTGTACCTGAGTAATAGCCTAGAGATCTACGCATGTGACTGA
P65-1	PY01695	H2-Kd	VYIKVYKEI	30.84	YRKSVYIKVYKEIAKIE*	TACCGTAAGTCTGTGTACATAAAGGTGTATAAGGAGATAGCTAAGATAGAATGA
P65-2	PY01695	H2-Kd	VYIPILGEL	35.06	PVRAVYIPILGELIPEW*	CCCGTGAGGGCAGTGTACATCCCTATCCTAGGTGAGCTGATACCTGAATGGTGA
P65-3	PY01695	H2-Kd	YYEQVQNEL	35.24	FPHSYYEQVQNELEGAE*	TTCCCACATAGCTACTATGAGCAGGTGCAGAATGAGCTAGAAGGTGCTGAGTGA
P65-4	PY01695	H2-Ld	YPYINYLKM	13.17	MWVEYPYINYLKMPILL*	ATGTGGGTAGAGTACCCTTACATAAACTACCTGAAGATGCCAATTTTGCTTTGA
P65-5	PY01712	H2-Kd	KWQNLSAYI	34.41	DSKPKWQNLSAYIALEC*	GATTCTAAACCTAAGTGGCAGAACCTGAGCGCCTACATAGCACTAGAATGCTGA
P65-6	PY01717	H2-Kd	FYFTSDYNL	9.71	IYRSFYFTSDYNLEFKC*	ATTTATCGATCCTTCTACTTCACTAGTGACTATAACCTAGAGTTTAAGTGCTGA
P65-7	PY01717	H2-Kd	NYMNWFEKI	9.83	KALTNYMNWFEKISITQ*	AAAGCCTTGACTAACTACATGAACTGGTTTGAGAAGATCTCGATAACTCAGTGA
P65-8	PY01717	H2-Kd	FYISSKILL	18.77	ASMQFYISSKILLVSFK*	GCTAGTATGCAATTCTACATAAGTAGTAAGATCCTGCTAGTATCCTTTAAGTGA
P65-9	PY01750	H2-Kd	KYINVNHIL	4.34	LLVRKYINVNHILARTS*	CTCCTAGTTCGTAAGTACATAAACGTGAACCACATCCTAGCTCGAACCTCCTGA
P65-10	PY01750	H2-Kd	IYFFYIFII	34.02	QRGVIYFFYIFIIGARV*	CAGCGGGGTGTAATCTACTTCTTCTACATCTTCATAATAGGGGCACGGGTCTGA
P66-1	PY01754	H2-Kd	LYMAHPNYL	8.26	VSSTLYMAHPNYLGLAV*	GTGTCCTCCACCCTGTACATGGCCCACCCTAACTACCTAGGTCTAGCTGTGTGA
P66-2	PY01754	H2-Kd	KYAPHNKEI	27.92	DIRHKYAPHNKEIAATV*	GACATAAGGCATAAGTACGCCCCTCATAATAAGGAGATAGCAGCTACAGTATGA
P66-3	PY01754	H2-Kd	KYKKVLLPI	32.26	MFKTKYKKVLLPILLKA*	ATGTTTAAAACTAAGTATAAGAAGGTGCTGCTGCCTATCCTCCTGAAAGCCTGA
P66-4	PY01761	H2-Kd	KYLNNFIMI	6.1	RTGRKYLNNFIMIALDE*	CGAACTGGACGTAAGTACCTGAATAACTTCATAATGATAGCTCTAGATGAATGA
P66-5	PY01761	H2-Kd	YYYENNNIL	6.95	QNQCYYYENNNILTAGV*	CAGAATCAGTGTTACTACTATGAGAATAATAACATCCTGACAGCGGGCGTCTGA
P66-6	PY01761	H2-Kd	KYYYENNNI	10.41	RVEYKYYYENNNINCSN*	CGTGTAGAATATAAGTACTACTATGAGAATAATAACATAAACTGTAGTAACTGA
P66-7	PY01761	H2-Kd	KYINYYLCI	11.5	QSKAKYINYYLCIERDH*	CAAAGTAAGGCTAAGTACATAAACTACTACCTGTGCATAGAAAGAGATCATTGA
P66-8	PY01761	H2-Kd	YQFYNNTFI	12.81	WDLSYQFYNNTFIDMQR*	TGGGACCTGTCCTACCAGTTCTATAATAACACCTTCATAGACATGCAGAGGTGA
P66-9	PY01761	H2-Kd	FYNNTFIFL	12.87	RLKHFYNNTFIFLDDLL*	AGACTGAAACATTTCTATAATAACACCTTCATCTTCCTAGATGACCTCCTGTGA
P66-10	PY01761	H2-Kd	KYLYLFNKL	35.58	LDHPKYLYLFNKLKPIG*	CTAGATCACCCTAAGTACCTGTACCTGTTTAATAAGCTGAAGCCGATAGGTTGA
P67-1	PY01770	H2-Kd	YYYESTLSL	5.32	VSKWYYYESTLSLIRPV*	GTGTCTAAGTGGTACTACTATGAGAGCACCCTGAGCCTGATTCGCCCCGTGTGA
P67-2	PY01779	H2-Kd	RYHSYFTPL	6.22	ADAMRYHSYFTPLAGLG*	GCTGACGCAATGAGATACCATAGCTACTTCACCCCTCTAGCAGGACTAGGCTGA
P67-3	PY01779	H2-Kd	IYLSRIYRI	35.05	LISEIYLSRIYRILGEG*	TTGATCTCTGAGATCTACCTGAGTAGAATCTATAGAATCCTAGGTGAGGGGTGA
P67-4	PY01779	H2-Kd	SYFTPLNYV	43.49	FSIDSYFTPLNYVLDEW*	TTCTCGATAGATAGCTACTTCACCCCTCTGAACTACGTGCTAGATGAGTGGTGA
P67-5	PY01786	H2-Kd	NYNYNLDII	35.53	LAASNYNYNLDIIEHVV*	TTAGCCGCGTCTAACTATAACTATAACCTAGACATAATAGAGCATGTAGTGTGA
P67-6	PY01824	H2-Kd	IYLPETFTL	37.34	KSYWIYLPETFTLVTLA*	AAATCCTACTGGATCTACCTGCCTGAGACCTTCACCCTAGTAACTCTAGCCTGA
P67-7	PY01855	H2-Kd	RYFFYMYEL	13.28	EGEGRYFFYMYELGLEV*	GAGGGTGAAGGTAGATACTTCTTCTACATGTATGAGCTAGGACTAGAAGTGTGA
P67-8	PY01855	H2-Kd	SYYVNKKSL	19.4	HDKHSYYVNKKSLTQLH*	CATGATAAGCATAGCTACTACGTGAATAAGAAGAGCCTGACTCAGCTGCACTGA
P67-9	PY01855	H2-Kd	HYITVSLCI	32.25	GRVPHYITVSLCIELPP*	GGCCGTGTGCCACACTACATAACCGTGAGCCTGTGCATAGAACTTCCTCCATGA
P67-10	PY01855	H2-Kd	TMFESNSFI	37.73	FTNHTMFESNSFIGETL*	TTCACTAACCACACCATGTTTGAGAGTAATAGCTTCATAGGTGAGACACTGTGA
P68-1	PY01855	H2-Kd	YFFYMYELI	38.03	KKVPYFFYMYELIRCFG*	AAAAAGGTACCGTACTTCTTCTACATGTATGAGCTGATAAGGTGTTTTGGATGA
P68-2	PY01855	H2-Kd	SYSFHTGFL	45.63	YECGSYSFHTGFLICEP*	TATGAGTGTGGTAGCTATAGCTTCCACACCGGCTTCCTGATCTGTGAACCGTGA
P68-3	PY01876	H2-Kd	TYLCKPETI	40.53	TSCHTYLCKPETIGGQV*	ACCTCATGCCACACCTACCTGTGTAAGCCTGAGACCATAGGCGGCCAGGTATGA
P68-4	PY01912	H2-Kd	LYNKLTDII	41.37	SCNPLYNKLTDIICPPI*	TCATGTAACCCCCTGTATAATAAGCTGACTGACATAATCTGCCCCCCAATCTGA
P68-5	PY01912	H2-Kd	KQLEPTWSI	47.01	TLVSKQLEPTWSILKRE*	ACCCTAGTGTCTAAGCAGCTAGAGCCTACCTGGAGCATCCTGAAAAGGGAGTGA
P68-6	PY01912	H2-Kd	QYAKVFDFL	49.09	AAWLQYAKVFDFLASAE*	GCCGCCTGGCTCCAGTACGCTAAGGTGTTTGACTTCCTAGCTAGCGCTGAGTGA
P68-7	PY01922	H2-Kd	NYLNNYTSI	3.15	ELLVNYLNNYTSIEYFD*	GAGCTGCTAGTGAACTACCTGAATAACTACACTAGCATAGAGTACTTTGATTGA
P68-8	PY01922	H2-Kd	KYMILLFSI	6.73	EASHKYMILLFSIKVRR*	GAAGCTAGCCATAAGTACATGATCCTGCTGTTTAGCATAAAGGTGAGGCGCTGA
P68-9	PY01922	H2-Kd	LYYFISTQI	16.85	SYCPLYYFISTQIQCRN*	AGCTATTGTCCCCTGTACTACTTCATAAGCACCCAGATCCAGTGTCGTAACTGA
P68-10	PY01922	H2-Kd	NYFFTYNEL	18.87	APKQNYFFTYNELVNFP*	GCACCTAAGCAAAACTACTTCTTCACCTATAATGAGCTAGTGAATTTTCCCTGA
P69-1	PY01922	H2-Kd	YYKKAMCAI	34.37	LLLDYYKKAMCAIQDIR*	TTGCTGCTAGATTACTATAAGAAGGCCATGTGCGCCATCCAAGATATCCGCTGA
P69-2	PY01922	H2-Kd	SEYEYSYYI	41.72	LGDHSEYEYSYYISQSS*	CTAGGTGACCATAGTGAGTATGAGTATAGCTACTACATCTCTCAGTCTAGCTGA
P69-3	PY01922	H2-Ld	IPFFTFDQL	38.34	AYYPIPFFTFDQLPSLS*	GCGTATTATCCAATCCCTTTCTTCACCTTTGACCAGCTGCCTAGCCTGAGTTGA
P69-4	PY01925	H2-Kd	SYHTTLIMI	13.39	HGNSSYHTTLIMIDSLV*	CATGGTAACTCTAGCTACCACACCACCCTGATAATGATAGACTCACTAGTCTGA
P69-5	PY01938	H2-Kd	LYYLMHTSM	47.15	EHAKLYYLMHTSMTVAP*	GAGCATGCTAAACTGTACTACCTGATGCACACTAGCATGACCGTAGCGCCCTGA
P69-6	PY01947	H2-Kd	KYLSSLSCI	4.79	ATKCKYLSSLSCISLNL*	GCTACTAAGTGTAAGTACCTGAGTAGCCTGAGCTGCATAAGTTTGAATCTATGA
P69-7	PY01947	H2-Kd	SYIETVKEI	9.76	IFRESYIETVKEIHFDI*	ATTTTTAGAGAGAGCTACATAGAGACCGTGAAGGAGATCCACTTTGACATCTGA
P69-8	PY01947	H2-Kd	LYIVVLFSI	16.19	ALIKLYIVVLFSITLEK*	GCCTTGATAAAGCTGTACATAGTAGTGCTGTTTAGCATAACCCTAGAGAAGTGA
P69-9	PY01983	H2-Kd	KYMLQIDTI	6.97	FALLKYMLQIDTIVNKW*	TTTGCTCTCCTGAAGTACATGCTGCAGATAGACACCATAGTGAATAAGTGGTGA
P69-10	PY01983	H2-Kd	YYSYMCIYI	9.36	WQKLYYSYMCIYIVGDC*	TGGCAGAAGCTGTACTATAGCTACATGTGCATCTACATAGTAGGTGACTGTTGA
P70-1	PY01983	H2-Kd	YQLLNYSSI	12.56	AQSGYQLLNYSSILKEK*	GCTCAGTCTGGATACCAGCTGCTGAACTATAGTAGCATCCTGAAGGAAAAGTGA
P70-2	PY01983	H2-Kd	SYFFNFSSF	14.68	NVTTSYFFNFSSFAPEA*	AATGTAACAACTAGCTACTTCTTTAACTTTAGTAGCTTCGCACCTGAGGCCTGA
P70-3	PY01983	H2-Kd	KYNDQINYI	16.28	QTLTKYNDQINYIKFTT*	CAAACTTTGACTAAGTATAATGACCAGATAAACTACATAAAGTTCACCACCTGA
P70-4	PY01983	H2-Kd	GYMTYSSPV	21.63	FLGQGYMTYSSPVFSKR*	TTCCTAGGGCAGGGCTACATGACCTATAGTAGCCCTGTGTTTAGTAAGCGATGA
P70-5	PY01983	H2-Kd	SYMCIYIFL	25.34	LVLVSYMCIYIFLDAFE*	CTAGTCCTAGTGAGCTACATGTGCATCTACATCTTCCTAGATGCTTTTGAGTGA
P70-6	PY01983	H2-Kd	KYTIHDNYI	29.08	STKEKYTIHDNYIISKH*	TCCACTAAGGAAAAGTACACCATCCATGATAACTACATAATTTCTAAGCACTGA
P70-7	PY01983	H2-Kd	FYHKEYVQI	30.06	ACQCFYHKEYVQIAHPN*	GCATGTCAGTGTTTCTACCATAAGGAGTACGTGCAGATAGCCCATCCTAATTGA
P70-8	PY01983	H2-Kd	NYVNDPNYI	37.53	ANPNNYVNDPNYIFMSG*	GCTAATCCTAATAACTACGTGAATGACCCTAACTACATCTTCATGTCCGGGTGA
P70-9	PY01983	H2-Kd	KYYYIYQLL	40.22	LMSHKYYYIYQLLKLQP*	CTAATGTCCCATAAGTACTACTACATCTACCAGCTGCTGAAGTTGCAGCCCTGA
P70-10	PY01983	H2-Kd	IYESNRYNI	42.75	QDKDIYESNRYNISYYR*	CAAGATAAGGATATCTATGAGAGTAATAGATATAACATCTCCTATTATAGATGA
P71-1	PY01983	H2-Kd	KYAQCFLIL	46.71	VPKYKYAQCFLILPAGL*	GTGCCTAAATATAAGTACGCCCAGTGCTTCCTGATCCTGCCAGCTGGCCTCTGA
P71-2	PY01983	H2-Kd	SYKFNIFLL	48.24	MAYGSYKFNIFLLDRCI*	ATGGCTTACGGTAGCTATAAGTTTAACATCTTCCTGCTAGACCGCTGTATCTGA
P71-3	PY01983	H2-Kd	KYISNFIFF	49.74	IKSLKYISNFIFFSEAV*	ATAAAGAGCCTGAAGTACATAAGTAACTTCATCTTCTTCTCTGAGGCGGTGTGA

P71-4	PY01989	H2-Kd	KYTCDFSII	6.49	LQAVKYTCDFSIINWER*	CTGCAGGCCGTGAAGTACACCTGTGACTTTAGCATAATAAATTGGGAGAGATGA
P71-5	PY01999	H2-Kd	KYMYKNDII	9.7	FTMLKYMYKNDIIPCRV*	TTCACTATGCTGAAGTACATGTATAAGAATGACATAATCCCATGTAGGGTGTGA
P71-6	PY02022	H2-Kd	MYMLTFSFI	3.64	GGPNMYMLTFSFICFDA*	GGCGGGCCTAACATGTACATGCTGACCTTTAGCTTCATCTGTTTTGACGCTTGA
P71-7	PY02022	H2-Kd	RYCWPFSQI	10.02	VLRCRYCWPFSQIMRYP*	GTGCTTCGCTGTAGATACTGCTGGCCTTTTAGCCAGATAATGAGGTATCCCTGA
P71-8	PY02022	H2-Kd	IYSNTNLSI	16.43	EGLKIYSNTNLSIPLGA*	GAGGGCCTGAAGATCTATAGTAACACTAACCTGAGCATCCCATTAGGGGCCTGA
P71-9	PY02022	H2-Kd	FYNFYLYPL	21.74	GGNFFYNFYLYPLESRD*	GGGGGTAATTTTTTCTATAACTTCTACCTGTACCCTCTAGAGTCTAGGGATTGA
P71-10	PY02022	H2-Kd	IYIFNLRKI	26.39	AYLLIYIFNLRKIEVST*	GCATATTTGTTGATCTACATCTTTAACCTGAGAAAGATAGAGGTGTCCACCTGA
P72-1	PY02022	H2-Ld	FPMIFSFIF	18.3	HKFVFPMIFSFIFKLRN*	CATAAGTTCGTCTTCCCTATGATCTTTAGCTTCATCTTTAAGCTGCGTAACTGA
P72-2	PY02022	H2-Ld	WPFSQIYIF	37.34	DKAPWPFSQIYIFLLVF*	GATAAAGCCCCATGGCCTTTTAGCCAGATCTACATCTTCCTGCTAGTGTTTTGA
P72-3	PY02029	H2-Kd	LYNHVLVNI	24.11	LPTQLYNHVLVNIVSPT*	CTGCCCACCCAGCTGTATAACCACGTGCTAGTGAACATAGTGAGTCCCACATGA
P72-4	PY02029	H2-Kd	CWTKNNSTI	42.71	SKWRCWTKNNSTIDNPR	TCTAAGTGGAGATGCTGGACTAAGAATAATAGCACCATAGATAACCCCCGGTGA
P72-5	PY02029	H2-Kd	KYFSALRCL	49.93	KILSKYFSALRCLEDLL*	AAGATTCTGAGTAAGTACTTTAGCGCCCTGAGATGCCTAGAGGATTTGCTCTGA
P72-6	PY02032	H2-Kd	SYISSTEKL	13.31	MMNLSYISSTEKLSESH*	ATGATGAACCTGAGCTACATAAGTAGCACTGAGAAGCTGAGTGAGTCACATTGA
P72-7	PY02047	H2-Kd	SYFHYQNFI	2.93	PQELSYFHYQNFIAEHR*	CCACAAGAGCTGAGCTACTTCCACTACCAGAACTTCATAGCTGAGCATCGCTGA
P72-8	PY02047	H2-Kd	TFIPNDTTI	17.71	KLFRTFIPNDTTIGRQI*	AAGCTCTTTCGGACCTTCATCCCTAATGACACCACCATAGGTAGACAGATTTGA
P72-9	PY02076	H2-Kd	LYIHLNFTL	19.64	LTSLLYIHLNFTLRKEE*	TTGACCTCCCTGCTGTACATCCACCTGAACTTCACCCTGCGTAAAGAGGAGTGA
P72-10	PY02084	H2-Kd	SYGTYYVRI	30.5	IQSPSYGTYYVRISPTG*	ATTCAGAGTCCTAGCTACGGCACCTACTACGTGAGAATCTCACCAACCGGATGA
P73-1	PY02084	H2-Kd	NYTGVFNAI	31.77	LGVTNYTGVFNAIGKFG*	CTAGGCGTGACTAACTACACCGGCGTGTTTAACGCCATAGGTAAATTCGGATGA
P73-2	PY02110	H2-Kd	KYFKKFYNI	8.62	QSMAKYFKKFYNIDAPY*	CAATCTATGGCTAAGTACTTTAAGAAGTTCTATAACATAGACGCACCCTACTGA
P73-3	PY02120	H2-Kd	LYVASISYI	4.68	QQESLYVASISYILQWK*	CAACAGGAATCCCTGTACGTAGCTAGCATAAGCTACATCTTGCAATGGAAGTGA
P73-4	PY02120	H2-Ld	IPLIFSYVL	45.54	PSPAIPLIFSYVLPDSF*	CCCTCCCCTGCTATCCCTCTGATCTTTAGCTACGTGCTGCCTGACTCGTTCTGA
P73-5	PY02143	H2-Kd	SYVNLSGYI	17.32	LSVYSYVNLSGYIEAPR*	CTCTCTGTGTATAGCTACGTGAACCTGAGCGGCTACATAGAAGCTCCACGCTGA
P73-6	PY02143	H2-Kd	VYTPNLVMI	23.84	LDQKVYTPNLVMIGEEH*	CTAGACCAGAAAGTGTACACCCCTAACCTAGTGATGATAGGTGAAGAGCACTGA
P73-7	PY02175	H2-Kd	KYLSIHEYL	18.12	RVKKKYLSIHEYLISYM*	CGAGTGAAGAAGAAGTACCTGAGCATCCATGAGTACCTGATAAGCTACATGTGA
P73-8	PY02175	H2-Kd	KYNLNYVSL	18.25	ESVEKYNLNYVSLHTLL*	GAGTCAGTAGAGAAGTATAACCTGAACTACGTGAGCCTGCATACATTGCTGTGA
P73-9	PY02180	H2-Kd	SYCEYCSYI	8.8	LVKLSYCEYCSYIPALV*	CTAGTGAAGCTGAGCTACTGTGAGTACTGTAGCTACATCCCTGCCCTAGTGTGA
P73-10	PY02180	H2-Kd	SYIKINYFL	9.55	FGGNSYIKINYFLDWAT*	TTTGGAGGTAATAGCTACATAAAGATAAACTACTTCCTAGACTGGGCAACATGA
P74-1	PY02180	H2-Kd	KQTNNFESI	34.13	GPPMKQTNNFESISDKE*	GGACCTCCTATGAAGCAGACTAATAACTTTGAGAGCATCTCTGATAAGGAATGA
P74-2	PY02180	H2-Kd	HYGPYNQNI	37.91	QVNSHYGPYNQNISERG*	CAAGTGAATTCCCACTACGGCCCTTATAACCAGAACATCTCTGAGAGAGGATGA
P74-3	PY02180	H2-Kd	FYSCVSNGL	38.49	TNEEFYSCVSNGLMISR*	ACTAATGAAGAGTTCTATAGCTGCGTGAGTAACGGCCTGATGATATCTAGATGA
P74-4	PY02181	H2-Kd	IYYGSRITI	7.04	VSPHIYYGSRITILFIA*	GTTTCCCCCCACATCTACTACGGTAGTAGAATAACCATCCTGTTCATAGCCTGA
P74-5	PY02181	H2-Kd	AYGQNYTFI	10.83	CMCVAYGQNYTFISPVQ*	TGTATGTGCGTAGCCTACGGCCAGAACTACACCTTCATCTCCCCTGTACAGTGA
P74-6	PY02181	H2-Kd	IYICSENSL	12.45	VRFNIYICSENSLKRKR*	GTGAGGTTTAATATCTACATCTGTAGTGAGAATAGCCTGAAGAGAAAGAGGTGA
P74-7	PY02181	H2-Kd	AYYTISHYL	16.17	SLINAYYTISHYLLHNH*	TCACTAATAAATGCCTACTACACCATAAGCCACTACCTGTTACATAACCACTGA
P74-8	PY02181	H2-Kd	QYFEGIMKI	19.15	FIAPQYFEGIMKINPSY*	TTCATAGCTCCTCAGTACTTTGAGGGCATAATGAAGATAAACCCTAGCTATTGA
P74-9	PY02181	H2-Kd	PYMNGLLHI	28.8	VTYDPYMNGLLHIWDST*	GTAACGTATGACCCTTACATGAACGGCCTGCTGCACATCTGGGATAGTACCTGA
P74-10	PY02189	H2-Kd	SYIDTFYSI	2.11	ERTASYIDTFYSIPTAN*	GAGAGGACCGCTAGCTACATAGACACCTTCTATAGCATCCCAACTGCTAATTGA
P75-1	PY02189	H2-Kd	YYLNGYYLI	3.75	QEHDYYLNGYYLISISN*	CAGGAACATGATTACTACCTGAACGGCTACTACCTGATCTCCATCTCTAACTGA
P75-2	PY02189	H2-Kd	YYIQYIFNI	4.9	FLITYYIQYIFNIGIAR*	TTCCTGATAACCTACTACATCCAGTACATCTTTAACATAGGTATAGCTAGATGA
P75-3	PY02189	H2-Kd	YYFKAIKNI	11.39	DSGGYYFKAIKNIQSPT*	GATAGCGGGGGATACTACTTTAAGGCCATAAAGAACATCCAGTCTCCGACCTGA
P75-4	PY02189	H2-Kd	YYINVIDNV	20.92	VRIEYYINVIDNVAAEA*	GTTCGTATAGAATACTACATAAACGTGATAGATAACGTAGCGGCTGAGGCGTGA
P75-5	PY02189	H2-Kd	AYSKNNTSL	21.4	LTLAAYSKNNTSLLEHA*	CTAACACTAGCCGCCTATAGTAAGAATAACACTAGCCTGCTAGAGCATGCTTGA
P75-6	PY02189	H2-Kd	QYLEGILPL	31.44	ETAIQYLEGILPLVQTE*	GAAACAGCCATACAGTACCTAGAGGGCATCCTGCCTCTAGTGCAGACTGAATGA
P75-7	PY02189	H2-Kd	AYLDILHLI	32.33	KLLWAYLDILHLIFVLV*	AAGCTGCTGTGGGCCTACCTAGACATCCTGCACCTGATCTTCGTGCTAGTGTGA
P75-8	PY02189	H2-Kd	RFYFMLSLI	32.61	AESNRFYFMLSLIIPIT*	GCTGAATCTAATAGATTCTACTTCATGCTGAGCCTGATAATACCCATAACGTGA
P75-9	PY02189	H2-Kd	FYGKVREII	34.56	GWMWFYGKVREIIKTWS	GGATGGATGTGGTTCTACGGTAAGGTGAGAGAGATAATAAAGACCTGGTCTTGA
P75-10	PY02189	H2-Kd	CYKDNVNNI	38.68	EESKCYKDNVNNIHLRN*	GAAGAAAGTAAGTGCTATAAGGATAACGTGAATAACATCCACCTGCGTAATTGA
P76-1	PY02189	H2-Kd	IYSPNDNHL	41.58	QLNNIYSPNDNHLVVNK*	CAGCTGAATAATATCTATAGCCCTAATGATAACCACCTAGTAGTGAATAAATGA
P76-2	PY02189	H2-Kd	SYLLNQKNI	43.35	ARTLSYLLNQKNIHCPP*	GCTAGAACACTGAGCTACCTGCTGAACCAGAAGAACATCCACTGCCCCCCTTGA
P76-3	PY02189	H2-Kd	SYSHLFIKI	48.52	LDKLSYSHLFIKISPNS*	TTAGATAAGCTGAGCTATAGCCACCTGTTCATAAAGATCTCGCCTAATTCGTGA
P76-4	PY02196	H2-Kd	CYSCNLCPI	8.09	SAYTCYSCNLCPIGLAG*	AGCGCCTATACGTGCTATAGCTGTAACCTGTGCCCTATAGGCCTAGCAGGATGA
P76-5	PY02196	H2-Kd	NYYEMTDNI	11.28	LLRDNYYEMTDNISSSR*	CTTCTGCGTGATAACTACTATGAGATGACTGATAACATAAGTAGTAGTAGATGA
P76-6	PY02196	H2-Kd	KYTHGLKAI	15.62	LHKWKYTHGLKAISVEQ*	CTTCATAAGTGGAAGTACACCCACGGCCTGAAGGCCATAAGCGTAGAACAGTGA
P76-7	PY02196	H2-Kd	GYIFNEKTI	25.95	QAMQGYIFNEKTIRMRA*	CAAGCCATGCAGGGCTACATCTTTAATGAGAAGACCATAAGAATGCGCGCCTGA
P76-8	PY02196	H2-Kd	KYKNLFIPI	39.81	NGDFKYKNLFIPIDYNY*	AACGGTGATTTTAAGTATAAGAACCTGTTCATCCCTATAGATTATAATTATTGA
P76-9	PY02196	H2-Kd	FFHKNYYHI	47.62	SIEIFFHKNYYHITSST*	TCCATAGAAATCTTCTTCCATAAGAACTACTACCACATAACCTCATCCACCTGA
P76-10	PY02230	H2-Kd	FYIGNFTTL	2.6	RAARFYIGNFTTLEVIM*	AGAGCCGCACGATTCTACATAGGTAACTTCACCACCCTAGAGGTAATAATGTGA
P77-1	PY02230	H2-Kd	SYFNYQNEI	2.91	KLWASYFNYQNEIARLV*	AAGCTGTGGGCTAGCTACTTTAACTACCAGAATGAGATAGCTAGGTTAGTTTGA
P77-2	PY02230	H2-Kd	KYSNLETSI	4.97	YGLLKYSNLETSIPGLF*	TATGGACTGCTGAAGTATAGTAACCTAGAGACTAGCATCCCTGGGCTATTTTGA
P77-3	PY02230	H2-Kd	SYYVMDTIL	8.49	VPNASYYVMDTILNFLP*	GTTCCTAACGCTAGCTACTACGTGATGGACACCATCCTGAACTTTCTTCCATGA
P77-4	PY02230	H2-Kd	KYIDDKYNL	20.06	EPNYKYIDDKYNLPRIA*	GAACCTAATTATAAGTACATAGATGATAAGTATAACCTGCCCCGGATAGCGTGA
P77-5	PY02230	H2-Kd	KEMPVIEYI	31.44	TYLTKEMPVIEYISLVR*	ACATATCTGACTAAGGAGATGCCTGTGATAGAGTACATCTCCCTAGTGAGATGA
P77-6	PY02230	H2-Ld	FPLININYF	22.67	DKRVFPLININYFSSPQ*	GATAAGCGTGTTTTCCCTCTGATAAACATAAACTACTTCTCGTCTCCACAATGA
P77-7	PY02239	H2-Kd	FYNHAKMMI	20.82	WLRLFYNHAKMMIQAFR*	TGGTTGCGTTTATTCTATAACCACGCTAAGATGATGATCCAGGCATTCCGCTGA
P77-8	PY02258	H2-Kd	IYANSLLNI	18.53	TIPHIYANSLLNINIPL*	ACCATTCCGCACATCTACGCTAATAGCCTGCTGAACATAAATATCCCGCTGTGA
P77-9	PY02258	H2-Kd	GYAGLVYEI	30.96	CDVAGYAGLVYEIAEVS*	TGTGACGTAGCTGGCTACGCCGGCCTAGTGTATGAGATAGCTGAAGTGTCCTGA
P77-10	PY02294	H2-Kd	HYLRAIPNL	31.91	MCPRHYLRAIPNLSNTL*	ATGTGCCCTCGCCACTACCTGAGAGCCATCCCTAACCTGTCTAATACTTTATGA
P78-1	PY02297	H2-Kd	RYNNNNTNI	4.61	VTHSRYNNNNTNIVGNQ*	GTAACCCACTCTAGATATAATAATAATAACACTAACATAGTAGGTAACCAGTGA
P78-2	PY02297	H2-Kd	MYNRMEYVI	10.75	SIVMMYNRMEYVILILL*	TCAATAGTGATGATGTATAATAGAATGGAGTACGTGATCCTAATCCTACTTTGA
P78-3	PY02297	H2-Ld	LPNVNNYNM	34.23	GSTKLPNVNNYNMQTAM	GGTAGCACTAAGCTGCCTAACGTGAATAACTATAACATGCAAACGGCCATGTGA
P78-4	PY02297	H2-Ld	HPMNMYNRM	46.38	TSIPHPMNMYNRMYPMT	ACATCTATCCCACACCCTATGAACATGTATAATAGAATGTATCCCATGACTTGA
P78-5	PY02310	H2-Kd	SYYINGNSI	4.75	IGVISYYINGNSIVYCN*	ATAGGCGTGATAAGCTACTACATAAACGGTAATAGCATAGTGTATTGTAACTGA
P78-6	PY02310	H2-Kd	SYNYYIENI	9.59	HTLASYNYYIENILEKI*	CACACCTTAGCTAGCTATAACTACTACATAGAGAACATCCTAGAGAAGATTTGA
P78-7	PY02310	H2-Kd	SYESSDSYI	13.58	WPLTSYESSDSYISLSL*	TGGCCACTGACTAGCTATGAGAGTAGTGATAGCTACATCTCCCTGAGCCTGTGA
P78-8	PY02310	H2-Kd	CYINNEKNI	31.65	QCLECYINNEKNINCSG*	CAATGCCTAGAGTGCTACATAAATAATGAGAAGAACATAAACTGCTCAGGGTGA
P78-9	PY02320	H2-Kd	YYLYYKNII	10.27	LKCHYYLYYKNIIDLIS*	CTGAAATGCCATTACTACCTGTACTATAAGAACATAATAGATCTAATAAGTTGA
P78-10	PY02320	H2-Kd	YYIKKIQFI	11.16	VCKRYYIKKIQFIREGM*	GTGTGTAAACGGTACTACATAAAGAAGATCCAGTTCATAAGGGAAGGGATGTGA
P79-1	PY02320	H2-Kd	LYHTIYNPI	12.5	VYTSLYHTIYNPINHTA*	GTGTACACATCCCTGTACCACACCATCTATAACCCTATAAACCACACTGCTTGA
P79-2	PY02320	H2-Kd	IYLGIVTPL	25.27	SVEVIYLGIVTPLSTCA*	TCTGTAGAAGTGATCTACCTAGGCATAGTGACCCCTCTGAGTACTTGCGCTTGA
P79-3	PY02320	H2-Kd	KYANLEDNI	32.67	LFNKKYANLEDNIKPEH*	CTCTTTAATAAAAAGTACGCTAACCTAGAGGATAACATAAAGCCTGAACACTGA
P79-4	PY02320	H2-Kd	IYQICNYPI	36.37	HNQLIYQICNYPIIPKQ*	CATAACCAGCTAATCTACCAGATCTGTAACTACCCTATAATTCCTAAGCAGTGA
P79-5	PY02320	H2-Kd	KYIIIYLNI	36.97	SESVKYIIIYLNIVPKG*	TCTGAAAGCGTGAAGTACATAATAATCTACCTGAACATAGTGCCTAAGGGCTGA
P79-6	PY02320	H2-Ld	HPACSFPTL	39.13	CQVVHPACSFPTLLTDG*	TGTCAGGTAGTGCACCCTGCCTGTAGCTTCCCTACCCTGCTAACTGACGGATGA
P79-7	PY02325	H2-Kd	KYHGNYTNI	4.39	MQGGKYHGNYTNICLFK*	ATGCAGGGCGGTAAGTACCACGGTAACTACACTAACATCTGCCTTTTTAAATGA
P79-8	PY02338	H2-Kd	KYAWVLDKL	18.36	DTNIKYAWVLDKLHHKM*	GACACTAATATAAAGTACGCCTGGGTGCTAGATAAGCTGCACCATAAGATGTGA
P79-9	PY02348	H2-Kd	FYFSYYYNL	6.11	YARRFYFSYYYNLFADS*	TACGCACGTAGATTCTACTTTAGCTACTACTATAACCTGTTCGCTGACTCCTGA
P79-10	PY02348	H2-Kd	YYYNLTVSL	6.26	FAVAYYYNLTVSLFTPG*	TTCGCAGTAGCCTACTACTATAACCTGACCGTGAGCCTGTTCACGCCCGGGTGA
P80-1	PY02348	H2-Kd	KFYKSWSSI	8.59	KPVRKFYKSWSSIAFFD*	AAACCCGTGAGAAAGTTCTATAAGAGCTGGAGTAGCATAGCCTTCTTTGACTGA
P80-2	PY02348	H2-Kd	KYNKIMNVI	9.16	SYSAKYNKIMNVIEIDK*	TCTTATAGTGCTAAGTATAATAAGATAATGAACGTGATAGAGATAGATAAATGA
P80-3	PY02348	H2-Kd	SYVKSTLKI	10.19	TYQGSYVKSTLKIDTPD*	ACGTATCAGGGTAGCTACGTGAAGAGCACCCTGAAGATAGATACTCCTGACTGA
P80-4	PY02348	H2-Kd	GYAFVIFPI	15.81	TLDLGYAFVIFPIPRIY*	ACCCTAGACCTAGGCTACGCCTTCGTGATCTTCCCTATCCCTAGGATCTACTGA
P80-5	PY02348	H2-Kd	FYKSWSSII	20.25	DDTNFYKSWSSIIHFSM*	GATGACACTAATTTCTATAAGAGCTGGAGTAGCATAATCCACTTTAGTATGTGA
P80-6	PY02348	H2-Kd	SYIIIRGSI	21.99	DSIDSYIIIRGSIKNGK*	GATAGCATAGATAGCTACATAATAATAAGAGGTAGCATAAAAAACGGTAAATGA
P80-7	PY02348	H2-Kd	NWINNANAI	36.62	SYDVNWINNANAIIYSF*	TCCTATGATGTGAACTGGATAAATAACGCTAACGCCATAATATACTCCTTTTGA
P80-8	PY02366	H2-Kd	FYFSNEFNI	4.54	IVNGFYFSNEFNIIHAY*	ATAGTGAATGGCTTCTACTTTAGTAATGAGTTTAACATAATTCACGCCTATTGA
P80-9	PY02366	H2-Kd	IYMNNNGHI	6.78	IHTNIYMNNNGHILGEC*	ATACATACTAACATCTACATGAATAATAACGGCCACATCCTAGGTGAGTGCTGA
P80-10	PY02366	H2-Kd	KYTNSCSDI	11.83	QQDTKYTNSCSDISFND*	CAGCAGGACACTAAGTACACTAATAGCTGTAGTGACATCTCATTTAATGACTGA
P81-1	PY02366	H2-Kd	HYNNGQMFL	17.93	GPPAHYNNGQMFLMCCS	GGACCACCTGCTCACTATAATAACGGCCAGATGTTCCTGATGTGCTGCTCTTGA
P81-2	PY02366	H2-Kd	NYNPNINNL	22.86	LCPKNYNPNINNLVASI*	CTTTGTCCTAAGAACTATAACCCTAACATAAATAACCTAGTAGCTTCTATTTGA
P81-3	PY02366	H2-Kd	SAYNMNYYI	43.7	KSRTSAYNMNYYIQFPH*	AAATCCCGGACTAGCGCCTATAACATGAACTACTACATCCAGTTTCCCCACTGA
P81-4	PY02373	H2-Kd	YYTNHVDTI	6	QEKGYYTNHVDTIIVHF*	CAGGAAAAGGGATACTACACTAACCACGTAGACACCATAATAGTGCACTTCTGA

P81-5	PY02373	H2-Kd	QYMHMTLII	8.91	ANEGQYMHMTLIIILSK*	GCTAATGAGGGGCAGTACATGCACATGACCCTGATAATAATTCTGAGTAAGTGA
P81-6	PY02373	H2-Kd	YYYKYLEIL	12.65	YELSYYYKYLEILAEGS*	TATGAACTTTCATACTACTATAAGTACCTAGAGATCCTAGCTGAGGGCTCTTGA
P81-7	PY02373	H2-Kd	YYTYFNNFI	12.95	SDEKYYTYFNNFISHAR*	AGTGATGAGAAGTACTACACCTACTTTAATAACTTCATCTCACACGCTCGATGA
P81-8	PY02373	H2-Kd	YYYDDENTL	15.39	SKRRYYYDDENTLANLL*	TCTAAGCGACGATACTACTATGATGATGAGAACACCCTAGCTAACCTGTTGTGA
P81-9	PY02373	H2-Kd	KYNINDNNI	18.19	LLIYKYNINDNNIVCDT*	CTGCTAATTTATAAGTATAACATAAATGATAATAACATAGTGTGTGATACTTGA
P81-10	PY02373	H2-Kd	KYTNINEEI	21.14	IGTGKYTNINEEIRMHS*	ATAGGTACTGGTAAGTACACTAACATAAATGAGGAGATCCGTATGCATTCCTGA
P82-1	PY02373	H2-Kd	NYNFVNSFL	25.65	FVMHNYNFVNSFLKHLD*	TTTGTGATGCATAACTATAACTTCGTGAATAGCTTCCTGAAGCATCTAGACTGA
P82-2	PY02373	H2-Kd	SFINLNETI	38.27	ACPLSFINLNETIRQSH*	GCGTGCCCCCTGAGCTTCATAAACCTGAATGAGACCATAAGACAGAGCCACTGA
P82-3	PY02373	H2-Kd	IYNFTSTIL	38.44	IRKDIYNFTSTILLTLI*	ATAAGAAAAGACATCTATAACTTCACTAGCACCATCCTGTTGACATTAATATGA
P82-4	PY02376	H2-Kd	CYEYMINFI	24.06	CPLSCYEYMINFIHKQK*	TGCCCCCTGTCGTGCTATGAGTACATGATAAACTTCATCCATAAGCAGAAGTGA
P82-5	PY02388	H2-Kd	KYSDSKSTI	4.98	LLWKKYSDSKSTIKGTK*	CTGCTGTGGAAGAAGTATAGTGATAGTAAGAGCACCATAAAAGGGACTAAGTGA
P82-6	PY02388	H2-Kd	MYSQIKCLI	31.8	RDDSMYSQIKCLIVTPL*	AGGGATGACTCTATGTATAGCCAGATAAAGTGCCTGATAGTGACACCCCTGTGA
P82-7	PY02388	H2-Kd	SYSQKTNLI	33.27	SDATSYSQKTNLILAGL*	TCTGATGCTACTAGCTATAGCCAGAAGACTAACCTGATCCTAGCCGGGCTGTGA
P82-8	PY02411	H2-Kd	CYVYNKNII	13.76	PTSGCYVYNKNIITAPT*	CCGACCTCGGGCTGCTACGTGTATAATAAGAACATAATAACTGCCCCTACATGA
P82-9	PY02411	H2-Kd	FYNMNIKSI	21.78	VISTFYNMNIKSITCKR*	GTGATATCTACCTTCTATAACATGAACATAAAGAGCATAACCTGTAAGCGCTGA
P82-10	PY02411	H2-Kd	SFMNNDDSI	25.23	HSTASFMNNDDSISRQL*	CATAGTACAGCTAGCTTCATGAATAATGATGAGCATCTCTAGGCAGTTATGA
P83-1	PY02411	H2-Kd	VYNKNIIEI	29.4	ACDFVYNKNIIEIYKYD*	GCATGTGACTTCGTGTATAATAAGAACATAATAGAGATCTATAAGTATGACTGA
P83-2	PY02411	H2-Kd	IYNLDINSI	32.66	LLVAIYNLDINSIWHWS*	CTACTAGTAGCTATCTATAACCTAGACATAAATAGCATCTGGCACTGGTCATGA
P83-3	PY02442	H2-Kd	KYYFYDSNI	4.68	EKAEKYYFYDSNIISQR*	GAGAAGGCTGAGAAGTACTACTTCTATGATAGTAACATAATTTCCCAGCGGTGA
P83-4	PY02442	H2-Kd	YYFNKKLTI	5.89	PDFVYYFNKKLTIEECP*	CCTGACTTTGTATACTACTTTAATAAGAAGCTGACCATAGAGGAGTGCCCATGA
P83-5	PY02442	H2-Kd	IYNCTYTNI	7.66	PTIPIYNCTYTNIGIVV*	CCGACAATACCAATCTATAACTGCACCTACACTAACATAGGAATAGTAGTGTGA
P83-6	PY02442	H2-Kd	IYQNYNNPI	7.93	KVEDIYQNYNNPICKFP*	AAGGTAGAAGACATCTACCAGAACTATAATAACCCTATCTGTAAATTCCCTTGA
P83-7	PY02442	H2-Kd	FYYNYDYVI	8.46	LYKPFYYNYDYVIGNKA*	CTCTATAAGCCCTTCTACTATAACTATGACTACGTGATAGGTAATAAGGCGTGA
P83-8	PY02442	H2-Kd	YYFKDNYII	9.29	SKQTYYFKDNYIIIPIK*	TCTAAGCAGACTTACTACTTTAAGGATAACTACATAATAATTCCAATAAAGTGA
P83-9	PY02442	H2-Kd	KYFEYNMLL	10.57	IPSEKYFEYNMLLESPE*	ATCCCTTCTGAGAAGTACTTTGAGTATAACATGCTGCTAGAGTCTCCTGAGTGA
P83-10	PY02442	H2-Kd	IYLNGSVNI	10.98	RLGAIYLNGSVNIEDPF*	CGCCTAGGCGCCATCTACCTGAACGGTAGCGTGAACATAGAGGACCCATTTTGA
P84-1	PY02442	H2-Kd	IYIYNKHNL	11.77	AMSQIYIYNKHNLALKT*	GCCATGTCTCAAATCTACATCTATAATAAGCATAACCTAGCACTGAAGACTTGA
P84-2	PY02442	H2-Kd	KYNLYINNI	14.64	QKDIKYNLYINNIYNSK*	CAAAAGGACATAAAGTATAACCTGTACATAAATAACATCTATAACTCTAAGTGA
P84-3	PY02442	H2-Kd	IYIKKYVTI	16.22	SPEIIYIKKYVTIVYGQ*	TCCCCTGAGATAATCTACATAAAGAAGTACGTGACCATAGTGTACGGGCAGTGA
P84-4	PY02442	H2-Kd	NYIIANSFI	16.51	PQDQNYIIANSFINKVA*	CCCCAGGACCAAAACTACATAATAGCTAATAGCTTCATAAATAAAGTAGCATGA
P84-5	PY02442	H2-Kd	LYACNKYTL	16.87	HQQSLYACNKYTLNNSP*	CACCAGCAAAGCCTGTACGCCTGTAATAAGTACACCCTGAATAACTCTCCATGA
P84-6	PY02442	H2-Kd	YYFYDSNIL	18.66	QSRAYYFYDSNILQELK*	CAGAGCCGCGCATACTACTTCTATGATAGTAACATCCTGCAGGAACTGAAGTGA
P84-7	PY02442	H2-Kd	IYNISKTNI	21.69	EDVSIYNISKTNISPLA*	GAAGACGTGAGCATCTATAACATAAGTAAGACTAACATAAGCCCCTTAGCGTGA
P84-8	PY02442	H2-Kd	KYINYSDYV	23.43	QAPKKYINYSDYVFCRC*	CAGGCCCCTAAGAAGTACATAAACTATAGTGACTACGTGTTTTGCCGATGTTGA
P84-9	PY02442	H2-Kd	YYCKDISIL	31.42	LQTEYYCKDISILSKGH*	CTACAAACTGAGTACTACTGTAAGGACATAAGCATCCTGTCTAAAGGCCACTGA
P84-10	PY02442	H2-Kd	MYLINKFII	31.53	LKEHMYLINKFIINPEL*	CTGAAGGAGCACATGTACCTGATAAATAAGTTCATAATAAATCCTGAGTTGTGA
P85-1	PY02442	H2-Kd	SYTHADNNI	32.05	RLFSSYTHADNNIMMPI*	AGGCTATTCTCTAGCTACACCCACGCTGATAATAACATAATGATGCCCATTTGA
P85-2	PY02442	H2-Kd	EYFPNYYIL	32.94	KNDSEYFPNYYILSIVD*	AAGAATGATAGTGAGTACTTCCCTAACTACTACATCCTGAGTATAGTAGACTGA
P85-3	PY02442	H2-Kd	IYYFKDNYI	39.78	EPLRIYYFKDNYIGEYG*	GAGCCTCTGAGGATCTACTACTTTAAGGATAACTACATAGGTGAGTACGGATGA
P85-4	PY02442	H2-Kd	IYYCKDISI	46.81	LANCIYYCKDISIEVIP*	TTAGCTAATTGCATCTACTACTGTAAGGACATAAGCATAGAGGTAATACCCTGA
P85-5	PY02460	H2-Kd	MYIIYVQNI	18.78	IVFQMYIIYVQNIEVDC*	ATAGTCTTCCAGATGTACATAATCTACGTGCAGAACATAGAAGTAGACTGTTGA
P85-6	PY02476	H2-Kd	TYMRYHSSV	6.17	VGSQTYMRYHSSVTGND	GTAGGTAGCCAAACCTACATGAGATACCATAGTAGCGTGACGGGTAATGACTGA
P85-7	PY02481	H2-Kd	YYINMDSRL	3.82	FQNVYYINMDSRLLESD*	TTCCAAAATGTGTACTACATAAACATGGAGTATGAGACTGCTAGAGAGTGATTGA
P85-8	PY02481	H2-Kd	RYLDILNNL	21.88	CRHNRYLDILNNLPLVL*	TGTCGTCATAATAGATACCTAGACATCCTGAATAACCTGCCCTTAGTTCTCTGA
P85-9	PY02481	H2-Ld	SPYLHLILF	49.08	RWRKSPYLHLILFNWVG*	AGGTGGAGAAAAAGCCCTTACCTGCACCTGATCCTGTTTAACTGGGTAGGCTGA
P85-10	PY02590	H2-Kd	KYIGESARI	21.78	GSCWKYIGESARIGPWY*	GGATCATGTTGGAAGTACATAGGTGAGAGCGCTAGAATAGGCCCCTGGTACTGA
P86-1	PY02590	H2-Ld	LPILNPFLF	20.33	RNSKLPILNPFLFQVHL*	CGTAATTCTAAACTGCCTATCCTGAACCCTTTCCTGTTCCAGGTCCATCTTTGA
P86-2	PY02592	H2-Kd	SYSYILSIL	20.56	QGVMSYSYILSILLKYE*	CAAGGGGTGATGAGCTATAGCTACATCCTGAGCATCCTGCTGAAGTATGAGTGA
P86-3	PY02597	H2-Kd	KYGKSYSEI	6.31	EYFCKYGKSYSEIIPQE*	GAGTATTTCTGTAAGTACGGTAAGAGCTATAGTGAGATAATTCCCCAGGAATGA
P86-4	PY02597	H2-Kd	FYFFTFLLL	37.18	VDKIFYFFTFLLLDYKK*	GTAGATAAAATATTCTACTTCTTCACCTTCCTGCTGCTAGATTATAAGAAATGA
P86-5	PY02606	H2-Kd	NYIDMFCQI	5.26	RVSDNYIDMFCQIPNPR*	AGGGTGAGTGATAACTACATAGACATGTTCTGCCAGATCCCTAATCCTAGGTGA
P86-6	PY02606	H2-Kd	TYYPSDHEI	7.57	NYPETYYPSDHEIQVGT*	AATTATCCTGAAACCTACTACCCTAGTGACCATGAGATCCAAGTAGGGACCTGA
P86-7	PY02606	H2-Kd	SYFKKKSLI	11.59	AASLSYFKKKSLIYPPP*	GCTGCTAGCCTGAGCTACTTTAAGAAGAAGAGCCTGATCTATCCTCCCCCTTGA
P86-8	PY02606	H2-Kd	NYASYQTYI	21.04	HQWLNYASYQTYISFGF*	CACCAGTGGTTGAACTACGCTAGCTACCAGACCTACATCTCCTTTGGGTTCTGA
P86-9	PY02606	H2-Kd	FYVNRNNPL	22.34	SRRNFYVNRNNPLGTSL*	TCGCGTCGTAACTTCTACGTGAATAGAAATAACCCTCTAGGTACTAGCCTGTGA
P86-10	PY02606	H2-Kd	FYSDISSIL	26.68	LEFPFYSDISSILVIGV*	CTAGAGTTTCCTTTCTATAGTGACATAAGTAGCATCCTAGTAATAGGCGTGTGA
P87-1	PY02606	H2-Kd	KYSKEVNKI	35.22	QDQEKYSKEVNKIIVLS*	CAGGATCAGGAGAAGTATAGTAAGGAGGTGAATAAGATAATAGTGCTCTCGTGA
P87-2	PY02606	H2-Kd	YYQGLSGNL	42.02	DKNQYYQGLSGNLGAKS	GATAAGAACCAGTACTACCAGGGCCTGAGCGGTAACCTAGGAGCTAAGTCTTGA
P87-3	PY02606	H2-Kd	NYIFDNNMI	42.84	RGVKNYIFDNNMIPFLT*	CGGGGCGTGAAGAACTACATCTTTGATAATAACATGATCCCTTTTCTAACCTGA
P87-4	PY02606	H2-Kd	IYSLSIQYI	43.41	TCDRIYSLSIQYILIEA*	ACATGTGATCGTATCTATAGCCTGAGCATCCAGTACATCTTGATAGAGGCATGA
P87-5	PY02631	H2-Kd	CYMNTPFKI	5.93	SGPACYMNTPFKIYLQI*	TCCGGACCAGCTTGCTACATGAACACCCCTTTTAAGATCTACCTGCAGATCTGA
P87-6	PY02631	H2-Kd	YYLFNFEII	6.84	FHPRYYLFNFEIIRSAL*	TTCCATCCTCGGTACTACCTGTTTAACTTTGAGATAATAAGGAGCGCGCTGTGA
P87-7	PY02631	H2-Kd	RYSNVHTLL	7.38	CSAERYSNVHTLLVGLP*	TGCTCTGCTGAAAGATATAGTAACGTGCACACCCTGCTAGTAGGACTGCCATGA
P87-8	PY02631	H2-Kd	SYICNKDML	23.42	HMYRSYICNKDMLTALK*	CACATGTATAGGAGCTACATCTGTAATAAGGACATGCTGACCGCCCTGAAGTGA
P87-9	PY02638	H2-Kd	YYYWIPMVL	12.17	MQQVYYYWIPMVLLSDT*	ATGCAGCAAGTCTACTACTACTGGATCCCTATGGTGCTGCTTTCTGACACCTGA
P87-10	PY02638	H2-Ld	IPMVLGYYF	17.48	VPESIPMVLGYYFQKIM*	GTTCCTGAATCTATCCCTATGGTGCTAGGCTACTACTTCCAGAAAATAATGTGA
P88-1	PY02638	H2-Ld	NPSANVYHF	48.78	VGRKNPSANVYHFQTCK*	GTAGGACGTAAAAACCCTAGCGCTAACGTGTACCACTTCCAGACATGTAAGTGA
P88-2	PY02679	H2-Kd	IYFKYANEL	12.02	FELAIYFKYANELLFNN*	TTTGAGCTAGCTATCTACTTTAAGTACGCTAATGAGCTGCTCTTTAATAACTGA
P88-3	PY02679	H2-Kd	NYIDIYIQI	23.23	VQDLNYIDYIQIIRAMG*	GTCCAAGACCTGAACTACATAGACTACATCCAGATAATAAGAGCGATGGGGTGA
P88-4	PY02679	H2-Kd	KYANELQAL	27.63	PIVNKYANELQALRILS*	CCAATAGTGAATAAGTACGCTAATGAGCTGCAGGCCCTGAGAATCCTGAGCTGA
P88-5	PY02679	H2-Kd	IYYIVNNSL	32.94	DFLFIYYIVNNSLAVDN*	GATTTTCTGTTCATCTACTACATAGTGAATAATAGCCTAGCCGTAGATAATTGA
P88-6	PY02679	H2-Kd	KYTEINDII	36.57	GSTNKYTEINDIIVITQ*	GGCTCCACTAATAAGTACACTGAGATAAATGACATAATAGTAATAACTCAGTGA
P88-7	PY02679	H2-Kd	IYDPNYETI	44.11	HNTPIYDPNYETILRLK*	CATAATACTCCGATCTATGACCCTAACTATGAGACCATCCTTCGCCTGAAGTGA
P88-8	PY02679	H2-Ld	FPNINYLRL	28.43	KAVGFPNINYLRLGGFC*	AAGGCCGTAGGCTTCCCTAACATAAACTACCTGAGACTAGGGGGATTCTGTTGA
P88-9	PY02683	H2-Kd	KYLPLFSTL	3.64	RLYAKYLPLFSTLAAQT*	CGGTTATATGCTAAGTACCTGCCTCTGTTTAGCACCCTAGCCGCTCAGACCTGA
P88-10	PY02683	H2-Kd	HYINHINYI	3.72	PDMTHYINHINYILERH*	CCTGATATGACACACTACATAAACCACATAAACTACATCCTAGAGAGGCATTGA
P89-1	PY02683	H2-Kd	IYANTAYTL	12.49	RRRPIYANTAYTLRTPA*	CGTAGGCGACCAATCTACGCTAACACCGCCTACACCCTGAGGACCCCGCTTGA
P89-2	PY02691	H2-Kd	TFIRSCQYI	40.7	NIGLTFIRSCQYISVPE*	AATATAGGTCTGACCTTCATAAGAAGCTGCCAGTACATCTCTGTCCCTGAATGA
P89-3	PY02696	H2-Kd	KYNASLETI	4.65	SLIHKYNASLETIKEQN*	AGCTTGATCCATAAGTATAACGCTAGCCTAGAGACCATAAAGGAGCAGAACTGA
P89-4	PY02696	H2-Kd	YFVSAFSQI	22.58	LTFLYFVSAFSQIDARE*	CTGACATTTTTATACTTCGTGAGCGCCTTTAGCCAGATAGATGCTAGAGAGTGA
P89-5	PY02715	H2-Kd	YYVNIESTI	3.63	NPSIYYVNIESTIKPGV*	AATCCTAGCATATACTACGTGAACATAGAGAGCACCATAAAGCCAGGCGTCTGA
P89-6	PY02715	H2-Kd	KYFFDDNSI	4.57	TPERKYFFDDNSITVAE*	ACGCCTGAGCGTAAGTACTTCTTTGATGATAATAGCATAACAGTAGCTGAGTGA
P89-7	PY02715	H2-Kd	FYSYLLPFI	21.66	KGWTFYSYLLPFIATQS*	AAAGGGTGGACATTCTATAGCTACCTGCTGCCTTTCATAGCAACCCAATCATGA
P89-8	PY02715	H2-Kd	TYNDIIYNI	28.15	MTVQTYNDIIYNINESQ*	ATGACCGTGCAGACCTATAATGACATAATCTATAACATAAATGAGTCCCAGTGA
P89-9	PY02715	H2-Kd	YYSKFSLYI	46.04	DSNQYYSKFSLYIGARS*	GACTCTAACCAGTACTATAGTAAGTTTAGCCTGTACATAGGAGCTAGGTCCTGA
P89-10	PY02722	H2-Kd	SYLKSKFTL	5.35	NMQKSYLKSKFTLAMFL*	AACATGCAGAAAAGCTACCTGAAGAGTAAGTTCACCCTAGCAATGTTTCTCTGA
P90-1	PY02724	H2-Ld	SPLKITHVL	36.75	TVGTSPLKITHVLRSLG*	ACGGTAGGAACTAGCCCTCTGAAGATAACCCACGTGCTGAGGTCGTTAGGCTGA
P90-2	PY02725	H2-Kd	RYMNYSDAV	26.55	VWLGRYMNYSDAVPGNI	GTGTGGCTAGGTAGATACATGAACTATAGTGACGCCGTGCCAGGTAACCATTGA
P90-3	PY02788	H2-Kd	SYNNTNSRL	10.49	REPHSYNNTNSRLSSTL*	CGTGAACCTCATAGCTATAATAACACTAATAGTAGACTGAGCTCCACCCTGTGA
P90-4	PY02788	H2-Kd	NYINDGNTI	18.07	KKLENYINDGNTILYFN*	AAGAAATTAGAAAACTACATAAATGACGGTAACACCATCTTATATTTTAACTGA
P90-5	PY02788	H2-Kd	FYNNQNNNI	22.15	LSALFYNNQNNNIGAIV*	CTGTCAGCACTGTTCTATAATAACCAGAATAATAACATAGGCGCCATAGTCTGA
P90-6	PY02788	H2-Kd	LYAQKINTI	26.95	KQLPLYAQKINTIRVSC*	AAGCAGCTGCCCCTGTACGCCCAGAAGATAAACACCATCCGTGTGTCATGTTGA
P90-7	PY02799	H2-Kd	KYQKNPATI	4.47	RFAEKYQKNPATIPIGE*	AGGTTTGCTGAGAAGTACCAGAAGAACCCTGCCACCATCCCTATAGGTGAGTGA
P90-8	PY02799	H2-Kd	KWLSDNSTI	15.58	KNSEKWLSDNSTIAQGT*	AAAAATAGTGAGAAGTGGCTGAGTGATAATAGCACCATAGCTCAGGGTACATGA
P90-9	PY02799	H2-Kd	KYWDTYLKL	31.63	RFEIKYWDTYLKLALVK*	CGCTTTGAAATAAAGTACTGGGACACCTACCTGAAGCTAGCGCTAGTGAAGTGA
P90-10	PY02799	H2-Kd	IYYPTTWEM	38.96	MSFQIYYPTTWEMSGCE*	ATGAGCTTTCAGATCTACTACCCTACCACCTGGGAGATGAGTGGATGTGAATGA
P91-1	PY02799	H2-Kd	MYSECCDYL	41.49	DSTSMYSECCDYLPSLF*	GATAGTACTAGTATGTATAGTGAGTGCTGTGACTACCTGCCTAGCCTGTTTTGA
P91-2	PY02799	H2-Ld	LPIFSCFVF	39.68	QHELLPIFSCFVFHEVL*	CAGCATGAACTGCTGCCTATCTTTAGCTGCTTCGTGTTCCATGAGGTCCTATGA
P91-3	PY02880	H2-Kd	KYYSTNPEI	5.35	RKELKYYSTNPEITGAS*	AGAAAGGAATTGAAGTACTATAGCACTAACCCTGAGATAACAGGCGCTTCCTGA
P91-4	PY02880	H2-Ld	CPSKNFFGM	44.31	SKQICPSKNFFGMADYW*	AGTAAACAGATTTGCCCTAGTAAGAACTTCTTCGGCATGGCTGATTATTGGTGA
P91-5	PY02891	H2-Kd	QYNWFISTL	14.17	AVGKQYNWFISTLAGQL*	GCTGTAGGTAAACAGTATAACTGGTTCATAAGCACCCTAGCTGGACAGCTCTGA

P91-6	PY02891	H2-Kd	YYGKNYPFL	18.26	SGNMYYGKNYPFLISDA*	TCCGGTAATATGTACTACGGTAAGAACTACCCTTTCCTGATAAGTGACGCCTGA
P91-7	PY02891	H2-Kd	SYTSDYFQL	29.4	GSNPSYTSDYFQLSSET*	GGTAGTAACCCTAGCTACACTAGTGACTACTTCCAGCTGTCTAGTGAAACCTGA
P91-8	PY02891	H2-Kd	MYYTQKIYI	38.75	TSSPMYYTQKIYIIQIK*	ACTAGCTCCCCAATGTACTACACCCAGAAGATCTACATAATACAGATAAAGTGA
P91-9	PY02891	H2-Ld	YPFLCRTVF	25.58	VGIFYPFLCRTVFRRDL*	GTAGGAATTTTCTACCCTTTCCTGTGTAGAACCGTGTTTAGGCGTGACCTGTGA
P91-10	PY02892	H2-Kd	KYMAVVIII	9.45	LKKDKYMAVVIIILLIL*	CTGAAGAAAGATAAGTACATGGCCGTAGTGATAATAATCCTCTTGATACTATGA
P92-1	PY02896	H2-Kd	KYGTRSNSL	41.17	KKTLKYGTRSNSLCSDG*	AAGAAGACACTGAAGTACGGCACTAGAAGTAATAGCCTGTGTAGTGATGGATGA
P92-2	PY02896	H2-Ld	YPGFNSYPM	17.09	PMSMYPGFNSYPMTVGS	CCAATGTCGATGTACCCTGGCTTTAATAGCTACCCTATGACCGTAGGGTCCTGA
P92-3	PY02896	H2-Ld	FPYVNNDIL	35.06	PMQTFPYVNNDILSCMD*	CCTATGCAGACTTTCCCTTACGTGAATAATGACATCCTGTCTTGCATGGACTGA
P92-4	PY02899	H2-Kd	YFFRNICKI	24.69	HQDIYFFRNICKISSEE*	CACCAGGATATTTACTTCTTTAGAAACATCTGTAAGATAAGCTCTGAAGAGTGA
P92-5	PY02920	H2-Kd	FYVDTINLL	17.01	QQLSFYVDTINLLTSGN*	CAACAGCTGAGTTTCTACGTAGACACCATAAACCTGCTGACGTCAGGTAACTGA
P92-6	PY02920	H2-Kd	SYIILYAVI	19.62	YDIKSYIILYAVIRSFD*	TATGATATAAAGAGCTACATAATCCTGTACGCCGTGATAAGGTCCTTTGATTGA
P92-7	PY02920	H2-Kd	GYIFNEPGI	20.21	FRALGYIFNEPGIRVQI*	TTTAGAGCTCTAGGCTACATCTTTAATGAGCCTGGCATAAGAGTTCAAATCTGA
P92-8	PY02920	H2-Kd	FFLNSYSII	26.65	RECCFFLNSYSIIILEG*	CGTGAGTGCTGCTTCTTCCTGAATAGCTATAGCATAATAATCCTAGAGGGCTGA
P92-9	PY02920	H2-Kd	NYSENVYNI	35.11	EDYLNYSENVYNILGIA*	GAGGACTACTTAAACTATAGTGAGAACGTGTATAACATCCTAGGAATAGCATGA
P92-10	PY02920	H2-Kd	SYSKNEYEL	41.12	AKFQSYSKNEYELGVGD*	GCTAAATTCCAGAGCTATAGTAAGAATGAGTATGAGCTAGGCGTAGGTGACTGA
P93-1	PY02920	H2-Kd	YYNYKNEQI	47.31	TDRDYYNYKNEQISRLN*	ACTGACCGTGACTACTATAACTATAAGAATGAGCAGATCTCACGACTGAACTGA
P93-2	PY02920	H2-Ld	FPQKNKPCF	40.28	SEEAFPQKNKPCFSVSA*	TCTGAGGAAGCCTTCCCTCAGAAGAATAAGCCTTGCTTCTCTGTGAGCGCCTGA
P93-3	PY02920	H2-Ld	YPHLLKFYL	48.96	TFSRYPHLLKFYLHLQT*	ACTTTTTCACGGTACCCTCACCTGCTGAAGTTCTACCTGCAACCTCCAGACTTGA
P93-4	PY02926	H2-Kd	YYSANNANL	19.85	PGCVYYSANNANLGSWG	CCGGGGTGTGTGTACTATAGCGCTAATAACGCTAACCTAGGCTCATGGGGGTGA
P93-5	PY02926	H2-Kd	KYKNHLCLI	25.91	EDLCKYKNHLCLIEAWQ*	GAAGATCTGTGTAAGTATAAGAACCACCTGTGCCTGATAGAAGCATGGCAGTGA
P93-6	PY02930	H2-Kd	YYVSHCDKL	36.04	PQNLYYVSHCDKLPGEM*	CCCCAAAACTTGACTACGTGAGCCACTGTGATAAGCTGCCTGGTGAGATGTGA
P93-7	PY02935	H2-Kd	KYLKLHEYI	9.89	SKHVKYLKLHEYIPTIR*	TCTAAGCATGTGAAGTACCTGAAGCTGCATGAGTACATCCCTACAATAAGATGA
P93-8	PY02935	H2-Kd	TYINYKTRL	10.52	KMGSTYINYKTRLILHT*	AAGATGGGTAGTACCTACATAAACTATAAGACTAGACTGATTCTGCACACCTGA
P93-9	PY02935	H2-Kd	RYLKERNEI	19.3	QSPSRYLKERNEIFPTP*	CAGAGCCCTAGTAGATACCTGAAGGAGAGAAATGAGATCTTCCCTACTCCCTGA
P93-10	PY02936	H2-Kd	KYISACRLI	9.07	FSEAKYISACRLIVNPS*	TTCTCTGAAGCTAAGTACATAAGCGCCTGTAGACTGATAGTGAATCCTAGCTGA
P94-1	PY02936	H2-Kd	GYIMDNAEI	39.61	SSGAGYIMDNAEIEVRV*	AGTAGTGGAGCCGGCTACATAATGGATAACGCTGAGATAGAGGTGAGGGTGTGA
P94-2	PY02945	H2-Kd	KYIKSIFPL	3.47	YRPEKYIKSIFPLEPCP*	TATAGGCCTGAGAAGTACATAAAGAGCATCTTCCCTCTAGAACCCTGCCCCTGA
P94-3	PY02945	H2-Kd	SYNETRNTI	3.89	QCLVSYNETRNTISQLG*	CAGTGTTTAGTGAGCTATAATGAGACTAGAAACACCATCTCACAGCTAGGATGA
P94-4	PY02945	H2-Kd	IYIPSFFYI	5.48	VECIIYIPSFFYICTPL*	GTAGAGTGTATAATCTACATCCCTAGCTTCTTCTACATCTGTACTCCAGTCTGA
P94-5	PY02945	H2-Kd	KYYNKYFPI	6.08	ESSFKYYNKYFPIDDGG*	GAGAGTAGTTTTAAGTACTATAATAAGTACTTCCCTATAGATGATGGTGGCTGA
P94-6	PY02945	H2-Kd	FYIEYNSIL	6.93	SKKSFYIEYNSILLTIV*	TCTAAGAAGAGTTTCTACATAGAGTATAATAGCATCCTGCTAACCATAGTATGA
P94-7	PY02945	H2-Kd	YYYFSWINI	7.57	ATWRYYYFSWINIEPSP*	GCCACATGGCGATACTACTACTTTAGCTGGATAAACATAGAACCGTCTCCTTGA
P94-8	PY02945	H2-Kd	GYYSNPISI	8.1	FTCKGYYSNPISIISDR*	TTTACCTGTAAGGGCTACTATAGTAACCCTATAAGCATAATTTCTGATAGGTGA
P94-9	PY02945	H2-Kd	TYMCGRKYI	10.28	NGFITYMCGRKYILSND*	AACGGATTCATAACCTACATGTGCGGTAGAAAGTACATCCTGAGTAATGACTGA
P94-10	PY02945	H2-Kd	SYYSTDKSI	10.48	TMYPSYYSTDKSIGHYG*	ACTATGTATCCTAGCTACTATAGCACTGATAAGAGCATAGGCCACTATGGGTGA
P95-1	PY02945	H2-Kd	LYIKLFNYI	12.27	GVQQLYIKLFNYIKACQ*	GGTGTACAGCAACTGTACATAAAGCTGTTTAACTACATAAAGGCCTGCCAGTGA
P95-2	PY02945	H2-Kd	VYYGCQSFL	12.99	ENIEVYYGCQSFLLGYN*	GAGAATATAGAAGTGTACTACGGCTGCCAGAGCTTCCTGCTAGGCTATAACTGA
P95-3	PY02945	H2-Kd	NYLENKSTL	15.38	GKTLNYLENKSTLAFAF*	GGTAAGACACCTGAACTACCTAGAGAATAAGAGCACCCTAGCCTTTGCCTTCTGA
P95-4	PY02945	H2-Kd	SYYRRHNSM	16.43	HDAASYYRRHNSMYLAV*	CATGATGCGGCTAGCTACTATAGAAGACATAATAGCATGTATCTAGCAGTGTGA
P95-5	PY02945	H2-Kd	YFNANFSSL	17.71	GMSIYFNANFSSLWSSL*	GGGATGAGTATATACTTTAACGCTAACTTTAGTAGCCTGTGGAGTTCCCTGTGA
P95-6	PY02945	H2-Kd	MYTFIFSEL	22.44	DILHMYTFIFSELFKTD*	GATATACTCCACATGTACACCTTCATCTTTAGTGAGCTGTTTAAGACTGACTGA
P95-7	PY02945	H2-Kd	LYALMLNEI	24.3	EGNALYALMLNEIKLTK*	GAGGGTAACGCCCTGTACGCCCTGATGCTGAATGAGATAAAGTTGACTAAGTGA
P95-8	PY02945	H2-Kd	HYNTNDNII	27.88	HLVFHYNTNDNIIIQTG*	CATTTAGTGTTTCACTATAACACTAATGATAACATAATAATCCAGACGGGGTGA
P95-9	PY02945	H2-Kd	IYHGNTKSI	30.74	ESIPIYHGNTKSIAQVY*	GAATCTATCCCCATCTACCACGGTAACACTAAGAGCATAGCACAGGTTTACTGA
P95-10	PY02945	H2-Kd	YYRRHNSMI	30.92	GLLDYYRRHNSMICFIL*	GGACTTCTAGACTACTATAGAAGACATAATAGCATGATCTGCTTTATTCTATGA
P96-1	PY02945	H2-Kd	NFINSHNFI	35.36	ALRQNFINSHNFILERL*	GCTTTGAGGCAGAACTTCATAAATAGCCATAACTTCATCCTAGAACGATTGTGA
P96-2	PY02945	H2-Kd	TYIFGDFIL	35.43	FESWTYIFGDFILHWEF*	TTTGAATCTTGGACCTACATCTTCGGTGACTTCATCCTGCATTGGGAGTTCTGA
P96-3	PY02945	H2-Kd	KYSNLNNDI	36.22	VRFTKYSNLNNDIECTA*	GTGAGGTTCACTAAGTATAGTAACCTGAATAATGACATAGAGTGTACCGCGTGA
P96-4	PY02945	H2-Kd	KWHHRESTI	37.14	CDSLKWHHRESTILDAV*	TGTGATAGCCTGAAGTGGCACCATAGAGAGAGCACCATCCTAGATGCGGTGTGA
P96-5	PY02945	H2-Kd	LYFENYNDL	37.92	ILPVLYFENYNDLRCYG*	ATCCTTCCAGTGCTGTACTTTGAGAACTATAATGACCTGCGCTGTTACGGCTGA
P96-6	PY02945	H2-Kd	SQNKNFPQI	38.42	TQSESQNKNFPQIDIEN*	ACCCAGAGTGAGAGCCAGAATAAGAACTTCCCTCAGATAGATATAGAGAATTGA
P96-7	PY02945	H2-Kd	IYNKENNYI	39.84	EDAMIYNKENNYINGLD*	GAGGACGCTATGATCTATAATAAGGAGAATAACTACATAAACGGTCTAGACTGA
P96-8	PY02945	H2-Kd	YYKNSRNEL	43.89	YPHMYYKNSRNELFDEK*	TACCCACACATGTACTATAAGAATAGTAGAAATGAGCTGTTTGATGAGAAGTGA
P96-9	PY02945	H2-Kd	NYLNRHTVL	44.1	HELSNYLNRHTVLQSLP*	CATGAACTCTCTAACTACCTGAATAGACACCGTGCTGCAGTCACTCCCCTGA
P96-10	PY02945	H2-Kd	SEMNHICKI	49.75	NDERSEMNHICKIILVS*	AATGATGAAAGGAGTGAGATGAACCACATCTGTAAGATAATTTTAGTATCTTGA
P97-1	PY02945	H2-Kd	HAVPMYTFI	49.77	GTGTHAVPMYTFISEGR*	GGCACAGGCACACACGCCGTGCCTATGTACACCTTCATCTCTGAAGGTAGATGA
P97-2	PY02945	H2-Ld	LPISSFYNF	14.24	VFMVLPISSFYNFNMGL*	GTCTTCATGGTTCTGCCTATAAGTAGCTTCTATAACTTTAACATGGGTCTGTGA
P97-3	PY03020	H2-Kd	IYIKRASHL	10.67	MTRTIYIKRASHLDIAG*	ATGACCCGGACAATCTACATAAAGAGAGCTAGCCACCTAGACATAGCTGGCTGA
P97-4	PY03020	H2-Kd	FYVAISVFI	15.77	SDEGFYVAISVFIVAVK*	AGTGATGAAGGATTCTACGTAGCCATAAGCGTGTTCATAGTAGCAGTGAAGTGA
P97-5	PY03020	H2-Kd	FYNQIKDKI	23.93	HALSFYNQIKDKIVAIT*	CATGCCCTCTCATTCTATAACCAGATAAAGGATAAGATAGTAGCCATAACTTGA
P97-6	PY03020	H2-Kd	FYLKQNSKI	28.98	SESDFYLKQNSKIISGF*	TCTGAGAGTGACTTCTACCTGAAGCAGAATAGTAAGATAATCTCCGGGTTCTGA
P97-7	PY03020	H2-Kd	KYYQKDDLI	39.2	GDPLKYYQKDDLIHNSM*	GGTGATCCACTGAAGTACTACCAGAAGGATGACCTGATCCATAATTCTATGTGA
P97-8	PY03025	H2-Ld	SPYENGVYF	14.19	ASKQSPYENGVYFTREV*	GCTAGTAAACAGAGCCCTTATGAGAACGGCGTGTACTTCACTAGAGAAGTGTGA
P97-9	PY03038	H2-Kd	IYNFNTYEI	8.22	LDILIYNFNTYEILSGS*	CTAGATATCCTAATCTATAACTTTAACACCTATGAGATCCTGTCCGGCTCCTGA
P97-10	PY03049	H2-Kd	FYFKWPYFI	5.24	AEQHFYFKWPYFIVLVT*	GCTGAACAGCATTTCTACTTTAAGTGGCCTTACTTCATAGTTCTAGTGACATGA
P98-1	PY03049	H2-Kd	IYIYYESCI	21.85	PEHFIYIYYESCIVKLR*	CCTGAACATTTCATCTACATCTACTATGAGAGCTGCATAGTGAAGCTGAGATGA
P98-2	PY03105	H2-Kd	FYQCVKLAL	24.89	PITSFYQCVKLALKENL*	CCTATAACTAGCTTCTACCAGTGCGTGAAGCTAGCCCTGAAAGAGAACCTGTGA
P98-3	PY03114	H2-Kd	FYNYTFSII	4.64	LEIHFYNYTFSIITDTA*	CTAGAAATTCACTTCTATAACTACACCTTTAGCATAATAACTGACACTGCCTGA
P98-4	PY03114	H2-Kd	IYIHDYFFI	18.76	VTPMIYIHDYFFIERRL*	GTAACACCCATGATCTACATCCATGACTACTTCTTCATAGAAAGGAGGTTGTGA
P98-5	PY03114	H2-Kd	IYCTILSII	35.26	TFSWIYCTILSIIYLML*	ACTTTCTCATGGATCTACTGCACCATCCTGAGCATAATCTACCTAATGCTTTGA
P98-6	PY03114	H2-Kd	SYNSFPLFL	40.66	AHILSYNSFPLFLNMTK*	GCCCACATCCTGAGCTATAATAGCTTCCCTCTGTTCCTGAACATGACTAAGTGA
P98-7	PY03114	H2-Kd	AFYNYTFSI	45.07	FEFSAFYNYTFSISNFR*	TTTGAATTCTCGGCCTTCTATAACTACACCTTTAGCATCTCTAACTTTCGCTGA
P98-8	PY03131	H2-Kd	IYMSSTHTL	2.86	AETQIYMSSTHTLKCLN*	GCTGAGACACAAATCTACATGAGTAGCACCCACACCCTGAAGTGTCTGAACTGA
P98-9	PY03131	H2-Kd	RYYKSKFHL	9.37	QIDRRYYKSKFHLNDLI*	CAGATAGATAGGAGATACTATAAGAGTAAGTTCCACCTGAATGATCTGATCTGA
P98-10	PY03131	H2-Kd	MYLDMNGII	15.05	HIYDMYLDMNGIIKDHK*	CATATCTATGATATGTACCTAGACATGAACGGCATAATAAAGGATCATAAGTGA
P99-1	PY03131	H2-Kd	NYNNNYPPL	20.38	PAISNYNNNYPPLLALS*	CCCGCTATAAGTAACTATAATAATAACTACCCTCCTCTGCTAGCTCTGAGTTGA
P99-2	PY03131	H2-Kd	YYAPLSSDL	30.02	TSNEYYAPLSSDLQEPL*	ACTAGTAATGAGTACTACGCCCCTCTGAGTAGTGACCTGCAAGAGCCCCTTTGA
P99-3	PY03131	H2-Kd	KYIEGLAWV	43.11	MYPSKYIEGLAWVAQVE*	ATGTACCCTAGTAAGTACATAGAGGGCCTAGCCTGGGTAGCACAGGTAGAGTGA
P99-4	PY03131	H2-Kd	LYQKVLPVL	48.67	YSETLYQKVLPVLNFYA*	TATAGTGAAACCCTGTACCAGAAGGTGCTGCCTGTGCTGAACTTCTACGCTTGA
P99-5	PY03140	H2-Kd	FYKNNKLEI	44.36	SRLQFYKNNKLEIYKLE*	AGTAGACTACAATTCTATAAGAATAATAAGCTAGAGATCTATAAGCTAGAGTGA
P99-6	PY03140	H2-Ld	VPYLHDFPF	42.99	SRKEVPYLHDFPFRQLG*	TCCCGTAAGGAGGTGCCTTACCTGCATGACTTCCCTTTCCGCCAGCTAGGTTGA
P99-7	PY03153	H2-Ld	IPSPNSYFM	14.39	VWNHIPSPNSYFMNVSL*	GTGTGGAATCACATCCCTAGCCCTAATAGCTACTTCATGAATGTGAGCCTCTGA
P99-8	PY03155	H2-Kd	YYLNVKSEI	3.32	FSIKYYLNVKSEIQQRK*	TTTAGCATAAAGTACTACCTGAACGTGAAGAGTGAGATCCAGCAGAGAAAATGA
P99-9	PY03155	H2-Kd	KYFAKENSI	4.13	FVKVKYFAKENSIAIQM*	TTCGTGAAAGTGAAGTACTTCGCTAAGGAGAATAGCATAGCGATTCAGATGTGA
P99-10	PY03155	H2-Kd	KYYRNNLFI	5.79	VLPFKYYRNNLFICGPD*	GTACTGCCTTTTAAGTACTATAGAAATAACCTGTTCATCTGCGGACCTGACTGA
P100-1	PY03155	H2-Kd	KYIYAFCNL	7.02	ESPKKYIYAFCNLGGEK*	GAGAGCCCTAAGAAGTACATCTACGCCTTCTGTAACCTAGGGGGTGAAAAGTGA
P100-2	PY03155	H2-Kd	FYLRLNSFL	7.63	SHHIFYLRLNSFLGCPY*	TCTCACCACATCTTCTACCTGAGACTGAATAGCTTCCTAGGATGCCCGTATTGA
P100-3	PY03155	H2-Kd	LYIENYNIL	10.41	SILELYIENYNILNSLP*	TCTATCCTAGAGCTGTACATAGAGAACTATAACATCCTGAACTCTCTGCCTTGA
P100-4	PY03155	H2-Kd	NYCNSLYSI	12.45	DLDTNYCNSLYSIWMHE*	GACCTAGATACTAACTACTGTAATAGCCTGTATAGCATCTGGATGCATGAGTGA
P100-5	PY03155	H2-Kd	VYNNGVYNI	13.27	VKGVVYNNGVYNICGLE*	GTGAAAGGTGTAGTGTATAATAACGGCGTGTATAACATCTGTGGTCTAGAATGA
P100-6	PY03155	H2-Kd	FYNHNLDGI	16.37	PGGLFYNHNLDGICLPV*	CCTGGCGGCCTCTTCTATAACCATAACCTAGACGGCATCTGTCTTCCCGTGTGA
P100-7	PY03155	H2-Kd	YYRNNLFIL	16.73	WWVEYYRNNLFILAVCY*	TGGTGGGTAGAATACTATAGAAATAACCTGTTCATCCTAGCGGTGTGCTACTGA
P100-8	PY03155	H2-Kd	YYVCFCDYI	16.89	LSLRYYVCFCDYIVGKS*	CTGAGTCTGAGATACTACGTGTGCTTCTGTGACTACATAGTAGGTAAATCCTGA
P100-9	PY03155	H2-Kd	KYIPDENNL	18	LLLPKYIPDENNLAPLL*	CTGCTACTGCCTAAGTACATCCCTGATGAGAATAACCTAGCGCCACTGCTCTGA
P100-10	PY03155	H2-Kd	SFQRNMTNI	20.21	VDPPSFQRNMTNIWNPP*	GTAGATCCCCCTAGCTTCCAGAGAAACATGACTAACATCTGGAACCCACCCTGA
P101-1	PY03155	H2-Kd	RYGCSYNFL	23.49	PESLRYGCSYNFLDYLA*	CCTGAATCCCTGAGATACGGCTGTAGCTATAACTTCCTAGATTACCTAGCTTGA
P101-2	PY03155	H2-Kd	YYFKNVTFF	28.22	RATLYYFKNVTFFALMT*	AGAGCAACACTGTACTACTTTAAGAACGTGACCTTCTTCGCACTAATGACTTGA
P101-3	PY03155	H2-Kd	KYDYSKQSI	29.58	DRKMKYDYSKQSIPLCM*	GACCGTAAGATGAAGTATGACTATAGTAAGCAGAGCATCCCCCTTTGCATGTGA
P101-4	PY03155	H2-Kd	NYIPIKNAL	30.76	PHQFNYIPIKNALEDFC*	CCCCATCAGTTTAACTACATCCCTATAAAGAACGCCCTAGAGGACTTTTGTTGA
P101-5	PY03155	H2-Kd	SLYRTYSHI	37.38	KVKFSLYRTYSHILVDV*	AAAGTGAAGTTTAGCCTGTATAGAACCTATAGCCACATCCTAGTAGATGTCTGA
P101-6	PY03155	H2-Kd	NYNFVLDEI	38.49	TVLANYNFVLDEIQLPA*	ACGGTGTTAGCTAACTATAACTTCGTGCTAGATGAGATCCAGCTCCCCGCCTGA

P101-7	PY03155	H2-Kd	KMIDNINSL	42.25	VSLEKMIDNINSLQHLT*	GTGAGTCTAGAGAAGATGATAGATAACATAAATAGCCTGCAGCACCTAACATGA
P101-8	PY03155	H2-Kd	LYGLYLSSI	46.42	ATSGLYGLYLSSIVHVE*	GCCACATCCGGTCTGTACGGCCTGTACCTGAGTAGCATAGTCCCTATGAGAATGA
P101-9	PY03155	H2-Ld	IPIKNALIF	23.17	AKWQIPIKNALIFSLGR*	GCTAAATGGCAGATCCCTATAAAGAACGCCCTGATCTTCTCTCTAGGTAGGTGA
P101-10	PY03155	H2-Ld	LPINNNYNF	28.89	DGPSLPINNNYNFRNEG*	GACGGACCTTCACTGCCTATAAATAATAACTTCCGTAATGAAGGATGA
P102-1	**PY03168**	**H2-Kd**	**SYVPSAEQI**	**7.47**	**EIDFSYVPSAEQIGLSE***	**GAAATAGACTTTAGCTACGTGCCTAGCGCTGAGCAGATAGGCCTGAGTGAGTGA**
P102-2	PY03187	H2-Kd	FYNNDLSNL	10.55	SATFFYNNDLSNLAIWD*	TCTGCGACTTTCTTCTATAATAATGACCTGAGTAACCTAGCCATCTGGGACTGA
P102-3	PY03187	H2-Kd	VYMREESKI	23.58	LEQRVYMREESKIPTAP*	CTAGAGCAAAGGGTGTACATGAGAGAGGAGAGTAAGATCCCTACTGCCCCTTGA
P102-4	PY03187	H2-Kd	TYLNSKLLI	25.6	AVKETYLNSKLLIKLNR*	GCCGTGAAGGAGACCTACCTGAATAGTAAGCTGCTGATAAAATTAAATAGGTGA
P102-5	PY03187	H2-Kd	SQFPFIPVI	26.13	KSFNSQFPFIPVIKFYA*	AAATCATTTAATAGCCAGTTCCCTTTCATCCCTGTGATAAAGTTTTATGCCTGA
P102-6	PY03187	H2-Kd	KQLTSHAQI	37.1	VKAAKQLTSHAQILKRG*	GTGAAGGCTGCTAAGCAGCTGACTAGCCACGCCCAGATCTTGAAAAGAGGATGA
P102-7	PY03187	H2-Ld	SPNPMIDIF	31.18	WKNASPNPMIDIFHVEQ*	TGGAAAAATGCTAGCCCTAACCCTATGATAGACATCTTCCACGTAGAGCAGTGA
P102-8	PY03214	H2-Kd	SYKEGHTYI	7.72	KESDSYKEGHTYIPCGS*	AAAGAAAGTGATAGCTATAAGGAGGGCCACACCTACATCCCATGCGGGTCCTGA
P102-9	PY03214	H2-Kd	AYIKWARFI	25.26	SSSTAYIKWARFIVLQD*	TCTAGTAGTACCGCCTACATAAAGTGGGCTAGATTCATAGTGCTCCAAGACTGA
P102-10	PY03214	H2-Kd	YYYSEYFSV	29.26	DAGNYYYSEYFSVVESN*	GACGCCGGTAACTACTACTATAGTGAGTACTTTAGCGTAGTAGAGTCTAATTGA
P103-1	PY03215	H2-Kd	AYINNVTNL	6.04	DLTIAYINNVTNLHLFR*	GACCTAACAATAGCCTACATAAATAACGTGACTAACCTGCACCTGTTTCGGTGA
P103-2	PY03223	H2-Kd	HYFSILFHI	6.48	VGTRHYFSILFHIQGGS*	GTAGGTACTAGACACTACTTTAGCATCCTGTTCCACATCCAGGGGGGGTCGTGA
P103-3	PY03223	H2-Kd	FYIGRSLEI	14.46	SVELFYIGRSLEIPARN*	TCCGTAGAACTGTTCTACATAGGTAGAAGCCTAGAGATCCCCGCACGTAACTGA
P103-4	PY03223	H2-Ld	LPLVSGNTF	38.46	TCVHLPLVSGNTFLTDN*	ACTTGTGTCCACCTGCCTCTAGTGAGCGGTAACACCTTCCTAACTGATAATTGA
P103-5	PY03237	H2-Kd	YYSPTVKSI	8.95	LAKCYYSPTVKSIRQDC*	CTAGCTAAATGCTACTATAGCCCTACCGTGAAGAGCATAAGGCAGGACTGCTGA
P103-6	PY03237	H2-Kd	QYYYSLFFI	13.02	TIEGQYYYSLFFIPGPY*	ACCATAGAGGGGCAGTACTACTATAGCCTGTTCTTCATCCCTGGTCCCTATTGA
P103-7	PY03237	H2-Kd	KFMWNYQMI	14.68	QFMAKFMWNYQMIQCNL	CAGTTTATGGCTAAGTTCATGTGGAACTACCAGATGATCCAGTGTAATTTGTGA
P103-8	PY03237	H2-Kd	YYYSLFFIL	15.97	CHTRYYYSLFFILAMKS*	TGTCACACTAGATACTACTATAGCCTGTTCTTCATCCTAGCTATGAAGAGCTGA
P103-9	PY03237	H2-Kd	NYGNNIYYI	24.92	SSILNYGNNIYYIVGMG*	AGTTCAATTCTGAACTACGGTAATAACATCTACTACATAGTAGGAATGGGATGA
P103-10	PY03237	H2-Kd	YFFPNNYGI	26.63	PQQSYFFPNNYGITLRF*	CCCCAGCAGTCATACTTCTTCCCTAATAACTACGGCATAACCTTGCGCTTTTGA
P104-1	PY03237	H2-Kd	NYIEYDFHI	38.39	QDDVNYIEYDFHIDRSE*	CAGGATGACGTGAACTACATAGAGTATGACTTCCACATAGATCGTTCTGAATGA
P104-2	PY03237	H2-Kd	KEYFYDSYI	44.21	TCVSKEYFYDSYIDTPI*	ACGTGTGTGTCTAAGGAGTACTTCTATGATAGCTACATAGATACCCCTATTTGA
P104-3	PY03243	H2-Kd	FYMSDILPV	41.19	ISLGFYMSDILPVQSPH*	ATATCGTTAGGATTCTACATGAGTGACATCCTGCCTGTGCAGTCACCACATTGA
P104-4	PY03255	H2-Kd	RYYEFVNSI	5.09	VELRRYYEFVNSIKLTA*	GTAGAGCTCCGTAGATACTATGAGTTCGTGAATAGCATAAAATTAACCGCCTGA
P104-5	PY03255	H2-Kd	KYLHLYSRL	9.15	FIQTKYLHLYSRLSSNT*	TTCATCCAGACTAAGTACCTGCACCTGTATAGTAGACTGAGCTCTAATACGTGA
P104-6	PY03255	H2-Kd	LYNSINNPI	12.99	GHIPLYNSINNPIMEFC*	GGCCACATTCCGCTGTATAATAGCATAAATAACCCTATAATGGAGTTCTGCTGA
P104-7	PY03255	H2-Kd	YYEFVNSII	13.83	PIVGYYEFVNSIIPMHK*	CCAATAGTAGGTTACTATGAGTTCGTGAATAGCATAATCCCTATGCATAAGTGA
P104-8	PY03255	H2-Kd	FQYNPYTYI	20.88	ISKGFQYNPYTYIPISG*	ATTTCTAAGGGTTTCCAGTATAACCCTTACACCTACATCCCTATAAGCGGGTGA
P104-9	PY03255	H2-Kd	NYNENFDSL	29.81	SHSFNYNENFDSLDLPY*	AGTCACTCCTTTAACTATAATGAGAACTTTGATAGCCTAGACCTCCCGTACTGA
P104-10	PY03255	H2-Kd	LYCNDIYTI	37.11	KDLLLYCNDIYTIRNKC*	AAGGATCTTCTGCTGTACTGTAATGACATCTACACCATCCGTAATAAATGCTGA
P105-1	PY03255	H2-Kd	YQLKSLNEI	45.86	AELYYQLKSLNEISELK*	GCTGAGCTGTACTACCAGCTGAAGAGCCTGAATGAGATCTCTGAACTGAAATGA
P105-2	PY03255	H2-Kd	KYKFDISKL	48.03	LLENKYKFDISKLFSKN*	CTCCTAGAGAATAAGTATAAGTTTGACATAAGTAAGCTGTTTTCTAAAAACTGA
P105-3	PY03267	H2-Kd	SQNNLFHSI	17.88	PNHDSQNNLFHSIEHAV*	CCTAACCATGATAGCCAGAATAACCTGTTCCATAGCATAGAACACGCAGTATGA
P105-4	PY03267	H2-Kd	KYIKNVQKV	20.17	DHEIKYIKNVQKVKGYV*	GACCATGAGATAAAGTACATAAAGAACGTGCAGAAGGTGAAAGGCTATGTGTGA
P105-5	PY03267	H2-Kd	QYIADQLNI	44.71	LVLPQYIADQLNITQCA*	CTAGTTCTCCCCCAGTACATAGCTGACCAGCTGAACATAACTCAATGTGCCTGA
P105-6	PY03269	H2-Kd	SYICCNSAL	5.79	CVSVSYICCNSALVLNY*	TGCGTCTCTGTGAGCTACATCTGCTGTAATAGCGCCCTAGTGCTGAACTACTGA
P105-7	PY03269	H2-Kd	HYQMMINNI	6.22	WSEFHYQMMINNISQLQ*	TGGAGTGAGTTCCACTACCAGATGATGATAAATAACATCTCTCAACTGCAGTGA
P105-8	PY03269	H2-Kd	NYLTMNSLI	8.4	RPLRNYLTMNSLIRLRH*	CGGCCACTGAGGAACTACCTGACCATGAATAGCCTGATAAGACTGAGACACTGA
P105-9	PY03269	H2-Kd	FYNYFTSTL	9.23	RPLKFYNYFTSTLGMTK*	AGACCCTTAAAGTTCTATAACTACTTCACTAGCACCCTAGGGATGACTAAGTGA
P105-10	PY03269	H2-Kd	NYFNSNMNI	9.98	FLQVNYFNSNMNIPLSH*	TTTCTGCAGGTGAACTACTTTAATAGTAACATGAACATCCCCCTGAGCCATTGA
P106-1	PY03269	H2-Kd	YYIKNNFDI	10.47	GFVHYYIKNNFDIKDVH*	GGCTTTGTGCACTACTACATAAAGAATAACTTTGACATAAAGGATGTCCACTGA
P106-2	PY03269	H2-Kd	IYMNDTMQL	15.31	SHKLIYMNDTMQLKKSL*	AGTCATAAGCTAATCTACATGAATGACACCATAGTCAGCTGAAAAAAAGTTTGTGA
P106-3	PY03269	H2-Kd	QYYANNKFI	19.31	KLDFQYYANNKFIGMSR*	AAACTAGACTTCCAGTACTACGCTAATAATAAGTTCATAGGAATGTCTAGATGA
P106-4	PY03269	H2-Kd	IQYNTTYSI	22.57	VRYTIQYNTTYSITQFV*	GTGCGCTATACCATCCAGTATAACACCACCTATAGCATAACCCAGTTTGTGTGA
P106-5	PY03269	H2-Kd	YYHTNNPDI	30.28	KVVAYYHTNNPDILDLG*	AAAGTAGTAGCATACTACCACACTAATAACCCTGACATCTTAGACTTAGGCTGA
P106-6	PY03269	H2-Kd	HYFFKLIYI	37.34	VGRFHYFFKLIYIVLHL*	GTAGGTAGGTTTCACTACTTCTTTAAGCTGATCTACATAGTGCTTCATCTGTGA
P106-7	PY03269	H2-Ld	IPIKNYYNL	11.38	IGAWIPIKNYYNLCKTA*	ATAGGTGCTTGGATCCCTATAAAGAACTACTATAACCTGTGTAAGACCGCTTGA
P106-8	PY03280	H2-Kd	KYNSSQTIV	36.18	DVFTKYNSSQTIVNIDW*	GACGTGTTTACTAAGTATAATAGTAGCCAGACCATAGTGAATATAGACTGGTGA
P106-9	PY03292	H2-Kd	IYNEVLTAL	11.87	GRILIYNEVLTALNLVV*	GGTAGGATTCTAATCTATAATGAGGTGCTGACCGCCCTGAACTTAGTAGTATGA
P106-10	PY03325	H2-Kd	SYFQNIKDI	18.61	VSLQSYFQNIKDISLDA*	GTGAGCCTGCAGAGCTACTTCCAGAACATAAAGGACATCTCACTAGATGCATGA
P107-1	PY03329	H2-Kd	KYNKTKDEL	41.05	SPTSKYNKTKDELPIGY*	TCACCTACCTCTAAGTATAATAAGACTAAGGATGAGCTGCCCATAGGCTATTGA
P107-2	PY03350	H2-Kd	TYYSYFSHI	3.28	QLKATYYSYFSHIHWEW*	CAGCTGAAGGCAACCTACTATAGCTACTTTAGCCACATCCACTGGGAGTGGTGA
P107-3	PY03350	H2-Kd	YYTNNNFPL	9.15	HVQDYYTNNNFPLAASP*	CATGTGCAAGACTACTACACTAATAATAACTTCCCTCTAGCCGCTAGCCCTTGA
P107-4	PY03350	H2-Ld	HPVQLFYIL	30.51	YPLLHPVQLFYILGGED*	TATCCTCTTCTTCACCCTGTGCAGCTGTTCTACATCCTAGGAGGTGAGGACTGA
P107-5	PY03350	H2-Ld	FPLSNLKYL	44.62	HAVLFPLSNLKYLILAK*	CATGCAGTCCTGTTCCCTCTGAGTAACCTGAAGTACCTGATACTAGCTAAATGA
P107-6	PY03353	H2-Kd	GYFPLLSII	4.5	RGYKGYFPLLSIIQCGY*	AGGGGCTATAAGGGCTACTTCCCTCTGCTGAGCATAATCCAGTGTGGGTATTGA
P107-7	PY03353	H2-Kd	IYIESKNII	8.2	SFGLIYIESKNIISAGG*	TCATTCGGGCTGATCTACATAGAGAGTAAGAACATAATCTCTGCAGGCGGCTGA
P107-8	PY03353	H2-Kd	KYLKNYFLI	8.42	LNVVKYLKNYFLIAGWQ*	CTGAACGTAGTGAAGTACCTGAAGAACTACTTCCTGATAGCCGGGTGGCAGTGA
P107-9	PY03353	H2-Kd	YYSIMNFFI	9.22	GVLFYYSIMNFFIEDTF*	GGCGTCCTCTTCTACTATAGCATAATGAACTTCTTCATAGAGGATACATTCTGA
P107-10	PY03353	H2-Kd	KYISPYIYI	11.97	QLLDKYISPYIYISFLY*	CAATTGCTAGATAAGTACATAAGCCCTTACATCTACATAAGTTTCCTGTACTGA
P108-1	PY03353	H2-Kd	KYSKGYFPL	12.72	AAYEKYSKGYFPLRQVK*	GCAGCCTATGAAAAGTATAGTAAGGGCTACTTCCCTCTGAGACAGGTGAAATGA
P108-2	PY03353	H2-Kd	LYFKITNII	19.42	TLAVLYFKITNIIDLRR*	ACCCTAGCCGTCCTGTACTTTAAGATAACTAACATAATAGACCTGAGGAGGTGA
P108-3	PY03353	H2-Kd	SYNYKNTEI	22.86	FKQASYNYKNTEIGLAG*	TTTAAGCAGGCTAGCTATAACTATAAGAACACTGAGATAGGCCTAGCCGGATGA
P108-4	PY03353	H2-Kd	SFFLSYSNI	26.31	CKTESFFLSYSNITLKI*	TGTAAAACTGAGAGCTTCTTCCTGAGCTATAGTAACATAACACTGAAAATTTGA
P108-5	PY03353	H2-Kd	TYIEYYYIL	26.64	ARQLTYIEYYYILDENS*	GCTCGCCAGCTAACCTACATAGAGTACTACTACATCCTAGATGAGAACTCTTGA
P108-6	PY03353	H2-Kd	KYILLFLNI	27.32	GLEGKYILLFLNIFFHC*	GGGCTAGAAGGTAAGTACATCCTGCTGTTCCTGAACATCTTCTTCCACTGTTGA
P108-7	PY03353	H2-Kd	KFIKKINSI	32.19	SQGVKFIKKINSISDAF*	AGTCAAGGCGTGAAGTTCATAAAGAAGATAAATAGCATCTCTGACGCCTTCTGA
P108-8	PY03353	H2-Kd	NYFKLPYGI	35.48	ASLTNYFKLPYGIRPSA*	GCTAGTCTAACTAACTACTTTAAGCTGCCTTACGGCATCCGCCCTAGCGCATGA
P108-9	PY03353	H2-Kd	TYQKLNEEI	47.59	RSKVTYQKLNEEITILT*	CGATCTAAAGTAACCTACCAGAAGCTGAATGAGGAGATAACAATCTTGACCTGA
P108-10	PY03353	H2-Ld	YPWLYKYIL	37.29	SGWVYPWLYKYILRIHG*	TCTGGATGGGTGTACCCTTGGCTGTATAAGTACATCCTGAGAATCCACGGGTGA
P109-1	PY03361	H2-Kd	FYYKICSHI	5.7	SLQTFYYKICSHIELLE*	AGCCTCCAAACCTTCTACTATAAGATCTGTAGCCACATAGAACTGCTAGAGTGA
P109-2	PY03361	H2-Kd	FYNNLKHKI	11.55	FWNIFYNNLKHKIAQPH*	TTCTGGAATATCTTCTATAATAACCTGAAGCATAAGATAGCCCAACCACACTGA
P109-3	PY03361	H2-Kd	AYFNNVIEL	15.26	IVSLAYFNNVIELSTRA*	ATAGTGTCTCTAGCCTACTTTAATAACGTGATAGAGCTGAGTACCCGCGCTTGA
P109-4	PY03361	H2-Kd	FYSKSTNAL	18.35	YWYDFYSKSTNALAPEL*	TACTGGTATGATTTCTATAGTAAGAGCACTAACGCCCTAGCACCTGAACTGTGA
P109-5	PY03361	H2-Kd	KMINDLNYI	20.03	LRFRKMINDLNYIPYGS*	CTGAGGTTTAGAAAGATGATAAATGACCTGAACTACATCCCATACGGTAGCTGA
P109-6	PY03361	H2-Kd	YYQDKINEL	48.77	TECGYYQDKINELRGLN*	ACTGAGTGTGGATACTACCAGGATAAGATAAATGAGCTGCGCGGCTTGAATTGA
P109-7	PY03361	H2-Ld	VPMDNSIFL	46.91	KPLTVPMDNSIFLEEYQ*	AAACCACTAACTGTGCCTATGGATAATAGCATCTTCCTAGAAGAGTACCAGTGA
P109-8	PY03377	H2-Kd	SYKPHYVTI	8.28	LVSISYKPHYVTIKGSP*	TTAGTGAGTATAAGCTATAAGCCTCACTACGTGACCATAAAAGGCTCCCCCTGA
P109-9	PY03377	H2-Kd	HYVTIIFSI	8.64	SPGGHYVTIIFSIQDNV*	AGTCCTGGAGGGCACTACGTGACCATAATCTTTAGCATCCAGGATAATGTTTGA
P109-10	PY03379	H2-Kd	SYLNSQNEI	4.01	VGRLSYLNSQNEIGPLL*	GTAGGTAGATTGAGCTACCTGAATAGCCAGAATGAGATAGGGCCTCTGCTGTGA
P110-1	PY03379	H2-Kd	YYFDKDSFI	4.86	EVVLYYFDKDSFIHLKG*	GAGGTAGTCCTGTACTACTTTGATAAGGATAGCTTCATCCACTTAAAGGGGTGA
P110-2	PY03379	H2-Kd	LYFINKSNI	7.33	PTTELYFINKSNIKEDW*	CCAACGACTGAACTGTACTTCATAAATAAGAGTAACATAAAGGAGGACTGGTGA
P110-3	PY03379	H2-Kd	KYISLYLYI	9.67	GAAAKYISLYLYIVADQ*	GGCGCCGCCGCTAAGTACATAAGCCTGTACCTGTACATAGTAGCTGACCAGTGA
P110-4	PY03379	H2-Kd	TYIKILRTI	11.7	MRALTYIKILRTIALVK*	ATGCGTGCCCTGACCTACATAAAGATCCTGAGAACCATAGCTCTAGTGAAATGA
P110-5	PY03379	H2-Kd	NYLDMLSLL	13.92	SFECNYLDMLSLLSAYI*	TCCTTTGAGTGTAACTACCTAGACATGCTGAGCCTGCTGTCCGCTTATATTTGA
P110-6	PY03379	H2-Kd	LYLYILSNI	18.77	PSCHLYLYILSNIKTQQ*	CCTTCTTGCCACCCTGTACCTGTACATCCTGAGTAACATAAAAACACAGCAGTGA
P110-7	PY03379	H2-Kd	YYYFKMNLI	19.78	PEMIYYYFKMNLIGKGE*	CCTGAAATGATTTACTACTACTTTAAGATGAACCTGATAGGTAAGGGTGAATGA
P110-8	PY03379	H2-Kd	KYLACSENL	37.87	AANEKYLACSENLLMGL*	GCCGCTAATGAAAAGTACCTAGCCTGTAGTGAGAACCTGTTAATGGGGCTGTGA
P110-9	PY03379	H2-Kd	KFFDIICEI	41.39	DNLCKFFDIICEILLKL*	GATAACCTGTGTAAGTTCTTTGACATAATCTGTGAGATCTTACTGAAGCTCTGA
P110-10	PY03379	H2-Kd	FLFPTYSKI	45.81	NHAKFLFPTYSKIAMLA*	AACCATGCTAAGTTCCTGTTCCCTACCTATAGTAAGATAGCTATGCTAGCTTGA
P111-1	PY03426	H2-Kd	NYIPSFNLL	8.9	HKEANYIPSFNLLKPQE*	CATAAGGAAGCTAACTACATCCCTAGCTTTAACCTGCTGAAGCCTCAGGAGTGA
P111-2	PY03426	H2-Kd	IYQGDIAYI	24.15	NIKLIYQGDIAYIIENS*	AACATAAAACTGATCTACCAGGGTGACATAGCCTACATAATAGAAAATAGCTGA
P111-3	PY03426	H2-Kd	FYHEVKRSL	30.91	RTHRFYHEVKRSLSAWE*	AGAACCCACCGCTTCTACCATGAGGTGAAGAGAAGCCTGTCCGCCTGGGAGTGA
P111-4	PY03461	H2-Kd	KYSASIFLI	11.92	MQLPKYSASIFLIPKDD*	ATGCAATTGCCTAAGTATAGCGCTAGCATCTTCCTGATCCCTAAGGATGATTGA
P111-5	PY03463	H2-Kd	KYLTYRIFL	28.2	GLTMKYLTYRIFLSRNV*	GGACTGACTATGAAGTACCTGACCTATAGAATCTTCCTGTCTAGGAACGTATGA
P111-6	PY03463	H2-Kd	SYIKIREKL	28.66	DVHASYIKIREKLLRAI*	GATGTACACGCTAGCTACATAAAGATAAGAGAGAAGCTGCTGAGAGCTATTTGA
P111-7	PY03463	H2-Kd	RYKNGFIKI	39.94	QLIERYKNGFIKIGLTL*	CAGCTGATAGAGAGATATAAGAACGGCTTCATAAAGATAGGTCTGACGCTTTGA

P111-8	PY03463	H2-Ld	YPNDNGRIF	44.41	AEADYPNDNGRIFFTEE*	GCTGAAGCTGACTACCCTAATGATAACGGTAGAATCTTCTTCACTGAGGAGTGA
P111-9	PY03464	H2-Kd	VYMIYLDSL	30.85	TMGKVYMIYLDSLLELH*	ACTATGGGTAAAGTGTACATGATCTACCTAGATAGCCTGCTAGAGCTGCACTGA
P111-10	PY03464	H2-Kd	CYSEMNVKI	34.2	QGIACYSEMNVKIKVQP*	CAGGGTATAGCCTGCTATAGTGAGATGAACGTGAAGATAAAGGTCCAGCCATGA
P112-1	PY03464	H2-Kd	KYVFIPINI	35.55	SRPTKYVFIPINIAAME*	TCTAGACCCACTAAGTACGTGTTCATCCCTATAAACATAGCCGCTATGGAATGA
P112-2	PY03473	H2-Kd	SYIRGTNGI	3	RATYSYIRGTNGIPSVM*	AGGGCAACATATAGCTACATAAGAGGCACTAACGGCATCCCATCTGTAATGTGA
P112-3	PY03473	H2-Ld	RPQMSSCFL	49.17	VSERRPQMSSCFLRRLV*	GTGAGTGAAAGGAGACCTCAGATGAGTAGCTGCTTCCTGCGTAGACTAGTCTGA
P112-4	PY03479	H2-Kd	SYYKIPHDI	10.47	LCTVSYYKIPHDIKYGF*	CTGTGTACAGTGAGCTACTATAAGATCCCTCATGACATAAAGTATGGGTTTTGA
P112-5	PY03479	H2-Kd	YFIENKIPI	47.89	HSPVYFIENKIPIESVK*	CATAGTCCAGTGTACTTCATAGAGAATAAGATCCCTATAGAGTCAGTGAAGTGA
P112-6	PY03480	H2-Kd	KYFLSPGFI	10.19	STLLKYFLSPGFIVVQP*	TCCACCCTCTTGAAGTACTTCCTGAGCCCTGGCTTCATAGTAGTCCAGCCATGA
P112-7	PY03480	H2-Kd	IYLYTMGTI	14.88	DGCPIYLYTMGTIEVAT*	GATGGGTGTCCTATCTACCTGTACACCATGGGCACCATAGAAGTAGCCACATGA
P112-8	PY03480	H2-Kd	KYDKGLYTI	15.25	PMPTKYDKGLYTICRNS*	CCCATGCCGACTAAGTATGATAAGGGCCTGTACACCATCTGTAGAAATTCTTGA
P112-9	PY03480	H2-Kd	SYLNFSTDI	18.59	TESSSYLNFSTDIEMSQ*	ACTGAGTCTAGTAGCTACCTGAACTTTAGCACTGACATAGAAATGTCTCAGTGA
P112-10	PY03480	H2-Kd	SYEEYLSFL	19.71	IPFVSYEEYLSFLLQNE*	ATCCCTTTCGTGAGCTATGAGGAGTACCTGAGCTTCCTGCTCCAGAATGAATGA
P113-1	PY03480	H2-Kd	VYIDNPNEL	25.1	EQRAVYIDNPNELKACE*	GAGCAGAGGGCTGTGTACATAGATAACCCTAATGAGCTGAAGGCTTGTGAATGA
P113-2	PY03480	H2-Kd	NYFPEIQFL	29.37	RPPMNYFPEIQFLSLPQ*	AGGCCCCCTATGAACTACTTCCCTGAGATCCAGTTCCTGAGCCTCCCACAGTGA
P113-3	PY03480	H2-Kd	KQLYYLVTI	30.42	LNTRKQLYYLVTISFKC*	CTGAATACACGTAAGCAGCTGTACTACCTAGTGACCATAAGCTTTAAGTGTTGA
P113-4	PY03480	H2-Kd	SQNNVINFI	37.07	SSKPSQNNVINFINGNT*	TCTAGTAAACCTAGCCAGAATAACGTGATAAACTTCATAAACGGTAATACTTGA
P113-5	PY03480	H2-Kd	HYSESTESL	38.5	PSQLHYSESTESLQSQV*	CCGTCTCAACTACACTATAGTGAGAGCACTGAGAGCCTGCAGTCGCAAGTATGA
P113-6	PY03491	H2-Kd	SYMFNEMSL	6.2	GHMFSYMFNEMSLDWVS	GGGCATATGTTTAGCTACATGTTTAATGAGATGAGCCTAGACTGGGTCTCGTGA
P113-7	PY03491	H2-Kd	NYINNFENI	6.41	NYPHNYINNFENIGEEK*	AATTACCCCCATAACTACATAAATAACTTTGAGAACATAGGTGAGGAGAAGTGA
P113-8	PY03491	H2-Kd	KYKSELSSI	9.3	IQASKYKSELSSILVSQ*	ATCCAAGCGTCTAAGTATAAGAGTGAGCTGAGTAGCATCCTAGTGAGCCAATGA
P113-9	PY03491	H2-Kd	KFLDNLSSI	9.66	VTPNKFLDNLSSIQSHG*	GTAACCCCTAATAAGTTCCTAGATAACCTGAGTAGCATCCAGAGCCACGGATGA
P113-10	PY03491	H2-Kd	SYRNDCNSI	12.79	PILRSYRNDCNSIWERA*	CCCATATTAAGGAGCTATAGAAATGACTGTAATAGCATCTGGGAGAGAGCCTGA
P114-1	PY03491	H2-Kd	VYLDGWPHI	16.77	RSAPVYLDGWPHIFVTF*	AGGTCTGCCCCGGTGTACCTAGACGGCTGGCCTCACATCTTTGTAACCTTCTGA
P114-2	PY03491	H2-Kd	MYLNQNkYI	24.61	DDSDMYLNQNKYISVDD*	GATGATAGTGACATGTACCTGAACCAGAATAAGTACATCTCTGTAGATGATTGA
P114-3	PY03491	H2-Kd	AYYNYMMKL	36.78	DCAYAYYNYMMKLGSLE*	GACTGCGCATATGCCTACTATAACTACATGATGAAGCTAGGATCACTAGAATGA
P114-4	PY03491	H2-Kd	IQHSHLSYI	39.19	LVQIIQHSHLSYITLMR*	CTAGTGCAGATAATCCAGCATAGCCACCTGAGCTACATAACACTAATGCGCTGA
P114-5	PY03493	H2-Kd	KYVNSIIYL	11.23	PLSMKYVNSIIYLGLEQ*	CCTCTGAGTATGAAGTACGTGAATAGCATAATCTACCTAGGGTTAGAGCAGTGA
P114-6	PY03493	H2-Kd	RYSINLYFI	12.15	QPSARYSINLYFIKCKS*	CAGCCCTCAGCTAGATATAGCATAAACCTGTACTTCATAAAGTGTAAAAGTTGA
P114-7	PY03493	H2-Kd	RYFKEVFHI	12.31	QIYNRYFKEVFHILDPF*	CAAATTTATAATAGATACTTTAAGGAGGTGTTCCACATCCTAGACCCCTTTTGA
P114-8	PY03493	H2-Kd	LYINMLINL	16.29	TLDKLYINMLINLRKYR*	ACGTTAGATAAGCTGTACATAAACATGCTGATAAACCTGAGGAAATACCGCTGA
P114-9	PY03493	H2-Kd	YYHIISCFL	42.14	PNAPYYHIISCFLGWQD*	CCTAACGCCCCTTACTACCACATAATAAGCTGCTTCCTAGGGTGGCAGGACTGA
P114-10	PY03493	H2-Ld	VPNISTYIL	44.99	SRAGVPNISTYILWYLT*	AGTCGAGCCGGGGTGCCTAACATAAGCACCTACATCCTGTGGTATCTGACATGA
P115-1	PY03513	H2-Kd	RYLKLITSL	8.33	SCESRYLKLITSLCRKG*	AGCTGTGAATCTAGATACCTGAAGCTGATAACTAGCCTGTGTAGGAAAGGTTGA
P115-2	PY03513	H2-Kd	FYKDIWNFL	39.98	FYSEFYKDIWNFLTEDR*	TTTTACTCTGAATTCTATAAGGACATCTGGAACTTCCTGACTGAGGATAGGTGA
P115-3	PY03513	H2-Kd	KYRISLPHI	41.92	CPRAKYRISLPHIMTGR*	TGCCCTCGAGCTAAGTATAGAATAAGCCTGCCTCACATAATGACAGGGCGCTGA
P115-4	PY03513	H2-Ld	IPFFSVFYM	16.22	KNMKIPFFSVFYMVLGR*	AAGAACATGAAGATCCCTTTCTTTAGCGTGTTCTACATGGTGCTAGGACGGTGA
P115-5	PY03521	H2-Kd	KYLRMFYAL	8.15	GKRIKYLRMFYALELNE*	GGTAAGAGAATAAAGTACCTGAGAATGTTCTACGCCCTAGAACTGAATGAGTGA
P115-6	PY03521	H2-Kd	KYNNSEDSI	9.36	VNPCKYNNSEDSIAYVL*	GTGAATCCCTGTAAGTATAATAATAGTGAGGATAGCATAGCATACGTGCTCTGA
P115-7	PY03521	H2-Kd	KYDHILSQL	31.32	LLSDKYDHILSQLLGAE*	TTATTGAGTGATAAGTATGACCACATCCTGAGCCAGCTGCTAGGAGCTGAGTGA
P115-8	PY03523	H2-Kd	KYFVYVDKI	7.66	AVPDKYFVYVDKICEKP*	GCTGTCCCTGATAAGTACTTCGTGTACGTAGATAAGATCTGTGAAAAGCCATGA
P115-9	PY03523	H2-Kd	SYITVEINI	10.28	QSMPSYITVEINIPDQV*	CAGTCCATGCCTAGCTACATAACCGTAGAGATAAACATCCCTGATCAGGTATGA
P115-10	PY03523	H2-Kd	YYCGMKNDI	45.82	NGKNYYCGMKNDILILA*	AACGGTAAAAATTACTACTGCGGCATGAAGAATGACATCCTGATCCTAGCGTGA
P116-1	PY03533	H2-Kd	MMISGTTVI	24.51	ITKAMMISGTTVIPPKD*	ATAACTAAAGCGATGATGATAAGCGGCACCACCGTGATCCCGCCTAAGGATTGA
P116-2	PY03581	H2-Kd	KYYPHTLNL	5.63	KSAIKYYPHTLNLGAPG*	AAATCAGCTATAAAGTACTACCCTCACACCCTGAACCTAGGTGCCCCTGGATGA
P116-3	PY03581	H2-Kd	KYDENYSNI	11.96	IQAMKYDENYSNIAKEK*	ATTCAGGCTATGAAGTATGATGAGAACTATAGTAACATAGCTAAGGAGAAATGA
P116-4	PY03581	H2-Kd	KYNYIKLEI	17.86	AETGKYNYIKLEISMEV*	GCTGAAACTGGTAAGTATAACTACATAAAGCTAGAGATAAGCATGGAGGTCTGA
P116-5	PY03582	H2-Kd	RYMKSNVTI	2.89	SPVIRYMKSNVTIVVAP*	AGCCCCGTAATAAGATACATGAAGAGTAACGTGACCATAGTAGTAGCCCCATGA
P116-6	PY03582	H2-Kd	KYYFWKENI	8.67	LVINKYYFWKENIAFDW*	CTAGTGATAAATAAGTACTACTTCTGGAAGGAGAACATAGCCTTTGATTGGTGA
P116-7	PY03582	H2-Kd	FYFSNTICL	29.48	KDSFFYFSNTICLEYRG*	AAAGATTCCTTCTTCTACTTTAGTAACACCATCTGCCTAGAATACCGAGGATGA
P116-8	PY03590	H2-Kd	SYYKNTNLV	31.27	SSQLSYYKNTNLVRAVA*	TCTAGCCAGCTGAGCTACTATAAGAACACTAACCTAGTGCGCGCAGTAGCTTGA
P116-9	PY03590	H2-Kd	IFISIFTSI	31.63	FDIKIFISIFTSIGKAF*	TTTGATATAAAAATCTTCATAAGCATCTTCACTAGCATAGGTAAAGCTTTCTGA
P116-10	PY03599	H2-Kd	LYLYNNNYI	8.89	CAVKLYLYNNNYIIPPG*	TGCGCCGTGAAACTGTACCTGTATAATAATAACTACATAATTCCTCCCGGATGA
P117-1	PY03599	H2-Kd	LYITEIGPI	37.73	STNPLYITEIGPIAVSS*	TCAACTAACCCTCTGTACATAACTGAGATAGGCCCTATAGCCGTGTCGTCTTGA
P117-2	PY03600	H2-Kd	FYTDILYRI	23.7	QMVLFYTDILYRILPVD*	CAGATGGTCTTGTTCTACACTGACATCCTGTATAGAATCCTGCCCGTAGATTGA
P117-3	PY03600	H2-Kd	LYFLNDITI	37.18	FIPILYFLNDITICPKA*	TTCATCCCTATTCTGTACTTCCTGAATGACATAACCATCTGCCCTAAGGCTTGA
P117-4	PY03616	H2-Kd	KYINVDDYI	4.98	CDSMKYINVDDYIKGQC*	TGTGATTCAATGAAGTACATAAACGTAGATGACTACATAAAAGGCCAGTGCTGA
P117-5	PY03616	H2-Kd	LYIMHMPSL	44.07	FPETLYIMHMPSLSQHL*	TTCCCTGAAACACTGTACATAATGCACATGCCTAGCCTGTCTCAGCACTTATGA
P117-6	PY03622	H2-Kd	CYTNNVSIL	12.75	PENRCYTNNVSILYEQT*	CCTGAGAATCGCTGCTACACTAATAACGTGAGCATCCTGTATGAGCAAACATGA
P117-7	PY03622	H2-Kd	CYTNNVSIL	12.75	SKSQCYTNNVSILLPIL*	AGTAAGAGCCAATGCTACACTAATAACGTGAGCATCCTGTTGCCCATACTGTGA
P117-8	PY03684	H2-Kd	SYNRTKQFL	12.94	CSYKSYNRTKQFLEPVE*	TGCTCTTATAAAAGCTATAATAGAACTAAGCAGTTCCTAGAACCTGTAGAATGA
P117-9	PY03684	H2-Kd	TYMTEQYII	18.28	LSINTYMTEQYIIRLET*	CTGTCAATAAACACCTACATGACTGAGCAGTACATAATAAGATTAGAGACATGA
P117-10	PY03684	H2-Kd	VYQKWRNLI	27.72	SRPCVYQKWRNLILGKP*	TCTAGACCATGCGTGTACCAGAAGTGGAGAAACCTGATCCTAGGTAAACCTTGA
P118-1	PY03684	H2-Kd	KYLHIQTYM	34.94	SQNNKYLHIQTYMPRTL*	AGCCAGAATAATAAGTACCTGCACATCCAGACCTACATGCCTCGCACTCTCTGA
P118-2	PY03694	H2-Kd	YYIKIMHNL	7.47	NSLEYYIKIMHNLMGPQ*	AATTCACTAGAGTACTACATAAAGATAATGCATAACCTGATGGGGCCCCAGTGA
P118-3	PY03694	H2-Kd	TYHYALSFL	9.01	YSFSTYHYALSFLDQLT*	TATTCTTTTAGCACCTACCACTACGCCCTGAGCTTCCTAGATCAGCTAACCTGA
P118-4	PY03694	H2-Kd	FYMDNSGKI	12.77	GEPSFYMDNSGKIPSAL*	GGTGAGCCATCATTCTACATGGATAATAGCGGTAAGATCCCTAGCGCACTCTGA
P118-5	PY03694	H2-Kd	KYITIDDII	13.7	VRGMKYITIDDIIVGTC*	GTGCGTGGCATGAAGTACATAACCATAGATGACATAATAGTAGGTACTTGCTGA
P118-6	PY03694	H2-Kd	KYVNSLFNV	29.14	KLAQKYVNSLFNVIQGA*	AAGCTAGCTCAGAAGTACGTGAATAGCCTGTTTAACGTGATCCAGGGCGCGTGA
P118-7	PY03694	H2-Kd	LYTHFTSPI	31.11	DRRWLYTHFTSPIIDVS*	GATAGGCGTTGGCTGTACACCCACTTCACTAGCCCTATAATAGACGTGAGTTGA
P118-8	PY03694	H2-Kd	PYFRACFSI	32.34	FHCAPYFRACFSIGSNS*	TTTCACTGCGCACCTTACTTTAGAGCCTGCTTTAGCATAGGATCTAACTCCTGA
P118-9	PY03694	H2-Kd	SYGSFKHKI	33.7	DFVSSYGSFKHKISRSV*	GATTTCGTCTCTAGCTACGGTAGCTTTAAGCATAAGATAAGTAGAAGTGTTTGA
P118-10	PY03694	H2-Kd	LQFNNNSNI	41.81	CRGDLQFNNNSNIDCSG*	TGTAGAGGTGACCTGCAGTTTAATAATAATGTAACATAGACTGTAGCGGTTGA
P119-1	PY03716	H2-Kd	SYGSLINSI	7.23	SIAASYGSLINSILAYR*	AGTATAGCGGCTAGCTACGGTAGCCTGATAAATAGCATCCTAGCGTATAGATGA
P119-2	PY03716	H2-Kd	KYFKIYNSM	22.29	NILMKYFKIYNSMPLCQ*	AACATTTTGATGAAGTACTTTAAGATCTATAATAGCATGCCTCTGTGTCAATGA
P119-3	PY03733	H2-Kd	SYIKSLTDI	4.3	DDNISYIKSLTDINCNE*	GATGATAACATAAGCTACATAAAGAGCCTGACTGACATAAATTGTAATGAGTGA
P119-4	PY03733	H2-Kd	KYFDKICSI	4.93	YESQKYFDKICSIISFL*	TATGAAAGTCAGAAGTACTTTGATAAGATCTGTAGCATAATCTCCTTCTTGTGA
P119-5	PY03733	H2-Kd	FFIPNSHSL	24.56	ETLNFFIPNSHSLSKCV*	GAGACACTGAATTTCTTCATCCCTAATAGCCATAGCCTGAGTAAATGCGTATGA
P119-6	PY03733	H2-Kd	KYALDISVL	32.17	PVTEKYALDISVLTVST*	CCTGTGACTGAAAAGTACGCCCTAGACATAAGCGTGCTGACCGTGAGCACCTGA
P119-7	PY03733	H2-Kd	TYICFWQLI	36.48	PKLRTYICFWQLITIKE*	CCTAAGCTGAGGACCTACATCTGCTTCTGGCAGCTGATAACCATAAAGGAATGA
P119-8	PY03745	H2-Kd	YYNENVGQI	10.47	VKGFYYNENVGQIRTMK*	GTGAAGGGATTCTACTATAATGAGAACGTAGGCCAGATAAGGACCATGAAGTGA
P119-9	PY03745	H2-Kd	SYDKYTSAL	49.71	SSLMSYDKYTSALPTVI*	AGCTCGCTGATGAGCTATGATAAGTACACTAGCGCCCTGCCAACCGTGATTTGA
P119-10	PY03755	H2-Kd	KYKYLLHAI	19.35	SEGLKYKYLLHAIDRQF*	AGTGAAGGGCTGAAGTATAAGTACCTGCTGCACGCCATAGACCGGCAGTTTTGA
P120-1	PY03769	H2-Kd	LYISTTNRL	13.41	RMSSLYISTTNRLAKRE*	CGGATGTCTTCCCTGTACATAAGCACCACTAATAGACTAGCTAAGAGGGAGTGA
P120-2	PY03769	H2-Kd	KQFKNYNSL	16.08	LCFDKQFKNYNSLSSAR*	CTTTGCTTTGATAAGCAGTTTAAGAACTATAATAGCCTGAGTTCCGCCCGTTGA
P120-3	PY03769	H2-Kd	IYKNIHHTI	19.43	CAAKIYKNIHHTIERLK*	TGCGCCGCTAAGATCTATAAGAACATCCACCACACCATAGAGAGACTGAAGTGA
P120-4	PY03769	H2-Kd	YYIIECLPI	25.57	TILAYYIIECLPINPCG*	ACTATACTAGCATACTACATAATAGAGTGCCTGCCTATAAATCCCTGCGGCTGA
P120-5	PY03769	H2-Kd	KYINEQKVI	27.09	ESWAKYINEQKVIMVIV*	GAGTCGTGGGCTAAGTACATAAATGAGCAGAAGGTGATAATGGTAATAGTCTGA
P120-6	PY03769	H2-Kd	CYNETGYNI	33.48	GLITCYNETGYNILRLF*	GGCCTGATAACATGCTATAATGAGACCGGCTATAACATCCTCCGTTTGTTCTGA
P120-7	PY03769	H2-Ld	SPQFNFDTF	14.04	IAGSSPQFNFDTFMSEL*	ATAGCGGGTAGTAGCCCTCAGTTTAACTTTGACACCTTCATGTCTGAGCTCTGA
P120-8	PY03769	H2-Ld	FPNNNILLL	32.4	VEELFPNNNILLLQFQR*	GTAGAGGAGTTGTTCCCTAATAATAACATCCTGCTGCTGCAGTTCCAGAGATGA
P120-9	PY03770	H2-Kd	SFNNTYHSI	9.95	GGSLSFNNTYHSIIEED*	GGTGGCTCTCTGAGCTTTAATAACACCTACCATAGCATAATAGAAGAAGACTGA
P120-10	PY03770	H2-Kd	KYSYFDHAI	11.56	PSQKKYSYFDHAIRATS*	CCCTCACAGAAAAAGTATAGCTACTTTGACCACGCCATAAGAGCCACTAGTTGA
P121-1	PY03791	H2-Kd	IYLRAPHPI	7.54	QDLEIYLRAPHPIMGSG*	CAGGACCTAGAGATCTACCTGAGAGCCCCTCACCCTATAATGGGTAGCGGATGA
P121-2	PY03791	H2-Kd	GYIKKEYSI	12.56	ISPWGYIKKEYSILCQL*	ATTTCACCCTGGGGCTACATAAAGAAGGAGTATAGCATCTTATGTCAACTGTGA
P121-3	PY03791	H2-Kd	RYINNNIKL	14.49	PVPLRYINNNIKLQNAG*	CCGGTCCCTCTGAGATACATAAATAATAACATAAAGCTGCAGAACGCGGGATGA
P121-4	PY03791	H2-Kd	KYIIVALPL	25.72	MPFDKYIIVALPLIEDD*	ATGCCCTTTGATAAGTACATAATAGTAGCCCTGCCTCTGATAGAAGATGATTGA
P121-5	PY03791	H2-Ld	YPFNFIWPF	37.31	ESRPYPFNFIWPFSLSR*	GAGAGTCGGCCTTACCCTTTTAACTTCATCTGGCCTTTCTCACTTTCCCGCTGA
P121-6	PY03808	H2-Kd	KYNLFENFI	30.02	QECGKYNLFENFIEAKV*	CAGGAGTGCGGTAAGTATAACCTGTTTGAGAACTTCATAGAAGCTAAAGTGTGA
P121-7	PY03808	H2-Kd	KYQEFSFIL	41.73	QIVDKYQEFSFILALRP*	CAAATAGTAGATAAGTACCAGGAGTTTAGCTTCATCCTAGCACTGAGACCATGA
P121-8	PY03814	H2-Kd	YYYVNDSFL	4.6	RDNAYYYVNDSFLDEVP*	AGAGATAACGCATACTACTACGTGAATGATAGCTTCCTAGATGAGGTCCCGTGA

P121-9	PY03814	H2-Kd	AYNQNYASI	5.68	KSASAYNQNYASIKVQQ*	AAAAGTGCTTCTGCCTATAACCAGAACTACGCTAGCATAAAAGTGCAGCAGTGA
P121-10	PY03814	H2-Kd	SYIKKFFKI	9.77	TLEVSYIKKFFKIKNAA*	ACGCTAGAGGTGAGCTACATAAAGAAGTTCTTTAAGATAAAAAACGCCGCTTGA
P122-1	PY03814	H2-Kd	KYTHMIYRL	10.93	VLGIKYTHMIYRLILLR*	GTGCTAGGCATAAAGTACACCCACATGATCTATAGACTGATCCTGTTGCGCTGA
P122-2	PY03814	H2-Kd	NYFSLFDHI	11.12	DLQLNYFSLFDHINNQD*	GACCTCCAATTGAACTACTTTAGCCTGTTTGACCACATAAATAACCAGGATTGA
P122-3	PY03814	H2-Kd	EYMDNYFSL	20.36	TVLLEYMDNYFSLAVQE*	ACCGTTCTGCTAGAGTACATGGATAACTACTTTAGCCTAGCCGTGCAGGAGTGA
P122-4	PY03814	H2-Kd	GYINTTLDI	23.02	EAPMGYINTTLDIELHI*	GAGGCTCCAATGGGCTACATAAACACCACCCTAGACATAGAACTGCACATCTGA
P122-5	PY03814	H2-Kd	FYFNTDDNL	25.8	ENRGFYFNTDDNLYEVS*	GAGAATAGAGGGTTCTACTTTAACACTGATGATAACCTGTATGAAGTCTCATGA
P122-6	PY03814	H2-Kd	IYRSTLSYL	30.26	IHKDIYRSTLSYLVLDS*	ATTCATAAGGACATCTATAGAAGCACCCTGAGCTACCTAGTACTAGACTCCTGA
P122-7	PY03814	H2-Kd	IYNDLNTGI	33.23	NDCYIYNDLNTGIPQCS*	AATGACTGCTACATCTATAATGACCTGAACACCGGCATCCCACAGTGTAGTTGA
P122-8	PY03814	H2-Kd	MYVLAMSAI	33.96	LSGLMYVLAMSAIKKTP*	CTGTCTGGCCTAATGTACGTGCTAGCCATGAGCGCCATAAAGAAGACCCCCTGA
P122-9	PY03816	H2-Kd	KYIKTKNMI	3.51	GQIAKYIKTKNMITGWK*	GGACAAATAGCTAAGTACATAAAGACTAAGAACATGATAACCGGATGGAAATGA
P122-10	PY03816	H2-Kd	FYHQNGEII	44.01	SGATFYHQNGEIIHDGL*	TCTGGTGCCACTTTCTACCACCAGAACGGTGAGATAATCCATGACGGTCTGTGA
P123-1	PY03817	H2-Kd	RYFTIISEI	3.36	GGNLRYFTIISEIKFLI*	GGAGGTAATTTGAGATACTTCACCATAATAAGTGAGATAAAAATTCCTAATCTGA
P123-2	PY03817	H2-Kd	KYINLCETL	5.2	QFDIKYINLCETLDPLQ*	CAGTTTGACATAAAGTACATAAACCTGTGTGAGACCCTAGACCCCCTGCAATGA
P123-3	PY03817	H2-Kd	IYITGNAYI	5.2	QGSLIYITGNAYILATD*	CAGGGCTCGCTGATCTACATAACCGGTAACGCCTACATCTTAGCCACTGACTGA
P123-4	PY03817	H2-Kd	RYINDNNKI	7.65	PIFYRYINDNNKIVTTH*	CCAATTTTCTATAGATACATAAATGATAAATAAGATAGTGACAACACACTGA
P123-5	PY03817	H2-Kd	TYLTMLFNI	7.77	AISDTYLTMLFNILDSL*	GCTATAAGTGACACCTACCTGACCATGCTGTTTAACATCCTAGATTCCCTGTGA
P123-6	PY03817	H2-Kd	IYYRNVIYI	14.79	YLLFIYYRNVIYINAIG*	TACCTCCTGTTTATCTACTATAGAAACGTGATCTACATAAACGCAATAGGCTGA
P123-7	PY03817	H2-Kd	IYFSNNIKI	15.24	RKRDIYFSNNIKISAIK*	CGTAAGCGTGATATCTACTTTAGTAATAACATAAAGATCTCCGCTATAAAGTGA
P123-8	PY03817	H2-Kd	KYNIINNSNL	15.88	FSFQKYNINNSNLPTGV*	TTTTCGTTTCAGAAGTATAACATAAATAATAGTAACCTGCCAACCGGGGTGTGA
P123-9	PY03817	H2-Kd	SYIFTKYCL	20.92	SLMESYIFTKYCLQNSP*	TCGCTAATGGAGAGCTACATCTTCACTAAGTACTGCCTGCAGAATAGCCCATGA
P123-10	PY03817	H2-Kd	IYIATRRII	23.07	IAAAIYIATRRIINLTH*	ATAGCCGCAGCTATCTACATAGCCACTAGAAGAATAATAAATCTGACCCACTGA
P124-1	PY03817	H2-Kd	KYNSTDFEL	23.73	FTGLKYNSTDFELCFTP*	TTCACGGGGTTGAAGTATAATAGCACTGACTTTGAGCTGTGTTTTACACCTTGA
P124-2	PY03817	H2-Kd	SYNKNEIII	30.85	TSVVSYNKNEIIIFSIT*	ACTTCAGTAGTGAGCTATAATAAGAATGAGATAATAATCTTCTCAATAACCTGA
P124-3	PY03817	H2-Kd	IYISNIFAM	38.4	KGTSIYISNIFAMHIIK*	AAAGGTACCTCCATCTACATAAGTAACATCTTCGCCATGCATATAATAAAGTGA
P124-4	PY03817	H2-Ld	KPIKMSFNL	44.69	LRKGKPIKMSFNLFSSQ*	CTGAGGAAGGGTAAGCCTATAAAGATGAGCTTTAACCTGTTTAGCTCACAGTGA
P124-5	PY03832	H2-Kd	YYQTPLSEI	3.95	VYQHYYQTPLSEISHDN*	GTGTATCAGCACTACTACCAGACCCCTCTGAGTGAGATCTCCCATGATAATTGA
P124-6	PY03832	H2-Kd	AYINDFYSI	4.19	QTNRAYINDFYSIDILW*	CAGACTAATAGGGCCTACATAAATGACTTCTATAGCATAGATATCCTCTGGTGA
P124-7	PY03832	H2-Kd	LYYFDSSNI	12.94	NRRGLYYFDSSNIHECF*	AACCGTAGGGGACTGTACTACTTTGATAGTAGTAACATCCATGAATGTTTTTGA
P124-8	PY03832	H2-Kd	IYKQNFDSI	19.49	ASTDIYKQNFDSIITGS*	GCTAGTACTGATATCTATAAGCAGAACTTTGATAGCATAATAACAGGTAGCTGA
P124-9	PY03832	H2-Kd	FFINSINNI	22.51	GYRTFFINSINNIKSAM*	GGTTATAGAACCTTCTTCATAAATAGCATAAATAACATAAAATCCGCAATGTGA
P124-10	PY03832	H2-Kd	FYKTYKNTI	25.89	FGQFFYKTYKNTISQPT*	TTCGGTCAGTTCTTCTATAAGACCTATAAGAACACCATCTCTCAGCCAACTTGA
P125-1	PY03832	H2-Kd	FYFQFFYDI	27.64	EKTKFYFQFFYDIRIKA*	GAGAAGACTAAGTTCTACTTCCAGTTCTTCTATGACATAAGAATAAAAGCATGA
P125-2	PY03832	H2-Kd	LYQLTIESI	33.47	KVKDLYQLTIESIPGVK*	AAGGTGAAGGACCTGTACCAGCTGACCATAGAGAGCATCCCTGGAGTGAAATGA
P125-3	PY03843	H2-Kd	KKMNMFTAI	32.61	GSGMKKMNMFTAIGCES*	GGTAGCGGAATGAAGAAGATGAACATGTTCACCGCCATAGGCTGTGAGTCCTGA
P125-4	PY03843	H2-Kd	CFYNLNSPI	44.37	EANRCFYNLNSPICLQQ*	GAGGCTAATCGTTGCTTCTATAACCTGAATAGCCCTATCTGTCTCCAGCAGTGA
P125-5	PY03875	H2-Ld	SPFYNIYIF	8.98	ERKESPFYNIYIFMKSV*	GAGCGTAAAGAAAGCCCTTTCTATAACATCTACATCTTCATGAAGTCAGTGTGA
P125-6	PY03911	H2-Kd	LYYVNISKI	7.49	TKLPLYYVNISKISIIP*	ACTAAACTTCCTCTGTACTACGTGAACATAAGTAAGTATAATCCCATGA
P125-7	PY03911	H2-Kd	RFINLTSSL	26.01	RATPRFINLTSSLQMEQ*	CGGGCCACGCCTAGATTCATAAACCTGACTAGTAGCCTGCAAATGGAACAGTGA
P125-8	PY03923	H2-Kd	SYFMSKNDI	8.34	YPDKSYFMSKNDIRDNQ*	TATCCTGATAAGAGCTACTTCATGAGTAAGAATGACATCCGTGATAATCAATGA
P125-9	PY03923	H2-Kd	KQILKMSSI	15.02	MLNTKQILKMSSIRHLL*	ATGCTGAACACTAAGCAGATCCTGAAGATGAGTAGCATAAGACATCTGCTGTGA
P125-10	PY03941	H2-Kd	SYVYIQNFL	24	ATAVSYVYIQNFLVYQI*	GCTACAGCCGTGAGCTACGTGTACATCCAGAACTTCCTAGTGTACCAGATCTGA
P126-1	PY03941	H2-Kd	KYISENSCL	27.06	REMDKYISENSCLSMES*	CGTGAAATGGATAAGTACATAAGTGAGAATAGCTGCCTGAGCATGGAGTCCTGA
P126-2	PY03941	H2-Kd	KYKPFVVSL	32.73	LAYKKYKPFVVSLHEQQ*	TTAGCCTATAAGAAGTATAAGCCTTTCGTAGTGAGCCTGCATGAGCAACAGTGA
P126-3	PY03941	H2-Kd	LYQFPLNSL	42.92	AHENLYQFPLNSLAESS*	GCACATGAAAACCTGTACCAGTTCCCTCTGAATAGCCTAGCTGAATCATCCTGA
P126-4	PY03941	H2-Ld	LPSVNYYNF	14.65	IGVLLPSVNYYNFNLAH*	ATAGGCGTTCTCCTGCCTAGCGTGAACTACTATAACTTTAACTTAGCCCACTGA
P126-5	PY03941	H2-Ld	FPLNSLTLF	34.87	EQHQFPLNSLTLFVAVK*	GAACAACACCAGTTCCCTCTGAATAGCCTGACCCTGTTCGTAGCAGTGAAATGA
P126-6	PY03952	H2-Kd	SYFEVFSSI	1.86	GVDESYFEVFSSIKLND*	GGGGTAGATGAGAGCTACTTTGAGGTGTTTAGTAGCATAAAACTGAATGACTGA
P126-7	PY03995	H2-Kd	YYCPIYNLI	8.65	AKNLYYCPIYNLISSIE*	GCTAAGAATCTCTACTACTGCCCTATCTATAACCTGATCTCTTCCATAGAGTGA
P126-8	PY03995	H2-Kd	LFMNGKNTI	21.26	ERSPLFMNGKNTIQLFA*	GAGCGTTCACCCCTGTTCATGAACGGTAAGAACACCATCCAGCTCTTTGCCTGA
P126-9	PY03995	H2-Kd	HYYCPIYNL	34.24	QNVYHYYCPIYNLCHDI*	CAGAACGTGTACCACTACTACTGCCCTATCTATAACCTGTGCCATGACATCTGA
P126-10	PY04008	H2-Kd	FYNNVWNQI	3.91	IPPMFYNNVWNQINENG*	ATTCCTCCCATGTTCTATAATAACGTGTGGAACCAGATAAATGAGAACGGTTGA
P127-1	PY04008	H2-Kd	KYLNNKDMI	8.4	KAPQKYLNNKDMILREF*	AAAGCACCCCAAAAGTACCTGAATAATAAGGACATGATCTTAAGGGAGTTCTGA
P127-2	PY04008	H2-Kd	KYYEHIIFI	12.01	HLRRKYYEHIIFITLML*	CACTTACGCCGTAAGTACTATGAGCACATAATCTTCATAACACTAATGCTGTGA
P127-3	PY04008	H2-Kd	KYENLIPSI	12.99	LGRGKYENLIPSILQDP*	CTAGGTAGAGGTAAGTATGAGAACCTGATCCCTAGCATCTTGCAGGACCCTTGA
P127-4	PY04008	H2-Kd	TYLKNNINI	27.53	LNAMTYLKNNINIGFFG*	CTGAATGCAATGACCTACCTGAAGAATAACATAAACATAGGATTTTTCGGATGA
P127-5	PY04008	H2-Ld	SPVDTVYIF	49.47	VGQSSPVDTVYIFDVKW*	GTAGGGCAGTCTAGCCCTGTAGACACCGTGTACATCTTTGACGTGAAGTGGTGA
P127-6	PY04034	H2-Kd	KYNNSIRNI	11.95	LCDYKYNNSIRNIRMLS*	CTTTGTGATTATAAGTATAATAATAGCATAAGAAACATAAGAATGCTCTCTTGA
P127-7	PY04034	H2-Kd	IYMDYDTWL	19.56	PDGVIYMDYDTWLDDVE*	CCTGACGGCGTAATCTACATGGACTATGACACCTGGCTAGATGACGTAGAATGA
P127-8	PY04034	H2-Kd	SYGNFSNYI	20.53	PTLSSYGNFSNYISHIS*	CCAACCCTGTCTAGCTACGGTAACTTTAGTAACTACATCTCTCATATCTCCTGA
P127-9	PY04034	H2-Kd	SYANLKPKI	24.81	LSKFSYANLKPKIRVHS*	CTCTCTAAGTTTAGCTACGCTAACCTGAAGCCTAAGATCCGCGTGCATAGCTGA
P127-10	PY04034	H2-Kd	IMFNNFQNI	30.5	QRSDIMFNNFQNILLKG*	CAACGATCTGATATAATGTTTAATAACTTCCAGAACATCCTTCTGAAAGGATGA
P128-1	PY04034	H2-Kd	NYIGTRNNL	44.4	ELYSNYIGTRNNLPVFI*	GAGCTATATAGTAACTACATAGGCACTAGAAATAACCTGCCAGTGTTTATTTGA
P128-2	PY04034	H2-Ld	FPFVNPVLL	23.56	VCQTFPFVNPVLLKALW*	GTGTGCCAGACTTTCCCTTTCGTGAACCCTGTGCTGCTGAAAGCCCTTTGGTGA
P128-3	PY04051	H2-Kd	KYLRAPAYI	7.91	ISEHKYLRAPAYIQRKI*	ATAAGTGAGCATAAGTACCTGAGAGCCCCTGCCTACATCCAAAGGAAGATTTGA
P128-4	PY04051	H2-Kd	SYEKTQSSL	20.52	QRDASYEKTQSSLSSDG*	CAGCGTGACGCTAGCTATGAAGAACCCAGAGTAGCCTGTCTTCTGACGGATGA
P128-5	PY04051	H2-Kd	SYVKQLPPL	25.62	RNMKSYVKQLPPLEPNG*	CGTAATATGAAGAGCTACGTGAAGCAGCTGCCTCCTCTAGAACCTAATGGCTGA
P128-6	PY04058	H2-Kd	QYIFSFRSL	34.05	YKVLQYIFSFRSLNSTA*	TATAAAGTCTTGCAGTACATCTTTAGCTTTAGAAGCCTGAATAGCACAGCCTGA
P128-7	PY04062	H2-Kd	KYLKLHNKI	10.35	GATRKYLKLHNKIVERN*	GGCGCCACTAGGAAGTACCTGAAGCTGCATAATAAGATAGTAGAGCGTAACTGA
P128-8	PY04062	H2-Kd	WYFIKTSSI	10.46	ICNRWYFIKTSSILTDF*	ATCTGTAACCGCTGGTACTTCATAAAGACTAGTAGCATCCTAACTGACTTTTGA
P128-9	PY04065	H2-Kd	KYFKSLLHI	4.17	LLLFKYFKSLLHICEAA*	TTACTATTGTTTAAGTACTTTAAGAGCCTGCTGCACATCTGTGAGGCCGCGTGA
P128-10	PY04081	H2-Kd	KFINVVNYI	9.48	ARWYKFINVVNYIERMS*	GCGCGCTGGTATAAGTTCATAAACGTAGTGAACTACATAGAAAGAATGTCCTGA
P129-1	PY04081	H2-Kd	KYEQTRMSI	11.52	LLIYKYEQTRMSIRFRK*	CTTCTAATCTATAAGTATGAGCAGACTAGAATGAGCATAAGGTTTAGAAAGTGA
P129-2	PY04081	H2-Kd	SYLNIKELI	20.3	NVDASYLNIKELIGVAS*	AATGTAGATGCTAGCTACCTGAACATAAAGGAGCTGATAGGCGTAGCCTCCTGA
P129-3	PY04081	H2-Kd	HYVEAESEI	20.91	LTNLHYVEAESEILADF*	CTGACTAACCTGCACTACGTAGAGGCTGAGAGTGAGATCCTAGCTGATTTTTGA
P129-4	PY04097	H2-Kd	KYFSSLSQF	17.28	ETTGKYFSSLSQFQLQK*	GAGACCACAGGTAAGTACTTTAGTAGCCTGAGCCAGTTCCAGCTGCAAAAATGA
P129-5	PY04097	H2-Kd	IYLENKMFL	36.97	EVFRIYLENKMFLCNLV*	GAGGTTTTTAGGATCTACCTAGAGAATAAGATGTTCCTGTGTAATCTAGTATGA
P129-6	PY04097	H2-Kd	EYISVVSRI	47.18	ATTSEYISVVSRIWSFI*	GCCACGACATCTGAGTACATAAGCGTAGTGAGTAGAATCTGGAGCTTTATTTGA
P129-7	PY04100	H2-Kd	IYQNMSVFI	8.53	MCDNIYQNMSVFISESF*	ATGTGTGATAATATCTACCAGAACATGAGCGTGTTCATAAGTGAGTCATTTTGA
P129-8	PY04100	H2-Kd	FYINPKYII	9.99	GGSKFYINPKYIITFKR*	GGCGGATCTAAGTTCTACATAAACCCTAAGTACATAATAACATTTAAACGTTGA
P129-9	PY04100	H2-Kd	MYNAENSKI	23.39	GVIPMYNAENSKIGNQS*	GGAGTAATCCCAATGTATAACGCTGAGAATAGTAAGATAGGTAATCAGTCCTGA
P129-10	PY04100	H2-Kd	KYLIYSDSL	27.03	GRENKYLIYSDSLLLVD*	GGGCGTGAAAATAAGTACCTGATCTATAGTGATAGCCTGCTTTTAGTAGATTGA
P130-1	PY04103	H2-Kd	KYIKLCQKI	5.65	LSRVKYIKLCQKICRPY*	CTGAGCCGCGTGAAGTACATAAAGCTGTGCCAGAAGATCTGCCGCCCATATTGA
P130-2	PY04103	H2-Kd	KYIYDKYNI	6.21	KFRGKYIYDKYNILESY*	AAGTTTAGAGGTAAGTACATCTATGATAAGTATAACATCCTAGAGAGCTATTGA
P130-3	PY04103	H2-Kd	GYIISSFVI	24.62	SMSRGYIISSFVISGGE*	TCCATGTCTAGGGGCTACATAATAAGTAGCTTCGTGATCTCAGGGGGTGAGTGA
P130-4	PY04146	H2-Kd	YYFYLYDTI	3.51	VAHSYYFYLYDTIVIVI*	GTAGCTCATAGTTACTACTTCTACCTGTATGACACCATAGTGATAGTAATTTGA
P130-5	PY04146	H2-Kd	KYNSVKNKI	9.3	SSPVKYNSVKNKIGLDN*	AGTTCCCCTGTGAAGTATAATAGCGTGAAGAATAAGATAGGCCTAGATAACTGA
P130-6	PY04173	H2-Kd	TYNEMYNHI	5.04	YMGNTYNEMYNHIQIMC*	TACATGGGTAATACCTATAATGAGATGTATAACCACATCCAAATAATGTGTTGA
P130-7	PY04173	H2-Kd	KYYGILLEL	20.1	GLYSKYYGILLELLTLF*	GGTCTTTACTCTAAGTACTACGGCATCCTGCTAGAGCTGCTAACCCTGTTTTGA
P130-8	PY04173	H2-Kd	KMINNNFQL	41.4	SQRAKMINNNFQLPGLG*	TCACAGCGTGCTAAGATGATAAATAATAACTTCCAGCTGCCAGGCCTAGGATGA
P130-9	PY04181	H2-Kd	YWFYDKYYI	32.1	LFIIYWFYDKYYIGGSF*	CTGTTTATAATCTACTGGTTCTATGATAAGTACTACATAGGTGGGTCCTTTTGA
P130-10	PY04181	H2-Ld	YPYIYFFFF	27	KSELYPYIYFFFFYVWL*	AAAAGTGAGCTCTACCCTTACATCTACTTCTTCTTCTTCTACGTTTGGCTCTGA
P131-1	PY04194	H2-Kd	KYWSTVIDI	27.84	VAFKKYWSTVIDIVLFP*	GTAGCTTTTAAAAAGTACTGGAGCACCGTGATAGACATAGTTCTCTTCCCGTGA
P131-2	PY04199	H2-Kd	GYFPNFDTI	3.15	NAIPGYFPNFDTIWFTA*	AACGCAATCCCGGGCTACTTCCCTAACTTTGACACCATCTGGTTCACAGCCTGA
P131-3	PY04199	H2-Kd	YYQNNVNFL	4.84	EQEFYYQNNVNFLSPYT*	GAACAGGAATTTTACTACCAGAATAACGTGAACTTCCTGTCTCCATACACATGA
P131-4	PY04199	H2-Kd	CYLNSYETL	10.74	CRSKCYLNSYETLCRTT*	TGTAGGTCTAAGTGCTACCTGAATAGCTATGAGACCCTGTGTAGAACCACCTGA
P131-5	PY04199	H2-Kd	IYLCGSEHI	21.2	FNPVIYLCGSEHIVGED*	TTTAATCCTGTAATCTACCTGTGCGGTAGTGAGCACATAGTAGGTGAGGACTGA
P131-6	PY04199	H2-Kd	RYLNVSEIL	33.1	ALKFRYLNVSEILVLRQ*	GCCCTGAAGTTTAGATACCTGAACGTGAGTGAGATCCTAGTCCTGAGACAGTGA
P131-7	PY04214	H2-Kd	KYYENELNI	8.99	FGGTKYYENELNITKPH*	TTTGGGGGCACTAAGTACTATGAGAATGAGCTGAACATAACTAAGCCCCATTGA
P131-8	PY04242	H2-Kd	IYYTARFPL	16.26	RIFNIYYTARFPLQGLK*	CGAATCTTTAACATCTACTACACCGCTAGATTCCCTCTGCAGGGCTTGAAGTGA
P131-9	PY04242	H2-Kd	YYTARFPLI	16.83	DLSDYYTARFPLIVFYD*	GATCTGTCTGACTACTACACCGCTAGATTCCCTCTGATAGTTTTTTATGACTGA

P131-10	PY04242	H2-Kd	YYKQFSNQI	26.04	RDSAYYKQFSNQITETM*	CGTGATAGCGCTTACTATAAGCAGTTTAGTAACCAGATAACTGAAACGATGTGA
P132-1	PY04244	H2-Kd	CYYFYRTAL	8.98	AITECYYFYRTALRVNQ*	GCTATAACTGAGTGCTACTACTTCTATAGAACCGCCCTGCGCGTGAATCAATGA
P132-2	PY04257	H2-Kd	MYINNNFEI	3.53	SIVAMYINNNFEIDPLQ*	TCTATAGTAGCAATGTACATAAATAATAACTTTGAGATAGACCCCCTCCAGTGA
P132-3	PY04257	H2-Kd	KYSDYFYNI	12.07	LEAEKYSDYFYNIMAMR*	CTAGAGGCTGAAAAGTATAGTGACTACTTCTATAACATAATGGCAATGCGTTGA
P132-4	PY04257	H2-Kd	IYNKDIPYI	31.69	RVPRIYNKDIPYIIWKV*	CGCGTACCTCGAATCTATAATAAGGACATCCCTTACATAATTTGGAAAGTGTGA
P132-5	PY04260	H2-Kd	LYYVNERTI	48.81	LLGNLYYVNERTIDVDD*	CTACTAGGTAATCTGTACTACGTGAATGAGAGAACCATAGATGTAGATGATTGA
P132-6	PY04273	H2-Kd	SFIANTNHI	10.34	GQLASFIANTNHIPVAY*	GGGCAGCTAGCTAGCTTCATAGCTAACACTAACCACATCCCTGTAGCTTACTGA
P132-7	PY04273	H2-Kd	KYSNTAIPL	24.22	IELSKYSNTAIPLPFML*	ATAGAACTGAGTAAGTATAGTAACACCGCCATCCCTCTGCCCTTCATGCTATGA
P132-8	PY04273	H2-Kd	KYALYRDYL	36.82	FWHMKYALYRDYLLPMG	TTTTGGCATATGAAGTACGCCCTGTATAGAGACTACCTGCTCCCCATGGGGTGA
P132-9	PY04273	H2-Ld	FPYLLRHSF	22.31	FPKHFPYLLRHSFYVLL*	TTCCCTAAGCATTTCCCTTACCTGCTGAGACATAGCTTCTACGTGCTGCTGTGA
P132-10	PY04302	H2-Kd	KYFAGFFTL	2.74	TNDGKYFAGFFTLTHCG*	ACTAATGACGGTAAGTACTTCGCCGGCTTCTTCACCCTGACCCATTGCGGGTGA
P133-1	PY04302	H2-Kd	YYNYSDYLI	8.66	ELFVYYNYSDYLIGNWR*	GAGCTGTTTGTGTACTATAACTATAGTGACTACCTGATAGGTAATTGGAGGTGA
P133-2	PY04302	H2-Kd	SYLRAGANI	9.61	ARGLSYLRAGANIYHDN*	GCTAGAGGATTAAGCTACCTGAGAGCCGGCGCTAACATCTATCATGATAATTGA
P133-3	PY04302	H2-Kd	NYFQYLFNI	9.83	SPRVNYFQYLFNITDES*	TCTCCACGAGTGAACTACTTCCAGTACCTGTTTAACATAACTGATGAGTCTTGA
P133-4	PY04302	H2-Kd	SYLQNKYAV	21.95	AGPRSYLQNKYAVNKAI*	GCAGGCCCCCGTAGCTACCTGCAGAATAAGTACGCCGTGAATAAGGCTATCTGA
P133-5	PY04302	H2-Kd	KYSLNNANI	24.79	ATDKKYSLNNANIGHAQ*	GCGACTGATAAGAAGTATAGCCTGAATAACGCTAACATAGGTCATGCCCAGTGA
P133-6	PY04302	H2-Kd	NYYNYSDYL	28.37	NITKNYYNYSDYLTSEL*	AACATAACTAAAAAACTACTATAACTATAGTGACTACCTGACATCTGAGTTATGA
P133-7	PY04302	H2-Kd	KYVYLRLII	29.71	ADQIKYVYLRLIILIIR*	GCTGACCAGATAAAGTACGTGTACCTGAGACTGATAATCCTGATAATCCGCTGA
P133-8	PY04302	H2-Kd	FYLDIIREI	39.08	PASEFYLDIIREIYLVG*	CCCGCCTCTGAGTTCTACCTAGACATAATAAGAGAGATCTATTTAGTAGGCTGA
P133-9	PY04302	H2-Kd	IYQNITENL	41.05	TDVTIYQNITENLQIGP*	ACTGACGTAACCATCTACCAGAACATAACTGAGAACCTGCAAATAGGACCCTGA
P133-10	PY04302	H2-Ld	VPYANFNDL	27.4	YTCFVPYANFNDLPPLP*	TATACCTGTTTCGTGCCTTACGCTAACTTTAATGACCTGCCCCCACTTCCTTGA
P134-1	PY04318	H2-Kd	KYISTIKSL	7.24	VNKTKYISTIKSLLLID*	GTGAATAAGACTAAGTACATAAGCACCATAAAGAGCCTGCTCCTGATAGACTGA
P134-2	PY04318	H2-Kd	NYYNLANLI	21.83	SKEANYYNLANLIKRKL*	TCTAAAGAAGCTAACTACTATAACCTAGCTAACCTGATAAAGCGTAAATTATGA
P134-3	PY04318	H2-Kd	HYIVKgEHI	42.03	GNRGHYIVKGEHIGRAK*	GGTAATAGAGGGCACTACATAGTGAAGGGTGAGCACATAGGGCGTGCTAAGTGA
P134-4	PY04318	H2-Kd	HYIVKvEHI	42.03	GIQFHYIVKVEHIHCTE*	GGCATTCAGTTTCACTACATAGTGAAGGTAGAGCACATCCATTGTACTGAGTGA
P134-5	PY04324	H2-Kd	IYNDIDTFL	30.35	QQVLIYNDIDTFLCCFV*	CAGCAGGTCTTAATCTATAATGACATAGACACCTTCCTGTGTTGTTTCGTCTGA
P134-6	PY04330	H2-Kd	SYTYHSVNI	26.75	SSKWSYTYHSVNIAGTR*	TCCTCTAAGTGGAGCTACACCTACCATAGCGTGAACATAGCAGGGACCGCTGA
P134-7	PY04338	H2-Kd	SYFFVTDHL	6.03	LGNRSYFFVTDHLDTPM*	CTAGGTAACCGTAGCTACTTCTTCGTGACTGACCACCTAGATACCCCCATGTGA
P134-8	PY04338	H2-Kd	KFFDYGYYI	40.33	QAQSKFFDYGYYILGPL*	CAAGCACAGAGTAAGTTCTTTGACTACGGCTACTACATCCTAGGTCCTCTCTGA
P134-9	PY04338	H2-Kd	YYLMSIGLL	42.56	ESDQYYLMSIGLLPLGD*	GAGTCTGATCAGTACTACCTGATGAGCATAGGCCTGCTGCCTCTAGGTGATTGA
P134-10	PY04343	H2-Kd	KYIRNMFEV	19.18	SSAWKYIRNMFEVKQEE*	TCATCGGCCTGGAAGTACATAAGAAACATGTTTGAGGTGAAGCAGGAGGAGTGA
P135-1	PY04357	H2-Kd	KYINVIMNL	4.77	RVVGKYINVIMNLGLLG*	CGGGTAGTAGGTAAGTACATAAACGTGATAATGAACCTAGGGCTCTTAGGATGA
P135-2	PY04357	H2-Kd	SYMDQKLEI	15.3	FAVPSYMDQKLEIGMFS*	TTTGCAGTCCCTAGCTACATGGACCAGAAGCTAGAGATAGGTATGTTTAGCTGA
P135-3	PY04357	H2-Kd	QYVNVMNPL	31.97	GASPQYVNVMNPLQHGL	GGCGCTAGCCCCCAGTACGTGAACGTGATGAACCCTCTGCAGCACGGCCTCTGA
P135-4	PY04357	H2-Kd	KYSIYSDNI	41.43	GLLCKYSIYSDNIFTGN*	GGCTTACTGTGTAAGTATAGCATCTATTGAGTATAACATCTTTACCGGTAATTGA
P135-5	PY04385	H2-Ld	LPQLGRFTL	48.13	GCLELPQLGRFTLLDPR*	GGATGCCTAGAGCTGCCTCAGCTAGGTAGATTCACCCTGCTAGATCCCCGCTGA
P135-6	PY04387	H2-Kd	IYQTKINTI	18.37	VEKKIYQTKINTIQRFF*	GTAGAGAAAAAAATCTACCAGACTAAGATAAACACCATCCAAAGGTTCTTTTGA
P135-7	PY04387	H2-Kd	GYQKMLTPM	22.48	AKNDGYQKMLTPMQGVF	GCTAAAAATGACGGCTACCAGAAGATGCTGACCCCTATGCAGGGGGTGAGGTGA
P135-8	PY04387	H2-Kd	NYSSLTYTI	26.08	QFDRNYSSLTYTIQDAG*	CAATTTGATCGTAACTATAGTAGCCTGACCTACACCATCCAAGATGCTGGATGA
P135-9	PY04387	H2-Ld	LPYYNPYLM	14.33	DVDGLPYYNPYLMGFKQ'	GATGTAGATGGGCTGCCTTACTATAACCCTTACCTGATGGGGTTTAAGCAGTGA
P135-10	PY04390	H2-Kd	SYLGLYFSI	4.51	YPESSYLGLYFSIFGSG*	TACCCTGAGTCTAGCTACCTAGGCCTGTACTTTAGCATCTTTGGATCTGGATGA
P136-1	PY04390	H2-Kd	KYLYMKNKL	13.46	SQSGKYLYMKNKLPNNI*	AGCCAGTCAGGTAAGTACCTGTACATGAAGAATAAGCTGCCTAATAATATCTGA
P136-2	PY04390	H2-Kd	YYIFRINLL	13.87	LLLTYYIFRINLLLVVG*	CTGCTTCTAACCTACTACATCTTTAGAATAAACCTGCTGCTAGTAGTAGGATGA
P136-3	PY04390	H2-Kd	KYIYLAEIL	22.83	RWFFKYIYLAEILESQW*	CGGTGGTTCTTTAAGTACATCTACCTAGCTGAGATCCTAGAGTCCCAGTGGTGA
P136-4	PY04437	H2-Kd	RYFNDKTII	4.2	QFKKRYFNDKTIICGNE*	CAGTTTAAGAAGAGATACTTTAATGATAAGACCATAATCTGTGGTAATGAGTGA
P136-5	PY04437	H2-Kd	YYFGSKDNI	4.95	AMSKYYFGSKDNITSDM*	GCTATGTCTAAGTACTACTTCGGTAGTAAGGATAACATAACTAGTGATATGTGA
P136-6	PY04437	H2-Kd	SYLKNAPII	5.38	TSFVSYLKNAPIISVED*	ACTAGCTTTGTGAGCTACCTGAAGAACGCCCCTATAATAAGTGTAGAAGACTGA
P136-7	PY04437	H2-Kd	KYIPSLAYM	6.74	GNFRKYIPSLAYMALED*	GGTAATTTTAGAAAGTACATCCCTAGCCTAGCCTACATGGCCTTAGAAGACTGA
P136-8	PY04437	H2-Kd	SYIHKKNNI	14.48	FEHTSYIHKKNNIRKVS*	TTTGAACACACTAGCTACATCCATAAGAAGAATAACATAAGGAAAGTGTCCTGA
P136-9	PY04437	H2-Kd	KYYKKNEEI	18.15	TEVEKYYKKNEEIQEVG*	ACTGAAGTAGAGAAGTACTATAAGAAGAATGAGGAGATCCAGGAGGTAGGATGA
P136-10	PY04437	H2-Kd	AYMTNSYHV	43	FYAQAYMTNSYHVQDRF'	TTCTACGCCCAGGCCTACATGACTAATAGCTACCACGTGCAGGATAGGTTCTGA
P137-1	PY04445	H2-Kd	IYFKYEQNI	19.25	SPTLIYFKYEQNIFKCF*	AGTCCAACACTGATCTACTTTAAGTATGAGCAGAACATCTTTAAGTGCTTTTGA
P137-2	PY04447	H2-Kd	HYFKSNTYM	18.85	EDPLHYFKSNTYMEIKS*	GAAGATCCTTTGCACTACTTTAAGAGTAACACCTACATGGAGATAAAGTCCTGA
P137-3	PY04447	H2-Kd	IYNEYDSNI	21.72	PSTEIYNEYDSNIFVNQ*	CCTAGCACTGAAATCTATAATGAGTATGATAGTAACATCTTCGTGAACCAGTGA
P137-4	PY04459	H2-Kd	YYMFLQHNL	5.69	PSVTYYMFLQHNLRPSA*	CCTTCAGTAACATACTACATGTTCCTGCAGCATAACCTGAGACCTAGCGCCTGA
P137-5	PY04459	H2-Kd	KYIILYSNI	6.81	YSNYKYIILYSNIRLMG*	TACTCTAACTATAAGTACATAATCCTGTATAGTAACATAAGGCTGATGGGATGA
P137-6	PY04459	H2-Kd	FYNWTIIGI	13.73	RASLFYNWTIIGIDDIL*	CGGGCTAGCCTGTTCTATAACTGGACCATAATAGGCATAGATGACATTCTGTGA
P137-7	PY04459	H2-Kd	LYYYKHSSI	14.59	FEEWLYYYKHSSIFGLI*	TTTGAAGAGTGGCTGTACTACTATAAGCATAGTAGCATCTTCGGACTAATCTGA
P137-8	PY04459	H2-Kd	SYKNNDSYL	18.52	KKGTSYKNNDSYLLFPR*	AAAAAGGGGACTAGCTATAAGAATAATGATAGCTACCTGTTGTTTCCTAGATGA
P137-9	PY04459	H2-Kd	KYKHGTNLL	19.8	PAGMKYKHGTNLLSIES*	CCTGCTGGCATGAAGTATAAGCACGGCACTAACCTGCTGAGCATAGAGAGCTGA
P137-10	PY04459	H2-Kd	RYLNEKETI	20.41	NSADRYLNEKETIDHSQ*	AATTCTGCTGATAGATACCTGAATGAGAAGGAGACCATAGACCATTCTCAATGA
P138-1	PY04459	H2-Kd	SYIKNTDYV	29.74	TKVQSYIKNTDYVHDHE*	ACTAAGGTTCAAAGCTACATAAAGAACACTGACTACGTGCATGATCATGAATGA
P138-2	PY04459	H2-Kd	TYIFDKNYL	30.65	NCGDTYIFDKNYLTYGK*	AACTGCGGTGACACCTACATCTTTGATAAGAACTACCTGACCTACGGTAAATGA
P138-3	PY04459	H2-Kd	SYLGYRLIL	38.74	ILVGSYLGYRLILKAEK*	ATTCTAGTAGGTAGCTACCTAGGCTATAGACTGATCCTGAAAGCTGAGAAGTGA
P138-4	PY04459	H2-Kd	SYSINQAFL	40.47	KSKRSYSINQAFLEFQS*	AAATCTAAGAGGAGCTATAGCATAAACCAGGCCTTCCTAGAGTTCCAAAGCTGA
P138-5	PY04474	H2-Kd	LYNIVTHNI	29.24	NSQLLYNIVTHNIKVWA*	AATAGTCAGCTCCTGTATAACATAGTGACCCATAACATAAAGGTGTGGGCCTGA
P138-6	PY04474	H2-Kd	KFASRLWHI	48.52	SSILKFASRLWHIEQIL*	TCATCTATTCTGAAGTTCGCTAGTAGACTGTGGCACATAGAGCAGATCCTGTGA
P138-7	PY04495	H2-Kd	KFISINNNI	33.74	SRGKKFISINNNILDGI*	AGTAGGGGTAAGAAGTTCATAAGCATAAATAATAACATCCTAGATGGGATCTGA
P138-8	PY04496	H2-Kd	KYMITSGFL	14.38	LKLAKYMITSGFLQHYT*	CTGAAGCTAGCTAAGTACATGATAACTAGCGGCTTCCTGCAGCACTACACATGA
P138-9	PY04499	H2-Kd	YYQAMSNLI	2.8	WQETYYQAMSNLIAYDK*	TGGCAGGAGACTTACTACCAGGCCATGAGTAACCTGATAGCCTATGATAAGTGA
P138-10	PY04499	H2-Kd	KYIKIPLTI	4.58	TVPAKYIKIPLTIREPC*	ACGGTTCCTGCTAAGTACATAAAGATCCCTCTGACCATCCGTGAGCCTTGTTGA
P139-1	PY04499	H2-Kd	RYYQAMSNL	7.15	TLRGRYYQAMSNLKCKL*	ACACTGAGGGGTAGATACTACCAGGCCATGAGTAACCTGAAATGTAAGCTGTGA
P139-2	PY04499	H2-Kd	KYYNHQNGL	8.03	RDKEKYYNHQNGLMGGF	AGAGATAAGGAAAAGTACTATAACCACCAGAACGGCCTGATGGGCGGGCGGTGA
P139-3	PY04499	H2-Kd	HYNFVYNKI	18.04	EFSQHYNFVYNKIFLSE*	GAATTCTCTCAGCACTATAACTTCGTGTATAATAAGATCTTCCTCTCTGAATGA
P139-4	PY04499	H2-Kd	KYMDKYFSV	23.52	SNGYKYMDKYFSVSATI*	AGTAACGGATATAAGTACATGGATAAGTACTTTAGCGTGAGCGCAACCATCTGA
P139-5	PY04499	H2-Kd	KYILLEDVI	45.64	HLPPKYILLEDVITPLQ*	CATCTCCCGCCTAAGTACATCCTGCTAGAGGACGTGATAACCCCTCTCCAGTGA
P139-6	PY04499	H2-Kd	SYNKKSNII	46.02	GLESSYNKKSNIIGNED*	GGCCTAGAGAGTAGCTATAATAAGAAGAGTAACATAATAGGTAATGAAGACTGA
P139-7	PY04499	H2-Ld	SPNNEFHTF	41.65	RDIDSPNNEFHTFTSQM*	CGTGATATAGATAGCCCTAATAATGAGTTCCACACCTTCACTAGCCAGATGTGA
P139-8	PY04500	H2-Kd	KYLEEKYSI	10.41	GLPLKYLEEKYSISYDV*	GGATTGCCCTTGAAGTACCTAGAGGAGAAGTATAGCATAAGCTATGATGTATGA
P139-9	PY04507	H2-Kd	KYNIRTLPI	29.15	PLPGKYNIRTLPIRTAE*	CCATTGCCAGGTAAGTATAACATAAGAACCCTGCCTATCCGCACCGCTGAATGA
P139-10	PY04546	H2-Kd	RYIEFCLYL	22.46	GGWFRYIEFCLYLDQLR*	GGGGGCTGGTTTAGATACATAGAGTTCTGCCTGTACCTAGATCAGCTGAGGTGA
P140-1	PY04546	H2-Kd	NYISIDYFI	28.79	PQVTNYISIDYFILHVF*	CCACAAGTGACTAACTACATAAGCATAGACTACTTCATCTTACATGTCTTCTGA
P140-2	PY04551	H2-Kd	KWYQMLHSI	4.83	AHALKWYQMLHSIEAYT*	GCCCATGCTTTGAAGTGGTACCAGATGCTGCATAGCATAGAGGCTTATACCTGA
P140-3	PY04605	H2-Kd	KYYPDFTSV	5.48	KNISKYYPDFTSVQQCL*	AAAAACATATCTAAGTACTACCCTGACTTCACTAGCGTGCAGCAATGCTTGTGA
P140-4	PY04605	H2-Kd	KYFVSTGFL	6.67	VKPLKYFVSTGFLVKGS*	GTGAAGCCCTTGAAGTACTTCGTGAGCACCGGCTTCCTAGTGAAGGGGTCCTGA
P140-5	PY04610	H2-Kd	LYGPTQTTI	8.46	MDLELYGPTQTTITLKL*	ATGGATTTAGAACTGTACGGCCCTACCCAGACCACCATAACTCTGAAACTCTGA
P140-6	PY04610	H2-Kd	NYINNKLEI	13.42	RRRENYINNKLEIEPIE*	CGTAGGAGGGAGAACTACATAAATAATAAGCTAGAGATAGAGCCCATAGAATGA
P140-7	PY04610	H2-Kd	SMINNNSMI	17.25	VKEPSMINNNSMILPES*	GTGAAAGAGCCTAGCATGATAAATAATAATAGCATGATCCTGCCTGAGAGCTGA
P140-8	PY04610	H2-Kd	SMINNNSMI	17.25	KSAFSMINNNSMIACLY*	AAGTCTGCTTTTAGCATGATAAATAATAATAGCATGATAGCCTGTCTCTACTGA
P140-9	PY04610	H2-Kd	YYQKILVII	17.27	YLVYYYQKILVIIKECE*	TATCTAGTCTATTACTACCAGAAGATCCTAGTGATAATAAAAGAATGTGAGTGA
P140-10	PY04610	H2-Kd	SMINNNSLI	18.42	TVIGSMINNNSLIALQL*	ACGGTAATAGGTAGCATGATAAATAATAATAGCCTGATAGCCCTGCAACTATGA
P141-1	PY04610	H2-Kd	SMINNNNMI	26.41	LNAYSMINNNNMIGPIM*	CTGAACGCTTATAGCATGATAAATAATAATAACATGATAGGACCAATAATGTGA
P141-2	PY04648	H2-Kd	LYYYYLQVI	25.6	DKGALYYYLQVIQMYL*	GATAAAGGCGCTCTGTACTACTACTACCTGCAGGTGATCCAAATGTATCTCTGA
P141-3	PY04648	H2-Kd	YQLKYIFYI	46.69	ETYSYQLKYIFYILKGH*	GAGACGTACTCCTACCAGCTGAAGTACATCTTCTACATCCTGAAAGGGCATTGA
P141-4	PY04652	H2-Kd	YYYSKRGII	46.74	MCLWYYYSKRGIIGMGG*	ATGTGCCTTTGGTACTACTATAGTAAGAGAGGCATAATAGGCATGGGAGGCTGA
P141-5	PY04657	H2-Kd	AYSPLISRL	25.71	AGQIAYSPLISRLVMLQ*	GCAGGGCAGATAGCCTATAGCCCTCTGATAAGTAGACTAGTAATGCTGCAGTGA
P141-6	PY04670	H2-Kd	GYSYVSTSI	9.47	EYAWGYSYVSTSIQSTP*	GAATACGCCTGGGGCTATAGCTACGTGAGCACTAGCATCCAATCCACCCCGTGA
P141-7	PY04670	H2-Kd	KYNNNSVQL	11.3	MYIEKYNNNSVQLQEQY*	ATGTACATAGAGAAGTATAATAATAATAGCGTGCAGCTGCAAGAGCAATATTGA
P141-8	PY04670	H2-Kd	KHFAMHSTL	19.27	QYCYKHFAMHSTLFVLA*	CAGTACTGTTATAAGCACTTCGCCATGCATAGCACCCTGTTCGTACTAGCATGA
P141-9	PY04670	H2-Kd	FYISSLKNL	19.47	FWYPFYISSLKNLLIGF*	TTTTGGTATCCATTCTACATAAGTAGCCTGAAGAACCTGCTAATAGGGTTCTGA
P141-10	PY04670	H2-Kd	IYLCYSNFL	46.82	GNVWIYLCYSNFLRDRG*	GGTAATGTGTGGATCTACCTGTGCTATAGTAACTTCCTGAGAGATAGGGGCTGA

P142-1	PY04689	H2-Kd	KYKDTTNSI	9.73	GAGQKYKDTTNSIQPTQ* GGGGCAGGGCAGAAGTATAAGGACACCACTAATAGCATCCAACCGACTCAGTGA
P142-2	PY04689	H2-Kd	FYVDNDSEI	16.44	PPAKFYVDNDSEICKGP* CCTCCTGCTAAGTTCTACGTAGATAATGATAGTGAAGGGACCATGA
P142-3	PY04691	H2-Kd	YYSHIESVI	7.09	AVGLYYSHIESVIDSLG* GCCGTAGGCCTCTACTATAGCCACATAGAGAGCGTGATAGATTCTCTAGGATGA
P142-4	PY04691	H2-Kd	KYIKKQNLI	10.34	PPSEKYIKKQNLITVME* CCCCCTAGTGAGAAGTACATAAAGAAGCAGAACCTGATAACGGTGATGGAGTGA
P142-5	PY04691	H2-Kd	NYGTTNSTI	21.37	LSAYNYGTTNSTIEGSD* CTGTCAGCTTATAACTACGGCACCACTAATAGCACCATAGAAGGTTCTGATTGA
P142-6	PY04734	H2-Kd	TFIRSCQYI	40.7	TERVTFIRSCQYIIHGE* ACTGAACGCGTGACCTTCATAAGAAGCTGCCAGTACATAATACACGGTGAATGA
P142-7	PY04750	H2-Kd	YYYPLYNII	3.68	GSTVYYYPLYNIIVREH* GGCTCTACAGTGTACTACTACCCTCTGTATAACATAATAGTCCGTGAACACTGA
P142-8	PY04750	H2-Kd	IYITMLHRI	4.22	WAESIYITMLHRISLLY* TGGGCTGAGAGTATCTACATAACCATGCTGCATAGAATCTCTCTCCTTTATTGA
P142-9	PY04750	H2-Kd	KYLGKICTI	8.17	GQMLKYLGKICTIQGDM* GGTCAGATGCTGAAGTACCTAGGTAAGATCTGCACCATCCAGGGTGACATGTGA
P142-10	PY04750	H2-Kd	FYYYPLYNI	11.76	EQFKFYYYPLYNIVFYV* GAGCAATTTAAGTTCTACTACTACCCTCTGTATAACATAGTGTTTTATGTGTGA
P143-1	PY04750	H2-Kd	FYFFYFKEI	24.2	MEDSFYFFYFKEIVENM* ATGGAAGATAGTTTCTACTTCTTCTACTTTAAGGAGATAGTAGAAAATATGTGA
P143-2	PY04750	H2-Kd	SYIDKFDRL	32.73	LVTLSYIDKFDRLLQHA* CTAGTAACACTGAGCTACATAGATAAGTTTGATAGACTGCTGCAGCACGCTTGA
P143-3	PY04754	H2-Kd	KYHPTCSLL	4.7	QLARKYHPTCSLLIDVK* CAACTAGCACGTAAGTACCACCCTACCTGTAGCCTGCTGATAGACGTGAAATGA
P143-4	PY04754	H2-Kd	SYISNEETI	5.87	IEATSYISNEETITCQK* ATAGAGGCCACTAGCTACATAAGTAATGAGGAGACCATAACATGCCAAAAGTGA
P143-5	PY04754	H2-Kd	RYNYYSYYI	12.01	VFGRRYNYYSYYIVQGT* GTCTTTGGACGTAGATATAACTACTATAGCTACTACATAGTGCAGGGCACGTGA
P143-6	PY04754	H2-Kd	YYRNNRVEI	29.06	MKDMYYRNNRVEIKYQS* ATGAAGGACATGTACTATAGAAATAATAGAGTAGAGATAAAGTACCAGTCTTGA
P143-7	PY04754	H2-Kd	VYLLSESSL	38.66	SLMKVYLLSESSLQRLQ* TCCCTAATGAAAGTGTACCTGCTGAGTGAGAGTAGCCTGCAGCGTCTCCAATGA
P143-8	PY04757	H2-Kd	KYISADVGL	26.38	MQRFKYISADVGLAERP* ATGCAGCGATTTAAGTACATAAGCGCTGACGTAGGCCTAGCTGAGAGGCCATGA
P143-9	PY04757	H2-Kd	KYLDLVGNL	44.14	KFYLKYLDLVGNLMQTE* AAATTTTACTTGAAGTACCTAGACCTAGTAGGTAACCTGATGCAGACTGAGTGA
P143-10	PY04760	H2-Kd	SYTLLVCSI	35.26	PQQESYTLLVCSIGRCM* CCTCAACAGGAAAGCTACACCCTGCTAGTGTGTAGCATAGGTAGGTGTATGTGA
P144-1	PY04766	H2-Kd	IYFKNNYNI	7.26	IVGGIYFKNNYNIGTVG* ATAGTAGGGGGCATCTACTTTAAGAATAACTATAACATAGGGACTGTAGGCTGA
P144-2	PY04766	H2-Kd	VYRPSCCYL	30.6	YDAAVYRPSCCYLWYPI* TATGATGCTGCCGTGTATAGACCTAGCTGCTGCTACCTGTGGTACCCCATTTGA
P144-3	PY04766	H2-Kd	SFIQNFLVI	32.54	SRVGSFIQNFLVIKHEM* TCTAGGGTAGGTAGCTTCATCCAGAACTTCCTAGTGATAAAACATGAAATGTGA
P144-4	PY04766	H2-Kd	VHFNGITSI	32.87	ANLGVHFNGITSIQPRG* GCTAACCTAGGCGTGCACTTTAACGGCATAAGCATCCAGCCTAGAGGGTGA
P144-5	PY04792	H2-Kd	YYFYIFSLI	3.99	RYLSYYFYIFSLIGWGA* CGATACCTGTCTTACTACTTCTACATCTTTAGCCTGATAGGGTGGGGCGCTTGA
P144-6	PY04792	H2-Kd	SYYFYIFSL	6.23	SLQRSYYFYIFSLFFAP* AGCCTACAGAGGAGCTACTACTTCTACATCTTTAGCCTGTTCTTCGCCCCTTGA
P144-7	PY04792	H2-Kd	LYNENKDYI	20.6	RVFFLYNENKDYIGWDD* AGAGTATTTTTTCTGTATAATGAGAATAAGGACTACATAGGATGGGATGATTGA
P144-8	PY04792	H2-Kd	KYISADVGL	26.38	LVMRKYISADVGLPALE* CTAGTGATGCGTAAGTACATAAGCGCTGACGTAGGCCTGCCGGCGTTAGAATGA
P144-9	PY04792	H2-Kd	KYLDLVGNL	44.14	EVGGKYLDLVGNLSLRV* GAGGTAGGTGGTAAGTACCTAGACCTAGTAGGTAACCTGTCCCTGAGGGTGTGA
P144-10	PY04793	H2-Kd	KFMFNTSII	8.26	TGLLKFMFNTSIIENLA* ACAGGCCTGCTGAAGTTCATGTTTAACACTAGCATAATAGAAAACCTAGCTTGA
P145-1	PY04793	H2-Kd	KEIPKTMSI	35.89	ATSGKEIPKTMSIELCL* GCCACCTCCGGTAAGGAGATCCCTAAGACCATGAGCATAGAGCTGTGCCTGTGA
P145-2	PY04813	H2-Kd	KQIPNQNTL	22.27	METLKQIPNQNTLYSET* ATGGAAACCCTGAAGCAGATCCCTAACCAGAACACCCTGTATAGTGAAACTTGA
P145-3	PY04813	H2-Kd	KYHKNLNNM	32.11	LLLDKYHKNLNNMLAFS* CTTCTGCTAGATAAGTACCATAAGAACCTGAATAACATGCTAGCTTTCTCCTGA
P145-4	PY04813	H2-Kd	HYSKANFSL	43.61	IKSSHYSKANFSLAQSL* ATAAAGAGTTCACACTATAGTAAGGCTAACTTTAGCCTAGCCCAGAGTTTGTGA
P145-5	PY04813	H2-Kd	NYNKNNNFL	48.57	GLLRNYNKNNNFLRGSC* GGTCTGTTGCGTAACTATAATAAGAATAATAACTTCCTGAGGGGTAGCTGTTGA
P145-6	PY04831	H2-Kd	NYIENHSML	8.37	IRRGNYIENHSMLAYCL* ATTCGTCGCGGTAACTACATAGAGAACCATAGCATGCTAGCTTATTGCCTCTGA
P145-7	PY04831	H2-Kd	FYFFIIQNI	10.05	KELAFYFFIIQNILNQN* AAAGAACTAGCCTTCTACTTCTTCATAATCCAGAACATCCTGAACCAGAACTGA
P145-8	PY04831	H2-Kd	NYFCHATNL	13.07	INKENYFCHATNLSLRP* ATAAATAAGGAAAACTACTTCTGCCACGCCACTAACCTGTCTTTGAGACCGTGA
P145-9	PY04831	H2-Kd	IYNGVVTHL	14.57	LCNGIYNGVVTHLRHSD* CTGTGTAATGGAATCTATAACGGCGTAGTGACCCACCTGAGACACTCTGACTGA
P145-10	PY04831	H2-Kd	SQIKNIFAI	14.71	VQVFSQIKNIFAILRPH* GTACAGGTCTTTAGCCAGATAAAGAACATCTTCGCCATCCTGCGCCCTCATTGA
P146-1	PY04831	H2-Kd	YYYTQLNLL	15.28	APIDYYYTQLNLLNDSC* GCTCCCATAGACTACTACACACCCAGCTGAACCTGCTGAATGACTCCTGCTGA
P146-2	PY04831	H2-Kd	LYYNFKSII	16.68	LTTLLYYNFKSIIQTKS* CTAACTACCCTCCTGTACTATAACTTTAAGAGCATAATCCAGACTAAAAGCTGA
P146-3	PY04831	H2-Kd	KYYYTQLNL	18.67	VEKGKYYYTQLNLACKP* GTAGAGAAGGGTAAGTACTACTACACCCAGCTGAACCTAGCATGTAAACCCTGA
P146-4	PY04831	H2-Kd	KYYTENGQI	19.77	LRTSKYYTENGQIVNRI* CTACGCACTAGTAAGTACTACACTGAGAACGGCCAGATAGTGAATAGGATCTGA
P146-5	PY04831	H2-Kd	KYHSKKHHI	23.99	AYFVKYHSKKHHIEPGE* GCTTACTTCGTGAAGTACCATAGTAAGAAGCACCACATAGAGCCCGGTGAGTGA
P146-6	PY04831	H2-Kd	YYNCIKTDI	25.37	SQHNYYNCIKTDIRSVL* TCCCAGCATAATTACTATAACTGCATAAAGACTGACATCCGCTCTGTGCTCTGA
P146-7	PY04831	H2-Kd	FYYELLINI	25.45	WRNTFYYELLINILSSS* TGGAGAAACACTTTCTACTATGAGCTGCTGATAAACATCCTGAGTAGTAGCTGA
P146-8	PY04831	H2-Kd	YYIISRINL	25.97	LTSPYYIISRINLQGRG* TTGACCTCTCCCTACTACATAATAAGTAGAATAAACCTGCAGGGTAGGGGGTGA
P146-9	PY04831	H2-Kd	FYYNDNLNL	30.6	PSGDFYYNDNLNLKQDI* CCTAGCGGTGACTTCTACTATAATGATAACCTGAACCTGAAACAGGATATCTGA
P146-10	PY04831	H2-Kd	YYINILKLL	34.36	PRLLYYINILKLLKTFD* CCACGCTTGCTGTACTACATAAACATCCTGAAGCTGCTGAAGACTTTTGACTGA
P147-1	PY04831	H2-Kd	IYVELFDSL	34.67	VRNGIYVELFDSLNTAW* GTGCGTAATGGGATCTACGTAGAGCTGTTTGATAGCCTGAACACCGCGTGGTGA
P147-2	PY04831	H2-Kd	TYNYCLTIL	35.91	RKQLTYNYCLTILRVFA* CGTAAGCAACTGACCTATAACTACTGCCTGACCATCCTGAGAGTATTTGCCTGA
P147-3	PY04831	H2-Kd	YYHKYLKYL	38.31	PRAIYYHKYLKYLFRMK* CCACGCGCTATCTACTACCATAAGTACCTGAAGTACCTGTTTAGGATGAAGTGA
P147-4	PY04831	H2-Kd	IYIETKRNI	44.11	HATAIYIETKRNINVFR* CATGCCACAGCAATCTACATAGAGACTAAGAGAAACATAAATGTGTTTCGATGA
P147-5	PY04837	H2-Kd	YYIFSFSLI	2.5	PAGAYYIFSFSLINTHP* CCGGCCGGAGCCTACTACATCTTTAGCTTTAGCCTGATAAACACTCACCCTTGA
P147-6	PY04837	H2-Kd	YYSNNHSNI	2.68	TRHKYYSNNHSNISSDS* ACACGTCATAAGTACTATAGTAATAACCATAGTAACATAAGCTCTGATAGTTGA
P147-7	PY04837	H2-Kd	YYFLLFSQI	5.87	CSHDYYFLLFSQITISH* TGTAGCCATGATTACTACTTCCTGCTGTTTAGCCAGATAACTATCTCTCACTGA
P147-8	PY04837	H2-Kd	FYLWPIELI	29.78	HVFFFYLWPIELISFCC* CATGTCTTCTTCTTCTACCTGTGGCCTATAGAGCTGATCTCATTTTGTTGCTGA
P147-9	PY04837	H2-Kd	SYSDLREII	35.01	MEGTSYSDLREIISAIV* ATGGAAGGCACTAGCTATAGTGACCTGAGAGAGATAATCTCAGCCATAGTTTGA
P147-10	PY04837	H2-Ld	LPFTFFIYL	39.74	PRKALPFTFFIYLSSAQ* CCTAGAAAGGCTCTGCCTTTCACCTTCTTCATCTACCTGTCTAGTGCTCAGTGA
P148-1	PY04854	H2-Kd	KYYFYKSVI	4.81	CEGLKYYFYKSVIHTEP* TGTGAGGGACTGAAGTACTACTTCTATAAGAGCGTGATCCATACTGAGCCATGA
P148-2	PY04854	H2-Kd	RYNNSKEYI	8.71	LARTRYNNSKEYIVPLE* CTAGCACGTACTAGATATAATAATAGTAAGGAGTACATAGTTCCCCTAGAGTGA
P148-3	PY04854	H2-Kd	IYNENINNI	10.35	GRFLIYNENINNIVHKQ* GGTAGATTCTTAATCTATAATGAGAACATAAATAACATAGTACATAAACAGTGA
P148-4	PY04854	H2-Kd	LYNNSKVEI	15.76	GLKPLYNNSKVEIVKGC* GGCTTGAAGCCACTGTATAATAATAGTAAGGTAGAGATAGTGAAGGGCTGTTGA
P148-5	PY04854	H2-Kd	KLINNYNSI	21.12	CSHLKLINNYNSIQGNG* TGTAGCCATTTGAAGCTGATAAATAACTATAATAGCATCCAGGGTAACGGTTGA
P148-6	PY04854	H2-Kd	FYVSPILNI	28.79	SLAGFYVSPILNIGDAV* TCTCTAGCTGGCTTCTACGTGAGCCCTATCCTGAACATAGGTGATGCCGTATGA
P148-7	PY04854	H2-Kd	VYTNNNTNL	42.93	KFGKVYTNNNTNLVKLF* AAATTCGGTAAGGTGTACACTAATAATAACACTAACCTAGTGAAGCTGTTTTGA
P148-8	PY04854	H2-Kd	KYLNNDIDI	45.11	VAYPKYLNNDIDIGSPM* GTAGCCTATCCTAAGTACCTGAATAATGACATAGACATAGGCTCCCCTATGTGA
P148-9	PY04854	H2-Ld	SPILNIYSL	9.97	LSTPSPILNIYSLPGLL* CTCTCGACTCCTAGCCCTATCCTGAACATCTATAGCCTGCCTGGGCTGTTGTGA
P148-10	PY04895	H2-Kd	CYTYVVEFI	32.46	FPHPCYTYVVEFISITA* TTCCCGCATCCCTGCTACACCTACGTAGTAGAGTTCATCTCAATAACCGCCTGA
P149-1	PY04895	H2-Kd	IYISYIVGL	41.81	TKQVIYISYIVGLEAGH* ACTAAGCAGGTAATCTACAATAAGCTACATAGTAGGCCTAGAGGCCGGACATTGA
P149-2	PY04895	H2-Kd	FYSHVGWLL	44.99	VRSEFYSHVGWLLILTI* GTGAGAAGTGAATTCTATAGCCACGTAGGCTGGCTGCTGATATTGACAATTTGA
P149-3	PY04895	H2-Kd	KYLNINTRV	48.97	GLVWKYLNINTRVSMGR* GGGCTAGTATGGAAGTACCTGAACATAAACACTAGAGTGTCAATGGGTAGATGA
P149-4	PY04912	H2-Kd	YYLKTKGNL	28.3	ECVEYYLKTKGNLTGPE* GAATGTGTAGAGTACTACCTGAAGACTAAGGGTAACCTGACTGGACCTGAGTGA
P149-5	PY04917	H2-Kd	IYQNLILNI	34.03	KIGLIYQNLILNIRTLR* AAGATAGGACTGATCTACCAGAACCTGATCCTGAACATAAGAACACTGAGATGA
P149-6	PY04917	H2-Ld	NPIFNHYLF	33.84	LEAKNPIFNHYLFKCAR* CTAGAGGCTAAAAACCCTATCTTTAACCACTACCTGTTTAAATGTGCTAGATGA
P149-7	PY04921	H2-Ld	HPLPNLYIM	8.33	FDVKHPLPNLYIMPELL* TTTGATGTGAAGCACCCTCTGCCTAACCTGTACATAATGCCTGAACTTCTGTGA
P149-8	PY04935	H2-Kd	KYLKNNTNI	4.03	RQSHKYLKNNTNILGGY* CGACAATCACATAAGTACCTGAAGAATAACACTAACATCCTAGGCGGGTACTGA
P149-9	PY04935	H2-Kd	KYFSYFQCI	5.86	SLLRKYFSYFQCIFGDT* AGTCTCCTCCGTAAGTACTTTAGCTACTTCCAGTGCATCTTTGGTGACACCTGA
P149-10	PY04935	H2-Kd	NYMVNNTNI	5.88	VGGPNYMVNNTNIEHQR* GTAGGAGGGCCTAACTACATGGTGAATAACACTAACATAGAACATCAGAGGTGA
P150-1	PY04935	H2-Kd	KYINYYYGI	6.11	SLIAKYINYYYGITGRR* AGTCTAATAGCTAAGTACATAAACTACTACTACGGCATAACCGGTAGAAGATGA
P150-2	PY04935	H2-Kd	VYCKTYSFL	30.19	GLPKVYCKTYSFLSFAT* GGGCTCCCTAAGGTGTACTGTAAGACCTATAGCTTCCTGTCCTTTGCCACATGA
P150-3	PY04935	H2-Kd	YYEYSINML	44.02	AGEPYYEYSINMLQTKA* GCTGGTGAGCCATACTATGAGTATAGCATAAACATGCTGCAAACTAAGGCATGA
P150-4	PY04937	H2-Kd	YYNDAVNKL	34.69	KLLAYYNDAVNKLSLQV* AAGTTGTTAGCCTACTATAATGACGCCGTGAATAAGCTGTCATTGCAGGTGTGA
P150-5	PY04969	H2-Kd	SYSNNYLAI	5.62	DDRASYSNNYLAILVLC* GATGATAGGGCTAGCTATAGTAATAACTACCTAGCCATCCTAGTCCTGTGCTGA
P150-6	PY04969	H2-Kd	YYNFLKPSL	14.36	QPLPYYNFLKPSLFLER* CAGCCTTTGCCCTACTATAACTTCCTGAAGCCTAGCCTGTTCCTAGAGAGGTGA
P150-7	PY04969	H2-Kd	NYLNIKSNI	25.08	QQNSNYLNIKSNILASE* CAGCAAAATAGTAACTACCTGAACATAAAGAGTAACATCCTAGCTAGTGAGTGA
P150-8	PY04969	H2-Kd	NYLTLYSGI	28.22	HKYTNYLTLYSGIMSFK* CATAAGTACACTAACTACCTGACCCTGTATAGCGGCATAATGAGCTTTAAGTGA
P150-9	PY04969	H2-Kd	NYNGWFSLL	39.32	NRNSNYNGWFSLLLVTM* AATAGAAACTCTAACTATAACGGCTGGTTTAGCCTGCTGCTAGTGACGATGTGA
P150-10	PY04969	H2-Kd	KLINASSSI	44.24	DAGAKLINASSSILAAK* GACGCAGGGGCTAAGCTGATAAACGCTAGTAGTAGCATCCTAGCAGCTAAATGA
P151-1	PY04985	H2-Kd	YYVCEKNII	26.56	PLKKYYVCEKNIIYMGN* CCGCTGAAGAAGTACTACGTGTGTGAGAAGAACATAATCTACATGGTGAATTGA
P151-2	PY04990	H2-Kd	HYNNTFFPL	7.33	ANGNHYNNTFFPLSILK* GCTAATGGTAACCACTATAATAACACCTTCTTCCCTCTGTCTATCTTAAAATGA
P151-3	PY05001	H2-Kd	TYFSFSYFL	28.06	RPIRTYFSFSYFLPKQK* AGGCCAATAAGAACCTACTTTAGCTTTAGCTACTTCCTGCCTAAACAGAAGTGA
P151-4	PY05002	H2-Kd	KYANTSRTI	13.39	WKRMKYANTSRTIKLEQ* TGGAAACGGATGAAGTACGCTAACACTAGTAGAACCATAAAGCTAGAACAGTGA
P151-5	PY05002	H2-Kd	SYIYNKIKL	19.9	AGVTSYIYNKIKLRPKR* GCGGGGGTGACTAGCTACATCTATAATAAGATAAAGCTGAGGCCTAAAAGATGA
P151-6	PY05002	H2-Kd	SYINKKNEL	29.69	LYQRSYINKKNELLSRK* TTGTACCAAAGGAGCTACATAAATAAGAAGAATGAGCTGTTGTCTAGAAAGTGA
P151-7	PY05002	H2-Kd	SYLFKTGNI	45.19	KYVMSYLFKTGNIEPFV* AAGTACGTAATGAGCTACCTGTTTAAGACCGGTAACATAGAACCTTTTGTGTGA
P151-8	PY05002	H2-Kd	VFINSLSYL	47.09	TQVVVFINSLSYLEARS* ACCCAAGTAGTAGTGTTCATAAATAGCCTGAGCTACCTAGAGGCACGATCGTGA
P151-9	PY05002	H2-Ld	VPYVLRYLL	39.24	GQGPVPYVLRYLLTCRE* GGGCAGGGTCCCGTGCCTTACGTGCTGAGATACCTGCTGACCTGTCGTGAGTGA
P151-10	PY05002	H2-Ld	VPLQAHIFF	44.92	EILKVPLQAHIFFGNSL* GAAATCCTGAAGGTGCCTCTGCAGGCCCACATCTTCTTCGGTAATAGCCTTTGA
P152-1	PY05006	H2-Kd	NYFKLFPSI	8.23	LFDANYFKLFPSIVQEA* CTTTTTGATGCTAACTACTTTAAGCTGTTCCCTAGCATAGTTCAGGAGGCGTGA

P152-2	PY05006	H2-Kd	GYVNKLYSL	22.42	RFPQGYVNKLYSLVYIR*	CGTTTTCCTCAGGGCTACGTGAATAAGCTGTATAGCCTAGTGTACATAAGATGA
P152-3	PY05006	H2-Kd	YYNSETNHL	25.17	LHQPYYNSETNHLTQEL*	CTGCATCAACCCTACTATAATAGTGAGACTAACCACCTGACACAGGAACTGTGA
P152-4	PY05006	H2-Kd	FYQKKDTNI	30.07	RPLPFYQKKDTNINPST*	AGGCCTCTGCCCTTCTACCAGAAGAAGGACACTAACATAAACCCCTCCACATGA
P152-5	PY05006	H2-Kd	NYNDAYNMI	48.82	LIGYNYNDAYNMIVQDS*	TTGATAGGGTATAACTATAATGACGCCTATAACATGATAGTGCAAGATTCTTGA
P152-6	PY05008	H2-Kd	HYMGNLLDI	10.34	VVREHYMGNLLDISACQ*	GTAGTCCGTGAACACTACATGGGTAACCTGCTAGACATCTCTGCCTGTCAATGA
P152-7	PY05008	H2-Kd	SYNSDLYII	11.69	EANLSYNSDLYIIQAES*	GAAGCTAATTTAAGCTATAATAGTGACCTGTACATAATCCAAGCTGAAAGCTGA
P152-8	PY05008	H2-Kd	HYMHLKPLI	12.29	AARGHYMHLKPLIEGYN*	GCCGCTAGGGGTCACTACATGCACCTGAAGCCTCTGATAGAAGGCTATAATTGA
P152-9	PY05008	H2-Kd	MYHYGRCII	22.44	KGKNMYHYGRCIIPEKK*	AAGGGTAAGAATATGTACCACTACGGTAGATGCATAATCCCTGAAAAGAAATGA
P152-10	PY05008	H2-Kd	RYLYRHFFL	35.18	ACTLRYLYRHFFLFVML*	GCTTGCACCCTGAGATACCTGTATAGACACTTCTTCCTGTTCGTGATGCTTTGA
P153-1	PY05008	H2-Ld	LPSLAFHVF	27.25	NRRSLPSLAFHVFPDPE*	AATAGGAGGTCTCTGCCTAGCCTAGCCTTCCACGTGTTCCCTGATCCTGAGTGA
P153-2	PY05031	H2-Kd	MYNKTSFVI	16.04	VMSMMYNKTSFVILTVF*	GTAATGTCCATGATGTATAATAAGACTAGCTTCGTGATCCTAACTGTCTTTTGA
P153-3	PY05031	H2-Kd	IYYTYNQEL	22.82	ILHGIYYTYNQELAEIG*	ATCCTCCATGGTATCTACTACACCTATAACCAGGAGCTAGCTGAAATAGGGTGA
P153-4	PY05031	H2-Kd	LYFTKNTII	24	QMLKLYFTKNTIIDSVG*	CAGATGTTGAAACTGTACTTCACTAAGAACACCATAATAGACTCGGTAGGCTGA
P153-5	PY05031	H2-Kd	KYFKSLSNF	30.74	WLLFKYFKSLSNFAVTS*	TGGCTGCTCTTTAAGTACTTTAAGAGCCTGAGTAACTTCGCCGTAACTTCCTGA
P153-6	PY05031	H2-Kd	HYFNFFLKL	47.5	SDTSHYFNFFLKLYRCF*	AGTGACACATCCCACTACTTTAACTTCTTCCTGAAGCTGTATAGGTGTTTTTGA
P153-7	PY05035	H2-Kd	GYLCSHSPI	3.27	MWSRGYLCSHSPISQLY*	ATGTGGAGTAGGGGCTACCTGTGTAGCCATAGCCCTATCTCCCAGTTATATTGA
P153-8	PY05035	H2-Kd	SYMHSKLII	3.86	YCAPSYMHSKLIIKSIA*	TACTGTGCTCCTAGCTACATGCATAGTAAGCTGATAATAAAGTCGATAGCTTGA
P153-9	PY05035	H2-Kd	SYMVIAHGI	5.39	VFSTSYMVIAHGITKED*	GTGTTCTCTACTAGCTACATGGTGATAGCCCACGGCATAACTAAAGAGGACTGA
P153-10	PY05035	H2-Kd	FYMSMSLEL	5.71	GRTEFYMSMSLELCGNM	GGTAGAACTGAGTTCTACATGAGCATGAGCCTAGAGCTGTGTGGTAACATGTGA
P154-1	PY05035	H2-Kd	FYSHNIGNI	15.47	GLHHFYSHNIGNIKENR*	GGACTACACCATTTCTATAGCCATAACATAGGTAACATAAAAGAGAATAGATGA
P154-2	PY05035	H2-Kd	NYFKHITVL	16.14	GGLENYFKHITVLSYSQ*	GGAGGGCTAGAGAACTACTTTAAGCACATAACCGTGCTGTCGTATTCTCAATGA
P154-3	PY05035	H2-Kd	KYFIILPSL	19.42	QNEVKYFIILPSLPLMI*	CAAAATGAAGTGAAGTACTTCATAATCCTGCCTAGCCTGCCGCTAATGATATGA
P154-4	PY05035	H2-Kd	HYTYYNNYI	20.29	HMKSHYTYYNNYIPCMS*	CATATGAAATCACACTACACCTACTATAATAACTACATCCCCTGCATGAGCTGA
P154-5	PY05035	H2-Kd	NYISYSEVI	20.82	IRDGNYISYSEVIPWHL*	ATCCGTGACGGTAACTACATAAGCTATAGTGAGGTGATCCCATGGCACCTTTGA
P154-6	PY05035	H2-Kd	RYVNDEHSL	24.42	DSKSRYVNDEHSLHNGM	GACTCTAAAAGTAGATACGTGAATGATGAGCATAGCCTGCATAACGGAATGTGA
P154-7	PY05035	H2-Kd	FYTSFLNMI	26.92	AYDSFYTSFLNMIGDIF*	GCGTATGACTCGTTCTACACTAGCTTCCTGAACATGATAGGTGACATCTTTTGA
P154-8	PY05035	H2-Kd	SYSDLQFLI	34.63	LVGVSYSDLQFLIQVTQ*	TTAGTAGGGGTGAGCTATAGTGACCTGCAGTTCCTGATCCAGGTAACTCAGTGA
P154-9	PY05035	H2-Kd	SHWNIRTYI	37.31	KHSVSHWNIRTYIQLST*	AAGCATTCAGTGAGCCACTGGAACATAAGAACCTACATCCAGTTGAGCACTTGA
P154-10	PY05035	H2-Kd	TYIMLPFII	39.4	SCLRTYIMLPFIIRTRK*	TCCTGTTTGAGGACCTACATAATGCTGCCTTTCATAATAAGAAACCGTAAGTGA
P155-1	PY05035	H2-Kd	SFVFSHWNI	43.66	ALSGSFVFSHWNICSQA*	GCACTTTCTGGTAGCTTCGTGTTTAGCCACTGGAACATCTGTAGCCAGGCTTGA
P155-2	PY05035	H2-Kd	KYGIDKNTI	47.09	HDPQKYGIDKNTIINNL*	CATGACCCCCAGAAGTACGGCATAGATAAGAACACCATAATAAATAATCTGTGA
P155-3	PY05035	H2-Kd	KYRIYLSSL	48.79	VRSKKYRIYLSSLKKFS*	GTGAGGTCTAAGAAGTATAGAATCTACCTGAGTAGCCTGAAGAAGTTTAGCTGA
P155-4	PY05038	H2-Kd	YYIYVCAII	5.87	GSVEYYIYVCAIIEFAV*	GGTAGTGTAGAATACTACATCTACGTGTGCGCCATAATAGAGTTTGCAGTGTGA
P155-5	PY05038	H2-Kd	KYYIYVCAI	11.69	WITRKYYIYVCAIVYEN*	TGGATAACTAGGAAGTACTACATCTACGTGTGCGCCATAGTCTATGAGAACTGA
P155-6	PY05038	H2-Kd	MYAYDYIFI	47.58	SEIVMYAYDYIFIENTD*	AGTGAAATAGTGATGTACGCCTATGACTACATCTTCATAGAAAATACTGATTGA
P155-7	PY05047	H2-Kd	LYYDDHNEI	13.82	VQQLLYYDDHNEIRLYS*	GTCCAGCAGTTGCTGTACTATGATGACCATAATGAGATCCGTCTCTACTCTTGA
P155-8	PY05048	H2-Kd	RYYKGPELL	28	CGGVRYYKGPELLVLLL*	TGCGGTGGCGTGAGATACTATAAGGGCCCTGAGCTGCTAGTGCTGTTACTCTGA
P155-9	PY05049	H2-Kd	IYNVMKDII	29.98	VRWPIYNVMKDIIVSKV*	GTGAGGTGGCCTATCTATAACGTGATGAAGGACATAATAGTATCTAAAGTGTGA
P155-10	PY05063	H2-Kd	KFYSNKCEI	31.04	DHTDKFYSNKCEISRNL*	GACCACACTGATAAGTTCTATAGTAATAAGTGTGAGATCTCTCGTAATCTCTGA
P156-1	PY05063	H2-Kd	IYNFSEAEI	38.03	AGSNIYNFSEAEIGTTP*	GCCGGGTCTAATATCTATAACTTTAGTGAGGCTGAGATAGGCACCACACCGTGA
P156-2	PY05103	H2-Kd	SYLINFINL	37.33	GWPESYLINFINLGAKK*	GGTTGGCCTGAGAGCTACCTGATAAACTTCATAAACCTAGGAGCTAAAAAGTGA
P156-3	PY05129	H2-Kd	KYLYSFIDI	27.8	LTPMKYLYSFIDIRGTF*	CTGACGCCCATGAAGTACCTGTATAGCTTCATAGACATAAGGGGTACCTTCTGA
P156-4	PY05136	H2-Kd	KFISVATTL	10.81	AKAPKFISVATTLSAHM*	GCTAAAGCTCCTAAGTTCATAAGCGTAGCCACCACCCTGAGCGCACACATGTGA
P156-5	PY05136	H2-Kd	YYSDAESFL	11.91	DAEGYYSDAESFLDDDN*	GACGCTGAAGGATACTATAGTGACGCTGAGAGCTTCCTAGATGATGATAATTGA
P156-6	PY05141	H2-Kd	SYFGDVDEI	9.8	YDGASYFGDVDEIHEME*	TATGATGGAGCTAGCTACTTCGGTGACGTAGATGAGATCCATGAGATGGAGTGA
P156-7	PY05241	H2-Kd	SYHSVNSFI	2.56	AIFFSYHSVNSFIKETA*	GCCATTTTCTTTAGCTACCATAGCGTGAAGTAGCTTCATAAAGGAGACAGCTTGA
P156-8	PY05241	H2-Kd	KYFKLLGQL	14.53	LLESKYFKLLGQLEATN*	CTGCTAGAATCTAAGTACTTTAAGCTGCTAGGCCAGCTAGAGGCCACTAATTGA
P156-9	PY05241	H2-Kd	FYNEVIEEL	19.92	LSQEFYNEVIEELKFEA*	CTTTCCCAGGAGTTCTATAATGAGGTGATAGAGGAGCTGAAATTTGAGGCGTGA
P156-10	PY05248	H2-Kd	KYIYNTSII	2.21	YGAAKYIYNTSIIYQSP*	TATGGGGCTGCTAAGTACATCTATAACACTAGCATAATCTATCAGTCCCCTTGA
P157-1	PY05248	H2-Kd	YYYSYKNKI	4.82	SDKGYYYSYKNKIEQLK*	TCTGATAAAGGGTACTACATAGCTATAAGAATAAGATAGAACAGCTGAAGTGA
P157-2	PY05248	H2-Kd	SYIISKPPI	5.09	LVRLSYIISKPPICTDF*	CTAGTCCGTCTGAGCTACATAATAAGTAAGCCTCCTATCTGTACTGATTTCTGA
P157-3	PY05248	H2-Kd	KYIKILWNL	8.75	RAQEKYIKILWNLPTDM*	AGGGCTCAGGAGAAGTACATAAAGATCCTGTGGAACCTGCCCACTGATATGTGA
P157-4	PY05248	H2-Kd	SYHHLTVVI	11.64	VSNLSYHHLTVVIKAKC*	GTCTCTAACCTGAGCTACCACCACCTGACCGTAGTGATAAAAGCTAAGTGTTGA
P157-5	PY05248	H2-Kd	CYFGCIYII	20.23	ILLPCYFGCIYIIAYFD*	ATCCTGTTACCTTGCTACTTCGGCTGCATCCTACATAATAGCCTATTTTGACTGA
P157-6	PY05248	H2-Kd	KYEPIILTI	24.01	PKYWKYEPIILTIIMAV*	CCTAAGTATTGGAAGTATGAGCCTATAATCCTGACCATAATAATGGCAGTCTGA
P157-7	PY05248	H2-Kd	HYFVFLNLI	25.46	CTVSHYFVFLNLIEELS*	TGTACAGTGAGCCACTACTTCGTGTTCCTGAACCTGATAGAGGAGTTGTCTTGA
P157-8	PY05248	H2-Kd	IYYSNMALL	35.92	RVTMIYYSNMALLLALG*	CGCGTAACCATGATCTACTATAGTAACATGGCCCTGCTGCTAGCATTAGGCTGA
P157-9	PY05248	H2-Kd	YQNYNLFYI	40.89	WKERYQNYNLFYICPLR*	TGGAAAGAGAGGTACCAGAACTATAACCTGTTCTACATCTGTCCATTGAGGTGA
P157-10	PY05279	H2-Kd	SYNSIINII	8.8	VGQPSYNSIINIIGQSP*	GTAGGCCAGCCTAGCTATAATAGCATAATAAACATAATAGGGCAGAGCCCGTGA
P158-1	PY05279	H2-Kd	SYNNRCSFV	29.2	QFTDSYNNRCSFVYDST*	CAGTTCACTGATAGCTATAATAATAGATGTAGCTTCGTGTATGATTCAACATGA
P158-2	PY05328	H2-Kd	LYFHFYSKL	31.47	KIAELYFHFYSKLPVRE*	AAGATAGCTGAACTGTACTTCCACTTCTATAGTAAGCTGCCCGTGCGTGAGTGA
P158-3	PY05329	H2-Kd	SYKQMGLSI	18.32	LHKESYKQMGLSITKGC*	CTCCATAAGGAAAGCTATAAGCAGATGGGCCTGAGCATAACTAAGGGCTGTTGA
P158-4	PY05329	H2-Kd	IYYKSPNIL	21.48	PILIIYYKSPNILSRMI*	CCAATACTGATAATCTACTATAAGAGCCCTAACATCCTGAGTAGGATGATTTGA
P158-5	PY05353	H2-Kd	IYINIFHTL	5.2	SGPDIYINIFHTLSEDF*	AGTGGGCCTGATATCTACATAAACATCTTCCACACCCTGTCTGAAGACTTCTGA
P158-6	PY05353	H2-Kd	IYINNYNPL	6.15	SVQRIYINNYNPLKVLK*	AGCGTGCAGCGGATCTACATAAATAACTATAACCCTCTGAAAGTGCTGAAATGA
P158-7	PY05353	H2-Kd	MYNAQGYLI	46	VKPLMYNAQGYLIADDP*	GTGAAGCCCCTAATGTATAACGCCCAGGGCTACCTGATAGCTGATGATCCTTGA
P158-8	PY05353	H2-Kd	SFLFALCSI	46.66	PTSSSFLFALCSILAPR*	CCCACATCCTCTAGCTTCCTGTTCGCCCTGTGTAGCATCCTAGCTCCTAGGTGA
P158-9	PY05356	H2-Kd	KYTKMLQNI	5.06	KESGKYTKMLQNINSLQ*	AAAGAATCTGGTAAGTACACTAAGATGCTGCAGAACATAAATTCCCTTCAGTGA
P158-10	PY05356	H2-Kd	KQIRNMSVI	11.16	HFRPKQIRNMSVIGLDK*	CACTTCCGCCCTAAGCAGATAAGAAACATGAGCGTGATAGGCCTAGATAAATGA
P159-1	PY05356	H2-Kd	IYQTFARTI	42.24	TVLLIYQTFARTISDTK*	ACAGTCCTCCTAATCTACCAGACCTTCGCTAGAACCATAAGTGATACTAAATGA
P159-2	PY05383	H2-Kd	SYQPGFFTI	2.63	QSSHSYQPGFFTISANP*	CAGAGCTCCCATAGCTACCAGCCTGGCTTCTTCACCATAAGCGCTAATCCCTGA
P159-3	PY05383	H2-Kd	SFFFSLATI	13.58	HLKLSFFFSLATILVKL*	CACCTGAAGCTGAGCTTCTTCTTTAGCCTAGCCACCATCCTAGTGAAGCTCTGA
P159-4	PY05383	H2-Kd	KEFENINEI	31.2	LHDKKEFENINEIFDDD*	CTGCATGATAAGAAGGAGTTTGAGAACATAAATGAGATCTTTGATGATGACTGA
P159-5	PY05395	H2-Kd	FYYNDISFL	4.9	LANNFYYNDISFLTEFT*	TTAGCTAATAACTTCTACTATAATGACATAAGCTTCCTGACTGAGTTCACTTGA
P159-6	PY05395	H2-Kd	TYFYLTNLI	13.46	DPEMTYFYLTNLIPLTC*	GACCCTGAAATGACCTACTTCTACCTGACTAACCTGATCCCACTAACATGCTGA
P159-7	PY05395	H2-Kd	SYFYQVLFL	37.32	SSCLSYFYQVLFLSVRI*	TCCTCTTGCCTGAGCTACTTCTACCAGGTGCTGTTCCTGTCAGTGAGGATATGA
P159-8	PY05398	H2-Kd	NYVNNLLSL	19.04	SDYRNYVNNLLSLDLLM*	TCTGATTATCGTAACTACGTGAATAACCTGCTGAGCCTAGATCTGCTAATGTGA
P159-9	PY05398	H2-Kd	RMHPIRHHI	35.5	ELFRRMHPIRHHIINVA*	GAATTGTTTAGAAGAATGCACCCTATAAGACACCACATAATAAATGTAGCTTGA
P159-10	PY05401	H2-Kd	TYVDRIASI	21.95	LEISTYVDRIASIIRLS*	CTAGAAATAAGTACCTACGTAGATAGAATAGCTAGCATAATAAGACTGAGCTGA
P160-1	PY05401	H2-Kd	RYQEFSAKI	25.9	DFTFRYQEFSAKIVGFE*	GACTTCACCTTTAGATACCAGGAGTTTAGCGCTAAGATAGTAGGGTTTGAATGA
P160-2	PY05430	H2-Kd	LYIPGTKMI	14.46	TSGKLYIPGTKMIGGEI*	ACTAGCGGTAAACTGTACATCCCTGGCACTAAGATGATAGGGGGTGAAATCTGA
P160-3	PY05447	H2-Kd	FYIKNSPYI	3.7	WPAEFYIKNSPYIHFKL*	TGGCCAGCTGAATTCTACATAAAGAATAGCCCTTACATCCACTTTAAGCTGTGA
P160-4	PY05447	H2-Kd	SYINQVNFI	4.19	GTCCSYINQVNFITGVG*	GGCACCTGCTGTAGCTACATAAACCAGGTGAACTTCATAACGGGAGTAGGATGA
P160-5	PY05447	H2-Kd	KYIENSEKI	11.18	TESAKYIENSEKIAAML*	ACTGAAAGTGCTAAGTACATAGAGAATAGTGAGAAGATAGCTGCGATGTTATGA
P160-6	PY05447	H2-Kd	KYIKNVEKL	11.47	TSTLKYIKNVEKLVIKF*	ACCTCCACATTGAAGTACATAAAGAACGTAGAGAAGCTAGTGATAAAGTTTTGA
P160-7	PY05447	H2-Kd	YYNNINLPL	12.05	VLCPYYNNINLPLVAQK*	GTATTGTGCCCGTACTATAATAACATAAACCTGCCTCTAGTAGCTCAAAAATGA
P160-8	PY05447	H2-Kd	KYNVAYNGI	13.22	TLPKKYNVAYNGIMWPA*	ACCCTGCCTAAAAAGTATAACGTAGCCTATAACGGCATAATGTGGCCAGCCTGA
P160-9	PY05447	H2-Kd	VYYINWTII	13.22	PAPPVYYINWTIISSRL*	CCCGCGCCACCCGTGTACTACATAAACTGGACCATAATCTCGTCTCGACTGTGA
P160-10	PY05447	H2-Kd	KYIYFFFII	19.17	TPEVKYIYFFFIIGQME*	ACTCCTGAAGTGAAGTACATCTACTTCTTCTTCATAATAGGGCAGATGGAGTGA
P161-1	PY05447	H2-Kd	YYIYNNIDI	21.12	LEWVYYIYNNIDIASYN*	CTAGAGTGGGTGTACTACATCTATAATAACATAGACATAGCTAGCTATAATTGA
P161-2	PY05447	H2-Kd	KAINTFFSI	25.63	VEEKKAINTFFSISRSN*	GTAGAAGAGAAAAAGGCCATAAACACCTTCTTTAGCATCTCCCGGTCTAACTGA
P161-3	PY05447	H2-Kd	IYYEDFHLL	26.63	CAHGIYYEDFHLLQTKL*	TGCGCGCACGGGATCTACTATGAGGACTTCCACCTGCTGCAGACTAAGCTTTGA
P161-4	PY05447	H2-Kd	KMYEWINEI	37.81	IRTAKMYEWINEISVRL*	ATAAGAACTGCTAAGATGTATGAGTGGATAAATGAGATCTCTGTGAGGTTGTGA
P161-5	PY05447	H2-Kd	IYHTKINHI	45.41	SRKFIYHTKINHISAKR*	AGCCGTAAGTTCATCTACCACACTAAGATAAACCACATCTCTGCTAAGCGCTGA
P161-6	PY05447	H2-Kd	LYIYCLLFI	48.69	GMVLLYIYCLLFIRGLL*	GGGATGGTTCTTCTGTACATCTACTGCCTGCTGTTCATCCGCGGGCTGCTGTGA
P161-7	PY05447	H2-Kd	FWFFILNEI	49.24	YSNIFWFFILNEIYDRV*	TATAGTAACATTTTCTGGTTCTTCATCCTGAATGAGATCTATGATCGAGTCTGA
P161-8	PY05447	H2-Ld	HPIPNFANI	22.2	TPTLHPIPNFANIGCGG*	ACACCAACACTCCACCCTATCCCTAACTTCGCTAACATAGGCTGTGGCGGCTGA
P161-9	PY05484	H2-Kd	KYIHNMNKI	3.26	TRTTKYIHNMNKICWFS*	ACTAGAACCACTAAGTACATCCATAACATGAATAAGATCTGCTGGTTTTCTTGA
P161-10	PY05484	H2-Kd	YYINNENVI	3.94	AIDQYYINNENVIVDDY*	GCAATAGACCAATACTACATAAATAATGAGAACGTGATAGTAGATGACTACTGA
P162-1	PY05484	H2-Kd	IYFNYAHNI	4.46	SEADIYFNYAHNISYFP*	AGTGAAGCTGACATCTACTTTAACTACGCCCATAACATCTCCTACTTCCCGTGA
P162-2	PY05484	H2-Kd	YYNGNGHPI	7.21	ANPKYYNGNGHPIAALF*	GCTAATCCTAAGTACTATAACGGTAACGGCCACCCTATAGCTGCTTTGTTTTGA

P162-3	PY05484	H2-Kd	IYFYNNEEI	11.87	ACILIYFYNNEEIAKVL*	GCGTGTATCCTAATCTACTTCTATAATAATGAGGAGATAGCTAAAGTCCTGTGA
P162-4	PY05484	H2-Kd	SYSSMHSIV	12.56	ANPESYSSMHSIVQMFQ*	GCTAACCCTGAGAGCTATAGTAGCATGCAATAGCTGCAGATGTTCCAGTGA
P162-5	PY05484	H2-Kd	SYNPETVLI	21.69	QWKVSYNPETVLIVFVE*	CAGTGGAAAGTGAGCTATAACCCTGAGACCGTGCTGATAGTATTCGTAGAATGA
P162-6	PY05484	H2-Kd	FYNERKYEI	35.47	ANAAFYNERKYEIPSDE*	GCTAATGCAGCCTTCTATAATGAGAGAAAGTATGAGATCCCTAGTGATGAGTGA
P162-7	PY05522	H2-Kd	FYNNMSNKI	5.65	MKSRFYNNMSNKISLHP*	ATGAAGTCTAGATTCTATAATAACATGAGTAATAAGATAAGCCTTCATCCCTGA
P162-8	PY05522	H2-Kd	MYYKNEYLL	28.21	VIYSMYYKNEYLLKLEN*	GTGATTTACTCAATGTACTATAAGAATGAGTACCTGCTGAAGCTAGAGAACTGA
P162-9	PY05522	H2-Kd	KEMKFYTPI	31.66	EVPQKEMKFYTPIVCSE*	GAAGTGCCTCAGAAGGAGATGAAGTTCTACACCCCTATAGTGTGCTCTGAGTGA
P162-10	PY05537	H2-Kd	YYHNNTYRV	42.95	ESLCYYHNNTYRVLLPW*	GAAAGTCTGTGCTACTACCATAATAACACCTATAGAGTGCTGCTTCCATGGTGA
P163-1	PY05542	H2-Kd	SYIYHTPVL	9.87	ENASSYIYHTPVLKSVM*	GAAAATGCCTCTAGCTACATCTACCACACCCCTGTGCTGAAATCAGTGATGTGA
P163-2	PY05544	H2-Kd	SYKRGAHSL	10.72	ADQDSYKRGAHSLLFIA*	GCTGACCAGGATAGCTATAAGAGAGGCGCCCATAGCCTGCTCTTCATAGCATGA
P163-3	PY05544	H2-Kd	GYIQLMTYI	12.34	ILFLGYIQLMTYIYIAS*	ATCCTGTTTCTAGGCTACATCCAGCTGATGACCTACATCTACATAGCTAGCTGA
P163-4	PY05544	H2-Kd	EYYFYRTTI	28.62	YAGPEYYFYRTTIYMQH*	TACGCAGGGCCTGAGTACTACTTCTATAGAACCACCATCTATATGCAGCACTGA
P163-5	PY05545	H2-Kd	NYIDMKNTI	4.65	PPWENYIDMKNTIRVLI*	CCTCCTTGGGAAAACTACATAGACATGAAGAACACCATCCGCGTCTTGATCTGA
P163-6	PY05545	H2-Kd	KYMLDENEI	9.85	VEYSKYMLDENEIAQLQ*	GTAGAATATAGTAAGTACATGCTAGATGAGAATGAGATAGCTCAACTGCAGTGA
P163-7	PY05545	H2-Kd	WYWNIFYAI	10.65	KQILWYWNIFYAIAARP*	AAGCAGATTCTATGGTACTGGAACATCTTCTACGCCATAGCAGCTAGACCTTGA
P163-8	PY05545	H2-Kd	SYGNNFPHL	15.78	EIDGSYGNNFPHLTTQD*	GAAATAGATGGTAGCTACGGTAATAACTTCCCTCACCTGACTACCCAAGACTGA
P163-9	PY05545	H2-Kd	KHIQSFNPI	17.38	EKWDKHIQSFNPIPKPR*	GAGAAGTGGGATAAGCACATCCAGAGCTTTAACCCTATCCCTAAACCTAGATGA
P163-10	PY05545	H2-Kd	IYFNIIYHL	19.17	PIEGIYFNIIYHLRARF*	CCTATAGAGGGGATCTACTTTAACATAATCTACCACCTGAGAGCTAGATTCTGA
P164-1	PY05545	H2-Kd	FYDYAKSYI	20.07	AHAKFYDYAKSYIFSPT*	GCCCATGCTAAGTTCTATGACTACGCTAAGAGCTACATCTTCTCTCCCACCTGA
P164-2	PY05545	H2-Kd	RFMRTFENI	31.76	YEHERFMRTFENINDYQ*	TATGAGCATGAGAGATTCATGAGAACCTTTGAGAACATAAATGACTACCAGTGA
P164-3	PY05545	H2-Kd	IYYSKMENI	34.74	EAEEIYYSKMENIDRMD*	GAGGCTGAGGAGATCTACTATAGTAAGATGGAGAACATAGATCGGATGGATTGA
P164-4	PY05545	H2-Ld	IPMNYIFQM	33.39	VVEKIPMNYIFQMVQIA*	GTAGTAGAGAAAATCCCTATGAACTACATCTTCCAGATGGTGCAGATAGCATGA
P164-5	PY05556	H2-Kd	IYNNNNTIL	19.86	DMLPIYNNNNTILQDLD*	GACATGCTGCCAATCTATAATAATAATAACACCATCCTGCAGGACCTAGACTGA
P164-6	PY05564	H2-Kd	YYGNMNFNI	7.18	EELLYYGNMNFNIIRVD*	GAGGAACTCTTGTACTACGGTAACATGAACTTTAACATAATAAGGGTAGACTGA
P164-7	PY05565	H2-Kd	YYFNNIMSI	2.31	VSGTYYFNNIMSIYGSM*	GTGAGCGGGACCTACTACTTTAATAACATAATGAGCATCTACGGGTCAATGTGA
P164-8	PY05565	H2-Kd	YYIHHMHML	6.88	EPVTYYIHHMHMLGLQR*	GAGCCAGTGACCTACTACATCCACCACATGCACATGCTAGGGCTACAGAGGTGA
P164-9	PY05565	H2-Kd	KYLNEQNEI	11.41	LNLLKYLNEQNEIMRGF*	TTAAACCTATTAAAGTACCTGAATGAGCAGAATGAGATAATGAGGGGGTTTTGA
P164-10	PY05565	H2-Kd	GYNYYFNNI	12.15	YADIGYNYYFNNIHQGY*	TATGCTGACATAGGCTATAACTACTACTTTAATAACATCCACCAAGGGTACTGA
P165-1	PY05565	H2-Kd	IYVSSKHII	13	AVVLIYVSSKHIIASGP*	GCCGTAGTACTAATCTACGTGAGTAGTAAGCACATAATAGCGTCAGGGCCGTGA
P165-2	PY05565	H2-Kd	LYNNYLNNI	13.53	NTMSLYNNYLNNIRVQA*	AACACCATGAGTCTGTATAATAACTACCTGAATAACATAAGGGTCCAAGCCTGA
P165-3	PY05565	H2-Kd	YYYKVAKKI	22.91	TGEFYYYKVAKKIFEPK*	ACTGGTGAATTCTACTACTATAAGGTAGCTAAGAAGATCTTTGAACCTAAGTGA
P165-4	PY05565	H2-Kd	IQTNNYSSI	25.48	HSLFIQTNNYSSICESN*	CATTCGCTGTTCATCCAGACTAATAACTATAGTAGCATCTGTGAGAGTAATTGA
P165-5	PY05565	H2-Kd	KYNTNQNDI	26.34	VPGEKYNTNQNDIKGDQ*	GTGCCTGGTGAGAAGTATAACACTAACCAGAATGACATAAAGGGTGACCAGTGA
P165-6	PY05565	H2-Ld	IPNYNIPPF	21.55	VTASIPNYNIPPFQQDD*	GTAACCGCTAGCATCCCTAACTATAACATCCCTCCTTTCCAGCAGGATGACTGA
P165-7	PY05567	H2-Kd	FYIGLVVVL	29.38	GLHEFYIGLVVVLRAGK*	GGCCTTCATGAATTCTACATAGGCCTAGTAGTAGTGCTGCGCGCCGGTAAGTGA
P165-8	PY05567	H2-Kd	AYFMTRLVL	49.4	VQLVAYFMTRLVLGRRK*	GTGCAACTAGTAGCCTACTTCATGACTAGACTAGTGCTAGGTCGCCGTAAATGA
P165-9	PY05610	H2-Kd	YYLYYFYNI	9.25	RLPLYYLYYFYNIPPHG*	AGACTGCCCTTATACTACCTGTACTACTTCTATAACATCCCTCCACATGGGTGA
P165-10	PY05610	H2-Kd	LYLNALYFI	18.47	HVAILYLNALYFIRRLC*	CATGTAGCGATCCTGTACCTGAACGCCCTGTACTTCATAAGAAGGCTGTGTTGA
P166-1	PY05610	H2-Kd	KYHMNNELI	23.23	CTKKKYHMNNELILCGV*	TGTACTAAAAAGAAGTACCACATGAATAATGAGCTGATCTTGTGTGGAGTGTGA
P166-2	PY05610	H2-Ld	MPMLVNYIL	24.98	LNVAMPMLVNYILLQPS*	CTGAACGTAGCCATGCCTATGCTAGTGAACTACATCCTGCTGCAACCTTCCTGA
P166-3	PY05612	H2-Kd	NYMNSKTYL	5.99	RYEANYMNSKTYLLEKT*	AGATATGAGGCTAACTACATGAATAGTAAGACCTACCTGCTAGAGAAAACATGA
P166-4	PY05612	H2-Kd	MYQNAHNML	10.93	LFLSMYQNAHNMLWDHH	CTGTTTCTGAGCATGTACCAGAACGCCCATAACATGCTGTGGGATCACCATTGA
P166-5	PY05612	H2-Kd	YAMNNFAPI	32.31	TFEEYAMNNFAPIYALV*	ACCTTTGAGGAGTACGCCATGAATAACTTCGCCCCTATCTACGCCCTAGTCTGA
P166-6	PY05620	H2-Kd	KYKHNPSLI	10.15	FCEQKYKHNPSLIGFVD*	TTCTGTGAGCAGAAGTATAAGCATAACCCTAGCCTGATAGGTTTTGTAGACTGA
P166-7	PY05633	H2-Kd	YYNSSVEKI	16.79	SKGWYYNSSVEKIVFWK*	AGTAAGGGCTGGTACTATAATAGTAGCGTAGAGAAGATAGTGTTTTGGAAATGA
P166-8	PY05642	H2-Kd	SYHVSCLGL	41.3	LTRQSYHVSCLGLGSTN*	CTGACTCGACAAAGCTACCACGTGAGCTGCCTAGGCCTAGGCTCAACTAATTGA
P166-9	PY05680	H2-Kd	SYLENESHI	4.46	YPQLSYLENESHIQLPD*	TATCCTCAGCTGAGCTACCTAGAGAATGAGAGCCACATCCAGCTGCCTGATTGA
P166-10	PY05680	H2-Kd	CYLVDTSSI	7.68	ATCVCYLVDTSSINLPE*	GCCACGTGTGTTTGCTACCTAGTAGACACTAGTAGCATAAACCTGCCTGAATGA
P167-1	PY05680	H2-Kd	SYNYKHNNI	24.62	GRILSYNYKHNNIIEDL*	GGGCGCATTCTGAGCTATAACTATAAGCATAATAACATAATAGAGGACTTGTGA
P167-2	PY05680	H2-Kd	MYEPLIGPI	41.15	TSEKMYEPLIGPIFVDD*	ACTTCTGAAAAGATGTATGAGCCTCTGATAGGCCCTATCTTCGTAGATGACTGA
P167-3	PY05680	H2-Ld	YPYQYSFFL	22.29	KCDDYPYQYSFFLAQRM'	AAGTGTGATGACTACCCTTACCAGTATAGCTTCTTCCTAGCGCAGCGCATGTGA
P167-4	PY05683	H2-Kd	SYHSDTSEI	5.65	VKRSSYHSDTSEIHENP*	GTGAAGCGCTCTAGCTACCATAGTGAGATCCATGAGAACCCGTGA
P167-5	PY05683	H2-Kd	LYVPYSYII	27.11	YGGSLYVPYSYIITSHT*	TACGGTGGATCTCTGTACGTGCCTTATAGCTACATAATAACGTCTCACACATGA
P167-6	PY05696	H2-Kd	SYFSAIPTI	2.27	YQSMSYFSAIPTITSDD*	TACCAATCCATGAGCTACTTTAGCGCCATCCCTACCATAACTAGTGATGACTGA
P167-7	PY05696	H2-Kd	YYISFRNEI	4.53	NSSLYYISFRNEIKQPI*	AACTCCTCTCTCTACTACATAAGCTTTAGAAATGAGATAAAGCAGCCAATATGA
P167-8	PY05696	H2-Kd	FYLDNPSAL	7.15	AMVHFYLDNPSALLVPC*	GCCATGGTGCACTTCTACCTAGATAACCCTAGCGCCCTGCTAGTGCCCTGCTGA
P167-9	PY05696	H2-Kd	KYFINYFQL	8.97	ETRCKYFINYFQLMRVH*	GAGACCCGCTGTAAGTACTTCATAAACTACTTCCAGCTGATGAGGGTGCACTGA
P167-10	PY05696	H2-Kd	YYKNVLNSL	12.43	NETPYYKNVLNSLFLTL*	AATGAAACCCCATACTATAAGAACGTGCTGAATAGCCTGTTCCTGACCCTCTGA
P168-1	PY05696	H2-Kd	QYFPQFNFL	16.6	LYFQQYFPQFNFLAEKQ*	CTGTACTTCCAACAGTACTTCCCTCAGTTTAACTTCCTAGCTGAAAAGCAGTGA
P168-2	PY05696	H2-Kd	NYIDNNLTL	21.64	GYRANYIDNNLTLSANF*	GGATATCGCGCTAACTACATAGATAATAACCTGACCCTGAGTGCTAATTTCTGA
P168-3	PY05696	H2-Kd	LYNYVIPQI	24.99	DLFSLYNYVIPQIDQRI*	GACCTGTTCTCTCTGTATAACTACGTGATCCCTCAGATAGATCAGAGAATATGA
P168-4	PY05696	H2-Kd	SYAELCEEI	30.58	KFFTSYAELCEEIGKPR*	AAGTTCTTCACTAGCTACGCTGAGCTGTGTGAGGAGATAGGTAAGCCACGTTGA
P168-5	PY05696	H2-Ld	SPYNFYFNF	20.48	LGQPSPYNFYFNFHTCT*	CTAGGCCAACCTAGCCCTTATAACTTCTACTTTAACTTCCACACATGTACCTGA
P168-6	PY05748	H2-Kd	IYQAMYNVI	4.7	ERRYIYQAMYNVIAASS*	GAGCGGCGCTACATCTACCAGGCCATGTATAACGTGATAGCTGCCTCTAGCTGA
P168-7	PY05748	H2-Kd	KYIPILEDL	31.23	HVIIKYIPILEDLLSGA*	CACGTGATAATAAAGTACATCCCTATCCTAGAGGACCTGTTGTCTGGCGCGTGA
P168-8	PY05748	H2-Kd	SYSCHKYVL	37.37	LMVQSYSCHKYVLYLQV*	TTAATGGTGCAGAGCTATAGCTGCCATAAGTACGTGCTGTATCTTCAGGTTTGA
P168-9	PY05748	H2-Ld	YPNGISYPL	37.86	KFWAYPNGISYPLDVYV*	AAATTCTGGGCCTACCCTAACGGCATAAGCTACCCTCTAGATGTTTACGTTTGA
P168-10	PY05772	H2-Kd	KYICNSYNI	2.94	CHSTKYICNSYNIRKAF*	TGCCATTCTACTAAGTACATCTGTAATAGCTATAACATCCGTAAGGCCTTCTGA
P169-1	PY05772	H2-Kd	KYYVNNYYL	6.77	VHIKKYYVNNYYLHKFE*	GTGCACATAAAGAAGTACTACGTGAATAACTACTACCTGCATAAGTTTGAGTGA
P169-2	PY05772	H2-Kd	FFMNSKFNI	17.22	KSPAFFMNSKFNIVRQI*	AAAAGCCCCGCATTCTTCATGAATAGTAAGTTTAACATAGTGAGACAGATCTGA
P169-3	PY05772	H2-Kd	FYNAYVDVL	22.23	HLDDFYNAYVDVLFKST*	CACCTAGATGACTTCTATAACGCCTACGTAGACGTGCTGTTTAAGTCAACCTGA
P169-4	PY05772	H2-Kd	IYNHRYTNI	23.08	LANYIYNHRYTNIYTGM*	CTAGCTAACTATATCTATAACCATAGATACACTAACATCTATACAGGAATGTGA
P169-5	PY05772	H2-Kd	FYYELTGLI	28.81	AKDLFYYELTGLICEER*	GCTAAGGATCTCTTCTACTATGAGCTGACCGGCCTGATCTGTGAAGAACGCTGA
P169-6	PY05772	H2-Kd	NYNNVKNEI	31.98	EVSLNYNNVKNEISQDL*	GAGGTGTCACTGAACTATAATAACGTGAAGAATGAGATCTCCCAGGACTTGTGA
P169-7	PY05811	H2-Kd	IYKNNLLSI	19.64	QHKKIYKNNLLSIWIER*	CAGCATAAGAAGATCTATAAGAATAACCTGCTGAGCATCTGGATAGAGCGCTGA
P169-8	PY05811	H2-Kd	VYYVNLFNL	33.07	FATQVYYVNLFNLNPEY*	TTCGCTACTCAGGTGTACTACGTGAACCTGTTTAACCTGAATCCTGAGTACTGA
P169-9	PY05811	H2-Kd	KSFSNISNI	44.73	VLPAKSFSNISNIDDSG*	GTGCTGCCCGCTAAGAGCTTTAGTAACATAAGTAACATAGATGACTCGGGGTGA
P169-10	PY05818	H2-Kd	MYFCVAQKI	8.74	IVKTMYFCVAQKIGRAI*	ATAGTGAAAACAATGTACTTCTGCGTAGCCCAGAAGATAGGACGGGCTATCTGA
P170-1	PY05841	H2-Kd	FYYYIITNI	8.02	GKFVFYYYIITNINVAL*	GGTAAATTCGTTTTCTACTACTACATAATAACTAACATAAACGTAGCACTGTGA
P170-2	PY05841	H2-Kd	IYNITNSNI	16.25	QGILIYNITNSNIPSDG*	CAGGGCATCCTGATCTATAACATAACTAATAGTAACATCCCTAGTGACGGGTGA
P170-3	PY05841	H2-Kd	MYRNYYDYI	22	ALEMMYRNYYDYIGWIS*	GCCCTAGAGATGATGTATAGAAACTACTATGACTACATAGGCTGGATAAGTTGA
P170-4	PY05841	H2-Kd	IYLTSFCIL	33.13	TPRSIYLTSFCILPWIE*	ACCCCCCGGTCCATCTACCTGACTAGCTTCTGCATCCTGCCCTGGATAGAGTGA
P170-5	PY05843	H2-Kd	FYNNQDSFI	11.93	SCDNFYNNQDSFITLFD*	TCATGTGATAATTTCTATAATAACCAGGATAGCTTCATAACCCTCTTTGATTGA
P170-6	PY05843	H2-Kd	NYLSYRHPI	12.31	EPGHNYLSYRHPIRELS*	GAGCCTGGACATAACTACCTGAGCTATAGACACCCTATCCGTGAACTTTCATGA
P170-7	PY05843	H2-Kd	NYINPFSLL	19.4	VRRNNYINPFSLLVAEP*	GTGAGAAGGAATAACTACATAAACCCTTTTAGCCTGCTAGTAGCTGAACCATGA
P170-8	PY05853	H2-Kd	FYSSNKINI	15.26	EATEFYSSNKINIFEID*	GAAGCGACTGAATTCTATAGTAGTAATAAGATAAACATCTTTGAGATAGATTGA
P170-9	PY05853	H2-Kd	HYFNLDNYL	20.87	MRMQHYFNLDNYLHAVA	ATGAGAATGCAGCACTACTTTAACCTAGATAACTACCTGCATGCCGTAGCATGA
P170-10	PY05859	H2-Kd	SYNKNNNGI	9.52	RMISSYNKNNNGIMGLQ*	CGGATGATCTCTAGCTATAATAAGAATAATAACGGCATAATGGGTCTCCAGTGA
P171-1	PY05859	H2-Kd	KYLTSQFFL	9.87	EDANKYLTSQFFLVSFP*	GAAGATGCTAATAAGTACCTGACTAGCCAGTTCTTCCTAGTGTCCTTCCCTTGA
P171-2	PY05859	H2-Kd	NYLDNYFII	17.74	DHFVNYLDNYFIIEEWG*	GATCACTTCGTGAACTACCTAGATAACTACTTCATAATAGAGGAGTGGGGTTGA
P171-3	**PY05881**	**H2-Kd**	**GYKSGMSHI**	**20.26**	**LLRPGYKSGMSHIKRTS***	**TTGTTAAGACCTGGCTATAAGAGCGGCATGAGCCACATAAAGCGCACTAGCTGA**
P171-4	PY05897	H2-Kd	SYINTFCEL	3.88	PNATSYINTFCELNTSL*	CCTAATGCAACTAGCTACATAAACACCTTCTGTGAGCTGAACACATCCCTTTGA
P171-5	PY05897	H2-Kd	AYILNVNVI	12.06	RGVPAYILNVNVISCLG*	CGAGGAGTGCCTGCCTACATCCTGAACGTGAACGTGATCTCATGTCTAGGCTGA
P171-6	PY05897	H2-Kd	GYMNKVYML	26.81	VRQCGYMNKVYMLMKLP	GTCCGTCAGTGCGGCTACATGAATAAGGTGTACATGCTGATGAAGCTCCCGTGA
P171-7	PY05897	H2-Kd	FYFRKNYKL	36.44	LFTKFYFRKNYKLALTY*	CTGTTTACTAAGTTCTACTTTAGAAAGAACTATAAGCTAGCCCTGACCTATTGA
P171-8	PY05897	H2-Kd	KHNNNYSYI	43.59	VITHKHNNNYSYILHSH*	GTGATAACACATAAGCATAATAATAACTATAGCTACATCCTCCATTCACATTGA
P171-9	PY05908	H2-Kd	MYNNNINVI	4.87	LADCMYNNNINVIDDHP*	TTAGCTGATTGCATGTATAATAATAACATAAACGTGATAGATGACCACCCCTGA
P171-10	PY05908	H2-Kd	FYLNSKNEI	6.19	NDFAFYLNSKNEIKPVF*	AATGACTTTGCTTTCTACCTGAATAGTAAGAATGAGATAAAGCCAGTGTTCTGA
P172-1	PY05908	H2-Kd	KYFNISFDI	13.42	DKNFKYFNISFDISYPE*	GATAAGAATTTTAAGTACTTTAACATAAGCTTTGACATCTCATACCCTGAGTGA
P172-2	PY05908	H2-Kd	KQFRDHTNI	22.73	LTCKKQFRDHTNIAILL*	CTGACCTGTAAGAAGCAGTTTAGAGACCACACTAACATAGCAATTCTGCTGTGA
P172-3	PY05908	H2-Kd	YYINHFKKL	26.32	LLYLYYINHFKKLFQVG*	TTGCTCTACTTGTACTACATAAACCACTTTAAGAAGCTGTTCCAGGTAGGTTGA

P172-4	PY05908	H2-Kd	LQFHNFHII	31.14	LQKSLQFHNFHIILTGS*	CTGCAGAAGTCTCTGCAGTTCCATAACTTCCACATAATCCTAACCGGCTCATGA
P172-5	PY05908	H2-Kd	KYSAIFSFF	36.92	EASEKYSAIFSFFAGQA*	GAGGCTTCTGAGAAGTATAGCGCCATCTTTAGCTTCTTCGCTGGACAGGCGTGA
P172-6	PY05911	H2-Kd	SYFCTEKNI	15.69	EVKDSYFCTEKNILTQS*	GAGGTGAAGGATAGCTACTTCTGCACTGAGAAGAACATCCTAACCCAATCATGA
P172-7	PY05911	H2-Kd	IYILNFGEI	19.9	QSREIYILNFGEIYCPL*	CAGTCTCGTGAAATCTACATCCTGAACTTCGGTGAGATCTATTGTCCATTGTGA
P172-8	PY05911	H2-Kd	YYTNYISAV	29.65	FAAHYYTNYISAVFKAH*	TTTGCAGCTCACTACTACACTAACTACATAAGCGCCGTGTTTAAAGCACATTGA
P172-9	PY05911	H2-Kd	YYSFDTLFI	31.67	EDESYYSFDTLFIFGLY*	GAGGATGAGTCCTACTATAGCTTTGACACCCTGTTCATCTTCGGGTTGTATTGA
P172-10	PY05911	H2-Ld	IPHPALSLF	20.23	AKKNIPHPALSLFANNC*	GCTAAAAAGAACATCCCTCACCCTGCCCTGAGCCTGTTCGCTAATAATTGCTGA
P173-1	PY05915	H2-Kd	KYHDLYGPI	17.39	PDCYKYHDLYGPILPPL*	CCTGACTGCTATAAGTACCATGACCTGTACGGCCCTATCCTACCACCGCTTTGA
P173-2	PY05925	H2-Kd	FYYNMEKSL	12.97	YETSFYYNMEKSLTRLL*	TATGAGACTTCCTTCTACTATAACATGGAGAAGAGCCTGACTCGACTTTTATGA
P173-3	PY05925	H2-Kd	KYNELIDEL	33.59	KPKRKYNELIDELHELG*	AAACCTAAGCGTAAGTATAATGAGCTGATAGATGAGCTGCATGAACTAGGGTGA
P173-4	PY05947	H2-Kd	FYQSTLSLV	18.32	RPFCFYQSTLSLVTGPK*	AGGCCTTTCTGCTTCTACCAGAGCACCCTGAGCCTAGTGACCGGCCCTAAGTGA
P173-5	PY05957	H2-Kd	LYFANEREI	35.45	AGFRLYFANEREIPLYS*	GCCGGGTTTAGACTGTACTTCGCTAATGAGAGAGAGATCCCGCTGTACTCATGA
P173-6	PY05957	H2-Kd	IYQSTLSLV	43.57	MCAGIYQSTLSLVPAVS*	ATGTGTGCTGGCATCTACCAGAGCACCCTGAGCCTAGTGCCCGCAGTGAGCTGA
P173-7	PY05971	H2-Kd	KYDALKYTI	28.05	DLGAKYDALKYTIMEGE*	GATCTAGGTGCTAAGTATGACGCCCTGAAGTACACCATAATGGAAGGTGAGTGA
P173-8	PY05971	H2-Kd	IYAATKDYL	38.32	LLVPIYAATKDYLFKAL*	CTACTAGTGCCTATCTACGCCGCCACTAAGGACTACCTGTTTAAGGCCTTGTGA
P173-9	PY05975	H2-Kd	KYIKYHGPI	5.32	AKGDKYIKYHGPINVMV*	GCTAAGGGTGATAAGTACATAAAGTACCACGGCCCTATAAACGTGATGGTATGA
P173-10	PY05975	H2-Kd	FYNPLKMNI	8.07	SSYQFYNPLKMNISSHL*	TCTAGCTACCAGTTCTATAACCCTCTGAAGATGAACATAAGCTCACATTTGTGA
P174-1	PY05975	H2-Kd	KYHGPINEL	26.03	HQVIKYHGPINELGLLE*	CATCAGGTGATAAAGTACCACGGCCCTATAAATGAGCTAGGGCTGCTAGAGTGA
P174-2	PY05975	H2-Kd	MYAAKIHKI	31.73	FQTDMYAAKIHKISEKL*	TTCCAGACTGATATGTACGCCGCTAAGATCCATAAGATAAGTGAAAAGCTATGA
P174-3	PY05975	H2-Kd	QYYNGGGTL	35.27	STGTQYYNGGGTLQLVS*	TCTACAGGCACACAGTACTATAACGGCGGCGGCACCCTGCAGCTAGTGAGCTGA
P174-4	PY05975	H2-Ld	YPIFNYFNI	22.46	LLLYYPIFNYFNITNTL*	CTATTGCTTTACTACCCTATCTTTAACTACTTTAACATAACTAATACCTTGTGA
P174-5	PY05977	H2-Kd	KYMKSNVEL	5.83	KHAMKYMKSNVELILMI*	AAACACGCCATGAAGTACATGAAGAGTAACGTAGAGCTGATCCTAATGATTTGA
P174-6	PY05977	H2-Kd	VYFAGAGII	13.32	GNGAVYFAGAGIIPGSD*	GGTAACGGAGCTGTGTACTTCGCCGGCGCCGGCATAATCCCCGGTAGTGACTGA
P174-7	PY05977	H2-Kd	NYFDNNQNI	19.84	RIKANYFDNNQNILIAM*	CGGATAAAAGCTAACTACTTTGATAATAACCAGAACATCCTAATAGCGATGTGA
P174-8	PY05977	H2-Kd	NYLWGVWVL	23.72	YLRKNYLWGVWVLGPRD	TACCTTCGTAAGAACTACCTGTGGGGCGTGTGGGTGCTAGGCCCTCGTGACTGA
P174-9	PY05977	H2-Kd	LYNYPITPI	26.49	RDIELYNYPITPIQWTS*	CGTGACATAGAGCTGTATAACTACCCTATAACCCCTATCCAGTGGACTTCCTGA
P174-10	PY05977	H2-Kd	KYGLYNYPI	31.99	PISFKYGLYNYPITSAI*	CCGATAAGCTTTAAGTACGGCCTGTATAACTACCCTATAACATCCGCCATTTGA
P175-1	PY05977	H2-Kd	KFYSNKQNI	36.81	LGRGKFYSNKQNILENE*	TTAGGTAGGGGTAAGTTCTATAGTAATAAGCAGAACATCCTAGAGAATGAGTGA
P175-2	PY06001	H2-Ld	WPIYNRHPI	33.24	TKPPWPIYNRHPILSLV*	ACTAAACCTCCATGGCCTATCTATAATAGACACCCATCCTTTCACTAGTCTGA
P175-3	PY06005	H2-Kd	LYYANERTI	21.25	LESELYYANERTISFVI*	CTAGAATCTGAGCTGTACTACGCTAATGAGAGAACCATCTCTTTTGTGATCTGA
P175-4	PY06010	H2-Kd	KYNDWYTTL	5.17	SSKIKYNDWYTTLSFAA*	AGTTCTAAGATAAAGTATAATGACTGGTACACCACCCTGAGCTTCGCTGCCTGA
P175-5	PY06010	H2-Kd	WYTTLYETL	29.37	FGDSWYTTLYETLCGPG*	TTTGGTGATAGCTGGTACACCACCCTGTATGAGACCCTGTGCGGACCTGGCTGA
P175-6	PY06037	H2-Kd	FYYENRNYV	36	SYPMFYYENRNYVGRTQ	AGTTACCCCATGTTCTACTATGAGAATAGAAACTACGTAGGTAGAACCCAATGA
P175-7	PY06041	H2-Kd	SYSNNTNGL	19.52	SSANSYSNNTNGLLADI*	TCCTCTGCTAATAGCTATAGTAATAACACTAACGGCCTGCTAGCTGACATATGA
P175-8	PY06041	H2-Kd	RYMSLSNCL	33.04	SLDPRYMSLSNCLAYNG*	TCTCTAGACCCTAGATACATGAGCCTGAGTAACTGCCTAGCATATAATGGATGA
P175-9	PY06041	H2-Kd	SFFENFEKI	49.23	FVPGSFFENFEKILNDT*	TTCGTGCCTGGTAGCTTCTTTGAGAACTTTGAGAAGATCCTGAATGATACCTGA
P175-10	PY06045	H2-Kd	FYESTLSLI	12.76	DADSFYESTLSLIGEEL*	GACGCTGACTCCTTCTATGAGAGCACCCTGAGCCTGATAGGTGAAGAGCTGTGA
P176-1	PY06045	H2-Kd	LYFVNERSI	26.46	VTIILYFVNERSILSGN*	GTAACCATAATCCTGTACTTCGTGAATGAGAGAAGCATCTTATCCGGTAACTGA
P176-2	PY06049	H2-Kd	QYINLNETI	11.08	IMTYQYINLNETIEYRS*	ATAATGACTTACCAGTACATAAACCTGAATGAGACCATAGAATATAGATCCTGA
P176-3	PY06049	H2-Kd	NYFCNYFEL	12.85	GESLNYFCNYFELRLCE*	GGTGAATCACTGAACTACTTCTGTAACTACTTTGAGCTGAGGCTCTGTGAATGA
P176-4	PY06049	H2-Kd	IYLKNIYYL	29.99	DEIVIYLKNIYYLGGER*	GATGAAATAGTGATCTACCTGAAGAACATCTACTACCTAGGGGGTGAACGTTGA
P176-5	PY06049	H2-Kd	NYINKNNII	45.64	HPDCNYINKNNIIELTQ*	CACCCTGACTGTAACTACATAAATAAGAATAACATAATAGAGCTGACACAGTGA
P176-6	PY06049	H2-Ld	NPMINNYNF	17.76	PISQNPMINNYNFGLVI*	CCCATAAGCCAAAACCCTATGATAAATAACTATAACTTCGGCTTAGTGATTTGA
P176-7	PY06067	H2-Kd	KYIVNIASL	4.24	NEEKKYIVNIASLLIVQ*	AATGAAGAAAAAAAGTACATAGTGAACATAGCTAGCCTGTTAATAGTGCAGTGA
P176-8	PY06067	H2-Kd	KYYIDNSNI	6.89	PHKPKYYIDNSNIWNLV*	CCCCATAAGCCTAAGTACTACATAGATAATAGTAACATCTGGAACCTAGTGTGA
P176-9	PY06067	H2-Kd	KYKSLCEYI	18.36	CAECKYKSLCEYIPDHD*	TGCGCTGAATGTAAGTATAAGAGCCTGTGTGAGTACATCCCTGACCATGATTGA
P176-10	PY06076	H2-Kd	FYNNIYTYI	3.19	YVPSFYNNIYTYIKINC*	TACGTTCCTAGCTTCTATAATAACATCTACACCTACATAAAAATAAATTGCTGA
P177-1	PY06076	H2-Kd	TYSNTKTSI	8.62	GSGATYSNTKTSIIPLF*	GGTTCAGGCGCAACCTATAGTAACACTAAGACTAGCATAATTCCTCTCTTCTGA
P177-2	PY06076	H2-Kd	SYYFNDFII	8.7	TVALSYYFNDFIITGHL*	ACTGTAGCCTTGAGCTACTACTTTAATGACTTCATAATAACCGGGCATCTGTGA
P177-3	PY06076	H2-Kd	YYNINLYTL	10.01	TSFGYYNINLYTLCSYK*	ACTAGCTTTGGATACTATAACATAAACCTGTACACCCTGTGTAGTTATAAATGA
P177-4	PY06076	H2-Kd	FYNSYPFII	12.61	ALATFYNSYPFIIWVAD*	GCCCTAGCGACATTCTATAATAGCTACCCTTTCATAATCTGGGTAGCTGACTGA
P177-5	PY06076	H2-Kd	IYASNFENI	16.03	GVHGIYASNFENIDQVG*	GGCGTCCACGGAATCTACGCTAGTAACTTTGAGAACATAGACCAGGTAGGATGA
P177-6	PY06076	H2-Kd	YFYNSYPFI	18.48	VFSCYFYNSYPFISCQE*	GTTTTTTCTTGCTACTTCTATAATAGCTACCCTTTCATCTCCTGTCAGGAGTGA
P177-7	PY06076	H2-Kd	RYETTNISI	37.78	VTGLRYETTNISIQATA*	GTGACCGGTCTGAGATATGAGACCACTAACATAAGCATCCAAGCTACTGCCTGA
P177-8	PY06087	H2-Kd	HYINVIKSI	7.21	FGSLHYINVIKSIESVK*	TTCGGTAGCCTCCACTACATAAACGTGATAAAGAGCATAGAGTCCGTGAAATGA
P177-9	PY06087	H2-Kd	YYMYNNIKL	14.96	AVKHYYMYNNIKLLVYD*	GCCGTGAAACATTACTACATGTATAATAACATAAAGCTGCTAGTTTATGACTGA
P177-10	PY06087	H2-Kd	YYYYNLNNM	15.85	AHEQYYYYNLNNMQHDP	GCACATGAGCAGTACTACTACTATAACCTGAATAACATGCAGCATGATCCTTGA
P178-1	PY06087	H2-Kd	MYNNIKLNI	26.13	REQLMYNNIKLNIEGSE*	CGTGAGCAGTTGATGTATAATAACATAAAGCTGAACATAGAAGGATCTGAGTGA
P178-2	PY06110	H2-Kd	KYGFVITTL	11.72	LASLKYGFVITTLSALL*	CTAGCTAGTCTGAAGTACGGCTTCGTGATAACCACCCTGTCAGCCTTGCTGTGA
P178-3	PY06110	H2-Kd	KYNFLFEFI	12.02	QPVDKYNFLFEFIIQSW*	CAGCCAGTAGATAAGTATAACTTCCTGTTTGAGTTCATAATCCAGAGCTGGTGA
P178-4	PY06117	H2-Kd	RYYNYVTQI	2.74	LEYPRYYNYVTQIQEEF*	CTAGAATACCCTAGATACTATAACTACGTGACCCAGATCCAGGAGGAATTCTGA
P178-5	PY06117	H2-Kd	HYIALGHFI	5.79	TLYIHYIALGHFISAKS*	ACTCTCTATATCCACTACATAGCCCTAGGCCACTTCATCTCTGCTAAAAGTTGA
P178-6	PY06117	H2-Kd	YYNYVTQIL	12.93	MSTRYYNYVTQILPVFP*	ATGTCTACTCGCTACTATAACTACGTGACCCAGATCCTGCCAGTGTTCCCCTGA
P178-7	PY06117	H2-Kd	RYQEIHESL	14.87	TSSARYQEIHESLRMVL*	ACATCGTCAGCTAGATACCAGGAGATCCATGAGAGCCTGCGCATGGTGTTATGA
P178-8	PY06117	H2-Kd	YYKKLANEI	20.87	NHAAYYKKLANEIYFTS*	AATCATGCCGCCTACTATAAGAAGCTAGCTAATGAGATCTACTTCACTAGCTGA
P178-9	PY06117	H2-Kd	KFFSSTPKI	27.26	ITWEKFFSSTPKIQMTV*	ATAACCTGGGAGAAGTTCTTTAGTAGCACCCCTAAGATCCAAATGACAGTGTGA
P178-10	PY06117	H2-Kd	SYQPNVEYM	32.32	DVDESYQPNVEYMPLVI*	GACGTAGATGAGAGCTACCAGCCTAACGTAGAGTACATGCCACTAGTGATATGA
P179-1	PY06117	H2-Kd	IYVHILNLI	32.75	LQKEIYVHILNLIFTLA*	CTGCAAAAGGAAATCTACGTGCACATCCTGAACCTGATCTTTCACTTTAGCCTGA
P179-2	PY06117	H2-Kd	RSMFNRCTI	45.15	NIPHRSMFNRCTIKHAG*	AATATTCCACATAGAAGCATGTTTAATAGATGCACCATAAAACACGCAGGCTGA
P179-3	PY06117	H2-Kd	CYSRRSSAL	45.39	AQKMCYSRRSSALLRFT*	GCACAAAAAATGTGCTATAGTAGAAGAAGTAGCGCCCTGCTGCGCTTTACTTGA
P179-4	PY06142	H2-Kd	SYYNMRNNL	4.06	DGSCSYYNMRNNLNEEK	GACGGTTCCTGTAGCTACTATAACATGAGAAATAACCTGAATGAGGAGAAGTGA
P179-5	PY06142	H2-Kd	FYLYITNTI	6.92	DIHGFYLYITNTIAPLM*	GATATCCATGGCTTCTACCTGTACATAACTAACACCATAGCGCCTCTAATGTGA
P179-6	PY06142	H2-Kd	SYNLFSSNI	17.98	KRGRSYNLFSSNIRLLE*	AAAAGAGGTAGGAGCTATAACCTGTTTAGTAGTAACATAAGACTGTTAGAGTGA
P179-7	PY06146	H2-Kd	TYFSNQSSI	2.79	IPVSTYFSNQSSIASDA*	ATCCCAGTGAGTACCTACTTTAGTAACCAGAGTAGCATAGCTAGTGACGCTTGA
P179-8	PY06146	H2-Kd	YYVTSIVII	7.54	ESSYYYVTSIVIIHHDA*	GAAAGTTCTTATTACTACGTGACTAGCATAGTGATAATCCACCATGATGCCTGA
P179-9	PY06146	H2-Kd	WFNKVISTI	23.21	LAPPWFNKVISTIRSGY*	CTAGCACCACCTTGGTTTAATAAGGTGATAAGCACCATAAGATCAGGCTACTGA
P179-10	PY06160	H2-Kd	RWYNHISSL	11.27	NIVGRWYNHISSLWLFS*	AACATAGTAGGTAGATGGTATAACCACATAAGTAGCCTGTGGCTTTTTTCGTGA
P180-1	PY06160	H2-Kd	IYNQIKCVI	34.76	SNLAIYNQIKCVIPYYT*	TCTAATTTAGCAATCTATAACCAGATAAAGTGCGTGATCCCCTACTATACTTGA
P180-2	PY06161	H2-Kd	KYLEIHTLV	44.78	HTRQKYLEIHTLVVFFS*	CACACTAGGCAGAAGTACCTAGAGATCCACACCCTAGTAGTGTTTTTTAGCTGA
P180-3	PY06175	H2-Kd	SQLHLLSAI	39.44	TVGNSQLHLLSAIISLE*	ACTGTAGGTAATAGCCAGCTGCACCTGCTGAGCGCCATAATAAGCTTAGAATGA
P180-4	PY06175	H2-Kd	LYAYCHALI	47.46	ERQDLYAYCHALISCGK*	GAGAGGCAGGACCTGTACGCCTACTGCCACGCCCTGATCTCATGCGGTAAGTGA
P180-5	PY06191	H2-Kd	KYCNIYNFI	9.77	KRLDKYCNIYNFIISNL*	AAGCGGCTAGATAAGTACTGTAACATCTATAACTTCATAATAAGTAATTTGTGA
P180-6	PY06191	H2-Kd	KYILDNDYI	18.48	PTPSKYILDNDYIISVI*	CCAACTCCTAGTAAGTACATCCTAGATAATGACTACATAATAAGTGTAATCTGA
P180-7	PY06191	H2-Kd	KYNNNWNNV	25.95	CLKEKYNNNWNNVTLAL*	TGCTTGAAAGAGAAGTATAATAATAACTGGAATAACGTGACCTTAGCATTGTGA
P180-8	PY06191	H2-Kd	FYSKDMSNL	29.54	AEFTFYSKDMSNLDKLQ*	GCTGAGTTCACGTTCTATAGTAAGGACATGAGTAACCTAGATAAACTGCAGTGA
P180-9	PY06193	H2-Kd	KYSKKFNRI	26.92	HSELKYSKKFNRIQVLA*	CATAGTGAGCTGAAGTATAGTAAGAAGTTTAATAGAATCCAGGTACTAGCCTGA
P180-10	PY06193	H2-Kd	FYEGNSNEI	48.99	NEVIFYEGNSNEIRPFL*	AATGAGGTAATCTTCTATGAGGGTAATAGTAATGAGATCCGCCCTTTTCTCTGA
P181-1	PY06198	H2-Kd	SYFKNYIHI	4.9	SFWKSYFKNYIHIDIAN*	TCTTTTTGGAAGAGCTACTTTAAGAACTACATCCACATAGACATAGCTAACTGA
P181-2	PY06198	H2-Kd	SYIHRNTFL	5.36	LQDHSYIHRNTFLGDQV*	CTGCAGGACCATAGCTACATCCATAGAAACACCTTCCTAGGTGACCAGGTATGA
P181-3	PY06198	H2-Kd	NYITNYSEL	7.83	VERQNYITNYSELSKSG*	GTAGAGAGGCAGAACTACATAACTAACTATAGTGAGCTGTCTAAGTCTGGTTGA
P181-4	PY06198	H2-Kd	KYTNDMTYL	15.79	VARSKYTNDMTYLAKVH*	GTAGCTAGGTCTAAGTACACTAATGACATGACCTACCTAGCTAAGGTGCATTGA
P181-5	PY06198	H2-Kd	RYLLFQYPI	29.65	CLVDRYLLFQYPIKRQT*	TGTCTAGTAGATAGATACCTGCTGTTCCAGTACCCTATAAAAAGGCAAACCTGA
P181-6	PY06198	H2-Kd	KYSYIYAII	31.13	NRIEKYSYIYAIIEGSV*	AACCGGATAGAGAAGTATAGCTACATCTACGCCATAATAGAGGGTAGTGTTTGA
P181-7	PY06209	H2-Kd	KYLFYQSII	6.35	STVGKYLFYQSIIMGRV*	TCAACGGTAGGTAAGTACCTGTTCTACCAGAGCATAATAATGGGTAGAGTGTGA
P181-8	PY06209	H2-Kd	SYFDRKDTL	8.58	VFLLSYFDRKDTLKHVQ*	GTCTTCCTGCTGAGCTACTTTGATAGAAAGGACACCCTGAAGCACGTCCAGTGA
P181-9	PY06209	H2-Kd	SYFINMYYL	12.77	RSGDSYFINMYYLIILK*	CGTAGTGGTGATAGCTACTTCATAAACATGTACTACCTGATAATTTTGAAGTGA
P181-10	PY06209	H2-Kd	SFFNFIHHI	17.02	LQVYSFFNFIHHIRSLY*	CTACAGGTATATAGCTTCTTTAACTTCATCCACCACATAAGATCTCTCTATTGA
P182-1	PY06209	H2-Kd	KYYMMYNNM	22.27	NGRVKYYMMYNNMDKAF	AACGGTAGGGTGAAGTACTACATGATGTATAATAACATGGATAAAGCTAGGTGA
P182-2	PY06209	H2-Kd	SYVDKMAEI	38.95	NQDESYVDKMAEIEDAL*	AATCAGGATGAGAGCTACGTAGATAAGATGGCTGAGATAGAGGATGCTTTGTGA
P182-3	PY06210	H2-Kd	RYNVSFNFI	4.69	NDPPRYNVSFNFIHYGL*	AATGACCCTCCTAGATATAACGTGAGCTTTAACTTCATCCATTATGGTCTGTGA
P182-4	PY06214	H2-Kd	SYMYILASL	5.71	QKPGSYMYILASLTGET*	CAGAAACCAGGTAGCTACATGTACATCCTAGCTAGCCTGACCGGTGAAACATGA

P182-5	PY06214	H2-Kd	WQFPHFYSL	13.27	KAGRWQFPHFYSLTQSE	AAGGCTGGTAGATGGCAGTTCCCTCACTTCTATAGCCTGACACAGTCTGAGTGA
P182-6	PY06214	H2-Kd	IYYKFQQII	43.17	LSWNIYYKFQQIILGYL*	CTGAGTTGGAACATCTACTATAAGTTCCAGCAGATAATCCTAGGCTACTTATGA
P182-7	PY06214	H2-Kd	LYTCLYTPL	47.79	HQTVLYTCLYTPLKGSP*	CATCAGACTGTACTGTACACCTGCCTGTACACCCCTCTGAAAGGCTCTCCATGA
P182-8	PY06225	H2-Kd	KYVTKKHYI	10.43	VRCDKYVTKKHYIKYSG*	GTGAGATGTGATAAGTACGTGACTAAGAAGCACTACATAAAGTATTCTGGCTGA
P182-9	PY06225	H2-Kd	YYNGIATSV	24.97	CAYAYYNGIATSVGRFP*	TGCGCATACGCGTACTATAACGGCATAGCCACTAGCGTAGGCCGGTTCCCGTGA
P182-10	PY06225	H2-Ld	KPLANVYSI	23.52	YYFMKPLANVYSISKNE*	TACTACTTCATGAAGCCTCTAGCTAACGTGTATAGCATCTCTAAGAATGAGTGA
P183-1	PY06252	H2-Kd	KYINNKESL	5.41	TRQRKYINNKESLTFQK*	ACCCGTCAAAGAAAGTACATAAATAATAAGGAGAGCCTGACTTTCCAGAAGTGA
P183-2	PY06252	H2-Kd	IYVDSALSI	13.75	DALSIYVDSALSIALPP*	GACGCACTGAGCATCTACGTAGATAGCGCCCTGAGCATAGCGCTTCCTCCCTGA
P183-3	PY06252	H2-Kd	LYNFLLCPI	29.52	TDRVLYNFLLCPIFQSD*	ACTGACCGCGTGCTGTATAACTTCCTGCTGTGCCCTATCTTCCAGTCTGATTGA
P183-4	PY06252	H2-Kd	SYQYLRYLL	31.86	EDCDSYQYLRYLLVQLR*	GAAGATTGTGATAGCTACCAGTACCTGAGATACCTGCTAGTGCAGCTGAGATGA
P183-5	PY06260	H2-Kd	KYLDNTNHL	7.25	YAENKYLDNTNHLPKQL*	TACGCTGAGAATAAGTACCTAGATAACACTAACCACCTGCCTAAACAGCTCTGA
P183-6	PY06260	H2-Kd	IYNDNNLPI	23.07	ESRFIYNDNNLPIEIRG*	GAATCTAGATTCATCTATAATGATAATAACCTGCCTATAGAGATTCGCGGCTGA
P183-7	PY06307	H2-Kd	KYFPDKNML	7.71	EQPSKYFPDKNMLTWLS	GAGCAGCCGTCTAAGTACTTCCCTGATAAGAACATGCTGACCTGGTTAAGCTGA
P183-8	PY06307	H2-Kd	KYLNICDSV	26.56	FHKQKYLNICDSVTRMK*	TTCCATAAGCAGAAGTACCTGAACATCTGTGATAGCGTGACTCGTATGAAATGA
P183-9	PY06311	H2-Kd	KYIYNENTL	5.91	WPRSKYIYNENTLMAPK*	TGGCCTCGCTCTAAGTACATCTATAATGAGAACACCCTGATGGCTCCTAAGTGA
P183-10	PY06311	H2-Kd	MYFSTHNAL	7.26	VGCDMYFSTHNALRFML	GTAGGATGTGACATGTACTTTAGCACCCATAACGCCCTGCGCTTCATGCTGTGA
P184-1	PY06311	H2-Kd	GYILDLAEI	39.28	DLPVGYILDLAEIRITG*	GACCTCCCCGTAGGCTACATCCTAGACCTAGCTGAGATCCGCATAACAGGATGA
P184-2	PY06348	H2-Kd	KYITGNTRI	2.77	IREKKYITGNTRIPLPQ*	ATAAGAGAGAAAAAGTACATAACCGGTAACACTAGAATCCCTCTGCCACAGTGA
P184-3	PY06348	H2-Kd	KQFLNIYSI	11.36	NIQPKQFLNIYSIQDVF*	AACATCCAGCCTAAGCAGTTCCTGAACATCTATAGCATCCAGGATGTATTCTGA
P184-4	PY06348	H2-Kd	YYIKSDRFI	11.69	YFVPYYIKSDRFIAICA*	TATTTTGTACCGTACTACATAAAGAGTGATAGATTCATAGCCATATGCGCTTGA
P184-5	PY06348	H2-Ld	IPFENLQPL	39.35	SAEPIPFENLQPLRGQQ*	AGCGCTGAGCCGATCCCTTTTGAGAACCTGCAGCCTCTGCGTGGTCAGCAGTGA
P184-6	PY06362	H2-Kd	SQFFNFQKI	13.36	KENQSQFFNFQKIDLRF*	AAAGAGAACCAGAGCCAGTTCTTTAACTTCCAGAAGATAGATTTGCGCTTCTGA
P184-7	PY06362	H2-Kd	FYGNGNNNI	16.89	NEKEFYGNGNNNITLWK*	AATGAAAAAGAATTCTACGGTAACGGTAATAATAACATAACCCTGTGGAAGTGA
P184-8	PY06362	H2-Kd	FYNPNLCYV	19.97	KFPVFYNPNLCYVKIIQ*	AAGTTCCCGGTCTTCTATAACCCTAACCTGTGCTACGTGAAAATAATACAATGA
P184-9	PY06362	H2-Kd	YMIKYIFSI	34.26	SAQLYMIKYIFSIHIGP*	TCAGCTCAGCTGTACATGATAAAGTACATCTTTAGCATCCACATAGGCCCTTGA
P184-10	PY06362	H2-Kd	MFIKNLTHL	43.84	EGCLMFIKNLTHLSLTR*	GAGGGATGCTTGATGTTCATAAAGAACCTGACCCACCTGTCCCTGACCCGTTGA
P185-1	PY06422	H2-Kd	SYITNFNAL	3.77	QKAQSYITNFNALEKHE*	CAGAAGGCTCAGAGCTACATAACTAACTTTAACGCCCTAGAAAAACATGAGTGA
P185-2	PY06422	H2-Kd	AYNSNTNKI	15.84	IFDEAYNSNTNKIGTTP*	ATCTTTGATGAAGCCTATAATAGTAACACTAATAAGATAGGTACAACGCCATGA
P185-3	PY06422	H2-Kd	NYVQNRSVI	25.2	NNIGNYVQNRSVISLLS*	AATAATATAGGTAACTACGTGCAGAATAGAAGCGTGATAAGTCTGCTGAGCTGA
P185-4	PY06422	H2-Kd	TYISKNDII	39.58	MVKTTYISKNDIIGYVM*	ATGGTGAAGACAACCTACATAAGTAAGAATGACATAATAGGGTACGTAATGTGA
P185-5	PY06422	H2-Kd	YYAYKKNVI	42.24	KMEIYYAYKKNVIRQAL*	AAGATGGAGATTTACTACGCCTATAAGAAGAACGTGATAAGGCAGGCCCTCTGA
P185-6	PY06434	H2-Kd	RYYENISNI	2.83	SGTLRYYENISNIRFVH*	AGCGGTACTCTGAGATACTATGAGAACATAAGTAACATAAGATTTGTCCATTGA
P185-7	PY06434	H2-Kd	KFMNGLSKI	5.14	LNESKFMNGLSKIPMGL*	CTGAATGAGTCTAAGTTCATGAACGGCCTGAGTAAGATCCCCATGGGTCTGTGA
P185-8	PY06434	H2-Kd	SYNINCSFL	6.82	AEMHSYNINCSFLRTQD*	GCTGAGATGCATAGCTATAACATAAACTGTAGCTTCCTGCGCACGCAGGATTGA
P185-9	PY06434	H2-Kd	SYIQNEIVI	10.38	QNWVSYIQNEIVILCER*	CAGAACTGGGTGAGCTACATCCAGAATGAGATGATCCTCTGTGAGAGGTGA
P185-10	PY06434	H2-Kd	LYYIHNSYI	11.21	KVSYLYYIHNSYIRAQE*	AAGGTGAGCTATCTGTACTACATCCATAATAGCTACATAAGAGCACAAGAATGA
P186-1	PY06434	H2-Kd	NYIISHLTI	12.46	TNKVNYIISHLTILRSF*	ACTAATAAGGTGAACTACATAATAAGCCACCTGACCATCCTGAGGTCCTTCTGA
P186-2	PY06434	H2-Kd	FYSSTLFVL	13.9	SRVVFYSSTLFVLFLHW*	TCACGAGTAGTGTTCTATAGTAGCACCCTGTTCGTGCTGTTCCTACACTGGTGA
P186-3	PY06434	H2-Kd	SYNSSSEQI	16.6	KQSTSYNSSSEQINCIL*	AAACAGTCCACTAGCTATAATAGTAGTAGTGAGCAGATAAACTGTATCCTCTGA
P186-4	PY06434	H2-Kd	KYVILTDTI	16.96	APQPKYVILTDTIVYLL*	GCTCCACAGCCTAAGTACGTGATCCTGACTGACACCATAGTCTATCTGCTGTGA
P186-5	PY06434	H2-Kd	KYVINLNNL	19.94	PDERKYVINLNNLGAEV*	CCTGATGAGAGAAAGTACGTGATAAACCTGAATAACCTAGGGGCTGAAGTATGA
P186-6	PY06434	H2-Kd	KWLSSQSII	20.71	EAKKKWLSSQSIITHVV*	GAAGCTAAGAAGAAGTGGCTGAGTAGCCAGAGCATAATAACTCACGTAGTCTGA
P186-7	PY06434	H2-Kd	LYNLNFNFL	33.52	CAYQLYNLNFNFLRHGP*	TGTGCTTATCAACTGTATAACCTGAACTTTAACTTCCTGAGGCATGGACCTTGA
P186-8	PY06434	H2-Kd	LFMKNFNYI	46.82	LQAALFMKNFNYISLDR*	CTTCAAGCAGCCCTGTTCATGAAGAACTTTAACTACATAAGTCTAGATCGGTGA
P186-9	PY06434	H2-Kd	IFSNNISPI	49.47	NVSEIFSNNISPISTQT*	AACGTGAGTGAGATCTTTAGTAATAACATAAGCCCTATCTCGACACAGACCTGA
P186-10	PY06434	H2-Ld	LPIFNFIPI	24.25	WSVALPIFNFIPILYLD*	TGGTCCGTAGCTCTGCCTATCTTTAACTTCATCCCTATCCTGTACTTAGACTGA
P187-1	PY06446	H2-Kd	IYVEIITPL	20.54	SSKYIYVEIITPLFCRD*	AGTTCTAAATATATCTACGTAGAGATAATAACCCCTCTGTTCTGTAGAGATTGA
P187-2	PY06459	H2-Kd	MYLTAHEKI	17.37	DESKMYLTAHEKITTIP*	GATGAAAGTAAGATGTACCTGACCGCCCATGAGAAGATAACCACAATTCCATGA
P187-3	PY06460	H2-Kd	YYLLLSHQL	42.15	RLGVYYLLLSHQLPLED*	CGTTTAGGTGTCTACTACCTGCTGCTGAGCCACCAGCTGCCTCTAGAAGATTGA
P187-4	PY06465	H2-Kd	KYLNSLVMI	5.38	ADGQKYLNSLVMIDEES*	GCTGACGGCCAGAAGTACCTGAATAGCCTAGTGATGATAGATGAAGAGTCTTGA
P187-5	PY06587	H2-Kd	IYIQISNFI	8.43	YSEMIYIQISNFIGFHT*	TATAGTGAAATGATCTACATCCAGATAAGTAACTTCATAGGATTTCACACTTGA
P187-6	PY06587	H2-Kd	KYLLTIISI	12.82	NKRAKYLLTIISILAES*	AATAAGCGGGCTAAGTACCTGCTGACCATAATAAGCATCCTAGCTGAGTCATGA
P187-7	PY06587	H2-Kd	FYSKYLLTI	17.61	LPNRFYSKYLLTILRKE*	CTGCCTAATAGGTTCTATAGTAAGTACCTGCTGACCATCCTGAGGAAGGAGTGA
P187-8	PY06587	H2-Kd	SFIGNINNI	23.9	FSLCSFIGNINNICAES*	TTCTCACTGTGTAGCTTCATAGGTAACATAAATAACATCTGCGCTGAGTCTTGA
P187-9	PY06601	H2-Kd	RQWGNWNYI	15.29	LLNPRQWGNWNYIDGQI	CTACTGAACCCTAGACAGTGGGGTAACTGGAACTACATAGACGGACAGATCTGA
P187-10	PY06601	H2-Kd	MYHYFMTEI	19.41	TGYMMYHYFMTEIETSL*	ACTGGCTACATGATGTACCACTACTTCATGACTGAGATAGAGACCTCCTTGTGA
P188-1	PY06601	H2-Ld	YPWEISIPF	27.26	WQHMYPWEISIPFFFAC*	TGGCAGCATATGTACCCTTGGGAGATAAGCATCCCTTTCTTTTTTGCATGTTGA
P188-2	PY06632	H2-Kd	RYKNNLTII	9.3	GTSERYKNNLTIITSIA*	GGAACTAGTGAGAGATATAAGAATAACCTGACCATAATAACCTCCATAGCCTGA
P188-3	PY06632	H2-Kd	NYYCNLDYL	21.61	LACINYYCNLDYLGYRA*	CTAGCATGTATAAACTACTACTGTAACCTAGACTACCTAGGCTACCGGGCTTGA
P188-4	PY06632	H2-Kd	IYLRHLYII	30.8	CVRTIYLRHLYIICRLQ*	TGTGTCCGTACCATCTACCTGAGACACCTGTACATAATCTGTAGGCTGCAGTGA
P188-5	PY06638	H2-Kd	IYFYEQNSI	10.73	HIGFIYFYEQNSIFCPT*	CACATAGGCTTTATCTACTTCTATGAGCAGAATAGCATCTTCTGCCCGACATGA
P188-6	PY06638	H2-Kd	NYIKNNGNI	42.38	LENINYIKNNGNIIRGI*	CTAGAGAACATAAACTACATAAAGAATAACGGTAACATAATACGTGGAATATGA
P188-7	PY06638	H2-Kd	GYYRQNNKI	45.53	SRTIGYYRQNNKIRSKA*	TCTAGGACCATAGGCTACTATAGACAGAATAATAAGATAAGGTCTAAAGCTTGA
P188-8	PY06648	H2-Kd	YYLDVKENI	11.89	VPEAYYLDVKENIMSKC*	GTCCCTGAGGCGTACTACCTAGACGTGAAGGAGAACATAATGTCTAAGTGCTGA
P188-9	PY06648	H2-Kd	KYLKSKLDI	42.94	YAEDKYLKSKLDILKQL*	TATGCTGAAGATAAGTACCTGAAGAGTAAGCTAGACATCCTGAAGCAACTGTGA
P188-10	PY06695	H2-Kd	EYITIYFTI	25.74	INFKEYITIYFTIRGNS*	ATAAATTTTAAAGAGTACATAACCATCTACTTCACCATAAGGGGTAACTCTTGA
P189-1	PY06703	H2-Kd	LYNIGNSEI	18.44	LPRCLYNIGNSEIMSQG*	CTGCCCCGGTGTCTGTATAACATAGGTAATAGTGAGATAATGTCTCAAGGGTGA
P189-2	PY06739	H2-Kd	KYLDAIYSI	4.62	EPVDKYLDAIYSIARAE*	GAACCAGTAGATAAGTACCTAGACGCCATCTATAGCATAGCCCGGGCTGAGTGA
P189-3	PY06739	H2-Kd	FYVYVNISI	16.58	LTLGFYVYVNISIAYMP*	CTGACTCTAGGATTCTACGTGTACGTGAACATAAGCATAGCCTATATGCCTTGA
P189-4	PY06739	H2-Kd	kYANSNYnL	34.2	AQIRKYANSNYNLVDGE*	GCCCAGATACGTAAGTACGCTAATAGTAACTATAACCTAGTAGACGGTGAATGA
P189-5	PY06739	H2-Kd	rYANSNYtL	34.2	PGSRRYANSNYTLGDTT*	CCCGGCTCACGTAGATACGCTAATAGTAACTACACCCTAGGTGACACAACCTGA
P189-6	PY06739	H2-Kd	kYANSNYtL	34.2	STVAKYANSNYTLILTS*	TCCACTGTAGCTAAGTACGCTAATAGTAACTACACCCTGATCTTAACTTCATGA
P189-7	PY06739	H2-Kd	rYANSNYnL	34.2	KSRFRYANSNYNLRSIS*	AAGAGTAGATTTAGATACGCTAATAGTAACTATAACCTGCGTAGCATCTCATGA
P189-8	PY06767	H2-Kd	QYHGYNSVI	17.67	NMWLQYHGYNSVIDDSP	AACATGTGGCTTCAGTACCACGGCTATAATAGCGTGATAGATGACTCCCCATGA
P189-9	PY06767	H2-Kd	KYLGQIIKI	46.53	SAQTKYLGQIIKIFMEL*	TCCGCTCAAACTAAGTACCTAGGCCAGATAATAAAGATCTTCATGGAACTATGA
P189-10	PY06772	H2-Kd	RYIYSYGDI	19.81	HNSGRYIYSYGDILLAM*	CATAACTCGGGTAGATACATCTATAGCTACGGTGACATCCTGCTAGCTATGTGA
P190-1	PY06772	H2-Kd	KYIGLLKKL	42.19	KALDKYIGLLKKLHLTI*	AAAGCTCTAGATAAGTACATAGGCCTGCTGAAGAAGCTGCATCTGACTATCTGA
P190-2	PY06781	H2-Kd	KYNFSPGKI	34.49	SIPTKYNFSPGKIPTWN*	AGCATACCCACTAAGTATAACTTTAGCCCTGGTAAGATCCCCACATGGAATTGA
P190-3	PY06844	H2-Kd	SYISNNIFI	4.37	WRGISYISNNIFIPPDQ*	TGGAGAGGTATAAGCTACATAAGTAATAACATCTTCATCCCTCCTGATCAGTGA
P190-4	PY06844	H2-Kd	YYNAISSIL	7.42	LQDVYYNAISSILMPIM*	CTGCAGGACGTATACTATAACGCCATAAGTAGCATCCTGATGCCCATAATGTGA
P190-5	PY06844	H2-Kd	EYYNAISSI	16.43	TAQAEYYNAISSIKSDG*	ACTGCTCAGGCTGAGTACTATAACGCCATAAGTAGCATAAAGTCTGACGGGTGA
P190-6	PY06844	H2-Kd	CYFEYRFIL	19.8	IEVECYFEYRFILRVMG*	ATAGAAGTAGAATGCTACTTTGAGTATAGATTCATCCTGAGGGTAATGGGATGA
P190-7	PY06844	H2-Kd	VYNDFYYTI	21.25	KNKEVYNDFYYTICPLV*	AAGAATAAAGAAGTGTATAATGACTTCTACTACACCATCTGTCCCTTAGTGTGA
P190-8	PY06844	H2-Kd	KYLFCLFML	30.46	MVTRKYLFCLFMLKASN*	ATGGTAACTAGGAAGTACCTGTTCTGCCTGTTCATGCTGAAGGCTTCTAACTGA
P190-9	PY06861	H2-Kd	KFYDAFSTL	19.94	VLVTKFYDAFSTLKFQN*	GTGCTAGTGACTAAGTTCTATGACGCCTTTAGCACCCTGAAATTCCAGAACTGA
P190-10	PY06861	H2-Kd	YYTKNNINI	22.25	QGSSYYTKNNINIIHAT*	CAGGGTAGTAGCTACTACACTAAGAATAACATAAACATAATTCATGCCACGTGA
P191-1	PY06861	H2-Kd	FYIVLYISL	49.35	FTKEFYIVLYISLVDKG*	TTCACTAAGGAATTCTACATAGTGCTGTACATAAGCCTAGTAGATAAAGGATGA
P191-2	PY06873	H2-Kd	FYMLTAHSL	5.35	ADSNFYMLTAHSLLLSF*	GCTGATAGTAATTTCTACATGCTGACCGCCCATAGCCTGCTCCTGAGCTTTTGA
P191-3	PY06873	H2-Kd	AYSNLCVYI	25.93	DLEDAYSNLCVYIDVPF*	GATCTAGAGGATGCCTATAGTAACCTGTGCGTGTACATAGATGTTCCCTTCTGA
P191-4	PY06873	H2-Kd	TYYFTIPKL	29.03	LPAQTYYFTIPKLQTNH*	CTCCCAGCTCAGACCTACTACTTCACCATCCCTAAGCTGCAGACTAATCACTGA
P191-5	PY06924	H2-Kd	YYSYVCGEL	30.95	ESALYYSYVCGELPSGS*	GAATCCGCCCTGTACTATAGCTACGTGTGCGGTGAGCTGCCATCTGGCTCATGA
P191-6	PY06924	H2-Kd	SYVCGELNL	44.11	FPGSSYVCGELNLFPWC	TTCCCAGGGTCTAGCTACGTGTGCGGTGAGCTGAACCTGTTTCCCTGGTGCTGA
P191-7	PY06925	H2-Kd	KMNKHFSSI	20.57	NRQGKMNKHFSSIPQNP	AACCGCCAGGGTAAGATGAATAAGCACTTTAGTAGCATCCCCCAGAATCCATGA
P191-8	PY06986	H2-Kd	FYQSTLSLV	18.32	ESIGFYQSTLSLVQISR*	GAGAGCATAGGATTCTACCAGAGCACCCTGAGCCTAGTGCAGATCTCTAGGTGA
P191-9	PY06986	H2-Kd	LYFVNERSI	26.46	LLSPLYFVNERSIGDRI*	CTGCTGAGTCCTCTGTACTTCGTGAATGAGAGAAGCATAGGTGATCGGATCTGA
P191-10	PY07005	H2-Kd	MYNSSLHII	5.66	HNLCMYNSSLHIIMSLK*	CATAACCTGTGCATGTATAATAGTAGCCTGCACATAATAATGTCGCTGAAGTGA
P192-1	PY07005	H2-Kd	KYQGINDSI	6.76	MNELKYQGINDSITQIC*	ATGAATGAACTGAAGTACCAGGGCATAAATGATAGCATAACGCAGATCTGTTGA
P192-2	PY07005	H2-Kd	YYISLVKNI	13.59	TVLAYYISLVKNILRDL*	ACGGTGCTAGCATACTACATAAGCCTAGTGAAGAACATCCTGAGGGACCTGTGA
P192-3	PY07005	H2-Kd	FYFNIYLFL	18.15	KSLIFYFNIYLFLTKGT*	AAATCCCTGATATTCTACTTTAACATCTACCTGTTCCTGACTAAAGGTACTTGA
P192-4	PY07005	H2-Kd	RYKQHLNNL	43.98	LYVTRYKQHLNNLGRLT*	TTATATGTGACTAGATATAAGCAGCACCTGAATAACCTAGGTAGACTGACCTGA
P192-5	PY07026	H2-Kd	NYIFVHISL	43.64	LYEVNYIFVHISLLEPR*	CTGTATGAGGTGAACTACATCTTCGTGCACATAAGCCTGCTAGAACCTAGATGA

P192-6	PY07039	H2-Kd	IYLCCFSNI	7.74	DVPHIYLCCFSNINYHC*	GACGTTCCTCATATCTACCTGTGCTGCTTTAGTAACATAAATTACCATTGTTGA
P192-7	PY07039	H2-Kd	YYLNIKKNI	38.13	FGQLYYLNIKKNIPLEE*	TTCGGACAACTGTACTACCTGAACATAAAGAAGAACATCCCGCTAGAGGAGTGA
P192-8	PY07039	H2-Kd	KSIFMYSLI	40.83	SLTTKSIFMYSLIHTDA*	TCTCTGACCACTAAGAGCATCTTCATGTATAGCCTGATCCATACTGACGCATGA
P192-9	PY07061	H2-Kd	FYTLTLSEI	11.84	LKSIFYTLTLSEINFSK*	CTGAAGTCTATCTTCTACACCCTGACCCTGAGTGAGATAAATTTCTCTAAGTGA
P192-10	PY07061	H2-Kd	IYSQNINKI	14.27	HCRYIYSQNINKIEAVV*	CACTGTCGGTATATCTATAGCCAGAACATAAATAAGATAGAGGCCGTAGTATGA
P193-1	PY07061	H2-Kd	YYKDTHPQI	17.77	SVVIYYKDTHPQIGSLL*	TCTGTAGTGATTTACTATAAGGACACCCACCCTCAGATAGGTAGTCTGCTGTGA
P193-2	PY07061	H2-Kd	FYSFYTLTL	39.03	SRSFFYSFYTLTLYRFY*	TCTAGGTCCTTTTTCTATAGCTTCTACACCCTGACCCTGTATAGGTTCTACTGA
P193-3	PY07067	H2-Kd	SYFFLLYAI	5.49	FFSASYFFLLYAILDQC*	TTTTTTAGTGCTAGCTACTTCTTCCTGCTGTACGCCATCCTAGACCAGTGCTGA
P193-4	PY07067	H2-Kd	SYRSSNSSI	8.77	KEQNSYRSSNSSITGHG*	AAGGAACAGAATAGCTATAGAAGTAGTAATAGTAGCATAACAGGCCACGGTTGA
P193-5	PY07067	H2-Ld	KPNANLSLF	31.98	HLQQKPNANLSLFGNAP*	CACCTCCAGCAGAAGCCTAACGCTAACCTGAGCCTGTTCGGTAACGCTCCATGA
P193-6	PY07101	H2-Kd	VYIWGTFYI	4.87	IMAFVYIWGTFYIYNGY*	ATAATGGCGTTCGTGTACATCTGGGGCACCTTCTACATCTATAACGGCTATTGA
P193-7	PY07101	H2-Kd	SYNSYIHKL	9.57	FVDQSYNSYIHKLQGGL*	TTCGTAGATCAGAGCTATAATAGCTACATCCATAAGCTGCAAGGGGGTCTCTGA
P193-8	PY07154	H2-Kd	NYFKAAVEL	40.95	AYAKNYFKAAVELASRV*	GCATACGCTAAAAACTACTTTAAGGCCGCCGTAGAGCTAGCCTCTAGAGTCTGA
P193-9	PY07154	H2-Ld	IPFYNKLIL	43.67	LMLQIPFYNKLILRPSR*	CTAATGCTTCAGATCCCTTTCTATAATAAGCTGATCCTGCGCCCCTCTAGATGA
P193-10	PY07179	H2-Kd	KYNGIHSYI	3.48	IRNQKYNGIHSYIDGDH*	ATAAGAAACCAGAAGTATAACGGCATCCATAGCTACATAGACGGTGACCATTGA
P194-1	PY07179	H2-Kd	SYNNFNSII	5.3	FLSVSYNNFNSIIDTPG*	TTTCTCTCAGTGAGCTATAATAACTTTAATAGCATAATAGACACCCCAGGCTGA
P194-2	PY07179	H2-Kd	SYSTTICNI	7.42	GGSGSYSTTICNIQYNF*	GGCGGATCTGGTAGCTATAGCACCACCATCTGTAACATCCAGTATAATTTCTGA
P194-3	PY07179	H2-Kd	NYIHNKYQI	9.12	VLGQNYIHNKYQITSLP*	GTGTTAGGGCAGAACTACATCCATAATAAGTACCAGATAACATCCCTTCCCTGA
P194-4	PY07179	H2-Kd	KYIYIKYGI	10.94	SALWKYIYIKYGIPPEV*	TCTGCACTGTGGAAGTACATCTACATAAAGTACGGCATCCCACCTGAGGTGTGA
P194-5	PY07179	H2-Kd	SYFLACDNI	12.01	LHKKSYFLACDNIQAAG*	CTGCATAAAAAAAGCTACTTCCTAGCCTGTGATAACATCCAAGCAGCCGGTTGA
P194-6	PY07179	H2-Kd	KYIDFKKSL	24.56	IEEPKYIDFKKSLDQSK*	ATAGAAGAGCCTAAGTACATAGACTTTAAGAAGAGCCTAGATCAGTCTAAGTGA
P194-7	PY07179	H2-Kd	NYIDNDFLI	30.5	SRAWNYIDNDFLIHLLQ*	TCTAGGGCCTGGAACTACATAGATAATGACTTCCTGATCCATTTGCTACAGTGA
P194-8	PY07179	H2-Kd	YSYNNFNSI	32.77	TDHTYSYNNFNSIKIPK*	ACTGATCATACTTATAGCTATAATAACTTTAATAGCATAAAAATTCCTAAGTGA
P194-9	PY07179	H2-Kd	AYMDSNGKI	34.98	ERLTAYMDSNGKISGSP*	GAGCGGTTGACAGCCTACATGGATAGTAACGGTAAGATCTCAGGATCCCCTTGA
P194-10	PY07196	H2-Kd	YYINSNYFI	2.66	FQLSYYINSNYFIAASP*	TTTCAGCTGAGCTACTACATAAATAGTAACTACTTCATAGCTGCTAGCCCCTGA
P195-1	PY07196	H2-Kd	IYNDNTNFI	7.09	IPMPIYNDNTNFITDRH*	ATTCCTATGCCAATCTATAATGATAACACTAACTTCATAACTGACCGCCATTGA
P195-2	PY07196	H2-Kd	SYNAIAYVI	8.04	SDQNSYNAIAYVICGQT*	TCTGACCAAAATAGCTATAACGCCATAGCCTACGTGATCTGTGGTCAGACCTGA
P195-3	PY07196	H2-Kd	YYVPIRGKI	11.49	IRDTYYVPIRGKIIFNP*	ATTCGTGATACGTACTACGTGCCTATAAGAGGTAAGATAATATTTAATCCTTGA
P195-4	PY07196	H2-Kd	LYFYDFPFI	15.96	SERDLYFYDFPFITLEC*	TCTGAAAGGGATCTGTACTTCTATGACTTCCCTTTCATAACTCTAGAGTGTTGA
P195-5	PY07196	H2-Kd	LYFVSQLAI	23.29	EQFSLYFVSQLAIRKCV*	GAACAATTTTCCCTGTACTTCGTGAGCCAGCTAGCCATCCGTAAATGCGTTTGA
P195-6	PY07196	H2-Kd	KYVVIVSIL	38.41	IFIDKYVVIVSILGRLH*	ATTTTCATAGATAAGTACGTAGTGATAGTGAGCATCCTAGGGCGCCTGCACTGA
P195-7	PY07214	H2-Kd	KYIFQSSLL	11.07	YAAMKYIFQSSLLGLRF*	TATGCTGCTATGAAGTACATCTTCCAGAGTAGCCTGCTAGGGTTGAGATTTTGA
P195-8	PY07214	H2-Kd	KFLYTLNFI	43.02	LYQDKFLYTLNFILFTR*	CTGTACCAGGATAAGTTCCTGTACACCCTGAACTTCATCCTCTTTACTCGATGA
P195-9	PY07228	H2-Ld	SPYLSSFFL	21.21	WKKGSPYLSSFFLSSHH*	TGGAAGAAAGGTAGCCCTTACCTGAGTAGCTTCTTCCTGTCCTCCCACCATTGA
P195-10	PY07248	H2-Kd	IYIENSNQL	12.72	EASAIYIENSNQLNSLL*	GAGGCATCCGCTATCTACATAGAGAATAGTAACCAGCTGAATAGCCTACTTTGA
P196-1	PY07248	H2-Kd	SEFGFFHNI	33.66	FELLSEFGFFHNIIKCG*	TTTGAGCTGCTGAGTGAGTTCGGCTTCTTCCATAACATAATAAAATGCGGGTGA
P196-2	PY07248	H2-Kd	HYNEIVWEL	46.2	SGKKHYNEIVWELIGTD*	TCAGGTAAAAAACACTATAATGAGATAGTGTGGGAGCTGATAGGCACTGATTGA
P196-3	PY07292	H2-Kd	IYYSNIPQI	4.57	ARSRIYYSNIPQIPTPQ*	GCTCGTTCCCGAATCTACTATAGTAACATCCCTCAGATCCCCACTCCGCAGTGA
P196-4	PY07320	H2-Kd	KYRYNFNKI	20.36	AHFQKYRYNFNKIGTFF*	GCCCACTTCCAGAAGTATAGATATAACTTTAATAAGATAGGGACGTTTTTCTGA
P196-5	PY07326	H2-Kd	SYINGDLNL	12.86	DANFSYINGDLNLQPLR*	GATGCTAACTTTAGCTACATAAACGGTGACCTGAACCTGCAGCCGTTAAGATGA
P196-6	PY07326	H2-Kd	TYIHHINEL	13.75	YIPLTYIHHINELFHPK*	TATATTCCCCTGACCTACATCCACCACATAAATGAGCTGTTCCATCCTAAATGA
P196-7	PY07326	H2-Kd	IYNTGKGSI	23.78	ESDSIYNTGKGSIGAGT*	GAGTCTGACTCAATCTATAACACCGGTAAGGGTAGCATAGGAGCTGGGACGTGA
P196-8	PY07326	H2-Kd	GYLLDVSEI	28.17	SSQYGYLLDVSEILSQE*	TCTTCTCAGTACGGCTACCTGCTAGACGTGAGTGAGATCCTGAGCCAGGAATGA
P196-9	PY07326	H2-Kd	NYHCNFVCI	46.64	NATENYHCNFVCITACL*	AACGCAACTGAAAACTACCACTGTAACTTCGTGTGCATAACAGCCTGTCTGTGA
P196-10	PY07355	H2-Kd	NYFVNYINI	18.72	LDEGNYFVNYINISQEL*	CTAGATGAGGGTAACTACTTCGTGAACTACATAAACATCTCCCAAGAACTTTGA
P197-1	PY07355	H2-Kd	EYFAMPNII	26.59	VFEPEYFAMPNIIKCEN*	GTTTTTGAGCCTGAGTACTTCGCCATGCCTAACATAATAAAGTGTGAGAATTGA
P197-2	PY07390	H2-Kd	SYIPFHFPI	3.17	EFFQSYIPFHFPIIYLL*	GAATTCTTCCAGAGCTACATCCCTTTCCACTTCCCTATAATATACCTGCTGTGA
P197-3	PY07392	H2-Kd	LYFYMSCVI	7.91	QKTFLYFYMSCVITFWS*	CAGAAGACTTTCCTGTACTTCTACATGAGCTGCGTGATAACCTTCTGGTCATGA
P197-4	PY07392	H2-Kd	YYENRISSL	20.11	NFEKYYENRISSLQLII*	AACTTTGAAAAGTACTATGAGAATAGAATAAGTAGCCTGCAACTAATAATCTGA
P197-5	PY07392	H2-Kd	YYLQTGNDI	32.74	VLVDYYLQTGNDIAPNS*	GTGCTAGTAGATTACTACCTGCAGACCGGTAATGACATAGCTCCTAACTCATGA
P197-6	PY07392	H2-Kd	TYISNYGYV	38.51	CARDTYISNYGYVELHL*	TGCGCCCGTGACACCTACATAAGTAACTACGGCTACGTAGAGTTGCACTTGTGA
P197-7	PY07392	H2-Kd	IYSDTPYII	40.79	GIQLIYSDTPYIIFYTS*	GGAATTCAGCTAATCTATAGTGACACCCCTTACATAATCTTTTACACTAGCTGA
P197-8	PY07392	H2-Kd	FYRTVDDNI	49.39	LYTSFYRTVDDNIVEYV*	CTTTACACCTCTTTCTATAGAACCGTAGATGATAACATAGTAGAATATGTGTGA
P197-9	PY07416	H2-Kd	IYQNNRINI	13.91	RHSRIYQNNRINILFLA*	AGACATTCACGCATCTACCAGAATAATAGAATAAACATCCTGTTTCTAGCTTGA
P197-10	PY07416	H2-Kd	SYTEIYENI	17.47	RHVISYTEIYENIVVTD*	AGGCACGTAATAAGCTACACTGAGATCTATGAGAACATAGTAGTAACTGACTGA
P198-1	PY07416	H2-Kd	GYNNNNMLI	26.67	CQFGGYNNNNMLICGSI*	TGTCAGTTCGGCGGCTATAATAATAATAACATGCTGATCTGCGGATCCATCTGA
P198-2	PY07416	H2-Kd	NYNNIYPNI	31.02	QAPANYNNIYPNICATA*	CAGGCACCCGCTAACTATAATAACATCTACCCTAACATCTGCGCTACCGCCTGA
P198-3	PY07424	H2-Kd	YYSPSSYAI	4.5	PMKHYYSPSSYAIFGQG*	CCAATGAAGCACTACTATAGCCCTAGTAGCTACGCCATCTTCGGGCAGGGGTGA
P198-4	PY07424	H2-Kd	FYHDHFVNI	12.72	LVLKFYHDHFVNIHSEL*	TTAGTGTTAAAGTTCTACCATGACCACTTCGTGAACATCCATAGTGAGCTGTGA
P198-5	PY07424	H2-Kd	AYFRNSNLL	19.64	HGAKAYFRNSNLLTASR*	CATGGCGCTAAGGCCTACTTTAGAAATAGTAACCTGCTGACAGCGTCTCGATGA
P198-6	PY07428	H2-Kd	TYIKNVQNL	17.37	ELTCTYIKNVQNLEEKT*	GAACTGACTTGCACCTACATAAAGAACGTGCAGAACCTAGAGGAGAAAACTTGA
P198-7	PY07453	H2-Kd	IYNNLLNNI	13.8	GAEVIYNNLLNNIETKE*	GGTGCTGAAGTAATCTATAATAACCTGCTGAATAACATAGAGACTAAGGAGTGA
P198-8	PY07453	H2-Kd	LYIEQMDPI	39.59	SPATLYIEQMDPIQRVM*	TCTCCTGCTACGCTGTACATAGAGCAGATGGACCCTATCCAGCGGGTGATGTGA
P198-9	PY07453	H2-Ld	RPLAESFNM	45.59	VHQFRPLAESFNMRIAA*	GTCCATCAATTTAGACCTCTAGCTGAGAGCTTTAACATGCGCATAGCTGCCTGA
P198-10	PY07489	H2-Kd	VYNKVCDVL	44.08	IGFGVYNKVCDVLMRDM*	ATAGGGTTTGGTGTGTATAATAAGGTGTGTGACGTGCTGATGCGTGACATGTGA
P199-1	PY07492	H2-Kd	SYYENGEII	13.93	YESKSYYENGEIIKCTA*	TATGAGTCTAAGAGCTACTATGAGAACGGTGAGATAATAAAGTGTACTGCCTGA
P199-2	PY07549	H2-Kd	YYVTLLRFI	21.62	SPRGYYVTLLRFIPPPA*	AGTCCCCGCGGATACTACGTGACCCTGCTGAGATTCATCCCTCCCCCCGCTTGA
P199-3	PY07584	H2-Kd	IYFFNKIFI	11.95	IPQAIYFFNKIFILAGS*	ATCCCACAGGCGATCTACTTCTTTAATAAGATCTTCATCCTAGCAGGATCCTGA
P199-4	PY07596	H2-Kd	VYINNDSYI	5.42	SQFIVYINNDSYIAPAV*	AGTCAGTTTATAGTGTACATAAATAATGATAGCTACATAGCACCTGCCGTATGA
P199-5	PY07596	H2-Kd	SFFNTINQI	11.85	DIATSFFNTINQIDPMA*	GACATAGCCACTAGCTTCTTTAACACCATAAACCAGATAGATCCAATGGCATGA
P199-6	PY07596	H2-Kd	AYSYNNHNI	18.21	LDQTAYSYNNHNIALNA*	CTAGACCAGACCGCCTATAGCTATAATAACCATAACATAGCCCTGAACGCATGA
P199-7	PY07598	H2-Kd	EYNNNLYSI	20.81	HVSLEYNNNLYSIRQVT*	CACGTGAGCTTAGAGTATAATAATAACCTGTATAGCATCCGCCAAGTAACATGA
P199-8	PY07654	H2-Ld	FPWKNHLVV	45.56	DGLPFPWKNHLVVPYSS*	GACGGACTGCCCTTCCCTTGGAAGAACCACCTAGTAGTGCCATATAGTTCTTGA