



NetMHCII 2.0 Server - prediction results

Technical University of Denmark

Input is in FSA format
NetMHCII version 2.0.

Strong binder threshold 50.00. Weak binder threshold 500.00.

Allele	pos	peptide	core	1-log50k(aff)	affinity(nM)	Bind	Level	%Random	Identity
DRB1_0101	188	YRAWRHFIAMRASEH	WRHFIAMRA	0.8860	3.4	SB	0.40	Rv2754c, T	
DRB1_0101	189	RAWRHFIAMRASEHA	WRHFIAMRA	0.8808	3.6	SB	0.80	Rv2754c, T	
DRB1_0101	187	NYRAWRHFIAMRASE	WRHFIAMRA	0.8802	3.7	SB	0.80	Rv2754c, T	
DRB1_0101	186	GYRAWRHFIAMRAS	WRHFIAMRA	0.8783	3.7	SB	0.80	Rv2754c, T	
DRB1_0101	212	IECLRQLAAVAPAVF	LRQLAAVAP	0.8739	3.9	SB	0.80	Rv2754c, T	
DRB1_0101	185	TGNRYAWRHFIAMRA	WRHFIAMRA	0.8717	4.0	SB	1.00	Rv2754c, T	
DRB1_0101	191	WRHFIAMRASEHADV	FIAMRASEH	0.8702	4.1	SB	1.00	Rv2754c, T	
DRB1_0101	190	AWRHFIAMRASEHAD	WRHFIAMRA	0.8668	4.2	SB	2.00	Rv2754c, T	
DRB1_0101	66	VGHFSVLEHASVSFY	FSVLEHASV	0.8637	4.4	SB	2.00	Rv2754c, T	
DRB1_0101	211	AIECLRQLAAVAPAV	LRQLAAVAP	0.8611	4.5	SB	2.00	Rv2754c, T	
DRB1_0101	213	ECLRQLAAVAPAVFA	LRQLAAVAP	0.8570	4.7	SB	2.00	Rv2754c, T	
DRB1_0101	127	LRHILTEAADAARAT	ILTEAADAA	0.8412	5.6	SB	4.00	Rv2754c, T	
DRB1_0101	214	CLRQLAAVAPAVFAD	LRQLAAVAP	0.8405	5.6	SB	4.00	Rv2754c, T	
DRB1_0101	192	RHFIAMRASEHADVE	FIAMRASEH	0.8398	5.7	SB	4.00	Rv2754c, T	
DRB1_0101	67	GHFSVLEHASVSFYI	FSVLEHASV	0.8397	5.7	SB	4.00	Rv2754c, T	
DRB1_0101	65	DVGHFSVLEHASVSF	FSVLEHASV	0.8392	5.7	SB	4.00	Rv2754c, T	
DRB1_0101	179	ETRIVVTGNYRAWRH	IVVTGNYRA	0.8317	6.2	SB	4.00	Rv2754c, T	
DRB1_0101	76	SVSFYITGISRSCTH	FYITGISRS	0.8316	6.2	SB	4.00	Rv2754c, T	
DRB1_0101	210	LAIECLRQLAAVAPA	LRQLAAVAP	0.8311	6.2	SB	4.00	Rv2754c, T	
DRB1_0101	180	TRIVVTGNYRAWRHF	IVVTGNYRA	0.8154	7.4	SB	8.00	Rv2754c, T	
DRB1_0101	215	LRQLAAVAPAVFADF	LRQLAAVAP	0.8144	7.4	SB	8.00	Rv2754c, T	
DRB1_0101	126	DLRHILTEAADAARA	ILTEAADAA	0.8106	7.8	SB	8.00	Rv2754c, T	
DRB1_0101	209	RLAIECLRQLAAVAP	IECLRQLAA	0.8099	7.8	SB	8.00	Rv2754c, T	
DRB1_0101	77	VSFYITGISRSCTHE	FYITGISRS	0.8096	7.8	SB	8.00	Rv2754c, T	
DRB1_0101	68	HFSVLEHASVSFYIT	FSVLEHASV	0.8066	8.1	SB	8.00	Rv2754c, T	
DRB1_0101	193	HFIAMRASEHADVEI	FIAMRASEH	0.8029	8.4	SB	8.00	Rv2754c, T	
DRB1_0101	128	RHILTEAADAARATY	ILTEAADAA	0.7999	8.7	SB	8.00	Rv2754c, T	
DRB1_0101	97	HFSYSQLSQRYVPEK	YSQLSQRYV	0.7947	9.2	SB	8.00	Rv2754c, T	
DRB1_0101	75	ASVSFYITGISRSCT	FYITGISRS	0.7946	9.2	SB	8.00	Rv2754c, T	
DRB1_0101	64	IDVGHFSVLEHASVS	FSVLEHASV	0.7892	9.8	SB	8.00	Rv2754c, T	
DRB1_0101	208	RRLAIECLRQLAAVA	IECLRQLAA	0.7885	9.9	SB	8.00	Rv2754c, T	
DRB1_0101	178	TRIVVTGNYRAWRHF	IVVTGNYRA	0.7883	9.9	SB	8.00	Rv2754c, T	
DRB1_0101	181	RIVVTGNYRAWRHF	IVVTGNYRA	0.7741	11.5	SB	16.00	Rv2754c, T	
DRB1_0101	125	ADLRHILTEAADAAR	ILTEAADAA	0.7740	11.5	SB	16.00	Rv2754c, T	
DRB1_0101	96	RHFSYSQLSQRYVPE	YSQLSQRYV	0.7701	12.0	SB	16.00	Rv2754c, T	
DRB1_0101	194	FIAMRASEHADVEIR	FIAMRASEH	0.7695	12.1	SB	16.00	Rv2754c, T	
DRB1_0101	78	SFYITGISRSCTHEL	FYITGISRS	0.7691	12.2	SB	16.00	Rv2754c, T	
DRB1_0101	150	EAKFADQPNAILRRK	FADQPNAIL	0.7666	12.5	SB	16.00	Rv2754c, T	
DRB1_0101	129	HILTEAADAARATYS	ILTEAADAA	0.7622	13.1	SB	16.00	Rv2754c, T	
DRB1_0101	69	FSVLEHASVSFYITG	FSVLEHASV	0.7593	13.5	SB	16.00	Rv2754c, T	
DRB1_0101	98	HFSYSQLSQRYVPEKD	YSQLSQRYV	0.7570	13.9	SB	16.00	Rv2754c, T	
DRB1_0101	95	HRHFSYSQLSQRYVP	YSQLSQRYV	0.7490	15.1	SB	16.00	Rv2754c, T	
DRB1_0101	94	RHRHFSYSQLSQRYV	YSQLSQRYV	0.7455	15.7	SB	16.00	Rv2754c, T	
DRB1_0101	74	HASVSFYITGISRSC	FYITGISRS	0.7417	16.4	SB	16.00	Rv2754c, T	
DRB1_0101	151	EAKFADQPNAILRRKQ	FADQPNAIL	0.7374	17.1	SB	16.00	Rv2754c, T	
DRB1_0101	124	DADLRHILTEAADAAR	LRHILTEAA	0.7373	17.2	SB	16.00	Rv2754c, T	
DRB1_0101	207	IRRLAIECLRQLAAV	IECLRQLAA	0.7351	17.6	SB	16.00	Rv2754c, T	
DRB1_0101	63	IDVGHFSVLEHASV	FSVLEHASV	0.7307	18.4	SB	16.00	Rv2754c, T	
DRB1_0101	149	LEAKFADQPNAILRR	FADQPNAIL	0.7307	18.4	SB	16.00	Rv2754c, T	
DRB1_0101	158	NAILRRKQARQAARA	LRRKQARQA	0.7290	18.8	SB	16.00	Rv2754c, T	
DRB1_0101	104	SQRYVPEKDSRVVVP	YVPEKDSRV	0.7239	19.8	SB	16.00	Rv2754c, T	
DRB1_0101	177	ATETRIVVTGNYRAW	IVVTGNYRA	0.7201	20.7	SB	16.00	Rv2754c, T	
DRB1_0101	204	DVEIRRLAIECLRQL	IRRLAIECL	0.7182	21.1	SB	16.00	Rv2754c, T	
DRB1_0101	103	LSQRYVPEKDSRVVV	YVPEKDSRV	0.7162	21.5	SB	16.00	Rv2754c, T	
DRB1_0101	79	FYITGISRSCTHEL	FYITGISRS	0.7122	22.5	SB	16.00	Rv2754c, T	
DRB1_0101	167	QAAARAVLPNATETR	ARAVLPNAT	0.7120	22.5	SB	16.00	Rv2754c, T	
DRB1_0101	130	ILTEAADAARATYSE	ILTEAADAA	0.7102	23.0	SB	16.00	Rv2754c, T	
DRB1_0101	182	IVVTGNYRAWRHFIA	IVVTGNYRA	0.7041	24.6	SB	32.00	Rv2754c, T	
DRB1_0101	206	EIRRLAIECLRQLAA	IRRLAIECL	0.7039	24.6	SB	32.00	Rv2754c, T	
DRB1_0101	139	RATYSELLAKLEAKF	YSELLAKLE	0.7025	25.0	SB	32.00	Rv2754c, T	
DRB1_0101	159	AILRRKQARQAARAV	LRRKQARQA	0.7012	25.4	SB	32.00	Rv2754c, T	
DRB1_0101	160	ILRRKQARQAARAVL	LRRKQARQA	0.6971	26.5	SB	32.00	Rv2754c, T	
DRB1_0101	205	VEIRRLAIECLRQLA	IRRLAIECL	0.6952	27.1	SB	32.00	Rv2754c, T	
DRB1_0101	99	SYSQLSQRYVPEKDS	YSQLSQRYV	0.6907	28.4	SB	32.00	Rv2754c, T	
DRB1_0101	73	EHASVSFYITGISRS	FYITGISRS	0.6860	29.9	SB			
DRB1_0101	152	KFADQPNAILRRKQA	FADQPNAIL	0.6823	31.1	SB			

DRB1_0101	162	RRKQARQAARAVLPN	QARQAARAV	0.6720	34.8	SB	32.00	Rv2754c, T
DRB1_0101	138	ARATYSELLAKLEAK	YSELLAKLE	0.6713	35.0	SB	32.00	Rv2754c, T
DRB1_0101	11	IAKTDFLAPPDVPWT	TDFLAPPDV	0.6697	35.6	SB	32.00	Rv2754c, T
DRB1_0101	203	ADVEIRRLAIECLRQ	IRRLAIECL	0.6683	36.2	SB	32.00	Rv2754c, T
DRB1_0101	105	QRYVPEKDSRVVPP	YVPEKDSRV	0.6679	36.4	SB	32.00	Rv2754c, T
DRB1_0101	161	LRRKQARQAARAVLP	QARQAARAV	0.6625	38.5	SB	32.00	Rv2754c, T
DRB1_0101	216	RQLAAVAPAVFADF	LAAVAPAVF	0.6582	40.4	SB	32.00	Rv2754c, T
DRB1_0101	140	ATYSELLAKLEAKFA	YSELLAKLE	0.6568	41.0	SB	32.00	Rv2754c, T
DRB1_0101	93	IRHRHFSYSQLSQRY	RHFSYSQLS	0.6561	41.3	SB	32.00	Rv2754c, T
DRB1_0101	148	KLEAKFADQPNAILR	FADQPNAIL	0.6544	42.1	SB	32.00	Rv2754c, T
DRB1_0101	157	PNAILRRKQARQAAR	LRRKQARQA	0.6520	43.2	SB	32.00	Rv2754c, T
DRB1_0101	166	ARQAARAVLPNATET	ARAVLPNAT	0.6484	44.9	SB	32.00	Rv2754c, T
DRB1_0101	164	KQARQAARAVLPNAT	RQAARAVLP	0.6470	45.6	SB	32.00	Rv2754c, T
DRB1_0101	0	VAETAPLRVQLIAKT	TAPLRVQLI	0.6454	46.4	SB	32.00	Rv2754c, T
DRB1_0101	123	DDADLRHILTEAADA	LRHILTEAA	0.6420	48.1	SB	32.00	Rv2754c, T
DRB1_0101	176	NATETRIVVTGNYRA	IVVTGNYRA	0.6395	49.4	SB	32.00	Rv2754c, T
DRB1_0101	142	YSELLAKLEAKFADQ	LAKLEAKFA	0.6378	50.4	WB	32.00	Rv2754c, T
DRB1_0101	137	AARATYSELLAKLEA	YSELLAKLE	0.6346	52.1	WB	32.00	Rv2754c, T
DRB1_0101	168	QAARAVLPNATETRI	ARAVLPNAT	0.6326	53.3	WB	32.00	Rv2754c, T
DRB1_0101	202	HADVEIRRLAIECLR	IRRLAIECL	0.6298	54.9	WB	32.00	Rv2754c, T
DRB1_0101	143	SELLAKLEAKFADQP	LAKLEAKFA	0.6284	55.7	WB	32.00	Rv2754c, T
DRB1_0101	141	TYSELLAKLEAKFAD	YSELLAKLE	0.6209	60.5	WB	32.00	Rv2754c, T
DRB1_0101	3	TAPLRVQLIAKTDFL	LRVQLIAKT	0.6183	62.2	WB	32.00	Rv2754c, T
DRB1_0101	163	RKQARQAARAVLPNA	QARQAARAV	0.6163	63.5	WB	32.00	Rv2754c, T
DRB1_0101	100	YSQLSQRYVPEKDSR	YSQLSQRYV	0.6145	64.8	WB	32.00	Rv2754c, T
DRB1_0101	106	RYVPEKDSRVVPPG	YVPEKDSRV	0.6107	67.5	WB	32.00	Rv2754c, T
DRB1_0101	165	QAARAVLPNATE	ARAVLPNAT	0.6078	69.6	WB	32.00	Rv2754c, T
DRB1_0101	81	ITGISRSCTHELIRH	ISRSCTHEL	0.6067	70.5	WB	32.00	Rv2754c, T
DRB1_0101	135	ADAARATYSELLAKL	ARATYSELL	0.6033	73.1	WB	32.00	Rv2754c, T
DRB1_0101	4	APLRVQLIAKTDFLA	RVQLIAKTD	0.6017	74.4	WB	32.00	Rv2754c, T
DRB1_0101	1	AETAPLRVQLIAKTD	TAPLRVQLI	0.5970	78.3	WB	50.00	Rv2754c, T
DRB1_0101	102	QLSQRYVPEKDSRVV	YVPEKDSRV	0.5966	78.7	WB	50.00	Rv2754c, T
DRB1_0101	92	LIRHRHFSYSQLSQR	RHFSYSQLS	0.5938	81.1	WB	50.00	Rv2754c, T
DRB1_0101	136	DAARATYSELLAKLE	YSELLAKLE	0.5912	83.3	WB	50.00	Rv2754c, T
DRB1_0101	70	SVLEHASVSFYITGI	EHASVSFYI	0.5909	83.6	WB	50.00	Rv2754c, T
DRB1_0101	10	LIAKTDFLAPPDVPW	TDFLAPPDV	0.5891	85.2	WB	50.00	Rv2754c, T
DRB1_0101	80	YITGISRSCTHELIR	YITGISRSC	0.5885	85.8	WB	50.00	Rv2754c, T
DRB1_0101	153	FADQPNAILRRKQAR	FADQPNAIL	0.5874	86.9	WB	50.00	Rv2754c, T
DRB1_0101	2	ETAPLRVQLIAKTD	TAPLRVQLI	0.5852	89.0	WB	50.00	Rv2754c, T
DRB1_0101	12	AKTDFLAPPDVPWTT	TDFLAPPDV	0.5842	90.0	WB	50.00	Rv2754c, T
DRB1_0101	131	LTEAADAARATYSEL	TEAADAARA	0.5799	94.2	WB	50.00	Rv2754c, T
DRB1_0101	121	MEDDADLRHILTEAA	LRHILTEAA	0.5706	104.1	WB	50.00	Rv2754c, T
DRB1_0101	235	ADGTEVATSPATEA	TEVATSPLA	0.5696	105.4	WB	50.00	Rv2754c, T
DRB1_0101	184	VTGNYRAWRHFIAMR	YRAWRHFIA	0.5694	105.5	WB	50.00	Rv2754c, T
DRB1_0101	169	AARAVLPNATETRIV	ARAVLPNAT	0.5640	111.8	WB	50.00	Rv2754c, T
DRB1_0101	147	AKLEAKFADQPNAIL	FADQPNAIL	0.5618	114.5	WB	50.00	Rv2754c, T
DRB1_0101	217	QLAAVAPAVFADFEV	QLAAVAPAV	0.5609	115.7	WB	50.00	Rv2754c, T
DRB1_0101	201	EHADVEIRRLAIECL	IRRLAIECL	0.5607	116.0	WB	50.00	Rv2754c, T
DRB1_0101	156	QPNAILRRKQARQAA	LRRKQARQA	0.5603	116.4	WB	50.00	Rv2754c, T
DRB1_0101	122	EDDADLRHILTEAAD	LRHILTEAA	0.5591	117.9	WB	50.00	Rv2754c, T
DRB1_0101	60	LRHIIDVGHFVLEH	IIDVGHFV	0.5584	118.9	WB	50.00	Rv2754c, T
DRB1_0101	5	PLRVQLIAKTDFLAP	RVQLIAKTD	0.5539	124.8	WB	50.00	Rv2754c, T
DRB1_0101	132	TEAADAARATYSELL	ADAARATYS	0.5528	126.3	WB	50.00	Rv2754c, T
DRB1_0101	71	VELEHASVSFYITGIS	EHASVSFYI	0.5514	128.3	WB	50.00	Rv2754c, T
DRB1_0101	144	ELLAKLEAKFADQPN	LAKLEAKFA	0.5407	143.9	WB	50.00	Rv2754c, T
DRB1_0101	59	YLRHIIDVGHFVLE	IIDVGHFV	0.5394	146.1	WB	50.00	Rv2754c, T
DRB1_0101	82	TGISRSCTHELIRHR	ISRSCTHEL	0.5365	150.6	WB	50.00	Rv2754c, T
DRB1_0101	107	YVPEKDSRVVPPG	YVPEKDSRV	0.5299	161.8	WB	50.00	Rv2754c, T
DRB1_0101	58	GYLRHIIDVGHFVLE	IIDVGHFV	0.5287	164.0	WB	50.00	Rv2754c, T
DRB1_0101	183	VVTGNYRAWRHFIAM	YRAWRHFIA	0.5279	165.3	WB	50.00	Rv2754c, T
DRB1_0101	91	ELIRHRHFSYSQLSQ	HRHFSYSQL	0.5269	167.1	WB	50.00	Rv2754c, T
DRB1_0101	31	GPLVEFAGRACYQS	LVEFAGRAC	0.5259	169.0	WB	50.00	Rv2754c, T
DRB1_0101	6	LRVQLIAKTDFLAPP	LIAKTDFLA	0.5255	169.6	WB	50.00	Rv2754c, T
DRB1_0101	229	FEVTTLADGTEVATS	TTLADGTEV	0.5241	172.3	WB	50.00	Rv2754c, T
DRB1_0101	72	LEHASVSFYITGISR	HASVSFYIT	0.5208	178.5	WB	50.00	Rv2754c, T
DRB1_0101	30	GGPALVEFAGRACYQ	ALVEFAGRA	0.5205	179.1	WB	50.00	Rv2754c, T
DRB1_0101	134	AADAARATYSELLAK	ARATYSELL	0.5137	192.8	WB	50.00	Rv2754c, T
DRB1_0101	89	THELIRHRHFSYSQL	LIRHRHFSY	0.5127	195.0	WB	50.00	Rv2754c, T
DRB1_0101	50	NPKTATNAGYLRHI	TATNAGYLR	0.5097	201.2	WB	50.00	Rv2754c, T
DRB1_0101	90	HELIRHRHFSYSQLS	HRHFSYSQL	0.5076	205.9	WB	50.00	Rv2754c, T
DRB1_0101	8	VQLIAKTDFLAPPDV	TDFLAPPDV	0.5049	212.0	WB	50.00	Rv2754c, T
DRB1_0101	61	RHIIDVGHFVLEHA	IIDVGHFV	0.5016	219.8	WB	50.00	Rv2754c, T
DRB1_0101	9	QLIAKTDFLAPPDVP	TDFLAPPDV	0.4989	226.4	WB	50.00	Rv2754c, T
DRB1_0101	13	KTDFLAPPDVPWTTD	TDFLAPPDV	0.4987	226.7	WB	50.00	Rv2754c, T
DRB1_0101	170	ARAVLPNATETRIVV	ARAVLPNAT	0.4963	232.6	WB	50.00	Rv2754c, T
DRB1_0101	57	AGYLRHIIDVGHFV	YLRHIIDVG	0.4937	239.3	WB	50.00	Rv2754c, T
DRB1_0101	56	NAGYLRHIIDVGHF	YLRHIIDVG	0.4861	259.9	WB	50.00	Rv2754c, T
DRB1_0101	133	EADAARATYSELLA	ADAARATYS	0.4826	270.0	WB	50.00	Rv2754c, T
DRB1_0101	195	IAMRASEHADVEIRR	MRASEHADV	0.4818	272.3	WB	50.00	Rv2754c, T
DRB1_0101	101	SQLSQRYVPEKDSRV	YVPEKDSRV	0.4792	280.1	WB	50.00	Rv2754c, T
DRB1_0101	145	LLAKLEAKFADQPN	LAKLEAKFA	0.4781	283.4	WB	50.00	Rv2754c, T
DRB1_0101	32	PALVEFAGRACYQSW	LVEFAGRAC	0.4763	289.1	WB	50.00	Rv2754c, T
DRB1_0101	7	RVQLIAKTDFLAPPD	LIAKTDFLA	0.4703	308.2	WB	50.00	Rv2754c, T
DRB1_0101	155	DQPNAILRRKQARQA	LRRKQARQA	0.4701	309.0	WB	50.00	Rv2754c, T
DRB1_0101	83	GISRSCTHELIRHRH	ISRSCTHEL	0.4678	316.6	WB	50.00	Rv2754c, T

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DRB1_0101	234	LADGTEVATSPLATE	TEVATSPLA	0.4677	317.2	WB	50.00	Rv2754c, T
DRB1_0101	33	ALVEFAGRACYQSW	EFAGRACYQ	0.4650	326.4	WB	50.00	Rv2754c, T
DRB1_0101	29	DGGPALVEFAGRACY	ALVEFAGRA	0.4641	329.7	WB	50.00	Rv2754c, T
DRB1_0101	52	KTATNAGYLRHIIDV	NAGYLRHII	0.4635	331.9	WB	50.00	Rv2754c, T
DRB1_0101	218	LAAPAVFADFEV	LAAPAVFV	0.4587	349.6	WB	50.00	Rv2754c, T
DRB1_0101	87	SCTHELIRHRHFSYS	HELIRHRHF	0.4577	353.4	WB	50.00	Rv2754c, T
DRB1_0101	51	PKTATNAGYLRHIID	TATNAGYLR	0.4575	354.0	WB	50.00	Rv2754c, T
DRB1_0101	62	HIIDVGHFSVLEHAS	IIDVGHFSV	0.4538	368.5	WB	50.00	Rv2754c, T
DRB1_0101	55	TNAGYLRHIIDVGHF	YLRHIIDVG	0.4522	375.1	WB	50.00	Rv2754c, T
DRB1_0101	84	ISRSCTHELIRHRHF	SRSCTHELI	0.4434	412.6	WB	50.00	Rv2754c, T
DRB1_0101	49	PNPKTATNAGYLRHI	KTATNAGYL	0.4419	419.3	WB	50.00	Rv2754c, T
DRB1_0101	85	SRSCTHELIRHRHFS	CTHELIRHR	0.4402	426.9	WB	50.00	Rv2754c, T
DRB1_0101	88	CTHELIRHRHFSYSQ	HELIRHRHF	0.4381	436.7	WB	50.00	Rv2754c, T
DRB1_0101	228	DFEVTTLADGTEVAT	TTLADGTEV	0.4373	440.6	WB	50.00	Rv2754c, T
DRB1_0101	223	PAVFADFEVTTLADG	FADFEVTTL	0.4362	445.7	WB	50.00	Rv2754c, T
DRB1_0101	221	VAPAVFADFEVTTLA	FADFEVTTL	0.4354	450.0	WB	50.00	Rv2754c, T
DRB1_0101	224	AVFADFEVTTLADGT	ADFEVTTLA	0.4350	451.8	WB	50.00	Rv2754c, T
DRB1_0101	86	RSCTHELIRHRHFSY	HELIRHRHF	0.4330	461.5	WB	50.00	Rv2754c, T
DRB1_0101	53	TATNAGYLRHIIDVG	NAGYLRHII	0.4296	478.7	WB	50.00	Rv2754c, T
DRB1_0101	233	TLADGTEVATSPLAT	TEVATSPLA	0.4259	498.7	WB	50.00	Rv2754c, T
DRB1_0101	34	LVEFAGRACYQSWSK	FAGRACYQS	0.4257	499.8	WB	50.00	Rv2754c, T
DRB1_0101	54	ATNAGYLRHIIDVGH	NAGYLRHII	0.4196	533.6		50.00	Rv2754c, T
DRB1_0101	230	EVTTLADGTEVATSP	TTLADGTEV	0.4126	575.5		50.00	Rv2754c, T
DRB1_0101	222	APAVFADFEVTTLAD	FADFEVTTL	0.4119	580.2		50.00	Rv2754c, T
DRB1_0101	200	SEHADVEIRRLAIEC	DVEIRRLAI	0.4111	585.4		50.00	Rv2754c, T
DRB1_0101	43	YQSWSKPNPKTATNA	WSKPNPKTA	0.4091	598.0		50.00	Rv2754c, T
DRB1_0101	28	ADGGPALVEFAGRAC	ALVEFAGRA	0.4073	609.7		50.00	Rv2754c, T
DRB1_0101	171	RAVLPNATETRIVVT	PNATETRIV	0.3976	677.0		50.00	Rv2754c, T
DRB1_0101	196	AMRASEHADVEIRRL	MRASEHADV	0.3916	722.2		50.00	Rv2754c, T
DRB1_0101	199	ASEHADVEIRRLAIE	DVEIRRLAI	0.3906	730.0		50.00	Rv2754c, T
DRB1_0101	110	EKDSRVVPPGMEDD	SRVVVPPGM	0.3881	750.7		50.00	Rv2754c, T
DRB1_0101	109	PEKDSRVVPPGMED	SRVVVPPGM	0.3874	756.0		50.00	Rv2754c, T
DRB1_0101	226	FADFEVTTLADGTEV	FEVTTLADG	0.3866	762.9		50.00	Rv2754c, T
DRB1_0101	108	VPEKDSRVVPPGMED	SRVVVPPGM	0.3862	766.3		50.00	Rv2754c, T
DRB1_0101	172	AVLPNATETRIVVTG	PNATETRIV	0.3852	774.6		50.00	Rv2754c, T
DRB1_0101	225	VFADFEVTTLADGTE	FADFEVTTL	0.3844	781.4		50.00	Rv2754c, T
DRB1_0101	227	ADFEVTTLADGTEVA	TTLADGTEV	0.3830	792.7		50.00	Rv2754c, T
DRB1_0101	14	TDFLAPPDVPWTTDA	TDFLAPPDV	0.3821	800.4		50.00	Rv2754c, T
DRB1_0101	220	AVAPAVFADFEVTTL	AVFADFEVT	0.3818	803.7		50.00	Rv2754c, T
DRB1_0101	231	VTTLADGTEVATSPL	TTLADGTEV	0.3723	890.2		50.00	Rv2754c, T
DRB1_0101	24	WTTDADGGPALVEFA	DADGGPALV	0.3719	894.2		50.00	Rv2754c, T
DRB1_0101	146	LAKLEAKFADQPNAI	LAKLEAKFA	0.3664	949.4		50.00	Rv2754c, T
DRB1_0101	198	RASEHADVEIRRLAIE	DVEIRRLAI	0.3662	950.9		50.00	Rv2754c, T
DRB1_0101	44	QSWSKPNPKTATNAG	WSKPNPKTA	0.3647	966.6		50.00	Rv2754c, T
DRB1_0101	42	CYQSWSKPNPKTATN	WSKPNPKTA	0.3624	990.5		50.00	Rv2754c, T
DRB1_0101	27	DADGGPALVEFAGRA	ALVEFAGRA	0.3593	1024.2		50.00	Rv2754c, T
DRB1_0101	173	VLPNATETRIVVTGN	NATETRIVV	0.3585	1033.9		50.00	Rv2754c, T
DRB1_0101	219	AAVAPAVFADFEVTT	AVAPAVFAD	0.3538	1087.2		50.00	Rv2754c, T
DRB1_0101	197	MRASEHADVEIRRLA	MRASEHADV	0.3517	1112.0		50.00	Rv2754c, T
DRB1_0101	25	TTDADGGPALVEFAG	DADGGPALV	0.3489	1147.0		50.00	Rv2754c, T
DRB1_0101	232	TTLADGTEVATSPLA	TTLADGTEV	0.3454	1191.4		50.00	Rv2754c, T
DRB1_0101	23	PWTTDADGGPALVEF	TDADGGPAL	0.3449	1197.4		50.00	Rv2754c, T
DRB1_0101	111	KDSRVVPPGMEDDA	SRVVVPPGM	0.3434	1216.7		50.00	Rv2754c, T
DRB1_0101	120	GMEDDADLRHILTEA	DADLRHILT	0.3414	1243.6		50.00	Rv2754c, T
DRB1_0101	48	KPNPKTATNAGYLRH	KTATNAGYL	0.3388	1278.9		50.00	Rv2754c, T
DRB1_0101	41	ACYQSWSKPNPKTAT	WSKPNPKTA	0.3336	1354.0		50.00	Rv2754c, T
DRB1_0101	39	GRACYQSWSKPNPKT	CYQSWSKPN	0.3316	1382.6		50.00	Rv2754c, T
DRB1_0101	40	RACYQSWSKPNPKTA	CYQSWSKPN	0.3304	1400.4		50.00	Rv2754c, T
DRB1_0101	26	TDADGGPALVEFAGR	DADGGPALV	0.3292	1419.9		50.00	Rv2754c, T
DRB1_0101	35	VEFAGRACYQSWSKP	FAGRACYQS	0.3266	1460.3		50.00	Rv2754c, T
DRB1_0101	45	SWSKPNPKTATNAGY	WSKPNPKTA	0.3265	1461.7		50.00	Rv2754c, T
DRB1_0101	36	EFAGRACYQSWSKPN	CYQSWSKPN	0.3144	1666.4		50.00	Rv2754c, T
DRB1_0101	174	LPNATETRIVVTGNY	NATETRIVV	0.3118	1713.9		50.00	Rv2754c, T
DRB1_0101	46	WSKPNPKTATNAGYL	WSKPNPKTA	0.2988	1972.3		50.00	Rv2754c, T
DRB1_0101	22	VPWTTDADGGPALVE	WTTDADGGP	0.2970	2011.1		50.00	Rv2754c, T
DRB1_0101	37	FAGRACYQSWSKPNP	CYQSWSKPN	0.2961	2030.9		50.00	Rv2754c, T
DRB1_0101	38	AGRACYQSWSKPNPK	CYQSWSKPN	0.2934	2091.5		50.00	Rv2754c, T
DRB1_0101	175	PNATETRIVVTGNYR	NATETRIVV	0.2918	2126.8		50.00	Rv2754c, T
DRB1_0101	119	PGMEDDADLRHILTE	DADLRHILT	0.2877	2223.5		50.00	Rv2754c, T
DRB1_0101	21	DVPWTTDADGGPALV	WTTDADGGP	0.2789	2446.8		50.00	Rv2754c, T
DRB1_0101	112	DSRVVPPGMEDDAD	SRVVVPPGM	0.2774	2486.4		50.00	Rv2754c, T
DRB1_0101	47	SKPNPKTATNAGYLR	KTATNAGYL	0.2696	2703.7		50.00	Rv2754c, T
DRB1_0101	118	PPGMEDDADLRHILT	DADLRHILT	0.2647	2851.0		50.00	Rv2754c, T
DRB1_0101	154	ADQPNAILRRKQARQ	PNAILRRKQ	0.2632	2899.6		50.00	Rv2754c, T
DRB1_0101	20	PDVPWTTDADGGPAL	WTTDADGGP	0.2600	3000.5		50.00	Rv2754c, T
DRB1_0101	113	SRVVVPPGMEDDADL	SRVVVPPGM	0.2577	3075.4		50.00	Rv2754c, T
DRB1_0101	19	PPDVPWTTDADGGPA	WTTDADGGP	0.2493	3369.0		50.00	Rv2754c, T
DRB1_0101	18	APPDVPWTTDADGGP	WTTDADGGP	0.2259	4339.6		50.00	Rv2754c, T
DRB1_0101	117	VPPGMEDDADLRHIL	MEDDADLRH	0.2126	5010.6		50.00	Rv2754c, T
DRB1_0101	15	DFLAPPDVPWTTDAD	FLAPPDVPW	0.2114	5078.2		50.00	Rv2754c, T
DRB1_0101	16	FLAPPDVPWTTDADG	FLAPPDVPW	0.1952	6047.1		50.00	Rv2754c, T
DRB1_0101	114	RVVPPGMEDDADLRH	VVVPPGMED	0.1786	7236.1		50.00	Rv2754c, T
DRB1_0101	116	VVPPGMEDDADLRHI	MEDDADLRH	0.1779	7293.4		50.00	Rv2754c, T
DRB1_0101	115	VVVPPGMEDDADLRH	MEDDADLRH	0.1759	7452.5		50.00	Rv2754c, T
DRB1_0101	17	LAPPDVPWTTDADGG	PDVPWTTDA	0.1507	9786.3		50.00	Rv2754c, T

Allele: DRB1_0101. Number of high binders 82. Number of weak binders 90. Number of peptides 236

Allele	pos	peptide	core	1-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
DRB1_0301	127	LRHILTEAADAARAT	LRHILTEAA	0.5952	79.8	WB	4.00	Rv2754c, T
DRB1_0301	181	RIVVTGNYRAWRHFI	RIVVTGNYR	0.5942	80.7	WB	4.00	Rv2754c, T
DRB1_0301	180	TRIVVTGNYRAWRHF	RIVVTGNYR	0.5721	102.5	WB	4.00	Rv2754c, T
DRB1_0301	126	DLRHILTEAADAARA	LRHILTEAA	0.5541	124.5	WB	4.00	Rv2754c, T
DRB1_0301	179	ETRIVVTGNYRAWRH	RIVVTGNYR	0.5429	140.6	WB	8.00	Rv2754c, T
DRB1_0301	207	IRRLAIECLRQLAAV	IRRLAIECL	0.5227	174.9	WB	8.00	Rv2754c, T
DRB1_0301	222	APAVFADFVETTLAD	APAVFADFE	0.5152	189.7	WB	8.00	Rv2754c, T
DRB1_0301	125	ADLRHILTEAADAAR	LRHILTEAA	0.5099	201.0	WB	8.00	Rv2754c, T
DRB1_0301	78	SFYITGISRSCTHEL	FYITGISRS	0.5093	202.2	WB	8.00	Rv2754c, T
DRB1_0301	206	EIRRLAIECLRQLAA	RRLAIECLR	0.4991	225.7	WB	8.00	Rv2754c, T
DRB1_0301	221	VPAVAFADFVETTLA	APAVFADFE	0.4960	233.4	WB	8.00	Rv2754c, T
DRB1_0301	178	TETRIVVTGNYRAWR	RIVVTGNYR	0.4866	258.4	WB	8.00	Rv2754c, T
DRB1_0301	191	WRHFIAMRASEHADV	WRHFIAMRA	0.4835	267.3	WB	8.00	Rv2754c, T
DRB1_0301	128	RHILTEAADAARATY	ILTEAADAA	0.4802	276.9	WB	8.00	Rv2754c, T
DRB1_0301	77	VSFYITGISRSCTHE	FYITGISRS	0.4750	293.1	WB	16.00	Rv2754c, T
DRB1_0301	79	FYITGISRSCTHELI	FYITGISRS	0.4661	322.7	WB	16.00	Rv2754c, T
DRB1_0301	205	VEIRRLAIECLRQLA	RRLAIECLR	0.4643	329.1	WB	16.00	Rv2754c, T
DRB1_0301	220	AVAPAVFADFVETTL	APAVFADFE	0.4522	374.9	WB	16.00	Rv2754c, T
DRB1_0301	7	RVQLIAKTDNFLAPP	RVQLIAKTD	0.4495	386.0	WB	16.00	Rv2754c, T
DRB1_0301	6	LRVQLIAKTDNFLAPP	RVQLIAKTD	0.4489	388.6	WB	16.00	Rv2754c, T
DRB1_0301	129	HILTEAADAARATYS	ILTEAADAA	0.4439	410.4	WB	16.00	Rv2754c, T
DRB1_0301	189	RAWRHFIAMRASEHA	WRHFIAMRA	0.4388	433.6	WB	16.00	Rv2754c, T
DRB1_0301	119	PGMEDDADLRHILTE	GMEDDADLR	0.4387	434.1	WB	16.00	Rv2754c, T
DRB1_0301	117	VPPGMEDDADLRHIL	GMEDDADLR	0.4381	436.8	WB	16.00	Rv2754c, T
DRB1_0301	76	SVSFYITGISRSCTH	FYITGISRS	0.4370	442.1	WB	16.00	Rv2754c, T
DRB1_0301	118	PPGMEDDADLRHILT	GMEDDADLR	0.4366	443.8	WB	16.00	Rv2754c, T
DRB1_0301	5	PLRVQLIAKTDNFLAP	RVQLIAKTD	0.4327	463.4	WB	16.00	Rv2754c, T
DRB1_0301	192	RHFIAMRASEHADVE	FIAMRASEH	0.4326	463.9	WB	16.00	Rv2754c, T
DRB1_0301	95	HRHFSYSQLSQRYVP	FSYSQLSQR	0.4317	468.0	WB	16.00	Rv2754c, T
DRB1_0301	124	DADLRHILTEAADAA	LRHILTEAA	0.4265	495.1	WB	16.00	Rv2754c, T
DRB1_0301	190	AWRHFIAMRASEHAD	WRHFIAMRA	0.4261	497.2	WB	16.00	Rv2754c, T
DRB1_0301	204	DVEIRRLAIECLRQL	RRLAIECLR	0.4151	560.4		16.00	Rv2754c, T
DRB1_0301	193	HFIAMRASEHADVEI	FIAMRASEH	0.4145	564.2		16.00	Rv2754c, T
DRB1_0301	170	ARAVLPNATETRIVV	VLPNATETR	0.4128	574.3		16.00	Rv2754c, T
DRB1_0301	120	GMEDDADLRHILTEA	GMEDDADLR	0.4068	613.2		16.00	Rv2754c, T
DRB1_0301	86	RSCTHELIRHRHFSY	RSCTHELIR	0.4051	624.4		16.00	Rv2754c, T
DRB1_0301	81	ITGISRSCTHELIRH	ITGISRSCT	0.4042	630.4		16.00	Rv2754c, T
DRB1_0301	208	RRLAIECLRQLAAVA	RRLAIECLR	0.4034	635.9		16.00	Rv2754c, T
DRB1_0301	92	LIRHRHFSYSQLSQR	HRHFSYSQL	0.4030	639.0		16.00	Rv2754c, T
DRB1_0301	94	RHRHFSYSQLSQRYV	FSYSQLSQR	0.3994	664.2		16.00	Rv2754c, T
DRB1_0301	59	YLRHIIDVGHFSVLE	LRHIIDVGH	0.3952	694.8		32.00	Rv2754c, T
DRB1_0301	194	FIAMRASEHADVEIR	FIAMRASEH	0.3938	705.6		32.00	Rv2754c, T
DRB1_0301	200	SEHADVEIRRLAIEC	SEHADVEIR	0.3936	706.8		32.00	Rv2754c, T
DRB1_0301	188	YRAWRHFIAMRASEH	WRHFIAMRA	0.3936	707.1		32.00	Rv2754c, T
DRB1_0301	219	AAVAPAVFADFVETT	APAVFADFE	0.3899	736.0		32.00	Rv2754c, T
DRB1_0301	157	PNAILRRKQARQAAR	NAILRRKQA	0.3845	780.2		32.00	Rv2754c, T
DRB1_0301	60	LRHIIDVGHFSVLEH	LRHIIDVGH	0.3836	787.6		32.00	Rv2754c, T
DRB1_0301	80	YITGISRSCTHELIR	ITGISRSCT	0.3835	789.0		32.00	Rv2754c, T
DRB1_0301	89	THELIRHRHFSYSQL	THELIRHRH	0.3820	802.0		32.00	Rv2754c, T
DRB1_0301	182	IVVTGNYRAWRHFI	IVVTGNYR	0.3802	817.1		32.00	Rv2754c, T
DRB1_0301	96	RHFSYSQLSQRYVPE	FSYSQLSQR	0.3799	819.8		32.00	Rv2754c, T
DRB1_0301	198	RASEHADVEIRRLAI	SEHADVEIR	0.3777	840.1		32.00	Rv2754c, T
DRB1_0301	199	ASEHADVEIRRLAIE	SEHADVEIR	0.3774	842.8		32.00	Rv2754c, T
DRB1_0301	88	CTHELIRHRHFSYSQ	LIRHRHFSY	0.3774	842.8		32.00	Rv2754c, T
DRB1_0301	197	MRASEHADVEIRRLA	MRASEHADV	0.3773	843.9		32.00	Rv2754c, T
DRB1_0301	4	APLRVQLIAKTDFLA	RVQLIAKTD	0.3772	844.3		32.00	Rv2754c, T
DRB1_0301	58	GYLRHIIDVGHFSVL	LRHIIDVGH	0.3770	846.0		32.00	Rv2754c, T
DRB1_0301	93	IRHRHFSYSQLSQRY	FSYSQLSQR	0.3768	848.0		32.00	Rv2754c, T
DRB1_0301	158	NAILRRKQARQAARA	NAILRRKQA	0.3734	879.8		32.00	Rv2754c, T
DRB1_0301	130	ILTEAADAARATYSE	ILTEAADAA	0.3684	928.8		32.00	Rv2754c, T
DRB1_0301	177	ATETRIVVTGNYRAW	RIVVTGNYR	0.3662	950.6		32.00	Rv2754c, T
DRB1_0301	223	PAVADFVETTLADG	VFADFVETT	0.3648	965.2		32.00	Rv2754c, T
DRB1_0301	169	AARAVLPNATETRIV	VLPNATETR	0.3627	987.3		32.00	Rv2754c, T
DRB1_0301	156	QPNAILRRKQARQAA	NAILRRKQA	0.3617	998.1		32.00	Rv2754c, T
DRB1_0301	116	VVPPGMEDDADLRHI	GMEDDADLR	0.3586	1032.8		32.00	Rv2754c, T
DRB1_0301	83	GISRSTHELIRHRH	RSCTHELIR	0.3585	1033.9		32.00	Rv2754c, T
DRB1_0301	66	VGHFSVLEHASVSFY	HFSVLEHAS	0.3577	1042.6		32.00	Rv2754c, T
DRB1_0301	75	ASVSFYITGISRSCT	FYITGISRS	0.3551	1072.7		32.00	Rv2754c, T
DRB1_0301	87	SCTHELIRHRHFSYS	CTHELIRHR	0.3541	1084.5		32.00	Rv2754c, T
DRB1_0301	67	GHSVLEHASVSFYI	HFSVLEHAS	0.3509	1122.0		32.00	Rv2754c, T
DRB1_0301	224	AVFADFVETTLADGT	VFADFVETT	0.3502	1130.5		32.00	Rv2754c, T
DRB1_0301	57	AGYLRHIIDVGHFSV	LRHIIDVGH	0.3458	1186.2		32.00	Rv2754c, T
DRB1_0301	91	ELIRHRHFSYSQLSQ	LIRHRHFSY	0.3436	1214.9		32.00	Rv2754c, T
DRB1_0301	82	TGISRSCTHELIRHR	GISRSTHELI	0.3421	1234.7		32.00	Rv2754c, T
DRB1_0301	195	IAMRASEHADVEIRR	IAMRASEHA	0.3412	1247.1		32.00	Rv2754c, T
DRB1_0301	97	HFSYSQLSQRYVPEK	FSYSQLSQR	0.3395	1269.4		32.00	Rv2754c, T
DRB1_0301	172	AVLPNATETRIVVTG	VLPNATETR	0.3350	1333.1		32.00	Rv2754c, T

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DRB1_0301	171	RAVLPNATETRIVVVT	VLPNATETR	0.3341	1346.4	32.00	Rv2754c, T
DRB1_0301	90	HELIRHRHFSYSQLS	LIRHRHFSY	0.3322	1374.5	32.00	Rv2754c, T
DRB1_0301	155	DQPNAILRRKQARQA	NAILRRKQA	0.3316	1382.9	32.00	Rv2754c, T
DRB1_0301	84	ISRSCTHELIRHRHF	RSCCTHELIR	0.3307	1396.4	32.00	Rv2754c, T
DRB1_0301	203	ADVEIRRLAIECLRQ	IRRLAIECL	0.3304	1400.5	32.00	Rv2754c, T
DRB1_0301	8	VQLIAKTDFLAPPDV	QLIAKTDFL	0.3287	1426.7	32.00	Rv2754c, T
DRB1_0301	68	HFSVLEHASVSFYIT	HFSVLEHAS	0.3271	1452.0	32.00	Rv2754c, T
DRB1_0301	196	AMRASEHADVEIRRL	MRASEHADV	0.3270	1453.4	32.00	Rv2754c, T
DRB1_0301	142	YSELLAKLEAKFADQ	LLAKLEAKF	0.3226	1523.7	32.00	Rv2754c, T
DRB1_0301	230	EVTTLADGTEVATSP	TLADGTEVA	0.3226	1524.1	32.00	Rv2754c, T
DRB1_0301	65	DVGHFVLEHASVSF	VGHFVLEH	0.3223	1529.0	32.00	Rv2754c, T
DRB1_0301	201	EHADVEIRRLAIECL	EHADVEIRR	0.3210	1550.4	32.00	Rv2754c, T
DRB1_0301	123	DDADLRHILTEAADA	LRHILTEAA	0.3181	1600.4	32.00	Rv2754c, T
DRB1_0301	85	SRSCTHELIRHRHFS	RSCCTHELIR	0.3141	1670.6	32.00	Rv2754c, T
DRB1_0301	173	VLPNATETRIVVTGN	VLPNATETR	0.3137	1677.8	32.00	Rv2754c, T
DRB1_0301	202	HADVEIRRLAIECLR	RRLAIECLR	0.3082	1781.8	32.00	Rv2754c, T
DRB1_0301	61	RHIIDVGHFVLEHA	RHIIDVGHF	0.3082	1781.9	32.00	Rv2754c, T
DRB1_0301	168	QAARAVLPNATETRI	VLPNATETR	0.3081	1782.5	32.00	Rv2754c, T
DRB1_0301	176	NATETRIVVTGNRYR	RIVVTGNRYR	0.3073	1799.0	32.00	Rv2754c, T
DRB1_0301	229	FEVTTLADGTEVATS	TLADGTEVA	0.3068	1807.9	32.00	Rv2754c, T
DRB1_0301	187	NYRAWRHFIAMRASE	WRHFIAMRA	0.3063	1817.9	32.00	Rv2754c, T
DRB1_0301	225	VFADFEVTTLADGTE	VFADFEVTT	0.3061	1822.7	32.00	Rv2754c, T
DRB1_0301	98	FYSYQLSQRYVPEKD	FYSYQLSQR	0.3030	1884.8	32.00	Rv2754c, T
DRB1_0301	154	ADQPNAILRRKQARQ	NAILRRKQA	0.2979	1990.6	50.00	Rv2754c, T
DRB1_0301	141	TYSELLAKLEAKFAD	LLAKLEAKF	0.2977	1996.0	50.00	Rv2754c, T
DRB1_0301	209	RLAIECLRQLAAVAP	RLAIECLRQ	0.2972	2006.3	50.00	Rv2754c, T
DRB1_0301	63	IDVGHFVLEHASV	VGHFVLEH	0.2949	2056.2	50.00	Rv2754c, T
DRB1_0301	3	TAPLRVQLIAKTDFL	LRVQLIAKT	0.2922	2119.1	50.00	Rv2754c, T
DRB1_0301	74	HASVSFYITGISRSC	SFYITGISR	0.2911	2143.5	50.00	Rv2754c, T
DRB1_0301	115	VVVPPGMEDDADLRH	GMEDDADLR	0.2894	2182.0	50.00	Rv2754c, T
DRB1_0301	143	SELLAKLEAKFADQP	LLAKLEAKF	0.2857	2273.0	50.00	Rv2754c, T
DRB1_0301	62	HIIDVGHFVLEHAS	IDVGHFVSL	0.2856	2275.5	50.00	Rv2754c, T
DRB1_0301	64	IDVGHFVLEHASVS	VGHFVLEH	0.2834	2329.1	50.00	Rv2754c, T
DRB1_0301	167	RQAARAVLPNATETR	VLPNATETR	0.2834	2329.6	50.00	Rv2754c, T
DRB1_0301	56	NAGYLRHIIDVGHFS	LRHIIDVGH	0.2807	2398.7	50.00	Rv2754c, T
DRB1_0301	104	SQRYVPEKDSRVVVP	YVPEKDSRV	0.2743	2571.4	50.00	Rv2754c, T
DRB1_0301	139	RATYSELLAKLEAKF	YSELLAKLE	0.2731	2602.9	50.00	Rv2754c, T
DRB1_0301	121	MEDDADLRHILTEAA	MEDDADLRH	0.2694	2709.8	50.00	Rv2754c, T
DRB1_0301	122	EDDADLRHILTEAAD	LRHILTEAA	0.2694	2710.1	50.00	Rv2754c, T
DRB1_0301	140	ATYSELLAKLEAKFA	YSELLAKLE	0.2662	2805.2	50.00	Rv2754c, T
DRB1_0301	9	QLIAKTDFLAPPDVP	QLIAKTDFL	0.2656	2825.2	50.00	Rv2754c, T
DRB1_0301	159	AILRRKQARQAARAV	AILRRKQAR	0.2653	2833.4	50.00	Rv2754c, T
DRB1_0301	69	FVLEHASVSFYITG	FVLEHASV	0.2650	2844.2	50.00	Rv2754c, T
DRB1_0301	228	DFEVTTLADGTEVAT	TLADGTEVA	0.2630	2906.4	50.00	Rv2754c, T
DRB1_0301	231	VTTLADGTEVATSPL	TLADGTEVA	0.2602	2995.9	50.00	Rv2754c, T
DRB1_0301	210	LAIECLRQLAAVAPA	IECLRQLAA	0.2600	3000.7	50.00	Rv2754c, T
DRB1_0301	232	TTLADGTEVATSPLA	TLADGTEVA	0.2536	3215.7	50.00	Rv2754c, T
DRB1_0301	212	IECLRQLAAVAPAVF	IECLRQLAA	0.2526	3251.3	50.00	Rv2754c, T
DRB1_0301	105	QRYVPEKDSRVVPP	RYVPEKDSR	0.2521	3269.4	50.00	Rv2754c, T
DRB1_0301	211	ATIECLRQLAAVAPAV	IECLRQLAA	0.2507	3316.9	50.00	Rv2754c, T
DRB1_0301	138	ARATYSELLAKLEAK	ARATYSELL	0.2505	3323.9	50.00	Rv2754c, T
DRB1_0301	137	AARATYSELLAKLEA	ARATYSELL	0.2493	3368.0	50.00	Rv2754c, T
DRB1_0301	0	VAETAPLRVQLIAKT	VAETAPLRV	0.2484	3403.1	50.00	Rv2754c, T
DRB1_0301	103	LSQRYVPEKDSRVVV	RYVPEKDSR	0.2469	3456.5	50.00	Rv2754c, T
DRB1_0301	106	RYVPEKDSRVVPPG	RYVPEKDSR	0.2426	3621.6	50.00	Rv2754c, T
DRB1_0301	153	FADQPNAILRRKQAR	ADQPNAILR	0.2369	3854.7	50.00	Rv2754c, T
DRB1_0301	149	LEAKFADQPNAILRR	LEAKFADQP	0.2350	3931.3	50.00	Rv2754c, T
DRB1_0301	213	ECLRQLAAVAPAVFA	CLRQLAAVA	0.2348	3939.3	50.00	Rv2754c, T
DRB1_0301	186	GNYRAWRHFIAMRAS	WRHFIAMRA	0.2316	4079.4	50.00	Rv2754c, T
DRB1_0301	144	ELLAKLEAKFADQPN	LLAKLEAKF	0.2297	4163.3	50.00	Rv2754c, T
DRB1_0301	214	CLRQLAAVAPAVFAD	LRQLAAVAP	0.2283	4230.4	50.00	Rv2754c, T
DRB1_0301	136	DAARATYSELLAKLE	ARATYSELL	0.2271	4285.6	50.00	Rv2754c, T
DRB1_0301	55	TNAGYLRHIIDVGHF	LRHIIDVGH	0.2232	4467.6	50.00	Rv2754c, T
DRB1_0301	135	ADAARATYSELLAKL	ARATYSELL	0.2222	4518.4	50.00	Rv2754c, T
DRB1_0301	233	TLADGTEVATSPLAT	TLADGTEVA	0.2178	4737.1	50.00	Rv2754c, T
DRB1_0301	145	LLAKLEAKFADQPNA	LLAKLEAKF	0.2161	4823.8	50.00	Rv2754c, T
DRB1_0301	227	ADFEVTTLADGTEVA	TLADGTEVA	0.2159	4836.2	50.00	Rv2754c, T
DRB1_0301	131	LTEAADAARATYSEL	LTEAADAAR	0.2156	4849.5	50.00	Rv2754c, T
DRB1_0301	114	RVVVPPGMEDDADLR	GMEDDADLR	0.2154	4861.8	50.00	Rv2754c, T
DRB1_0301	107	YVPEKDSRVVPPPG	YVPEKDSRV	0.2143	4921.0	50.00	Rv2754c, T
DRB1_0301	2	ETAPLRVQLIAKTDF	RVQLIAKTD	0.2137	4950.0	50.00	Rv2754c, T
DRB1_0301	148	KLEAKFADQPNAILR	LEAKFADQP	0.2118	5057.1	50.00	Rv2754c, T
DRB1_0301	215	LRQLAAVAPAVFADF	LRQLAAVAP	0.2109	5103.0	50.00	Rv2754c, T
DRB1_0301	52	KTATNAGYLRHIIDV	TATNAGYLR	0.2102	5145.5	50.00	Rv2754c, T
DRB1_0301	73	EHASVSFYITGISR	SFYITGISR	0.2093	5193.9	50.00	Rv2754c, T
DRB1_0301	175	PNATETRIVVTGNRYR	RIVVTGNRYR	0.2076	5290.4	50.00	Rv2754c, T
DRB1_0301	218	LAAPAVFADFEVTT	APAVFADFE	0.2062	5368.3	50.00	Rv2754c, T
DRB1_0301	32	PLVEFAGRACYQSW	ALVEFAGRA	0.2061	5376.7	50.00	Rv2754c, T
DRB1_0301	102	QLSQRYVPEKDSRVV	RYVPEKDSR	0.2045	5473.0	50.00	Rv2754c, T
DRB1_0301	160	ILRRKQARQAARAVL	ILRRKQARQ	0.2042	5489.5	50.00	Rv2754c, T
DRB1_0301	152	KFADQPNAILRRKQA	KFADQPNAI	0.1990	5807.1	50.00	Rv2754c, T
DRB1_0301	21	DVPWTTDADGGPALV	VPWTTDADG	0.1985	5839.5	50.00	Rv2754c, T
DRB1_0301	33	ALVEFAGRACYQSW	ALVEFAGRA	0.1943	6108.1	50.00	Rv2754c, T
DRB1_0301	51	PKTATNAGYLRHIID	TATNAGYLR	0.1917	6280.1	50.00	Rv2754c, T
DRB1_0301	151	AKFADQPNAILRRKQ	KFADQPNAI	0.1914	6305.2	50.00	Rv2754c, T

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DRB1_0301	10	LIAKTDFLAPPDVPW	LIAKTDFLA	0.1892	6456.0	50.00	Rv2754c, T
DRB1_0301	20	PDVPTTADGGPAL	VPWTTDADG	0.1889	6476.6	50.00	Rv2754c, T
DRB1_0301	72	LEHASVSFYITGISR	SFYITGISR	0.1887	6491.3	50.00	Rv2754c, T
DRB1_0301	70	SVLEHASVSFYITGI	SVLEHASVS	0.1886	6498.9	50.00	Rv2754c, T
DRB1_0301	174	LPNATETRIVVTGNY	LPNATETRI	0.1883	6515.8	50.00	Rv2754c, T
DRB1_0301	101	SQLSQRYVPEKDSRV	RYVPEKDSR	0.1844	6799.5	50.00	Rv2754c, T
DRB1_0301	147	LAKLEAKFADQPNAIL	LEAKFADQP	0.1844	6802.2	50.00	Rv2754c, T
DRB1_0301	34	LVEFAGRACYQSWSK	VEFAGRACY	0.1810	7052.2	50.00	Rv2754c, T
DRB1_0301	31	GPALVEFAGRACYQS	ALVEFAGRA	0.1801	7125.8	50.00	Rv2754c, T
DRB1_0301	108	VPEKDSRVVPPGME	VPEKDSRVV	0.1800	7127.7	50.00	Rv2754c, T
DRB1_0301	146	LAKLEAKFADQPNAIL	LAKLEAKFA	0.1795	7166.8	50.00	Rv2754c, T
DRB1_0301	22	VPWTTDADGGPALVE	VPWTTDADG	0.1776	7316.6	50.00	Rv2754c, T
DRB1_0301	185	TGNYRAWRHFIAMRA	WRHFIAMRA	0.1715	7814.2	50.00	Rv2754c, T
DRB1_0301	150	EAKFADQPNAILRRK	KFADQPNAIL	0.1703	7923.7	50.00	Rv2754c, T
DRB1_0301	50	NPKTATNAGYLRHII	KTATNAGYL	0.1698	7960.1	50.00	Rv2754c, T
DRB1_0301	54	ATNAGYLRHIIIDVGH	LRHIIIDVGH	0.1688	8050.5	50.00	Rv2754c, T
DRB1_0301	35	VEFAGRACYQSWSKP	VEFAGRACY	0.1684	8086.3	50.00	Rv2754c, T
DRB1_0301	134	AADAARATYSELLAK	ADAARATYS	0.1679	8127.2	50.00	Rv2754c, T
DRB1_0301	71	VLEHASVSFYITGIS	VLEHASVSF	0.1675	8166.3	50.00	Rv2754c, T
DRB1_0301	217	QLAAVAPAVFADFEV	APAVFADFE	0.1606	8794.5	50.00	Rv2754c, T
DRB1_0301	30	GGPALVEFAGRACYQ	ALVEFAGRA	0.1594	8908.9	50.00	Rv2754c, T
DRB1_0301	109	PEKDSRVVPPGMED	PEKDSRVVV	0.1593	8922.8	50.00	Rv2754c, T
DRB1_0301	183	VVTGNYRAWRHFIAM	VTGNYRAWR	0.1587	8980.3	50.00	Rv2754c, T
DRB1_0301	19	PPDVPWTTDADGGPA	VPWTTDADG	0.1578	9071.2	50.00	Rv2754c, T
DRB1_0301	184	VTGNYRAWRHFIAMR	VTGNYRAWR	0.1567	9180.7	50.00	Rv2754c, T
DRB1_0301	11	IAKTDFLAPPDVPWPT	IAKTDFLAP	0.1555	9294.0	50.00	Rv2754c, T
DRB1_0301	166	AQAARAVLNPATET	RQAARAVLP	0.1523	9619.9	50.00	Rv2754c, T
DRB1_0301	216	RQLAAVAPAVFADFE	RQLAAVAPA	0.1498	9884.6	50.00	Rv2754c, T
DRB1_0301	99	SYSQSQLSQRYVPEKDS	SYSQSQLSQRY	0.1479	10093.1	50.00	Rv2754c, T
DRB1_0301	164	KQARQAARAVLPNAT	KQARQAARA	0.1467	10222.0	50.00	Rv2754c, T
DRB1_0301	132	TEAADAARATYSELL	TEAADAARA	0.1461	10293.5	50.00	Rv2754c, T
DRB1_0301	53	TATNAGYLRHIIIDVG	TATNAGYLR	0.1446	10461.5	50.00	Rv2754c, T
DRB1_0301	226	FADFEVTTLADGTEV	FEVTTLADG	0.1443	10498.8	50.00	Rv2754c, T
DRB1_0301	13	KTDFLAPPDVPWTTD	DFLAPPDVP	0.1442	10504.8	50.00	Rv2754c, T
DRB1_0301	133	EAADAARATYSELLA	ADAARATYS	0.1439	10539.0	50.00	Rv2754c, T
DRB1_0301	163	RKQARQAARAVLPNA	RKQARQAAR	0.1437	10557.1	50.00	Rv2754c, T
DRB1_0301	161	LRRKQARQAARAVLP	RKQARQAAR	0.1420	10754.4	50.00	Rv2754c, T
DRB1_0301	41	ACYQSWSKPNPKTAT	ACYQSWSKP	0.1408	10896.0	50.00	Rv2754c, T
DRB1_0301	12	AKTDFLAPPDVPWTT	KTDFLAPPD	0.1408	10899.7	50.00	Rv2754c, T
DRB1_0301	113	SRVVVPPGMEDDADL	SRVVVPPGM	0.1400	10995.0	50.00	Rv2754c, T
DRB1_0301	49	PNPKTATNAGYLRHI	KTATNAGYL	0.1345	11666.5	50.00	Rv2754c, T
DRB1_0301	100	YSQSQLSQRYVPEKDSR	SQLSQRYVP	0.1331	11841.5	50.00	Rv2754c, T
DRB1_0301	162	RKQARQAARAVLPNA	RKQARQAAR	0.1320	11990.5	50.00	Rv2754c, T
DRB1_0301	1	AETAPLRVQLIAKTD	PLRVQLIAK	0.1316	12039.1	50.00	Rv2754c, T
DRB1_0301	29	DGGPALVEFAGRACY	ALVEFAGRA	0.1280	12514.6	50.00	Rv2754c, T
DRB1_0301	165	QARQAARAVLPNATE	RQAARAVLP	0.1266	12708.1	50.00	Rv2754c, T
DRB1_0301	14	TDFLAPPDVPWTTDA	DFLAPPDVP	0.1252	12896.6	50.00	Rv2754c, T
DRB1_0301	40	RACYQSWSKPNPKTA	CYQSWSKPN	0.1247	12972.7	50.00	Rv2754c, T
DRB1_0301	18	APPDVPWTTDADGGP	DVPWTTDAD	0.1241	13056.2	50.00	Rv2754c, T
DRB1_0301	234	LADGTEVATSPLATE	LADGTEVAT	0.1167	14141.5	50.00	Rv2754c, T
DRB1_0301	23	PWTTDADGGPALVEF	PWTTDADGG	0.1097	15264.8	50.00	Rv2754c, T
DRB1_0301	42	CYQSWSKPNPKTATN	QSWSKPNPK	0.1066	15774.0	50.00	Rv2754c, T
DRB1_0301	39	GRACYQSWSKPNPKT	ACYQSWSKP	0.1045	16138.3	50.00	Rv2754c, T
DRB1_0301	112	DSRVVVPPGMEDDAD	SRVVVPPGM	0.1042	16185.5	50.00	Rv2754c, T
DRB1_0301	36	EFAGRACYQSWSKPN	FAGRACYQS	0.1042	16195.5	50.00	Rv2754c, T
DRB1_0301	235	ADGTEVATSPLATEA	GTEVATSPL	0.1025	16492.7	50.00	Rv2754c, T
DRB1_0301	48	KPNPKTATNAGYLRH	KTATNAGYL	0.1024	16504.5	50.00	Rv2754c, T
DRB1_0301	110	EKDSRVVVPPGMEDD	SRVVVPPGM	0.1008	16794.5	50.00	Rv2754c, T
DRB1_0301	24	WTTDADGGPALVEFA	TDADGGPAL	0.1003	16886.7	50.00	Rv2754c, T
DRB1_0301	37	FAGRACYQSWSKPNP	FAGRACYQS	0.1002	16916.7	50.00	Rv2754c, T
DRB1_0301	111	KDSRVVVPPGMEDDA	SRVVVPPGM	0.0998	16976.0	50.00	Rv2754c, T
DRB1_0301	15	DFLAPPDVPWTTDAD	DFLAPPDVP	0.0941	18069.6	50.00	Rv2754c, T
DRB1_0301	25	TTDADGGPALVEFAG	TDADGGPAL	0.0909	18703.3	50.00	Rv2754c, T
DRB1_0301	38	AGRACYQSWSKPNPK	ACYQSWSKP	0.0825	20484.1	50.00	Rv2754c, T
DRB1_0301	17	LAPPDVPWTTDADGG	VPWTTDADG	0.0780	21494.8	50.00	Rv2754c, T
DRB1_0301	26	TDADGGPALVEFAGR	TDADGGPAL	0.0777	21575.2	50.00	Rv2754c, T
DRB1_0301	43	QSWSKPNPKTATNA	QSWSKPNPK	0.0723	22878.0	50.00	Rv2754c, T
DRB1_0301	47	SKPNPKTATNAGYLR	KPNPKTATN	0.0721	22910.9	50.00	Rv2754c, T
DRB1_0301	44	QSWSKPNPKTATNAG	QSWSKPNPK	0.0713	23115.9	50.00	Rv2754c, T
DRB1_0301	28	ADGGPALVEFAGRAC	ALVEFAGRA	0.0712	23150.7	50.00	Rv2754c, T
DRB1_0301	16	FLAPPDVPWTTDADG	VPWTTDADG	0.0645	24885.0	50.00	Rv2754c, T
DRB1_0301	46	WSKPNPKTATNAGYL	WSKPNPKTA	0.0575	26837.8	50.00	Rv2754c, T
DRB1_0301	27	DADGGPALVEFAGRA	ALVEFAGRA	0.0541	27839.5	50.00	Rv2754c, T
DRB1_0301	45	SWSKPNPKTATNAGY	WSKPNPKTA	0.0531	28153.6	50.00	Rv2754c, T

Allele: DRB1_0301. Number of high binders 0. Number of weak binders 31. Number of peptides 236

Allele	pos	peptide	core	1-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
DRB1_0401	191	WRHFIAMRASEHADV	WRHFIAMRA	0.8101	7.8	SB	0.15	Rv2754c, T
DRB1_0401	189	RAWRHFIAMRASEHA	WRHFIAMRA	0.8082	8.0	SB	0.15	Rv2754c, T
DRB1_0401	190	AWRHFIAMRASEHAD	WRHFIAMRA	0.8008	8.6	SB	0.15	Rv2754c, T

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DRB1_0401	188	YRAWRHFIAMRASEH	WRHFIAMRA	0.7776	11.1	SB	0.40	Rv2754c, T
DRB1_0401	95	HRHFSYSQLSQRYPV	RHFSYSQLS	0.7388	16.9	SB	0.80	Rv2754c, T
DRB1_0401	187	NYRAWRHFIAMRASE	WRHFIAMRA	0.7384	17.0	SB	0.80	Rv2754c, T
DRB1_0401	94	RHRHFSYSQLSQRYPV	RHFSYSQLS	0.7347	17.6	SB	1.00	Rv2754c, T
DRB1_0401	96	RHFSYSQLSQRYPVE	HFSYSQLSQ	0.7268	19.2	SB	1.00	Rv2754c, T
DRB1_0401	93	IRHRHFSYSQLSQRY	RHFSYSQLS	0.7054	24.2	SB	2.00	Rv2754c, T
DRB1_0401	186	GNYRAWRHFIAMRAS	WRHFIAMRA	0.7034	24.8	SB	2.00	Rv2754c, T
DRB1_0401	192	RHFIAMRASEHADVE	RHFIAMRAS	0.6971	26.5	SB	2.00	Rv2754c, T
DRB1_0401	92	LIRHRHFSYSQLSQR	RHFSYSQLS	0.6605	39.4	SB	4.00	Rv2754c, T
DRB1_0401	212	IECLRQLAAVAPAVF	IECLRQLAA	0.6213	60.2	WB	8.00	Rv2754c, T
DRB1_0401	211	AIECLRQLAAVAPAV	IECLRQLAA	0.6034	73.0	WB	8.00	Rv2754c, T
DRB1_0401	209	RLAIECLRQLAAVAP	IECLRQLAA	0.5957	79.4	WB	8.00	Rv2754c, T
DRB1_0401	150	EAKFADQPNAILRRK	KFADQPNAI	0.5922	82.4	WB	8.00	Rv2754c, T
DRB1_0401	210	LAIIECLRQLAAVAPA	IECLRQLAA	0.5845	89.6	WB	8.00	Rv2754c, T
DRB1_0401	185	TGNYRAWRHFIAMRA	WRHFIAMRA	0.5803	93.8	WB	8.00	Rv2754c, T
DRB1_0401	151	AKFADQPNAILRRKQ	KFADQPNAI	0.5784	95.8	WB	8.00	Rv2754c, T
DRB1_0401	149	LEAKFADQPNAILRR	KFADQPNAI	0.5784	95.8	WB	8.00	Rv2754c, T
DRB1_0401	208	RRLAIECLRQLAAVA	IECLRQLAA	0.5774	96.8	WB	8.00	Rv2754c, T
DRB1_0401	97	HFSYSQLSQRYPVEK	HFSYSQLSQ	0.5725	102.0	WB	8.00	Rv2754c, T
DRB1_0401	91	ELIRHRHFSYSQLSQ	RHFSYSQLS	0.5657	109.8	WB	16.00	Rv2754c, T
DRB1_0401	213	ECLRQLAAVAPAVFA	LRQLAAVAP	0.5637	112.2	WB	16.00	Rv2754c, T
DRB1_0401	148	KLEAKFADQPNAILR	KFADQPNAI	0.5512	128.4	WB	16.00	Rv2754c, T
DRB1_0401	207	IRRLAIECLRQLAAV	IECLRQLAA	0.5482	132.7	WB	16.00	Rv2754c, T
DRB1_0401	206	EIRRLAIECLRQLAA	RLAIECLRQ	0.5437	139.4	WB	16.00	Rv2754c, T
DRB1_0401	126	DLRHILTEAADAARA	LRHILTEAA	0.5339	155.0	WB	16.00	Rv2754c, T
DRB1_0401	215	LRQLAAVAPAVFADF	LRQLAAVAP	0.5288	163.8	WB	16.00	Rv2754c, T
DRB1_0401	77	VSFYITGISRSCSTH	SFYITGISR	0.5284	164.4	WB	16.00	Rv2754c, T
DRB1_0401	125	ADLRHILTEAADAAR	LRHILTEAA	0.5268	167.3	WB	16.00	Rv2754c, T
DRB1_0401	214	CLRQLAAVAPAVFAD	LRQLAAVAP	0.5228	174.7	WB	16.00	Rv2754c, T
DRB1_0401	127	LRHILTEAADAARAT	LRHILTEAA	0.5203	179.5	WB	16.00	Rv2754c, T
DRB1_0401	76	SVSFYITGISRSCSTH	SFYITGISR	0.5192	181.7	WB	16.00	Rv2754c, T
DRB1_0401	193	HFIAMRASEHADVEI	FIAMRASEH	0.5147	190.8	WB	16.00	Rv2754c, T
DRB1_0401	40	RACYQSWSKPNPKTA	RACYQSWSK	0.5147	190.8	WB	16.00	Rv2754c, T
DRB1_0401	139	RATYSELLAKLEAKF	RATYSELLA	0.5119	196.6	WB	16.00	Rv2754c, T
DRB1_0401	39	GRACYQSWSKPNPKT	RACYQSWSK	0.5078	205.5	WB	16.00	Rv2754c, T
DRB1_0401	124	DADLRHILTEAADA	LRHILTEAA	0.5054	210.9	WB	16.00	Rv2754c, T
DRB1_0401	75	ASVSFYITGISRSCST	SFYITGISR	0.5051	211.5	WB	16.00	Rv2754c, T
DRB1_0401	59	YLRHIIIDVGHFVLE	RHIIIDVGHF	0.5031	216.2	WB	16.00	Rv2754c, T
DRB1_0401	58	GLRHIIIDVGHFVLE	RHIIIDVGHF	0.5029	216.7	WB	16.00	Rv2754c, T
DRB1_0401	38	AGRACYQSWSKPNPK	RACYQSWSK	0.4953	235.3	WB	16.00	Rv2754c, T
DRB1_0401	37	FAGRACYQSWSKPNP	RACYQSWSK	0.4940	238.7	WB	16.00	Rv2754c, T
DRB1_0401	147	AKLEAKFADQPNAIL	KFADQPNAI	0.4926	242.1	WB	16.00	Rv2754c, T
DRB1_0401	138	ARATYSELLAKLEAK	RATYSELLA	0.4906	247.6	WB	16.00	Rv2754c, T
DRB1_0401	152	KFADQPNAILRRKQA	KFADQPNAI	0.4855	261.6	WB	32.00	Rv2754c, T
DRB1_0401	78	SFYITGISRSCSTHEL	SFYITGISR	0.4819	272.1	WB	32.00	Rv2754c, T
DRB1_0401	205	VEIRRLAIECLRQLA	RLAIECLRQ	0.4758	290.5	WB	32.00	Rv2754c, T
DRB1_0401	74	HASVSFYITGISRSC	SFYITGISR	0.4738	296.9	WB	32.00	Rv2754c, T
DRB1_0401	66	VGHFSVLEHASVSVFY	FSVLEHASV	0.4733	298.6	WB	32.00	Rv2754c, T
DRB1_0401	57	AGYLRHIIIDVGHFV	RHIIIDVGHF	0.4681	315.9	WB	32.00	Rv2754c, T
DRB1_0401	137	AARATYSELLAKLEA	RATYSELLA	0.4585	350.2	WB	32.00	Rv2754c, T
DRB1_0401	167	RQAARAVLPNATETR	RQAARAVLP	0.4583	351.3	WB	32.00	Rv2754c, T
DRB1_0401	60	LRHIIIDVGHFVLEH	RHIIIDVGHF	0.4539	368.1	WB	32.00	Rv2754c, T
DRB1_0401	67	GHFVLEHASVSVFYI	FSVLEHASV	0.4521	375.3	WB	32.00	Rv2754c, T
DRB1_0401	90	HELIRHRHFSYSQLS	RHFSYSQLS	0.4508	380.6	WB	32.00	Rv2754c, T
DRB1_0401	123	DDADLRHILTEAADA	LRHILTEAA	0.4480	392.7	WB	32.00	Rv2754c, T
DRB1_0401	65	DVGHFVLEHASVSVF	FSVLEHASV	0.4455	403.1	WB	32.00	Rv2754c, T
DRB1_0401	136	DAARATYSELLAKLE	RATYSELLA	0.4430	414.1	WB	32.00	Rv2754c, T
DRB1_0401	204	VEIRRLAIECLRQL	RLAIECLRQ	0.4318	467.9	WB	32.00	Rv2754c, T
DRB1_0401	73	EHASVSVFYITGISR	SFYITGISR	0.4310	472.0	WB	32.00	Rv2754c, T
DRB1_0401	128	RHILTEAADAARATY	RHILTEAAD	0.4258	498.8	WB	32.00	Rv2754c, T
DRB1_0401	184	VTGNYRAWRHFIAMR	YRAWRHFI	0.4244	506.7	WB	32.00	Rv2754c, T
DRB1_0401	56	NAGYLRHIIIDVGHF	RHIIIDVGHF	0.4242	507.7	WB	32.00	Rv2754c, T
DRB1_0401	194	FIAMRASEHADVEIR	IAMRASEHA	0.4223	518.1	WB	32.00	Rv2754c, T
DRB1_0401	5	PLRVQLIAKTDFLAP	LRVQLIAKT	0.4223	518.3	WB	32.00	Rv2754c, T
DRB1_0401	166	ARQAARAVLPNATET	RQAARAVLP	0.4200	531.6	WB	32.00	Rv2754c, T
DRB1_0401	36	EFAGRACYQSWSKPN	RACYQSWSK	0.4188	538.5	WB	32.00	Rv2754c, T
DRB1_0401	143	SELLAKLEAKFADQP	ELLAKLEAK	0.4157	556.5	WB	32.00	Rv2754c, T
DRB1_0401	4	APLRVQLIAKTDFLA	LRVQLIAKT	0.4138	568.1	WB	32.00	Rv2754c, T
DRB1_0401	180	TRIVVTGNYRAWRH	RIVVTGNYR	0.4130	573.2	WB	32.00	Rv2754c, T
DRB1_0401	61	RHIIIDVGHFVLEHA	RHIIIDVGHF	0.4085	602.0	WB	32.00	Rv2754c, T
DRB1_0401	3	TAPLRVQLIAKTDFL	LRVQLIAKT	0.4081	604.4	WB	32.00	Rv2754c, T
DRB1_0401	179	ETRIVVTGNYRAWRH	RIVVTGNYR	0.4071	610.8	WB	32.00	Rv2754c, T
DRB1_0401	168	QAARAVLPNATETRI	RAVLPNATE	0.4065	614.7	WB	32.00	Rv2754c, T
DRB1_0401	68	HFSVLEHASVSVFYIT	FSVLEHASV	0.4044	628.8	WB	32.00	Rv2754c, T
DRB1_0401	165	QARQAARAVLPNATE	RQAARAVLP	0.4003	657.4	WB	32.00	Rv2754c, T
DRB1_0401	142	YSELLAKLEAKFADQ	ELLAKLEAK	0.3947	698.6	WB	32.00	Rv2754c, T
DRB1_0401	146	LAKLEAKFADQPNAI	KFADQPNAI	0.3908	728.5	WB	32.00	Rv2754c, T
DRB1_0401	64	IDVGHFVLEHASVSV	FSVLEHASV	0.3906	730.8	WB	32.00	Rv2754c, T
DRB1_0401	203	ADVEIRRLAIECLRQ	EIRRLAIEC	0.3897	737.6	WB	32.00	Rv2754c, T
DRB1_0401	178	TETRIVVTGNYRAWR	RIVVTGNYR	0.3850	776.0	WB	50.00	Rv2754c, T
DRB1_0401	223	PAVFADFEVTTLADG	VFADFEVTT	0.3839	785.4	WB	50.00	Rv2754c, T
DRB1_0401	135	ADAARATYSELLAKL	RATYSELLA	0.3832	790.9	WB	50.00	Rv2754c, T
DRB1_0401	72	LEHASVSVFYITGISR	SFYITGISR	0.3793	825.6	WB	50.00	Rv2754c, T
DRB1_0401	122	EDDADLRHILTEAAD	LRHILTEAA	0.3763	852.8	WB	50.00	Rv2754c, T
DRB1_0401	141	TYSELLAKLEAKFAD	ELLAKLEAK	0.3696	916.7	WB	50.00	Rv2754c, T

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DRB1_0401	6	LRVQLIAKTDFLAPP	LRVQLIAKT	0.3676	936.7	50.00	Rv2754c, T
DRB1_0401	183	VVTGNYRAWRHFIAM	YRAWRHFIAM	0.3650	963.9	50.00	Rv2754c, T
DRB1_0401	35	VEFAGRACYQSWSKP	RACYQSWSK	0.3640	973.5	50.00	Rv2754c, T
DRB1_0401	224	AVFADFEVTTLADGT	VFADFEVTT	0.3626	988.5	50.00	Rv2754c, T
DRB1_0401	144	ELLAKLEAKFADQPN	ELLAKLEAK	0.3625	989.9	50.00	Rv2754c, T
DRB1_0401	69	FSVLEHASVSFYITG	FSVLEHASV	0.3623	992.4	50.00	Rv2754c, T
DRB1_0401	225	VFADFEVTTLADGTE	VFADFEVTT	0.3570	1050.4	50.00	Rv2754c, T
DRB1_0401	181	RIVVTGNYRAWRHFI	RIVVTGNYR	0.3561	1060.8	50.00	Rv2754c, T
DRB1_0401	164	KQARQAARAVLPNAT	RQAARAVLP	0.3550	1073.6	50.00	Rv2754c, T
DRB1_0401	170	ARAVLPNATETRIVV	RAVLPNATE	0.3544	1080.7	50.00	Rv2754c, T
DRB1_0401	98	FSYSQLSQRYVPEKD	FSYSQLSQR	0.3534	1092.9	50.00	Rv2754c, T
DRB1_0401	222	APAVFADFEVTTLAD	VFADFEVTT	0.3533	1093.5	50.00	Rv2754c, T
DRB1_0401	160	ILRRKQARQAARAVL	ILRRKQARQ	0.3533	1094.1	50.00	Rv2754c, T
DRB1_0401	169	AARAVLPNATETRIV	RAVLPNATE	0.3501	1131.5	50.00	Rv2754c, T
DRB1_0401	55	TNAGYLRHIIDVGHF	YLRHIIDVG	0.3478	1160.1	50.00	Rv2754c, T
DRB1_0401	2	ETAPLRVQLIAKTDF	LRVQLIAKT	0.3418	1238.3	50.00	Rv2754c, T
DRB1_0401	159	AILRRKQARQAARAV	ILRRKQARQ	0.3418	1238.4	50.00	Rv2754c, T
DRB1_0401	140	ATYSELLAKLEAKFA	ELLAKLEAK	0.3411	1247.3	50.00	Rv2754c, T
DRB1_0401	177	FVADFEVTTGNYRAW	RIVVTGNYR	0.3367	1308.5	50.00	Rv2754c, T
DRB1_0401	71	VLEHASVSFYITGIS	VSFYITGIS	0.3348	1336.2	50.00	Rv2754c, T
DRB1_0401	63	IIDVGHFSVLEHASV	FSVLEHASV	0.3343	1343.4	50.00	Rv2754c, T
DRB1_0401	121	MEDDADLRHILTEAA	LRHILTEAA	0.3341	1345.6	50.00	Rv2754c, T
DRB1_0401	145	LLAKLEAKFADQPN	LAKLEAKFA	0.3255	1477.8	50.00	Rv2754c, T
DRB1_0401	171	RAVLPNATETRIVVT	RAVLPNATE	0.3232	1514.7	50.00	Rv2754c, T
DRB1_0401	162	RRKQARQAARAVLPN	RQAARAVLP	0.3204	1560.4	50.00	Rv2754c, T
DRB1_0401	163	RKQARQAARAVLPNA	RQAARAVLP	0.3202	1564.4	50.00	Rv2754c, T
DRB1_0401	195	IAMRASEHADVEIRR	IAMRASEHA	0.3196	1574.5	50.00	Rv2754c, T
DRB1_0401	42	CYQSWSKPNPKTATN	YQSWSKPNP	0.3190	1585.4	50.00	Rv2754c, T
DRB1_0401	89	THELIRHRHFSYSQL	LIRHRHFSY	0.3182	1598.8	50.00	Rv2754c, T
DRB1_0401	182	IVVTGNYRAWRHFI	IVVTGNYRA	0.3175	1611.4	50.00	Rv2754c, T
DRB1_0401	41	ACYQSWSKPNPKTAT	YQSWSKPNP	0.3169	1621.6	50.00	Rv2754c, T
DRB1_0401	221	VAPAVFADFEVTTLA	VFADFEVTT	0.3149	1656.5	50.00	Rv2754c, T
DRB1_0401	158	NAILRRKQARQAARA	ILRRKQARQ	0.3139	1675.4	50.00	Rv2754c, T
DRB1_0401	161	LRRKQARQAARAVLP	RRKQARQAA	0.3126	1698.3	50.00	Rv2754c, T
DRB1_0401	105	QRYVPEKDSRVVPPP	QRYVPEKDS	0.3113	1723.5	50.00	Rv2754c, T
DRB1_0401	34	LVEFAGRACYQSWSK	RACYQSWSK	0.3084	1778.4	50.00	Rv2754c, T
DRB1_0401	134	AADAARATYSELLAK	RATYSELLA	0.3048	1848.9	50.00	Rv2754c, T
DRB1_0401	202	HADVEIRRLAIECLR	EIRRLAIEC	0.3046	1851.8	50.00	Rv2754c, T
DRB1_0401	104	SQRYVPEKDSRVVVP	QRYVPEKDS	0.3045	1853.2	50.00	Rv2754c, T
DRB1_0401	201	EHADVEIRRLAIECLR	EHADVEIRR	0.3025	1895.5	50.00	Rv2754c, T
DRB1_0401	79	FYITGISRSCTHELI	FYITGISRS	0.3013	1918.5	50.00	Rv2754c, T
DRB1_0401	62	HIIDVGHFSVLEHAS	HIIDVGHFS	0.2959	2036.0	50.00	Rv2754c, T
DRB1_0401	103	LLQRYVPEKDSRVVV	QRYVPEKDS	0.2885	2205.2	50.00	Rv2754c, T
DRB1_0401	70	SVLEHASVSFYITGI	VLEHASVSF	0.2871	2238.8	50.00	Rv2754c, T
DRB1_0401	176	NATETRIVVTGNYRA	RIVVTGNYR	0.2863	2257.6	50.00	Rv2754c, T
DRB1_0401	157	PNAILRRKQARQAAR	ILRRKQARQ	0.2851	2286.2	50.00	Rv2754c, T
DRB1_0401	43	YQSWSKPNPKTATNA	YQSWSKPNP	0.2819	2366.5	50.00	Rv2754c, T
DRB1_0401	227	ADFEVTTLADGTEVA	DFEVTTLAD	0.2798	2422.3	50.00	Rv2754c, T
DRB1_0401	216	RQLAAVAPAVFADFE	RQLAAVAPA	0.2754	2541.5	50.00	Rv2754c, T
DRB1_0401	200	SEHADVEIRRLAIEC	EHADVEIRR	0.2747	2559.5	50.00	Rv2754c, T
DRB1_0401	228	DFEVTTLADGTEVAT	DFEVTTLAD	0.2720	2634.5	50.00	Rv2754c, T
DRB1_0401	1	AETAPLRVQLIAKTD	LRVQLIAKT	0.2716	2647.7	50.00	Rv2754c, T
DRB1_0401	226	FADFEVTTLADGTEV	DFEVTTLAD	0.2713	2654.7	50.00	Rv2754c, T
DRB1_0401	9	QLIAKTDFLAPPDVP	QLIAKTDFL	0.2688	2727.5	50.00	Rv2754c, T
DRB1_0401	88	THELIRHRHFSYSQ	LIRHRHFSY	0.2678	2758.3	50.00	Rv2754c, T
DRB1_0401	102	QLSQRYVPEKDSRVV	QRYVPEKDS	0.2651	2839.6	50.00	Rv2754c, T
DRB1_0401	153	FADQPNAILRRKQAR	FADQPNAIL	0.2649	2845.4	50.00	Rv2754c, T
DRB1_0401	129	HILTEAADAARATYS	ILTEAADAA	0.2623	2925.8	50.00	Rv2754c, T
DRB1_0401	220	AVAPAVFADFEVTTL	PAVFADFEV	0.2575	3084.6	50.00	Rv2754c, T
DRB1_0401	80	YITGISRSCTHELIR	YITGISRSC	0.2557	3144.8	50.00	Rv2754c, T
DRB1_0401	10	LIAKTDFLAPPDVPW	LIAKTDFLA	0.2555	3152.1	50.00	Rv2754c, T
DRB1_0401	54	ATNAGYLRHIIDVGH	GYLRHIIDV	0.2529	3240.3	50.00	Rv2754c, T
DRB1_0401	86	RSCTHELIRHRHFSY	LIRHRHFSY	0.2486	3393.0	50.00	Rv2754c, T
DRB1_0401	120	GMEDDADLRHILTEA	MEDDADLRH	0.2479	3420.9	50.00	Rv2754c, T
DRB1_0401	99	SYSQLSQRYVPEKDS	SYSQLSQRY	0.2467	3466.7	50.00	Rv2754c, T
DRB1_0401	8	VQLIAKTDFLAPPDVP	QLIAKTDFL	0.2462	3483.5	50.00	Rv2754c, T
DRB1_0401	133	EAADAARATYSELLA	RATYSELLA	0.2453	3518.1	50.00	Rv2754c, T
DRB1_0401	199	ASEHADVEIRRLAIE	EHADVEIRR	0.2444	3553.0	50.00	Rv2754c, T
DRB1_0401	7	RVQLIAKTDFLAPPD	LIAKTDFLA	0.2433	3595.2	50.00	Rv2754c, T
DRB1_0401	130	ILTEAADAARATYS	ILTEAADAA	0.2422	3638.6	50.00	Rv2754c, T
DRB1_0401	156	QPNAILRRKQARQAA	ILRRKQARQ	0.2415	3664.7	50.00	Rv2754c, T
DRB1_0401	84	ISRSCTHELIRHRHF	ISRSCTHEL	0.2408	3692.4	50.00	Rv2754c, T
DRB1_0401	233	TLADGTEVATSPLAT	LADGTEVAT	0.2408	3695.0	50.00	Rv2754c, T
DRB1_0401	234	LADGTEVATSPLATE	LADGTEVAT	0.2406	3701.8	50.00	Rv2754c, T
DRB1_0401	0	VAETAPLRVQLIAKTD	LRVQLIAKT	0.2371	3842.7	50.00	Rv2754c, T
DRB1_0401	106	RYVPEKDSRVVPPPG	RYVPEKDSR	0.2370	3848.5	50.00	Rv2754c, T
DRB1_0401	235	ADGTEVATSPLATEA	EVATSPLAT	0.2349	3937.4	50.00	Rv2754c, T
DRB1_0401	87	SCTHELIRHRHFSYS	LIRHRHFSY	0.2340	3973.6	50.00	Rv2754c, T
DRB1_0401	13	KTDFLAPPDVPWTTD	DFLAPPDVP	0.2337	3987.8	50.00	Rv2754c, T
DRB1_0401	83	GISRSCTHELIRHRH	GISRSCTHE	0.2326	4036.4	50.00	Rv2754c, T
DRB1_0401	14	TDFLAPPDVPWTTDA	DFLAPPDVP	0.2322	4053.6	50.00	Rv2754c, T
DRB1_0401	101	SQLSQRYVPEKDSRV	QRYVPEKDS	0.2293	4182.8	50.00	Rv2754c, T
DRB1_0401	229	FEVTTLADGTEVATS	FEVTTLADG	0.2270	4289.6	50.00	Rv2754c, T
DRB1_0401	12	AKTDFLAPPDVPWTT	DFLAPPDVP	0.2258	4343.1	50.00	Rv2754c, T
DRB1_0401	82	TGISRSCTHELIRHR	TGISRSCTH	0.2256	4355.6	50.00	Rv2754c, T

DRB1_0401	81	ITGISRSCTHELIRH	GISRSCTHE	0.2248	4391.3	50.00	Rv2754c, T
DRB1_0401	232	TTLADGTEVATSPLA	TLADGTEVA	0.2240	4431.9	50.00	Rv2754c, T
DRB1_0401	85	RSRCTHELIRHRHFS	RSRCTHELIR	0.2224	4507.5	50.00	Rv2754c, T
DRB1_0401	219	AAVAPAVFADFVTT	VFADFVTT	0.2194	4657.1	50.00	Rv2754c, T
DRB1_0401	230	EVTTLADGTEVATSP	TLADGTEVA	0.2181	4720.8	50.00	Rv2754c, T
DRB1_0401	11	IAKTDFLAPPDVPWT	DFLAPPDVP	0.2172	4769.2	50.00	Rv2754c, T
DRB1_0401	231	VTTLADGTEVATSPL	LADGTEVAT	0.2167	4792.1	50.00	Rv2754c, T
DRB1_0401	198	RASEHADVEIRRLAI	EHADVEIRR	0.2156	4853.1	50.00	Rv2754c, T
DRB1_0401	119	PGMEDDADLRHILTE	MEDDADLRH	0.2136	4959.2	50.00	Rv2754c, T
DRB1_0401	100	YSQLSQRYVPEKDSR	YSQLSQRYV	0.2078	5277.4	50.00	Rv2754c, T
DRB1_0401	197	MRASEHADVEIRRLA	EHADVEIRR	0.2070	5321.8	50.00	Rv2754c, T
DRB1_0401	118	PPGMEDDADLRHILT	MEDDADLRH	0.2064	5361.6	50.00	Rv2754c, T
DRB1_0401	53	TATNAGYLRHIIDVG	GYLRHIIDV	0.2060	5383.4	50.00	Rv2754c, T
DRB1_0401	175	PNATETRIVVTGNYSR	TRIVVTGNYS	0.2017	5636.3	50.00	Rv2754c, T
DRB1_0401	155	DQPNAILRRKQARQA	ILRRKQARQ	0.2013	5660.7	50.00	Rv2754c, T
DRB1_0401	33	ALVEFAGRACYQSW	FAGRACYQS	0.1938	6139.1	50.00	Rv2754c, T
DRB1_0401	15	DFLAPPDVPWTTDAD	DFLAPPDVP	0.1889	6479.2	50.00	Rv2754c, T
DRB1_0401	196	AMRASEHADVEIRRL	EHADVEIRR	0.1835	6863.0	50.00	Rv2754c, T
DRB1_0401	117	VPPGMEDDADLRHIL	GMEDDADLR	0.1787	7233.7	50.00	Rv2754c, T
DRB1_0401	32	PALVEFAGRACYQSW	FAGRACYQS	0.1695	7988.4	50.00	Rv2754c, T
DRB1_0401	107	YVPEKDSRVVPPGM	YVPEKDSRV	0.1584	9009.7	50.00	Rv2754c, T
DRB1_0401	218	LAAPAVFADFVTT	AAVAPAVFA	0.1560	9241.4	50.00	Rv2754c, T
DRB1_0401	110	EKDSRVVPPGMEDD	EKDSRVVVP	0.1547	9376.0	50.00	Rv2754c, T
DRB1_0401	154	ADQPNAILRRKQARQ	ILRRKQARQ	0.1499	9875.9	50.00	Rv2754c, T
DRB1_0401	217	QLAAVAPAVFADFV	QLAAVAPAV	0.1490	9969.9	50.00	Rv2754c, T
DRB1_0401	116	VVPPGMEDDADLRHI	MEDDADLRH	0.1488	9992.5	50.00	Rv2754c, T
DRB1_0401	31	GPALVEFAGRACYQS	FAGRACYQS	0.1464	10253.7	50.00	Rv2754c, T
DRB1_0401	131	LTEAADAARATYSEL	LTEAADAAR	0.1458	10321.7	50.00	Rv2754c, T
DRB1_0401	109	PEKDSRVVPPGMED	EKDSRVVVP	0.1454	10364.7	50.00	Rv2754c, T
DRB1_0401	44	QSWSKPNPKTATNAG	QSWSKPNPK	0.1403	10951.8	50.00	Rv2754c, T
DRB1_0401	52	KTATNAGYLRHIIDV	TATNAGYLR	0.1316	12042.5	50.00	Rv2754c, T
DRB1_0401	108	VPEKDSRVVPPGME	EKDSRVVVP	0.1291	12366.1	50.00	Rv2754c, T
DRB1_0401	111	KDSRVVPPGMEDDA	SRVVPPGM	0.1279	12527.8	50.00	Rv2754c, T
DRB1_0401	115	SRVVPPGMEDDADLRH	MEDDADLRH	0.1263	12751.1	50.00	Rv2754c, T
DRB1_0401	113	RVVVPPGMEDDADL	RVVVPPGME	0.1209	13514.8	50.00	Rv2754c, T
DRB1_0401	174	LPNATETRIVVTGNYS	TRIVVTGNYS	0.1204	13589.5	50.00	Rv2754c, T
DRB1_0401	173	VLPNATETRIVVTGN	VLPNATETR	0.1186	13864.6	50.00	Rv2754c, T
DRB1_0401	114	RVVVPPGMEDDADLR	RVVVPPGME	0.1172	14073.5	50.00	Rv2754c, T
DRB1_0401	172	AVLPNATETRIVVTG	VLPNATETR	0.1157	14292.6	50.00	Rv2754c, T
DRB1_0401	30	GGPALVEFAGRACYQ	PALVEFAGR	0.1141	14543.1	50.00	Rv2754c, T
DRB1_0401	112	DSRVVPPGMEDDAD	RVVVPPGME	0.1135	14635.6	50.00	Rv2754c, T
DRB1_0401	21	DVPWTTDADGGPALV	DVPWTTDAD	0.1116	14945.6	50.00	Rv2754c, T
DRB1_0401	16	FLAPPDVPWTTDADG	FLAPPDVPW	0.1089	15394.6	50.00	Rv2754c, T
DRB1_0401	20	PDVPWTTDADGGPAL	DVPWTTDAD	0.1062	15851.0	50.00	Rv2754c, T
DRB1_0401	19	PPDVPWTTDADGGPA	DVPWTTDAD	0.1055	15966.8	50.00	Rv2754c, T
DRB1_0401	29	DGGPALVEFAGRACY	PALVEFAGR	0.1046	16116.1	50.00	Rv2754c, T
DRB1_0401	51	PKTATNAGYLRHIID	TATNAGYLR	0.1044	16156.6	50.00	Rv2754c, T
DRB1_0401	50	NPKTATNAGYLRHI	TATNAGYLR	0.1037	16289.3	50.00	Rv2754c, T
DRB1_0401	22	VPWTTDADGGPALVE	WTTDADGGP	0.0984	17241.4	50.00	Rv2754c, T
DRB1_0401	45	WSKPNPKTATNAGY	WSKPNPKTA	0.0982	17278.6	50.00	Rv2754c, T
DRB1_0401	46	WSKPNPKTATNAGYL	WSKPNPKTA	0.0976	17386.2	50.00	Rv2754c, T
DRB1_0401	132	TEAADAARATYSELL	TEAADAARA	0.0931	18256.0	50.00	Rv2754c, T
DRB1_0401	49	PNPKTATNAGYLRHI	PKTATNAGY	0.0913	18612.1	50.00	Rv2754c, T
DRB1_0401	23	WTTDADGGPALVEF	WTTDADGGP	0.0885	19187.9	50.00	Rv2754c, T
DRB1_0401	48	KPNPKTATNAGYLRH	PKTATNAGY	0.0872	19472.5	50.00	Rv2754c, T
DRB1_0401	18	APPDVPWTTDADGGP	DVPWTTDAD	0.0870	19495.5	50.00	Rv2754c, T
DRB1_0401	47	SKPNPKTATNAGYLR	PKTATNAGY	0.0764	21873.9	50.00	Rv2754c, T
DRB1_0401	28	ADGGPALVEFAGRAC	PALVEFAGR	0.0762	21918.7	50.00	Rv2754c, T
DRB1_0401	24	WTTDADGGPALVEFA	WTTDADGGP	0.0749	22230.4	50.00	Rv2754c, T
DRB1_0401	17	LAPPDVPWTTDADGG	DVPWTTDAD	0.0703	23366.8	50.00	Rv2754c, T
DRB1_0401	27	DADGGPALVEFAGRA	PALVEFAGR	0.0620	25564.0	50.00	Rv2754c, T
DRB1_0401	26	TDADGGPALVEFAGR	PALVEFAGR	0.0508	28854.3	50.00	Rv2754c, T
DRB1_0401	25	TTDADGGPALVEFAG	TTDADGGPA	0.0430	31384.0	50.00	Rv2754c, T

Allele: DRB1_0401. Number of high binders 12. Number of weak binders 51. Number of peptides 236

Allele	pos	peptide	core	l-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
DRB1_0404	191	WRHFIAMRASEHADV	HFIAMRASE	0.7696	12.1	SB	0.80	Rv2754c, T
DRB1_0404	192	RHFIAMRASEHADVE	HFIAMRASE	0.7659	12.6	SB	0.80	Rv2754c, T
DRB1_0404	190	AWRHFIAMRASEHAD	HFIAMRASE	0.7615	13.2	SB	0.80	Rv2754c, T
DRB1_0404	193	HFIAMRASEHADVEI	HFIAMRASE	0.7444	15.9	SB	2.00	Rv2754c, T
DRB1_0404	189	RAWRHFIAMRASEHA	HFIAMRASE	0.7167	21.4	SB	2.00	Rv2754c, T
DRB1_0404	210	LAIECLRQLAAVAPA	LAIECLRQL	0.7002	25.6	SB	4.00	Rv2754c, T
DRB1_0404	209	RLAIECLRQLAAVAP	LAIECLRQL	0.6826	31.0	SB	4.00	Rv2754c, T
DRB1_0404	188	YRAWRHFIAMRASEH	HFIAMRASE	0.6668	36.8	SB	8.00	Rv2754c, T
DRB1_0404	211	AIECLRQLAAVAPAV	ECLRQLAAV	0.6627	38.4	SB	8.00	Rv2754c, T
DRB1_0404	208	RRLAIECLRQLAAVA	LAIECLRQL	0.6554	41.6	SB	8.00	Rv2754c, T
DRB1_0404	212	IECLRQLAAVAPAVF	ECLRQLAAV	0.6410	48.7	SB	8.00	Rv2754c, T
DRB1_0404	213	ECLRQLAAVAPAVFA	ECLRQLAAV	0.5932	81.6	WB	16.00	Rv2754c, T
DRB1_0404	207	IRRLAIECLRQLAAV	LAIECLRQL	0.5885	85.8	WB	16.00	Rv2754c, T
DRB1_0404	5	PLRVQLIAKTDFLAP	LRVQLIAKT	0.5771	97.1	WB	16.00	Rv2754c, T

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DRB1_0404	180	TRIVVTGNYRAWRFH	RIVVTGNYR	0.5760	98.3	WB	16.00	Rv2754c, T
DRB1_0404	4	APLRVQLIAKTDFLA	LRVQLIAKT	0.5755	98.8	WB	16.00	Rv2754c, T
DRB1_0404	187	NYRAWRHFIAMRASE	HFIAMRASE	0.5726	101.9	WB	16.00	Rv2754c, T
DRB1_0404	179	ETRIVVTGNYRAWRH	TRIVVTGNY	0.5672	108.0	WB	16.00	Rv2754c, T
DRB1_0404	3	TAPLRVQLIAKTDFL	LRVQLIAKT	0.5588	118.3	WB	16.00	Rv2754c, T
DRB1_0404	178	ETRIVVTGNYRAWR	TRIVVTGNY	0.5501	130.0	WB	16.00	Rv2754c, T
DRB1_0404	206	EIRRLAIECLRQLAA	LAIECLRQL	0.5493	131.1	WB	16.00	Rv2754c, T
DRB1_0404	6	LRVQLIAKTDFLAPP	LRVQLIAKT	0.5310	160.0	WB	16.00	Rv2754c, T
DRB1_0404	177	ATETRIVVTGNYRAW	TRIVVTGNY	0.5109	198.8	WB	32.00	Rv2754c, T
DRB1_0404	2	ETAPLRVQLIAKTDF	LRVQLIAKT	0.5104	199.8	WB	32.00	Rv2754c, T
DRB1_0404	214	CLRQLAAVAPAVFAD	CLRQLAAVA	0.5029	216.7	WB	32.00	Rv2754c, T
DRB1_0404	205	VEIRRLAIECLRQLA	EIRRLAIEC	0.4796	278.7	WB	32.00	Rv2754c, T
DRB1_0404	204	DVEIRRLAIECLRQL	EIRRLAIEC	0.4667	320.5	WB	32.00	Rv2754c, T
DRB1_0404	1	AETAPLRVQLIAKTD	LRVQLIAKT	0.4552	362.9	WB	32.00	Rv2754c, T
DRB1_0404	223	PAVFADFEVTTLDAG	AVFADFEVT	0.4443	408.6	WB	32.00	Rv2754c, T
DRB1_0404	176	NATETRIVVTGNYRA	TRIVVTGNY	0.4441	409.6	WB	32.00	Rv2754c, T
DRB1_0404	169	AARAVLPNATETRIV	AARAVLPNA	0.4436	411.5	WB	32.00	Rv2754c, T
DRB1_0404	181	RIVVTGNYRAWRHFI	RIVVTGNYR	0.4435	412.2	WB	32.00	Rv2754c, T
DRB1_0404	167	RQAAARAVLPNATETR	AARAVLPNA	0.4432	413.3	WB	32.00	Rv2754c, T
DRB1_0404	168	QAARAVLPNATETRI	AARAVLPNA	0.4410	423.5	WB	32.00	Rv2754c, T
DRB1_0404	224	AVFADFEVTTLDAGT	AVFADFEVT	0.4364	444.8	WB	32.00	Rv2754c, T
DRB1_0404	222	APAVFADFEVTTLDAG	AVFADFEVT	0.4279	487.7	WB	32.00	Rv2754c, T
DRB1_0404	58	GLRHHIIDVGHFVSVL	YLRHHIIDVG	0.4272	491.4	WB	32.00	Rv2754c, T
DRB1_0404	59	YLRHHIIDVGHFVSLE	YLRHHIIDVG	0.4215	522.9		32.00	Rv2754c, T
DRB1_0404	95	HRHFSYSQLSQRYVP	HRHFSYSQL	0.4206	528.1		32.00	Rv2754c, T
DRB1_0404	215	LRQLAAVAPAVFADF	QLAAVAPAV	0.4186	539.7		32.00	Rv2754c, T
DRB1_0404	221	VAPAVFADFEVTTLA	AVFADFEVT	0.4171	548.3		32.00	Rv2754c, T
DRB1_0404	76	SVSFYITGISRSCSTH	FYITGISRS	0.4158	556.1		32.00	Rv2754c, T
DRB1_0404	57	AGYLRHHIIDVGHFSV	YLRHHIIDVG	0.4149	561.3		32.00	Rv2754c, T
DRB1_0404	203	ADVEIRRLAIECLRQ	EIRRLAIEC	0.4148	562.2		32.00	Rv2754c, T
DRB1_0404	7	RVQLIAKTDFLAPPD	RVQLIAKTD	0.4119	580.3		32.00	Rv2754c, T
DRB1_0404	67	GHSVLEHASVSFYI	FSVLEHASV	0.4101	591.3		32.00	Rv2754c, T
DRB1_0404	75	ASVSFYITGISRSCST	SFYITGISR	0.4091	598.1		32.00	Rv2754c, T
DRB1_0404	94	RHRHFSYSQLSQRYV	HRHFSYSQL	0.4087	600.3		32.00	Rv2754c, T
DRB1_0404	166	ARQAARAVLPNATETR	AARAVLPNA	0.4086	601.4		32.00	Rv2754c, T
DRB1_0404	68	HFSVLEHASVSFYIT	FSVLEHASV	0.4071	611.1		32.00	Rv2754c, T
DRB1_0404	64	IDVGHFSVLEHASVS	FSVLEHASV	0.4057	620.1		50.00	Rv2754c, T
DRB1_0404	63	IIDVGHFSVLEHASV	IDVGHFSVL	0.4057	620.2		50.00	Rv2754c, T
DRB1_0404	66	VGHFSVLEHASVSFY	FSVLEHASV	0.4038	633.5		50.00	Rv2754c, T
DRB1_0404	92	LIRHRHFSYSQLSQR	HRHFSYSQL	0.4023	643.3		50.00	Rv2754c, T
DRB1_0404	143	SELLAKLEAKFADQP	ELLAKLEAK	0.3989	667.5		50.00	Rv2754c, T
DRB1_0404	56	NAGYLRHHIIDVGHFS	YLRHHIIDVG	0.3965	685.4		50.00	Rv2754c, T
DRB1_0404	142	YSELLAKLEAKFADQ	ELLAKLEAK	0.3962	687.6		50.00	Rv2754c, T
DRB1_0404	65	DVGHFSVLEHASVSF	FSVLEHASV	0.3959	690.0		50.00	Rv2754c, T
DRB1_0404	216	RQLAAVAPAVFADFE	QLAAVAPAV	0.3955	692.9		50.00	Rv2754c, T
DRB1_0404	77	VSFYITGISRSCSTHE	SFYITGISR	0.3908	728.5		50.00	Rv2754c, T
DRB1_0404	126	LRHILTEAADAARA	HILTEAADA	0.3892	741.5		50.00	Rv2754c, T
DRB1_0404	194	FIAMRASEHADVEIR	FIAMRASEH	0.3891	742.1		50.00	Rv2754c, T
DRB1_0404	74	HASVSFYITGISRSC	SFYITGISR	0.3890	743.5		50.00	Rv2754c, T
DRB1_0404	78	SFYITGISRSCSTHEL	YITGISRSC	0.3853	773.4		50.00	Rv2754c, T
DRB1_0404	141	TYSELLAKLEAKFAD	ELLAKLEAK	0.3853	773.8		50.00	Rv2754c, T
DRB1_0404	93	IRHRHFSYSQLSQRY	HRHFSYSQL	0.3824	798.3		50.00	Rv2754c, T
DRB1_0404	69	FSVLEHASVSFYITG	FSVLEHASV	0.3781	835.8		50.00	Rv2754c, T
DRB1_0404	96	RHFSYSQLSQRYVPE	FSYSQLSQR	0.3745	869.7		50.00	Rv2754c, T
DRB1_0404	125	ADLRHILTEAADAAR	LRHILTEAA	0.3725	888.0		50.00	Rv2754c, T
DRB1_0404	55	TNAGYLRHHIIDVGHF	YLRHHIIDVG	0.3663	949.9		50.00	Rv2754c, T
DRB1_0404	73	ENASVSFYITGISRS	ASVSFYITG	0.3659	954.2		50.00	Rv2754c, T
DRB1_0404	186	GNYRAWRHFIAMRAS	AWRHFIAMR	0.3658	955.0		50.00	Rv2754c, T
DRB1_0404	220	AVAPAVFADFEVTTL	AVFADFEVT	0.3647	967.0		50.00	Rv2754c, T
DRB1_0404	144	ELLAKLEAKFADQPN	ELLAKLEAK	0.3625	990.3		50.00	Rv2754c, T
DRB1_0404	37	FAGRACYQSWKPNP	RACYQSWSK	0.3577	1042.6		50.00	Rv2754c, T
DRB1_0404	0	VAETAPLRVQLIAKT	LRVQLIAKT	0.3576	1043.5		50.00	Rv2754c, T
DRB1_0404	91	ELIRHRHFSYSQLSQ	LIRHRHFSY	0.3564	1057.0		50.00	Rv2754c, T
DRB1_0404	62	HIIDVGHFSVLEHAS	IDVGHFSVL	0.3564	1057.1		50.00	Rv2754c, T
DRB1_0404	60	LRHHIIDVGHFSVLEH	LRHHIIDVGH	0.3563	1058.8		50.00	Rv2754c, T
DRB1_0404	170	ARAVLPNATETRIVV	RAVLPNATE	0.3553	1070.3		50.00	Rv2754c, T
DRB1_0404	165	QARQAARAVLPNATE	AARAVLPNA	0.3546	1078.4		50.00	Rv2754c, T
DRB1_0404	79	FYITGISRSCSTHELI	YITGISRSC	0.3545	1079.0		50.00	Rv2754c, T
DRB1_0404	61	RHHIIDVGHFSVLEHA	IDVGHFSVL	0.3537	1088.6		50.00	Rv2754c, T
DRB1_0404	127	LRHILTEAADAARAT	HILTEAADA	0.3534	1091.8		50.00	Rv2754c, T
DRB1_0404	202	HADVEIRRLAIECLR	EIRRLAIEC	0.3530	1096.6		50.00	Rv2754c, T
DRB1_0404	225	VFADFEVTTLDAGTE	FEVTTLDAG	0.3514	1116.5		50.00	Rv2754c, T
DRB1_0404	226	FADFEVTTLDAGTEV	EVTTLADGT	0.3491	1144.3		50.00	Rv2754c, T
DRB1_0404	227	ADFEVTTLDAGTEVA	EVTTLADGT	0.3471	1169.0		50.00	Rv2754c, T
DRB1_0404	229	FEVTTLDAGTEVATS	EVTTLADGT	0.3466	1176.4		50.00	Rv2754c, T
DRB1_0404	140	ATYSELLAKLEAKFA	ELLAKLEAK	0.3464	1178.5		50.00	Rv2754c, T
DRB1_0404	228	DFEVTTLDAGTEVAT	EVTTLADGT	0.3448	1199.4		50.00	Rv2754c, T
DRB1_0404	40	RACYQSWKPNPKTA	RACYQSWSK	0.3390	1276.0		50.00	Rv2754c, T
DRB1_0404	175	PNATETRIVVTGNYR	TRIVVTGNY	0.3389	1277.4		50.00	Rv2754c, T
DRB1_0404	39	GRACYQSWKPNPKT	RACYQSWSK	0.3389	1278.5		50.00	Rv2754c, T
DRB1_0404	124	DADLRHILTEAADA	LRHILTEAA	0.3388	1279.5		50.00	Rv2754c, T
DRB1_0404	97	HFSYSQLSQRYVPEK	FSYSQLSQR	0.3375	1297.1		50.00	Rv2754c, T
DRB1_0404	54	ATNAGYLRHHIIDVGH	YLRHHIIDVG	0.3308	1394.2		50.00	Rv2754c, T
DRB1_0404	150	EAKFADQPNAILRRK	KFADQPNAI	0.3300	1407.7		50.00	Rv2754c, T
DRB1_0404	72	LEHASVSFYITGISR	ASVSFYITG	0.3298	1410.7		50.00	Rv2754c, T

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DRB1_0404	139	RATYSELLAKLEAKF	ELLAKLEAK	0.3288	1424.7	50.00	Rv2754c, T
DRB1_0404	149	LEAKFADQPNAILRR	KFADQPNAI	0.3274	1446.9	50.00	Rv2754c, T
DRB1_0404	217	QLAAVAPAVFADFEV	QLAAVAPAV	0.3257	1474.3	50.00	Rv2754c, T
DRB1_0404	151	AKFADQPNAILRRKQ	KFADQPNAI	0.3244	1495.0	50.00	Rv2754c, T
DRB1_0404	36	EFAGRACYQSWSKPN	RACYQSWSK	0.3206	1556.9	50.00	Rv2754c, T
DRB1_0404	38	AGRACYQSWSKPNPK	RACYQSWSK	0.3203	1562.2	50.00	Rv2754c, T
DRB1_0404	219	AAVAPAVFADFEVTT	AVFADFEVT	0.3156	1644.2	50.00	Rv2754c, T
DRB1_0404	128	RHILTEAADAARATY	HILTEAADA	0.3131	1688.6	50.00	Rv2754c, T
DRB1_0404	185	TGNYRAWRHFIAMRA	AWRHFIAMR	0.3123	1704.3	50.00	Rv2754c, T
DRB1_0404	80	YITGISRSCSTHELIR	YITGISRSC	0.3105	1736.7	50.00	Rv2754c, T
DRB1_0404	148	KLEAKFADQPNAILR	KFADQPNAI	0.3094	1759.0	50.00	Rv2754c, T
DRB1_0404	71	VLEHASVSFYITGIS	ASVSFYITG	0.3048	1848.7	50.00	Rv2754c, T
DRB1_0404	90	HELIRHRHFSYSQLS	LIRHRHFSY	0.3031	1882.7	50.00	Rv2754c, T
DRB1_0404	98	FSYSQLSQRYVPEKD	FSYSQLSQR	0.2981	1987.4	50.00	Rv2754c, T
DRB1_0404	164	KQARQAARAVLPNAT	RQAARAVLP	0.2979	1990.5	50.00	Rv2754c, T
DRB1_0404	152	KFADQPNAILRRKQA	KFADQPNAI	0.2945	2065.5	50.00	Rv2754c, T
DRB1_0404	138	ARATYSELLAKLEAK	ELLAKLEAK	0.2932	2096.2	50.00	Rv2754c, T
DRB1_0404	70	SVLEHASVSFYITGI	VLEHASVSF	0.2928	2104.3	50.00	Rv2754c, T
DRB1_0404	8	VQLIAKTDFLAPPDVP	QLIAKTDFL	0.2914	2136.6	50.00	Rv2754c, T
DRB1_0404	9	QLIAKTDFLAPPDVP	QLIAKTDFL	0.2879	2219.0	50.00	Rv2754c, T
DRB1_0404	201	EHADVEIRRLAIECL	EIRRLAIEC	0.2872	2236.9	50.00	Rv2754c, T
DRB1_0404	123	DDADLRHILTEAADA	LRHILTEAA	0.2860	2266.0	50.00	Rv2754c, T
DRB1_0404	171	RAVLPNATETRIVVT	RAVLPNATE	0.2849	2293.3	50.00	Rv2754c, T
DRB1_0404	11	IAKTDFLAPPDVPWPT	IAKTDFLAP	0.2758	2530.3	50.00	Rv2754c, T
DRB1_0404	35	VEFAGRACYQSWSKP	FAGRACYQS	0.2751	2549.7	50.00	Rv2754c, T
DRB1_0404	13	KTDFLAPPDVPWTTD	DFLAPPDVP	0.2734	2594.9	50.00	Rv2754c, T
DRB1_0404	12	AKTDFLAPPDVPWTT	DFLAPPDVP	0.2731	2605.5	50.00	Rv2754c, T
DRB1_0404	147	AKLEAKFADQPNAIL	KFADQPNAI	0.2706	2675.1	50.00	Rv2754c, T
DRB1_0404	129	HILTEAADAARATYS	HILTEAADA	0.2700	2694.2	50.00	Rv2754c, T
DRB1_0404	112	DSRVVVPVPGMEDDAD	SRVVVPPGM	0.2688	2727.3	50.00	Rv2754c, T
DRB1_0404	113	SRVVVPPGMEDDADL	SRVVVPPGM	0.2688	2727.5	50.00	Rv2754c, T
DRB1_0404	111	KDSRVVVPVPGMEDDA	SRVVVPPGM	0.2645	2857.5	50.00	Rv2754c, T
DRB1_0404	53	TATNAGYLRHI IDVG	YLRHI IDVG	0.2628	2910.4	50.00	Rv2754c, T
DRB1_0404	230	EVTTLADGTEVATSP	EVTTLADGT	0.2610	2967.4	50.00	Rv2754c, T
DRB1_0404	184	VTGNYRAWRHFIAMR	YRAWRHFIA	0.2595	3017.9	50.00	Rv2754c, T
DRB1_0404	10	LIAKTDFLAPPDVPW	IAKTDFLAP	0.2568	3108.0	50.00	Rv2754c, T
DRB1_0404	14	TDFLAPPDVPWTTDA	DFLAPPDVP	0.2567	3108.8	50.00	Rv2754c, T
DRB1_0404	218	LAAVAPAVFADFEVT	AVFADFEVT	0.2557	3144.5	50.00	Rv2754c, T
DRB1_0404	15	DFLAPPDVPWTTDAD	DFLAPPDVP	0.2555	3150.7	50.00	Rv2754c, T
DRB1_0404	34	LVEFAGRACYQSWSK	FAGRACYQS	0.2466	3468.5	50.00	Rv2754c, T
DRB1_0404	110	EKDSRVVVPVPGMEDD	SRVVVPPGM	0.2461	3486.9	50.00	Rv2754c, T
DRB1_0404	182	IVVTGNYRAWRHFI	IVVTGNYRA	0.2431	3604.5	50.00	Rv2754c, T
DRB1_0404	145	LLAKLEAKFADQPNA	LLAKLEAKF	0.2391	3762.4	50.00	Rv2754c, T
DRB1_0404	41	ACYQSWSKPNPKTAT	YQSWSKPNP	0.2366	3864.1	50.00	Rv2754c, T
DRB1_0404	137	AARATYSELLAKLEA	RATYSELLA	0.2330	4016.9	50.00	Rv2754c, T
DRB1_0404	81	ITGISRSCSTHELIRH	TGISRSCTH	0.2313	4094.6	50.00	Rv2754c, T
DRB1_0404	146	LAKLEAKFADQPNAI	KFADQPNAI	0.2295	4173.7	50.00	Rv2754c, T
DRB1_0404	89	THELIRHRHFSYSQL	LIRHRHFSY	0.2256	4353.1	50.00	Rv2754c, T
DRB1_0404	99	SYSQLSQRYVPEKDS	SQLSQRYVP	0.2253	4368.8	50.00	Rv2754c, T
DRB1_0404	183	VVTGNYRAWRHFIAM	NYRAWRHFI	0.2252	4373.8	50.00	Rv2754c, T
DRB1_0404	163	KQARQAARAVLPN	RQAARAVLP	0.2240	4429.6	50.00	Rv2754c, T
DRB1_0404	122	EDDADLRHILTEAAD	LRHILTEAA	0.2229	4482.1	50.00	Rv2754c, T
DRB1_0404	136	DAARATYSELLAKLE	RATYSELLA	0.2218	4536.1	50.00	Rv2754c, T
DRB1_0404	100	YLSQLSQRYVPEKDSR	QLSQRYVPE	0.2204	4607.5	50.00	Rv2754c, T
DRB1_0404	82	TGISRSCTHELIRHR	TGISRSCTH	0.2156	4849.4	50.00	Rv2754c, T
DRB1_0404	114	RVVVVPPGMEDDADLR	RVVVVPPGM	0.2117	5061.8	50.00	Rv2754c, T
DRB1_0404	32	PALVEFAGRACYQSW	PALVEFAGR	0.2109	5103.1	50.00	Rv2754c, T
DRB1_0404	16	FLAPPDVPWTTDADG	FLAPPDVPW	0.2100	5157.0	50.00	Rv2754c, T
DRB1_0404	135	ADAARATYSELLAKL	AARATYSEL	0.2099	5159.1	50.00	Rv2754c, T
DRB1_0404	18	APPDVPWTTDADGGP	DVPWTTDAD	0.2055	5413.5	50.00	Rv2754c, T
DRB1_0404	109	PEKDSRVVVPVPGMED	SRVVVPPGM	0.2047	5461.6	50.00	Rv2754c, T
DRB1_0404	19	PPDVPWTTDADGGPA	DVPWTTDAD	0.2039	5504.5	50.00	Rv2754c, T
DRB1_0404	200	SEHADVEIRRLAIEC	EIRRLAIEC	0.2031	5552.5	50.00	Rv2754c, T
DRB1_0404	158	NAILRRKQARQAARA	AILRRKQAR	0.2027	5575.5	50.00	Rv2754c, T
DRB1_0404	17	LAPPDVPWTTDADGG	DVPWTTDAD	0.2015	5652.6	50.00	Rv2754c, T
DRB1_0404	101	SQLSQRYVPEKDSRV	SQLSQRYVP	0.2012	5669.9	50.00	Rv2754c, T
DRB1_0404	31	GPALVEFAGRACYQS	PALVEFAGR	0.2008	5695.9	50.00	Rv2754c, T
DRB1_0404	157	PNAILRRKQARQAAR	AILRRKQAR	0.2005	5713.5	50.00	Rv2754c, T
DRB1_0404	42	CYQSWSKPNPKTATN	YQSWSKPNP	0.1923	6243.3	50.00	Rv2754c, T
DRB1_0404	235	ADGTEVATSPATEA	EVATSPATE	0.1921	6255.7	50.00	Rv2754c, T
DRB1_0404	156	QPNAILRRKQARQA	AILRRKQAR	0.1920	6265.5	50.00	Rv2754c, T
DRB1_0404	33	ALVEFAGRACYQSW	FAGRACYQS	0.1914	6306.1	50.00	Rv2754c, T
DRB1_0404	174	LPNATETRIVVTGNY	TRIVVTGNY	0.1888	6485.1	50.00	Rv2754c, T
DRB1_0404	134	ADAARATYSELLAK	AARATYSEL	0.1872	6599.6	50.00	Rv2754c, T
DRB1_0404	20	DVPWTTDADGGPAL	DVPWTTDAD	0.1860	6681.5	50.00	Rv2754c, T
DRB1_0404	172	AVLPNATETRIVVTG	VLPNATETR	0.1794	7178.2	50.00	Rv2754c, T
DRB1_0404	102	QLSQRYVPEKDSRVV	QLSQRYVPE	0.1787	7231.1	50.00	Rv2754c, T
DRB1_0404	162	RRKQARQAARAVLPN	QARQAARAV	0.1780	7286.8	50.00	Rv2754c, T
DRB1_0404	121	MEDDADLRHILTEAA	LRHILTEAA	0.1746	7557.2	50.00	Rv2754c, T
DRB1_0404	161	LRRKQARQAARAVLP	QARQAARAV	0.1742	7595.1	50.00	Rv2754c, T
DRB1_0404	234	LADGTEVATSPATE	EVATSPATE	0.1689	8037.0	50.00	Rv2754c, T
DRB1_0404	232	TTLADGTEVATSPLA	TTLADGTEV	0.1689	8037.8	50.00	Rv2754c, T
DRB1_0404	155	DPNAILRRKQARQA	AILRRKQAR	0.1688	8053.7	50.00	Rv2754c, T
DRB1_0404	159	AILRRKQARQAARAV	AILRRKQAR	0.1685	8073.6	50.00	Rv2754c, T
DRB1_0404	88	CHELIRHRHFSYSQ	LIRHRHFSY	0.1675	8165.6	50.00	Rv2754c, T

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DRB1_0404	30	GGPALVEFAGRACYQ	PALVEFAGR	0.1660	8295.3	50.00	Rv2754c, T
DRB1_0404	108	VPEKDSRVVPPGME	SRVVVPPGM	0.1660	8299.3	50.00	Rv2754c, T
DRB1_0404	231	VTTLADGTEVATSPL	TTLADGTEV	0.1609	8763.5	50.00	Rv2754c, T
DRB1_0404	153	FADQPNAILRRKQAR	NAILRRKQA	0.1585	9003.0	50.00	Rv2754c, T
DRB1_0404	133	EAADAARATYSELLA	AARATYSEL	0.1551	9338.7	50.00	Rv2754c, T
DRB1_0404	173	VLPNATETRIVVVTGN	VLPNATETR	0.1531	9542.9	50.00	Rv2754c, T
DRB1_0404	104	SQRYVPEKDSRVVVP	RYVPEKDSR	0.1522	9637.9	50.00	Rv2754c, T
DRB1_0404	106	RYVPEKDSRVVPPG	RYVPEKDSR	0.1466	10232.5	50.00	Rv2754c, T
DRB1_0404	160	ILRRKQARQAARAVL	QARQAARAV	0.1448	10433.1	50.00	Rv2754c, T
DRB1_0404	105	QRYVPEKDSRVVPPP	RYVPEKDSR	0.1445	10468.8	50.00	Rv2754c, T
DRB1_0404	21	DVPWTTDADGGPALV	DVPWTTDAD	0.1445	10474.8	50.00	Rv2754c, T
DRB1_0404	103	LSQRYVPEKDSRVVV	RYVPEKDSR	0.1444	10487.2	50.00	Rv2754c, T
DRB1_0404	29	DGGPALVEFAGRACY	PALVEFAGR	0.1439	10544.0	50.00	Rv2754c, T
DRB1_0404	233	TLADGTEVATSPLAT	LADGTEVAT	0.1429	10650.6	50.00	Rv2754c, T
DRB1_0404	195	IAMRASEHADVEIRR	IAMRASEHA	0.1390	11107.2	50.00	Rv2754c, T
DRB1_0404	43	YQSWSKPNPKTATNA	YQSWSKPNP	0.1385	11168.7	50.00	Rv2754c, T
DRB1_0404	87	SCTHELIRHRHFSYS	LIRHRHFSY	0.1377	11272.7	50.00	Rv2754c, T
DRB1_0404	154	ADQPNAILRRKQARQ	AILRRKQAR	0.1376	11287.8	50.00	Rv2754c, T
DRB1_0404	107	YVPEKDSRVVPPGM	SRVVVPPGM	0.1359	11491.3	50.00	Rv2754c, T
DRB1_0404	52	KTATNAGYLRHIIDV	NAGYLRHII	0.1303	12215.5	50.00	Rv2754c, T
DRB1_0404	130	ILTEAADAARATYSE	ILTEAADAA	0.1267	12699.8	50.00	Rv2754c, T
DRB1_0404	47	SKPNPKTATNAGYLR	NPKTATNAG	0.1250	12929.2	50.00	Rv2754c, T
DRB1_0404	48	KPNPKTATNAGYLRH	NPKTATNAG	0.1183	13899.6	50.00	Rv2754c, T
DRB1_0404	83	GISRSCTHELIRRRH	GISRSCTHE	0.1180	13946.6	50.00	Rv2754c, T
DRB1_0404	46	WSKPNPKTATNAGYL	NPKTATNAG	0.1166	14164.5	50.00	Rv2754c, T
DRB1_0404	132	TEAADAARATYSELL	AARATYSEL	0.1158	14283.3	50.00	Rv2754c, T
DRB1_0404	120	GMEDDADLRHILTEA	DLRHILTEA	0.1141	14551.2	50.00	Rv2754c, T
DRB1_0404	44	QSWSKPNPKTATNAG	QSWSKPNPK	0.1135	14637.8	50.00	Rv2754c, T
DRB1_0404	115	VVVPPGMEDDADLRH	VVVPPGMED	0.1112	15017.9	50.00	Rv2754c, T
DRB1_0404	49	PNPKTATNAGYLRHI	NPKTATNAG	0.1104	15139.3	50.00	Rv2754c, T
DRB1_0404	86	RSCTHELIRHRHFSY	LIRHRHFSY	0.1104	15142.2	50.00	Rv2754c, T
DRB1_0404	199	ASEHADVEIRRLAIE	DVEIRRLAI	0.1101	15189.1	50.00	Rv2754c, T
DRB1_0404	28	ADGGPALVEFAGRAC	PALVEFAGR	0.1095	15292.4	50.00	Rv2754c, T
DRB1_0404	45	SWSKPNPKTATNAGY	NPKTATNAG	0.1077	15586.0	50.00	Rv2754c, T
DRB1_0404	131	LTEAADAARATYSEL	LTEAADAAR	0.1038	16264.0	50.00	Rv2754c, T
DRB1_0404	51	PKTATNAGYLRHIID	NAGYLRHII	0.1034	16341.2	50.00	Rv2754c, T
DRB1_0404	50	NPKTATNAGYLRHII	NPKTATNAG	0.0993	17079.1	50.00	Rv2754c, T
DRB1_0404	116	VVPPGMEDDADLRHI	PGMEDDADL	0.0978	17351.1	50.00	Rv2754c, T
DRB1_0404	84	ISRSCTHELIRHRHF	ISRSCTHEL	0.0971	17489.2	50.00	Rv2754c, T
DRB1_0404	118	PPGMEDDADLRHILT	PGMEDDADL	0.0962	17652.5	50.00	Rv2754c, T
DRB1_0404	117	VPPGMEDDADLRHIL	PGMEDDADL	0.0911	18663.7	50.00	Rv2754c, T
DRB1_0404	119	PGMEDDADLRHILTE	PGMEDDADL	0.0901	18862.6	50.00	Rv2754c, T
DRB1_0404	196	AMRASEHADVEIRRL	AMRASEHAD	0.0884	19221.3	50.00	Rv2754c, T
DRB1_0404	85	SRSCTHELIRHRHFS	HELIRHRHF	0.0830	20367.2	50.00	Rv2754c, T
DRB1_0404	27	DADGGPALVEFAGRA	PALVEFAGR	0.0824	20502.8	50.00	Rv2754c, T
DRB1_0404	198	RASEHADVEIRRLAI	DVEIRRLAI	0.0739	22466.6	50.00	Rv2754c, T
DRB1_0404	22	VPWTTDADGGPALVE	VPWTTDADG	0.0678	24003.3	50.00	Rv2754c, T
DRB1_0404	197	MRASEHADVEIRRLA	MRASEHADV	0.0664	24379.5	50.00	Rv2754c, T
DRB1_0404	26	TDADGGPALVEFAGR	PALVEFAGR	0.0597	26200.0	50.00	Rv2754c, T
DRB1_0404	23	PWTTDADGGPALVEF	PWTTDADGG	0.0436	31197.1	50.00	Rv2754c, T
DRB1_0404	25	TTDADGGPALVEFAG	DADGGPALV	0.0361	33833.1	50.00	Rv2754c, T
DRB1_0404	24	WTTDADGGPALVEFA	DADGGPALV	0.0336	34766.8	50.00	Rv2754c, T

Allele: DRB1_0404. Number of high binders 11. Number of weak binders 26. Number of peptides 236

Allele	pos	peptide	core	1-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
DRB1_0405	95	HRHFSYSQLSQRYVP	FSYSQLSQR	0.7551	14.1	SB	0.80	Rv2754c, T
DRB1_0405	94	RHRHFSYSQLSQRYV	FSYSQLSQR	0.7432	16.1	SB	1.00	Rv2754c, T
DRB1_0405	189	RAWRHFIAMRASEHA	WRHFIAMRA	0.7167	21.4	SB	2.00	Rv2754c, T
DRB1_0405	188	YRAWRHFIAMRASEH	WRHFIAMRA	0.7129	22.3	SB	2.00	Rv2754c, T
DRB1_0405	96	RHFSYSQLSQRYVPE	FSYSQLSQR	0.7075	23.7	SB	4.00	Rv2754c, T
DRB1_0405	97	HFSYSQLSQRYVPEK	FSYSQLSQR	0.6972	26.5	SB	4.00	Rv2754c, T
DRB1_0405	187	NYRAWRHFIAMRASE	WRHFIAMRA	0.6926	27.8	SB	4.00	Rv2754c, T
DRB1_0405	211	AIECLRQLAAVAPAV	ECLRQLAAV	0.6871	29.5	SB	4.00	Rv2754c, T
DRB1_0405	212	IECLRQLAAVAPAVF	ECLRQLAAV	0.6859	29.9	SB	4.00	Rv2754c, T
DRB1_0405	210	LAIECLRQLAAVAPA	CLRQLAAVA	0.6848	30.3	SB	4.00	Rv2754c, T
DRB1_0405	190	AWRHFIAMRASEHAD	WRHFIAMRA	0.6795	32.1	SB	4.00	Rv2754c, T
DRB1_0405	124	DADLRHILTEAADAA	DLRHILTEA	0.6775	32.8	SB	4.00	Rv2754c, T
DRB1_0405	123	DDADLRHILTEAADA	DLRHILTEA	0.6761	33.3	SB	4.00	Rv2754c, T
DRB1_0405	209	RLAIECLRQLAAVAP	CLRQLAAVA	0.6719	34.8	SB	8.00	Rv2754c, T
DRB1_0405	93	IRHRHFSYSQLSQRY	FSYSQLSQR	0.6701	35.5	SB	8.00	Rv2754c, T
DRB1_0405	213	ECLRQLAAVAPAVFA	ECLRQLAAV	0.6686	36.1	SB	8.00	Rv2754c, T
DRB1_0405	186	GNYRAWRHFIAMRAS	WRHFIAMRA	0.6614	39.0	SB	8.00	Rv2754c, T
DRB1_0405	98	FSYSQLSQRYVPEKDS	FSYSQLSQR	0.6568	41.0	SB	8.00	Rv2754c, T
DRB1_0405	125	ADLRHILTEAADAAAR	DLRHILTEA	0.6562	41.3	SB	8.00	Rv2754c, T
DRB1_0405	92	LIRHRHFSYSQLSQR	FSYSQLSQR	0.6493	44.5	SB	8.00	Rv2754c, T
DRB1_0405	191	WRHFIAMRASEHADV	WRHFIAMRA	0.6406	48.8	SB	8.00	Rv2754c, T
DRB1_0405	57	AGYLRHIIDVGHFVS	YLRHIIDVG	0.6397	49.3	SB	8.00	Rv2754c, T
DRB1_0405	56	NAGYLRHIIDVGHFVS	YLRHIIDVG	0.6367	51.0	WB	8.00	Rv2754c, T
DRB1_0405	58	GYLRHIIDVGHFVSL	YLRHIIDVG	0.6276	56.2	WB	8.00	Rv2754c, T
DRB1_0405	122	EDDADLRHILTEAAD	DLRHILTEA	0.6258	57.3	WB	8.00	Rv2754c, T

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DRB1_0405	208	RRLAIECLRQLAAVA	CLRQLAAVA	0.6224	59.5	WB	16.00	Rv2754c, T
DRB1_0405	185	TGNYRAWRHFIAMRA	WRHFIAMRA	0.6193	61.5	WB	16.00	Rv2754c, T
DRB1_0405	55	TNAGYLRHIIDVGHF	YLRHIIDVG	0.6057	71.2	WB	16.00	Rv2754c, T
DRB1_0405	126	DLRHILTEAADAARA	LRHILTEAA	0.5953	79.7	WB	16.00	Rv2754c, T
DRB1_0405	76	SVSFYITGISRSTH	FYITGISRS	0.5695	105.4	WB	16.00	Rv2754c, T
DRB1_0405	54	ATNAGYLRHIIDVGH	YLRHIIDVG	0.5654	110.1	WB	16.00	Rv2754c, T
DRB1_0405	75	ASVSFYITGISRSTH	FYITGISRS	0.5623	113.9	WB	32.00	Rv2754c, T
DRB1_0405	121	MEDDADLRHILTEAA	DLRHILTEA	0.5603	116.4	WB	32.00	Rv2754c, T
DRB1_0405	59	YLRHIIDVGHFSVLE	YLRHIIDVG	0.5587	118.5	WB	32.00	Rv2754c, T
DRB1_0405	207	IRRLAIECLRQLAAV	AIECLRQLA	0.5540	124.7	WB	32.00	Rv2754c, T
DRB1_0405	149	LEAKFADQPNAILRR	AKFADQPNA	0.5522	127.2	WB	32.00	Rv2754c, T
DRB1_0405	150	EAKFADQPNAILRRK	FADQPNAIL	0.5484	132.5	WB	32.00	Rv2754c, T
DRB1_0405	148	KLEAKFADQPNAILR	AKFADQPNA	0.5462	135.7	WB	32.00	Rv2754c, T
DRB1_0405	192	RHFIAMRASEHADVE	FIAMRASEH	0.5459	136.0	WB	32.00	Rv2754c, T
DRB1_0405	74	HASVSFYITGISRSC	FYITGISRS	0.5422	141.6	WB	32.00	Rv2754c, T
DRB1_0405	91	ELIRHRHFSYSQSLQ	HRHFSYSQL	0.5337	155.3	WB	32.00	Rv2754c, T
DRB1_0405	137	AARATYSELLAKLEA	ATYSELLAK	0.5317	158.7	WB	32.00	Rv2754c, T
DRB1_0405	77	VSFYITGISRSTH	FYITGISRS	0.5203	179.4	WB	32.00	Rv2754c, T
DRB1_0405	147	AKLEAKFADQPNAIL	AKFADQPNA	0.5190	182.0	WB	32.00	Rv2754c, T
DRB1_0405	151	AKFADQPNAILRRKQ	FADQPNAIL	0.5163	187.4	WB	32.00	Rv2754c, T
DRB1_0405	205	VEIRRLAIECLRQLA	VEIRRLAIE	0.5128	194.7	WB	32.00	Rv2754c, T
DRB1_0405	73	EHASVSFYITGISR	FYITGISRS	0.5101	200.5	WB	32.00	Rv2754c, T
DRB1_0405	136	DAARATYSELLAKLE	RATYSELLA	0.5098	201.1	WB	32.00	Rv2754c, T
DRB1_0405	206	EIRRLAIECLRQLAA	LAIECLRQL	0.5061	209.2	WB	32.00	Rv2754c, T
DRB1_0405	204	DVEIRRLAIECLRQL	VEIRRLAIE	0.5061	209.3	WB	32.00	Rv2754c, T
DRB1_0405	214	CLRQLAAVAPAVFAD	CLRQLAAVA	0.5009	221.5	WB	32.00	Rv2754c, T
DRB1_0405	179	ETRIVVTGNYRAWRH	TRIVVTGNY	0.4972	230.5	WB	32.00	Rv2754c, T
DRB1_0405	193	HFIAMRASEHADVEI	HFIAMRASE	0.4948	236.7	WB	32.00	Rv2754c, T
DRB1_0405	178	TETRIVVTGNYRAWR	TRIVVTGNY	0.4943	237.7	WB	32.00	Rv2754c, T
DRB1_0405	4	APLRVQLIAKTDFLA	LRVQLIAKT	0.4884	253.6	WB	32.00	Rv2754c, T
DRB1_0405	78	SFYITGISRSTH	FYITGISRS	0.4882	254.2	WB	32.00	Rv2754c, T
DRB1_0405	180	TRIVVTGNYRAWRHF	TRIVVTGNY	0.4866	258.5	WB	32.00	Rv2754c, T
DRB1_0405	226	FADFEVTTLDGTEV	FEVTTLDG	0.4850	263.0	WB	32.00	Rv2754c, T
DRB1_0405	5	PLRVQLIAKTDFLAP	RVQLIAKT	0.4807	275.7	WB	32.00	Rv2754c, T
DRB1_0405	138	ARATYSELLAKLEAK	RATYSELLA	0.4806	275.9	WB	32.00	Rv2754c, T
DRB1_0405	90	HELIRHRHFSYSQSL	HRHFSYSQL	0.4800	277.6	WB	32.00	Rv2754c, T
DRB1_0405	225	VFADFEVTTLDGTE	FEVTTLDG	0.4799	278.1	WB	32.00	Rv2754c, T
DRB1_0405	203	ADVEIRRLAIECLRQ	VEIRRLAIE	0.4797	278.4	WB	32.00	Rv2754c, T
DRB1_0405	177	ATETRIVVTGNYRAW	TRIVVTGNY	0.4791	280.3	WB	32.00	Rv2754c, T
DRB1_0405	3	TAPLRVQLIAKTDFL	LRVQLIAKT	0.4787	281.4	WB	32.00	Rv2754c, T
DRB1_0405	184	VTGNYRAWRHFIAMR	RAWRHFIAM	0.4734	298.2	WB	50.00	Rv2754c, T
DRB1_0405	53	TATNAGYLRHIIDVG	YLRHIIDVG	0.4714	304.8	WB	50.00	Rv2754c, T
DRB1_0405	2	ETAPLRVQLIAKTDF	LRVQLIAKT	0.4707	307.1	WB	50.00	Rv2754c, T
DRB1_0405	139	RATYSELLAKLEAKF	RATYSELLA	0.4679	316.3	WB	50.00	Rv2754c, T
DRB1_0405	100	YSQLSQRYVPEKDSR	YSQLSQRYV	0.4666	321.0	WB	50.00	Rv2754c, T
DRB1_0405	99	SYSQLSQRYVPEKDS	YSQLSQRYV	0.4607	342.3	WB	50.00	Rv2754c, T
DRB1_0405	227	ADFEVTTLDGTEVA	FEVTTLDG	0.4594	347.1	WB	50.00	Rv2754c, T
DRB1_0405	224	AVFADFEVTTLDGTE	DFEVTTLDG	0.4588	349.2	WB	50.00	Rv2754c, T
DRB1_0405	69	FSVLEHASVSFYITG	SVLEHASVS	0.4576	353.6	WB	50.00	Rv2754c, T
DRB1_0405	68	HFSVLEHASVSFYIT	SVLEHASVS	0.4545	365.6	WB	50.00	Rv2754c, T
DRB1_0405	223	PAVFADFEVTTLDG	FEVTTLDG	0.4544	366.2	WB	50.00	Rv2754c, T
DRB1_0405	176	NATETRIVVTGNYRA	TRIVVTGNY	0.4497	385.3	WB	50.00	Rv2754c, T
DRB1_0405	135	ADAARATYSELLAKL	RATYSELLA	0.4482	391.8	WB	50.00	Rv2754c, T
DRB1_0405	67	GHFVLEHASVSFYIT	FSVLEHASV	0.4480	392.6	WB	50.00	Rv2754c, T
DRB1_0405	66	VGHFVLEHASVSFY	FSVLEHASV	0.4473	395.3	WB	50.00	Rv2754c, T
DRB1_0405	228	DFEVTTLDGTEVAT	FEVTTLDG	0.4437	411.0	WB	50.00	Rv2754c, T
DRB1_0405	6	LRVQLIAKTDFLAPP	LRVQLIAKT	0.4428	415.3	WB	50.00	Rv2754c, T
DRB1_0405	1	AETAPLRVQLIAKT	LRVQLIAKT	0.4397	429.5	WB	50.00	Rv2754c, T
DRB1_0405	64	IDVGHFVLEHASVS	VGHFVLEH	0.4375	439.7	WB	50.00	Rv2754c, T
DRB1_0405	60	LRHIIDVGHFVLEH	LRHIIDVGH	0.4353	450.2	WB	50.00	Rv2754c, T
DRB1_0405	120	GMEDDADLRHILTEA	ADLRHILTE	0.4333	460.3	WB	50.00	Rv2754c, T
DRB1_0405	202	HADVEIRRLAIECLR	VEIRRLAIE	0.4326	463.8	WB	50.00	Rv2754c, T
DRB1_0405	127	LRHILTEAADAARAT	LRHILTEAA	0.4302	476.0	WB	50.00	Rv2754c, T
DRB1_0405	146	LAKLEAKFADQPNAI	AKFADQPNA	0.4255	500.5	WB	50.00	Rv2754c, T
DRB1_0405	63	IIDVGHFVLEHASV	VGHFVLEH	0.4250	503.5	WB	50.00	Rv2754c, T
DRB1_0405	72	LEHASVSFYITGISR	SVSFYITGI	0.4248	504.3	WB	50.00	Rv2754c, T
DRB1_0405	134	AADAARATYSELLAK	AARATYSEL	0.4239	509.4	WB	50.00	Rv2754c, T
DRB1_0405	65	DVGHFVLEHASVSF	VGHFVLEH	0.4198	532.5	WB	50.00	Rv2754c, T
DRB1_0405	70	SVLEHASVSFYITGI	SVLEHASVS	0.4192	535.8	WB	50.00	Rv2754c, T
DRB1_0405	71	VLEHASVSFYITGIS	VSFYITGIS	0.4177	545.0	WB	50.00	Rv2754c, T
DRB1_0405	39	GRACYQSWSKPNPKT	CYQSWSKPN	0.4133	571.1	WB	50.00	Rv2754c, T
DRB1_0405	36	EFAGRACYQSWSKPN	FAGRACYQS	0.4113	583.6	WB	50.00	Rv2754c, T
DRB1_0405	37	FAGRACYQSWSKPNP	CYQSWSKPN	0.4104	589.8	WB	50.00	Rv2754c, T
DRB1_0405	62	HIIDVGHFVLEHAS	VGHFVLEH	0.4100	592.4	WB	50.00	Rv2754c, T
DRB1_0405	79	FYITGISRSTH	FYITGISRS	0.4098	593.1	WB	50.00	Rv2754c, T
DRB1_0405	34	LVEFAGRACYQSWSK	FAGRACYQS	0.4035	634.9	WB	50.00	Rv2754c, T
DRB1_0405	61	RHIIDVGHFVLEHA	HIIDVGHFS	0.4032	637.2	WB	50.00	Rv2754c, T
DRB1_0405	194	FIAMRASEHADVEIR	IAMRASEHA	0.4013	650.3	WB	50.00	Rv2754c, T
DRB1_0405	38	AGRACYQSWSKPNPK	CYQSWSKPN	0.3992	665.2	WB	50.00	Rv2754c, T
DRB1_0405	175	PNATETRIVVTGNYR	TRIVVTGNY	0.3970	681.5	WB	50.00	Rv2754c, T
DRB1_0405	0	VAETAPLRVQLIAKT	LRVQLIAKT	0.3967	683.6	WB	50.00	Rv2754c, T
DRB1_0405	222	APAVFADFEVTTLDG	FADFEVTTL	0.3960	689.0	WB	50.00	Rv2754c, T
DRB1_0405	140	ATYSELLAKLEAKFA	ATYSELLAK	0.3951	695.6	WB	50.00	Rv2754c, T
DRB1_0405	102	QLSQRYVPEKDSRVV	SQRYVPEKD	0.3896	738.1	WB	50.00	Rv2754c, T
DRB1_0405	101	QLSQRYVPEKDSRV	SQRYVPEKD	0.3892	741.7	WB	50.00	Rv2754c, T

DRB1_0405	201	EHADVEIRRLAIECL	VEIRRLAIE	0.3890	743.1	50.00	Rv2754c, T
DRB1_0405	183	VVTGNYRAWRHFIAM	YRAWRHFIAM	0.3887	745.4	50.00	Rv2754c, T
DRB1_0405	10	LIAKTDFLAPPDVPW	TDFLAPPDV	0.3878	752.8	50.00	Rv2754c, T
DRB1_0405	35	VEFAGRACYQSWSKP	FAGRACYQS	0.3878	753.2	50.00	Rv2754c, T
DRB1_0405	40	RACYQSWSKPNPKTA	CYQSWSKPN	0.3871	758.5	50.00	Rv2754c, T
DRB1_0405	119	PGMEDDADLRHILTE	GMEDDADLR	0.3861	766.7	50.00	Rv2754c, T
DRB1_0405	103	LSQRYVPEKDSRVVV	QRYVPEKDS	0.3859	768.9	50.00	Rv2754c, T
DRB1_0405	152	KFADQPNAILLRKQA	FADQPNAIL	0.3837	787.2	50.00	Rv2754c, T
DRB1_0405	235	ADGTEVATSPLATEA	GTEVATSPL	0.3796	822.5	50.00	Rv2754c, T
DRB1_0405	33	ALVEFAGRACYQSW	FAGRACYQS	0.3781	835.9	50.00	Rv2754c, T
DRB1_0405	234	LADGTEVATSPLATE	GTEVATSPL	0.3763	852.9	50.00	Rv2754c, T
DRB1_0405	104	SQRYVPEKDSRVVVP	QRYVPEKDS	0.3759	856.3	50.00	Rv2754c, T
DRB1_0405	181	RIVVTGNYRAWRHFI	RIVVTGNYR	0.3715	897.6	50.00	Rv2754c, T
DRB1_0405	9	QLIAKTDFLAPPDVP	LIAKTDFLA	0.3677	935.6	50.00	Rv2754c, T
DRB1_0405	89	THELIRHRHFSYSQL	HRHFSYSQL	0.3667	945.5	50.00	Rv2754c, T
DRB1_0405	11	IAKTDFLAPPDVPWT	TDFLAPPDV	0.3657	956.0	50.00	Rv2754c, T
DRB1_0405	7	RVQLIAKTDFLAPPD	RVQLIAKTD	0.3619	996.7	50.00	Rv2754c, T
DRB1_0405	41	ACYQSWSKPNPKTAT	CYQSWSKPN	0.3611	1005.2	50.00	Rv2754c, T
DRB1_0405	8	VQLIAKTDFLAPPDVP	LIAKTDFLA	0.3598	1019.6	50.00	Rv2754c, T
DRB1_0405	42	CYQSWSKPNPKTATN	YQSWSKPNP	0.3531	1095.7	50.00	Rv2754c, T
DRB1_0405	110	EKDSRVVPPGMEDD	SRVVPPGM	0.3442	1206.9	50.00	Rv2754c, T
DRB1_0405	12	AKTDFLAPPDVPWTT	TDFLAPPDV	0.3437	1213.7	50.00	Rv2754c, T
DRB1_0405	13	KTDFLAPPDVPWTTD	TDFLAPPDV	0.3424	1230.1	50.00	Rv2754c, T
DRB1_0405	168	QAARAVLPNATETRI	AARAVLPNA	0.3418	1238.7	50.00	Rv2754c, T
DRB1_0405	141	TYSELLAKLEAKFAD	TYSELLAKL	0.3402	1260.0	50.00	Rv2754c, T
DRB1_0405	109	PEKDSRVVPPGMED	SRVVPPGM	0.3392	1273.9	50.00	Rv2754c, T
DRB1_0405	167	RQAARAVLPNATETR	AARAVLPNA	0.3372	1301.2	50.00	Rv2754c, T
DRB1_0405	111	KDSRVVPPGMEDDA	SRVVPPGM	0.3325	1369.5	50.00	Rv2754c, T
DRB1_0405	169	AARAVLPNATETRIV	AARAVLPNA	0.3320	1377.6	50.00	Rv2754c, T
DRB1_0405	32	PALVEFAGRACYQSW	FAGRACYQS	0.3305	1399.5	50.00	Rv2754c, T
DRB1_0405	145	LLAKLEAKFADQPN	AKFADQPN	0.3296	1413.0	50.00	Rv2754c, T
DRB1_0405	105	QRYVPEKDSRVVPPP	QRYVPEKDS	0.3270	1454.1	50.00	Rv2754c, T
DRB1_0405	112	DSRVVPPGMEDDAD	SRVVPPGM	0.3263	1465.1	50.00	Rv2754c, T
DRB1_0405	200	SEHADVEIRRLAIEC	VEIRRLAIE	0.3252	1482.5	50.00	Rv2754c, T
DRB1_0405	166	AQAARAVLPNATET	AARAVLPNA	0.3251	1484.1	50.00	Rv2754c, T
DRB1_0405	233	TLADGTEVATSPLAT	GTEVATSPL	0.3249	1487.2	50.00	Rv2754c, T
DRB1_0405	142	YSELLAKLEAKFADQ	ELLAKLEAK	0.3241	1499.2	50.00	Rv2754c, T
DRB1_0405	118	PGMEDDADLRHILT	PGMEDDADL	0.3229	1520.0	50.00	Rv2754c, T
DRB1_0405	174	LPNATETRIVVTGNY	TRIVVTGNY	0.3183	1596.4	50.00	Rv2754c, T
DRB1_0405	108	VPEKDSRVVPPGME	DSRVVPPG	0.3145	1663.4	50.00	Rv2754c, T
DRB1_0405	117	VPPGMEDDADLRHIL	PGMEDDADL	0.3134	1684.4	50.00	Rv2754c, T
DRB1_0405	143	SELLAKLEAKFADQP	ELLAKLEAK	0.3131	1690.2	50.00	Rv2754c, T
DRB1_0405	165	QARQAARAVLPNATE	RAVLPNATE	0.3122	1706.4	50.00	Rv2754c, T
DRB1_0405	144	ELLAKLEAKFADQPN	ELLAKLEAK	0.3115	1718.8	50.00	Rv2754c, T
DRB1_0405	133	EAADAARATYSELLA	AARATYSEL	0.3099	1749.5	50.00	Rv2754c, T
DRB1_0405	115	VVVPPGMEDDADLRH	PGMEDDADL	0.3084	1778.4	50.00	Rv2754c, T
DRB1_0405	229	FEVTTLADGTEVATS	FEVTTLADG	0.3083	1779.9	50.00	Rv2754c, T
DRB1_0405	182	IVVTGNYRAWRHFI	IVVTGNYRA	0.3068	1809.3	50.00	Rv2754c, T
DRB1_0405	232	TTLADGTEVATSPLA	GTEVATSPL	0.3067	1811.1	50.00	Rv2754c, T
DRB1_0405	113	SRVVVPPGMEDDADL	SRVVVPPGM	0.3046	1851.4	50.00	Rv2754c, T
DRB1_0405	221	VAPAVFADFEVTTLA	FADFEVTTL	0.3024	1895.9	50.00	Rv2754c, T
DRB1_0405	116	VVPPGMEDDADLRHI	PGMEDDADL	0.3016	1913.7	50.00	Rv2754c, T
DRB1_0405	80	YITGISRSCTHELIR	GISRSCTHE	0.3005	1935.1	50.00	Rv2754c, T
DRB1_0405	215	LRQLAAVAPAVFADP	LRQLAAVAP	0.2970	2011.6	50.00	Rv2754c, T
DRB1_0405	195	IAMRASEHADVEIRR	IAMRASEHA	0.2938	2082.0	50.00	Rv2754c, T
DRB1_0405	107	YVPEKDSRVVPPGME	YVPEKDSRV	0.2933	2093.9	50.00	Rv2754c, T
DRB1_0405	114	RVVVPPGMEDDADLR	RVVVPPGME	0.2929	2101.6	50.00	Rv2754c, T
DRB1_0405	88	CTHELIRHRHFSYSQ	IRHRHFSYS	0.2921	2119.6	50.00	Rv2754c, T
DRB1_0405	82	TGISRSCTHELIRHR	ISRSCTHEL	0.2881	2213.4	50.00	Rv2754c, T
DRB1_0405	31	GPALVEFAGRACYQS	FAGRACYQS	0.2860	2265.3	50.00	Rv2754c, T
DRB1_0405	81	ITGISRSCTHELIRH	ISRSCTHEL	0.2858	2269.7	50.00	Rv2754c, T
DRB1_0405	128	RHILTEAADAARATY	HILTEAADA	0.2834	2329.1	50.00	Rv2754c, T
DRB1_0405	83	GISRSCTHELIRHRH	ISRSCTHEL	0.2814	2380.4	50.00	Rv2754c, T
DRB1_0405	52	KTATNAGYLRHIIDV	GYLRHIIDV	0.2809	2394.0	50.00	Rv2754c, T
DRB1_0405	170	ARAVLPNATETRIVV	RAVLPNATE	0.2805	2405.0	50.00	Rv2754c, T
DRB1_0405	106	RYVPEKDSRVVPPG	YVPEKDSRV	0.2778	2473.8	50.00	Rv2754c, T
DRB1_0405	158	NAILRRKQARQAARA	LRRKQARQA	0.2775	2482.5	50.00	Rv2754c, T
DRB1_0405	231	VTTLADGTEVATSPL	GTEVATSPL	0.2763	2514.7	50.00	Rv2754c, T
DRB1_0405	220	AVAPAVFADFEVTTL	FADFEVTTL	0.2707	2671.9	50.00	Rv2754c, T
DRB1_0405	14	TDFLAPPDVPWTTDA	FLAPPDVPW	0.2689	2724.6	50.00	Rv2754c, T
DRB1_0405	157	PNAILRRKQARQAAR	LRRKQARQA	0.2680	2752.4	50.00	Rv2754c, T
DRB1_0405	84	ISRSCTHELIRHRHF	ISRSCTHEL	0.2668	2786.8	50.00	Rv2754c, T
DRB1_0405	87	SCTHELIRHRHFSYS	IRHRHFSYS	0.2605	2984.2	50.00	Rv2754c, T
DRB1_0405	159	AILRRKQARQAARAV	ILRRKQARQ	0.2602	2995.6	50.00	Rv2754c, T
DRB1_0405	171	RAVLPNATETRIVVT	RAVLPNATE	0.2589	3035.3	50.00	Rv2754c, T
DRB1_0405	199	ASEHADVEIRRLAIE	VEIRRLAIE	0.2589	3037.0	50.00	Rv2754c, T
DRB1_0405	19	PPDVPWTTDADGGPA	DVPWTTDAD	0.2562	3127.8	50.00	Rv2754c, T
DRB1_0405	43	YQSWSKPNPKTATNA	YQSWSKPNP	0.2549	3172.7	50.00	Rv2754c, T
DRB1_0405	160	ILRRKQARQAARAVL	LRRKQARQA	0.2548	3175.3	50.00	Rv2754c, T
DRB1_0405	18	APPDVPWTTDADGGP	DVPWTTDAD	0.2502	3336.7	50.00	Rv2754c, T
DRB1_0405	20	PDVPWTTDADGGPAL	DVPWTTDAD	0.2464	3475.0	50.00	Rv2754c, T
DRB1_0405	16	FLAPPDVPWTTDADG	DVPWTTDAD	0.2456	3508.1	50.00	Rv2754c, T
DRB1_0405	153	FADQPNAILRRKQAR	FADQPNAIL	0.2433	3595.0	50.00	Rv2754c, T
DRB1_0405	15	DFLAPPDVPWTTDAD	FLAPPDVPW	0.2429	3610.5	50.00	Rv2754c, T
DRB1_0405	86	RSCTHELIRHRHFSY	CTHELIRHR	0.2324	4045.8	50.00	Rv2754c, T

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DRB1_0405	156	QPNAILRRKQARQAA	LRRKQARQA	0.2316	4078.1	50.00	Rv2754c, T
DRB1_0405	17	LAPPDVFWTTDADGG	DVPWTTDAD	0.2298	4159.3	50.00	Rv2754c, T
DRB1_0405	173	VLPNATETRIVVVTGN	LPNATETRI	0.2233	4463.5	50.00	Rv2754c, T
DRB1_0405	21	DVPWTTDADGGPALV	DVPWTTDAD	0.2205	4598.8	50.00	Rv2754c, T
DRB1_0405	164	KQARQAARAVLPNAT	AARAVLPNA	0.2205	4601.7	50.00	Rv2754c, T
DRB1_0405	172	AVLSPNATETRIVVVTG	LPNATETRI	0.2186	4694.0	50.00	Rv2754c, T
DRB1_0405	85	SRSCTHELIRHRHFS	CHELIRHR	0.2176	4748.3	50.00	Rv2754c, T
DRB1_0405	132	TEAADAARATYSELL	AARATYSEL	0.2168	4789.2	50.00	Rv2754c, T
DRB1_0405	196	AMRASEHADVEIRRL	AMRASEHAD	0.2139	4939.0	50.00	Rv2754c, T
DRB1_0405	129	HILTEAADAARATYS	HILTEAADA	0.2104	5130.3	50.00	Rv2754c, T
DRB1_0405	155	DQPNAILRRKQARQA	LRRKQARQA	0.2065	5352.7	50.00	Rv2754c, T
DRB1_0405	161	LRRKQARQAARAVLP	LRRKQARQA	0.2060	5385.3	50.00	Rv2754c, T
DRB1_0405	30	GGPALVEFAGRACYQ	LVEFAGRAC	0.2045	5469.5	50.00	Rv2754c, T
DRB1_0405	216	RQLAAVAPAVFADFE	RQLAAVAPA	0.1944	6104.0	50.00	Rv2754c, T
DRB1_0405	29	DGGPALVEFAGRACY	LVEFAGRAC	0.1913	6307.3	50.00	Rv2754c, T
DRB1_0405	219	AAVAPAVFADFEVTT	AVFADFEVT	0.1889	6479.8	50.00	Rv2754c, T
DRB1_0405	230	EVTTLADGTEVATSP	ADGTEVATS	0.1880	6536.4	50.00	Rv2754c, T
DRB1_0405	198	RASEHADVEIRRLAI	DVEIRRLAI	0.1853	6730.6	50.00	Rv2754c, T
DRB1_0405	163	RKQARQAARAVLPNA	QARQAARAV	0.1766	7401.3	50.00	Rv2754c, T
DRB1_0405	197	MRASEHADVEIRRLA	MRASEHADV	0.1761	7437.8	50.00	Rv2754c, T
DRB1_0405	44	QSWSKPNPKTATNAG	QSWSKPNPK	0.1742	7589.1	50.00	Rv2754c, T
DRB1_0405	218	LAAVAPAVFADFEVTT	AVFADFEVT	0.1741	7597.9	50.00	Rv2754c, T
DRB1_0405	217	QLAAVAPAVFADFEV	QLAAVAPAV	0.1729	7699.2	50.00	Rv2754c, T
DRB1_0405	22	VPWTTDADGGPALVE	VPWTTDADG	0.1697	7975.8	50.00	Rv2754c, T
DRB1_0405	28	ADGGPALVEFAGRAC	LVEFAGRAC	0.1647	8412.7	50.00	Rv2754c, T
DRB1_0405	26	TDADGGPALVEFAGR	DADGGPALV	0.1629	8577.8	50.00	Rv2754c, T
DRB1_0405	45	SWSKPNPKTATNAGY	NPKTATNAG	0.1588	8973.1	50.00	Rv2754c, T
DRB1_0405	51	PKTATNAGYLRHIID	KTATNAGYL	0.1565	9195.7	50.00	Rv2754c, T
DRB1_0405	24	WTTDADGGPALVEFA	WTTDADGGP	0.1533	9523.0	50.00	Rv2754c, T
DRB1_0405	25	TTDADGGPALVEFAG	DADGGPALV	0.1511	9752.2	50.00	Rv2754c, T
DRB1_0405	27	DADGGPALVEFAGRA	PALVEFAGR	0.1488	9998.1	50.00	Rv2754c, T
DRB1_0405	131	LTEAADAARATYSEL	AARATYSEL	0.1458	10325.2	50.00	Rv2754c, T
DRB1_0405	154	ADQPNAILRRKQARQ	ILRRKQARQ	0.1422	10730.7	50.00	Rv2754c, T
DRB1_0405	50	NPKTATNAGYLRHII	KTATNAGYL	0.1378	11260.4	50.00	Rv2754c, T
DRB1_0405	46	WSPKPNPKTATNAGYL	NPKTATNAG	0.1376	11284.5	50.00	Rv2754c, T
DRB1_0405	162	RRKQARQAARAVLPN	QARQAARAV	0.1346	11652.1	50.00	Rv2754c, T
DRB1_0405	23	PWTDDADGGPALVEF	WTTDADGGP	0.1303	12208.3	50.00	Rv2754c, T
DRB1_0405	49	PNPKTATNAGYLRHI	KTATNAGYL	0.1279	12530.9	50.00	Rv2754c, T
DRB1_0405	48	KPNPKTATNAGYLRH	NPKTATNAG	0.1240	13076.8	50.00	Rv2754c, T
DRB1_0405	47	SKPNPKTATNAGYLR	NPKTATNAG	0.1169	14110.5	50.00	Rv2754c, T
DRB1_0405	130	ILTEAADAARATYSE	ILTEAADAA	0.0917	18546.7	50.00	Rv2754c, T

Allele: DRB1_0405. Number of high binders 22. Number of weak binders 66. Number of peptides 236

Allele	pos	peptide	core	1-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
DRB1_0701	67	GHFSVLEHASVSFYI	LEHASVSFY	0.7457	15.7	SB	8.00	Rv2754c, T
DRB1_0701	188	YRAWRHFIAMRASEH	FIAMRASEH	0.7449	15.8	SB	8.00	Rv2754c, T
DRB1_0701	78	SFYITGISRSCTHEL	ISRSCTHEL	0.7448	15.8	SB	8.00	Rv2754c, T
DRB1_0701	132	TEAADAARATYSELL	ARATYSELL	0.7442	15.9	SB	8.00	Rv2754c, T
DRB1_0701	79	FYITGISRSCTHELI	ISRSCTHEL	0.7383	17.0	SB	8.00	Rv2754c, T
DRB1_0701	66	VGHFSVLEHASVSFY	LEHASVSFY	0.7357	17.4	SB	8.00	Rv2754c, T
DRB1_0701	133	EAADAARATYSELLA	ARATYSELL	0.7200	20.7	SB	8.00	Rv2754c, T
DRB1_0701	68	HFSVLEHASVSFYIT	LEHASVSFY	0.7169	21.4	SB	8.00	Rv2754c, T
DRB1_0701	189	RAWRHFIAMRASEHA	FIAMRASEH	0.7138	22.1	SB	8.00	Rv2754c, T
DRB1_0701	80	YITGISRSCTHELIR	ISRSCTHEL	0.7021	25.1	SB	16.00	Rv2754c, T
DRB1_0701	191	WRHFIAMRASEHADV	FIAMRASEH	0.6927	27.8	SB	16.00	Rv2754c, T
DRB1_0701	134	AADAARATYSELLAK	ARATYSELL	0.6809	31.6	SB	16.00	Rv2754c, T
DRB1_0701	69	FSVLEHASVSFYITG	LEHASVSFY	0.6773	32.8	SB	16.00	Rv2754c, T
DRB1_0701	65	DVGHFSVLEHASVSF	VLEHASVSF	0.6756	33.4	SB	16.00	Rv2754c, T
DRB1_0701	94	RHRHFSYSQLSQRYV	YSQLSQRYV	0.6715	35.0	SB	16.00	Rv2754c, T
DRB1_0701	176	NATETRIVVVTGNRYA	IVVTGNRYA	0.6679	36.4	SB	16.00	Rv2754c, T
DRB1_0701	101	SQLSQRYVPEKDSRV	YVPEKDSRV	0.6630	38.3	SB	16.00	Rv2754c, T
DRB1_0701	190	AWRHFIAMRASEHAD	FIAMRASEH	0.6624	38.6	SB	16.00	Rv2754c, T
DRB1_0701	84	ISRSCTHELIRHRHF	ISRSCTHEL	0.6541	42.2	SB	16.00	Rv2754c, T
DRB1_0701	63	IIDVGHFSVLEHASV	FSVLEHASV	0.6519	43.2	SB	16.00	Rv2754c, T
DRB1_0701	135	ADAARATYSELLAKL	ARATYSELL	0.6505	43.9	SB	16.00	Rv2754c, T
DRB1_0701	81	ITGISRSCTHELIRH	ISRSCTHEL	0.6491	44.6	SB	16.00	Rv2754c, T
DRB1_0701	102	QLSQRYVPEKDSRVV	YVPEKDSRV	0.6469	45.6	SB	16.00	Rv2754c, T
DRB1_0701	86	RSCTHELIRHRHFSY	LIRHRHFSY	0.6401	49.1	SB	16.00	Rv2754c, T
DRB1_0701	177	ATETRIVVVTGNRYAW	IVVTGNRYA	0.6393	49.5	SB	16.00	Rv2754c, T
DRB1_0701	192	RHFIAMRASEHADVE	FIAMRASEH	0.6315	53.9	WB	16.00	Rv2754c, T
DRB1_0701	136	DAARATYSELLAKLE	ARATYSELL	0.6308	54.3	WB	16.00	Rv2754c, T
DRB1_0701	87	SCTHELIRHRHFSYS	LIRHRHFSY	0.6269	56.7	WB	16.00	Rv2754c, T
DRB1_0701	95	HRHFSYSQLSQRYVP	YSQLSQRYV	0.6209	60.4	WB	16.00	Rv2754c, T
DRB1_0701	103	LSQRYVPEKDSRVVV	YVPEKDSRV	0.6166	63.3	WB	16.00	Rv2754c, T
DRB1_0701	90	HELIRHRHFSYSQLS	LIRHRHFSY	0.6166	63.3	WB	16.00	Rv2754c, T
DRB1_0701	82	TGISRSCTHELIRHR	ISRSCTHEL	0.6138	65.3	WB	16.00	Rv2754c, T
DRB1_0701	70	SVLEHASVSFYITGI	LEHASVSFY	0.6129	65.9	WB	16.00	Rv2754c, T
DRB1_0701	137	AAARATYSELLAKLEA	ARATYSELL	0.6072	70.1	WB	16.00	Rv2754c, T
DRB1_0701	185	TGNRYAWRHFIAMRA	WRHFIAMRA	0.6055	71.4	WB	16.00	Rv2754c, T
DRB1_0701	0	VAETAPLRVQLIAKT	VAETAPLRV	0.6001	75.7	WB	16.00	Rv2754c, T

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DRB1_0701	88	CTHELIRHRHFSYSQ	LIRHRHFSY	0.5998	75.9	WB	32.00	Rv2754c, T
DRB1_0701	3	TAPLRVQLIAKTDFL	QLIAKTDFL	0.5979	77.5	WB	32.00	Rv2754c, T
DRB1_0701	193	HFIAMRASEHADVEI	FIAMRASEH	0.5939	81.0	WB	32.00	Rv2754c, T
DRB1_0701	178	TETRIVVVTGNYRAWR	IVVTGNYRA	0.5920	82.6	WB	32.00	Rv2754c, T
DRB1_0701	64	IDVGHFVLEHASVS	FVLEHASV	0.5890	85.4	WB	32.00	Rv2754c, T
DRB1_0701	89	THELIRHRHFSYSQL	LIRHRHFSY	0.5876	86.7	WB	32.00	Rv2754c, T
DRB1_0701	71	VLEHASVSFYITGIS	LEHASVSFY	0.5867	87.5	WB	32.00	Rv2754c, T
DRB1_0701	83	GISRSCTHELIRHRH	ISRSCTHEL	0.5860	88.2	WB	32.00	Rv2754c, T
DRB1_0701	182	IVVTGNYRAWRHFI	IVVTGNYRA	0.5834	90.7	WB	32.00	Rv2754c, T
DRB1_0701	4	APLRVQLIAKTDFLA	QLIAKTDFL	0.5754	98.9	WB	32.00	Rv2754c, T
DRB1_0701	138	ARATYSELLAKLEAK	ARATYSELL	0.5733	101.2	WB	32.00	Rv2754c, T
DRB1_0701	57	AGYLRHIIDVGHFV	IIDVGHFV	0.5725	102.0	WB	32.00	Rv2754c, T
DRB1_0701	92	LIRHRHFSYSQLSQR	LIRHRHFSY	0.5680	107.2	WB	32.00	Rv2754c, T
DRB1_0701	96	RHFSYSQLSQRYVPE	YSQLSQRYV	0.5675	107.7	WB	32.00	Rv2754c, T
DRB1_0701	186	GNYRAWRHFIAMRAS	WRHFIAMRA	0.5672	108.1	WB	32.00	Rv2754c, T
DRB1_0701	181	RIVVTGNYRAWRHFI	IVVTGNYRA	0.5640	111.9	WB	32.00	Rv2754c, T
DRB1_0701	231	VTTLDAGTEVATSPL	GTEVATSPL	0.5622	114.1	WB	32.00	Rv2754c, T
DRB1_0701	232	TTLADGTEVATSPLA	GTEVATSPL	0.5599	116.9	WB	32.00	Rv2754c, T
DRB1_0701	91	ELIRHRHFSYSQLSQ	LIRHRHFSY	0.5591	118.0	WB	32.00	Rv2754c, T
DRB1_0701	104	SQRYVPEKDSRVVVP	YVPEKDSRV	0.5542	124.4	WB	32.00	Rv2754c, T
DRB1_0701	58	GYLRHIIDVGHFV	IIDVGHFV	0.5530	126.0	WB	32.00	Rv2754c, T
DRB1_0701	179	ETRIVVVTGNYRAWRH	IVVTGNYRA	0.5416	142.6	WB	32.00	Rv2754c, T
DRB1_0701	194	FIAMRASEHADVEIR	FIAMRASEH	0.5363	151.0	WB	32.00	Rv2754c, T
DRB1_0701	10	LIAKTDFLAPPDVPW	FLAPPDVPW	0.5300	161.6	WB	32.00	Rv2754c, T
DRB1_0701	233	TLADGTEVATSPLAT	GTEVATSPL	0.5261	168.5	WB	32.00	Rv2754c, T
DRB1_0701	180	TRIVVTGNYRAWRH	IVVTGNYRA	0.5242	172.1	WB	32.00	Rv2754c, T
DRB1_0701	59	YLRHIIDVGHFV	IIDVGHFV	0.5232	174.0	WB	32.00	Rv2754c, T
DRB1_0701	187	NYRAWRHFIAMRASE	WRHFIAMRA	0.5232	174.1	WB	32.00	Rv2754c, T
DRB1_0701	105	QRYVPEKDSRVVPP	YVPEKDSRV	0.5151	189.8	WB	32.00	Rv2754c, T
DRB1_0701	72	LEHASVSFYITGISR	LEHASVSFY	0.5108	199.0	WB	32.00	Rv2754c, T
DRB1_0701	74	HASVSFYITGISRSC	YITGISRSC	0.5095	201.8	WB	32.00	Rv2754c, T
DRB1_0701	5	PLRVQLIAKTDFLAP	QLIAKTDFL	0.5033	215.8	WB	32.00	Rv2754c, T
DRB1_0701	212	IECLRQLAAVAPAVF	LAAVAPAVF	0.5007	221.9	WB	32.00	Rv2754c, T
DRB1_0701	97	HFSYSQLSQRYVPEK	YSQLSQRYV	0.4916	244.8	WB	32.00	Rv2754c, T
DRB1_0701	2	ETAPLRVQLIAKTDF	VQLIAKTDF	0.4887	252.8	WB	32.00	Rv2754c, T
DRB1_0701	213	ECLRQLAAVAPAVFA	LAAVAPAVF	0.4883	253.8	WB	32.00	Rv2754c, T
DRB1_0701	169	AARAVLPNATETRIV	PNATETRIV	0.4858	260.7	WB	32.00	Rv2754c, T
DRB1_0701	60	LRHIIDVGHFVLEH	IIDVGHFV	0.4852	262.3	WB	32.00	Rv2754c, T
DRB1_0701	46	WSKPNPKTATNAGYL	KTATNAGYL	0.4836	267.0	WB	32.00	Rv2754c, T
DRB1_0701	75	ASVSFYITGISRSC	YITGISRSC	0.4830	268.8	WB	32.00	Rv2754c, T
DRB1_0701	11	IAKTDFLAPPDVPWT	FLAPPDVPW	0.4816	272.8	WB	32.00	Rv2754c, T
DRB1_0701	147	AKLEAKFADQPNAIL	FADQPNAIL	0.4810	274.8	WB	32.00	Rv2754c, T
DRB1_0701	106	RYVPEKDSRVVPPG	YVPEKDSRV	0.4775	285.4	WB	32.00	Rv2754c, T
DRB1_0701	73	EHASVSFYITGISRS	FYITGISRS	0.4729	299.9	WB	32.00	Rv2754c, T
DRB1_0701	234	LADGTEVATSPLATE	GTEVATSPL	0.4634	332.2	WB	32.00	Rv2754c, T
DRB1_0701	161	LRRKQARQAARAVLP	RQAARAVLP	0.4624	335.8	WB	32.00	Rv2754c, T
DRB1_0701	202	HADVEIRRLAIECLR	IRRLAIECL	0.4552	363.2	WB	32.00	Rv2754c, T
DRB1_0701	98	FSYSQLSQRYVPEKD	YSQLSQRYV	0.4547	365.2	WB	32.00	Rv2754c, T
DRB1_0701	107	YVPEKDSRVVPPGM	YVPEKDSRV	0.4533	370.5	WB	50.00	Rv2754c, T
DRB1_0701	6	LRVQLIAKTDFLAPP	QLIAKTDFL	0.4522	375.1	WB	50.00	Rv2754c, T
DRB1_0701	170	AARAVLPNATETRIV	PNATETRIV	0.4482	391.4	WB	50.00	Rv2754c, T
DRB1_0701	61	RHIIDVGHFVLEHA	IIDVGHFV	0.4450	405.6	WB	50.00	Rv2754c, T
DRB1_0701	201	EHADVEIRRLAIECL	IRRLAIECL	0.4441	409.4	WB	50.00	Rv2754c, T
DRB1_0701	214	CLRQLAAVAPAVFAD	LAAVAPAVF	0.4429	415.0	WB	50.00	Rv2754c, T
DRB1_0701	148	KLEAKFADQPNAILR	FADQPNAIL	0.4405	425.7	WB	50.00	Rv2754c, T
DRB1_0701	47	SKPNPKTATNAGYLR	KTATNAGYL	0.4398	429.0	WB	50.00	Rv2754c, T
DRB1_0701	160	ILRRKQARQAARAVL	ARQAARAVL	0.4382	436.5	WB	50.00	Rv2754c, T
DRB1_0701	76	ASVSFYITGISRSC	YITGISRSC	0.4362	446.0	WB	50.00	Rv2754c, T
DRB1_0701	12	AKTDFLAPPDVPWTT	FLAPPDVPW	0.4320	466.8	WB	50.00	Rv2754c, T
DRB1_0701	183	VVTGNYRAWRHFIAM	NYRAWRHFI	0.4274	490.6	WB	50.00	Rv2754c, T
DRB1_0701	49	PNPKTATNAGYLRHI	KTATNAGYL	0.4167	550.8	WB	50.00	Rv2754c, T
DRB1_0701	7	RVQLIAKTDFLAPPD	QLIAKTDFL	0.4127	575.2	WB	50.00	Rv2754c, T
DRB1_0701	85	SRSCHELIRHRHFS	HELIRHRHF	0.4122	577.9	WB	50.00	Rv2754c, T
DRB1_0701	235	ADGTEVATSPLATEA	GTEVATSPL	0.4103	590.0	WB	50.00	Rv2754c, T
DRB1_0701	215	LRQLAAVAPAVFADF	LAAVAPAVF	0.4094	595.8	WB	50.00	Rv2754c, T
DRB1_0701	62	HIIDVGHFVLEHAS	IIDVGHFV	0.4091	598.0	WB	50.00	Rv2754c, T
DRB1_0701	48	KPNPKTATNAGYLRH	KTATNAGYL	0.4032	637.5	WB	50.00	Rv2754c, T
DRB1_0701	171	RAVLPNATETRIVVT	PNATETRIV	0.4010	652.4	WB	50.00	Rv2754c, T
DRB1_0701	93	IRHRHFSYSQLSQRY	FSYSQLSQR	0.4009	653.4	WB	50.00	Rv2754c, T
DRB1_0701	77	VSFYITGISRSC	YITGISRSC	0.3996	662.9	WB	50.00	Rv2754c, T
DRB1_0701	226	FADFEVTTLDGTEV	TTLADGTEV	0.3966	692.1	WB	50.00	Rv2754c, T
DRB1_0701	50	NPKTATNAGYLRHII	KTATNAGYL	0.3955	692.9	WB	50.00	Rv2754c, T
DRB1_0701	149	LEAKFADQPNAILRR	FADQPNAIL	0.3944	701.0	WB	50.00	Rv2754c, T
DRB1_0701	162	RRKQARQAARAVLP	RQAARAVLP	0.3925	715.8	WB	50.00	Rv2754c, T
DRB1_0701	203	ADVEIRRLAIECLRQ	IRRLAIECL	0.3893	740.8	WB	50.00	Rv2754c, T
DRB1_0701	184	VTGNYRAWRHFIAMR	NYRAWRHFI	0.3858	769.1	WB	50.00	Rv2754c, T
DRB1_0701	216	RQLAAVAPAVFADFE	LAAVAPAVF	0.3819	802.1	WB	50.00	Rv2754c, T
DRB1_0701	99	SYSQLSQRYVPEKDS	YSQLSQRYV	0.3812	808.6	WB	50.00	Rv2754c, T
DRB1_0701	52	KTATNAGYLRHIIDV	KTATNAGYL	0.3810	810.3	WB	50.00	Rv2754c, T
DRB1_0701	204	DVEIRRLAIECLRQL	IRRLAIECL	0.3796	822.7	WB	50.00	Rv2754c, T
DRB1_0701	8	VQLIAKTDFLAPPDV	QLIAKTDFL	0.3739	875.3	WB	50.00	Rv2754c, T
DRB1_0701	13	KTDFLAPPDVPWTTD	FLAPPDVPW	0.3709	903.5	WB	50.00	Rv2754c, T
DRB1_0701	51	PKTATNAGYLRHII	KTATNAGYL	0.3673	939.7	WB	50.00	Rv2754c, T
DRB1_0701	195	IAMRASEHADVEIRR	MRASEHADV	0.3625	990.4	WB	50.00	Rv2754c, T
DRB1_0701	196	AMRASEHADVEIRRL	MRASEHADV	0.3563	1058.5	WB	50.00	Rv2754c, T

DRB1_0701	217	QLAAVAPAVFADFEV	LAAVAPAVF	0.3536	1090.1	50.00	Rv2754c, T
DRB1_0701	172	AVLPNATETRIVVVTG	PNATETRIV	0.3467	1174.6	50.00	Rv2754c, T
DRB1_0701	100	YSQLSQRYVPEKDSR	YSQLSQRYV	0.3453	1192.0	50.00	Rv2754c, T
DRB1_0701	150	EAKFADQPNAILRRK	FADQPNAIL	0.3442	1206.9	50.00	Rv2754c, T
DRB1_0701	211	AIECLRQLAAVAPAV	QLAAVAPAV	0.3441	1208.4	50.00	Rv2754c, T
DRB1_0701	168	QAARAVLPNATETRI	LPNATETRI	0.3420	1236.1	50.00	Rv2754c, T
DRB1_0701	109	PEKDSRVVPPGMED	VVVPPGMED	0.3416	1241.2	50.00	Rv2754c, T
DRB1_0701	163	RKQARQAARAVLPNA	RQAARAVLP	0.3370	1304.1	50.00	Rv2754c, T
DRB1_0701	227	ADFEVTTLADGTEVA	TTLADGTEV	0.3369	1306.2	50.00	Rv2754c, T
DRB1_0701	14	TDFLAPPDVPWTTDA	FLAPPDVPW	0.3334	1356.1	50.00	Rv2754c, T
DRB1_0701	175	PNATETRIVVVTGNR	RIVVVTGNR	0.3312	1388.5	50.00	Rv2754c, T
DRB1_0701	205	VEIRRLAIECLRQLA	IRRLAIECL	0.3309	1393.9	50.00	Rv2754c, T
DRB1_0701	197	MRASEHADVEIRRLA	MRASEHADV	0.3266	1459.6	50.00	Rv2754c, T
DRB1_0701	140	ATYSELLAKLEAKFA	LLAKLEAKF	0.3263	1464.1	50.00	Rv2754c, T
DRB1_0701	173	VLPNATETRIVVVTGN	PNATETRIV	0.3178	1606.0	50.00	Rv2754c, T
DRB1_0701	151	AKFADQPNAILRRKQ	FADQPNAIL	0.3170	1620.0	50.00	Rv2754c, T
DRB1_0701	9	QLIAKTDFLAPPDVP	QLIAKTDFL	0.3117	1714.8	50.00	Rv2754c, T
DRB1_0701	206	EIRRLAIECLRQLAA	IRRLAIECL	0.3046	1852.7	50.00	Rv2754c, T
DRB1_0701	220	AVAPAVFADFEVTTL	FADFEVTTL	0.3039	1867.0	50.00	Rv2754c, T
DRB1_0701	174	LPNATETRIVVVTGNY	PNATETRIV	0.3019	1906.7	50.00	Rv2754c, T
DRB1_0701	15	DFLAPPDVPWTTDAD	FLAPPDVPW	0.3013	1919.7	50.00	Rv2754c, T
DRB1_0701	36	EFAGRACYQSWSKPN	CYQSWSKPN	0.3010	1925.2	50.00	Rv2754c, T
DRB1_0701	164	KQARQAARAVLPNAT	RQAARAVLP	0.2936	2087.2	50.00	Rv2754c, T
DRB1_0701	110	EKDSRVVPPGMEDD	VVVPPGMED	0.2868	2245.7	50.00	Rv2754c, T
DRB1_0701	152	KFADQPNAILRRKQA	FADQPNAIL	0.2868	2246.2	50.00	Rv2754c, T
DRB1_0701	141	TYSELLAKLEAKFAD	LLAKLEAKF	0.2865	2252.2	50.00	Rv2754c, T
DRB1_0701	131	LTEAADAARATYSEL	AARATYSEL	0.2790	2443.5	50.00	Rv2754c, T
DRB1_0701	40	RACYQSWSKPNPKTA	WSKPNPKTA	0.2788	2447.2	50.00	Rv2754c, T
DRB1_0701	228	DFEVTTLADGTEVAT	TTLADGTEV	0.2788	2448.6	50.00	Rv2754c, T
DRB1_0701	218	LAAVAPAVFADFEVT	LAAVAPAVF	0.2778	2475.2	50.00	Rv2754c, T
DRB1_0701	155	DQPNAILRRKQARQA	LRRKQARQA	0.2746	2561.0	50.00	Rv2754c, T
DRB1_0701	207	IRRLAIECLRQLAAV	IRRLAIECL	0.2741	2574.9	50.00	Rv2754c, T
DRB1_0701	139	RATYSELLAKLEAKF	LLAKLEAKF	0.2735	2592.4	50.00	Rv2754c, T
DRB1_0701	55	TNAGYLRHIIDVGHF	LRHIIDVGH	0.2702	2688.6	50.00	Rv2754c, T
DRB1_0701	16	FLAPPDVPWTTDADG	FLAPPDVPW	0.2699	2696.5	50.00	Rv2754c, T
DRB1_0701	37	FAGRACYQSWSKPNP	CYQSWSKPN	0.2680	2751.2	50.00	Rv2754c, T
DRB1_0701	166	ARQAARAVLPNATET	RQAARAVLP	0.2654	2831.6	50.00	Rv2754c, T
DRB1_0701	108	VPEKDSRVVPPPGME	RVVVPPGME	0.2620	2938.1	50.00	Rv2754c, T
DRB1_0701	221	VPAVAFADFEVTTLA	FADFEVTTL	0.2612	2962.4	50.00	Rv2754c, T
DRB1_0701	153	FADQPNAILRRKQAR	FADQPNAIL	0.2569	3101.6	50.00	Rv2754c, T
DRB1_0701	165	QARQAARAVLPNATE	RQAARAVLP	0.2551	3165.8	50.00	Rv2754c, T
DRB1_0701	208	RRLAIECLRQLAAVA	CLRQLAAVA	0.2545	3183.5	50.00	Rv2754c, T
DRB1_0701	41	ACYQSWSKPNPKTAT	WSKPNPKTA	0.2540	3202.8	50.00	Rv2754c, T
DRB1_0701	31	GPALVEFAGRACYQS	FAGRACYQS	0.2532	3228.3	50.00	Rv2754c, T
DRB1_0701	142	YSELLAKLEAKFADQ	LAKLEAKFA	0.2466	3469.7	50.00	Rv2754c, T
DRB1_0701	54	ATNAGYLRHIIDVGH	LRHIIDVGH	0.2460	3492.6	50.00	Rv2754c, T
DRB1_0701	111	KDSRVVPPPGMEDDA	VVVPPGMED	0.2442	3561.1	50.00	Rv2754c, T
DRB1_0701	159	AILRRKQARQAARAV	QARQAARAV	0.2429	3609.6	50.00	Rv2754c, T
DRB1_0701	156	QPNAILRRKQARQAA	LRRKQARQA	0.2426	3623.7	50.00	Rv2754c, T
DRB1_0701	167	RQAARAVLPNATETR	RQAARAVLP	0.2415	3666.2	50.00	Rv2754c, T
DRB1_0701	198	RASEHADVEIRRLAI	DVEIRRLAI	0.2404	3709.0	50.00	Rv2754c, T
DRB1_0701	56	NAGYLRHIIDVGHFS	LRHIIDVGH	0.2374	3831.1	50.00	Rv2754c, T
DRB1_0701	125	ADLRHILTEAADAAR	LTEAADAAR	0.2340	3973.7	50.00	Rv2754c, T
DRB1_0701	42	CYQSWSKPNPKTATN	WSKPNPKTA	0.2295	4174.2	50.00	Rv2754c, T
DRB1_0701	32	PALVEFAGRACYQSW	FAGRACYQS	0.2280	4241.4	50.00	Rv2754c, T
DRB1_0701	200	SEHADVEIRRLAIEC	EIRRLAIEC	0.2276	4261.0	50.00	Rv2754c, T
DRB1_0701	229	FEVTTLADGTEVATS	TTLADGTEV	0.2219	4530.3	50.00	Rv2754c, T
DRB1_0701	38	AGRACYQSWSKPNPK	CYQSWSKPN	0.2189	4682.4	50.00	Rv2754c, T
DRB1_0701	124	DADLRHILTEAADA	ILTEAADA	0.2187	4692.1	50.00	Rv2754c, T
DRB1_0701	143	SELLAKLEAKFADQP	LLAKLEAKF	0.2145	4912.0	50.00	Rv2754c, T
DRB1_0701	33	ALVEFAGRACYQSW	FAGRACYQS	0.2137	4951.0	50.00	Rv2754c, T
DRB1_0701	157	PNAILRRKQARQAAR	LRRKQARQA	0.2136	4959.5	50.00	Rv2754c, T
DRB1_0701	222	APAVFADFEVTTLAD	FADFEVTTL	0.2129	4994.4	50.00	Rv2754c, T
DRB1_0701	199	ASEHADVEIRRLAIE	DVEIRRLAI	0.2126	5010.3	50.00	Rv2754c, T
DRB1_0701	126	DLRHILTEAADAARA	LTEAADAAR	0.2084	5244.3	50.00	Rv2754c, T
DRB1_0701	209	RLAIECLRQLAAVAP	CLRQLAAVA	0.2027	5576.5	50.00	Rv2754c, T
DRB1_0701	112	DSRVVPPPGMEDDAD	VVVPPGMED	0.1990	5808.4	50.00	Rv2754c, T
DRB1_0701	144	ELLAKLEAKFADQPN	LLAKLEAKF	0.1973	5916.4	50.00	Rv2754c, T
DRB1_0701	53	TATNAGYLRHIIDVG	TNAGYLRHI	0.1969	5937.7	50.00	Rv2754c, T
DRB1_0701	123	DDADLRHILTEAADA	HILTEAADA	0.1954	6038.6	50.00	Rv2754c, T
DRB1_0701	39	GRACYQSWSKPNPKT	CYQSWSKPN	0.1935	6159.0	50.00	Rv2754c, T
DRB1_0701	154	ADQPNAILRRKQARQ	ILRRKQARQ	0.1913	6309.8	50.00	Rv2754c, T
DRB1_0701	158	NAILRRKQARQAARA	LRRKQARQA	0.1895	6434.4	50.00	Rv2754c, T
DRB1_0701	223	PAVFADFEVTTLADG	FADFEVTTL	0.1877	6558.4	50.00	Rv2754c, T
DRB1_0701	29	DGGPALVEFAGRACY	VEFAGRACY	0.1860	6683.5	50.00	Rv2754c, T
DRB1_0701	230	EVTTLADGTEVATSP	TTLADGTEV	0.1850	6752.2	50.00	Rv2754c, T
DRB1_0701	145	LLAKLEAKFADQPN	LLAKLEAKF	0.1823	6954.5	50.00	Rv2754c, T
DRB1_0701	127	LRHILTEAADAARAT	LTEAADAAR	0.1815	7015.3	50.00	Rv2754c, T
DRB1_0701	34	LVEFAGRACYQSWSK	FAGRACYQS	0.1808	7066.9	50.00	Rv2754c, T
DRB1_0701	113	SRVVVPPGMEDDADL	VVVPPGMED	0.1789	7216.2	50.00	Rv2754c, T
DRB1_0701	210	LAIECLRQLAAVAPA	CLRQLAAVA	0.1780	7284.9	50.00	Rv2754c, T
DRB1_0701	121	MEDDADLRHILTEAA	LRHILTEAA	0.1761	7439.9	50.00	Rv2754c, T
DRB1_0701	224	AVFADFEVTTLADGT	FADFEVTTL	0.1750	7526.4	50.00	Rv2754c, T
DRB1_0701	43	YQSWSKPNPKTATNA	WSKPNPKTA	0.1711	7848.8	50.00	Rv2754c, T
DRB1_0701	114	RVVVPPGMEDDADLR	VVVPPGMED	0.1693	8004.2	50.00	Rv2754c, T

DRB1_0701	30	GGPALVEFAGRACYQ	VEFAGRACY	0.1630	8568.3	50.00	Rv2754c, T
DRB1_0701	225	VFADFEVTTLADGTE	FADFEVTTL	0.1626	8606.5	50.00	Rv2754c, T
DRB1_0701	28	ADGGPALVEFAGRAC	LVEFAGRAC	0.1613	8733.0	50.00	Rv2754c, T
DRB1_0701	45	SWSKPNPKTATNAGY	WSKPNPKTA	0.1607	8791.4	50.00	Rv2754c, T
DRB1_0701	129	HILTEAADAARATYS	ADAARATYS	0.1600	8856.5	50.00	Rv2754c, T
DRB1_0701	35	VEFAGRACYQSWSKP	FAGRACYQS	0.1560	9240.5	50.00	Rv2754c, T
DRB1_0701	44	QSWKPNPKTATNAG	WSKPNPKTA	0.1552	9327.3	50.00	Rv2754c, T
DRB1_0701	122	EDDADLRHILTEAAD	LRHILTEAA	0.1504	9827.4	50.00	Rv2754c, T
DRB1_0701	128	RHILTEAADAARATY	ILTEAADAA	0.1498	9885.6	50.00	Rv2754c, T
DRB1_0701	219	AAVAPAVFADFEVTT	AAVAPAVFA	0.1494	9928.3	50.00	Rv2754c, T
DRB1_0701	115	VVPPGMEDDADLRH	VVPPGMEDE	0.1372	11325.8	50.00	Rv2754c, T
DRB1_0701	1	AETAPLRVQLIAKTD	TAPLRVQLI	0.1357	11520.5	50.00	Rv2754c, T
DRB1_0701	130	ILTEAADAARATYSE	ADAARATYS	0.1303	12215.3	50.00	Rv2754c, T
DRB1_0701	146	LAKLEAKFADQPNAI	LAKLEAKFA	0.1217	13395.2	50.00	Rv2754c, T
DRB1_0701	116	VVPPGMEDDADLRHI	EDDADLRHI	0.1061	15863.7	50.00	Rv2754c, T
DRB1_0701	117	VPPGMEDDADLRHIL	EDDADLRHI	0.0961	17667.2	50.00	Rv2754c, T
DRB1_0701	118	PPGMEDDADLRHILT	EDDADLRHI	0.0883	19242.1	50.00	Rv2754c, T
DRB1_0701	27	DADGGPALVEFAGRA	ALVEFAGRA	0.0814	20724.0	50.00	Rv2754c, T
DRB1_0701	120	GMEDDADLRHILTEA	EDDADLRHI	0.0781	21478.0	50.00	Rv2754c, T
DRB1_0701	119	PGMEDDADLRHILTE	EDDADLRHI	0.0766	21830.6	50.00	Rv2754c, T
DRB1_0701	24	WTTDADGGPALVEFA	GGPALVEFA	0.0717	23007.1	50.00	Rv2754c, T
DRB1_0701	20	PDVPWTTDADGGPAL	TDADGGPAL	0.0683	23869.7	50.00	Rv2754c, T
DRB1_0701	22	VPWTTDADGGPALVE	TDADGGPAL	0.0677	24030.6	50.00	Rv2754c, T
DRB1_0701	21	DVPWTTDADGGPALV	TDADGGPAL	0.0640	25006.2	50.00	Rv2754c, T
DRB1_0701	23	PWTDDADGGPALVEF	TDADGGPAL	0.0638	25067.4	50.00	Rv2754c, T
DRB1_0701	25	TTDADGGPALVEFAG	GGPALVEFA	0.0624	25466.8	50.00	Rv2754c, T
DRB1_0701	19	PPDVWTTDADGGP	WTTDADGGP	0.0614	25730.5	50.00	Rv2754c, T
DRB1_0701	18	APPDVPWTTDADGGP	WTTDADGGP	0.0495	29264.0	50.00	Rv2754c, T
DRB1_0701	26	TDADGGPALVEFAGR	TDADGGPAL	0.0459	30425.0	50.00	Rv2754c, T
DRB1_0701	17	LAPPDVPWTTDADGG	VPWTTDADG	0.0427	31495.2	50.00	Rv2754c, T

Allele: DRB1_0701. Number of high binders 25. Number of weak binders 71. Number of peptides 236

Allele	pos	peptide	core	1-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
DRB1_0802	156	QPNAILRRKQARQAA	QPNAILRRK	0.6610	39.2	SB	0.80	Rv2754c, T
DRB1_0802	186	GNYRAWRHFIAMRAS	GNYRAWRHF	0.6396	49.4	SB	2.00	Rv2754c, T
DRB1_0802	157	PNAILRRKQARQAAR	PNAILRRKQ	0.6379	50.3	WB	2.00	Rv2754c, T
DRB1_0802	155	DQPNAILRRKQARQA	NAILRRKQA	0.6268	56.7	WB	2.00	Rv2754c, T
DRB1_0802	185	TGNYRAWRHFIAMRA	GNYRAWRHF	0.6195	61.4	WB	2.00	Rv2754c, T
DRB1_0802	182	IVVTGNYRAWRHFIA	GNYRAWRHF	0.6009	75.0	WB	4.00	Rv2754c, T
DRB1_0802	183	VVTGNYRAWRHFIAM	GNYRAWRHF	0.5990	76.6	WB	4.00	Rv2754c, T
DRB1_0802	158	NAILRRKQARQAARA	NAILRRKQA	0.5853	88.8	WB	4.00	Rv2754c, T
DRB1_0802	181	RIVVTGNYRAWRHF	RIVVTGNYR	0.5804	93.6	WB	4.00	Rv2754c, T
DRB1_0802	184	VTGNYRAWRHFIAMR	GNYRAWRHF	0.5773	96.9	WB	4.00	Rv2754c, T
DRB1_0802	187	NYRAWRHFIAMRASE	WRHFIAMRA	0.5738	100.6	WB	4.00	Rv2754c, T
DRB1_0802	188	YRAWRHFIAMRASEH	WRHFIAMRA	0.5484	132.4	WB	8.00	Rv2754c, T
DRB1_0802	79	FYITGISRSCTHELI	FYITGISRS	0.5477	133.4	WB	8.00	Rv2754c, T
DRB1_0802	159	AILRRKQARQAARAV	ILRRKQARQ	0.5457	136.4	WB	8.00	Rv2754c, T
DRB1_0802	154	ADQPNAILRRKQARQ	ILRRKQARQ	0.5407	144.0	WB	8.00	Rv2754c, T
DRB1_0802	160	ILRRKQARQAARAVL	ILRRKQARQ	0.5353	152.6	WB	8.00	Rv2754c, T
DRB1_0802	78	FYITGISRSCTHEL	FYITGISRS	0.5329	156.6	WB	8.00	Rv2754c, T
DRB1_0802	40	RACYQSWKPNPKTA	CYQSWSKPN	0.5322	157.8	WB	8.00	Rv2754c, T
DRB1_0802	209	RLAIECLRQLAAVAP	AIECLRQLA	0.5221	176.0	WB	8.00	Rv2754c, T
DRB1_0802	180	TRIVVTGNYRAWRHF	RIVVTGNYR	0.5186	182.8	WB	8.00	Rv2754c, T
DRB1_0802	189	RAWRHFIAMRASEHA	WRHFIAMRA	0.5170	186.0	WB	8.00	Rv2754c, T
DRB1_0802	77	VSFYITGISRSCTHE	FYITGISRS	0.5136	193.0	WB	8.00	Rv2754c, T
DRB1_0802	190	AWRHFIAMRASEHAD	WRHFIAMRA	0.5006	222.1	WB	8.00	Rv2754c, T
DRB1_0802	39	GRACYQSWKPNPKT	CYQSWSKPN	0.4923	243.1	WB	8.00	Rv2754c, T
DRB1_0802	210	LAIECLRQLAAVAPA	AIECLRQLA	0.4921	243.4	WB	8.00	Rv2754c, T
DRB1_0802	41	ACYQSWKPNPKTAT	CYQSWSKPN	0.4905	247.8	WB	8.00	Rv2754c, T
DRB1_0802	76	SVSFYITGISRSCTH	YITGISRS	0.4899	249.4	WB	8.00	Rv2754c, T
DRB1_0802	208	RRLAIECLRQLAAVA	AIECLRQLA	0.4883	253.9	WB	8.00	Rv2754c, T
DRB1_0802	37	FAGRACYQSWKPNP	CYQSWSKPN	0.4811	274.5	WB	16.00	Rv2754c, T
DRB1_0802	161	LRRKQARQAARAVLP	LRRKQARQA	0.4804	276.3	WB	16.00	Rv2754c, T
DRB1_0802	191	WRHFIAMRASEHADV	WRHFIAMRA	0.4789	281.1	WB	16.00	Rv2754c, T
DRB1_0802	38	AGRACYQSWKPNPK	CYQSWSKPN	0.4746	294.2	WB	16.00	Rv2754c, T
DRB1_0802	211	LAIECLRQLAAVAPV	AIECLRQLA	0.4746	294.3	WB	16.00	Rv2754c, T
DRB1_0802	75	ASVSFYITGISRSCT	YITGISRS	0.4709	306.4	WB	16.00	Rv2754c, T
DRB1_0802	153	FADQPNAILRRKQAR	NAILRRKQA	0.4704	308.0	WB	16.00	Rv2754c, T
DRB1_0802	80	YITGISRSCTHELIR	YITGISRS	0.4703	308.3	WB	16.00	Rv2754c, T
DRB1_0802	74	HASVSFYITGISRS	YITGISRS	0.4613	340.1	WB	16.00	Rv2754c, T
DRB1_0802	36	EFAGRACYQSWSKPN	FAGRACYQS	0.4518	376.6	WB	16.00	Rv2754c, T
DRB1_0802	96	RHFSYSQLSQRYVPE	YSQLSQRYV	0.4495	386.1	WB	16.00	Rv2754c, T
DRB1_0802	94	RHRHFSYSQLSQRYV	YSQLSQRYV	0.4456	403.0	WB	16.00	Rv2754c, T
DRB1_0802	179	ETRIVVTGNYRAWRH	RIVVTGNYR	0.4416	420.5	WB	16.00	Rv2754c, T
DRB1_0802	178	TETRIVVTGNYRAWR	RIVVTGNYR	0.4379	437.6	WB	16.00	Rv2754c, T
DRB1_0802	95	HRHFSYSQLSQRYVP	YSQLSQRYV	0.4370	442.1	WB	16.00	Rv2754c, T
DRB1_0802	42	CYQSWKPNPKTATN	CYQSWSKPN	0.4357	448.6	WB	16.00	Rv2754c, T
DRB1_0802	97	HFSYSQLSQRYVPEK	YSQLSQRYV	0.4352	450.9	WB	16.00	Rv2754c, T
DRB1_0802	66	VGHFSVLEHASVSFY	HFSVLEHAS	0.4347	453.4	WB	16.00	Rv2754c, T
DRB1_0802	67	GHFSVLEHASVSFYI	HFSVLEHAS	0.4308	472.9	WB	16.00	Rv2754c, T

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DRB1_0802	98	FSYSQLSQRYVPEKD	YSQLSQRYV	0.4233	512.6	16.00	Rv2754c, T
DRB1_0802	177	ATETRIVVTGNRYRAW	RIVVTGNRYR	0.4221	519.7	16.00	Rv2754c, T
DRB1_0802	152	KFADQPNAILRRKQA	NAILRRKQA	0.4213	524.1	16.00	Rv2754c, T
DRB1_0802	65	DVGHFVLEHASVSF	FVLEHASV	0.4184	540.6	16.00	Rv2754c, T
DRB1_0802	214	CLRQLAAVAPAVFAD	CLRQLAAVA	0.4184	540.9	16.00	Rv2754c, T
DRB1_0802	99	SYSQLSQRYVPEKDS	YSQLSQRYV	0.4149	561.7	16.00	Rv2754c, T
DRB1_0802	212	EICLRQLAAVAPAVF	CLRQLAAVA	0.4104	589.8	16.00	Rv2754c, T
DRB1_0802	213	EICLRQLAAVAPAVFA	CLRQLAAVA	0.4100	592.3	32.00	Rv2754c, T
DRB1_0802	91	ELIRHRHFSYSQLSQ	ELIRHRHFS	0.4073	609.8	32.00	Rv2754c, T
DRB1_0802	202	HADVEIRRLAIECLR	ADVEIRRLA	0.4069	612.5	32.00	Rv2754c, T
DRB1_0802	192	RHFIAMRASEHADVE	RHFIAMRAS	0.4054	622.4	32.00	Rv2754c, T
DRB1_0802	64	IDVGHFVLEHASVS	FVLEHASV	0.4046	627.6	32.00	Rv2754c, T
DRB1_0802	207	IRRLAIECLRQLAAV	AIECLRQLA	0.4027	640.6	32.00	Rv2754c, T
DRB1_0802	88	CHELIRHRHFSYSQ	CHELIRHR	0.4014	650.0	32.00	Rv2754c, T
DRB1_0802	90	HELIRHRHFSYSQLS	HELIRHRHF	0.4008	653.9	32.00	Rv2754c, T
DRB1_0802	5	PLRVQLIAKTDFLAP	LRVQLIAKT	0.3976	677.3	32.00	Rv2754c, T
DRB1_0802	203	ADVEIRRLAIECLRQ	ADVEIRRLA	0.3949	697.2	32.00	Rv2754c, T
DRB1_0802	33	ALVEFAGRACYQSW	ALVEFAGRA	0.3941	703.4	32.00	Rv2754c, T
DRB1_0802	6	LRVQLIAKTDFLAPP	RVQLIAKTD	0.3891	742.7	32.00	Rv2754c, T
DRB1_0802	4	APLRVQLIAKTDFLA	PLRVQLIAK	0.3867	761.7	32.00	Rv2754c, T
DRB1_0802	63	LIDVGHFVLEHASV	FVLEHASV	0.3853	773.3	32.00	Rv2754c, T
DRB1_0802	100	YSQLSQRYVPEKDSR	YSQLSQRYV	0.3836	788.1	32.00	Rv2754c, T
DRB1_0802	35	VEFAGRACYQSWSKP	FAGRACYQS	0.3829	794.0	32.00	Rv2754c, T
DRB1_0802	162	RRKQARQAARAVLPN	RRKQARQAA	0.3820	801.4	32.00	Rv2754c, T
DRB1_0802	92	LIRHRHFSYSQLSQR	RHFSYSQLS	0.3802	817.4	32.00	Rv2754c, T
DRB1_0802	34	LVEFAGRACYQSWSK	FAGRACYQS	0.3788	829.7	32.00	Rv2754c, T
DRB1_0802	68	HFSVLEHASVSFYIT	HFSVLEHAS	0.3782	834.9	32.00	Rv2754c, T
DRB1_0802	206	EIRRLAIECLRQLAA	AIECLRQLA	0.3772	844.6	32.00	Rv2754c, T
DRB1_0802	89	THELIRHRHFSYSQL	HELIRHRHF	0.3737	876.6	32.00	Rv2754c, T
DRB1_0802	201	EHADVEIRRLAIECL	ADVEIRRLA	0.3731	882.6	32.00	Rv2754c, T
DRB1_0802	55	TNAGYLRHIIDVGHF	YLRHIIDVG	0.3704	908.7	32.00	Rv2754c, T
DRB1_0802	93	IRHRHFSYSQLSQRY	RHRHFSYSQ	0.3697	915.3	32.00	Rv2754c, T
DRB1_0802	87	SCTHELIRHRHFSYS	CHELIRHR	0.3691	922.1	32.00	Rv2754c, T
DRB1_0802	3	TAPLRVQLIAKTDFL	LRVQLIAKT	0.3676	936.7	32.00	Rv2754c, T
DRB1_0802	54	ATNAGYLRHIIDVGH	YLRHIIDVG	0.3667	946.0	32.00	Rv2754c, T
DRB1_0802	1	AETAPLRVQLIAKTD	LRVQLIAKT	0.3634	979.8	32.00	Rv2754c, T
DRB1_0802	2	ETAPLRVQLIAKTDF	LRVQLIAKT	0.3609	1007.5	32.00	Rv2754c, T
DRB1_0802	176	NATETRIVVTGNRYA	RIVVTGNRYR	0.3593	1024.8	32.00	Rv2754c, T
DRB1_0802	56	NAGYLRHIIDVGHFS	YLRHIIDVG	0.3579	1040.1	32.00	Rv2754c, T
DRB1_0802	215	LRQLAAVAPAVFADF	QLAAVAPAV	0.3539	1086.0	32.00	Rv2754c, T
DRB1_0802	200	SEHADVEIRRLAIEC	ADVEIRRLA	0.3499	1134.7	32.00	Rv2754c, T
DRB1_0802	32	PALVEFAGRACYQSW	ALVEFAGRA	0.3492	1143.2	32.00	Rv2754c, T
DRB1_0802	53	TATNAGYLRHIIDVG	YLRHIIDVG	0.3484	1153.0	32.00	Rv2754c, T
DRB1_0802	57	AGYLRHIIDVGHFSV	YLRHIIDVG	0.3411	1248.0	32.00	Rv2754c, T
DRB1_0802	205	VEIRRLAIECLRQLA	AIECLRQLA	0.3402	1260.4	32.00	Rv2754c, T
DRB1_0802	86	RSCTHELIRHRHFSY	LIRHRHFSY	0.3350	1332.7	32.00	Rv2754c, T
DRB1_0802	0	VAETAPLRVQLIAKT	LRVQLIAKT	0.3343	1342.5	32.00	Rv2754c, T
DRB1_0802	31	GPALVEFAGRACYQS	ALVEFAGRA	0.3343	1343.4	32.00	Rv2754c, T
DRB1_0802	43	YQSWSKPNPKATNA	YQSWSKPNP	0.3332	1358.5	32.00	Rv2754c, T
DRB1_0802	58	KYLRHIIDVGHFSVL	YLRHIIDVG	0.3312	1388.9	32.00	Rv2754c, T
DRB1_0802	163	RKQARQAARAVLPNA	RKQARQAAR	0.3312	1388.9	32.00	Rv2754c, T
DRB1_0802	139	RATYSELLAKLEAKF	LLAKLEAKF	0.3278	1440.8	32.00	Rv2754c, T
DRB1_0802	62	HIIDVGHFVLEHAS	HIIDVGHFS	0.3277	1442.8	32.00	Rv2754c, T
DRB1_0802	73	EHASVSFYITGISRS	FYITGISRS	0.3260	1468.9	32.00	Rv2754c, T
DRB1_0802	193	HFIAMRASEHADVEI	HFIAMRASE	0.3239	1503.8	32.00	Rv2754c, T
DRB1_0802	151	AKFADQPNAILRRKQ	QPNAILRRK	0.3153	1650.1	50.00	Rv2754c, T
DRB1_0802	141	TYSELLAKLEAKFAD	TYSELLAKL	0.3149	1656.2	50.00	Rv2754c, T
DRB1_0802	7	RVQLIAKTDFLAPPD	RVQLIAKTD	0.3099	1749.2	50.00	Rv2754c, T
DRB1_0802	164	KQARQAARAVLPNAT	QARQAARAV	0.3097	1752.7	50.00	Rv2754c, T
DRB1_0802	175	PNATETRIVVTGNRYR	RIVVTGNRYR	0.3053	1838.3	50.00	Rv2754c, T
DRB1_0802	216	RQLAAVAPAVFADFE	RQLAAVAPA	0.3037	1869.3	50.00	Rv2754c, T
DRB1_0802	199	ASEHADVEIRRLAIE	ADVEIRRLA	0.3026	1893.5	50.00	Rv2754c, T
DRB1_0802	138	ARATYSELLAKLEAK	YSELLAKLE	0.3018	1908.8	50.00	Rv2754c, T
DRB1_0802	81	ITGISRSCTHELIRH	ITGISRSCT	0.3009	1927.1	50.00	Rv2754c, T
DRB1_0802	142	YSELLAKLEAKFADQ	YSELLAKLE	0.3001	1944.5	50.00	Rv2754c, T
DRB1_0802	140	ATYSELLAKLEAKFA	LLAKLEAKF	0.2992	1963.3	50.00	Rv2754c, T
DRB1_0802	30	GGPALVEFAGRACYQ	ALVEFAGRA	0.2919	2125.4	50.00	Rv2754c, T
DRB1_0802	59	YLRHIIDVGHFVLE	YLRHIIDVG	0.2896	2179.2	50.00	Rv2754c, T
DRB1_0802	198	RASEHADVEIRRLAI	ADVEIRRLA	0.2852	2285.6	50.00	Rv2754c, T
DRB1_0802	137	AARATYSELLAKLEA	YSELLAKLE	0.2823	2358.6	50.00	Rv2754c, T
DRB1_0802	9	QLIAKTDFLAPPDVP	QLIAKTDFL	0.2808	2395.9	50.00	Rv2754c, T
DRB1_0802	165	QARQAARAVLPNATE	QARQAARAV	0.2793	2435.1	50.00	Rv2754c, T
DRB1_0802	145	LLAKLEAKFADQPNA	LLAKLEAKF	0.2792	2438.2	50.00	Rv2754c, T
DRB1_0802	144	ELLAKLEAKFADQPN	LLAKLEAKF	0.2749	2553.0	50.00	Rv2754c, T
DRB1_0802	83	GISRSCTHELIRHRH	GISRSCTHE	0.2745	2564.1	50.00	Rv2754c, T
DRB1_0802	143	SELLAKLEAKFADQP	LAKLEAKFA	0.2722	2629.8	50.00	Rv2754c, T
DRB1_0802	204	DVEIRRLAIECLRQL	DVEIRRLAI	0.2688	2727.5	50.00	Rv2754c, T
DRB1_0802	69	FVLEHASVSFYITG	FVLEHASV	0.2673	2773.4	50.00	Rv2754c, T
DRB1_0802	29	DGGPALVEFAGRACY	ALVEFAGRA	0.2672	2777.1	50.00	Rv2754c, T
DRB1_0802	52	KTATNAGYLRHIIDV	KTATNAGYL	0.2671	2779.0	50.00	Rv2754c, T
DRB1_0802	8	VQLIAKTDFLAPPDVP	QLIAKTDFL	0.2653	2832.1	50.00	Rv2754c, T
DRB1_0802	61	RHIIDVGHFVLEHA	HIIDVGHFS	0.2624	2923.3	50.00	Rv2754c, T
DRB1_0802	194	FIAMRASEHADVEIR	IAMRASEHA	0.2594	3020.3	50.00	Rv2754c, T
DRB1_0802	136	DAARATYSELLAKLE	RATYSELLA	0.2583	3055.7	50.00	Rv2754c, T
DRB1_0802	101	SQLSQRYVPEKDSRV	SQLSQRYVP	0.2570	3098.2	50.00	Rv2754c, T

DRB1_0802	82	TGISRSCTHELIRHR	GISRSCTHE	0.2561	3130.3	50.00	Rv2754c, T
DRB1_0802	85	SRSCCTHELIRHRHFS	CTHELIRHR	0.2555	3151.3	50.00	Rv2754c, T
DRB1_0802	84	ISRSCTHELIRHRHF	CTHELIRHR	0.2499	3346.9	50.00	Rv2754c, T
DRB1_0802	44	QSWSKPNPKTATNAG	WSKPNPKTA	0.2485	3397.9	50.00	Rv2754c, T
DRB1_0802	167	RQAARAVLPNATETR	RQAARAVLP	0.2465	3474.1	50.00	Rv2754c, T
DRB1_0802	107	YVPEKDSRVVPPGPM	YVPEKDSRV	0.2460	3490.3	50.00	Rv2754c, T
DRB1_0802	45	WSKPNPKTATNAGY	WSKPNPKTA	0.2452	3523.5	50.00	Rv2754c, T
DRB1_0802	106	RYVPEKDSRVVPPG	YVPEKDSRV	0.2415	3667.2	50.00	Rv2754c, T
DRB1_0802	102	QLSQRYVPEKDSRVV	LSQRYVPEK	0.2409	3690.7	50.00	Rv2754c, T
DRB1_0802	166	ARQAARAVLPNATET	RQAARAVLP	0.2382	3798.8	50.00	Rv2754c, T
DRB1_0802	195	IAMRASEHADVEIRR	IAMRASEHA	0.2375	3829.0	50.00	Rv2754c, T
DRB1_0802	217	QLAAVAPAVFADFV	QLAAVAPAV	0.2371	3845.2	50.00	Rv2754c, T
DRB1_0802	51	PKTATNAGYLRHIID	KTATNAGYL	0.2349	3935.9	50.00	Rv2754c, T
DRB1_0802	105	QRYVPEKDSRVVPP	YVPEKDSRV	0.2326	4037.4	50.00	Rv2754c, T
DRB1_0802	103	LSQRYVPEKDSRVV	LSQRYVPEK	0.2310	4107.4	50.00	Rv2754c, T
DRB1_0802	150	EAKFADQPNAILRRK	QPNAILRRK	0.2261	4331.4	50.00	Rv2754c, T
DRB1_0802	10	LIAKTDFLAPPDVPW	LIAKTDFLA	0.2243	4413.4	50.00	Rv2754c, T
DRB1_0802	72	LEHASVSFYITGISR	HASVSFYIT	0.2241	4425.0	50.00	Rv2754c, T
DRB1_0802	197	IAMRASEHADVEIRRLA	ADVEIRRLA	0.2195	4653.3	50.00	Rv2754c, T
DRB1_0802	28	ADGGPALVEFAGRAC	ALVEFAGRA	0.2193	4663.0	50.00	Rv2754c, T
DRB1_0802	46	WSKPNPKTATNAGYL	WSKPNPKTA	0.2192	4665.0	50.00	Rv2754c, T
DRB1_0802	135	ADAARATYSELLAKL	RATYSELLA	0.2154	4863.2	50.00	Rv2754c, T
DRB1_0802	50	NPKTATNAGYLRHII	NAGYLRHII	0.2081	5259.7	50.00	Rv2754c, T
DRB1_0802	174	LPNATETRIVVTGNY	NATETRIVV	0.2066	5345.6	50.00	Rv2754c, T
DRB1_0802	146	LAKLEAKFADQPNAI	LAKLEAKFA	0.2060	5382.4	50.00	Rv2754c, T
DRB1_0802	108	VPEKDSRVVPPGME	KDSRVVPP	0.2055	5412.0	50.00	Rv2754c, T
DRB1_0802	173	VLPNATETRIVVTGN	NATETRIVV	0.2050	5441.7	50.00	Rv2754c, T
DRB1_0802	60	LRHIIDVGHFVSLEH	HIIDVGHFS	0.2043	5484.3	50.00	Rv2754c, T
DRB1_0802	71	VLEHASVSFYITGIS	HASVSFYIT	0.2037	5518.6	50.00	Rv2754c, T
DRB1_0802	104	SQRYVPEKDSRVVPP	YVPEKDSRV	0.1997	5764.7	50.00	Rv2754c, T
DRB1_0802	111	KDSRVVPPGMEDDA	KDSRVVPP	0.1890	6469.1	50.00	Rv2754c, T
DRB1_0802	70	SVLEHASVSFYITGI	HASVSFYIT	0.1888	6484.5	50.00	Rv2754c, T
DRB1_0802	110	EKDSRVVPPGMEDD	KDSRVVPP	0.1867	6632.4	50.00	Rv2754c, T
DRB1_0802	109	PEKDSRVVPPGME	KDSRVVPP	0.1841	6818.9	50.00	Rv2754c, T
DRB1_0802	172	AVLPNATETRIVVTG	NATETRIVV	0.1817	7004.8	50.00	Rv2754c, T
DRB1_0802	124	DADLRHILTEAADA	LRHILTEAA	0.1803	7105.2	50.00	Rv2754c, T
DRB1_0802	123	DDADLRHILTEAADA	LRHILTEAA	0.1800	7133.0	50.00	Rv2754c, T
DRB1_0802	27	DADGGPALVEFAGRA	ALVEFAGRA	0.1777	7308.2	50.00	Rv2754c, T
DRB1_0802	122	EDDADLRHILTEAAD	LRHILTEAA	0.1724	7740.9	50.00	Rv2754c, T
DRB1_0802	147	AKLEAKFADQPNAIL	LEAKFADQP	0.1695	7987.5	50.00	Rv2754c, T
DRB1_0802	148	KLEAKFADQPNAILR	LEAKFADQP	0.1695	7987.6	50.00	Rv2754c, T
DRB1_0802	121	MEDDADLRHILTEAA	LRHILTEAA	0.1690	8030.7	50.00	Rv2754c, T
DRB1_0802	233	TLADGTEVATSPLAT	TEVATSPLA	0.1688	8052.6	50.00	Rv2754c, T
DRB1_0802	168	QAARAVLPNATETRI	QAARAVLPN	0.1687	8055.2	50.00	Rv2754c, T
DRB1_0802	126	DLRHILTEAADAARA	LRHILTEAA	0.1682	8101.7	50.00	Rv2754c, T
DRB1_0802	127	LRHILTEAADAARAT	LRHILTEAA	0.1681	8111.1	50.00	Rv2754c, T
DRB1_0802	125	ADLRHILTEAADAAR	LRHILTEAA	0.1623	8636.4	50.00	Rv2754c, T
DRB1_0802	169	AARAVLPNATETRIV	ARAVLPNAT	0.1620	8662.2	50.00	Rv2754c, T
DRB1_0802	171	RANLPNATETRIVVT	NATETRIVV	0.1620	8666.6	50.00	Rv2754c, T
DRB1_0802	49	PNPKTATNAGYLRHI	KTATNAGYL	0.1618	8685.7	50.00	Rv2754c, T
DRB1_0802	11	IAKTDFLAPPDVPWT	IAKTDFLAP	0.1616	8704.6	50.00	Rv2754c, T
DRB1_0802	170	ARAVLPNATETRIVV	ARAVLPNAT	0.1613	8731.8	50.00	Rv2754c, T
DRB1_0802	235	ADGTEVATSPLATEA	GTEVATSPL	0.1609	8772.1	50.00	Rv2754c, T
DRB1_0802	232	TTLADGTEVATSPLA	TEVATSPLA	0.1585	9000.1	50.00	Rv2754c, T
DRB1_0802	149	LEAKFADQPNAILRR	LEAKFADQP	0.1545	9392.7	50.00	Rv2754c, T
DRB1_0802	134	AADAARATYSELLAK	RATYSELLA	0.1532	9529.5	50.00	Rv2754c, T
DRB1_0802	48	KPNPKTATNAGYLRH	KTATNAGYL	0.1485	10025.5	50.00	Rv2754c, T
DRB1_0802	234	FLADGTEVATSPLATE	TEVATSPLA	0.1455	10353.9	50.00	Rv2754c, T
DRB1_0802	16	FLAPPDVPWTTDADG	FLAPPDVPW	0.1432	10613.5	50.00	Rv2754c, T
DRB1_0802	133	EAADAARATYSELLA	RATYSELLA	0.1426	10686.7	50.00	Rv2754c, T
DRB1_0802	47	SKPNPKTATNAGYLR	KTATNAGYL	0.1410	10871.6	50.00	Rv2754c, T
DRB1_0802	225	VFADFEVTTLADGTE	VFADFEVTT	0.1354	11558.0	50.00	Rv2754c, T
DRB1_0802	224	AVFADFEVTTLADGT	VFADFEVTT	0.1345	11665.5	50.00	Rv2754c, T
DRB1_0802	12	AKTDFLAPPDVPWTT	FLAPPDVPW	0.1328	11880.2	50.00	Rv2754c, T
DRB1_0802	15	DFLAPPDVPWTTDAD	FLAPPDVPW	0.1321	11968.7	50.00	Rv2754c, T
DRB1_0802	228	DFEVTTLADGTEVAT	FEVTTLADG	0.1280	12510.8	50.00	Rv2754c, T
DRB1_0802	128	RHILTEAADAARATY	HILTEAADA	0.1270	12649.4	50.00	Rv2754c, T
DRB1_0802	13	KTDFLAPPDVPWTTD	FLAPPDVPW	0.1262	12767.5	50.00	Rv2754c, T
DRB1_0802	229	FEVTTLADGTEVATS	FEVTTLADG	0.1238	13103.8	50.00	Rv2754c, T
DRB1_0802	227	ADFEVTTLADGTEVA	FEVTTLADG	0.1237	13118.1	50.00	Rv2754c, T
DRB1_0802	196	AMRASEHADVEIRRL	HADVEIRRL	0.1205	13573.5	50.00	Rv2754c, T
DRB1_0802	14	TDFLAPPDVPWTTDA	FLAPPDVPW	0.1197	13687.1	50.00	Rv2754c, T
DRB1_0802	120	GMEDDADLRHILTEA	DLRHILTEA	0.1188	13832.8	50.00	Rv2754c, T
DRB1_0802	129	HILTEAADAARATYS	HILTEAADA	0.1146	14470.1	50.00	Rv2754c, T
DRB1_0802	112	DSRVVPPGMEDDAD	DSRVVPPG	0.1126	14780.4	50.00	Rv2754c, T
DRB1_0802	226	FADFEVTTLADGTEV	FEVTTLADG	0.1126	14782.5	50.00	Rv2754c, T
DRB1_0802	223	PAVFADFEVTTLADG	VFADFEVTT	0.1111	15035.5	50.00	Rv2754c, T
DRB1_0802	231	VTTLADGTEVATSPL	GTEVATSPL	0.1043	16178.0	50.00	Rv2754c, T
DRB1_0802	26	TDADGGPALVEFAGR	GPALVEFAG	0.1008	16795.6	50.00	Rv2754c, T
DRB1_0802	119	PGMEDDADLRHILTE	DADLRHILT	0.0988	17162.5	50.00	Rv2754c, T
DRB1_0802	19	PPDVPWTTDADGGPA	WTTDADGGP	0.0936	18153.8	50.00	Rv2754c, T
DRB1_0802	118	PPGMEDDADLRHILT	DADLRHILT	0.0929	18294.8	50.00	Rv2754c, T
DRB1_0802	25	TTDADGGPALVEFAG	GPALVEFAG	0.0918	18515.0	50.00	Rv2754c, T
DRB1_0802	20	PDVPWTTDADGGPAL	WTTDADGGP	0.0915	18585.7	50.00	Rv2754c, T
DRB1_0802	130	ILTEAADAARATYSE	ILTEAADAA	0.0885	19189.7	50.00	Rv2754c, T

DRB1_0802	132	TEAADAARATYSELL	ARATYSELL	0.0869	19518.5	50.00	Rv2754c, T
DRB1_0802	17	LAPPDVFWTTDADGG	LAPPDVFWTT	0.0839	20166.1	50.00	Rv2754c, T
DRB1_0802	18	APPDVFWTTDADGGP	WTTDADGGP	0.0820	20585.2	50.00	Rv2754c, T
DRB1_0802	222	APAVFADFEVTTLAD	VFADFEVTT	0.0762	21929.6	50.00	Rv2754c, T
DRB1_0802	219	AAVAPAVFADFEVTT	AAVAPAVFA	0.0736	22549.2	50.00	Rv2754c, T
DRB1_0802	24	WTTDADGGPALVEFA	WTTDADGGP	0.0730	22704.9	50.00	Rv2754c, T
DRB1_0802	21	DVPWTTDADGGPALV	WTTDADGGP	0.0724	22845.1	50.00	Rv2754c, T
DRB1_0802	113	SRVVVPPGMEDDADL	RVVVPPGME	0.0720	22954.8	50.00	Rv2754c, T
DRB1_0802	131	LTEAADAARATYSEL	LTEAADAAR	0.0710	23184.0	50.00	Rv2754c, T
DRB1_0802	230	EVTTLADGTEVATSP	TLADGTEVA	0.0710	23186.2	50.00	Rv2754c, T
DRB1_0802	22	VPWTTDADGGPALVE	WTTDADGGP	0.0704	23349.6	50.00	Rv2754c, T
DRB1_0802	221	VAPAVFADFEVTTLA	VFADFEVTT	0.0636	25119.8	50.00	Rv2754c, T
DRB1_0802	218	LAAVAPAVFADFEVT	AAVAPAVFA	0.0628	25337.1	50.00	Rv2754c, T
DRB1_0802	114	RVVVVPPGMEDDADLR	RVVVPPGME	0.0609	25863.4	50.00	Rv2754c, T
DRB1_0802	23	PWTTDADGGPALVEF	WTTDADGGP	0.0607	25932.0	50.00	Rv2754c, T
DRB1_0802	220	AVAPAVFADFEVTTL	VFADFEVTT	0.0556	27396.4	50.00	Rv2754c, T
DRB1_0802	117	VPPGMEDDADLRHIL	DDADLRHIL	0.0390	32785.5	50.00	Rv2754c, T
DRB1_0802	115	VVVPPGMEDDADLRH	VVVPPGMED	0.0371	33456.3	50.00	Rv2754c, T
DRB1_0802	116	VVPPGMEDDADLRHI	GMEDDADLR	0.0278	37030.5	50.00	Rv2754c, T

Allele: DRB1_0802. Number of high binders 2. Number of weak binders 45. Number of peptides 236

Allele	pos	peptide	core	l-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
DRB1_0901	190	AWRHFIAMRASEHAD	WRHFIAMRA	0.6579	40.5	SB	2.00	Rv2754c, T
DRB1_0901	191	WRHFIAMRASEHADV	WRHFIAMRA	0.6509	43.7	SB	2.00	Rv2754c, T
DRB1_0901	189	RAWRHFIAMRASEHA	WRHFIAMRA	0.6248	57.9	WB	4.00	Rv2754c, T
DRB1_0901	216	RQLAAVAPAVFADFE	QLAAVAPAV	0.6100	68.0	WB	4.00	Rv2754c, T
DRB1_0901	215	LRQLAAVAPAVFADF	QLAAVAPAV	0.6086	69.1	WB	4.00	Rv2754c, T
DRB1_0901	95	HRHFSYSQLSQRYVP	YSQLSQRYV	0.6043	72.3	WB	4.00	Rv2754c, T
DRB1_0901	188	YRAWRHFIAMRASEH	WRHFIAMRA	0.6039	72.7	WB	4.00	Rv2754c, T
DRB1_0901	78	SFYITGISRSCTHEL	FYITGISRS	0.5964	78.8	WB	4.00	Rv2754c, T
DRB1_0901	214	CLRQLAAVAPAVFAD	LAAVAPAVF	0.5935	81.3	WB	4.00	Rv2754c, T
DRB1_0901	94	RHRHFSYSQLSQRYV	YSQLSQRYV	0.5886	85.7	WB	8.00	Rv2754c, T
DRB1_0901	79	FYITGISRSCTHELI	FYITGISRS	0.5858	88.4	WB	8.00	Rv2754c, T
DRB1_0901	192	RHFIAMRASEHADVE	RHFIAMRAS	0.5706	104.2	WB	8.00	Rv2754c, T
DRB1_0901	187	NYRAWRHFIAMRASE	WRHFIAMRA	0.5698	105.1	WB	8.00	Rv2754c, T
DRB1_0901	96	RHFSYSQLSQRYVPE	YSQLSQRYV	0.5645	111.2	WB	8.00	Rv2754c, T
DRB1_0901	137	AARATYSELLAKLEA	RATYSELLA	0.5634	112.5	WB	8.00	Rv2754c, T
DRB1_0901	213	ECLRQLAAVAPAVFAD	QLAAVAPAV	0.5631	113.0	WB	8.00	Rv2754c, T
DRB1_0901	217	QLAAVAPAVFADFEV	LAAVAPAVF	0.5607	116.0	WB	8.00	Rv2754c, T
DRB1_0901	77	VSFYITGISRSCTHE	FYITGISRS	0.5599	117.0	WB	8.00	Rv2754c, T
DRB1_0901	186	GNYRAWRHFIAMRAS	WRHFIAMRA	0.5464	135.4	WB	16.00	Rv2754c, T
DRB1_0901	136	DAAARATYSELLAKLE	YSELLAKLE	0.5442	138.6	WB	16.00	Rv2754c, T
DRB1_0901	97	HFSYSQLSQRYVPEK	YSQLSQRYV	0.5430	140.4	WB	16.00	Rv2754c, T
DRB1_0901	100	YSQLSQRYVPEKDSR	YSQLSQRYV	0.5382	147.9	WB	16.00	Rv2754c, T
DRB1_0901	185	TGNYRAWRHFIAMRA	WRHFIAMRA	0.5370	149.8	WB	16.00	Rv2754c, T
DRB1_0901	138	AARATYSELLAKLEAK	RATYSELLA	0.5360	151.4	WB	16.00	Rv2754c, T
DRB1_0901	67	GHFSVLEHASVSFYI	VLEHASVSF	0.5232	174.0	WB	16.00	Rv2754c, T
DRB1_0901	76	VVSFYITGISRSCTH	FYITGISRS	0.5226	175.0	WB	16.00	Rv2754c, T
DRB1_0901	98	FYSQLSQRYVPEKDD	YSQLSQRYV	0.5170	186.0	WB	16.00	Rv2754c, T
DRB1_0901	93	IRHRHFSYSQLSQRY	RHFSYSQLS	0.5151	189.8	WB	16.00	Rv2754c, T
DRB1_0901	66	VGHFSVLEHASVSFY	FSVLEHASV	0.5146	191.0	WB	16.00	Rv2754c, T
DRB1_0901	204	DVEIRRLAIECLRQL	IRRLAIECL	0.5142	191.8	WB	16.00	Rv2754c, T
DRB1_0901	0	VAETAPLRVQLIAKT	VAETAPLRV	0.5128	194.7	WB	16.00	Rv2754c, T
DRB1_0901	92	LIRHRHFSYSQLSQR	HRHFSYSQL	0.5079	205.4	WB	16.00	Rv2754c, T
DRB1_0901	99	SYSQLSQRYVPEKDS	YSQLSQRYV	0.5031	216.1	WB	16.00	Rv2754c, T
DRB1_0901	139	RATYSELLAKLEAKF	RATYSELLA	0.5023	218.0	WB	16.00	Rv2754c, T
DRB1_0901	203	ADVEIRRLAIECLRQ	IRRLAIECL	0.5013	220.6	WB	16.00	Rv2754c, T
DRB1_0901	193	HFIAMRASEHADVEI	HFIAMRASE	0.4950	236.1	WB	16.00	Rv2754c, T
DRB1_0901	69	FSVLEHASVSFYITG	VLEHASVSF	0.4917	244.5	WB	32.00	Rv2754c, T
DRB1_0901	165	QARQAARAVLPNATE	QARQAARAV	0.4907	247.3	WB	32.00	Rv2754c, T
DRB1_0901	68	HFSVLEHASVSFYIT	VLEHASVSF	0.4897	249.9	WB	32.00	Rv2754c, T
DRB1_0901	212	IECLRQLAAVAPAVF	QLAAVAPAV	0.4896	250.2	WB	32.00	Rv2754c, T
DRB1_0901	202	HADVEIRRLAIECLR	IRRLAIECL	0.4881	254.4	WB	32.00	Rv2754c, T
DRB1_0901	91	ELIRHRHFSYSQLSQ	HRHFSYSQL	0.4867	258.1	WB	32.00	Rv2754c, T
DRB1_0901	101	SQLSQRYVPEKDSRV	SQRYVPEKD	0.4831	268.4	WB	32.00	Rv2754c, T
DRB1_0901	80	YITGISRSCTHELIR	YITGISRSC	0.4787	281.4	WB	32.00	Rv2754c, T
DRB1_0901	71	VLEHASVSFYITGIS	VLEHASVSF	0.4778	284.4	WB	32.00	Rv2754c, T
DRB1_0901	164	KQARQAARAVLPNAT	QARQAARAV	0.4764	288.8	WB	32.00	Rv2754c, T
DRB1_0901	65	DVGHFSVLEHASVSF	FSVLEHASV	0.4763	288.9	WB	32.00	Rv2754c, T
DRB1_0901	135	ADAARATYSELLAKL	ARATYSELL	0.4752	292.5	WB	32.00	Rv2754c, T
DRB1_0901	141	TYSELLAKLEAKFAD	YSELLAKLE	0.4752	292.5	WB	32.00	Rv2754c, T
DRB1_0901	205	VEIRRLAIECLRQLA	IRRLAIECL	0.4733	298.6	WB	32.00	Rv2754c, T
DRB1_0901	75	ASVSFYITGISRSCT	FYITGISRS	0.4711	305.8	WB	32.00	Rv2754c, T
DRB1_0901	140	ATYSELLAKLEAKFA	YSELLAKLE	0.4696	310.7	WB	32.00	Rv2754c, T
DRB1_0901	40	RACYQSWSKPNPKTA	WSKPNPKTA	0.4689	313.2	WB	32.00	Rv2754c, T
DRB1_0901	102	QLSQRYVPEKDSRVV	QRYVPEKDS	0.4688	313.2	WB	32.00	Rv2754c, T
DRB1_0901	111	KDSRVVVPPGMEDDA	RVVVPPGME	0.4686	314.2	WB	32.00	Rv2754c, T
DRB1_0901	70	SVLEHASVSFYITGI	VLEHASVSF	0.4632	332.8	WB	32.00	Rv2754c, T
DRB1_0901	218	LAAVAPAVFADFEVT	LAAVAPAVF	0.4614	339.5	WB	32.00	Rv2754c, T
DRB1_0901	112	DSRVVVPPGMEDDAD	RVVVPPGME	0.4558	360.6	WB	32.00	Rv2754c, T

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DRB1_0901	142	YSELLAKLEAKFADQ	YSELLAKLE	0.4548	364.7	WB	32.00	Rv2754c, T
DRB1_0901	128	RHILTEAADAARATY	ILTEAADAA	0.4546	365.6	WB	32.00	Rv2754c, T
DRB1_0901	90	HELIRHRHFSYSQLS	HRHFSYSQL	0.4525	373.8	WB	32.00	Rv2754c, T
DRB1_0901	194	FIAMRASEHADVEIR	FIAMRASEH	0.4514	378.4	WB	32.00	Rv2754c, T
DRB1_0901	113	SRVVVPPGMEDDADL	VVVPPGMED	0.4504	382.3	WB	32.00	Rv2754c, T
DRB1_0901	127	LRHILTEAADAARAT	ILTEAADAA	0.4480	392.4	WB	32.00	Rv2754c, T
DRB1_0901	234	LADGTEVATSPLATE	TEVATSPLA	0.4467	398.2	WB	32.00	Rv2754c, T
DRB1_0901	163	RKQARQAARAVLPNA	QARQAARAV	0.4466	398.3	WB	32.00	Rv2754c, T
DRB1_0901	195	IAMRASEHADVEIRR	IAMRASEHA	0.4459	401.4	WB	32.00	Rv2754c, T
DRB1_0901	160	ILRRKQARQAARAVL	QARQAARAV	0.4447	406.8	WB	32.00	Rv2754c, T
DRB1_0901	64	IDVGHFVLEHASVS	FVLEHASV	0.4430	414.3	WB	32.00	Rv2754c, T
DRB1_0901	211	AIECLRQLAAVAPAV	QLAAVAPAV	0.4414	421.5	WB	32.00	Rv2754c, T
DRB1_0901	206	EIRRLAIECLRQLAA	IRRLAIECL	0.4397	429.3	WB	32.00	Rv2754c, T
DRB1_0901	103	LSQRYVPEKDSRVVV	SQRYVPEKD	0.4395	430.1	WB	32.00	Rv2754c, T
DRB1_0901	201	EHADVEIRRLAIECL	IRRLAIECL	0.4384	435.2	WB	32.00	Rv2754c, T
DRB1_0901	162	RRKQARQAARAVLPN	QARQAARAV	0.4377	438.9	WB	32.00	Rv2754c, T
DRB1_0901	110	EKDSRVVVPPGMED	SRVVVPPGM	0.4366	443.9	WB	32.00	Rv2754c, T
DRB1_0901	143	SELLAKLEAKFADQP	LAKLEAKFA	0.4358	448.0	WB	32.00	Rv2754c, T
DRB1_0901	134	AADAARATYSELLAK	ARATYSELL	0.4356	448.7	WB	32.00	Rv2754c, T
DRB1_0901	41	ACYQSWSKPNPKTAT	WSKPNPKTA	0.4355	449.5	WB	32.00	Rv2754c, T
DRB1_0901	161	LRRKQARQAARAVLP	QARQAARAV	0.4353	450.3	WB	32.00	Rv2754c, T
DRB1_0901	166	ARQAARAVLPNATET	ARQAARAVL	0.4347	453.0	WB	32.00	Rv2754c, T
DRB1_0901	235	ADGTEVATSPLATEA	TEVATSPLA	0.4339	457.4	WB	32.00	Rv2754c, T
DRB1_0901	129	HILTEAADAARATYS	ILTEAADAA	0.4311	471.4	WB	32.00	Rv2754c, T
DRB1_0901	74	HASVSFYITGISRSC	FYITGISRS	0.4303	475.3	WB	32.00	Rv2754c, T
DRB1_0901	81	ITGISRSCTHELIRH	ISRSCTHEL	0.4289	482.5	WB	32.00	Rv2754c, T
DRB1_0901	232	EITLADGTEVATSPLA	GTEVATSPL	0.4251	502.8	WB	50.00	Rv2754c, T
DRB1_0901	126	DLRHILTEAADAARA	LRHILTEAA	0.4246	505.6	WB	50.00	Rv2754c, T
DRB1_0901	82	TGISRSCTHELIRHR	ISRSCTHEL	0.4226	516.6	WB	50.00	Rv2754c, T
DRB1_0901	73	EHASVSFYITGISRS	FYITGISRS	0.4207	527.2	WB	50.00	Rv2754c, T
DRB1_0901	144	ELLAKLEAKFADQPN	LAKLEAKFA	0.4199	532.0	WB	50.00	Rv2754c, T
DRB1_0901	4	APLRVQLIAKTDFLA	LRVQLIAKT	0.4194	534.9	WB	50.00	Rv2754c, T
DRB1_0901	42	CYQSWSKPNPKTATN	WSKPNPKTA	0.4186	539.7	WB	50.00	Rv2754c, T
DRB1_0901	233	TLADGTEVATSPLAT	LADGTEVAT	0.4183	541.0	WB	50.00	Rv2754c, T
DRB1_0901	207	IRRLAIECLRQLAAV	IRRLAIECL	0.4183	541.4	WB	50.00	Rv2754c, T
DRB1_0901	6	LRVQLIAKTDFLAPP	LRVQLIAKT	0.4181	542.2	WB	50.00	Rv2754c, T
DRB1_0901	159	AILRRKQARQAARAV	QARQAARAV	0.4159	555.4	WB	50.00	Rv2754c, T
DRB1_0901	145	LLAKLEAKFADQPN	LAKLEAKFA	0.4139	567.8	WB	50.00	Rv2754c, T
DRB1_0901	109	PEKDSRVVVPPGMED	VVVPPGMED	0.4134	570.7	WB	50.00	Rv2754c, T
DRB1_0901	63	IDVGHFVLEHASV	FVLEHASV	0.4134	570.8	WB	50.00	Rv2754c, T
DRB1_0901	5	PLRVQLIAKTDFLAP	LRVQLIAKT	0.4110	585.6	WB	50.00	Rv2754c, T
DRB1_0901	11	IAKTDFLAPPDVPWT	TDFLAPPDV	0.4103	589.9	WB	50.00	Rv2754c, T
DRB1_0901	12	AKTDFLAPPDVPWTT	TDFLAPPDV	0.4076	607.7	WB	50.00	Rv2754c, T
DRB1_0901	13	KTDFLAPPDVPWTTD	DFLAPPDVP	0.4071	611.0	WB	50.00	Rv2754c, T
DRB1_0901	43	YQSWSKPNPKTATNA	WSKPNPKTA	0.4068	612.7	WB	50.00	Rv2754c, T
DRB1_0901	219	AAVAPAVFADFEVTT	AAVAPAVFA	0.4067	613.4	WB	50.00	Rv2754c, T
DRB1_0901	184	VTGNYRAWRHFIAMR	AWRHFIAMR	0.4050	625.0	WB	50.00	Rv2754c, T
DRB1_0901	114	RVVVPPGMEDDADLR	RVVVPPGME	0.4047	626.7	WB	50.00	Rv2754c, T
DRB1_0901	125	ADLRHILTEAADAAR	HILTEAADA	0.4041	631.2	WB	50.00	Rv2754c, T
DRB1_0901	196	AMRASEHADVEIRRL	MRASEHADV	0.4017	648.0	WB	50.00	Rv2754c, T
DRB1_0901	231	VITLADGTEVATSPL	GTEVATSPL	0.4004	657.3	WB	50.00	Rv2754c, T
DRB1_0901	104	SQRYVPEKDSRVVVP	YVPEKDSRV	0.3979	675.0	WB	50.00	Rv2754c, T
DRB1_0901	3	TAPLRVQLIAKTDFL	LRVQLIAKT	0.3956	692.2	WB	50.00	Rv2754c, T
DRB1_0901	84	ISRSCTHELIRHRHF	ISRSCTHEL	0.3912	725.4	WB	50.00	Rv2754c, T
DRB1_0901	57	AGYLRHIIDVGHFV	YLRHIIDVG	0.3907	729.7	WB	50.00	Rv2754c, T
DRB1_0901	130	ILTEAADAARATYSE	ILTEAADAA	0.3905	731.4	WB	50.00	Rv2754c, T
DRB1_0901	10	LIAKTDFLAPPDVPW	TDFLAPPDV	0.3903	732.9	WB	50.00	Rv2754c, T
DRB1_0901	44	QSWSKPNPKTATNAG	WSKPNPKTA	0.3895	739.2	WB	50.00	Rv2754c, T
DRB1_0901	197	MRASEHADVEIRRLA	MRASEHADV	0.3877	754.0	WB	50.00	Rv2754c, T
DRB1_0901	133	EAADAARATYSELLA	ARATYSELL	0.3874	756.1	WB	50.00	Rv2754c, T
DRB1_0901	83	GISRSCTHELIRHRH	ISRSCTHEL	0.3873	756.7	WB	50.00	Rv2754c, T
DRB1_0901	124	DADLRHILTEAADAA	HILTEAADA	0.3853	773.6	WB	50.00	Rv2754c, T
DRB1_0901	72	LEHASVSFYITGISR	LEHASVSFY	0.3820	801.6	WB	50.00	Rv2754c, T
DRB1_0901	105	QRYVPEKDSRVVVP	YVPEKDSRV	0.3819	802.9	WB	50.00	Rv2754c, T
DRB1_0901	9	QLIAKTDFLAPPDVP	QLIAKTDFL	0.3798	820.5	WB	50.00	Rv2754c, T
DRB1_0901	58	GYLRHIIDVGHFVSL	YLRHIIDVG	0.3785	832.7	WB	50.00	Rv2754c, T
DRB1_0901	56	NAGYLRHIIDVGHFS	YLRHIIDVG	0.3767	849.3	WB	50.00	Rv2754c, T
DRB1_0901	167	RQAARAVLPNATETR	RQAARAVLP	0.3756	859.0	WB	50.00	Rv2754c, T
DRB1_0901	170	ARAVLPNATETRIVV	RAVLPNATE	0.3745	869.2	WB	50.00	Rv2754c, T
DRB1_0901	14	TDFLAPPDVPWTTDA	DFLAPPDVP	0.3733	880.8	WB	50.00	Rv2754c, T
DRB1_0901	89	THELIRHRHFSYSQL	HRHFSYSQL	0.3722	891.3	WB	50.00	Rv2754c, T
DRB1_0901	210	LAIECLRQLAAVAPA	CLRQLAAVA	0.3717	896.1	WB	50.00	Rv2754c, T
DRB1_0901	45	SWSKPNPKTATNAGY	WSKPNPKTA	0.3705	907.9	WB	50.00	Rv2754c, T
DRB1_0901	146	LAKLEAKFADQPNAI	LAKLEAKFA	0.3699	913.4	WB	50.00	Rv2754c, T
DRB1_0901	171	RAVLPNATETRIVVT	LPNATETRI	0.3691	921.7	WB	50.00	Rv2754c, T
DRB1_0901	34	LVEFAGRACYQSWSK	VEFAGRACY	0.3654	959.7	WB	50.00	Rv2754c, T
DRB1_0901	108	VPEKDSRVVVPPGME	RVVVPPGME	0.3649	964.1	WB	50.00	Rv2754c, T
DRB1_0901	39	GRACYQSWSKPNPKT	YQSWSKPNP	0.3639	975.0	WB	50.00	Rv2754c, T
DRB1_0901	1	AETAPLRVQLIAKTD	AETAPLRVQ	0.3634	980.1	WB	50.00	Rv2754c, T
DRB1_0901	37	FAGRACYQSWSKPNP	AGRACYQSW	0.3632	982.8	WB	50.00	Rv2754c, T
DRB1_0901	199	ASEHADVEIRRLAIE	ASEHADVEI	0.3630	984.3	WB	50.00	Rv2754c, T
DRB1_0901	169	AAAVLPNATETRIV	RAVLPNATE	0.3625	990.1	WB	50.00	Rv2754c, T
DRB1_0901	7	RVQLIAKTDFLAPPD	QLIAKTDFL	0.3620	995.8	WB	50.00	Rv2754c, T
DRB1_0901	158	NAILRRKQARQAARA	LRRKQARQA	0.3618	997.6	WB	50.00	Rv2754c, T
DRB1_0901	220	AVAPAVFADFEVTTL	AVAPAVFAD	0.3592	1025.6	WB	50.00	Rv2754c, T

DRB1_0901	153	FADQPNAILRRKQAR	FADQPNAIL	0.3591	1026.6	50.00	Rv2754c, T
DRB1_0901	38	AGRACYQSWSKPNPK	AGRACYQSW	0.3588	1030.8	50.00	Rv2754c, T
DRB1_0901	62	HIIDVGHFVLEHAS	IDVGHFVLE	0.3583	1035.8	50.00	Rv2754c, T
DRB1_0901	147	AKLEAKFADQPNAIL	FADQPNAIL	0.3580	1039.4	50.00	Rv2754c, T
DRB1_0901	59	YLRHIIDVGHFVLE	YLRHIIDVG	0.3572	1048.3	50.00	Rv2754c, T
DRB1_0901	36	EFAGRACYQSWSKPN	AGRACYQSW	0.3559	1063.6	50.00	Rv2754c, T
DRB1_0901	2	ETAPLVRQLIAKTDF	LRVQLIAKT	0.3554	1069.5	50.00	Rv2754c, T
DRB1_0901	208	RRLAIECLRQLAAVA	LAIECLRQL	0.3505	1126.7	50.00	Rv2754c, T
DRB1_0901	152	KFADQPNAILRRKQA	FADQPNAIL	0.3505	1127.1	50.00	Rv2754c, T
DRB1_0901	132	TEAADAARATYSELL	ARATYSELL	0.3486	1150.5	50.00	Rv2754c, T
DRB1_0901	55	TNAGYLRHIIDVGHF	YLRHIIDVG	0.3473	1166.8	50.00	Rv2754c, T
DRB1_0901	172	AVLPNATETRIIVVTG	LPNATETRI	0.3451	1195.3	50.00	Rv2754c, T
DRB1_0901	8	VQLIAKTDFLAPPDV	QLIAKTDFL	0.3445	1202.5	50.00	Rv2754c, T
DRB1_0901	35	VEFAGRACYQSWSKP	EFAGRACYQ	0.3430	1222.3	50.00	Rv2754c, T
DRB1_0901	33	ALVEFAGRACYQSW	EFAGRACYQ	0.3425	1229.1	50.00	Rv2754c, T
DRB1_0901	168	QAARAVLPNATETRI	RAVLPNATE	0.3418	1238.3	50.00	Rv2754c, T
DRB1_0901	209	RLAIECLRQLAAVAP	CLRQLAAVA	0.3399	1263.8	50.00	Rv2754c, T
DRB1_0901	32	PALVEFAGRACYQSW	LVEFAGRAC	0.3382	1287.6	50.00	Rv2754c, T
DRB1_0901	46	WSKPNPKTATNAGYL	WSKPNPKTA	0.3375	1297.2	50.00	Rv2754c, T
DRB1_0901	123	DDADLRHILTEAADA	RHILTEAAD	0.3331	1360.9	50.00	Rv2754c, T
DRB1_0901	54	ATNAGYLRHIIDVGH	YLRHIIDVG	0.3325	1369.2	50.00	Rv2754c, T
DRB1_0901	223	PAVFADFEVTTLADG	PAVFADFEV	0.3324	1370.8	50.00	Rv2754c, T
DRB1_0901	173	LPNATETRIIVVTGN	LPNATETRI	0.3315	1385.1	50.00	Rv2754c, T
DRB1_0901	221	VAPAVFADFEVTTLA	VAPAVFADF	0.3313	1387.8	50.00	Rv2754c, T
DRB1_0901	156	QPNAILRRKQARQAA	LRRKQARQA	0.3309	1393.5	50.00	Rv2754c, T
DRB1_0901	155	DQPNAILRRKQARQA	LRRKQARQA	0.3302	1404.0	50.00	Rv2754c, T
DRB1_0901	61	RHIIDVGHFVLEHA	IDVGHFVLE	0.3291	1421.2	50.00	Rv2754c, T
DRB1_0901	230	EVTTLADGTEVATSP	TTLADGTEV	0.3278	1440.2	50.00	Rv2754c, T
DRB1_0901	148	KLEAKFADQPNAILR	FADQPNAIL	0.3265	1460.9	50.00	Rv2754c, T
DRB1_0901	157	PNAILRRKQARQAAR	LRRKQARQA	0.3260	1469.4	50.00	Rv2754c, T
DRB1_0901	198	RASEHADVEIRRLAI	ASEHADVEI	0.3252	1481.4	50.00	Rv2754c, T
DRB1_0901	150	EAKFADQPNAILRRK	FADQPNAIL	0.3249	1486.9	50.00	Rv2754c, T
DRB1_0901	174	LPNATETRIIVVTGNY	LPNATETRI	0.3241	1499.8	50.00	Rv2754c, T
DRB1_0901	149	LEAKFADQPNAILRR	FADQPNAIL	0.3228	1521.9	50.00	Rv2754c, T
DRB1_0901	222	APAVFADFEVTTLAD	AVFADFEVT	0.3224	1527.4	50.00	Rv2754c, T
DRB1_0901	151	AKFADQPNAILRRKQ	FADQPNAIL	0.3210	1551.4	50.00	Rv2754c, T
DRB1_0901	53	TATNAGYLRHIIDVG	YLRHIIDVG	0.3209	1553.3	50.00	Rv2754c, T
DRB1_0901	131	LTEAADAARATYSEL	LTEAADAAR	0.3186	1592.1	50.00	Rv2754c, T
DRB1_0901	200	SEHADVEIRRLAIEC	VEIRRLAIE	0.3168	1623.4	50.00	Rv2754c, T
DRB1_0901	115	VVPPGMEDDADLRH	VVPPGMED	0.3137	1678.5	50.00	Rv2754c, T
DRB1_0901	224	AVFADFEVTTLADGT	AVFADFEVT	0.3135	1681.2	50.00	Rv2754c, T
DRB1_0901	87	SCTHELIRHRHFSYS	IRHRHFSYS	0.3135	1682.0	50.00	Rv2754c, T
DRB1_0901	183	VVTGNYRAWRHFIAM	YRAWRHFIA	0.3133	1686.6	50.00	Rv2754c, T
DRB1_0901	226	FADFEVTTLADGTEV	FADFEVTTL	0.3122	1705.6	50.00	Rv2754c, T
DRB1_0901	107	YVPEKDSRVVPPGM	YVPEKDSRV	0.3111	1727.2	50.00	Rv2754c, T
DRB1_0901	31	GPALVEFAGRACYQS	LVEFAGRAC	0.3101	1744.7	50.00	Rv2754c, T
DRB1_0901	106	RYVPEKDSRVVPPG	YVPEKDSRV	0.3086	1772.8	50.00	Rv2754c, T
DRB1_0901	229	FEVTTLADGTEVATS	TTLADGTEV	0.3052	1839.6	50.00	Rv2754c, T
DRB1_0901	228	DFEVTTLADGTEVAT	FEVTTLADG	0.3036	1871.9	50.00	Rv2754c, T
DRB1_0901	182	IVVTGNYRAWRHFI	IVVTGNYRA	0.2947	2060.4	50.00	Rv2754c, T
DRB1_0901	225	VFADFEVTTLADGTE	FADFEVTTL	0.2887	2200.5	50.00	Rv2754c, T
DRB1_0901	85	SRSCTHELIRHRHFS	SRSCTHELI	0.2872	2235.2	50.00	Rv2754c, T
DRB1_0901	154	ADQPNAILRRKQARQ	NAILRRKQA	0.2840	2314.2	50.00	Rv2754c, T
DRB1_0901	88	CHELIRHRHFSYSQ	IRHRHFSYS	0.2833	2331.3	50.00	Rv2754c, T
DRB1_0901	122	EDDADLRHILTEAAD	RHILTEAAD	0.2811	2387.7	50.00	Rv2754c, T
DRB1_0901	30	GGPALVEFAGRACYQ	LVEFAGRAC	0.2808	2396.1	50.00	Rv2754c, T
DRB1_0901	227	ADFEVTTLADGTEVA	FEVTTLADG	0.2805	2404.1	50.00	Rv2754c, T
DRB1_0901	180	TRIVVTGNYRAWRHFI	TRIVVTGNY	0.2800	2416.8	50.00	Rv2754c, T
DRB1_0901	15	DFLAPPDVPWTTDAD	DFLAPPDVP	0.2784	2459.5	50.00	Rv2754c, T
DRB1_0901	181	RIVVTGNYRAWRHFI	RIVVTGNYR	0.2761	2521.6	50.00	Rv2754c, T
DRB1_0901	60	LRHIIDVGHFVLEH	IDVGHFVLE	0.2721	2632.8	50.00	Rv2754c, T
DRB1_0901	176	NATETRIIVVTGNYRA	NATETRIIV	0.2603	2990.6	50.00	Rv2754c, T
DRB1_0901	27	DADGGPALVEFAGRA	DADGGPALV	0.2574	3086.3	50.00	Rv2754c, T
DRB1_0901	175	PNATETRIIVVTGNYR	PNATETRIV	0.2570	3099.9	50.00	Rv2754c, T
DRB1_0901	26	TDADGGPALVEFAGR	DADGGPALV	0.2511	3305.5	50.00	Rv2754c, T
DRB1_0901	28	ADGGPALVEFAGRAC	LVEFAGRAC	0.2503	3332.4	50.00	Rv2754c, T
DRB1_0901	52	KTATNAGYLRHIIDV	KTATNAGYL	0.2498	3352.4	50.00	Rv2754c, T
DRB1_0901	24	WTTDADGGPALVEFA	DADGGPALV	0.2497	3356.4	50.00	Rv2754c, T
DRB1_0901	47	SKPNPKTATNAGYLR	KTATNAGYL	0.2491	3376.9	50.00	Rv2754c, T
DRB1_0901	86	RSCTHELIRHRHFSY	RSCTHELIR	0.2468	3462.4	50.00	Rv2754c, T
DRB1_0901	22	VPWTTDADGGPALVE	DADGGPALV	0.2458	3500.1	50.00	Rv2754c, T
DRB1_0901	51	PKTATNAGYLRHIID	KTATNAGYL	0.2415	3667.7	50.00	Rv2754c, T
DRB1_0901	25	TTDADGGPALVEFAG	DADGGPALV	0.2414	3671.4	50.00	Rv2754c, T
DRB1_0901	29	DGGPALVEFAGRACY	DGGPALVEF	0.2397	3738.9	50.00	Rv2754c, T
DRB1_0901	48	KPNPKTATNAGYLRH	KTATNAGYL	0.2394	3752.0	50.00	Rv2754c, T
DRB1_0901	179	ETRIVVTGNYRAWRH	RIVVTGNYR	0.2387	3779.4	50.00	Rv2754c, T
DRB1_0901	178	TETRIVVTGNYRAWR	RIVVTGNYR	0.2385	3785.2	50.00	Rv2754c, T
DRB1_0901	21	DVPWTTDADGGPALV	DADGGPALV	0.2347	3946.1	50.00	Rv2754c, T
DRB1_0901	177	ATETRIVVTGNYRAW	RIVVTGNYR	0.2230	4480.0	50.00	Rv2754c, T
DRB1_0901	23	PWTTDADGGPALVEF	DADGGPALV	0.2216	4545.4	50.00	Rv2754c, T
DRB1_0901	50	NPKTATNAGYLRHI	KTATNAGYL	0.2182	4716.8	50.00	Rv2754c, T
DRB1_0901	16	FLAPPDVPWTTDADG	FLAPPDVPW	0.2137	4953.6	50.00	Rv2754c, T
DRB1_0901	49	PNPKTATNAGYLRHI	KTATNAGYL	0.2130	4987.3	50.00	Rv2754c, T
DRB1_0901	116	VVPPGMEDDADLRHI	VVPPGMEDD	0.2043	5483.2	50.00	Rv2754c, T
DRB1_0901	121	MEDDADLRHILTEAA	LRHILTEAA	0.1902	6387.7	50.00	Rv2754c, T

DRB1_0901	19	PPDVPWTTDADGGPA	DVPWTTDAD	0.1717	7803.2	50.00	Rv2754c, T
DRB1_0901	20	PDVVPWTTDADGGPAL	VPWTTDADG	0.1670	8209.2	50.00	Rv2754c, T
DRB1_0901	18	APPDVPWTTDADGGP	WTTDADGGP	0.1603	8824.4	50.00	Rv2754c, T
DRB1_0901	119	PGMEDDADLRHILTE	DADLRHILT	0.1422	10738.0	50.00	Rv2754c, T
DRB1_0901	17	LAPPDVPWTTDADGG	LAPPDVPWT	0.1415	10821.0	50.00	Rv2754c, T
DRB1_0901	120	GMEDDADLRHILTEA	DLRHILTEA	0.1392	11089.0	50.00	Rv2754c, T
DRB1_0901	117	VPPGMEDDADLRHIL	VPPGMEDDA	0.1355	11547.0	50.00	Rv2754c, T
DRB1_0901	118	PPGMEDDADLRHILT	PGMEDDADL	0.1134	14654.2	50.00	Rv2754c, T

Allele: DRB1_0901. Number of high binders 2. Number of weak binders 82. Number of peptides 236

Allele	pos	peptide	core	1-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
DRB1_1101	78	SFYITGISRSCTHEL	YITGISRSRC	0.7793	10.9	SB	0.80	Rv2754c, T
DRB1_1101	190	AWRHFIAMRASEHAD	HFIAMRASE	0.7784	11.0	SB	0.80	Rv2754c, T
DRB1_1101	209	RLAIECLRQLAAVAP	IECLRQLAA	0.7778	11.1	SB	0.80	Rv2754c, T
DRB1_1101	189	RAWRHFIAMRASEHA	HFIAMRASE	0.7669	12.5	SB	0.80	Rv2754c, T
DRB1_1101	77	VSFYITGISRSCTHE	YITGISRSRC	0.7619	13.1	SB	0.80	Rv2754c, T
DRB1_1101	210	LAIECLRQLAAVAPA	IECLRQLAA	0.7610	13.3	SB	0.80	Rv2754c, T
DRB1_1101	208	RLAIECLRQLAAVA	AIECLRQLA	0.7603	13.4	SB	0.80	Rv2754c, T
DRB1_1101	191	WRHFIAMRASEHADV	HFIAMRASE	0.7599	13.4	SB	1.00	Rv2754c, T
DRB1_1101	79	FYITGISRSCTHELI	YITGISRSRC	0.7490	15.1	SB	1.00	Rv2754c, T
DRB1_1101	188	YRAWRHFIAMRASEH	WRHFIAMRA	0.7405	16.6	SB	2.00	Rv2754c, T
DRB1_1101	76	SVSFYITGISRSCTH	YITGISRSRC	0.7173	21.3	SB	2.00	Rv2754c, T
DRB1_1101	207	IRRLAIECLRQLAAV	AIECLRQLA	0.7143	22.0	SB	2.00	Rv2754c, T
DRB1_1101	211	AIECLRQLAAVAPAV	IECLRQLAA	0.7045	24.5	SB	2.00	Rv2754c, T
DRB1_1101	187	NYRAWRHFIAMRASE	WRHFIAMRA	0.6985	26.1	SB	4.00	Rv2754c, T
DRB1_1101	192	RHFIAMRASEHADVE	HFIAMRASE	0.6944	27.3	SB	4.00	Rv2754c, T
DRB1_1101	66	VGHFVLEHASVVSFY	FSVLEHASV	0.6904	28.5	SB	4.00	Rv2754c, T
DRB1_1101	65	DVGHFVLEHASVSF	HFSVLEHAS	0.6769	33.0	SB	4.00	Rv2754c, T
DRB1_1101	88	CHELIRHRHFSYSQ	LIRHRHFSY	0.6757	33.4	SB	4.00	Rv2754c, T
DRB1_1101	80	YITGISRSCTHELIR	YITGISRSRC	0.6748	33.7	SB	4.00	Rv2754c, T
DRB1_1101	89	THELIRHRHFSYSQL	LIRHRHFSY	0.6731	34.4	SB	4.00	Rv2754c, T
DRB1_1101	75	ASVSFYITGISRSCT	YITGISRSRC	0.6538	42.4	SB	4.00	Rv2754c, T
DRB1_1101	206	EIRRLAIECLRQLAA	AIECLRQLA	0.6472	45.5	SB	4.00	Rv2754c, T
DRB1_1101	87	SCTHELIRHRHFSYS	LIRHRHFSY	0.6462	46.0	SB	4.00	Rv2754c, T
DRB1_1101	186	GNYRAWRHFIAMRAS	YRAWRHFIA	0.6399	49.2	SB	8.00	Rv2754c, T
DRB1_1101	64	IDVGHFVLEHASVS	HFSVLEHAS	0.6373	50.6	WB	8.00	Rv2754c, T
DRB1_1101	156	QPNAILRRKQARQAA	NAILRRKQA	0.6272	56.5	WB	8.00	Rv2754c, T
DRB1_1101	67	GHFVLEHASVVSFYI	FSVLEHASV	0.6271	56.6	WB	8.00	Rv2754c, T
DRB1_1101	157	PNAILRRKQARQAAR	NAILRRKQA	0.6264	57.0	WB	8.00	Rv2754c, T
DRB1_1101	185	TGNYRAWRHFIAMRA	YRAWRHFIA	0.6090	68.8	WB	8.00	Rv2754c, T
DRB1_1101	155	DQPNAILRRKQARQA	NAILRRKQA	0.6052	71.6	WB	8.00	Rv2754c, T
DRB1_1101	86	RCTHELIRHRHFSYS	LIRHRHFSY	0.5912	83.4	WB	8.00	Rv2754c, T
DRB1_1101	63	IDVGHFVLEHASV	HFSVLEHAS	0.5814	92.7	WB	8.00	Rv2754c, T
DRB1_1101	158	NAILRRKQARQAARA	NAILRRKQA	0.5768	97.4	WB	8.00	Rv2754c, T
DRB1_1101	193	HFIAMRASEHADVEI	HFIAMRASE	0.5740	100.4	WB	8.00	Rv2754c, T
DRB1_1101	68	HFSVLEHASVVSFYIT	FSVLEHASV	0.5574	120.2	WB	16.00	Rv2754c, T
DRB1_1101	154	ADQPNAILRRKQARQ	NAILRRKQA	0.5571	120.5	WB	16.00	Rv2754c, T
DRB1_1101	90	HELIRHRHFSYSQLS	LIRHRHFSY	0.5516	127.9	WB	16.00	Rv2754c, T
DRB1_1101	182	IVVTGNYRAWRHFI	IVVTGNYRA	0.5479	133.1	WB	16.00	Rv2754c, T
DRB1_1101	184	IVTGNYSRAWRHFI	NYRAWRHFI	0.5456	136.6	WB	16.00	Rv2754c, T
DRB1_1101	5	PLRVQLIAKTDFLAP	VQLIAKTDF	0.5437	139.4	WB	16.00	Rv2754c, T
DRB1_1101	183	VVTGNYRAWRHFIAM	YRAWRHFIA	0.5421	141.7	WB	16.00	Rv2754c, T
DRB1_1101	212	IECLRQLAAVAPAVF	IECLRQLAA	0.5357	151.9	WB	16.00	Rv2754c, T
DRB1_1101	74	HASVSFYITGISRSCT	YITGISRSRC	0.5341	154.6	WB	16.00	Rv2754c, T
DRB1_1101	6	LRVQLIAKTDFLAPP	VQLIAKTDF	0.5315	159.1	WB	16.00	Rv2754c, T
DRB1_1101	140	ATYSELLAKLEAKFA	SELLAKLEA	0.5215	177.2	WB	16.00	Rv2754c, T
DRB1_1101	205	VEIRRLAIECLRQLA	AIECLRQLA	0.5213	177.6	WB	16.00	Rv2754c, T
DRB1_1101	4	APLRVQLIAKTDFLA	RVQLIAKTD	0.5211	178.0	WB	16.00	Rv2754c, T
DRB1_1101	181	RIVVTGNYRAWRHFI	IVVTGNYRA	0.5163	187.5	WB	16.00	Rv2754c, T
DRB1_1101	180	TRIVVTGNYRAWRH	IVVTGNYRA	0.5089	203.1	WB	16.00	Rv2754c, T
DRB1_1101	33	ALVEFAGRACYQSW	VEFAGRACY	0.5058	209.9	WB	16.00	Rv2754c, T
DRB1_1101	32	PALVEFAGRACYQSW	VEFAGRACY	0.5052	211.4	WB	16.00	Rv2754c, T
DRB1_1101	141	TYSELLAKLEAKFAD	SELLAKLEA	0.5052	211.5	WB	16.00	Rv2754c, T
DRB1_1101	139	RATYSELLAKLEAKF	YSELLAKLE	0.4979	228.8	WB	16.00	Rv2754c, T
DRB1_1101	62	HIIDVGHFVLEHAS	VGHFVLEH	0.4958	233.9	WB	16.00	Rv2754c, T
DRB1_1101	34	LVEFAGRACYQSWSK	VEFAGRACY	0.4924	242.6	WB	16.00	Rv2754c, T
DRB1_1101	92	LIRHRHFSYSQLSQR	LIRHRHFSY	0.4889	252.0	WB	16.00	Rv2754c, T
DRB1_1101	97	HFSYSQLSQRVPEK	YSQLSQRV	0.4813	273.7	WB	16.00	Rv2754c, T
DRB1_1101	96	RHFSYSQLSQRVPE	YSQLSQRV	0.4812	273.9	WB	16.00	Rv2754c, T
DRB1_1101	91	ELIRHRHFSYSQLSQ	LIRHRHFSY	0.4741	296.1	WB	16.00	Rv2754c, T
DRB1_1101	179	ETRIVVTGNYRAWRH	IVVTGNYRA	0.4727	300.3	WB	32.00	Rv2754c, T
DRB1_1101	95	HRHFSYSQLSQRVVP	YSQLSQRV	0.4692	312.1	WB	32.00	Rv2754c, T
DRB1_1101	31	GPALVEFAGRACYQS	VEFAGRACY	0.4674	318.1	WB	32.00	Rv2754c, T
DRB1_1101	3	TAPLRVQLIAKTDFL	RVQLIAKTD	0.4671	319.3	WB	32.00	Rv2754c, T
DRB1_1101	142	YSELLAKLEAKFADQ	SELLAKLEA	0.4670	319.6	WB	32.00	Rv2754c, T
DRB1_1101	159	AILRRKQARQAARAV	ILRRKQARQ	0.4594	347.0	WB	32.00	Rv2754c, T
DRB1_1101	81	ITGISRSCTHELIRH	ITGISRSCT	0.4568	356.7	WB	32.00	Rv2754c, T
DRB1_1101	85	SCTHELIRHRHFS	THELIRHRH	0.4562	359.3	WB	32.00	Rv2754c, T
DRB1_1101	138	ARATYSELLAKLEAK	YSELLAKLE	0.4553	362.5	WB	32.00	Rv2754c, T
DRB1_1101	153	FADQPNAILRRKQAR	NAILRRKQA	0.4485	390.2	WB	32.00	Rv2754c, T

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DRB1_1101	98	FSYSQLSQRYVPEKD	YSQLSQRYV	0.4403	426.7	WB	32.00	Rv2754c, T
DRB1_1101	94	RHRHFSYSQLSQRYV	YSQLSQRYV	0.4373	440.8	WB	32.00	Rv2754c, T
DRB1_1101	178	TETRIVVVTGNYRAWR	IVVTGNYRA	0.4295	479.3	WB	32.00	Rv2754c, T
DRB1_1101	7	RVQLIAKTDFLAPPD	VQLIAKTDF	0.4295	479.3	WB	32.00	Rv2754c, T
DRB1_1101	35	VEFAGRACYQSWSKP	VEFAGRACY	0.4239	509.4		32.00	Rv2754c, T
DRB1_1101	202	LADVEIRRLAIECLR	ADVEIRRLA	0.4153	559.2		32.00	Rv2754c, T
DRB1_1101	60	HRHIIIDVGHFVLEH	HIIDVGHFS	0.4138	568.4		32.00	Rv2754c, T
DRB1_1101	204	DVEIRRLAIECLRQL	RRLAIECLR	0.4091	597.6		32.00	Rv2754c, T
DRB1_1101	2	ETAPLRVQLIAKTDF	RVQLIAKTD	0.4058	619.4		32.00	Rv2754c, T
DRB1_1101	203	ADVEIRRLAIECLRQ	DVEIRRLAI	0.4039	632.5		32.00	Rv2754c, T
DRB1_1101	84	ISRSCTHELIRHRHF	THELIRHRH	0.4008	654.0		32.00	Rv2754c, T
DRB1_1101	201	EHADVEIRRLAIECL	ADVEIRRLA	0.3999	660.3		32.00	Rv2754c, T
DRB1_1101	61	RHIIDVGHFVLEHA	VGHFVLEH	0.3968	682.6		32.00	Rv2754c, T
DRB1_1101	160	ILRRKQARQAARAVL	ILRRKQARQ	0.3947	699.0		32.00	Rv2754c, T
DRB1_1101	30	GGPALVEFAGRACYQ	VEFAGRACY	0.3938	705.4		32.00	Rv2754c, T
DRB1_1101	137	AARATYSELLAKLEA	YSELLAKLE	0.3906	730.4		32.00	Rv2754c, T
DRB1_1101	59	YLRHIIDVGHFVLE	LRHIIDVGH	0.3868	760.8		32.00	Rv2754c, T
DRB1_1101	99	SYSQLSQRYVPEKDS	YSQLSQRYV	0.3768	847.7		32.00	Rv2754c, T
DRB1_1101	143	SELLAKLEAKFADQP	SELLAKLEA	0.3761	854.9		32.00	Rv2754c, T
DRB1_1101	152	KFADQPNAILRRKQA	NAILRRKQA	0.3731	883.1		32.00	Rv2754c, T
DRB1_1101	69	FSVLEHASVVSFYITG	FSVLEHASV	0.3720	893.1		32.00	Rv2754c, T
DRB1_1101	58	GYLRHIIDVGHFVSL	LRHIIDVGH	0.3710	902.8		32.00	Rv2754c, T
DRB1_1101	93	IRHRHFSYSQLSQRY	RHFSYSQLS	0.3705	907.6		32.00	Rv2754c, T
DRB1_1101	177	ATETRIVVVTGNYRAW	TRIVVTGNY	0.3664	949.4		32.00	Rv2754c, T
DRB1_1101	200	SEHADVEIRRLAIEC	ADVEIRRLA	0.3594	1023.6		32.00	Rv2754c, T
DRB1_1101	57	AGYLRHIIDVGHFV	LRHIIDVGH	0.3498	1135.9		50.00	Rv2754c, T
DRB1_1101	194	FIAMRASEHADVEIR	FIAMRASEH	0.3491	1144.3		50.00	Rv2754c, T
DRB1_1101	73	EHASVVSFYITGISRS	SFYITGISR	0.3441	1207.6		50.00	Rv2754c, T
DRB1_1101	1	AETAPLRVQLIAKTD	RVQLIAKTD	0.3290	1422.0		50.00	Rv2754c, T
DRB1_1101	213	ECLRQLAAVAPAVFA	LRQLAAVAP	0.3257	1473.4		50.00	Rv2754c, T
DRB1_1101	124	DADLRHILTEAADAA	LRHILTEAA	0.3217	1540.0		50.00	Rv2754c, T
DRB1_1101	29	DGGPALVEFAGRACY	VEFAGRACY	0.3191	1583.7		50.00	Rv2754c, T
DRB1_1101	168	QAARAVLPNATETRI	RAVLPNATE	0.3188	1588.9		50.00	Rv2754c, T
DRB1_1101	125	ADLRHILTEAADAA	LRHILTEAA	0.3102	1743.9		50.00	Rv2754c, T
DRB1_1101	176	NATETRIVVVTGNYRA	IVVTGNYRA	0.3098	1751.1		50.00	Rv2754c, T
DRB1_1101	136	DAARATYSELLAKLE	YSELLAKLE	0.3072	1801.3		50.00	Rv2754c, T
DRB1_1101	83	GISRSCTHELIRHRH	THELIRHRH	0.3026	1893.3		50.00	Rv2754c, T
DRB1_1101	56	NAGYLRHIIDVGHFS	YLRHIIDVG	0.3019	1907.1		50.00	Rv2754c, T
DRB1_1101	169	AARAVLPNATETRIV	RAVLPNATE	0.3012	1920.7		50.00	Rv2754c, T
DRB1_1101	214	CLRQLAAVAPAVFAD	LRQLAAVAP	0.3001	1945.4		50.00	Rv2754c, T
DRB1_1101	126	DLRHILTEAADAA	LRHILTEAA	0.2997	1953.4		50.00	Rv2754c, T
DRB1_1101	100	YSQLSQRYVPEKDSR	YSQLSQRYV	0.2989	1969.6		50.00	Rv2754c, T
DRB1_1101	167	RQAARAVLPNATETR	ARAVLPNAT	0.2974	2002.1		50.00	Rv2754c, T
DRB1_1101	161	LRRKQARQAARAVLP	RKQARQAAR	0.2973	2003.9		50.00	Rv2754c, T
DRB1_1101	8	VQLIAKTDFLAPPDV	VQLIAKTDF	0.2958	2036.6		50.00	Rv2754c, T
DRB1_1101	199	ASEHADVEIRRLAIE	ADVEIRRLA	0.2943	2070.7		50.00	Rv2754c, T
DRB1_1101	82	TGISRSCTHELIRHR	TGISRSCTH	0.2880	2215.9		50.00	Rv2754c, T
DRB1_1101	55	TNAGYLRHIIDVGHF	YLRHIIDVG	0.2835	2325.9		50.00	Rv2754c, T
DRB1_1101	162	RRKQARQAARAVLPN	RKQARQAAR	0.2803	2410.0		50.00	Rv2754c, T
DRB1_1101	123	DDADLRHILTEADA	LRHILTEAA	0.2787	2450.8		50.00	Rv2754c, T
DRB1_1101	144	ELLAKLEAKFADQPN	LAKLEAKFA	0.2781	2465.8		50.00	Rv2754c, T
DRB1_1101	54	ATNAGYLRHIIDVGH	AGYLRHIID	0.2770	2497.9		50.00	Rv2754c, T
DRB1_1101	163	RKQARQAARAVLPN	ARQAARAVL	0.2729	2610.0		50.00	Rv2754c, T
DRB1_1101	127	LRHILTEAADAA	LRHILTEAA	0.2632	2897.9		50.00	Rv2754c, T
DRB1_1101	36	EFAGRACYQSWSKPN	FAGRACYQS	0.2610	2969.9		50.00	Rv2754c, T
DRB1_1101	170	ARAVLPNATETRIVV	RAVLPNATE	0.2593	3024.1		50.00	Rv2754c, T
DRB1_1101	166	QAARAVLPNATET	RAVLPNATE	0.2585	3049.7		50.00	Rv2754c, T
DRB1_1101	0	VAETAPLRVQLIAKT	TAPLRVQLI	0.2517	3283.7		50.00	Rv2754c, T
DRB1_1101	145	LLAKLEAKFADQPN	LAKLEAKFA	0.2505	3326.3		50.00	Rv2754c, T
DRB1_1101	215	LRQLAAVAPAVFADF	LRQLAAVAP	0.2485	3398.4		50.00	Rv2754c, T
DRB1_1101	40	RACYQSWSKPNPKTA	YQSWSKPNP	0.2453	3518.6		50.00	Rv2754c, T
DRB1_1101	165	QARQAARAVLPNATE	ARQAARAVL	0.2453	3519.0		50.00	Rv2754c, T
DRB1_1101	37	FAGRACYQSWSKPNP	FAGRACYQS	0.2409	3690.0		50.00	Rv2754c, T
DRB1_1101	164	KQARQAARAVLPNAT	ARQAARAVL	0.2404	3708.6		50.00	Rv2754c, T
DRB1_1101	122	EDDADLRHILTEAAD	LRHILTEAA	0.2362	3883.0		50.00	Rv2754c, T
DRB1_1101	41	ACYQSWSKPNPKTAT	YQSWSKPNP	0.2359	3895.5		50.00	Rv2754c, T
DRB1_1101	39	GRACYQSWSKPNPKT	YQSWSKPNP	0.2346	3948.2		50.00	Rv2754c, T
DRB1_1101	42	CYQSWSKPNPKTATN	YQSWSKPNP	0.2287	4211.2		50.00	Rv2754c, T
DRB1_1101	72	LEHASVVSFYITGISR	SFYITGISR	0.2287	4212.5		50.00	Rv2754c, T
DRB1_1101	53	TNAGYLRHIIDVGH	ATNAGYLRH	0.2277	4254.4		50.00	Rv2754c, T
DRB1_1101	175	PNATETRIVVVTGNYR	TRIVVTGNY	0.2234	4457.3		50.00	Rv2754c, T
DRB1_1101	198	RASEHADVEIRRLAI	ADVEIRRLA	0.2220	4526.0		50.00	Rv2754c, T
DRB1_1101	121	MEDDADLRHILTEAA	LRHILTEAA	0.2093	5195.1		50.00	Rv2754c, T
DRB1_1101	146	LAKLEAKFADQPN	LAKLEAKFA	0.2064	5359.2		50.00	Rv2754c, T
DRB1_1101	151	AKFADQPNAILRRKQ	AKFADQPN	0.2051	5435.6		50.00	Rv2754c, T
DRB1_1101	135	ADAARATYSELLAKL	RATYSELLA	0.1984	5840.9		50.00	Rv2754c, T
DRB1_1101	52	KTATNAGYLRHIIDV	ATNAGYLRH	0.1973	5910.7		50.00	Rv2754c, T
DRB1_1101	38	AGRACYQSWSKPNPK	YQSWSKPNP	0.1924	6237.4		50.00	Rv2754c, T
DRB1_1101	51	PKTATNAGYLRHIID	ATNAGYLRH	0.1906	6359.4		50.00	Rv2754c, T
DRB1_1101	149	LEAKFADQPNAILRR	AKFADQPN	0.1904	6369.3		50.00	Rv2754c, T
DRB1_1101	150	EAKFADQPNAILRRK	AKFADQPN	0.1817	7004.4		50.00	Rv2754c, T
DRB1_1101	148	KLEAKFADQPNAILR	AKFADQPN	0.1784	7255.0		50.00	Rv2754c, T
DRB1_1101	43	YQSWSKPNPKTATNA	YQSWSKPNP	0.1762	7431.3		50.00	Rv2754c, T
DRB1_1101	171	RAVLPNATETRIVVT	RAVLPNATE	0.1730	7696.0		50.00	Rv2754c, T
DRB1_1101	228	DFEVTTLADGTEVAT	FEVTTLADG	0.1721	7768.6		50.00	Rv2754c, T

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DRB1_1101	71	VLEHASVSFYITGIS	VLEHASVSF	0.1697	7975.0	50.00	Rv2754c, T
DRB1_1101	216	RQLAAVAPAVFADF	AAVAPAVFA	0.1695	7987.1	50.00	Rv2754c, T
DRB1_1101	227	ADFEVTTLADGTEVA	FEVTTLADG	0.1683	8094.1	50.00	Rv2754c, T
DRB1_1101	128	RHILTEAADAARATY	RHILTEAAD	0.1623	8631.7	50.00	Rv2754c, T
DRB1_1101	229	FEVTTLADGTEVATS	FEVTTLADG	0.1623	8636.9	50.00	Rv2754c, T
DRB1_1101	50	NPKTATNAGYLRHII	ATNAGYLRH	0.1545	9400.3	50.00	Rv2754c, T
DRB1_1101	226	FADFEVTTLADGTEV	FEVTTLADG	0.1539	9455.5	50.00	Rv2754c, T
DRB1_1101	70	SVLEHASVSFYITGI	VLEHASVSF	0.1513	9722.7	50.00	Rv2754c, T
DRB1_1101	225	VFADFEVTTLADGTE	VFADFEVTT	0.1493	9940.5	50.00	Rv2754c, T
DRB1_1101	111	KDSRVVPPGMEDDA	RVVVPPGME	0.1485	10027.2	50.00	Rv2754c, T
DRB1_1101	120	QMEDDADLRHILTEA	DADLRHILT	0.1483	10052.9	50.00	Rv2754c, T
DRB1_1101	9	QLIAKTDFLAPPDVP	IAKTDFLAP	0.1458	10321.8	50.00	Rv2754c, T
DRB1_1101	134	AADAARATYSELLAK	RATYSELLA	0.1455	10361.7	50.00	Rv2754c, T
DRB1_1101	174	LPNATETRIVVTGNY	TRIVVTGNY	0.1433	10607.6	50.00	Rv2754c, T
DRB1_1101	147	AKLEAKFADQPNAIL	AKFADQPNA	0.1430	10639.0	50.00	Rv2754c, T
DRB1_1101	110	EKDSRVVPPGMEDD	RVVVPPGME	0.1361	11461.3	50.00	Rv2754c, T
DRB1_1101	112	DSRVVPPGMEDDAD	RVVVPPGME	0.1356	11534.8	50.00	Rv2754c, T
DRB1_1101	224	AVFADFEVTTLADGT	VFADFEVTT	0.1328	11889.7	50.00	Rv2754c, T
DRB1_1101	102	LSQRYVPEKDSRVV	QRYVPEKDS	0.1310	12118.1	50.00	Rv2754c, T
DRB1_1101	101	SQLSQRYVPEKDSRV	QRYVPEKDS	0.1237	13107.9	50.00	Rv2754c, T
DRB1_1101	10	LIAKTDFLAPPDVPW	LIAKTDFLA	0.1228	13247.1	50.00	Rv2754c, T
DRB1_1101	113	SRVVVPPGMEDDADL	RVVVPPGME	0.1213	13463.5	50.00	Rv2754c, T
DRB1_1101	109	PMEDDADLRHILTE	RVVVPPGME	0.1172	14066.6	50.00	Rv2754c, T
DRB1_1101	119	PGMEDDADLRHILTE	DADLRHILT	0.1167	14150.6	50.00	Rv2754c, T
DRB1_1101	217	QLAAVAPAVFADF	AAVAPAVFA	0.1162	14221.0	50.00	Rv2754c, T
DRB1_1101	223	PAVFADFEVTTLADG	VFADFEVTT	0.1155	14329.6	50.00	Rv2754c, T
DRB1_1101	103	LSQRYVPEKDSRVV	QRYVPEKDS	0.1151	14389.7	50.00	Rv2754c, T
DRB1_1101	49	PNPKTATNAGYLRHI	ATNAGYLRH	0.1144	14500.5	50.00	Rv2754c, T
DRB1_1101	195	IAMRASEHADVEIRR	IAMRASEHA	0.1141	14555.7	50.00	Rv2754c, T
DRB1_1101	133	EADAARATYSELLA	AADAARATY	0.1093	15330.2	50.00	Rv2754c, T
DRB1_1101	28	ADGGPALVEFAGRAC	LVEFAGRAC	0.1082	15508.7	50.00	Rv2754c, T
DRB1_1101	44	QSWSKPNPKTATNAG	SWSKPNPKT	0.1074	15645.2	50.00	Rv2754c, T
DRB1_1101	108	VPEKDSRVVPPGME	DSRVVPPG	0.1007	16814.2	50.00	Rv2754c, T
DRB1_1101	197	MRASEHADVEIRRLA	ADVEIRRLA	0.0976	17389.4	50.00	Rv2754c, T
DRB1_1101	104	SQRYVPEKDSRVVVP	QRYVPEKDS	0.0973	17439.3	50.00	Rv2754c, T
DRB1_1101	118	PPGMEDDADLRHILT	DADLRHILT	0.0967	17555.6	50.00	Rv2754c, T
DRB1_1101	230	EVTTLADGTEVATSP	EVTTLADGT	0.0955	17794.2	50.00	Rv2754c, T
DRB1_1101	235	ADGTEVATSPLATEA	TEVATSPLA	0.0927	18341.2	50.00	Rv2754c, T
DRB1_1101	129	HILTEAADAARATYS	HILTEAADA	0.0926	18355.9	50.00	Rv2754c, T
DRB1_1101	173	VLPNATETRIVVTGN	NATETRIVV	0.0884	19204.5	50.00	Rv2754c, T
DRB1_1101	11	IAKTDFLAPPDVPWT	TDFLAPPDV	0.0878	19329.3	50.00	Rv2754c, T
DRB1_1101	48	KPNPKTATNAGYLRH	ATNAGYLRH	0.0878	19336.7	50.00	Rv2754c, T
DRB1_1101	45	SWSKPNPKTATNAGY	SWSKPNPKT	0.0856	19808.5	50.00	Rv2754c, T
DRB1_1101	105	QRYVPEKDSRVVPPP	QRYVPEKDS	0.0847	19992.1	50.00	Rv2754c, T
DRB1_1101	218	LAAVAPAVFADF	AAVAPAVFA	0.0846	20019.0	50.00	Rv2754c, T
DRB1_1101	107	YVPEKDSRVVPPGM	SRVVVPPGM	0.0844	20062.6	50.00	Rv2754c, T
DRB1_1101	172	AVLPNATETRIVVTG	VLPNATETR	0.0841	20117.3	50.00	Rv2754c, T
DRB1_1101	234	LADGTEVATSPLATE	GTEVATSPL	0.0820	20598.6	50.00	Rv2754c, T
DRB1_1101	222	APAVFADF	VFADFEVTT	0.0810	20809.2	50.00	Rv2754c, T
DRB1_1101	131	LTEAADAARATYSEL	AADAARATY	0.0803	20962.6	50.00	Rv2754c, T
DRB1_1101	13	KTDFLAPPDVPWTTD	FLAPPDVPW	0.0777	21571.0	50.00	Rv2754c, T
DRB1_1101	114	RVVVPPGMEDDADLR	RVVVPPGME	0.0774	21636.9	50.00	Rv2754c, T
DRB1_1101	132	TEAADAARATYSELL	AADAARATY	0.0766	21826.6	50.00	Rv2754c, T
DRB1_1101	12	AKTDFLAPPDVPWTT	FLAPPDVPW	0.0755	22094.2	50.00	Rv2754c, T
DRB1_1101	219	AAVAPAVFADF	AAVAPAVFA	0.0746	22313.5	50.00	Rv2754c, T
DRB1_1101	231	VTTLADGTEVATSPL	LADGTEVAT	0.0710	23186.5	50.00	Rv2754c, T
DRB1_1101	233	TLADGTEVATSPLAT	EVATSPLAT	0.0703	23364.0	50.00	Rv2754c, T
DRB1_1101	232	TTLADGTEVATSPLA	LADGTEVAT	0.0696	23556.4	50.00	Rv2754c, T
DRB1_1101	221	VAPAVFADF	VFADFEVTT	0.0668	24272.1	50.00	Rv2754c, T
DRB1_1101	196	AMRASEHADVEIRRL	AMRASEHAD	0.0667	24291.8	50.00	Rv2754c, T
DRB1_1101	130	ILTEAADAARATYSE	AADAARATY	0.0625	25430.8	50.00	Rv2754c, T
DRB1_1101	46	WSPKPNPKTATNAGYL	SKPNPKTAT	0.0619	25583.7	50.00	Rv2754c, T
DRB1_1101	47	SKPNPKTATNAGYLR	SKPNPKTAT	0.0600	26113.6	50.00	Rv2754c, T
DRB1_1101	14	TDFLAPPDVPWTTDA	FLAPPDVPW	0.0569	27016.7	50.00	Rv2754c, T
DRB1_1101	220	AVAPAVFADF	VFADFEVTT	0.0543	27787.8	50.00	Rv2754c, T
DRB1_1101	106	RYVPEKDSRVVPPG	YVPEKDSRV	0.0480	29757.0	50.00	Rv2754c, T
DRB1_1101	27	DADGGPALVEFAGRA	ALVEFAGRA	0.0475	29911.6	50.00	Rv2754c, T
DRB1_1101	15	DFLAPPDVPWTTDAD	FLAPPDVPW	0.0375	33334.9	50.00	Rv2754c, T
DRB1_1101	115	VVVPPGMEDDADLRH	VVVPPGMED	0.0327	35091.8	50.00	Rv2754c, T
DRB1_1101	16	FLAPPDVPWTTDADG	FLAPPDVPW	0.0295	36337.1	50.00	Rv2754c, T
DRB1_1101	26	TDADGGPALVEFAGR	GPALVEFAG	0.0257	37862.7	50.00	Rv2754c, T
DRB1_1101	22	VPWTTDADGGPALVE	VPWTTDADG	0.0231	38931.5	50.00	Rv2754c, T
DRB1_1101	21	DVPWTTDADGGPALV	VPWTTDADG	0.0221	39377.6	50.00	Rv2754c, T
DRB1_1101	20	PDVPWTTDADGGPAL	VPWTTDADG	0.0205	40036.2	50.00	Rv2754c, T
DRB1_1101	19	PPDVPWTTDADGGPA	VPWTTDADG	0.0180	41161.1	50.00	Rv2754c, T
DRB1_1101	25	TTDADGGPALVEFAG	ADGGPALVE	0.0180	41168.7	50.00	Rv2754c, T
DRB1_1101	23	PWTTDADGGPALVEF	PWTTDADGG	0.0177	41303.4	50.00	Rv2754c, T
DRB1_1101	117	VPPGMEDDADLRHIL	MEDDADLRH	0.0150	42519.6	50.00	Rv2754c, T
DRB1_1101	24	WTTDADGGPALVEFA	DADGGPALV	0.0146	42705.8	50.00	Rv2754c, T
DRB1_1101	18	APPDVPWTTDADGGP	VPWTTDADG	0.0141	42925.9	50.00	Rv2754c, T
DRB1_1101	17	LAPPDVPWTTDADGG	VPWTTDADG	0.0120	43935.7	50.00	Rv2754c, T
DRB1_1101	116	VVPPGMEDDADLRHI	MEDDADLRH	0.0111	44347.4	50.00	Rv2754c, T

Allele: DRB1_1101. Number of high binders 24. Number of weak binders 49. Number of peptides 73

Allele	pos	peptide	core	1-log50k(aff)	affinity(nM)	Bind	Level	%Random	Identity
DRB1_1302	177	ATETRIVVTGNYRAW	IVVTGNYRA	0.6148	64.6	WB	4.00	Rv2754c, T	
DRB1_1302	176	NATETRIVVTGNYRA	IVVTGNYRA	0.6041	72.5	WB	8.00	Rv2754c, T	
DRB1_1302	178	TETRIVVTGNYRAWR	IVVTGNYRA	0.5983	77.2	WB	8.00	Rv2754c, T	
DRB1_1302	179	ETRIVVTGNYRAWRH	IVVTGNYRA	0.5755	98.8	WB	8.00	Rv2754c, T	
DRB1_1302	212	IECLRQLAAVAPAVF	LAAVAPAVF	0.5684	106.7	WB	8.00	Rv2754c, T	
DRB1_1302	213	ECLRQLAAVAPAVFA	LAAVAPAVF	0.5615	114.9	WB	8.00	Rv2754c, T	
DRB1_1302	180	TRIVVTGNYRAWRHF	IVVTGNYRA	0.5535	125.3	WB	8.00	Rv2754c, T	
DRB1_1302	214	CLRQLAAVAPAVFAD	LAAVAPAVF	0.5500	130.2	WB	8.00	Rv2754c, T	
DRB1_1302	3	TAPLRVQLIAKTDFL	QLIAKTDFL	0.5317	158.6	WB	16.00	Rv2754c, T	
DRB1_1302	215	LRQLAAVAPAVFADF	LAAVAPAVF	0.5287	163.9	WB	16.00	Rv2754c, T	
DRB1_1302	66	VGHFSVLEHASVSFY	LEHASVSFY	0.5247	171.2	WB	16.00	Rv2754c, T	
DRB1_1302	181	RIVVTGNYRAWRHF	IVVTGNYRA	0.5244	171.8	WB	16.00	Rv2754c, T	
DRB1_1302	67	GHFSVLEHASVSFYI	LEHASVSFY	0.5163	187.4	WB	16.00	Rv2754c, T	
DRB1_1302	4	APLRVQLIAKTDFLA	QLIAKTDFL	0.5157	188.7	WB	16.00	Rv2754c, T	
DRB1_1302	5	PLRVQLIAKTDFLAP	QLIAKTDFL	0.5065	208.3	WB	16.00	Rv2754c, T	
DRB1_1302	161	LRRKQARQAARAVLP	ARQAARAVL	0.5045	212.9	WB	16.00	Rv2754c, T	
DRB1_1302	68	HFSVLEHASVSFYIT	LEHASVSFY	0.4982	228.0	WB	16.00	Rv2754c, T	
DRB1_1302	162	RKQARQAARAVLPN	QARQAARAV	0.4927	242.1	WB	16.00	Rv2754c, T	
DRB1_1302	160	ILRRKQARQAARAVL	QARQAARAV	0.4806	276.0	WB	16.00	Rv2754c, T	
DRB1_1302	69	FSVLEHASVSFYITG	LEHASVSFY	0.4784	282.4	WB	16.00	Rv2754c, T	
DRB1_1302	6	LRVQLIAKTDFLAPP	QLIAKTDFL	0.4771	286.6	WB	16.00	Rv2754c, T	
DRB1_1302	216	RQLAAVAPAVFADFE	LAAVAPAVF	0.4769	287.2	WB	16.00	Rv2754c, T	
DRB1_1302	163	RKQARQAARAVLPNA	QARQAARAV	0.4702	308.7	WB	16.00	Rv2754c, T	
DRB1_1302	70	SVLEHASVSFYITGI	LEHASVSFY	0.4678	316.9	WB	16.00	Rv2754c, T	
DRB1_1302	182	IVVTGNYRAWRHFIA	IVVTGNYRA	0.4448	406.3	WB	32.00	Rv2754c, T	
DRB1_1302	71	VLEHASVSFYITGIS	LEHASVSFY	0.4443	408.6	WB	32.00	Rv2754c, T	
DRB1_1302	217	QLAAVAPAVFADFEV	LAAVAPAVF	0.4408	424.4	WB	32.00	Rv2754c, T	
DRB1_1302	164	KQARQAARAVLPNAT	ARQAARAVL	0.4336	458.9	WB	32.00	Rv2754c, T	
DRB1_1302	0	VAETAPLRVQLIAKT	LRVQLIAKT	0.4334	459.7	WB	32.00	Rv2754c, T	
DRB1_1302	148	KLEAKFADQPNAILR	KFADQPNAI	0.4320	466.8	WB	32.00	Rv2754c, T	
DRB1_1302	149	LEAKFADQPNAILRR	KFADQPNAI	0.4316	468.7	WB	32.00	Rv2754c, T	
DRB1_1302	7	RVQLIAKTDFLAPPD	QLIAKTDFL	0.4297	478.5	WB	32.00	Rv2754c, T	
DRB1_1302	147	AKLEAKFADQPNAIL	KFADQPNAI	0.4285	484.6	WB	32.00	Rv2754c, T	
DRB1_1302	159	AILRRKQARQAARAV	QARQAARAV	0.4255	500.6	WB	32.00	Rv2754c, T	
DRB1_1302	165	QARQAARAVLPNATE	QARQAARAV	0.4221	519.3	WB	32.00	Rv2754c, T	
DRB1_1302	58	GYLRHIDVGHFSVL	RHIDVGHF	0.4187	538.6	WB	32.00	Rv2754c, T	
DRB1_1302	150	EAKFADQPNAILLRK	KFADQPNAI	0.4150	561.1	WB	32.00	Rv2754c, T	
DRB1_1302	55	TNAGYLRHIDVGHF	RHIDVGHF	0.4045	628.7	WB	32.00	Rv2754c, T	
DRB1_1302	52	KTATNAGYLRHIDV	KTATNAGYL	0.4000	659.8	WB	32.00	Rv2754c, T	
DRB1_1302	8	VQLIAKTDFLAPPDV	QLIAKTDFL	0.4000	660.1	WB	32.00	Rv2754c, T	
DRB1_1302	47	SKPNPKTATNAGYLR	KTATNAGYL	0.3989	667.4	WB	32.00	Rv2754c, T	
DRB1_1302	168	QAARAVLPNATETRI	LPNATETRI	0.3987	669.4	WB	32.00	Rv2754c, T	
DRB1_1302	57	AGYLRHIDVGHFSV	RHIDVGHF	0.3968	683.4	WB	32.00	Rv2754c, T	
DRB1_1302	56	NAGYLRHIDVGHFS	RHIDVGHF	0.3949	697.1	WB	32.00	Rv2754c, T	
DRB1_1302	151	AKFADQPNAILRRKQ	KFADQPNAI	0.3934	708.4	WB	32.00	Rv2754c, T	
DRB1_1302	59	YLRHIDVGHFSVLE	RHIDVGHF	0.3877	753.8	WB	32.00	Rv2754c, T	
DRB1_1302	49	PNPKTATNAGYLRHI	KTATNAGYL	0.3873	757.1	WB	32.00	Rv2754c, T	
DRB1_1302	211	AIECLRQLAAVAPAV	LRQLAAVAP	0.3863	764.9	WB	32.00	Rv2754c, T	
DRB1_1302	124	DADLRHILTEAADA	LRHILTEAA	0.3854	772.8	WB	32.00	Rv2754c, T	
DRB1_1302	48	KPNPKTATNAGYLRH	KTATNAGYL	0.3832	791.4	WB	32.00	Rv2754c, T	
DRB1_1302	218	LAAVAPAVFADFEVT	LAAVAPAVF	0.3823	799.0	WB	32.00	Rv2754c, T	
DRB1_1302	2	ETAPLRVQLIAKTDF	LRVQLIAKT	0.3819	802.6	WB	32.00	Rv2754c, T	
DRB1_1302	50	NPKTATNAGYLRHII	KTATNAGYL	0.3816	804.8	WB	32.00	Rv2754c, T	
DRB1_1302	46	WSKPNPKTATNAGYL	KTATNAGYL	0.3799	820.3	WB	32.00	Rv2754c, T	
DRB1_1302	125	ADLRHILTEAADAAR	LRHILTEAA	0.3790	827.7	WB	32.00	Rv2754c, T	
DRB1_1302	169	AARAVLPNATETRIV	LPNATETRI	0.3788	830.0	WB	32.00	Rv2754c, T	
DRB1_1302	60	LRHIDVGHFSVLEH	RHIDVGHF	0.3761	854.6	WB	32.00	Rv2754c, T	
DRB1_1302	170	ARAVLPNATETRIVV	LPNATETRI	0.3745	869.5	WB	32.00	Rv2754c, T	
DRB1_1302	175	PNATETRIVVTGNYR	RIVVTGNYR	0.3733	881.0	WB	32.00	Rv2754c, T	
DRB1_1302	152	KFADQPNAILRRKQA	KFADQPNAI	0.3730	883.2	WB	32.00	Rv2754c, T	
DRB1_1302	51	PKTATNAGYLRHIID	KTATNAGYL	0.3678	935.0	WB	32.00	Rv2754c, T	
DRB1_1302	166	ARQAARAVLPNATET	ARQAARAVL	0.3672	941.1	WB	32.00	Rv2754c, T	
DRB1_1302	65	DVGHFSVLEHASVSF	VLEHASVSF	0.3606	1010.3	WB	32.00	Rv2754c, T	
DRB1_1302	78	SFYITGISRSCSTHEL	ISRSCSTHEL	0.3603	1014.2	WB	32.00	Rv2754c, T	
DRB1_1302	210	LAIECLRQLAAVAPA	LRQLAAVAP	0.3589	1028.9	WB	32.00	Rv2754c, T	
DRB1_1302	126	DLRHILTEAADAARA	LRHILTEAA	0.3562	1059.2	WB	32.00	Rv2754c, T	
DRB1_1302	121	MEDDADLRHILTEAA	LRHILTEAA	0.3477	1162.3	WB	32.00	Rv2754c, T	
DRB1_1302	79	FYITGISRSCSTHELI	ISRSCSTHEL	0.3472	1167.6	WB	32.00	Rv2754c, T	
DRB1_1302	209	RLAIECLRQLAAVAP	LRQLAAVAP	0.3455	1189.7	WB	32.00	Rv2754c, T	
DRB1_1302	122	EDDADLRHILTEAAD	LRHILTEAA	0.3452	1194.0	WB	32.00	Rv2754c, T	
DRB1_1302	127	LRHILTEAADAARAT	LRHILTEAA	0.3440	1209.8	WB	32.00	Rv2754c, T	
DRB1_1302	72	LEHASVSFYITGISR	LEHASVSFY	0.3402	1259.8	WB	32.00	Rv2754c, T	
DRB1_1302	171	RAVLPNATETRIVVT	LPNATETRI	0.3400	1262.5	WB	32.00	Rv2754c, T	
DRB1_1302	123	DDADLRHILTEAADA	LRHILTEAA	0.3390	1276.2	WB	32.00	Rv2754c, T	
DRB1_1302	1	AETAPLRVQLIAKTD	LRVQLIAKT	0.3357	1323.1	WB	32.00	Rv2754c, T	
DRB1_1302	80	YITGISRSCSTHELIR	ISRSCSTHEL	0.3345	1340.1	WB	32.00	Rv2754c, T	
DRB1_1302	157	PNAILRRKQARQAAR	RKQARQAAR	0.3329	1364.0	WB	32.00	Rv2754c, T	
DRB1_1302	158	NAILRRKQARQAARA	RKQARQAAR	0.3313	1387.9	WB	32.00	Rv2754c, T	
DRB1_1302	9	QLIAKTDFLAPPDVP	QLIAKTDFL	0.3236	1507.8	WB	32.00	Rv2754c, T	
DRB1_1302	189	RAWRHFIAMRASEHA	WRHFIAMRA	0.3234	1510.9	WB	32.00	Rv2754c, T	

DRB1_1302	232	TTLADGTEVATSPLA	GTEVATSPL	0.3219	1535.1	50.00	Rv2754c, T
DRB1_1302	167	RQAARAVLPNATETR	AVLPNATET	0.3216	1541.1	50.00	Rv2754c, T
DRB1_1302	81	ITGISRSCTHELIRH	ISRSCTHEL	0.3170	1619.6	50.00	Rv2754c, T
DRB1_1302	188	YRAWRHFIAMRASEH	WRHFIAMRA	0.3168	1623.5	50.00	Rv2754c, T
DRB1_1302	54	ATNAGYLRHIIDVGH	LRHIIDVGH	0.3167	1624.0	50.00	Rv2754c, T
DRB1_1302	186	GNYRAWRHFIAMRAS	WRHFIAMRA	0.3146	1662.6	50.00	Rv2754c, T
DRB1_1302	61	RHIIDVGHFVSLEHA	RHIIDVGHF	0.3121	1707.0	50.00	Rv2754c, T
DRB1_1302	231	VTTLADGTEVATSPL	GTEVATSPL	0.3119	1711.1	50.00	Rv2754c, T
DRB1_1302	146	LAKLEAKFADQPNAI	KFADQPNAI	0.3097	1752.0	50.00	Rv2754c, T
DRB1_1302	234	LADGTEVATSPLATE	GTEVATSPL	0.3087	1772.5	50.00	Rv2754c, T
DRB1_1302	233	TLDGTEVATSPLAT	GTEVATSPL	0.3059	1825.9	50.00	Rv2754c, T
DRB1_1302	82	TGISRSCTHELIRHR	ISRSCTHEL	0.3001	1944.1	50.00	Rv2754c, T
DRB1_1302	174	LPNATETRIVVTGNY	LPNATETRI	0.2932	2096.3	50.00	Rv2754c, T
DRB1_1302	235	ADGTEVATSPLATEA	GTEVATSPL	0.2930	2099.5	50.00	Rv2754c, T
DRB1_1302	190	AWRHFIAMRASEHAD	WRHFIAMRA	0.2882	2212.9	50.00	Rv2754c, T
DRB1_1302	187	NYRAWRHFIAMRASE	WRHFIAMRA	0.2856	2275.5	50.00	Rv2754c, T
DRB1_1302	172	AVLPNATETRIVVTG	LPNATETRI	0.2809	2393.9	50.00	Rv2754c, T
DRB1_1302	155	DQPNAILRRKQARQA	ILRRKQARQ	0.2780	2470.8	50.00	Rv2754c, T
DRB1_1302	191	WRHFIAMRASEHADV	WRHFIAMRA	0.2772	2490.5	50.00	Rv2754c, T
DRB1_1302	156	QPNAILRRKQARQAA	ILRRKQARQ	0.2754	2539.8	50.00	Rv2754c, T
DRB1_1302	185	TGNYRAWRHFIAMRA	WRHFIAMRA	0.2753	2543.9	50.00	Rv2754c, T
DRB1_1302	83	GISRSCTHELIRHRH	ISRSCTHEL	0.2739	2581.4	50.00	Rv2754c, T
DRB1_1302	84	ISRSCTHELIRHRHF	ISRSCTHEL	0.2727	2614.9	50.00	Rv2754c, T
DRB1_1302	206	EIRRLAIECLRQLAA	LAIECLRQL	0.2671	2779.8	50.00	Rv2754c, T
DRB1_1302	204	DVEIRRLAIECLRQL	LAIECLRQL	0.2621	2933.6	50.00	Rv2754c, T
DRB1_1302	208	RRLAIECLRQLAAVA	IECLRQLAA	0.2620	2936.6	50.00	Rv2754c, T
DRB1_1302	183	VVTGNYRAWRHFIAM	VVTGNYRAW	0.2612	2962.3	50.00	Rv2754c, T
DRB1_1302	207	IRRLAIECLRQLAAV	IECLRQLAA	0.2526	3251.8	50.00	Rv2754c, T
DRB1_1302	154	ADQPNAILRRKQARQ	ILRRKQARQ	0.2444	3552.6	50.00	Rv2754c, T
DRB1_1302	153	FADQPNAILRRKQAR	FADQPNAIL	0.2394	3750.5	50.00	Rv2754c, T
DRB1_1302	102	LSQRYVPEKDSRVV	YVPEKDSRV	0.2381	3803.9	50.00	Rv2754c, T
DRB1_1302	94	RHRHFSYSQLSQRYV	YSQLSQRYV	0.2360	3889.1	50.00	Rv2754c, T
DRB1_1302	135	ADAARATYSELLAKL	ARATYSELL	0.2353	3919.5	50.00	Rv2754c, T
DRB1_1302	108	VPEKDSRVVPPGME	RVVVPPGME	0.2347	3944.7	50.00	Rv2754c, T
DRB1_1302	103	LSQRYVPEKDSRVV	YVPEKDSRV	0.2325	4042.0	50.00	Rv2754c, T
DRB1_1302	173	VLPNATETRIVVTGN	LPNATETRI	0.2322	4052.4	50.00	Rv2754c, T
DRB1_1302	133	EAADAARATYSELLA	ARATYSELL	0.2268	4299.8	50.00	Rv2754c, T
DRB1_1302	109	PEKDSRVVPPGMED	RVVVPPGME	0.2265	4310.4	50.00	Rv2754c, T
DRB1_1302	205	VEIRRLAIECLRQLA	LAIECLRQL	0.2257	4347.5	50.00	Rv2754c, T
DRB1_1302	45	SWSKPNPKTATNAGY	PKTATNAGY	0.2234	4458.0	50.00	Rv2754c, T
DRB1_1302	95	HRHFSYSQLSQRYV	YSQLSQRYV	0.2207	4588.8	50.00	Rv2754c, T
DRB1_1302	104	SQRYVPEKDSRVVVP	YVPEKDSRV	0.2204	4605.7	50.00	Rv2754c, T
DRB1_1302	134	AADAARATYSELLAK	ARATYSELL	0.2177	4741.0	50.00	Rv2754c, T
DRB1_1302	110	EKDSRVVPPGMEDD	RVVVPPGME	0.2161	4825.7	50.00	Rv2754c, T
DRB1_1302	63	IIDVGHFVSLEHASV	FSVLEHASV	0.2122	5031.6	50.00	Rv2754c, T
DRB1_1302	136	DAARATYSELLAKLE	ARATYSELL	0.2119	5048.7	50.00	Rv2754c, T
DRB1_1302	132	TEAADAARATYSELL	ARATYSELL	0.2097	5171.5	50.00	Rv2754c, T
DRB1_1302	140	ATYSELLAKLEAKFA	LLAKLEAKF	0.2070	5322.1	50.00	Rv2754c, T
DRB1_1302	107	YVPEKDSRVVPPG	YVPEKDSRV	0.2034	5538.7	50.00	Rv2754c, T
DRB1_1302	62	HIIDVGHFVSLEHAS	IDVGHFVS	0.2028	5572.4	50.00	Rv2754c, T
DRB1_1302	105	QRYVPEKDSRVVPP	YVPEKDSRV	0.2028	5572.9	50.00	Rv2754c, T
DRB1_1302	111	KDSRVVPPGMEDDA	RVVVPPGME	0.1985	5835.9	50.00	Rv2754c, T
DRB1_1302	137	AARATYSELLAKLEA	ARATYSELL	0.1984	5844.7	50.00	Rv2754c, T
DRB1_1302	101	SQLSQRYVPEKDSRV	YVPEKDSRV	0.1962	5986.6	50.00	Rv2754c, T
DRB1_1302	192	RHFIAMRASEHADVE	IAMRASEHA	0.1949	6068.3	50.00	Rv2754c, T
DRB1_1302	42	CYQSWKPNPKTATN	WSKPNPKTA	0.1939	6138.3	50.00	Rv2754c, T
DRB1_1302	141	TYSELLAKLEAKFAD	LLAKLEAKF	0.1931	6188.0	50.00	Rv2754c, T
DRB1_1302	106	RYVPEKDSRVVPPG	YVPEKDSRV	0.1865	6648.9	50.00	Rv2754c, T
DRB1_1302	53	TATNAGYLRHIIDV	GYLRHIIDV	0.1848	6767.5	50.00	Rv2754c, T
DRB1_1302	228	DFEVTTLADGTEVAT	TTLADGTEV	0.1844	6799.8	50.00	Rv2754c, T
DRB1_1302	43	YQSWKPNPKTATNA	WSKPNPKTA	0.1839	6839.3	50.00	Rv2754c, T
DRB1_1302	203	ADVEIRRLAIECLRQ	DVEIRRLAI	0.1838	6844.1	50.00	Rv2754c, T
DRB1_1302	112	DSRVVPPGMEDDAD	RVVVPPGME	0.1826	6935.5	50.00	Rv2754c, T
DRB1_1302	41	ACYQSWKPNPKTAT	WSKPNPKTA	0.1807	7080.1	50.00	Rv2754c, T
DRB1_1302	96	RHFSYSQLSQRYVPE	YSQLSQRYV	0.1797	7156.4	50.00	Rv2754c, T
DRB1_1302	90	HELIRHRHFSYSQLS	LIRHRHFSY	0.1776	7318.0	50.00	Rv2754c, T
DRB1_1302	139	RATYSELLAKLEAKF	LLAKLEAKF	0.1771	7356.6	50.00	Rv2754c, T
DRB1_1302	128	RHILTEAADAARATY	ILTEAADAA	0.1766	7401.0	50.00	Rv2754c, T
DRB1_1302	201	EHADVEIRRLAIECL	DVEIRRLAI	0.1765	7405.3	50.00	Rv2754c, T
DRB1_1302	91	ELIRHRHFSYSQLSQ	LIRHRHFSY	0.1760	7445.7	50.00	Rv2754c, T
DRB1_1302	142	YSELLAKLEAKFADQ	LLAKLEAKF	0.1750	7528.5	50.00	Rv2754c, T
DRB1_1302	227	ADFEVTTLADGTEVA	TTLADGTEV	0.1744	7573.6	50.00	Rv2754c, T
DRB1_1302	113	SRVVVPPGMEDDADL	RVVVPPGME	0.1743	7585.0	50.00	Rv2754c, T
DRB1_1302	44	QSWKPNPKTATNAG	WSKPNPKTA	0.1740	7611.0	50.00	Rv2754c, T
DRB1_1302	229	FEVTTLADGTEVATS	TTLADGTEV	0.1740	7612.2	50.00	Rv2754c, T
DRB1_1302	64	IDVGHFVSLEHASVS	FSVLEHASV	0.1701	7941.6	50.00	Rv2754c, T
DRB1_1302	93	IRHRHFSYSQLSQRY	SYSQLSQRY	0.1695	7989.2	50.00	Rv2754c, T
DRB1_1302	193	HFIAMRASEHADVEI	IAMRASEHA	0.1684	8083.7	50.00	Rv2754c, T
DRB1_1302	202	HADVEIRRLAIECLR	DVEIRRLAI	0.1676	8157.8	50.00	Rv2754c, T
DRB1_1302	92	LIRHRHFSYSQLSQR	LIRHRHFSY	0.1674	8176.3	50.00	Rv2754c, T
DRB1_1302	138	ARATYSELLAKLEAK	ARATYSELL	0.1645	8433.9	50.00	Rv2754c, T
DRB1_1302	199	ASEHADVEIRRLAIE	DVEIRRLAI	0.1624	8628.3	50.00	Rv2754c, T
DRB1_1302	129	HILTEAADAARATYS	ILTEAADAA	0.1600	8858.5	50.00	Rv2754c, T
DRB1_1302	226	FADFEVTTLADGTEV	TTLADGTEV	0.1586	8993.8	50.00	Rv2754c, T
DRB1_1302	230	EVTTLADGTEVATSP	TTLADGTEV	0.1580	9042.8	50.00	Rv2754c, T

DRB1_1302	194	FIAMRASEHADVEIR	IAMRASEHA	0.1566	9181.7	50.00	Rv2754c, T
DRB1_1302	89	THELIRHRHFSYSQL	LIRHRHFSY	0.1559	9258.3	50.00	Rv2754c, T
DRB1_1302	143	SELLAKLEAKFADQP	LLAKLEAKF	0.1532	9527.0	50.00	Rv2754c, T
DRB1_1302	200	SEHADVEIRRLAIEC	DVEIRRLAI	0.1528	9567.0	50.00	Rv2754c, T
DRB1_1302	76	SVSFYITGISRSCTH	TGISRSCTH	0.1523	9625.4	50.00	Rv2754c, T
DRB1_1302	114	RVVVPVPGMEDDADLR	RVVVPVPGME	0.1519	9661.3	50.00	Rv2754c, T
DRB1_1302	97	HFSYSQLSQRYVPEK	YSQLSQRYV	0.1519	9667.1	50.00	Rv2754c, T
DRB1_1302	86	RSCTHELIRHRHFSY	LIRHRHFSY	0.1513	9732.2	50.00	Rv2754c, T
DRB1_1302	87	SCTHELIRHRHFSYS	LIRHRHFSY	0.1476	10127.0	50.00	Rv2754c, T
DRB1_1302	40	RACYQSWSKPNPKTA	WSKPNPKTA	0.1476	10128.8	50.00	Rv2754c, T
DRB1_1302	198	RASEHADVEIRRLAI	DVEIRRLAI	0.1463	10272.3	50.00	Rv2754c, T
DRB1_1302	130	ILTEAADAARATYSE	ILTEAADAA	0.1435	10588.2	50.00	Rv2754c, T
DRB1_1302	88	CHELIRHRHFSYSQ	LIRHRHFSY	0.1427	10678.8	50.00	Rv2754c, T
DRB1_1302	144	ELLAKLEAKFADQPN	LLAKLEAKF	0.1404	10946.9	50.00	Rv2754c, T
DRB1_1302	184	VTGNYRAWRHFIAMR	NYRAWRHFI	0.1369	11368.4	50.00	Rv2754c, T
DRB1_1302	219	AAVAPAVFADFVTT	AAVAPAVFA	0.1362	11460.0	50.00	Rv2754c, T
DRB1_1302	98	FSYSQLSQRYVPEKD	YSQLSQRYV	0.1315	12047.2	50.00	Rv2754c, T
DRB1_1302	131	LTEAADAARATYSEL	AARATYSEL	0.1270	12649.5	50.00	Rv2754c, T
DRB1_1302	73	EHASVSFYITGISRS	SVSFYITGI	0.1266	12714.6	50.00	Rv2754c, T
DRB1_1302	75	ASVSFYITGISRSCT	SVSFYITGI	0.1244	13012.4	50.00	Rv2754c, T
DRB1_1302	27	DADGGPALVEFAGRA	ALVEFAGRA	0.1243	13022.7	50.00	Rv2754c, T
DRB1_1302	145	LLAKLEAKFADQPNA	LLAKLEAKF	0.1224	13305.8	50.00	Rv2754c, T
DRB1_1302	77	VSFYITGISRSCTHE	FYITGISRS	0.1203	13597.8	50.00	Rv2754c, T
DRB1_1302	21	DVPWTTDADGGPALV	DADGGPALV	0.1184	13883.2	50.00	Rv2754c, T
DRB1_1302	74	HASVSFYITGISRS	SVSFYITGI	0.1176	14001.5	50.00	Rv2754c, T
DRB1_1302	99	SYSQLSQRYVPEKDS	YSQLSQRYV	0.1166	14155.6	50.00	Rv2754c, T
DRB1_1302	29	DGGPALVEFAGRACY	ALVEFAGRA	0.1156	14313.0	50.00	Rv2754c, T
DRB1_1302	24	WTTDADGGPALVEFA	DADGGPALV	0.1149	14416.2	50.00	Rv2754c, T
DRB1_1302	22	VPWTTDADGGPALVE	DADGGPALV	0.1115	14956.9	50.00	Rv2754c, T
DRB1_1302	30	GGPALVEFAGRACYQ	ALVEFAGRA	0.1076	15602.1	50.00	Rv2754c, T
DRB1_1302	33	ALVEFAGRACYQSW	ALVEFAGRA	0.1072	15682.5	50.00	Rv2754c, T
DRB1_1302	23	PWTTDADGGPALVEF	DADGGPALV	0.1049	16063.7	50.00	Rv2754c, T
DRB1_1302	28	ADGGPALVEFAGRAC	ALVEFAGRA	0.1023	16527.9	50.00	Rv2754c, T
DRB1_1302	25	TTDADGGPALVEFAG	DADGGPALV	0.1009	16774.4	50.00	Rv2754c, T
DRB1_1302	195	IAMRASEHADVEIRR	IAMRASEHA	0.1001	16924.8	50.00	Rv2754c, T
DRB1_1302	10	LIAKTDFLAPPDVPW	LIAKTDFLA	0.0994	17055.5	50.00	Rv2754c, T
DRB1_1302	31	GPALVEFAGRACYQS	ALVEFAGRA	0.0957	17758.9	50.00	Rv2754c, T
DRB1_1302	32	PALVEFAGRACYQSW	ALVEFAGRA	0.0955	17798.5	50.00	Rv2754c, T
DRB1_1302	225	VFADFEVTTLADGTE	EVTTLADGT	0.0925	18377.7	50.00	Rv2754c, T
DRB1_1302	26	TDADGGPALVEFAGR	DADGGPALV	0.0919	18499.2	50.00	Rv2754c, T
DRB1_1302	100	YSQLSQRYVPEKDSR	YSQLSQRYV	0.0880	19287.8	50.00	Rv2754c, T
DRB1_1302	224	AVFADFEVTTLADGT	DFEVTTLAD	0.0835	20259.8	50.00	Rv2754c, T
DRB1_1302	34	LVEFAGRACYQSWSK	LVEFAGRAC	0.0785	21392.5	50.00	Rv2754c, T
DRB1_1302	196	AMRASEHADVEIRRL	MRASEHADV	0.0767	21816.9	50.00	Rv2754c, T
DRB1_1302	220	AVAPAVFADFVTTTL	VFADFEVTT	0.0763	21904.9	50.00	Rv2754c, T
DRB1_1302	223	PAVFADFEVTTLADG	VFADFEVTT	0.0748	22246.5	50.00	Rv2754c, T
DRB1_1302	197	MRASEHADVEIRRLA	MRASEHADV	0.0746	22300.2	50.00	Rv2754c, T
DRB1_1302	39	GRACYQSWSKPNPKT	QSWSKPNPK	0.0680	23957.9	50.00	Rv2754c, T
DRB1_1302	38	AGRACYQSWSKPNPK	QSWSKPNPK	0.0675	24095.2	50.00	Rv2754c, T
DRB1_1302	222	APAVFADFVTTLAD	VFADFEVTT	0.0673	24127.0	50.00	Rv2754c, T
DRB1_1302	115	VVVPVPGMEDDADLRH	VVVPVPGMED	0.0667	24294.4	50.00	Rv2754c, T
DRB1_1302	85	SRSCTHELIRHRHFS	HELIRHRHF	0.0640	25027.3	50.00	Rv2754c, T
DRB1_1302	11	IAKTDFLAPPDVPWT	FLAPPDVPW	0.0626	25393.9	50.00	Rv2754c, T
DRB1_1302	37	FAGRACYQSWSKPNP	RACYQSWSK	0.0617	25636.9	50.00	Rv2754c, T
DRB1_1302	36	EFAGRACYQSWSKPN	RACYQSWSK	0.0616	25676.3	50.00	Rv2754c, T
DRB1_1302	119	PGMEDDADLRHILTE	DADLRHILT	0.0609	25868.7	50.00	Rv2754c, T
DRB1_1302	221	VAPAVFADFVTTTLA	VFADFEVTT	0.0605	25976.4	50.00	Rv2754c, T
DRB1_1302	35	VEFAGRACYQSWSKP	RACYQSWSK	0.0601	26106.0	50.00	Rv2754c, T
DRB1_1302	120	GMEDDADLRHILTEA	DADLRHILT	0.0594	26303.6	50.00	Rv2754c, T
DRB1_1302	118	PPGMEDDADLRHILT	DADLRHILT	0.0539	27911.3	50.00	Rv2754c, T
DRB1_1302	117	VPPGMEDDADLRHIL	PGMEDDADL	0.0494	29312.5	50.00	Rv2754c, T
DRB1_1302	116	VVPPGMEDDADLRHI	EDDADLRHI	0.0465	30231.4	50.00	Rv2754c, T
DRB1_1302	12	AKTDFLAPPDVPWTT	FLAPPDVPW	0.0413	31970.3	50.00	Rv2754c, T
DRB1_1302	20	PDVPWTTDADGGPAL	TTDADGGPA	0.0413	31987.3	50.00	Rv2754c, T
DRB1_1302	13	KTDFLAPPDVPWTTD	FLAPPDVPW	0.0355	34060.1	50.00	Rv2754c, T
DRB1_1302	19	PPDVPWTTDADGGPA	TTDADGGPA	0.0352	34148.7	50.00	Rv2754c, T
DRB1_1302	15	DFLAPPDVPWTTDAD	FLAPPDVPW	0.0343	34510.1	50.00	Rv2754c, T
DRB1_1302	14	TDFLAPPDVPWTTDA	FLAPPDVPW	0.0337	34705.9	50.00	Rv2754c, T
DRB1_1302	16	FLAPPDVPWTTDADG	FLAPPDVPW	0.0312	35661.0	50.00	Rv2754c, T
DRB1_1302	18	APPDVPWTTDADGGP	WTTDADGGP	0.0260	37749.8	50.00	Rv2754c, T
DRB1_1302	17	LAPPDVPWTTDADGG	PDPWTTDA	0.0214	39648.7	50.00	Rv2754c, T

Allele: DRB1_1302. Number of high binders 0. Number of weak binders 33. Number of peptides 236

Allele	pos	peptide	core	l-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
DRB1_1501	181	RIVVTGNYRAWRHFI	VTGNYRAWR	0.7609	13.3	SB	0.80	Rv2754c, T
DRB1_1501	183	VVTGNYRAWRHFIAM	VTGNYRAWR	0.7559	14.0	SB	0.80	Rv2754c, T
DRB1_1501	184	TVGNYRAWRHFIAMR	VTGNYRAWR	0.7475	15.4	SB	0.80	Rv2754c, T
DRB1_1501	180	TRIVVTGNYRAWRHFI	VTGNYRAWR	0.7395	16.8	SB	0.80	Rv2754c, T
DRB1_1501	189	RAWRHFIAMRASEHA	AWRHFIAMR	0.7308	18.4	SB	0.80	Rv2754c, T
DRB1_1501	182	IVVTGNYRAWRHFIAM	VTGNYRAWR	0.7304	18.5	SB	0.80	Rv2754c, T

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DRB1_1501	188	YRAWRHFIAMRASEH	AWRHFIAMR	0.7116	22.6	SB	2.00	Rv2754c, T
DRB1_1501	190	AWRHFIAMRASEHAD	AWRHFIAMR	0.7080	23.6	SB	2.00	Rv2754c, T
DRB1_1501	179	ETRIVVTGNYRAWRH	VTGNYRAWR	0.7057	24.1	SB	2.00	Rv2754c, T
DRB1_1501	185	TGNYRAWRHFIAMRA	AWRHFIAMR	0.7012	25.4	SB	2.00	Rv2754c, T
DRB1_1501	187	NYRAWRHFIAMRASE	AWRHFIAMR	0.6849	30.2	SB	2.00	Rv2754c, T
DRB1_1501	186	GNYRAWRHFIAMRAS	AWRHFIAMR	0.6693	35.8	SB	4.00	Rv2754c, T
DRB1_1501	143	SELLAKLEAKFADQP	LLAKLEAKF	0.6522	43.1	SB	4.00	Rv2754c, T
DRB1_1501	142	YSELLAKLEAKFADQ	LLAKLEAKF	0.6516	43.4	SB	4.00	Rv2754c, T
DRB1_1501	178	TETRIVVTGNYRAWR	VVTGNYRAW	0.6488	44.7	SB	4.00	Rv2754c, T
DRB1_1501	90	HELIRHRHFSYSQLS	LIRHRHFSY	0.6469	45.6	SB	4.00	Rv2754c, T
DRB1_1501	89	THELIRHRHFSYSQL	LIRHRHFSY	0.6453	46.4	SB	4.00	Rv2754c, T
DRB1_1501	141	TYSELLAKLEAKFAD	LLAKLEAKF	0.6440	47.1	SB	4.00	Rv2754c, T
DRB1_1501	158	NAILRRKQARQAARA	AILRRKQAR	0.6359	51.4	WB	4.00	Rv2754c, T
DRB1_1501	140	ATYSELLAKLEAKFA	LLAKLEAKF	0.6355	51.6	WB	4.00	Rv2754c, T
DRB1_1501	157	PNAILRRKQARQAAR	AILRRKQAR	0.6320	53.6	WB	4.00	Rv2754c, T
DRB1_1501	91	ELIRHRHFSYSQLSQ	LIRHRHFSY	0.6245	58.1	WB	8.00	Rv2754c, T
DRB1_1501	159	AILRRKQARQAARAV	AILRRKQAR	0.6226	59.4	WB	8.00	Rv2754c, T
DRB1_1501	144	ELLAKLEAKFADQPN	LLAKLEAKF	0.6218	59.9	WB	8.00	Rv2754c, T
DRB1_1501	88	CHELIRHRHFSYSQ	LIRHRHFSY	0.6214	60.2	WB	8.00	Rv2754c, T
DRB1_1501	156	QPNAILRRKQARQAA	AILRRKQAR	0.6150	64.5	WB	8.00	Rv2754c, T
DRB1_1501	191	WRHFIAMRASEHADV	HFIAMRASE	0.6104	67.7	WB	8.00	Rv2754c, T
DRB1_1501	87	SCTHELIRHRHFSYS	LIRHRHFSY	0.5982	77.3	WB	8.00	Rv2754c, T
DRB1_1501	155	DQPNAILRRKQARQA	AILRRKQAR	0.5816	92.5	WB	8.00	Rv2754c, T
DRB1_1501	92	LIRHRHFSYSQLSQR	LIRHRHFSY	0.5773	96.9	WB	8.00	Rv2754c, T
DRB1_1501	86	RSCTHELIRHRHFSY	LIRHRHFSY	0.5758	98.5	WB	8.00	Rv2754c, T
DRB1_1501	192	RHFIAMRASEHADVE	HFIAMRASE	0.5548	123.6	WB	16.00	Rv2754c, T
DRB1_1501	139	RATYSELLAKLEAKF	LLAKLEAKF	0.5529	126.2	WB	16.00	Rv2754c, T
DRB1_1501	177	ATETRIVVTGNYRAW	IVVTGNYRA	0.5437	139.3	WB	16.00	Rv2754c, T
DRB1_1501	202	HADVEIRRLAIECLR	EIRRLAIEC	0.5400	145.1	WB	16.00	Rv2754c, T
DRB1_1501	64	IDVGHFSVLEHASVS	DVGHFSVLE	0.5386	147.3	WB	16.00	Rv2754c, T
DRB1_1501	203	ADVEIRRLAIECLRQ	EIRRLAIEC	0.5386	147.3	WB	16.00	Rv2754c, T
DRB1_1501	65	DVGHFSVLEHASVSF	DVGHFSVLE	0.5364	150.8	WB	16.00	Rv2754c, T
DRB1_1501	204	DVEIRRLAIECLRQL	EIRRLAIEC	0.5351	153.0	WB	16.00	Rv2754c, T
DRB1_1501	30	GGPALVEFAGRACYQ	ALVEFAGRA	0.5230	174.3	WB	16.00	Rv2754c, T
DRB1_1501	205	EIRRLAIECLRQLA	EIRRLAIEC	0.5184	183.2	WB	16.00	Rv2754c, T
DRB1_1501	154	ADQPNAILRRKQARQ	AILRRKQAR	0.5177	184.7	WB	16.00	Rv2754c, T
DRB1_1501	201	EHADVEIRRLAIECL	EIRRLAIEC	0.5153	189.5	WB	16.00	Rv2754c, T
DRB1_1501	31	GPALVEFAGRACYQS	ALVEFAGRA	0.5115	197.5	WB	16.00	Rv2754c, T
DRB1_1501	208	RRLAIECLRQLAAVA	CLRQLAAVA	0.5057	210.2	WB	16.00	Rv2754c, T
DRB1_1501	29	DGGPALVEFAGRACY	ALVEFAGRA	0.5000	223.7	WB	16.00	Rv2754c, T
DRB1_1501	63	IIDVGHFSVLEHASV	DVGHFSVLE	0.4990	226.0	WB	16.00	Rv2754c, T
DRB1_1501	209	RLAIECLRQLAAVAP	CLRQLAAVA	0.4983	227.9	WB	16.00	Rv2754c, T
DRB1_1501	211	AIECLRQLAAVAPAV	CLRQLAAVA	0.4974	230.0	WB	16.00	Rv2754c, T
DRB1_1501	193	HFIAMRASEHADVEI	HFIAMRASE	0.4961	233.2	WB	16.00	Rv2754c, T
DRB1_1501	32	PALVEFAGRACYQSW	ALVEFAGRA	0.4934	240.3	WB	16.00	Rv2754c, T
DRB1_1501	145	LLAKLEAKFADQPNA	LLAKLEAKF	0.4919	244.2	WB	16.00	Rv2754c, T
DRB1_1501	212	IECLRQLAAVAPAVF	CLRQLAAVA	0.4857	261.1	WB	32.00	Rv2754c, T
DRB1_1501	210	LAIECLRQLAAVAPA	CLRQLAAVA	0.4846	264.1	WB	32.00	Rv2754c, T
DRB1_1501	39	GRACYQSWSKPNPKT	RACYQSWSK	0.4825	270.1	WB	32.00	Rv2754c, T
DRB1_1501	67	VGHFSVLEHASVSFY	SVLEHASVS	0.4771	286.5	WB	32.00	Rv2754c, T
DRB1_1501	66	GHFSVLEHASVSFYI	VLEHASVSF	0.4745	294.6	WB	32.00	Rv2754c, T
DRB1_1501	62	HIIDVGHFSVLEHAS	DVGHFSVLE	0.4719	303.0	WB	32.00	Rv2754c, T
DRB1_1501	38	AGRACYQSWSKPNPK	RACYQSWSK	0.4693	311.6	WB	32.00	Rv2754c, T
DRB1_1501	213	ECLRQLAAVAPAVFA	ECLRQLAAV	0.4665	321.2	WB	32.00	Rv2754c, T
DRB1_1501	40	RACYQSWSKPNPKTA	RACYQSWSK	0.4646	328.0	WB	32.00	Rv2754c, T
DRB1_1501	33	ALVEFAGRACYQSW	ALVEFAGRA	0.4613	340.0	WB	32.00	Rv2754c, T
DRB1_1501	28	ADGGPALVEFAGRAC	ALVEFAGRA	0.4526	373.5	WB	32.00	Rv2754c, T
DRB1_1501	160	ILRRKQARQAARAVL	ILRRKQARQ	0.4482	391.6	WB	32.00	Rv2754c, T
DRB1_1501	206	EIRRLAIECLRQLAA	EIRRLAIEC	0.4433	413.0	WB	32.00	Rv2754c, T
DRB1_1501	207	IRRLAIECLRQLAAV	ECLRQLAAV	0.4430	414.3	WB	32.00	Rv2754c, T
DRB1_1501	61	RHIIDVGHFSVLEHA	DVGHFSVLE	0.4421	418.2	WB	32.00	Rv2754c, T
DRB1_1501	200	SEHADVEIRRLAIEC	VEIRRLAIE	0.4408	424.2	WB	32.00	Rv2754c, T
DRB1_1501	176	NATETRIVVTGNYRA	RIVVTGNYR	0.4380	437.2	WB	32.00	Rv2754c, T
DRB1_1501	37	FAGRACYQSWSKPNP	RACYQSWSK	0.4369	442.4	WB	32.00	Rv2754c, T
DRB1_1501	60	LRHIIDVGHFSVLEH	DVGHFSVLE	0.4277	488.9	WB	32.00	Rv2754c, T
DRB1_1501	68	HFSVLEHASVSFYIT	VLEHASVSF	0.4210	525.9	WB	32.00	Rv2754c, T
DRB1_1501	36	EFAGRACYQSWSKPN	RACYQSWSK	0.4154	558.2	WB	32.00	Rv2754c, T
DRB1_1501	153	FADQPNAILRRKQAR	AILRRKQAR	0.4152	560.0	WB	32.00	Rv2754c, T
DRB1_1501	124	DADLRHILTEAADA	DLRHILTEA	0.4092	597.1	WB	32.00	Rv2754c, T
DRB1_1501	123	DDADLRHILTEAADA	DLRHILTEA	0.4082	603.5	WB	32.00	Rv2754c, T
DRB1_1501	138	ARATYSELLAKLEAK	TYSELLAKL	0.4058	619.5	WB	32.00	Rv2754c, T
DRB1_1501	69	FSVLEHASVSFYITG	VLEHASVSF	0.4037	633.6	WB	32.00	Rv2754c, T
DRB1_1501	59	YLRHIIDVGHFSVLE	DVGHFSVLE	0.4001	658.9	WB	32.00	Rv2754c, T
DRB1_1501	70	SVLEHASVSFYITGI	VLEHASVSF	0.3989	667.6	WB	32.00	Rv2754c, T
DRB1_1501	125	ADLRHILTEAADAAR	DLRHILTEA	0.3941	703.3	WB	32.00	Rv2754c, T
DRB1_1501	1	AETAPLRVQLIAKTD	RVQLIAKTD	0.3833	790.5	WB	50.00	Rv2754c, T
DRB1_1501	122	EDDADLRHILTEAAD	DLRHILTEA	0.3812	808.8	WB	50.00	Rv2754c, T
DRB1_1501	93	IRHRHFSYSQLSQRY	IRHRHFSYS	0.3792	826.3	WB	50.00	Rv2754c, T
DRB1_1501	5	PLRVQLIAKTDFLAP	RVQLIAKTD	0.3723	890.1	WB	50.00	Rv2754c, T
DRB1_1501	4	APLRVQLIAKTDFLA	RVQLIAKTD	0.3699	914.0	WB	50.00	Rv2754c, T
DRB1_1501	6	LRVQLIAKTDFLAPP	RVQLIAKTD	0.3679	933.9	WB	50.00	Rv2754c, T
DRB1_1501	35	VEFAGRACYQSWSKP	RACYQSWSK	0.3629	985.1	WB	50.00	Rv2754c, T
DRB1_1501	121	MEDDADLRHILTEAA	DLRHILTEA	0.3610	1006.5	WB	50.00	Rv2754c, T
DRB1_1501	34	LVEFAGRACYQSWSK	RACYQSWSK	0.3603	1014.0	WB	50.00	Rv2754c, T
DRB1_1501	85	SRSCTHELIRHRHFS	ELIRHRHFS	0.3584	1035.3	WB	50.00	Rv2754c, T

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DRB1_1501	3	TAPLRVQLIAKTD	RVQLIAKTD	0.3546	1078.8	50.00	Rv2754c, T
DRB1_1501	2	ETAPLRVQLIAKTD	RVQLIAKTD	0.3532	1094.8	50.00	Rv2754c, T
DRB1_1501	71	VLEHASVSFYITGIS	VLEHASVSF	0.3504	1128.6	50.00	Rv2754c, T
DRB1_1501	214	CLRQLAAVAPAVFAD	CLRQLAAVA	0.3481	1156.9	50.00	Rv2754c, T
DRB1_1501	75	ASVSFYITGISRSC	ASVSFYITG	0.3473	1166.6	50.00	Rv2754c, T
DRB1_1501	221	VAPAVFADFEVTTLA	VFADFEVTT	0.3431	1221.0	50.00	Rv2754c, T
DRB1_1501	126	DLRHILTEAADAARA	DLRHILTEA	0.3401	1261.7	50.00	Rv2754c, T
DRB1_1501	220	AVAPAVFADFEVTTL	VFADFEVTT	0.3370	1304.7	50.00	Rv2754c, T
DRB1_1501	54	ATNAGYLRHIIDVGH	YLRHIIDVG	0.3347	1337.6	50.00	Rv2754c, T
DRB1_1501	175	PNATETRIVVTGNYS	RIVVTGNYS	0.3313	1387.0	50.00	Rv2754c, T
DRB1_1501	80	YITGISRSCHELIR	YITGISRSC	0.3304	1401.7	50.00	Rv2754c, T
DRB1_1501	41	ACYQSWSKPNPKTAT	ACYQSWSKP	0.3255	1477.1	50.00	Rv2754c, T
DRB1_1501	0	VAETAPLRVQLIAKT	ETAPLRVQL	0.3251	1483.6	50.00	Rv2754c, T
DRB1_1501	81	ITGISRSCHELIRH	GISRSCHE	0.3223	1529.0	50.00	Rv2754c, T
DRB1_1501	58	GLRHLIDVGHFVS	YLRHIIDVG	0.3215	1543.0	50.00	Rv2754c, T
DRB1_1501	74	HASVSFYITGISRSC	ASVSFYITG	0.3208	1553.9	50.00	Rv2754c, T
DRB1_1501	94	RHRHFSYSQLSQRYV	RHFSYSQLS	0.3202	1564.4	50.00	Rv2754c, T
DRB1_1501	137	AARATYSELLAKLEA	TYSELLAKL	0.3176	1608.6	50.00	Rv2754c, T
DRB1_1501	27	DADGGPALVEFAGRA	ALVEFAGRA	0.3171	1618.1	50.00	Rv2754c, T
DRB1_1501	7	RVQLIAKTDLAPPD	RVQLIAKTD	0.3125	1699.9	50.00	Rv2754c, T
DRB1_1501	55	TNAGYLRHIIDVGHF	YLRHIIDVG	0.3117	1714.4	50.00	Rv2754c, T
DRB1_1501	73	EHASVSFYITGISR	ASVSFYITG	0.3108	1731.1	50.00	Rv2754c, T
DRB1_1501	53	TATNAGYLRHIIDVG	YLRHIIDVG	0.3107	1733.9	50.00	Rv2754c, T
DRB1_1501	56	NAGYLRHIIDVGHFS	YLRHIIDVG	0.3082	1781.4	50.00	Rv2754c, T
DRB1_1501	79	FYITGISRSCHELIR	YITGISRSC	0.3081	1784.0	50.00	Rv2754c, T
DRB1_1501	76	SVSFYITGISRSCHE	VSFYITGIS	0.3062	1819.7	50.00	Rv2754c, T
DRB1_1501	78	SFYITGISRSCHELIR	YITGISRSC	0.3060	1824.9	50.00	Rv2754c, T
DRB1_1501	72	LEHASVSFYITGISR	ASVSFYITG	0.3041	1862.2	50.00	Rv2754c, T
DRB1_1501	222	APAVFADFEVTTLAD	VFADFEVTT	0.3017	1911.6	50.00	Rv2754c, T
DRB1_1501	77	VSFYITGISRSCHE	VSFYITGIS	0.2958	2038.1	50.00	Rv2754c, T
DRB1_1501	82	YITGISRSCHELIRH	GISRSCHE	0.2947	2061.1	50.00	Rv2754c, T
DRB1_1501	146	LAKLEAKFADQPNAI	KLEAKFADQ	0.2945	2066.2	50.00	Rv2754c, T
DRB1_1501	96	RHFSYSQLSQRYVPE	RHFSYSQLS	0.2937	2084.1	50.00	Rv2754c, T
DRB1_1501	219	AAVAPAVFADFEVTT	VFADFEVTT	0.2914	2137.3	50.00	Rv2754c, T
DRB1_1501	136	AARATYSELLAKLE	TYSELLAKL	0.2905	2156.3	50.00	Rv2754c, T
DRB1_1501	83	GISRSCHELIRHRH	GISRSCHE	0.2904	2160.0	50.00	Rv2754c, T
DRB1_1501	57	AGYLRHIIDVGHFVS	YLRHIIDVG	0.2902	2164.0	50.00	Rv2754c, T
DRB1_1501	95	HRHFSYSQLSQRYVP	RHFSYSQLS	0.2901	2167.4	50.00	Rv2754c, T
DRB1_1501	223	PAVFADFEVTTLADG	VFADFEVTT	0.2830	2339.4	50.00	Rv2754c, T
DRB1_1501	135	ADAARATYSELLAKL	TYSELLAKL	0.2829	2341.7	50.00	Rv2754c, T
DRB1_1501	199	ASEHADVEIRRLAIE	VEIRRLAIE	0.2820	2364.0	50.00	Rv2754c, T
DRB1_1501	194	FIAMRASEHADVEIR	FIAMRASEH	0.2796	2426.4	50.00	Rv2754c, T
DRB1_1501	169	AARAVLPNATETRIV	VLPNATETR	0.2748	2557.6	50.00	Rv2754c, T
DRB1_1501	161	LRRKQARQAARAVLP	RKQARQAAR	0.2723	2626.3	50.00	Rv2754c, T
DRB1_1501	84	ISRSCHELIRHRHF	RSCHELIR	0.2702	2687.3	50.00	Rv2754c, T
DRB1_1501	224	AVFADFEVTTLADGT	VFADFEVTT	0.2666	2795.4	50.00	Rv2754c, T
DRB1_1501	162	RKQARQAARAVLPN	QARQAARAV	0.2627	2914.9	50.00	Rv2754c, T
DRB1_1501	120	GMEDDADLRHILTEA	DLRHILTEA	0.2576	3079.9	50.00	Rv2754c, T
DRB1_1501	163	RKQARQAARAVLPNA	QARQAARAV	0.2560	3134.1	50.00	Rv2754c, T
DRB1_1501	173	VLPNATETRIVVTGN	VLPNATETR	0.2519	3275.7	50.00	Rv2754c, T
DRB1_1501	168	QARAVLPNATETRIV	VLPNATETR	0.2516	3287.5	50.00	Rv2754c, T
DRB1_1501	167	RQARAVLPNATETR	ARAVLPNAT	0.2486	3395.1	50.00	Rv2754c, T
DRB1_1501	170	ARAVLPNATETRIVV	VLPNATETR	0.2484	3401.1	50.00	Rv2754c, T
DRB1_1501	172	AVLPNATETRIVVTG	VLPNATETR	0.2435	3587.2	50.00	Rv2754c, T
DRB1_1501	171	RAVLPNATETRIVVT	VLPNATETR	0.2423	3634.5	50.00	Rv2754c, T
DRB1_1501	52	KTATNAGYLRHIIDV	NAGYLRHII	0.2362	3882.7	50.00	Rv2754c, T
DRB1_1501	97	HFSYSQLSQRYVPEK	YSQLSQRYV	0.2349	3935.5	50.00	Rv2754c, T
DRB1_1501	127	LRHILTEAADAARAT	LRHILTEAA	0.2346	3950.7	50.00	Rv2754c, T
DRB1_1501	134	AADAARATYSELLAK	AARATYSEL	0.2345	3953.8	50.00	Rv2754c, T
DRB1_1501	174	LPNATETRIVVTGNY	ETRIVVTGN	0.2344	3957.1	50.00	Rv2754c, T
DRB1_1501	148	KLEAKFADQPNAILR	KLEAKFADQ	0.2325	4038.6	50.00	Rv2754c, T
DRB1_1501	215	LRQLAAVAPAVFADF	RQLAAVAPA	0.2320	4061.7	50.00	Rv2754c, T
DRB1_1501	147	AKLEAKFADQPNAIL	KLEAKFADQ	0.2288	4205.8	50.00	Rv2754c, T
DRB1_1501	164	KQARQAARAVLPNAT	QARQAARAV	0.2275	4267.5	50.00	Rv2754c, T
DRB1_1501	98	FSYSQLSQRYVPEKD	YSQLSQRYV	0.2224	4506.5	50.00	Rv2754c, T
DRB1_1501	105	QRYVPEKDSRVVPP	RYVPEKDSR	0.2208	4586.9	50.00	Rv2754c, T
DRB1_1501	8	VQLIAKTDLAPPDV	AKTDFLAPP	0.2203	4610.1	50.00	Rv2754c, T
DRB1_1501	106	RYVPEKDSRVVPPG	RYVPEKDSR	0.2195	4652.2	50.00	Rv2754c, T
DRB1_1501	166	ARQAARAVLPNATET	AVLPNATET	0.2162	4821.7	50.00	Rv2754c, T
DRB1_1501	101	SQLSQRYVPEKDSRV	LSQRYVPEK	0.2130	4989.4	50.00	Rv2754c, T
DRB1_1501	42	CYQSWSKPNPKTATN	CYQSWSKPN	0.2118	5055.4	50.00	Rv2754c, T
DRB1_1501	165	QARQAARAVLPNATE	QARQAARAV	0.2115	5073.4	50.00	Rv2754c, T
DRB1_1501	218	LAAVAPAVFADFEVT	AVFADFEVT	0.2113	5081.7	50.00	Rv2754c, T
DRB1_1501	102	QLSQRYVPEKDSRVV	LSQRYVPEK	0.2104	5130.6	50.00	Rv2754c, T
DRB1_1501	9	QLIAKTDLAPPDVP	AKTDFLAPP	0.2072	5313.9	50.00	Rv2754c, T
DRB1_1501	99	SYSQLSQRYVPEKDS	SYSQLSQRY	0.2030	5563.1	50.00	Rv2754c, T
DRB1_1501	225	VFADFEVTTLADGTE	VFADFEVTT	0.1982	5856.0	50.00	Rv2754c, T
DRB1_1501	103	LSQRYVPEKDSRVVV	RYVPEKDSR	0.1979	5874.7	50.00	Rv2754c, T
DRB1_1501	100	YSQLSQRYVPEKDSR	LSQRYVPEK	0.1968	5944.3	50.00	Rv2754c, T
DRB1_1501	235	ADGTEVATSPLATEA	TEVATSPLA	0.1958	6010.8	50.00	Rv2754c, T
DRB1_1501	104	SQRYVPEKDSRVVPP	RYVPEKDSR	0.1928	6210.8	50.00	Rv2754c, T
DRB1_1501	216	RQLAAVAPAVFADFE	RQLAAVAPA	0.1899	6407.9	50.00	Rv2754c, T
DRB1_1501	11	IAKTDFLAPPDVPWT	AKTDFLAPP	0.1891	6461.9	50.00	Rv2754c, T
DRB1_1501	51	PKTATNAGYLRHIID	ATNAGYLRH	0.1881	6536.2	50.00	Rv2754c, T
DRB1_1501	133	EAADAARATYSELLA	AADAARATY	0.1848	6767.0	50.00	Rv2754c, T

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DRB1_1501	149	LEAKFADQPNAILRR	KFADQPNAI	0.1843	6808.3	50.00	Rv2754c, T
DRB1_1501	10	LIAKTDFLAPPDVPW	AKTDFLAPP	0.1816	7010.1	50.00	Rv2754c, T
DRB1_1501	50	NPKTATNAGYLRHI	ATNAGYLRH	0.1808	7072.6	50.00	Rv2754c, T
DRB1_1501	12	AKTDFLAPPDVPWTT	AKTDFLAPP	0.1769	7370.5	50.00	Rv2754c, T
DRB1_1501	195	IAMRASEHADVEIRR	IAMRASEHA	0.1615	8711.6	50.00	Rv2754c, T
DRB1_1501	107	YVPEKDSRVVPPGPM	EKDSRVVVP	0.1605	8806.0	50.00	Rv2754c, T
DRB1_1501	198	RASEHADVEIRRLAI	DVEIRRLAI	0.1551	9338.9	50.00	Rv2754c, T
DRB1_1501	132	TEAADAARATYSELL	AADAARATY	0.1549	9359.5	50.00	Rv2754c, T
DRB1_1501	150	EAKFADQPNAILRRK	KFADQPNAI	0.1506	9804.1	50.00	Rv2754c, T
DRB1_1501	128	RHILTEAADAARATY	HILTEAADA	0.1488	9995.5	50.00	Rv2754c, T
DRB1_1501	217	QLAAVAPAVFADFV	QLAAVAPAV	0.1484	10037.8	50.00	Rv2754c, T
DRB1_1501	49	PNPKTATNAGYLRHI	ATNAGYLRH	0.1463	10271.8	50.00	Rv2754c, T
DRB1_1501	152	KFADQPNAILRRKQA	NAILRRKQA	0.1436	10578.5	50.00	Rv2754c, T
DRB1_1501	129	HILTEAADAARATYS	HILTEAADA	0.1435	10580.3	50.00	Rv2754c, T
DRB1_1501	108	VPEKDSRVVPPGME	EKDSRVVVP	0.1416	10804.5	50.00	Rv2754c, T
DRB1_1501	229	FEVTTLADGTEVATS	EVTTLADGT	0.1396	11044.9	50.00	Rv2754c, T
DRB1_1501	119	PGMEDDADLRHILTE	ADLRHILTE	0.1385	11169.0	50.00	Rv2754c, T
DRB1_1501	131	LTEAADAARATYSEL	AADAARATY	0.1383	11195.7	50.00	Rv2754c, T
DRB1_1501	48	KPNPKTATNAGYLRH	ATNAGYLRH	0.1354	11553.4	50.00	Rv2754c, T
DRB1_1501	151	AKFADQPNAILRRKQ	KFADQPNAI	0.1338	11756.6	50.00	Rv2754c, T
DRB1_1501	234	LADGTEVATSPLATE	TEVATSPLA	0.1322	11962.9	50.00	Rv2754c, T
DRB1_1501	230	EVTTLADGTEVATSP	EVTTLADGT	0.1298	12279.1	50.00	Rv2754c, T
DRB1_1501	228	FEVTTLADGTEVAT	EVTTLADGT	0.1273	12606.5	50.00	Rv2754c, T
DRB1_1501	226	FADFVTTLADGTEV	EVTTLADGT	0.1265	12720.3	50.00	Rv2754c, T
DRB1_1501	227	ADFVTTLADGTEVA	EVTTLADGT	0.1251	12919.5	50.00	Rv2754c, T
DRB1_1501	233	TLADGTEVATSPLAT	TLADGTEVA	0.1247	12966.0	50.00	Rv2754c, T
DRB1_1501	130	ILTEAADAARATYSE	ILTEAADAA	0.1176	14002.7	50.00	Rv2754c, T
DRB1_1501	232	TTLADGTEVATSPLA	TLADGTEVA	0.1167	14138.0	50.00	Rv2754c, T
DRB1_1501	196	AMRASEHADVEIRRL	AMRASEHAD	0.1134	14651.2	50.00	Rv2754c, T
DRB1_1501	109	PEKDSRVVPPGMED	EKDSRVVVP	0.1123	14833.8	50.00	Rv2754c, T
DRB1_1501	231	VTTLADGTEVATSPL	TLADGTEVA	0.1057	15936.6	50.00	Rv2754c, T
DRB1_1501	13	KTDFLAPPDVPWTTD	DFLAPPDVP	0.1055	15964.1	50.00	Rv2754c, T
DRB1_1501	15	DFLAPPDVPWTTDAD	DFLAPPDVP	0.1055	15968.6	50.00	Rv2754c, T
DRB1_1501	14	TDFLAPPDVPWTTDA	DFLAPPDVP	0.1024	16506.3	50.00	Rv2754c, T
DRB1_1501	26	TDADGGPALVEFAGR	PALVEFAGR	0.0994	17055.3	50.00	Rv2754c, T
DRB1_1501	110	EKDSRVVPPGMEDD	EKDSRVVVP	0.0978	17354.4	50.00	Rv2754c, T
DRB1_1501	118	PPGMEDDADLRHILT	GMEDDADLR	0.0940	18091.7	50.00	Rv2754c, T
DRB1_1501	43	YQSWSKPNPKTATNA	YQSWSKPNP	0.0933	18215.6	50.00	Rv2754c, T
DRB1_1501	117	VPPGMEDDADLRHIL	GMEDDADLR	0.0916	18559.2	50.00	Rv2754c, T
DRB1_1501	44	QSWSKPNPKTATNAG	SWSKPNPKT	0.0856	19800.3	50.00	Rv2754c, T
DRB1_1501	46	WSKPNPKTATNAGYL	KTATNAGYL	0.0855	19823.9	50.00	Rv2754c, T
DRB1_1501	45	SWSKPNPKTATNAGY	SWSKPNPKT	0.0846	20012.7	50.00	Rv2754c, T
DRB1_1501	47	SKPNPKTATNAGYLR	TATNAGYLR	0.0819	20620.7	50.00	Rv2754c, T
DRB1_1501	16	FLAPPDVPWTTDADG	DVPWTTDAD	0.0810	20809.2	50.00	Rv2754c, T
DRB1_1501	116	VVPPGMEDDADLRHI	GMEDDADLR	0.0801	21021.2	50.00	Rv2754c, T
DRB1_1501	17	LAPPDVPWTTDADGG	DVPWTTDAD	0.0744	22345.2	50.00	Rv2754c, T
DRB1_1501	115	VVVPPGMEDDADLRH	GMEDDADLR	0.0732	22651.6	50.00	Rv2754c, T
DRB1_1501	114	RVVVPPGMEDDADLR	GMEDDADLR	0.0729	22722.8	50.00	Rv2754c, T
DRB1_1501	197	MRASEHADVEIRRLA	EHADVEIRR	0.0722	22883.4	50.00	Rv2754c, T
DRB1_1501	111	KDSRVVPPGMEDDA	KDSRVVPP	0.0704	23349.6	50.00	Rv2754c, T
DRB1_1501	112	DSRVVPPGMEDDAD	DSRVVPP	0.0611	25819.8	50.00	Rv2754c, T
DRB1_1501	113	SRVVVPPGMEDDADL	RVVVPPGME	0.0602	26080.6	50.00	Rv2754c, T
DRB1_1501	25	TTDADGGPALVEFAG	TTDADGGPA	0.0548	27626.2	50.00	Rv2754c, T
DRB1_1501	20	DVPWTTDADGGPAL	DVPWTTDAD	0.0548	27627.1	50.00	Rv2754c, T
DRB1_1501	18	APPDVPWTTDADGGP	DVPWTTDAD	0.0530	28171.3	50.00	Rv2754c, T
DRB1_1501	19	PPDVPWTTDADGGPA	DVPWTTDAD	0.0525	28326.3	50.00	Rv2754c, T
DRB1_1501	24	WTTDADGGPALVEFA	TTDADGGPA	0.0503	29014.9	50.00	Rv2754c, T
DRB1_1501	21	DVPWTTDADGGPALV	DVPWTTDAD	0.0470	30083.6	50.00	Rv2754c, T
DRB1_1501	23	PWTDDADGGPALVEF	TDADGGPAL	0.0417	31833.3	50.00	Rv2754c, T
DRB1_1501	22	VPWTTDADGGPALVE	TDADGGPAL	0.0332	34916.8	50.00	Rv2754c, T

Allele: DRB1_1501. Number of high binders 18. Number of weak binders 53. Number of peptides 236

Allele	pos	peptide	core 1-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
DRB3_0101	56	NAGYLRHIIDVGHFS	HIIDVGHFS	0.4874	256.1	WB	4.00 Rv2754c, T
DRB3_0101	57	AGYLRHIIDVGHFSV	HIIDVGHFS	0.4674	318.4	WB	4.00 Rv2754c, T
DRB3_0101	58	GYLRHIIDVGHFSVL	HIIDVGHFS	0.4619	337.6	WB	4.00 Rv2754c, T
DRB3_0101	59	YLRHIIDVGHFSVLE	HIIDVGHFS	0.4215	523.0		8.00 Rv2754c, T
DRB3_0101	60	LRHIIDVGHFSVLEH	HIIDVGHFS	0.3944	700.8		8.00 Rv2754c, T
DRB3_0101	61	RHIIDVGHFSVLEHA	HIIDVGHFS	0.3641	973.0		16.00 Rv2754c, T
DRB3_0101	147	AKLEAKFADQPNAIL	KFADQPNAI	0.3531	1095.8		16.00 Rv2754c, T
DRB3_0101	148	KLEAKFADQPNAILR	KFADQPNAI	0.3432	1219.3		16.00 Rv2754c, T
DRB3_0101	62	HIIDVGHFSVLEHAS	HIIDVGHFS	0.3244	1494.5		16.00 Rv2754c, T
DRB3_0101	67	GHFSVLEHASVSFYI	LEHASVSFY	0.3238	1505.1		16.00 Rv2754c, T
DRB3_0101	149	LEAKFADQPNAILRR	KFADQPNAI	0.3220	1534.2		16.00 Rv2754c, T
DRB3_0101	68	HFSVLEHASVSFYIT	LEHASVSFY	0.3213	1545.1		16.00 Rv2754c, T
DRB3_0101	66	VGHFSVLEHASVSFY	LEHASVSFY	0.3159	1639.1		16.00 Rv2754c, T
DRB3_0101	204	DVEIRRLAIEICLRQL	LAIEICLRQL	0.3046	1851.2		16.00 Rv2754c, T
DRB3_0101	150	EAKFADQPNAILRRK	KFADQPNAI	0.3016	1913.2		16.00 Rv2754c, T
DRB3_0101	117	VPPGMEDDADLRHIL	DDADLRHIL	0.2994	1959.9		16.00 Rv2754c, T
DRB3_0101	69	FSVLEHASVSFYITG	LEHASVSFY	0.2981	1987.9		16.00 Rv2754c, T

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DRB3_0101	205	VEIRRLAIECLRQLA	LAIECLRQL	0.2963	2025.4	16.00	Rv2754c, T
DRB3_0101	151	AKFADQPNAILRRKQ	KFADQPNAI	0.2909	2147.7	32.00	Rv2754c, T
DRB3_0101	118	PPGMEDDADLRHIL	DDADLRHIL	0.2900	2169.7	32.00	Rv2754c, T
DRB3_0101	206	EIRRLAIECLRQLAA	LAIECLRQL	0.2858	2268.7	32.00	Rv2754c, T
DRB3_0101	119	PGMEDDADLRHILTE	DDADLRHIL	0.2824	2354.0	32.00	Rv2754c, T
DRB3_0101	207	IRRLAIECLRQLAAV	LAIECLRQL	0.2821	2361.8	32.00	Rv2754c, T
DRB3_0101	79	FYITGISRSCSTHELI	ISRSCSTHEL	0.2808	2396.5	32.00	Rv2754c, T
DRB3_0101	92	LIRHRHFSYSQLSQR	FSYSQLSQR	0.2807	2398.2	32.00	Rv2754c, T
DRB3_0101	70	SVLEHASVSYFYITGI	LEHASVSYFY	0.2803	2408.3	32.00	Rv2754c, T
DRB3_0101	146	LAKLEAKFADQPNAI	KFADQPNAI	0.2798	2421.3	32.00	Rv2754c, T
DRB3_0101	152	KFADQPNAILRRKQA	KFADQPNAI	0.2791	2439.3	32.00	Rv2754c, T
DRB3_0101	78	SFYITGISRSCSTHEL	ISRSCSTHEL	0.2787	2450.7	32.00	Rv2754c, T
DRB3_0101	208	RRLAIECLRQLAAVA	LAIECLRQL	0.2764	2514.1	32.00	Rv2754c, T
DRB3_0101	80	YITGISRSCSTHELIR	ISRSCSTHEL	0.2718	2641.3	32.00	Rv2754c, T
DRB3_0101	93	IRHRHFSYSQLSQRY	FSYSQLSQR	0.2703	2685.7	32.00	Rv2754c, T
DRB3_0101	209	RLAIECLRQLAAVAP	LAIECLRQL	0.2690	2723.2	32.00	Rv2754c, T
DRB3_0101	81	ITGISRSCSTHELIRH	ISRSCSTHEL	0.2684	2740.8	32.00	Rv2754c, T
DRB3_0101	71	VLEHASVSYFYITGSI	LEHASVSYFY	0.2681	2747.8	32.00	Rv2754c, T
DRB3_0101	120	GMEDDADLRHILTEA	GMEDDADLR	0.2634	2892.4	32.00	Rv2754c, T
DRB3_0101	94	RHRHFSYSQLSQRVY	FSYSQLSQR	0.2606	2982.3	32.00	Rv2754c, T
DRB3_0101	72	LEHASVSYFYITGISR	LEHASVSYFY	0.2577	3075.2	32.00	Rv2754c, T
DRB3_0101	82	TGISRSCSTHELIRHR	ISRSCSTHEL	0.2576	3081.2	32.00	Rv2754c, T
DRB3_0101	83	GISRSCSTHELIRHRH	ISRSCSTHEL	0.2567	3110.0	32.00	Rv2754c, T
DRB3_0101	210	LAIECLRQLAAVAPA	LAIECLRQL	0.2560	3134.7	32.00	Rv2754c, T
DRB3_0101	103	LSQRYVPEKDSRVVV	YVPEKDSRV	0.2506	3321.9	32.00	Rv2754c, T
DRB3_0101	31	GPALVEFAGRACYQS	FAGRACYQS	0.2478	3422.7	32.00	Rv2754c, T
DRB3_0101	84	ISRSCSTHELIRHRHF	ISRSCSTHEL	0.2429	3611.7	32.00	Rv2754c, T
DRB3_0101	32	PALVEFAGRACYQSW	FAGRACYQS	0.2407	3696.8	32.00	Rv2754c, T
DRB3_0101	95	HRHFSYSQLSQRVVP	FSYSQLSQR	0.2397	3738.3	32.00	Rv2754c, T
DRB3_0101	104	SQRYVPEKDSRVVVP	YVPEKDSRV	0.2361	3884.7	32.00	Rv2754c, T
DRB3_0101	33	ALVEFAGRACYQSW	FAGRACYQS	0.2314	4089.6	32.00	Rv2754c, T
DRB3_0101	223	PAVFADFEVTTLDAG	FEVTTLDAG	0.2292	4187.3	32.00	Rv2754c, T
DRB3_0101	105	QRYVPEKDSRVVPPP	YVPEKDSRV	0.2257	4348.1	32.00	Rv2754c, T
DRB3_0101	220	AVAPAVFADFEVTTL	VFADFEVTT	0.2244	4411.9	32.00	Rv2754c, T
DRB3_0101	101	LSQRYVPEKDSRVV	YVPEKDSRV	0.2236	4450.5	32.00	Rv2754c, T
DRB3_0101	96	RHFSYSQLSQRVPE	FSYSQLSQR	0.2234	4457.3	32.00	Rv2754c, T
DRB3_0101	53	TATNAGYLRHIIDVG	YLRHIIDVG	0.2187	4693.1	32.00	Rv2754c, T
DRB3_0101	221	VAPAVFADFEVTTLA	VFADFEVTT	0.2183	4711.9	32.00	Rv2754c, T
DRB3_0101	34	LVEFAGRACYQSWSK	FAGRACYQS	0.2181	4720.8	32.00	Rv2754c, T
DRB3_0101	219	AAVAPAVFADFEVTT	VFADFEVTT	0.2174	4759.1	32.00	Rv2754c, T
DRB3_0101	102	QLSQRYVPEKDSRVV	YVPEKDSRV	0.2173	4761.5	32.00	Rv2754c, T
DRB3_0101	74	HASVSYFYITGISRSC	FYITGISRS	0.2172	4766.0	32.00	Rv2754c, T
DRB3_0101	224	AVFADFEVTTLDAGT	VFADFEVTT	0.2161	4825.0	32.00	Rv2754c, T
DRB3_0101	181	RIVVTGNRAWRHFI	NYRAWRHFI	0.2156	4853.9	32.00	Rv2754c, T
DRB3_0101	106	RYVPEKDSRVVPPG	YVPEKDSRV	0.2150	4884.7	32.00	Rv2754c, T
DRB3_0101	63	IIDVGHFSVLEHASV	FSVLEHASV	0.2131	4986.1	32.00	Rv2754c, T
DRB3_0101	35	VEFAGRACYQSWSKP	FAGRACYQS	0.2117	5061.4	32.00	Rv2754c, T
DRB3_0101	97	HFSYSQLSQRVPEK	FSYSQLSQR	0.2091	5207.5	32.00	Rv2754c, T
DRB3_0101	73	EHASVSYFYITGISRS	FYITGISRS	0.2085	5241.6	32.00	Rv2754c, T
DRB3_0101	123	DDADLRHILTEAADA	DDADLRHIL	0.2073	5308.9	32.00	Rv2754c, T
DRB3_0101	55	TNAGYLRHIIDVGHF	YLRHIIDVG	0.2068	5337.6	50.00	Rv2754c, T
DRB3_0101	54	ATNAGYLRHIIDVGH	YLRHIIDVG	0.2046	5465.7	50.00	Rv2754c, T
DRB3_0101	116	VVPPGMEDDADLRHI	GMEDDADLR	0.2024	5599.1	50.00	Rv2754c, T
DRB3_0101	64	IDVGHFSVLEHASVS	FSVLEHASV	0.2022	5606.9	50.00	Rv2754c, T
DRB3_0101	36	EFAGRACYQSWSKPN	FAGRACYQS	0.2019	5626.5	50.00	Rv2754c, T
DRB3_0101	75	ASVSYFYITGISRSC	FYITGISRS	0.2004	5717.4	50.00	Rv2754c, T
DRB3_0101	37	FAGRACYQSWSKPNP	FAGRACYQS	0.2004	5721.8	50.00	Rv2754c, T
DRB3_0101	225	VFADFEVTTLDAGTE	VFADFEVTT	0.1993	5787.6	50.00	Rv2754c, T
DRB3_0101	121	MEDDADLRHILTEAA	DDADLRHIL	0.1984	5846.6	50.00	Rv2754c, T
DRB3_0101	115	VVPPGMEDDADLRH	GMEDDADLR	0.1969	5942.0	50.00	Rv2754c, T
DRB3_0101	222	APAVFADFEVTTLD	VFADFEVTT	0.1953	6042.7	50.00	Rv2754c, T
DRB3_0101	182	IVVTGNRAWRHFI	NYRAWRHFI	0.1934	6169.2	50.00	Rv2754c, T
DRB3_0101	107	YVPEKDSRVVPPGM	YVPEKDSRV	0.1930	6194.5	50.00	Rv2754c, T
DRB3_0101	76	SVSFYITGISRSCSTH	FYITGISRS	0.1875	6572.0	50.00	Rv2754c, T
DRB3_0101	114	RVVPPGMEDDADLR	GMEDDADLR	0.1875	6572.3	50.00	Rv2754c, T
DRB3_0101	98	FSYSQLSQRVPEK	FSYSQLSQR	0.1875	6576.7	50.00	Rv2754c, T
DRB3_0101	65	DVGHFSVLEHASVSF	FSVLEHASV	0.1852	6743.6	50.00	Rv2754c, T
DRB3_0101	183	VVTGNRAWRRHFIAM	NYRAWRHFI	0.1846	6787.9	50.00	Rv2754c, T
DRB3_0101	124	DADLRHILTEAADA	ILTEAADA	0.1833	6883.6	50.00	Rv2754c, T
DRB3_0101	125	ADLRHILTEAADAAR	ILTEAADA	0.1800	7134.0	50.00	Rv2754c, T
DRB3_0101	12	AKTDFLAPPDVPWTT	FLAPPDVPW	0.1793	7181.6	50.00	Rv2754c, T
DRB3_0101	218	LAAPAVFADFEVTT	LAAPAVFAD	0.1784	7256.1	50.00	Rv2754c, T
DRB3_0101	122	EDDADLRHILTEAAD	DDADLRHIL	0.1781	7279.0	50.00	Rv2754c, T
DRB3_0101	153	FADQPNAILRRKQAR	FADQPNAIL	0.1754	7492.3	50.00	Rv2754c, T
DRB3_0101	215	LRQLAAVAPAVFADF	LAAPAVFAD	0.1714	7827.8	50.00	Rv2754c, T
DRB3_0101	77	VSYFYITGISRSCSTH	FYITGISRS	0.1703	7920.5	50.00	Rv2754c, T
DRB3_0101	14	TDFLAPPDVPWTTDA	FLAPPDVPW	0.1691	8026.5	50.00	Rv2754c, T
DRB3_0101	191	WRHFIAMRASEHADV	FIAMRASEH	0.1688	8053.2	50.00	Rv2754c, T
DRB3_0101	13	KTDFLAPPDVPWTTD	FLAPPDVPW	0.1686	8064.8	50.00	Rv2754c, T
DRB3_0101	212	IECLRQLAAVAPAVF	LAAPAVFAD	0.1677	8147.6	50.00	Rv2754c, T
DRB3_0101	127	LRHILTEAADAARAT	ILTEAADA	0.1671	8199.5	50.00	Rv2754c, T
DRB3_0101	216	QLAAVAPAVFADFE	LAAPAVFAD	0.1671	8203.5	50.00	Rv2754c, T
DRB3_0101	126	DLRHILTEAADAARA	ILTEAADA	0.1670	8209.1	50.00	Rv2754c, T
DRB3_0101	184	VTGNRAWRRHFIAMR	NYRAWRHFI	0.1666	8244.0	50.00	Rv2754c, T
DRB3_0101	15	DFLAPPDVPWTTDAD	FLAPPDVPW	0.1644	8438.9	50.00	Rv2754c, T

DRB3_0101	4	APLRVQLIAKTDFLA	VQLIAKTDF	0.1632	8554.2	50.00	Rv2754c, T
DRB3_0101	226	FADFEVTTLADGTEV	FEVTTLADG	0.1625	8616.3	50.00	Rv2754c, T
DRB3_0101	188	YRAWRHFIAMRASEH	FIAMRASEH	0.1625	8616.9	50.00	Rv2754c, T
DRB3_0101	185	TGNYRAWRHFIAMRA	NYRAWRHF	0.1620	8665.1	50.00	Rv2754c, T
DRB3_0101	192	RHFIAMRASEHADVE	FIAMRASEH	0.1618	8684.5	50.00	Rv2754c, T
DRB3_0101	217	QLAAVAPAVFADFEV	LAAVAPAVF	0.1604	8812.7	50.00	Rv2754c, T
DRB3_0101	213	ECLRQLAAVAPAVFA	LAAVAPAVF	0.1601	8843.5	50.00	Rv2754c, T
DRB3_0101	3	TAPLRVQLIAKTDFL	VQLIAKTDF	0.1598	8876.9	50.00	Rv2754c, T
DRB3_0101	189	RAWRHFIAMRASEHA	FIAMRASEH	0.1596	8891.4	50.00	Rv2754c, T
DRB3_0101	190	AWRHFIAMRASEHAD	FIAMRASEH	0.1593	8925.5	50.00	Rv2754c, T
DRB3_0101	16	FLAPPDVPWTTDADG	FLAPPDVPW	0.1592	8934.0	50.00	Rv2754c, T
DRB3_0101	193	HFIAMRASEHADVEI	FIAMRASEH	0.1588	8971.9	50.00	Rv2754c, T
DRB3_0101	11	IAKTDFLAPPDVPWT	FLAPPDVPW	0.1557	9273.9	50.00	Rv2754c, T
DRB3_0101	214	CLRQLAAVAPAVFAD	LAAVAPAVF	0.1548	9364.1	50.00	Rv2754c, T
DRB3_0101	194	FIAMRASEHADVEIR	FIAMRASEH	0.1542	9425.2	50.00	Rv2754c, T
DRB3_0101	128	RHILTEAADAARATY	ILTEAADAA	0.1522	9635.4	50.00	Rv2754c, T
DRB3_0101	10	LIAKTDFLAPPDVPW	FLAPPDVPW	0.1521	9641.4	50.00	Rv2754c, T
DRB3_0101	52	KTATNAGYLRHIIDV	GYLRHIIDV	0.1518	9676.3	50.00	Rv2754c, T
DRB3_0101	5	PLRVQLIAKTDFLAP	VQLIAKTDF	0.1516	9696.5	50.00	Rv2754c, T
DRB3_0101	186	GNYRAWRHFIAMRAS	NYRAWRHF	0.1515	9703.0	50.00	Rv2754c, T
DRB3_0101	2	ETAPLRVQLIAKTDF	VQLIAKTDF	0.1513	9725.8	50.00	Rv2754c, T
DRB3_0101	227	ADFEVTTLADGTEVA	FEVTTLADG	0.1486	10016.2	50.00	Rv2754c, T
DRB3_0101	129	HILTEAADAARATYS	ILTEAADAA	0.1480	10076.5	50.00	Rv2754c, T
DRB3_0101	6	LRVQLIAKTDFLAPP	VQLIAKTDF	0.1479	10095.8	50.00	Rv2754c, T
DRB3_0101	20	PDVPWTTDADGGPAL	TDADGGPAL	0.1458	10325.6	50.00	Rv2754c, T
DRB3_0101	228	DFEVTTLADGTEVAT	FEVTTLADG	0.1439	10540.8	50.00	Rv2754c, T
DRB3_0101	187	NYRAWRHFIAMRASE	NYRAWRHF	0.1391	11100.8	50.00	Rv2754c, T
DRB3_0101	197	MRASEHADVEIRRLA	MRASEHADV	0.1333	11819.2	50.00	Rv2754c, T
DRB3_0101	21	DVPWTTDADGGPALV	TDADGGPAL	0.1322	11959.3	50.00	Rv2754c, T
DRB3_0101	7	RVQLIAKTDFLAPPD	VQLIAKTDF	0.1293	12341.7	50.00	Rv2754c, T
DRB3_0101	90	HELIRHRHFSYSQLS	LIRHRHFSY	0.1283	12472.6	50.00	Rv2754c, T
DRB3_0101	8	VQLIAKTDFLAPPDV	VQLIAKTDF	0.1276	12572.2	50.00	Rv2754c, T
DRB3_0101	229	FEVTTLADGTEVATS	FEVTTLADG	0.1260	12795.6	50.00	Rv2754c, T
DRB3_0101	0	VAETAPLRVQLIAKT	LRVQLIAKT	0.1247	12970.2	50.00	Rv2754c, T
DRB3_0101	91	ELIRHRHFSYSQLSQ	LIRHRHFSY	0.1221	13348.4	50.00	Rv2754c, T
DRB3_0101	18	APPDVPWTTDADGGP	WTTDADGGP	0.1218	13383.8	50.00	Rv2754c, T
DRB3_0101	109	PEKDSRVVPPGMED	PEKDSRVVV	0.1192	13762.1	50.00	Rv2754c, T
DRB3_0101	108	VPEKDSRVVPPGME	PEKDSRVVV	0.1186	13864.3	50.00	Rv2754c, T
DRB3_0101	195	IAMRASEHADVEIRR	MRASEHADV	0.1184	13880.2	50.00	Rv2754c, T
DRB3_0101	176	NATETRIVVTGNYRA	TRIVVTGNY	0.1181	13925.6	50.00	Rv2754c, T
DRB3_0101	177	ATETRIVVTGNYRAW	TRIVVTGNY	0.1158	14280.7	50.00	Rv2754c, T
DRB3_0101	1	AETAPLRVQLIAKTD	LRVQLIAKT	0.1120	14874.8	50.00	Rv2754c, T
DRB3_0101	178	TETRIVVTGNYRAWR	TRIVVTGNY	0.1105	15119.5	50.00	Rv2754c, T
DRB3_0101	86	RSCTHELIRHRHFSY	LIRHRHFSY	0.1094	15300.0	50.00	Rv2754c, T
DRB3_0101	17	LAPPDVPWTTDADGG	APPDVPWTT	0.1090	15370.8	50.00	Rv2754c, T
DRB3_0101	22	VPWTTDADGGPALVE	TDADGGPAL	0.1085	15458.1	50.00	Rv2754c, T
DRB3_0101	175	PNATETRIVVTGNYR	TRIVVTGNY	0.1073	15651.3	50.00	Rv2754c, T
DRB3_0101	174	LPNATETRIVVTGNY	TRIVVTGNY	0.1068	15743.0	50.00	Rv2754c, T
DRB3_0101	196	AMRASEHADVEIRRL	MRASEHADV	0.1067	15758.7	50.00	Rv2754c, T
DRB3_0101	19	PPDVPWTTDADGGPA	WTTDADGGP	0.1064	15812.0	50.00	Rv2754c, T
DRB3_0101	179	ETRIVVTGNYRAWRH	TRIVVTGNY	0.1062	15843.3	50.00	Rv2754c, T
DRB3_0101	87	SCTHELIRHRHFSYS	LIRHRHFSY	0.1046	16127.5	50.00	Rv2754c, T
DRB3_0101	198	RASEHADVEIRRLAI	ADVEIRRLA	0.1038	16268.4	50.00	Rv2754c, T
DRB3_0101	89	THELIRHRHFSYSQL	LIRHRHFSY	0.1030	16412.4	50.00	Rv2754c, T
DRB3_0101	202	HADVEIRRLAIECLR	ADVEIRRLA	0.1024	16507.9	50.00	Rv2754c, T
DRB3_0101	180	TRIVVTGNYRAWRHF	TRIVVTGNY	0.1019	16593.5	50.00	Rv2754c, T
DRB3_0101	23	PWTTDADGGPALVEF	TDADGGPAL	0.1018	16610.6	50.00	Rv2754c, T
DRB3_0101	130	ILTEAADAARATYSE	ILTEAADAA	0.1015	16677.2	50.00	Rv2754c, T
DRB3_0101	9	QLIAKTDFLAPPDVP	LIAKTDFLA	0.0991	17119.3	50.00	Rv2754c, T
DRB3_0101	211	AIECLRQLAAVAPAV	QLAAVAPAV	0.0971	17482.6	50.00	Rv2754c, T
DRB3_0101	88	CTHELIRHRHFSYSQ	LIRHRHFSY	0.0970	17502.1	50.00	Rv2754c, T
DRB3_0101	203	ADVEIRRLAIECLRQ	ADVEIRRLA	0.0967	17561.3	50.00	Rv2754c, T
DRB3_0101	170	ARAVLPNATETRIVV	NATETRIVV	0.0925	18370.6	50.00	Rv2754c, T
DRB3_0101	51	PKTATNAGYLRHIID	TATNAGYLR	0.0915	18569.2	50.00	Rv2754c, T
DRB3_0101	171	RAVLPNATETRIVVT	NATETRIVV	0.0891	19068.2	50.00	Rv2754c, T
DRB3_0101	50	NPKTATNAGYLRHII	TATNAGYLR	0.0879	19321.4	50.00	Rv2754c, T
DRB3_0101	199	ASEHADVEIRRLAIE	ADVEIRRLA	0.0877	19363.7	50.00	Rv2754c, T
DRB3_0101	24	WTTDADGGPALVEFA	TDADGGPAL	0.0871	19481.6	50.00	Rv2754c, T
DRB3_0101	29	DGGPALVEFAGRACY	ALVEFAGRA	0.0857	19772.1	50.00	Rv2754c, T
DRB3_0101	201	EHADVEIRRLAIECL	ADVEIRRLA	0.0855	19821.3	50.00	Rv2754c, T
DRB3_0101	141	TYSELLAKLEAKFAD	LLAKLEAKF	0.0854	19851.6	50.00	Rv2754c, T
DRB3_0101	139	RATYSELLAKLEAKF	LLAKLEAKF	0.0840	20155.2	50.00	Rv2754c, T
DRB3_0101	49	PNPKTATNAGYLRHI	TATNAGYLR	0.0814	20720.0	50.00	Rv2754c, T
DRB3_0101	140	ATYSELLAKLEAKFA	LLAKLEAKF	0.0812	20778.1	50.00	Rv2754c, T
DRB3_0101	26	TDADGGPALVEFAGR	TDADGGPAL	0.0800	21035.1	50.00	Rv2754c, T
DRB3_0101	200	SEHADVEIRRLAIEC	ADVEIRRLA	0.0795	21144.2	50.00	Rv2754c, T
DRB3_0101	142	YSELLAKLEAKFADQ	LLAKLEAKF	0.0793	21208.1	50.00	Rv2754c, T
DRB3_0101	232	TTLADGTEVATSPLA	TEVATSPLA	0.0785	21374.9	50.00	Rv2754c, T
DRB3_0101	30	GGPALVEFAGRACYG	ALVEFAGRA	0.0776	21597.8	50.00	Rv2754c, T
DRB3_0101	25	TTDADGGPALVEFAG	TDADGGPAL	0.0776	21603.2	50.00	Rv2754c, T
DRB3_0101	231	VTTLADGTEVATSPL	TLADGTEVA	0.0773	21660.3	50.00	Rv2754c, T
DRB3_0101	172	AVLPNATETRIVVTG	NATETRIVV	0.0772	21685.2	50.00	Rv2754c, T
DRB3_0101	230	EVTTLADGTEVATSP	TLADGTEVA	0.0768	21782.5	50.00	Rv2754c, T
DRB3_0101	113	SRVVVPPGMEDDADL	PGMEDDADL	0.0753	22143.9	50.00	Rv2754c, T
DRB3_0101	136	DAARATYSELLAKLE	TYSELLAKL	0.0750	22203.9	50.00	Rv2754c, T

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DRB3_0101	135	ADAARATYSELLAKL	TYSELLAKL	0.0749	22225.8	50.00	Rv2754c, T
DRB3_0101	145	LLAKLEAKFADQPNA	LLAKLEAKF	0.0714	23083.6	50.00	Rv2754c, T
DRB3_0101	233	TLADGTEVATSPLAT	TLADGTEVA	0.0713	23110.6	50.00	Rv2754c, T
DRB3_0101	143	SELLAKLEAKFADQP	LLAKLEAKF	0.0709	23222.9	50.00	Rv2754c, T
DRB3_0101	137	AARATYSELLAKLEA	ARATYSELL	0.0707	23260.4	50.00	Rv2754c, T
DRB3_0101	38	AGRACYQSWSKPNPK	CYQSWSKPN	0.0706	23280.8	50.00	Rv2754c, T
DRB3_0101	99	YSQLSQRYVPEKDS	YSQLSQRYV	0.0698	23494.1	50.00	Rv2754c, T
DRB3_0101	132	TEAADAARATYSELL	ARATYSELL	0.0695	23567.9	50.00	Rv2754c, T
DRB3_0101	100	YSQLSQRYVPEKDSR	YSQLSQRYV	0.0692	23646.8	50.00	Rv2754c, T
DRB3_0101	41	ACYQSWSKPNPKTAT	CYQSWSKPN	0.0689	23728.1	50.00	Rv2754c, T
DRB3_0101	85	SRSCTHELIRHRHFS	ELIRHRHFS	0.0686	23806.0	50.00	Rv2754c, T
DRB3_0101	169	AARAVLPNATETRIV	PNATETRIV	0.0675	24099.6	50.00	Rv2754c, T
DRB3_0101	144	ELLAKLEAKFADQPN	LLAKLEAKF	0.0671	24201.8	50.00	Rv2754c, T
DRB3_0101	39	GRACYQSWSKPNPKT	CYQSWSKPN	0.0666	24326.5	50.00	Rv2754c, T
DRB3_0101	155	QPNAILRRKQARQA	LRRKQARQA	0.0664	24385.0	50.00	Rv2754c, T
DRB3_0101	173	VLPNATETRIVVTGN	NATETRIVV	0.0663	24397.1	50.00	Rv2754c, T
DRB3_0101	40	RACYQSWSKPNPKTA	CYQSWSKPN	0.0660	24482.3	50.00	Rv2754c, T
DRB3_0101	27	DADGGPALVEFAGRA	ALVEFAGRA	0.0658	24528.2	50.00	Rv2754c, T
DRB3_0101	47	SKPNPKTATNAGYLR	TATNAGYLR	0.0655	24626.3	50.00	Rv2754c, T
DRB3_0101	133	EAADAARATYSELLA	ARATYSELL	0.0645	24883.1	50.00	Rv2754c, T
DRB3_0101	156	QPNAILRRKQARQAA	LRRKQARQA	0.0640	25027.1	50.00	Rv2754c, T
DRB3_0101	157	PNAILRRKQARQAAR	LRRKQARQA	0.0628	25353.3	50.00	Rv2754c, T
DRB3_0101	28	ADGGPALVEFAGRAC	ALVEFAGRA	0.0627	25384.9	50.00	Rv2754c, T
DRB3_0101	138	ARATYSELLAKLEAK	ARATYSELL	0.0626	25385.7	50.00	Rv2754c, T
DRB3_0101	110	EKDSRVVPPGMEDD	SRVVVPPGM	0.0623	25476.5	50.00	Rv2754c, T
DRB3_0101	48	KPNPKTATNAGYLRH	TATNAGYLR	0.0610	25833.2	50.00	Rv2754c, T
DRB3_0101	111	KDSRVVPPGMEDDA	SRVVVPPGM	0.0598	26175.9	50.00	Rv2754c, T
DRB3_0101	158	NAILRRKQARQAARA	LRRKQARQA	0.0579	26723.3	50.00	Rv2754c, T
DRB3_0101	112	DSRVVPPGMEDDAD	SRVVVPPGM	0.0565	27128.8	50.00	Rv2754c, T
DRB3_0101	168	QAARAVLPNATETRI	VLPNATETR	0.0553	27492.6	50.00	Rv2754c, T
DRB3_0101	134	AAADAARATYSELLAK	ARATYSELL	0.0549	27619.6	50.00	Rv2754c, T
DRB3_0101	234	LADGTEVATSPLATE	TEVATSPLA	0.0537	27953.3	50.00	Rv2754c, T
DRB3_0101	161	LRRKQARQAARAVLP	LRRKQARQA	0.0535	28040.6	50.00	Rv2754c, T
DRB3_0101	131	LTEAADAARATYSEL	EAADAARAT	0.0534	28047.8	50.00	Rv2754c, T
DRB3_0101	42	CYQSWSKPNPKTATN	CYQSWSKPN	0.0533	28084.3	50.00	Rv2754c, T
DRB3_0101	160	ILRRKQARQAARAVL	LRRKQARQA	0.0524	28369.2	50.00	Rv2754c, T
DRB3_0101	159	AILRRKQARQAARAV	LRRKQARQA	0.0522	28419.9	50.00	Rv2754c, T
DRB3_0101	167	RQAARAVLPNATETR	VLPNATETR	0.0484	29628.5	50.00	Rv2754c, T
DRB3_0101	235	ADGTEVATSPLATEA	TEVATSPLA	0.0482	29686.2	50.00	Rv2754c, T
DRB3_0101	164	KQARQAARAVLPNAT	ARAVLPNAT	0.0447	30836.3	50.00	Rv2754c, T
DRB3_0101	165	QARQAARAVLPNATE	ARAVLPNAT	0.0422	31663.6	50.00	Rv2754c, T
DRB3_0101	166	ARQAARAVLPNATET	ARAVLPNAT	0.0421	31711.3	50.00	Rv2754c, T
DRB3_0101	162	RKQARQAARAVLPN	ARQAARAVL	0.0356	34024.0	50.00	Rv2754c, T
DRB3_0101	43	YQSWSKPNPKTATNA	SKPNPKTAT	0.0349	34280.4	50.00	Rv2754c, T
DRB3_0101	163	RKQARQAARAVLPNA	ARQAARAVL	0.0344	34459.7	50.00	Rv2754c, T
DRB3_0101	46	WSKPNPKTATNAGYL	SKPNPKTAT	0.0298	36234.6	50.00	Rv2754c, T
DRB3_0101	45	SWSKPNPKTATNAGY	PKTATNAGY	0.0291	36514.1	50.00	Rv2754c, T
DRB3_0101	154	ADQPNAILRRKQARQ	AILRRKQAR	0.0247	38280.3	50.00	Rv2754c, T
DRB3_0101	44	QSWSKPNPKTATNAG	SKPNPKTAT	0.0244	38416.4	50.00	Rv2754c, T

Allele: DRB3_0101. Number of high binders 0. Number of weak binders 3. Number of peptides 236

Allele	pos	peptide	core	1-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
DRB4_0101	3	TAPLRVQLIAKTDFL	APLRVQLIA	0.8074	8.0	SB	0.15	Rv2754c, T
DRB4_0101	2	ETAPLRVQLIAKTDF	APLRVQLIA	0.8035	8.4	SB	0.15	Rv2754c, T
DRB4_0101	4	APLRVQLIAKTDFLA	APLRVQLIA	0.7964	9.1	SB	0.15	Rv2754c, T
DRB4_0101	1	AETAPLRVQLIAKTD	APLRVQLIA	0.7797	10.8	SB	0.30	Rv2754c, T
DRB4_0101	0	VAETAPLRVQLIAKT	APLRVQLIA	0.7639	12.9	SB	0.40	Rv2754c, T
DRB4_0101	5	PLRVQLIAKTDFLAP	LRVQLIAKT	0.6968	26.6	SB	2.00	Rv2754c, T
DRB4_0101	206	EIRRLAIECLRQLAA	IRRLAIECL	0.6899	28.6	SB	2.00	Rv2754c, T
DRB4_0101	204	DVEIRRLAIECLRQL	IRRLAIECL	0.6863	29.8	SB	2.00	Rv2754c, T
DRB4_0101	205	VEIRRLAIECLRQLA	IRRLAIECL	0.6824	31.1	SB	2.00	Rv2754c, T
DRB4_0101	203	ADVEIRRLAIECLRQ	IRRLAIECL	0.6626	38.5	SB	4.00	Rv2754c, T
DRB4_0101	207	IRRLAIECLRQLAAV	IRRLAIECL	0.6607	39.3	SB	4.00	Rv2754c, T
DRB4_0101	90	HELIRHRHFSYSQLS	RHFSYSQLS	0.6576	40.6	SB	4.00	Rv2754c, T
DRB4_0101	91	ELIRHRHFSYSQLSQ	RHFSYSQLS	0.6438	47.2	SB	4.00	Rv2754c, T
DRB4_0101	6	LRVQLIAKTDFLAPP	LRVQLIAKT	0.6407	48.8	SB	4.00	Rv2754c, T
DRB4_0101	202	HADVEIRRLAIECLR	IRRLAIECL	0.6403	49.0	SB	4.00	Rv2754c, T
DRB4_0101	92	LIRHRHFSYSQLSQR	RHFSYSQLS	0.6328	53.1	WB	4.00	Rv2754c, T
DRB4_0101	201	EHADVEIRRLAIECL	IRRLAIECL	0.6201	61.0	WB	8.00	Rv2754c, T
DRB4_0101	89	THELIRHRHFSYSQL	IRHRHFSYS	0.6077	69.7	WB	8.00	Rv2754c, T
DRB4_0101	190	AWRHFIAMRASEHAD	RHFIAMRAS	0.6007	75.2	WB	8.00	Rv2754c, T
DRB4_0101	88	CTHELIRHRHFSYSQ	IRHRHFSYS	0.5933	81.5	WB	8.00	Rv2754c, T
DRB4_0101	209	RLAIECLRQLAAVAP	LAIECLRQL	0.5926	82.1	WB	8.00	Rv2754c, T
DRB4_0101	191	WRHFIAMRASEHADV	RHFIAMRAS	0.5922	82.4	WB	8.00	Rv2754c, T
DRB4_0101	95	HRHFSYSQLSQRYVP	RHFSYSQLS	0.5897	84.7	WB	8.00	Rv2754c, T
DRB4_0101	94	RHRHFSYSQLSQRYV	RHFSYSQLS	0.5871	87.1	WB	8.00	Rv2754c, T
DRB4_0101	93	IRHRHFSYSQLSQRY	RHFSYSQLS	0.5866	87.6	WB	8.00	Rv2754c, T
DRB4_0101	210	LAIECLRQLAAVAPA	LAIECLRQL	0.5823	91.7	WB	8.00	Rv2754c, T
DRB4_0101	87	SCTHELIRHRHFSYS	HELIRHRHF	0.5774	96.8	WB	8.00	Rv2754c, T
DRB4_0101	189	RAWRHFIAMRASEHA	RHFIAMRAS	0.5746	99.8	WB	8.00	Rv2754c, T

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DRB4_0101	208	RRLAIECLRQLAAVA	LAIECLRQL	0.5579	119.5	WB	16.00	Rv2754c, T
DRB4_0101	187	NYRAWRHFIAMRASE	RHFIAMRAS	0.5567	121.1	WB	16.00	Rv2754c, T
DRB4_0101	60	LRHIIDVGHFVSLEH	LRHIIDVGH	0.5483	132.6	WB	16.00	Rv2754c, T
DRB4_0101	186	GNYRAWRHFIAMRAS	RHFIAMRAS	0.5475	133.8	WB	16.00	Rv2754c, T
DRB4_0101	188	YRAWRHFIAMRASEH	RHFIAMRAS	0.5457	136.4	WB	16.00	Rv2754c, T
DRB4_0101	58	GYLRHIIDVGHFVSVL	LRHIIDVGH	0.5422	141.6	WB	16.00	Rv2754c, T
DRB4_0101	96	RHFSYSQLSQRYVPE	RHFSYSQLS	0.5375	149.1	WB	16.00	Rv2754c, T
DRB4_0101	126	DLRHILTEAADAARA	LRHILTEAA	0.5365	150.7	WB	16.00	Rv2754c, T
DRB4_0101	192	RHFIAMRASEHADVE	RHFIAMRAS	0.5355	152.3	WB	16.00	Rv2754c, T
DRB4_0101	213	ECLRQLAAVAPAVFA	LRQLAAVAP	0.5343	154.2	WB	16.00	Rv2754c, T
DRB4_0101	212	TECLRQLAAVAPAVF	CLRQLAAVA	0.5340	154.7	WB	16.00	Rv2754c, T
DRB4_0101	59	YLRHIIDVGHFVSLE	LRHIIDVGH	0.5289	163.6	WB	16.00	Rv2754c, T
DRB4_0101	125	ADLRHILTEAADAAR	LRHILTEAA	0.5287	163.9	WB	16.00	Rv2754c, T
DRB4_0101	57	AGYLRHIIDVGHFSV	LRHIIDVGH	0.5207	178.7	WB	16.00	Rv2754c, T
DRB4_0101	63	LIDVGHFVSLEHASV	FVSLEHASV	0.5181	183.8	WB	16.00	Rv2754c, T
DRB4_0101	124	DADLRHILTEAADAA	LRHILTEAA	0.5178	184.5	WB	16.00	Rv2754c, T
DRB4_0101	66	VGHFVSLEHASVSFY	FVSLEHASV	0.5104	199.7	WB	16.00	Rv2754c, T
DRB4_0101	65	DVGHFVSLEHASVSF	FVSLEHASV	0.5088	203.4	WB	16.00	Rv2754c, T
DRB4_0101	55	TNAGYLRHIIDVGHF	LRHIIDVGH	0.5054	211.0	WB	16.00	Rv2754c, T
DRB4_0101	56	NAGYLRHIIDVGHFS	LRHIIDVGH	0.5050	211.7	WB	16.00	Rv2754c, T
DRB4_0101	211	AIECLRQLAAVAPAV	LRQLAAVAP	0.5049	212.2	WB	16.00	Rv2754c, T
DRB4_0101	214	CLRQLAAVAPAVFAD	LRQLAAVAP	0.5047	212.6	WB	16.00	Rv2754c, T
DRB4_0101	127	LRHILTEAADAARAT	LRHILTEAA	0.5017	219.5	WB	16.00	Rv2754c, T
DRB4_0101	64	IDVGHFVSLEHASVS	FVSLEHASV	0.4973	230.3	WB	32.00	Rv2754c, T
DRB4_0101	123	DDADLRHILTEAADA	LRHILTEAA	0.4964	232.6	WB	32.00	Rv2754c, T
DRB4_0101	7	RVQLIAKTDFLAPPD	VQLIAKTDF	0.4922	243.3	WB	32.00	Rv2754c, T
DRB4_0101	61	RHIIDVGHFVSLEHA	RHIIDVGHF	0.4905	247.7	WB	32.00	Rv2754c, T
DRB4_0101	122	EDDADLRHILTEAAD	LRHILTEAA	0.4770	286.8	WB	32.00	Rv2754c, T
DRB4_0101	121	MEDDADLRHILTEAA	LRHILTEAA	0.4754	291.9	WB	32.00	Rv2754c, T
DRB4_0101	86	RGCTHELIRHRHFSY	HELIRHRHF	0.4735	297.8	WB	32.00	Rv2754c, T
DRB4_0101	185	TSNYRAWRHFIAMRA	WRHFIAMRA	0.4705	307.7	WB	32.00	Rv2754c, T
DRB4_0101	54	ATNAGYLRHIIDVGH	LRHIIDVGH	0.4691	312.5	WB	32.00	Rv2754c, T
DRB4_0101	8	VQLIAKTDFLAPPDV	VQLIAKTDF	0.4679	316.5	WB	32.00	Rv2754c, T
DRB4_0101	157	PNAILRRKQARQAAR	AILRRKQAR	0.4677	317.3	WB	32.00	Rv2754c, T
DRB4_0101	158	NAILRRKQARQAARA	AILRRKQAR	0.4583	351.0	WB	32.00	Rv2754c, T
DRB4_0101	156	QPNAILRRKQARQAA	LRRKQARQA	0.4553	362.5	WB	32.00	Rv2754c, T
DRB4_0101	62	HIIDVGHFVSLEHAS	GHFVSLEHA	0.4543	366.7	WB	32.00	Rv2754c, T
DRB4_0101	67	GHFVSLEHASVSFYI	FVSLEHASV	0.4375	439.8	WB	32.00	Rv2754c, T
DRB4_0101	200	SEHADVEIRRLAIEC	EIRRLAIEC	0.4349	452.1	WB	32.00	Rv2754c, T
DRB4_0101	193	HFIAMRASEHADVEI	IAMRASEHA	0.4338	457.8	WB	32.00	Rv2754c, T
DRB4_0101	155	DQPNAILRRKQARQA	LRRKQARQA	0.4312	470.7	WB	32.00	Rv2754c, T
DRB4_0101	159	AILRRKQARQAARAV	AILRRKQAR	0.4296	478.9	WB	32.00	Rv2754c, T
DRB4_0101	180	TRIVVTGNYPYRAWRH	TRIVVTGNY	0.4035	635.5	WB	32.00	Rv2754c, T
DRB4_0101	85	SRSCHELIRHRHFS	HELIRHRHF	0.4028	640.3	WB	32.00	Rv2754c, T
DRB4_0101	215	LRQLAAVAPAVFADF	LRQLAAVAP	0.4020	645.5	WB	32.00	Rv2754c, T
DRB4_0101	84	ISRSCHELIRHRHF	HELIRHRHF	0.4019	646.4	WB	50.00	Rv2754c, T
DRB4_0101	184	VTGNYRAWRHFIAMR	TGNYRAWRH	0.3997	661.9	WB	50.00	Rv2754c, T
DRB4_0101	79	FYITGISRSCTHELI	ITGISRSCT	0.3983	671.8	WB	50.00	Rv2754c, T
DRB4_0101	179	ETRIVVTGNYPYRAWRH	TRIVVTGNY	0.3932	709.9	WB	50.00	Rv2754c, T
DRB4_0101	68	HFSVLEHASVSFYIT	FVSLEHASV	0.3923	717.2	WB	50.00	Rv2754c, T
DRB4_0101	78	SFYITGISRSCTHEL	ITGISRSCT	0.3888	745.1	WB	50.00	Rv2754c, T
DRB4_0101	194	FIAMRASEHADVEIR	IAMRASEHA	0.3855	771.9	WB	50.00	Rv2754c, T
DRB4_0101	81	ITGISRSCTHELIRH	ITGISRSCT	0.3823	798.9	WB	50.00	Rv2754c, T
DRB4_0101	69	FVSLEHASVSFYITG	FVSLEHASV	0.3780	836.8	WB	50.00	Rv2754c, T
DRB4_0101	80	YITGISRSCTHELIR	ITGISRSCT	0.3774	842.8	WB	50.00	Rv2754c, T
DRB4_0101	77	VSFYITGISRSCTHE	ITGISRSCT	0.3748	866.3	WB	50.00	Rv2754c, T
DRB4_0101	97	HFSYSQLSQRYVPEK	FSYSQLSQR	0.3684	928.6	WB	50.00	Rv2754c, T
DRB4_0101	183	VVTGNYRAWRHFIAM	GNYPYRAWRH	0.3671	941.4	WB	50.00	Rv2754c, T
DRB4_0101	178	TRIVVTGNYPYRAWRH	TRIVVTGNY	0.3644	970.2	WB	50.00	Rv2754c, T
DRB4_0101	76	SVSFYITGISRSCTH	ITGISRSCT	0.3628	986.3	WB	50.00	Rv2754c, T
DRB4_0101	160	ILRRKQARQAARAVL	ILRRKQARQ	0.3624	990.6	WB	50.00	Rv2754c, T
DRB4_0101	53	TATNAGYLRHIIDVG	GYLRHIIDV	0.3606	1010.2	WB	50.00	Rv2754c, T
DRB4_0101	195	IAMRASEHADVEIRR	IAMRASEHA	0.3594	1023.4	WB	50.00	Rv2754c, T
DRB4_0101	182	IVVTGNYRAWRHFI	GNYPYRAWRH	0.3564	1057.5	WB	50.00	Rv2754c, T
DRB4_0101	177	ATETRIVVTGNYPYRAW	TRIVVTGNY	0.3531	1095.5	WB	50.00	Rv2754c, T
DRB4_0101	82	TGISRSCTHELIRHR	ISRSCHEL	0.3522	1106.2	WB	50.00	Rv2754c, T
DRB4_0101	199	ASEHADVEIRRLAIE	DVEIRRLAI	0.3436	1214.2	WB	50.00	Rv2754c, T
DRB4_0101	216	RQLAAVAPAVFADFE	LAAPAVAVF	0.3435	1215.5	WB	50.00	Rv2754c, T
DRB4_0101	154	ADQPNAILRRKQARQ	NAILRRKQA	0.3419	1237.5	WB	50.00	Rv2754c, T
DRB4_0101	176	NATETRIVVTGNYPY	TRIVVTGNY	0.3386	1282.7	WB	50.00	Rv2754c, T
DRB4_0101	83	GISRSCHELIRHRH	ISRSCHEL	0.3370	1304.8	WB	50.00	Rv2754c, T
DRB4_0101	52	KTATNAGYLRHIIDV	GYLRHIIDV	0.3358	1322.0	WB	50.00	Rv2754c, T
DRB4_0101	181	RIVVTGNYPYRAWRHFI	TGNYRAWRH	0.3332	1359.5	WB	50.00	Rv2754c, T
DRB4_0101	75	ASVSFYITGISRSCT	ITGISRSCT	0.3305	1399.7	WB	50.00	Rv2754c, T
DRB4_0101	98	FSYSQLSQRYVPEK	FSYSQLSQR	0.3276	1443.8	WB	50.00	Rv2754c, T
DRB4_0101	111	KDSRVVPPGMEDEDA	SRVVVPPGM	0.3256	1475.2	WB	50.00	Rv2754c, T
DRB4_0101	113	SRVVVPPGMEDEADL	SRVVVPPGM	0.3201	1565.4	WB	50.00	Rv2754c, T
DRB4_0101	120	GMEDDADLRHILTEA	DLRHILTEA	0.3164	1630.2	WB	50.00	Rv2754c, T
DRB4_0101	99	SYSQLSQRYVPEKDS	YSQLSQRYV	0.3151	1653.0	WB	50.00	Rv2754c, T
DRB4_0101	112	DSRVVPPGMEDEDA	SRVVVPPGM	0.3146	1661.4	WB	50.00	Rv2754c, T
DRB4_0101	161	LRRKQARQAARAVLP	LRRKQARQA	0.3063	1817.8	WB	50.00	Rv2754c, T
DRB4_0101	74	HASVSFYITGISRS	FYITGISRS	0.3060	1823.9	WB	50.00	Rv2754c, T
DRB4_0101	73	EHASVSFYITGISRS	EHASVSFYI	0.2994	1959.6	WB	50.00	Rv2754c, T
DRB4_0101	153	FADQPNAILRRKQAR	NAILRRKQA	0.2961	2029.4	WB	50.00	Rv2754c, T
DRB4_0101	142	YSELLAKLEAKFADQ	LLAKLEAKF	0.2941	2075.1	WB	50.00	Rv2754c, T

DRB4_0101	100	YSQLSQRYVPEKDSR	QRYVPEKDS	0.2937	2085.0	50.00	Rv2754c, T
DRB4_0101	128	RHILTEAADAARATY	RHILTEAAD	0.2926	2108.9	50.00	Rv2754c, T
DRB4_0101	217	QLAAVPAVFADFEV	LAAVPAVF	0.2881	2213.1	50.00	Rv2754c, T
DRB4_0101	143	SELLAKLEAKFADQP	SELLAKLEA	0.2873	2234.3	50.00	Rv2754c, T
DRB4_0101	110	EKDSRVVPPGMEDD	SRVVPPGM	0.2866	2251.4	50.00	Rv2754c, T
DRB4_0101	141	TYSELLAKLEAKFAD	ELLAKLEAK	0.2863	2256.6	50.00	Rv2754c, T
DRB4_0101	140	ATYSELLAKLEAKFA	ELLAKLEAK	0.2800	2415.7	50.00	Rv2754c, T
DRB4_0101	175	PNATETRIVVTGNYSR	TRIVVTGNY	0.2779	2471.6	50.00	Rv2754c, T
DRB4_0101	109	PEKDSRVVPPGMED	SRVVPPGM	0.2764	2512.8	50.00	Rv2754c, T
DRB4_0101	71	VLEHASVSFYITGISR	HASVSFYIT	0.2743	2569.8	50.00	Rv2754c, T
DRB4_0101	198	RASEHADVEIRRLAI	DVEIRRLAI	0.2729	2609.9	50.00	Rv2754c, T
DRB4_0101	108	VPEKDSRVVPPGME	SRVVPPGM	0.2705	2679.6	50.00	Rv2754c, T
DRB4_0101	101	SQLSQRYVPEKDSRV	QRYVPEKDS	0.2648	2848.7	50.00	Rv2754c, T
DRB4_0101	70	SVLEHASVSFYITGI	HASVSFYIT	0.2638	2879.1	50.00	Rv2754c, T
DRB4_0101	144	ELLAKLEAKFADQPN	ELLAKLEAK	0.2622	2931.4	50.00	Rv2754c, T
DRB4_0101	72	LEHASVSFYITGISR	EHASVSFYI	0.2614	2956.9	50.00	Rv2754c, T
DRB4_0101	139	RATYSELLAKLEAKF	SELLAKLEA	0.2587	3044.0	50.00	Rv2754c, T
DRB4_0101	165	QARQAARAVLPNATE	ARAVLPNAT	0.2586	3047.6	50.00	Rv2754c, T
DRB4_0101	166	ARQAARAVLPNATE	ARAVLPNAT	0.2568	3106.5	50.00	Rv2754c, T
DRB4_0101	164	KQARQAARAVLPNAT	ARAVLPNAT	0.2558	3138.9	50.00	Rv2754c, T
DRB4_0101	51	PKTATNAGYLRHIID	AGYLRHIID	0.2550	3166.9	50.00	Rv2754c, T
DRB4_0101	168	QAARAVLPNATETRI	ARAVLPNAT	0.2505	3327.2	50.00	Rv2754c, T
DRB4_0101	138	ARATYSELLAKLEAK	ARATYSELL	0.2483	3406.0	50.00	Rv2754c, T
DRB4_0101	174	LPNATETRIVVTGNY	TRIVVTGNY	0.2479	3420.4	50.00	Rv2754c, T
DRB4_0101	218	LAAVPAVFADFEV	LAAVPAVF	0.2478	3426.0	50.00	Rv2754c, T
DRB4_0101	103	LSQRYVPEKDSRVVV	QRYVPEKDS	0.2436	3585.2	50.00	Rv2754c, T
DRB4_0101	102	QLSQRYVPEKDSRVV	QRYVPEKDS	0.2434	3589.8	50.00	Rv2754c, T
DRB4_0101	145	LLAKLEAKFADQPN	LLAKLEAKF	0.2429	3610.5	50.00	Rv2754c, T
DRB4_0101	105	QRYVPEKDSRVVPPP	QRYVPEKDS	0.2415	3666.7	50.00	Rv2754c, T
DRB4_0101	167	RQAARAVLPNATETR	ARAVLPNAT	0.2413	3673.6	50.00	Rv2754c, T
DRB4_0101	9	QLIAKTDFLAPDPVP	QLIAKTDFL	0.2398	3734.9	50.00	Rv2754c, T
DRB4_0101	119	PGMEDDADLRHILTE	MEDDADLRH	0.2397	3736.1	50.00	Rv2754c, T
DRB4_0101	107	YVPEKDSRVVPPGM	SRVVPPGM	0.2359	3893.6	50.00	Rv2754c, T
DRB4_0101	104	SQRYVPEKDSRVVPP	QRYVPEKDS	0.2359	3894.5	50.00	Rv2754c, T
DRB4_0101	152	KFADQPNAILRRKQA	NAILRRKQA	0.2352	3923.3	50.00	Rv2754c, T
DRB4_0101	169	AARAVLPNATETRIV	ARAVLPNAT	0.2330	4020.8	50.00	Rv2754c, T
DRB4_0101	37	FAGRACYQSWSKPNP	AGRACYQSW	0.2273	4275.9	50.00	Rv2754c, T
DRB4_0101	117	VPPGMEDDADLRHIL	VPPGMEDDA	0.2268	4299.7	50.00	Rv2754c, T
DRB4_0101	18	APPDVPTTADGGGP	APPDVPTTT	0.2250	4380.4	50.00	Rv2754c, T
DRB4_0101	148	KLEAKFADQPNAILR	AKFADQPN	0.2237	4446.1	50.00	Rv2754c, T
DRB4_0101	36	EFAGRACYQSWSKPN	AGRACYQSW	0.2232	4467.2	50.00	Rv2754c, T
DRB4_0101	137	AARATYSELLAKLEA	ARATYSELL	0.2220	4524.6	50.00	Rv2754c, T
DRB4_0101	118	PPGMEDDADLRHILT	MEDDADLRH	0.2220	4525.1	50.00	Rv2754c, T
DRB4_0101	151	AKFADQPNAILRRKQ	AKFADQPN	0.2209	4581.9	50.00	Rv2754c, T
DRB4_0101	162	RRKQARQAARAVLPN	RRKQARQAA	0.2207	4591.7	50.00	Rv2754c, T
DRB4_0101	17	LAPPDVPTTADGGG	VPWTTDADG	0.2202	4615.7	50.00	Rv2754c, T
DRB4_0101	32	PALVEFAGRACYQSW	FAGRACYQS	0.2190	4677.5	50.00	Rv2754c, T
DRB4_0101	31	GPALVEFAGRACYQS	VEFAGRACY	0.2170	4778.2	50.00	Rv2754c, T
DRB4_0101	16	FLAPPDVPTTADADG	VPWTTDADG	0.2156	4848.9	50.00	Rv2754c, T
DRB4_0101	114	RVVVPPGMEDDADLR	VPPGMEDDA	0.2153	4866.0	50.00	Rv2754c, T
DRB4_0101	163	RKQARQAARAVLPNA	ARQAARAVL	0.2140	4935.9	50.00	Rv2754c, T
DRB4_0101	129	HILTEAADAARATYS	HILTEAADA	0.2126	5011.4	50.00	Rv2754c, T
DRB4_0101	116	VVPPGMEDDADLRHI	VPPGMEDDA	0.2121	5040.9	50.00	Rv2754c, T
DRB4_0101	196	AMRASEHADVEIRRL	MRASEHADV	0.2116	5063.9	50.00	Rv2754c, T
DRB4_0101	147	AKLEAKFADQPNAIL	KLEAKFADQ	0.2101	5150.6	50.00	Rv2754c, T
DRB4_0101	33	ALVEFAGRACYQSW	AGRACYQSW	0.2065	5354.7	50.00	Rv2754c, T
DRB4_0101	35	VEFAGRACYQSWSKP	AGRACYQSW	0.2061	5376.7	50.00	Rv2754c, T
DRB4_0101	38	AGRACYQSWSKPNPK	AGRACYQSW	0.2055	5411.6	50.00	Rv2754c, T
DRB4_0101	34	LVEFAGRACYQSWSK	AGRACYQSW	0.2028	5570.5	50.00	Rv2754c, T
DRB4_0101	150	EAKFADQPNAILRRK	AKFADQPN	0.2006	5707.2	50.00	Rv2754c, T
DRB4_0101	50	NPKTATNAGYLRHII	NAGYLRHII	0.1993	5790.0	50.00	Rv2754c, T
DRB4_0101	170	ARAVLPNATETRIVV	ARAVLPNAT	0.1985	5837.1	50.00	Rv2754c, T
DRB4_0101	136	DAARATYSELLAKLE	YSELLAKLE	0.1975	5901.9	50.00	Rv2754c, T
DRB4_0101	146	LAKLEAKFADQPNAI	LAKLEAKFA	0.1958	6010.9	50.00	Rv2754c, T
DRB4_0101	149	LEAKFADQPNAILRR	AKFADQPN	0.1948	6076.1	50.00	Rv2754c, T
DRB4_0101	19	PPDVPTTADADGGPA	VPWTTDADG	0.1942	6115.6	50.00	Rv2754c, T
DRB4_0101	20	PDPVPTTADADGGPAL	VPWTTDADG	0.1932	6179.6	50.00	Rv2754c, T
DRB4_0101	14	TDFLAPPDVPWTTDA	TDFLAPPDV	0.1914	6302.2	50.00	Rv2754c, T
DRB4_0101	197	MRASEHADVEIRRLA	ADVEIRRLA	0.1879	6548.9	50.00	Rv2754c, T
DRB4_0101	40	VACYQSWSKPNPKTA	CYQSWSKPN	0.1855	6717.1	50.00	Rv2754c, T
DRB4_0101	115	VVPPGMEDDADLRH	VPPGMEDDA	0.1843	6803.3	50.00	Rv2754c, T
DRB4_0101	221	VAPAVFADFEVTTLA	ADFEVTTLA	0.1832	6886.5	50.00	Rv2754c, T
DRB4_0101	13	KTDFLAPPDVPWTTD	TDFLAPPDV	0.1796	7161.0	50.00	Rv2754c, T
DRB4_0101	223	PAVFADFEVTTLADG	ADFEVTTLA	0.1783	7263.6	50.00	Rv2754c, T
DRB4_0101	39	GRACYQSWSKPNPKT	QSWSKPNPK	0.1732	7678.0	50.00	Rv2754c, T
DRB4_0101	135	ADAARATYSELLAKL	RATYSELLA	0.1714	7826.7	50.00	Rv2754c, T
DRB4_0101	134	AADAARATYSELLAK	RATYSELLA	0.1679	8131.2	50.00	Rv2754c, T
DRB4_0101	10	LIAKTDFLAPPDVPW	TDFLAPPDV	0.1671	8195.0	50.00	Rv2754c, T
DRB4_0101	12	AKTDFLAPPDVPWTT	TDFLAPPDV	0.1669	8218.1	50.00	Rv2754c, T
DRB4_0101	30	GGPALVEFAGRACYQ	VEFAGRACY	0.1666	8240.2	50.00	Rv2754c, T
DRB4_0101	41	ACYQSWSKPNPKTAT	CYQSWSKPN	0.1632	8553.1	50.00	Rv2754c, T
DRB4_0101	224	AVFADFEVTTLADGT	ADFEVTTLA	0.1619	8670.8	50.00	Rv2754c, T
DRB4_0101	227	ADFEVTTLADGTEVA	ADFEVTTLA	0.1615	8709.0	50.00	Rv2754c, T
DRB4_0101	42	CYQSWSKPNPKTATN	QSWSKPNPK	0.1612	8742.3	50.00	Rv2754c, T
DRB4_0101	133	EAADAARATYSELLA	RATYSELLA	0.1575	9097.8	50.00	Rv2754c, T

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DRB4_0101	11	IAKTDFLAPPDVPWT	TDFLAPPDV	0.1566	9188.2	50.00	Rv2754c, T
DRB4_0101	220	AVAPAVFADFEVTTL	VAPAVFADF	0.1565	9199.1	50.00	Rv2754c, T
DRB4_0101	15	DFLAPPDVPWTTDAD	APPDVPWTT	0.1565	9200.5	50.00	Rv2754c, T
DRB4_0101	219	AAVAPAVFADFEVTT	VAPAVFADF	0.1564	9210.3	50.00	Rv2754c, T
DRB4_0101	226	FADFEVTTLADGTEV	ADFEVTTLA	0.1558	9263.2	50.00	Rv2754c, T
DRB4_0101	222	APAVFADFEVTTLAD	ADFEVTTLA	0.1549	9356.3	50.00	Rv2754c, T
DRB4_0101	29	DGGPALVEFAGRACY	VEFAGRACY	0.1549	9359.0	50.00	Rv2754c, T
DRB4_0101	49	PNPKTATNAGYLRHI	ATNAGYLRH	0.1519	9669.0	50.00	Rv2754c, T
DRB4_0101	225	VFADFEVTTLADGTE	ADFEVTTLA	0.1516	9698.5	50.00	Rv2754c, T
DRB4_0101	228	DFEVTTLADGTEVAT	FEVTTLADG	0.1400	10988.8	50.00	Rv2754c, T
DRB4_0101	132	TEAADAARATYSELL	ARATYSELL	0.1376	11282.1	50.00	Rv2754c, T
DRB4_0101	173	VLPNATETRIVVVTGN	LPNATETRI	0.1354	11558.8	50.00	Rv2754c, T
DRB4_0101	106	RYVPEKDSRVVPPG	KDSRVVPPP	0.1334	11804.0	50.00	Rv2754c, T
DRB4_0101	28	ADGGPALVEFAGRAC	GPALVEFAG	0.1329	11871.2	50.00	Rv2754c, T
DRB4_0101	171	RAVLPNATETRIVVV	RAVLPNATE	0.1315	12048.2	50.00	Rv2754c, T
DRB4_0101	48	KPNPKTATNAGYLRH	ATNAGYLRH	0.1296	12298.0	50.00	Rv2754c, T
DRB4_0101	21	DVPWTTDADGGPALV	VPWTTDADG	0.1265	12715.9	50.00	Rv2754c, T
DRB4_0101	229	FEVTTLADGTEVATS	FEVTTLADG	0.1239	13088.6	50.00	Rv2754c, T
DRB4_0101	43	YQSWSKPNPKTATNA	YQSWSKPNP	0.1233	13165.0	50.00	Rv2754c, T
DRB4_0101	27	DADGGPALVEFAGRA	GPALVEFAG	0.1218	13383.4	50.00	Rv2754c, T
DRB4_0101	130	ILTEAADAARATYSE	ILTEAADAA	0.1217	13400.2	50.00	Rv2754c, T
DRB4_0101	172	AVLPNATETRIVVVTG	LPNATETRI	0.1194	13732.3	50.00	Rv2754c, T
DRB4_0101	22	VPWTTDADGGPALVE	VPWTTDADG	0.1139	14574.8	50.00	Rv2754c, T
DRB4_0101	26	TDADGGPALVEFAGR	GPALVEFAG	0.1057	15933.5	50.00	Rv2754c, T
DRB4_0101	235	ADGTEVATSPLATEA	GTEVATSPL	0.0967	17568.9	50.00	Rv2754c, T
DRB4_0101	44	QSWSKPNPKTATNAG	QSWSKPNPK	0.0966	17580.5	50.00	Rv2754c, T
DRB4_0101	234	LADGTEVATSPLATE	GTEVATSPL	0.0940	18084.6	50.00	Rv2754c, T
DRB4_0101	131	LTEAADAARATYSEL	AARATYSEL	0.0939	18111.0	50.00	Rv2754c, T
DRB4_0101	233	TLADGTEVATSPLAT	GTEVATSPL	0.0881	19279.4	50.00	Rv2754c, T
DRB4_0101	46	WSKPNPKTATNAGYL	WSKPNPKTA	0.0869	19523.8	50.00	Rv2754c, T
DRB4_0101	230	EVTTLADGTEVATSP	EVTTLADGT	0.0854	19839.8	50.00	Rv2754c, T
DRB4_0101	45	SWSKPNPKTATNAGY	WSKPNPKTA	0.0842	20112.1	50.00	Rv2754c, T
DRB4_0101	232	TTLADGTEVATSPLA	GTEVATSPL	0.0840	20139.8	50.00	Rv2754c, T
DRB4_0101	231	VTTLADGTEVATSPL	GTEVATSPL	0.0809	20839.4	50.00	Rv2754c, T
DRB4_0101	25	TTDADGGPALVEFAG	GPALVEFAG	0.0773	21658.0	50.00	Rv2754c, T
DRB4_0101	47	SKPNPKTATNAGYLR	KPNPKTATN	0.0742	22396.2	50.00	Rv2754c, T
DRB4_0101	24	WTTDADGGPALVEFA	GGPALVEFA	0.0531	28138.4	50.00	Rv2754c, T
DRB4_0101	23	PWTTDADGGPALVEF	DADGGPALV	0.0481	29710.3	50.00	Rv2754c, T

Allele: DRB4_0101. Number of high binders 15. Number of weak binders 55. Number of peptides 236

Allele	pos	peptide	core	1-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
DRB5_0101	189	RAWRHFIAMRASEHA	FIAMRASEH	0.8483	5.2	SB	0.15	Rv2754c, T
DRB5_0101	188	YRAWRHFIAMRASEH	FIAMRASEH	0.8390	5.7	SB	0.20	Rv2754c, T
DRB5_0101	190	AWRHFIAMRASEHAD	FIAMRASEH	0.8321	6.1	SB	0.20	Rv2754c, T
DRB5_0101	191	WRHFIAMRASEHADV	FIAMRASEH	0.8130	7.6	SB	0.40	Rv2754c, T
DRB5_0101	192	RHFIAMRASEHADVE	FIAMRASEH	0.7799	10.8	SB	0.80	Rv2754c, T
DRB5_0101	187	NYRAWRHFIAMRASE	WRHFIAMRA	0.7620	13.1	SB	1.00	Rv2754c, T
DRB5_0101	186	GNYRAWRHFIAMRAS	WRHFIAMRA	0.7538	14.4	SB	2.00	Rv2754c, T
DRB5_0101	185	TGNYRAWRHFIAMRA	WRHFIAMRA	0.7347	17.7	SB	2.00	Rv2754c, T
DRB5_0101	193	HFIAMRASEHADVEI	FIAMRASEH	0.7297	18.6	SB	2.00	Rv2754c, T
DRB5_0101	180	TRIVVTGNYRAWRHF	RIVVTGNYR	0.7215	20.4	SB	2.00	Rv2754c, T
DRB5_0101	95	RRHFSYSQLSQRYP	FSYSQLSQR	0.7182	21.1	SB	4.00	Rv2754c, T
DRB5_0101	96	RHFSYSQLSQRYPVE	FSYSQLSQR	0.7179	21.2	SB	4.00	Rv2754c, T
DRB5_0101	179	ETRIVVTGNYRAWRH	RIVVTGNYR	0.7171	21.4	SB	4.00	Rv2754c, T
DRB5_0101	94	RHRHFSYSQLSQRYP	FSYSQLSQR	0.7116	22.7	SB	4.00	Rv2754c, T
DRB5_0101	178	TETRIVVTGNYRAWR	RIVVTGNYR	0.7089	23.3	SB	4.00	Rv2754c, T
DRB5_0101	181	RIVVTGNYRAWRHF	RIVVTGNYR	0.7061	24.0	SB	4.00	Rv2754c, T
DRB5_0101	97	HFSYSQLSQRYPVEK	FSYSQLSQR	0.6833	30.8	SB	4.00	Rv2754c, T
DRB5_0101	93	IRHRHFSYSQLSQRYP	FSYSQLSQR	0.6728	34.5	SB	4.00	Rv2754c, T
DRB5_0101	177	ATETRIVVTGNYRAW	RIVVTGNYR	0.6685	36.1	SB	8.00	Rv2754c, T
DRB5_0101	76	SFSFYITGISRSCTH	SFYITGISR	0.6416	48.3	SB	8.00	Rv2754c, T
DRB5_0101	78	SFYITGISRSCTHEL	FYITGISRS	0.6390	49.7	SB	8.00	Rv2754c, T
DRB5_0101	77	VSFYITGISRSCTHE	SFYITGISR	0.6375	50.5	WB	8.00	Rv2754c, T
DRB5_0101	98	FSYSQLSQRYPVEKD	FSYSQLSQR	0.6325	53.3	WB	8.00	Rv2754c, T
DRB5_0101	92	LIRHRHFSYSQLSQR	FSYSQLSQR	0.6314	54.0	WB	8.00	Rv2754c, T
DRB5_0101	75	ASVSFYITGISRSCT	SFYITGISR	0.6243	58.2	WB	8.00	Rv2754c, T
DRB5_0101	176	NATETRIVVTGNYRA	RIVVTGNYR	0.6115	66.9	WB	8.00	Rv2754c, T
DRB5_0101	184	VTGNYRAWRHFIAMR	GNYRAWRHF	0.6020	74.2	WB	16.00	Rv2754c, T
DRB5_0101	74	HASVSFYITGISRSCT	SFYITGISR	0.5869	87.3	WB	16.00	Rv2754c, T
DRB5_0101	206	EIRRLAIECLRQLAA	RLAIECLRQ	0.5847	89.4	WB	16.00	Rv2754c, T
DRB5_0101	158	NAILRRKQARQAARA	ILRRKQARQ	0.5815	92.6	WB	16.00	Rv2754c, T
DRB5_0101	194	FIAMRASEHADVEIR	FIAMRASEH	0.5807	93.3	WB	16.00	Rv2754c, T
DRB5_0101	159	AILRRKQARQAARAV	ILRRKQARQ	0.5802	93.9	WB	16.00	Rv2754c, T
DRB5_0101	160	ILRRKQARQAARAVL	ILRRKQARQ	0.5754	98.9	WB	16.00	Rv2754c, T
DRB5_0101	205	VEIRRLAIECLRQLA	RLAIECLRQ	0.5747	99.6	WB	16.00	Rv2754c, T
DRB5_0101	157	PNAILRRKQARQAAR	ILRRKQARQ	0.5676	107.6	WB	16.00	Rv2754c, T
DRB5_0101	208	RLAIECLRQLAAVA	RLAIECLRQ	0.5649	110.8	WB	16.00	Rv2754c, T
DRB5_0101	207	IRRLAIECLRQLAAV	RLAIECLRQ	0.5611	115.4	WB	16.00	Rv2754c, T
DRB5_0101	86	RSCTHELIRHRHFSY	CTHELIRHR	0.5495	130.9	WB	16.00	Rv2754c, T
DRB5_0101	73	EHASVSFYITGISRS	SFYITGISR	0.5473	134.1	WB	16.00	Rv2754c, T

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DRB5_0101	204	DVEIRRLAIECLRQL	RLAIECLRQ	0.5455	136.7	WB	16.00	Rv2754c, T
DRB5_0101	175	PNATETRIVVTGNYSR	RIVVTGNYSR	0.5411	143.3	WB	16.00	Rv2754c, T
DRB5_0101	66	VGHFSVLEHASVSFY	FSVLEHASV	0.5393	146.1	WB	16.00	Rv2754c, T
DRB5_0101	67	GHFSVLEHASVSFYI	FSVLEHASV	0.5373	149.3	WB	16.00	Rv2754c, T
DRB5_0101	156	QPNAILRRKQARQAA	LRRKQARQA	0.5290	163.5	WB	16.00	Rv2754c, T
DRB5_0101	183	VVTGNYRAWRHFIAM	GNYRAWRHF	0.5231	174.2	WB	16.00	Rv2754c, T
DRB5_0101	79	FYITGISRSCTHELI	FYITGISRS	0.5199	180.3	WB	32.00	Rv2754c, T
DRB5_0101	85	SRSCTHELIRHRHFS	CTHELIRHR	0.5193	181.4	WB	32.00	Rv2754c, T
DRB5_0101	84	ISRSCTHELIRHRHF	CTHELIRHR	0.5182	183.6	WB	32.00	Rv2754c, T
DRB5_0101	182	IVVTGNYRAWRHFA	IVVTGNYRA	0.5141	191.9	WB	32.00	Rv2754c, T
DRB5_0101	209	RLAIECLRQLAAVAP	RLAIECLRQ	0.5136	192.9	WB	32.00	Rv2754c, T
DRB5_0101	68	HFSVLEHASVSFYIT	FSVLEHASV	0.5104	199.9	WB	32.00	Rv2754c, T
DRB5_0101	87	SCTHELIRHRHFSYS	CTHELIRHR	0.5025	217.8	WB	32.00	Rv2754c, T
DRB5_0101	83	GISRSCTHELIRHRH	CTHELIRHR	0.5006	222.2	WB	32.00	Rv2754c, T
DRB5_0101	65	DVGHFSVLEHASVSF	FSVLEHASV	0.4916	244.9	WB	32.00	Rv2754c, T
DRB5_0101	155	DQPNAILRRKQARQA	ILRRKQARQ	0.4900	249.1	WB	32.00	Rv2754c, T
DRB5_0101	88	CTHELIRHRHFSYSQ	CTHELIRHR	0.4853	262.1	WB	32.00	Rv2754c, T
DRB5_0101	161	LRRKQARQAARAVLP	LRRKQARQA	0.4762	289.4	WB	32.00	Rv2754c, T
DRB5_0101	82	TGISRSCTHELIRHR	CTHELIRHR	0.4721	302.4	WB	32.00	Rv2754c, T
DRB5_0101	69	FSVLEHASVSFYITG	FSVLEHASV	0.4688	313.5	WB	32.00	Rv2754c, T
DRB5_0101	64	IDVGHFSVLEHASVS	FSVLEHASV	0.4679	316.4	WB	32.00	Rv2754c, T
DRB5_0101	203	ADVEIRRLAIECLRQ	RRLAIECLR	0.4675	317.8	WB	32.00	Rv2754c, T
DRB5_0101	139	RATYSELLAKLEAKF	ATYSELLAK	0.4631	333.5	WB	32.00	Rv2754c, T
DRB5_0101	4	APLRVQLIAKTDFLA	LRVQLIAKT	0.4539	368.2	WB	32.00	Rv2754c, T
DRB5_0101	5	PLRVQLIAKTDFLAP	LRVQLIAKT	0.4439	410.4	WB	32.00	Rv2754c, T
DRB5_0101	3	TAPLRVQLIAKTDFL	LRVQLIAKT	0.4401	427.7	WB	32.00	Rv2754c, T
DRB5_0101	140	ATYSELLAKLEAKFA	LLAKLEAKF	0.4393	431.2	WB	32.00	Rv2754c, T
DRB5_0101	138	ARATYSELLAKLEAK	ATYSELLAK	0.4376	439.2	WB	32.00	Rv2754c, T
DRB5_0101	210	LAIECLRQLAAVAPA	CLRQLAAVA	0.4357	448.3	WB	32.00	Rv2754c, T
DRB5_0101	211	AIECLRQLAAVAPAV	LRQLAAVAP	0.4316	468.7	WB	32.00	Rv2754c, T
DRB5_0101	212	IECLRQLAAVAPAVF	LRQLAAVAP	0.4295	479.4	WB	32.00	Rv2754c, T
DRB5_0101	72	LEHASVSFYITGISR	SFYITGISR	0.4292	481.2	WB	32.00	Rv2754c, T
DRB5_0101	91	ELIRHRHFSYSQLSQ	RHFSYSQLS	0.4256	500.1		32.00	Rv2754c, T
DRB5_0101	63	IIDVGHFSVLEHASV	FSVLEHASV	0.4254	501.0		32.00	Rv2754c, T
DRB5_0101	169	AARAVLPNATETRIV	ARAVLPNAT	0.4249	503.9		32.00	Rv2754c, T
DRB5_0101	40	RACYQSWSKPNPKTA	RACYQSWSK	0.4247	504.8		32.00	Rv2754c, T
DRB5_0101	39	GRACYQSWSKPNPKT	RACYQSWSK	0.4226	516.6		32.00	Rv2754c, T
DRB5_0101	0	VAETAPLRVQLIAKT	VAETAPLRV	0.4218	521.2		32.00	Rv2754c, T
DRB5_0101	37	FAGRACYQSWSKPNP	RACYQSWSK	0.4209	526.1		32.00	Rv2754c, T
DRB5_0101	170	ARAVLPNATETRIVV	ARAVLPNAT	0.4207	527.4		32.00	Rv2754c, T
DRB5_0101	126	DLRHILTEAADAARA	HILTEADA	0.4190	537.2		32.00	Rv2754c, T
DRB5_0101	213	ECLRQLAAVAPAVFA	LRQLAAVAP	0.4188	538.5		32.00	Rv2754c, T
DRB5_0101	137	AARATYSELLAKLEA	ATYSELLAK	0.4182	541.8		32.00	Rv2754c, T
DRB5_0101	38	AGRACYQSWSKPNPK	RACYQSWSK	0.4177	545.0		32.00	Rv2754c, T
DRB5_0101	90	HELIRHRHFSYSQLS	HELIRHRHF	0.4175	545.8		32.00	Rv2754c, T
DRB5_0101	2	ETAPLRVQLIAKTDF	LRVQLIAKT	0.4146	563.7		32.00	Rv2754c, T
DRB5_0101	36	EFAGRACYQSWSKPN	RACYQSWSK	0.4143	564.9		32.00	Rv2754c, T
DRB5_0101	168	QAARAVLPNATETRI	ARAVLPNAT	0.4091	597.7		50.00	Rv2754c, T
DRB5_0101	104	SQRYVPEKDSRVVVP	YVPEKDSRV	0.4069	612.5		50.00	Rv2754c, T
DRB5_0101	125	ADLRHILTEAADAAR	HILTEADA	0.4048	626.7		50.00	Rv2754c, T
DRB5_0101	154	AQPNAILRRKQARQ	ILRRKQARQ	0.4034	635.7		50.00	Rv2754c, T
DRB5_0101	103	LSQRYVPEKDSRVVV	YVPEKDSRV	0.4023	643.2		50.00	Rv2754c, T
DRB5_0101	58	GYLRHIIIDVGHFSVL	LRHIIIDVGH	0.4020	646.0		50.00	Rv2754c, T
DRB5_0101	6	LRVQLIAKTDFLAPP	LRVQLIAKT	0.3995	663.3		50.00	Rv2754c, T
DRB5_0101	141	TYSELLAKLEAKFAD	LLAKLEAKF	0.3979	675.2		50.00	Rv2754c, T
DRB5_0101	35	VEFAGRACYQSWSKP	RACYQSWSK	0.3970	681.2		50.00	Rv2754c, T
DRB5_0101	59	YLRHIIIDVGHFSVLE	LRHIIIDVGH	0.3938	705.5		50.00	Rv2754c, T
DRB5_0101	105	QRYVPEKDSRVVVP	YVPEKDSRV	0.3930	711.9		50.00	Rv2754c, T
DRB5_0101	136	DAARATYSELLAKLE	ATYSELLAK	0.3926	715.0		50.00	Rv2754c, T
DRB5_0101	57	AGYLRHIIIDVGHFSV	LRHIIIDVGH	0.3910	727.1		50.00	Rv2754c, T
DRB5_0101	214	CLRQLAAVAPAVFAD	LRQLAAVAP	0.3886	746.5		50.00	Rv2754c, T
DRB5_0101	32	PALVEFAGRACYQSW	ALVEFAGRA	0.3873	757.0		50.00	Rv2754c, T
DRB5_0101	142	YSELLAKLEAKFADQ	LLAKLEAKF	0.3842	783.1		50.00	Rv2754c, T
DRB5_0101	31	GPALVEFAGRACYQS	ALVEFAGRA	0.3806	813.7		50.00	Rv2754c, T
DRB5_0101	127	LRHILTEAADAARAT	HILTEADA	0.3782	835.6		50.00	Rv2754c, T
DRB5_0101	1	AETAPLRVQLIAKT	LRVQLIAKT	0.3755	860.4		50.00	Rv2754c, T
DRB5_0101	33	ALVEFAGRACYQSW	ALVEFAGRA	0.3728	885.6		50.00	Rv2754c, T
DRB5_0101	89	THELIRHRHFSYSQL	HELIRHRHF	0.3727	886.7		50.00	Rv2754c, T
DRB5_0101	167	RQAARAVLPNATETR	ARAVLPNAT	0.3718	895.2		50.00	Rv2754c, T
DRB5_0101	106	RYVPEKDSRVVVP	YVPEKDSRV	0.3715	898.3		50.00	Rv2754c, T
DRB5_0101	171	RAVLPNATETRIVVT	LPNATETRI	0.3699	913.4		50.00	Rv2754c, T
DRB5_0101	56	NAGYLRHIIIDVGHFS	LRHIIIDVGH	0.3697	916.0		50.00	Rv2754c, T
DRB5_0101	124	DADLRHILTEAADA	LRHILTEAA	0.3695	917.6		50.00	Rv2754c, T
DRB5_0101	162	RRKQARQAARAVLPN	RKQARQAAR	0.3689	923.2		50.00	Rv2754c, T
DRB5_0101	143	SELLAKLEAKFADQP	LLAKLEAKF	0.3685	927.2		50.00	Rv2754c, T
DRB5_0101	102	QLSQRYVPEKDSRVV	YVPEKDSRV	0.3685	927.4		50.00	Rv2754c, T
DRB5_0101	202	HADVEIRRLAIECLR	RRLAIECLR	0.3625	989.5		50.00	Rv2754c, T
DRB5_0101	30	GGPALVEFAGRACYQ	ALVEFAGRA	0.3620	994.9		50.00	Rv2754c, T
DRB5_0101	60	LRHIIIDVGHFSVLEH	LRHIIIDVGH	0.3619	996.9		50.00	Rv2754c, T
DRB5_0101	163	RKQARQAARAVLPNA	RKQARQAAR	0.3608	1008.5		50.00	Rv2754c, T
DRB5_0101	55	TNAGYLRHIIIDVGHF	LRHIIIDVGH	0.3586	1032.8		50.00	Rv2754c, T
DRB5_0101	144	ELLAKLEAKFADQPN	LLAKLEAKF	0.3574	1046.2		50.00	Rv2754c, T
DRB5_0101	135	ADAARATYSELLAKL	ATYSELLAK	0.3556	1066.4		50.00	Rv2754c, T
DRB5_0101	99	SYSQLSQRYVPEKDS	SYSQLSQRY	0.3548	1076.3		50.00	Rv2754c, T
DRB5_0101	128	RHILTEAADAARATY	HILTEADA	0.3474	1165.3		50.00	Rv2754c, T

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DRB5_0101	54	ATNAGYLRHIIDVGH	LRHIIDVGH	0.3433	1219.0	50.00	Rv2754c, T
DRB5_0101	34	LVEFAGRACYQSWSK	FAGRACYQS	0.3349	1334.2	50.00	Rv2754c, T
DRB5_0101	166	ARQAARAVLPNATET	ARAVLPNAT	0.3336	1353.2	50.00	Rv2754c, T
DRB5_0101	153	FADQPNAILRRKQAR	AILRRKQAR	0.3331	1361.3	50.00	Rv2754c, T
DRB5_0101	123	DDADLRHILTEAADA	LRHILTEAA	0.3306	1397.6	50.00	Rv2754c, T
DRB5_0101	101	SQLSQRYVPEKDSRV	YVPEKDSRV	0.3297	1411.5	50.00	Rv2754c, T
DRB5_0101	165	QQAARAVLPNATE	ARAVLPNAT	0.3294	1416.4	50.00	Rv2754c, T
DRB5_0101	81	ITGISRSCTHELIRH	RSCTHELIR	0.3275	1445.4	50.00	Rv2754c, T
DRB5_0101	145	LLAKLEAKFADQPNA	LLAKLEAKF	0.3251	1483.9	50.00	Rv2754c, T
DRB5_0101	29	DGGPALVEFAGRACY	ALVEFAGRA	0.3234	1512.0	50.00	Rv2754c, T
DRB5_0101	80	YITGISRSCTHELIR	YITGISRSC	0.3152	1652.3	50.00	Rv2754c, T
DRB5_0101	215	LRQLAAVAPAVFADF	LRQLAAVAP	0.3127	1696.9	50.00	Rv2754c, T
DRB5_0101	70	SVLEHASVVSFYITGI	LEHASVVSFY	0.3087	1772.2	50.00	Rv2754c, T
DRB5_0101	41	ACYQSWSKPNPKTAT	QSWSKPNPK	0.3078	1788.3	50.00	Rv2754c, T
DRB5_0101	164	KQARQAARAVLPNAT	ARQAARAVL	0.3063	1818.3	50.00	Rv2754c, T
DRB5_0101	71	VLEHASVVSFYITGIS	LEHASVVSFY	0.2937	2084.4	50.00	Rv2754c, T
DRB5_0101	151	AKFADQPNAILRRKQ	FADQPNAIL	0.2894	2183.9	50.00	Rv2754c, T
DRB5_0101	152	KFADQPNAILRRKQA	FADQPNAIL	0.2882	2211.2	50.00	Rv2754c, T
DRB5_0101	150	EAKFADQPNAILRRK	FADQPNAIL	0.2877	2224.2	50.00	Rv2754c, T
DRB5_0101	172	AVLPNATETRIVVTG	VLPNATETR	0.2862	2259.4	50.00	Rv2754c, T
DRB5_0101	134	AADAARATYSELLAK	ATYSELLAK	0.2842	2309.6	50.00	Rv2754c, T
DRB5_0101	107	YVPEKDSRVVPPGM	YVPEKDSRV	0.2781	2468.3	50.00	Rv2754c, T
DRB5_0101	61	RHIIDVGHFVSLEHA	RHIIDVGHF	0.2764	2513.2	50.00	Rv2754c, T
DRB5_0101	62	HIIDVGHFVSLEHAS	HFSVLEHAS	0.2748	2557.3	50.00	Rv2754c, T
DRB5_0101	149	LEAKFADQPNAILRR	KFADQPNAI	0.2711	2661.6	50.00	Rv2754c, T
DRB5_0101	173	VLPNATETRIVVTGN	LPNATETRI	0.2703	2683.2	50.00	Rv2754c, T
DRB5_0101	28	ADGGPALVEFAGRAC	ALVEFAGRA	0.2672	2775.8	50.00	Rv2754c, T
DRB5_0101	201	EHADVEIRRLAIECL	HADVEIRRL	0.2560	3133.3	50.00	Rv2754c, T
DRB5_0101	53	TATNAGYLRHIIDVG	ATNAGYLRH	0.2558	3141.3	50.00	Rv2754c, T
DRB5_0101	122	EDDADLRHILTEAAD	LRHILTEAA	0.2534	3222.0	50.00	Rv2754c, T
DRB5_0101	200	SEHADVEIRRLAIEC	HADVEIRRL	0.2498	3351.2	50.00	Rv2754c, T
DRB5_0101	129	HILTEAADAARATYS	HILTEAADA	0.2488	3385.6	50.00	Rv2754c, T
DRB5_0101	100	YSQLSQRYVPEKDSR	YSQLSQRYV	0.2431	3604.2	50.00	Rv2754c, T
DRB5_0101	50	NPKTATNAGYLRHII	PKTATNAGY	0.2411	3681.9	50.00	Rv2754c, T
DRB5_0101	27	DADGGPALVEFAGRA	ALVEFAGRA	0.2346	3949.3	50.00	Rv2754c, T
DRB5_0101	226	FADFEVTTLDGTEV	FEVTTLDAG	0.2343	3962.8	50.00	Rv2754c, T
DRB5_0101	51	PKTATNAGYLRHII	ATNAGYLRH	0.2318	4072.5	50.00	Rv2754c, T
DRB5_0101	227	ADFEVTTLDGTEVA	FEVTTLDAG	0.2312	4096.6	50.00	Rv2754c, T
DRB5_0101	148	KLEAKFADQPNAILR	KFADQPNAI	0.2300	4152.0	50.00	Rv2754c, T
DRB5_0101	199	ASEHADVEIRRLAIE	HADVEIRRL	0.2288	4204.0	50.00	Rv2754c, T
DRB5_0101	216	RQLAAVAPAVFADFE	AAVAPAVFA	0.2284	4224.3	50.00	Rv2754c, T
DRB5_0101	42	CYQSWSKPNPKTATN	QSWSKPNPK	0.2254	4363.5	50.00	Rv2754c, T
DRB5_0101	174	LPNATETRIVVTGNY	LPNATETRI	0.2235	4454.5	50.00	Rv2754c, T
DRB5_0101	228	DFEVTTLDGTEVAT	FEVTTLDAG	0.2233	4465.8	50.00	Rv2754c, T
DRB5_0101	195	IAMRASEHADVEIRR	IAMRASEHA	0.2232	4466.9	50.00	Rv2754c, T
DRB5_0101	225	VFADFEVTTLDGTE	FEVTTLDAG	0.2227	4492.8	50.00	Rv2754c, T
DRB5_0101	52	KTATNAGYLRHII	ATNAGYLRH	0.2168	4788.6	50.00	Rv2754c, T
DRB5_0101	49	PNPKTATNAGYLRHI	PKTATNAGY	0.2141	4929.7	50.00	Rv2754c, T
DRB5_0101	111	KDSRVVPPGMEDDA	RVVVPPGME	0.2084	5245.3	50.00	Rv2754c, T
DRB5_0101	198	RASEHADVEIRRLAI	HADVEIRRL	0.2044	5476.7	50.00	Rv2754c, T
DRB5_0101	110	EKDSRVVPPGMEDD	RVVVPPGME	0.2010	5679.7	50.00	Rv2754c, T
DRB5_0101	121	MEDDADLRHILTEAA	LRHILTEAA	0.2006	5705.1	50.00	Rv2754c, T
DRB5_0101	224	AVFADFEVTTLDGHT	FEVTTLDAG	0.1989	5813.3	50.00	Rv2754c, T
DRB5_0101	48	KPNPKTATNAGYLRH	PKTATNAGY	0.1968	5944.7	50.00	Rv2754c, T
DRB5_0101	109	PEKDSRVVPPGMED	RVVVPPGME	0.1940	6131.2	50.00	Rv2754c, T
DRB5_0101	112	DSRVVPPGMEDDAD	RVVVPPGME	0.1914	6306.5	50.00	Rv2754c, T
DRB5_0101	133	EAADAARATYSELLA	ADAARATYS	0.1821	6973.5	50.00	Rv2754c, T
DRB5_0101	217	QLAAVAPAVFADFEV	AAVAPAVFA	0.1818	6991.8	50.00	Rv2754c, T
DRB5_0101	43	YQSWSKPNPKTATNA	QSWSKPNPK	0.1791	7203.3	50.00	Rv2754c, T
DRB5_0101	196	AMRASEHADVEIRRL	HADVEIRRL	0.1781	7280.9	50.00	Rv2754c, T
DRB5_0101	113	SRVVVPPGMEDDADL	RVVVPPGME	0.1768	7378.6	50.00	Rv2754c, T
DRB5_0101	7	RVQLIAKTDFLAPPD	LIAKTDFLA	0.1753	7504.2	50.00	Rv2754c, T
DRB5_0101	223	PAVFADFEVTTLDAG	FEVTTLDAG	0.1751	7518.6	50.00	Rv2754c, T
DRB5_0101	229	FEVTTLDAGTEVATS	FEVTTLDAG	0.1704	7907.8	50.00	Rv2754c, T
DRB5_0101	44	QSWSKPNPKTATNAG	QSWSKPNPK	0.1693	8003.1	50.00	Rv2754c, T
DRB5_0101	47	SKPNPKTATNAGYLR	PKTATNAGY	0.1630	8568.9	50.00	Rv2754c, T
DRB5_0101	146	LAKLEAKFADQPNAI	LAKLEAKFA	0.1630	8569.1	50.00	Rv2754c, T
DRB5_0101	235	ADGTEVATSPLATEA	EVATSPLAT	0.1624	8627.4	50.00	Rv2754c, T
DRB5_0101	130	ILTEAADAARATYSE	LTEAADAAR	0.1619	8677.5	50.00	Rv2754c, T
DRB5_0101	197	MRASEHADVEIRRLA	HADVEIRRL	0.1592	8927.8	50.00	Rv2754c, T
DRB5_0101	147	AKLEAKFADQPNAIL	FADQPNAIL	0.1577	9073.0	50.00	Rv2754c, T
DRB5_0101	131	LTEAADAARATYSEL	LTEAADAAR	0.1557	9272.4	50.00	Rv2754c, T
DRB5_0101	46	WSKPNPKTATNAGYL	PKTATNAGY	0.1540	9447.2	50.00	Rv2754c, T
DRB5_0101	234	LADGTEVATSPLATE	EVATSPLAT	0.1503	9836.6	50.00	Rv2754c, T
DRB5_0101	45	SWSKPNPKTATNAGY	WSKPNPKTA	0.1501	9858.0	50.00	Rv2754c, T
DRB5_0101	8	VQLIAKTDFLAPPDV	QLIAKTDFL	0.1478	10100.5	50.00	Rv2754c, T
DRB5_0101	114	RVVVPPGMEDDADLR	RVVVPPGME	0.1443	10494.9	50.00	Rv2754c, T
DRB5_0101	108	VPEKDSRVVPPGME	SRVVVPPGM	0.1438	10549.6	50.00	Rv2754c, T
DRB5_0101	12	AKTDFLAPPDVPWTT	FLAPPDVPW	0.1429	10653.0	50.00	Rv2754c, T
DRB5_0101	13	KTDFLAPPDVPWTTD	FLAPPDVPW	0.1419	10770.9	50.00	Rv2754c, T
DRB5_0101	11	IAKTDFLAPPDVPWT	FLAPPDVPW	0.1315	12047.5	50.00	Rv2754c, T
DRB5_0101	132	TEAADAARATYSELL	ADAARATYS	0.1299	12258.6	50.00	Rv2754c, T
DRB5_0101	218	LAAVAPAVFADFEV	AAVAPAVFA	0.1292	12361.3	50.00	Rv2754c, T
DRB5_0101	9	QLIAKTDFLAPPDVP	QLIAKTDFL	0.1281	12507.4	50.00	Rv2754c, T
DRB5_0101	14	TDFLAPPDVPWTTDA	FLAPPDVPW	0.1278	12541.2	50.00	Rv2754c, T

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DRB5_0101	10	LIAKTDFLAPPDVPW	LIAKTDFLA	0.1270	12647.9	50.00	Rv2754c, T
DRB5_0101	233	TLADGTEVATSPLAT	EVATSPLAT	0.1268	12682.0	50.00	Rv2754c, T
DRB5_0101	120	GMEDDADLRHILTEA	GMEDDADLR	0.1172	14076.1	50.00	Rv2754c, T
DRB5_0101	222	APAVFADFVEVTTLAD	FADFVEVTTL	0.1148	14445.3	50.00	Rv2754c, T
DRB5_0101	15	DFLAPPDVPWTTDAD	FLAPPDVPW	0.1039	16244.3	50.00	Rv2754c, T
DRB5_0101	219	AAVAPAVFADFVTT	AAVAPAVFA	0.1005	16848.2	50.00	Rv2754c, T
DRB5_0101	221	VAPAVFADFVEVTTLA	FADFVEVTTL	0.0960	17701.1	50.00	Rv2754c, T
DRB5_0101	232	TTLADGTEVATSPLA	GTEVATSPL	0.0906	18768.0	50.00	Rv2754c, T
DRB5_0101	220	AVAPAVFADFVEVTTL	FADFVEVTTL	0.0870	19513.0	50.00	Rv2754c, T
DRB5_0101	119	PGMEDDADLRHILTE	GMEDDADLR	0.0845	20035.9	50.00	Rv2754c, T
DRB5_0101	231	VTTLADGTEVATSPL	GTEVATSPL	0.0811	20785.3	50.00	Rv2754c, T
DRB5_0101	26	TDADGGPALVEFAGR	PALVEFAGR	0.0803	20964.0	50.00	Rv2754c, T
DRB5_0101	118	PPGMEDDADLRHILT	GMEDDADLR	0.0803	20966.0	50.00	Rv2754c, T
DRB5_0101	230	EVTTLADGTEVATSP	EVTTLADGT	0.0770	21723.2	50.00	Rv2754c, T
DRB5_0101	16	FLAPPDVPWTTDADG	FLAPPDVPW	0.0766	21821.0	50.00	Rv2754c, T
DRB5_0101	115	VVPPGMEDDADLRH	VVPPGMED	0.0753	22141.1	50.00	Rv2754c, T
DRB5_0101	117	VPPGMEDDADLRHIL	GMEDDADLR	0.0709	23218.6	50.00	Rv2754c, T
DRB5_0101	19	PPDVPWTTDADGGPA	VPWTTDADG	0.0617	25636.9	50.00	Rv2754c, T
DRB5_0101	116	VVPPGMEDDADLRHI	GMEDDADLR	0.0617	25658.5	50.00	Rv2754c, T
DRB5_0101	18	APPDVPWTTDADGGP	VPWTTDADG	0.0605	25995.8	50.00	Rv2754c, T
DRB5_0101	17	LAPPDVPWTTDADGG	VPWTTDADG	0.0603	26034.9	50.00	Rv2754c, T
DRB5_0101	21	DVPWTTDADGGPALV	VPWTTDADG	0.0591	26384.9	50.00	Rv2754c, T
DRB5_0101	20	PDPWTTDADGGPAL	VPWTTDADG	0.0576	26817.4	50.00	Rv2754c, T
DRB5_0101	22	VPWTTDADGGPALVE	VPWTTDADG	0.0486	29540.1	50.00	Rv2754c, T
DRB5_0101	23	PWTTDADGGPALVEF	PWTTDADGG	0.0386	32934.5	50.00	Rv2754c, T
DRB5_0101	24	WTTDADGGPALVEFA	WTTDADGGP	0.0383	33043.7	50.00	Rv2754c, T
DRB5_0101	25	TTDADGGPALVEFAG	DADGGPALV	0.0310	35754.8	50.00	Rv2754c, T

Allele: DRB5_0101. Number of high binders 21. Number of weak binders 50. Number of peptides 236

Allele	pos	peptide	core	l-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
IAb	215	LRQLAAVAPAVFADF	RQLAAVAPA	0.6798	32.0	SB	0.80	Rv2754c, T
IAb	214	CLRQLAAVAPAVFAD	RQLAAVAPA	0.6729	34.4	SB	0.80	Rv2754c, T
IAb	213	ECLRQLAAVAPAVFA	RQLAAVAPA	0.6608	39.3	SB	0.80	Rv2754c, T
IAb	216	QLAAVAPAVFADFE	QLAAVAPAV	0.6410	48.6	SB	1.00	Rv2754c, T
IAb	188	YRAWRHFIAMRASEH	WRHFIAMRA	0.6259	57.3	WB	2.00	Rv2754c, T
IAb	189	RAWRHFIAMRASEHA	WRHFIAMRA	0.6154	64.2	WB	2.00	Rv2754c, T
IAb	212	IECLRQLAAVAPAVF	RQLAAVAPA	0.6025	73.8	WB	2.00	Rv2754c, T
IAb	187	NYRAWRHFIAMRASE	WRHFIAMRA	0.5982	77.3	WB	2.00	Rv2754c, T
IAb	165	QARQAARAVLPNATE	ARAVLPNAT	0.5892	85.2	WB	2.00	Rv2754c, T
IAb	164	KQARQAARAVLPNAT	ARAVLPNAT	0.5857	88.5	WB	2.00	Rv2754c, T
IAb	190	AWRHFIAMRASEHAD	RHFIAMRAS	0.5761	98.1	WB	2.00	Rv2754c, T
IAb	191	WRHFIAMRASEHADV	RHFIAMRAS	0.5727	101.9	WB	4.00	Rv2754c, T
IAb	186	GNYRAWRHFIAMRAS	WRHFIAMRA	0.5720	102.6	WB	4.00	Rv2754c, T
IAb	235	ADGTEVATSPLATEA	EVATSPLAT	0.5676	107.6	WB	4.00	Rv2754c, T
IAb	167	RQAARAVLPNATETR	QAARAVLPN	0.5654	110.1	WB	4.00	Rv2754c, T
IAb	166	ARQAARAVLPNATET	QAARAVLPN	0.5584	118.8	WB	4.00	Rv2754c, T
IAb	217	QLAAVAPAVFADFEV	QLAAVAPAV	0.5560	122.0	WB	4.00	Rv2754c, T
IAb	163	RKQARQAARAVLPNA	QARQAARAV	0.5244	171.7	WB	4.00	Rv2754c, T
IAb	168	QAARAVLPNATETRI	QAARAVLPN	0.5152	189.6	WB	4.00	Rv2754c, T
IAb	211	AIECLRQLAAVAPAV	RQLAAVAPA	0.5109	198.7	WB	8.00	Rv2754c, T
IAb	185	TGNYRAWRHFIAMRA	RAWRHFIAM	0.5050	211.8	WB	8.00	Rv2754c, T
IAb	192	RHFIAMRASEHADVE	FIAMRASEH	0.5006	222.3	WB	8.00	Rv2754c, T
IAb	234	LADGTEVATSPLATE	EVATSPLAT	0.4857	261.0	WB	8.00	Rv2754c, T
IAb	162	RRKQARQAARAVLPN	QARQAARAV	0.4754	291.7	WB	8.00	Rv2754c, T
IAb	13	KTDFLAPPDVPWTTD	TDFLAPPDV	0.4694	311.4	WB	8.00	Rv2754c, T
IAb	113	SRVVVPPGMEDDADL	RVVVPPGME	0.4688	313.5	WB	8.00	Rv2754c, T
IAb	43	QSWSKPNPKTATNA	QSWSKPNPK	0.4647	327.8	WB	8.00	Rv2754c, T
IAb	112	DSRVVVPPGMEDDAD	RVVVPPGME	0.4634	332.2	WB	8.00	Rv2754c, T
IAb	12	AKTDFLAPPDVPWTT	TDFLAPPDV	0.4624	335.9	WB	8.00	Rv2754c, T
IAb	111	KDSRVVVPPGMEDDA	RVVVPPGME	0.4620	337.2	WB	8.00	Rv2754c, T
IAb	42	CYQSWSKPNPKTATN	QSWSKPNPK	0.4536	369.2	WB	8.00	Rv2754c, T
IAb	169	AARAVLPNATETRIV	ARAVLPNAT	0.4524	374.4	WB	8.00	Rv2754c, T
IAb	161	LRRKQARQAARAVLP	QARQAARAV	0.4473	395.4	WB	8.00	Rv2754c, T
IAb	11	IAKTDFLAPPDVPWPT	TDFLAPPDV	0.4449	405.7	WB	8.00	Rv2754c, T
IAb	41	ACYQSWSKPNPKTAT	QSWSKPNPK	0.4414	421.6	WB	8.00	Rv2754c, T
IAb	233	TLADGTEVATSPLAT	EVATSPLAT	0.4355	449.4	WB	8.00	Rv2754c, T
IAb	14	TDFLAPPDVPWTTDA	TDFLAPPDV	0.4293	480.3	WB	16.00	Rv2754c, T
IAb	170	ARAVLPNATETRIVV	ARAVLPNAT	0.4285	484.5	WB	16.00	Rv2754c, T
IAb	44	QSWSKPNPKTATNAG	WSKPNPKTA	0.4283	486.0	WB	16.00	Rv2754c, T
IAb	110	EKDSRVVVPPGMEDD	RVVVPPGME	0.4259	498.7	WB	16.00	Rv2754c, T
IAb	40	RACYQSWSKPNPKTA	QSWSKPNPK	0.4154	558.7	WB	16.00	Rv2754c, T
IAb	132	TEAADAARATYSELL	EAADAARAT	0.4103	590.1	WB	16.00	Rv2754c, T
IAb	130	ILTEAADAARATYSE	EAADAARAT	0.4058	619.6	WB	16.00	Rv2754c, T
IAb	131	LTEAADAARATYSEL	EAADAARAT	0.4050	625.2	WB	16.00	Rv2754c, T
IAb	218	LAAVAPAVFADFVEV	LAAVAPAVF	0.4033	636.4	WB	16.00	Rv2754c, T
IAb	76	SVSFYITGISRSTH	SFYITGISR	0.3996	662.9	WB	16.00	Rv2754c, T
IAb	95	HRHFSYSQLSQRYP	RHFSYSQLS	0.3923	716.8	WB	16.00	Rv2754c, T
IAb	109	PEKDSRVVVPPGMED	RVVVPPGME	0.3920	719.5	WB	16.00	Rv2754c, T
IAb	133	EAADAARATYSELLA	EAADAARAT	0.3895	738.9	WB	16.00	Rv2754c, T
IAb	94	RHRHFSYSQLSQRYP	RHFSYSQLS	0.3884	748.0	WB	16.00	Rv2754c, T

IAb	114	RVVVPPGMEDDADLR	RVVVPPGME	0.3882	749.7	16.00	Rv2754c, T
IAb	77	VSFYITGISRSCTHE	SFYITGISR	0.3865	763.3	16.00	Rv2754c, T
IAb	75	ASVSFYITGISRSCT	SFYITGISR	0.3857	770.2	16.00	Rv2754c, T
IAb	129	HILTEAADAARATYS	EAADAARAT	0.3822	800.1	16.00	Rv2754c, T
IAb	193	HFIAMRASEHADVEI	FIAMRASEH	0.3793	825.8	16.00	Rv2754c, T
IAb	93	IRHRHFSYSQLSQRY	RHFSYSQLS	0.3788	829.6	16.00	Rv2754c, T
IAb	210	LAIECLRQLAAVAPA	RQLAAVAPA	0.3756	859.1	16.00	Rv2754c, T
IAb	96	RHFSYSQLSQRYVPE	RHFSYSQLS	0.3679	933.6	16.00	Rv2754c, T
IAb	10	LIAKTDFLAPPDVPW	TDFLAPPDV	0.3676	936.7	16.00	Rv2754c, T
IAb	74	HASVSFYITGISRSCT	SFYITGISR	0.3595	1022.8	16.00	Rv2754c, T
IAb	15	DFLAPPDVPWTTDAD	DFLAPPDVP	0.3563	1058.1	16.00	Rv2754c, T
IAb	45	SWSKPNPKTATNAGY	WSKPNPKTA	0.3546	1078.0	16.00	Rv2754c, T
IAb	46	WSKPNPKTATNAGYL	WSKPNPKTA	0.3503	1129.1	16.00	Rv2754c, T
IAb	160	ILRRKQARQAARAVL	QARQAARAV	0.3503	1129.2	16.00	Rv2754c, T
IAb	92	LIRHRHFSYSQLSQR	RHFSYSQLS	0.3498	1136.2	16.00	Rv2754c, T
IAb	194	FIAMRASEHADVEIR	FIAMRASEH	0.3488	1147.7	16.00	Rv2754c, T
IAb	137	AARATYSELLAKLEA	ATYSELLAK	0.3478	1160.2	16.00	Rv2754c, T
IAb	149	LEAKFADQPNAILRR	KFADQPNAI	0.3418	1238.2	32.00	Rv2754c, T
IAb	171	RAVLPNATETRIVVV	RAVLPNATE	0.3406	1255.2	32.00	Rv2754c, T
IAb	135	ADAARATYSELLAKL	RATYSELLA	0.3399	1264.6	32.00	Rv2754c, T
IAb	39	GRACYQSWSKPNPKT	QSWSKPNPK	0.3346	1338.2	32.00	Rv2754c, T
IAb	136	DAARATYSELLAKLE	RATYSELLA	0.3310	1391.3	32.00	Rv2754c, T
IAb	148	KLEAKFADQPNAILR	KFADQPNAI	0.3291	1420.4	32.00	Rv2754c, T
IAb	108	VPEKDSRVVPPGME	RVVVPPGME	0.3279	1439.9	32.00	Rv2754c, T
IAb	138	ARATYSELLAKLEAK	ATYSELLAK	0.3279	1440.2	32.00	Rv2754c, T
IAb	128	RHILTEAADAARATY	TEAADAARA	0.3256	1475.4	32.00	Rv2754c, T
IAb	150	EAKFADQPNAILRRK	KFADQPNAI	0.3223	1528.7	32.00	Rv2754c, T
IAb	147	AKLEAKFADQPNAIL	KFADQPNAI	0.3213	1545.3	32.00	Rv2754c, T
IAb	146	LAKLEAKFADQPNAI	KFADQPNAI	0.3211	1549.6	32.00	Rv2754c, T
IAb	9	QLIAKTDFLAPPDVP	TDFLAPPDV	0.3187	1590.5	32.00	Rv2754c, T
IAb	78	SFYITGISRSCTHEL	SFYITGISR	0.3184	1595.5	32.00	Rv2754c, T
IAb	184	VTGNYPRAWRHFIAMR	RAWRHFIAM	0.3159	1639.1	32.00	Rv2754c, T
IAb	134	AADAARATYSELLAK	ADAARATYS	0.3141	1671.8	32.00	Rv2754c, T
IAb	73	EHASVSFYITGISRS	FYITGISRS	0.3064	1816.3	32.00	Rv2754c, T
IAb	38	AGRACYQSWSKPNPK	QSWSKPNPK	0.3038	1868.5	32.00	Rv2754c, T
IAb	127	LRHILTEAADAARAT	EAADAARAT	0.3003	1939.6	32.00	Rv2754c, T
IAb	159	AILRRKQARQAARAV	QARQAARAV	0.3002	1943.3	32.00	Rv2754c, T
IAb	139	RATYSELLAKLEAKF	ATYSELLAK	0.2919	2125.7	32.00	Rv2754c, T
IAb	183	VVTGNYPRAWRHFIAM	RAWRHFIAM	0.2875	2228.4	32.00	Rv2754c, T
IAb	66	VGHFSVLEHASVSFY	GHFSVLEHA	0.2847	2296.9	32.00	Rv2754c, T
IAb	67	GHFSVLEHASVSFYI	SVLEHASVS	0.2842	2308.6	32.00	Rv2754c, T
IAb	172	AVLPNATETRIVVVGT	AVLPNATET	0.2816	2375.2	32.00	Rv2754c, T
IAb	70	SVLEHASVSFYITGI	SVLEHASVS	0.2798	2421.8	32.00	Rv2754c, T
IAb	91	ELIRHRHFSYSQLSQ	RHFSYSQLS	0.2783	2462.0	32.00	Rv2754c, T
IAb	69	FSVLEHASVSFYITG	SVLEHASVS	0.2726	2617.4	32.00	Rv2754c, T
IAb	219	AAVAPAVFADFVETT	AAVAPAVFA	0.2659	2814.3	32.00	Rv2754c, T
IAb	68	HFSVLEHASVSFYIT	SVLEHASVS	0.2650	2843.0	32.00	Rv2754c, T
IAb	72	LEHASVSFYITGISR	VSFYITGIS	0.2637	2882.4	32.00	Rv2754c, T
IAb	0	VAETAPLRVQLIAKT	VAETAPLRV	0.2634	2891.4	32.00	Rv2754c, T
IAb	16	FLAPPDVPWTTDADG	APPDVPWTT	0.2591	3029.8	32.00	Rv2754c, T
IAb	151	AKFADQPNAILRRKQ	KFADQPNAI	0.2524	3256.8	32.00	Rv2754c, T
IAb	232	TTLADGTEVATSPLA	TEVATSPLA	0.2519	3276.1	32.00	Rv2754c, T
IAb	17	LAPPDVPWTTDADGG	APPDVPWTT	0.2511	3304.0	32.00	Rv2754c, T
IAb	223	PAVFADFEVTTLDAG	AVFADFEVT	0.2481	3412.9	32.00	Rv2754c, T
IAb	145	LLAKLEAKFADQPN	AKLEAKFAD	0.2466	3470.6	32.00	Rv2754c, T
IAb	224	AVFADFEVTTLDAGT	AVFADFEVT	0.2429	3609.1	50.00	Rv2754c, T
IAb	126	DLRHILTEAADAARA	ILTEAADAA	0.2372	3838.6	50.00	Rv2754c, T
IAb	144	ELLAKLEAKFADQPN	AKLEAKFAD	0.2367	3860.3	50.00	Rv2754c, T
IAb	140	ATYSELLAKLEAKFA	ATYSELLAK	0.2349	3938.5	50.00	Rv2754c, T
IAb	222	APAVFADFEVTTLD	AVFADFEVT	0.2346	3950.8	50.00	Rv2754c, T
IAb	8	VQLIAKTDFLAPPDV	TDFLAPPDV	0.2315	4086.8	50.00	Rv2754c, T
IAb	25	TTDADGGPALVEFAG	DADGGPALV	0.2286	4217.2	50.00	Rv2754c, T
IAb	221	VAPAVFADFEVTTLA	AVFADFEVT	0.2273	4276.1	50.00	Rv2754c, T
IAb	65	DVGHFSVLEHASVSF	GHFSVLEHA	0.2251	4379.5	50.00	Rv2754c, T
IAb	26	TDADGGPALVEFAGR	TDADGGPAL	0.2247	4395.2	50.00	Rv2754c, T
IAb	79	FYITGISRSCTHELI	FYITGISRS	0.2247	4398.3	50.00	Rv2754c, T
IAb	24	WTTDADGGPALVEFA	DADGGPALV	0.2225	4502.1	50.00	Rv2754c, T
IAb	71	VLEHASVSFYITGIS	VSFYITGIS	0.2220	4524.5	50.00	Rv2754c, T
IAb	152	KFADQPNAILRRKQA	KFADQPNAI	0.2202	4615.5	50.00	Rv2754c, T
IAb	90	HELIRHRHFSYSQLS	RHFSYSQLS	0.2189	4682.7	50.00	Rv2754c, T
IAb	195	IAMRASEHADVEIRR	IAMRASEHA	0.2162	4822.6	50.00	Rv2754c, T
IAb	37	FAGRACYQSWSKPNP	YQSWSKPNP	0.2142	4928.0	50.00	Rv2754c, T
IAb	231	VTTLDAGTEVATSPL	TLADGTEVA	0.2134	4970.3	50.00	Rv2754c, T
IAb	64	IDVGHFSVLEHASVS	GHFSVLEHA	0.2129	4996.0	50.00	Rv2754c, T
IAb	103	LSQRYVPEKDSRVVV	SQRYVPEKD	0.2124	5022.6	50.00	Rv2754c, T
IAb	209	RLAIECLRQLAAVAP	LRQLAAVAP	0.2120	5043.0	50.00	Rv2754c, T
IAb	220	AVAPAVFADFEVTTL	AVFADFEVT	0.2109	5104.7	50.00	Rv2754c, T
IAb	1	AETAPLRVQLIAKT	AETAPLRVQ	0.2089	5215.1	50.00	Rv2754c, T
IAb	173	VLPNATETRIVVVGTN	VLPNATETR	0.2072	5315.9	50.00	Rv2754c, T
IAb	104	SQRYVPEKDSRVVVP	SQRYVPEKD	0.2042	5489.5	50.00	Rv2754c, T
IAb	143	SELLAKLEAKFADQP	LAKLEAKFA	0.2036	5522.8	50.00	Rv2754c, T
IAb	102	QLSQRYVPEKDSRVV	SQRYVPEKD	0.2033	5539.5	50.00	Rv2754c, T
IAb	97	HFSYSQLSQRYVPEK	HFSYSQLSQ	0.2028	5573.2	50.00	Rv2754c, T
IAb	21	DVPWTTDADGGPALV	TDADGGPAL	0.1957	6019.5	50.00	Rv2754c, T
IAb	225	VFADFEVTTLDAGTE	ADFEVTTLA	0.1955	6029.9	50.00	Rv2754c, T

IAb	226	FADFEVTTLADGTEV	ADFEVTTLA	0.1953	6041.7	50.00	Rv2754c, T
IAb	47	SKPNPKTATNAGYLR	PNPKTATNA	0.1938	6143.7	50.00	Rv2754c, T
IAb	230	EVTTLADGTEVATSP	TLADGTEVA	0.1937	6145.7	50.00	Rv2754c, T
IAb	125	ADLRHILTEAADAAAR	ILTEAADAA	0.1937	6151.6	50.00	Rv2754c, T
IAb	158	NAILRRKQARQAARA	LRRKQARQA	0.1925	6227.6	50.00	Rv2754c, T
IAb	33	ALVEFAGRACYQSW	VEFAGRACY	0.1888	6482.2	50.00	Rv2754c, T
IAb	101	SQLSQRYVPEKDSRV	SQRYVPEKD	0.1880	6541.6	50.00	Rv2754c, T
IAb	23	PWTTDADGGPALVEF	TDADGGPAL	0.1876	6569.3	50.00	Rv2754c, T
IAb	63	IIDVGHFSVLEHASV	GHFSVLEHA	0.1870	6613.3	50.00	Rv2754c, T
IAb	32	PALVEFAGRACYQSW	VEFAGRACY	0.1862	6669.7	50.00	Rv2754c, T
IAb	142	YSELLAKLEAKFADQ	YSELLAKLE	0.1836	6858.4	50.00	Rv2754c, T
IAb	34	LVEFAGRACYQSWSK	VEFAGRACY	0.1825	6943.0	50.00	Rv2754c, T
IAb	141	TYSELLAKLEAKFAD	YSELLAKLE	0.1814	7024.8	50.00	Rv2754c, T
IAb	49	PNPKTATNAGYLRHI	PNPKTATNA	0.1814	7026.1	50.00	Rv2754c, T
IAb	27	DADGGPALVEFAGRA	DADGGPALV	0.1789	7213.8	50.00	Rv2754c, T
IAb	18	APPDVPWTTDADGGP	APPDVPWTT	0.1788	7221.4	50.00	Rv2754c, T
IAb	3	TAPLRVQLIAKTDFL	RVQLIAKTD	0.1788	7227.0	50.00	Rv2754c, T
IAb	182	IVVTGNYRAWRHFI	YRAWRHFI	0.1777	7314.6	50.00	Rv2754c, T
IAb	31	GPALVEFAGRACYQS	VEFAGRACY	0.1768	7381.7	50.00	Rv2754c, T
IAb	107	YVPEKDSRVVPPGM	SRVVVPPGM	0.1762	7429.2	50.00	Rv2754c, T
IAb	227	ADFEVTTLADGTEVA	ADFEVTTLA	0.1760	7446.6	50.00	Rv2754c, T
IAb	229	FEVTTLADGTEVATS	TLADGTEVA	0.1758	7458.7	50.00	Rv2754c, T
IAb	7	RVQLIAKTDFLAPPD	RVQLIAKTD	0.1746	7561.5	50.00	Rv2754c, T
IAb	124	DADLRHILTEAADAA	ILTEAADAA	0.1742	7594.7	50.00	Rv2754c, T
IAb	22	VPWTTDADGGPALVE	TDADGGPAL	0.1715	7817.5	50.00	Rv2754c, T
IAb	30	GGPALVEFAGRACYQ	GGPALVEFA	0.1714	7823.3	50.00	Rv2754c, T
IAb	100	YSQLSQRYVPEKDSR	SQRYVPEKD	0.1701	7940.3	50.00	Rv2754c, T
IAb	98	FSYSQLSQRYVPEKD	FSYSQLSQR	0.1689	8039.5	50.00	Rv2754c, T
IAb	2	ETAPLRVQLIAKTD	RVQLIAKTD	0.1661	8290.5	50.00	Rv2754c, T
IAb	62	HIIDVGHFSVLEHAS	GHFSVLEHA	0.1643	8455.6	50.00	Rv2754c, T
IAb	207	IRRLAIECLRQLAAV	IRRLAIECL	0.1604	8819.1	50.00	Rv2754c, T
IAb	228	DFEVTTLADGTEVAT	TTLADGTEV	0.1580	9047.0	50.00	Rv2754c, T
IAb	4	APLRVQLIAKTDFLA	RVQLIAKTD	0.1573	9112.4	50.00	Rv2754c, T
IAb	29	DGGPALVEFAGRACY	VEFAGRACY	0.1571	9140.1	50.00	Rv2754c, T
IAb	80	YITGISRSCTHELIR	YITGISRSC	0.1557	9273.7	50.00	Rv2754c, T
IAb	206	EIRRLAIECLRQLAA	IRRLAIECL	0.1540	9450.8	50.00	Rv2754c, T
IAb	28	ADGGPALVEFAGRAC	ADGGPALVE	0.1534	9504.1	50.00	Rv2754c, T
IAb	48	KPNPKTATNAGYLRH	PNPKTATNA	0.1508	9784.8	50.00	Rv2754c, T
IAb	99	YSQLSQRYVPEKDS	SQRYVPEKD	0.1504	9819.1	50.00	Rv2754c, T
IAb	5	PLRVQLIAKTDFLAP	RVQLIAKTD	0.1498	9881.6	50.00	Rv2754c, T
IAb	6	LRVQLIAKTDFLAPP	RVQLIAKTD	0.1492	9950.4	50.00	Rv2754c, T
IAb	20	PDVPWTTDADGGPAL	TDADGGPAL	0.1462	10276.8	50.00	Rv2754c, T
IAb	35	VEFAGRACYQSWSKP	VEFAGRACY	0.1462	10278.1	50.00	Rv2754c, T
IAb	61	RHIIDVGHFSVLEHA	GHFSVLEHA	0.1444	10476.2	50.00	Rv2754c, T
IAb	157	PNAILRRKQARQAAR	LRRKQARQA	0.1405	10934.6	50.00	Rv2754c, T
IAb	105	QRYVPEKDSRVVPPP	YVPEKDSRV	0.1323	11943.1	50.00	Rv2754c, T
IAb	123	DDADLRHILTEAADA	LRHILTEAA	0.1313	12074.7	50.00	Rv2754c, T
IAb	50	NPKTATNAGYLRHII	TNAGYLRHI	0.1310	12116.5	50.00	Rv2754c, T
IAb	181	RIVVTGNYRAWRHFI	IVVTGNYRA	0.1302	12219.2	50.00	Rv2754c, T
IAb	208	RRLAIECLRQLAAVA	RLAIECLRQ	0.1299	12265.0	50.00	Rv2754c, T
IAb	115	VVVPPGMEDDADLRH	VVVPPGMED	0.1298	12273.4	50.00	Rv2754c, T
IAb	53	TATNAGYLRHIIDVG	TNAGYLRHI	0.1276	12570.0	50.00	Rv2754c, T
IAb	52	KTATNAGYLRHIIDV	TNAGYLRHI	0.1246	12983.6	50.00	Rv2754c, T
IAb	54	ATNAGYLRHIIDVGH	AGYLRHIID	0.1242	13038.5	50.00	Rv2754c, T
IAb	205	VEIRRLAIECLRQLA	IRRLAIECL	0.1217	13397.3	50.00	Rv2754c, T
IAb	51	PKTATNAGYLRHIID	TATNAGYLR	0.1211	13492.1	50.00	Rv2754c, T
IAb	55	TNAGYLRHIIDVGHF	AGYLRHIID	0.1192	13762.1	50.00	Rv2754c, T
IAb	156	QPNAILRRKQARQA	LRRKQARQA	0.1183	13896.3	50.00	Rv2754c, T
IAb	19	PPDVPWTTDADGGPA	DVPWTTDAD	0.1164	14184.6	50.00	Rv2754c, T
IAb	36	EFAGRACYQSWSKPN	RACYQSWSK	0.1133	14677.2	50.00	Rv2754c, T
IAb	81	ITGISRSCTHELIRH	TGISRSCTH	0.1120	14889.3	50.00	Rv2754c, T
IAb	122	EDDADLRHILTEAAD	LRHILTEAA	0.1105	15128.0	50.00	Rv2754c, T
IAb	204	DVEIRRLAIECLRQL	IRRLAIECL	0.1092	15332.8	50.00	Rv2754c, T
IAb	180	TRIVVTGNYRAWRHF	IVVTGNYRA	0.1067	15757.1	50.00	Rv2754c, T
IAb	82	TGISRSCTHELIRHR	TGISRSCTH	0.1060	15877.4	50.00	Rv2754c, T
IAb	196	AMRASEHADVEIRRL	AMRASEHAD	0.1003	16882.5	50.00	Rv2754c, T
IAb	121	MEDDADLRHILTEAA	LRHILTEAA	0.0999	16968.8	50.00	Rv2754c, T
IAb	60	LRHIIDVGHFSVLEH	VGHFSVLEH	0.0939	18108.3	50.00	Rv2754c, T
IAb	56	NAGYLRHIIDVGHFS	AGYLRHIID	0.0893	19022.1	50.00	Rv2754c, T
IAb	106	RYVPEKDSRVVPPPG	YVPEKDSRV	0.0891	19063.9	50.00	Rv2754c, T
IAb	179	ETRIVVTGNYRAWRH	IVVTGNYRA	0.0887	19154.1	50.00	Rv2754c, T
IAb	57	AGYLRHIIDVGHFSV	AGYLRHIID	0.0877	19350.5	50.00	Rv2754c, T
IAb	203	ADVEIRRLAIECLRQ	IRRLAIECL	0.0869	19520.2	50.00	Rv2754c, T
IAb	155	DQPNAILRRKQARQA	LRRKQARQA	0.0822	20538.1	50.00	Rv2754c, T
IAb	153	FADQPNAILRRKQAR	FADQPNAIL	0.0816	20678.8	50.00	Rv2754c, T
IAb	178	TETRIVVTGNYRAWR	IVVTGNYRA	0.0771	21700.4	50.00	Rv2754c, T
IAb	174	LPNATETRIVVTGNY	LPNATETRI	0.0757	22042.8	50.00	Rv2754c, T
IAb	89	THELIRHRHFSYSQL	HRHFSYSQL	0.0752	22152.3	50.00	Rv2754c, T
IAb	202	HADVEIRRLAIECLR	IRRLAIECL	0.0743	22366.7	50.00	Rv2754c, T
IAb	177	ATETRIVVTGNYRAW	IVVTGNYRA	0.0709	23218.9	50.00	Rv2754c, T
IAb	83	GISRSCCTHELIRHRH	GISRSCCTH	0.0690	23710.9	50.00	Rv2754c, T
IAb	201	EHADVEIRRLAIECL	IRRLAIECL	0.0611	25807.7	50.00	Rv2754c, T
IAb	59	YLRHIIDVGHFSVLE	HIIDVGHFS	0.0585	26557.0	50.00	Rv2754c, T
IAb	197	MRASEHADVEIRRLA	RASEHADVE	0.0584	26578.0	50.00	Rv2754c, T
IAb	154	ADQPNAILRRKQARQ	ADQPNAILR	0.0555	27415.4	50.00	Rv2754c, T

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IAb	176	NATETRIVVTGNYRA	IVVTGNYRA	0.0543	27794.4	50.00	Rv2754c, T
IAb	175	PNATETRIVVTGNYR	PNATETRIV	0.0533	28096.7	50.00	Rv2754c, T
IAb	58	GYLRRHIDVGHFSVL	GYLRRHIDV	0.0531	28154.9	50.00	Rv2754c, T
IAb	198	RASEHADVEIRRLAI	RASEHADVE	0.0520	28498.1	50.00	Rv2754c, T
IAb	116	VPPGMEDDADLRHI	VPPGMEDD	0.0445	30894.1	50.00	Rv2754c, T
IAb	84	ISRSCTHELIRHRHF	ISRSCTHEL	0.0362	33782.3	50.00	Rv2754c, T
IAb	88	CTHELIRHRHFSYSQ	RHRHFSYSQ	0.0340	34610.6	50.00	Rv2754c, T
IAb	120	GMEDDADLRHILTEA	ADLRHILTE	0.0339	34645.5	50.00	Rv2754c, T
IAb	199	ASEHADVEIRRLAIE	ASEHADVEI	0.0312	35665.2	50.00	Rv2754c, T
IAb	200	SEHADVEIRRLAIEC	SEHADVEIR	0.0282	36843.5	50.00	Rv2754c, T
IAb	119	PGMEDDADLRHILTE	ADLRHILTE	0.0232	38900.0	50.00	Rv2754c, T
IAb	117	VPPGMEDDADLRHIL	VPPGMEDDA	0.0217	39540.3	50.00	Rv2754c, T
IAb	87	SCTHELIRHRHFSYS	IRHRHFSYS	0.0208	39902.6	50.00	Rv2754c, T
IAb	85	SRSCTHELIRHRHFS	SRSCTHELI	0.0200	40270.8	50.00	Rv2754c, T
IAb	118	PPGMEDDADLRHILT	PPGMEDDAD	0.0188	40779.9	50.00	Rv2754c, T
IAb	86	RSCTHELIRHRHFSY	HELIRHRHF	0.0165	41838.7	50.00	Rv2754c, T

Allele: IAb. Number of high binders 4. Number of weak binders 36. Number of peptides 236

Allele	pos	peptide	core	1-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
IAd	189	RAWRHFIAMRASEHA	RHFIAMRAS	0.5688	106.2	WB	0.15	Rv2754c, T
IAd	190	AWRHFIAMRASEHAD	WRHFIAMRA	0.5650	110.6	WB	0.15	Rv2754c, T
IAd	191	WRHFIAMRASEHADV	RHFIAMRAS	0.5421	141.8	WB	0.20	Rv2754c, T
IAd	213	ECLRQLAAVAVPAVFA	RQLAAVAPA	0.5275	166.0	WB	0.30	Rv2754c, T
IAd	188	YRAWRHFIAMRASEH	WRHFIAMRA	0.5250	170.6	WB	0.30	Rv2754c, T
IAd	186	GNYRAWRHFIAMRAS	WRHFIAMRA	0.5232	174.1	WB	0.30	Rv2754c, T
IAd	187	NYRAWRHFIAMRASE	WRHFIAMRA	0.5184	183.3	WB	0.40	Rv2754c, T
IAd	212	IECLRQLAAVAVPAVF	RQLAAVAPA	0.5175	185.1	WB	0.40	Rv2754c, T
IAd	211	AIECLRQLAAVAVPAV	RQLAAVAPA	0.5152	189.8	WB	0.40	Rv2754c, T
IAd	164	KQARQAARAVLPNAT	AARAVLPNA	0.5080	205.0	WB	0.40	Rv2754c, T
IAd	163	RKQARQAARAVLPNA	AARAVLPNA	0.4842	265.3	WB	0.80	Rv2754c, T
IAd	214	CLRQLAAVAVPAVFAD	RQLAAVAPA	0.4836	267.0	WB	0.80	Rv2754c, T
IAd	215	LRQLAAVAVPAVFADF	RQLAAVAPA	0.4792	280.1	WB	0.80	Rv2754c, T
IAd	165	QARQAARAVLPNATE	AARAVLPNA	0.4762	289.4	WB	0.80	Rv2754c, T
IAd	210	LAIECLRQLAAVAVPA	RQLAAVAPA	0.4756	291.1	WB	0.80	Rv2754c, T
IAd	185	TGNYRAWRHFIAMRA	WRHFIAMRA	0.4453	404.2	WB	2.00	Rv2754c, T
IAd	166	ARQAARAVLPNATET	AARAVLPNA	0.4359	447.3	WB	2.00	Rv2754c, T
IAd	216	RQLAAVAVPAVFADFE	RQLAAVAPA	0.4234	511.9		2.00	Rv2754c, T
IAd	167	RQAARAVLPNATETR	AARAVLPNA	0.4126	575.7		2.00	Rv2754c, T
IAd	161	LRRKQARQAARAVLP	LRRKQARQA	0.4033	636.8		2.00	Rv2754c, T
IAd	192	RHFIAMRASEHADVE	RHFIAMRAS	0.4026	641.2		4.00	Rv2754c, T
IAd	168	QAARAVLPNATETRI	AARAVLPNA	0.3881	750.3		4.00	Rv2754c, T
IAd	0	VAETAPLRVQLIAKT	LRVQLIAKT	0.3864	764.7		4.00	Rv2754c, T
IAd	160	ILRRKQARQAARAVL	LRRKQARQA	0.3856	770.7		4.00	Rv2754c, T
IAd	196	AMRASEHADVEIRRL	HADVEIRRL	0.3802	817.6		4.00	Rv2754c, T
IAd	162	RRKQARQAARAVLPN	RRKQARQA	0.3790	827.7		4.00	Rv2754c, T
IAd	197	MRASEHADVEIRRLA	HADVEIRRL	0.3770	846.5		4.00	Rv2754c, T
IAd	159	AILRRKQARQAARAV	LRRKQARQA	0.3609	1006.8		4.00	Rv2754c, T
IAd	1	AETAPLRVQLIAKTD	LRVQLIAKT	0.3572	1048.6		4.00	Rv2754c, T
IAd	169	AARAVLPNATETRIV	AARAVLPNA	0.3533	1093.2		8.00	Rv2754c, T
IAd	199	ASEHADVEIRRLAIE	HADVEIRRL	0.3503	1129.3		8.00	Rv2754c, T
IAd	126	DLRHILTEAADAARA	TEAADAARA	0.3498	1135.5		8.00	Rv2754c, T
IAd	198	RASEHADVEIRRLAI	HADVEIRRL	0.3482	1155.9		8.00	Rv2754c, T
IAd	5	PLRVQLIAKTDFLAP	LRVQLIAKT	0.3462	1180.4		8.00	Rv2754c, T
IAd	209	RLAIECLRQLAAVAP	RQLAAVAPA	0.3438	1211.6		8.00	Rv2754c, T
IAd	158	NAILRRKQARQAARA	LRRKQARQA	0.3415	1242.6		8.00	Rv2754c, T
IAd	200	SEHADVEIRRLAIEC	EHADVEIRR	0.3379	1292.3		8.00	Rv2754c, T
IAd	157	PNAILRRKQARQAAR	LRRKQARQA	0.3345	1340.0		8.00	Rv2754c, T
IAd	205	VEIRRLAIECLRQLA	IRRLAIECL	0.3279	1439.4		8.00	Rv2754c, T
IAd	195	IAMRASEHADVEIRR	IAMRASEHA	0.3261	1467.7		8.00	Rv2754c, T
IAd	6	LRVQLIAKTDFLAPP	LRVQLIAKT	0.3242	1497.5		8.00	Rv2754c, T
IAd	204	DVEIRRLAIECLRQL	IRRLAIECL	0.3240	1502.0		8.00	Rv2754c, T
IAd	206	EIRRLAIECLRQLAA	IRRLAIECL	0.3224	1528.3		8.00	Rv2754c, T
IAd	194	FIAMRASEHADVEIR	SEHADVEIR	0.3200	1568.4		8.00	Rv2754c, T
IAd	127	LRHILTEAADAARAT	TEAADAARA	0.3190	1584.9		8.00	Rv2754c, T
IAd	4	APLRVQLIAKTDFLA	LRVQLIAKT	0.3185	1593.7		8.00	Rv2754c, T
IAd	2	ETAPLRVQLIAKTD	LRVQLIAKT	0.3171	1617.1		8.00	Rv2754c, T
IAd	156	QPNAILRRKQARQAA	LRRKQARQA	0.3156	1644.8		8.00	Rv2754c, T
IAd	3	TAPLRVQLIAKTD	LRVQLIAKT	0.3097	1752.2		8.00	Rv2754c, T
IAd	202	HADVEIRRLAIECLR	HADVEIRRL	0.3055	1834.0		8.00	Rv2754c, T
IAd	135	ADAARATYSELLAKL	AARATYSEL	0.3044	1856.9		8.00	Rv2754c, T
IAd	207	IRRLAIECLRQLAAV	IRRLAIECL	0.3039	1865.3		8.00	Rv2754c, T
IAd	201	EHADVEIRRLAIECL	HADVEIRRL	0.3002	1943.1		16.00	Rv2754c, T
IAd	141	TYSELLAKLEAKFAD	LAKLEAKFA	0.2939	2080.0		16.00	Rv2754c, T
IAd	137	AARATYSELLAKLEA	AARATYSEL	0.2891	2190.3		16.00	Rv2754c, T
IAd	140	ATYSELLAKLEAKFA	LAKLEAKFA	0.2871	2237.4		16.00	Rv2754c, T
IAd	134	AADAARATYSELLAK	AARATYSEL	0.2849	2291.9		16.00	Rv2754c, T
IAd	133	EADAARATYSELLA	AARATYSEL	0.2803	2409.2		16.00	Rv2754c, T
IAd	131	LTEAADAARATYSEL	TEAADAARA	0.2800	2417.2		16.00	Rv2754c, T
IAd	208	RRLAIECLRQLAAVA	LAIECLRQL	0.2787	2451.7		16.00	Rv2754c, T
IAd	125	ADLRHILTEAADAAR	LRHILTEAA	0.2779	2472.9		16.00	Rv2754c, T

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IAd	129	HILTEAADAARATYS	TEAADAARA	0.2729	2609.8	16.00	Rv2754c, T
IAd	132	TEAADAARATYSELL	TEAADAARA	0.2726	2618.4	16.00	Rv2754c, T
IAd	136	DAARATYSELLAKLE	RATYSELLA	0.2674	2770.3	16.00	Rv2754c, T
IAd	128	RHILTEAADAARATY	TEAADAARA	0.2660	2813.3	16.00	Rv2754c, T
IAd	176	NATETRIVVTGNRYRA	ATETRIVVVT	0.2658	2817.6	16.00	Rv2754c, T
IAd	142	YSELLAKLEAKFADQ	LAKLEAKFA	0.2612	2961.5	16.00	Rv2754c, T
IAd	177	ATETRIVVTGNRYRAW	ATETRIVVVT	0.2593	3022.1	16.00	Rv2754c, T
IAd	58	GYLRHIIDVGHFSVL	RHIIDVGHF	0.2588	3040.7	16.00	Rv2754c, T
IAd	130	ILTEAADAARATYSE	TEAADAARA	0.2569	3104.5	16.00	Rv2754c, T
IAd	57	AGYLRHIIDVGHFSV	RHIIDVGHF	0.2567	3109.9	16.00	Rv2754c, T
IAd	203	ADVEIRRLAIECLRQ	RLAIECLRQ	0.2524	3257.4	16.00	Rv2754c, T
IAd	124	DADLRHILTEAADA	LRHILTEAA	0.2516	3287.1	16.00	Rv2754c, T
IAd	143	SELLAKLEAKFADQP	LAKLEAKFA	0.2488	3386.9	16.00	Rv2754c, T
IAd	193	HFIAMRASEHADVEI	IAMRASEHA	0.2486	3395.1	16.00	Rv2754c, T
IAd	155	DQPNAILRRKQARQA	LRRKQARQA	0.2437	3580.5	32.00	Rv2754c, T
IAd	56	NAGYLRHIIDVGHFS	RHIIDVGHF	0.2405	3707.2	32.00	Rv2754c, T
IAd	55	TNAGYLRHIIDVGHF	RHIIDVGHF	0.2389	3772.3	32.00	Rv2754c, T
IAd	59	YLRHIIDVGHFSVLE	RHIIDVGHF	0.2378	3814.7	32.00	Rv2754c, T
IAd	174	LPNATETRIVVTGNY	ATETRIVVVT	0.2307	4119.4	32.00	Rv2754c, T
IAd	60	LRHIIDVGHFSVLEH	RHIIDVGHF	0.2272	4281.3	32.00	Rv2754c, T
IAd	123	DDADLRHILTEAADA	LRHILTEAA	0.2216	4547.1	32.00	Rv2754c, T
IAd	61	RHIIDVGHFSVLEHA	RHIIDVGHF	0.2205	4603.2	32.00	Rv2754c, T
IAd	144	ELLAKLEAKFADQPN	LAKLEAKFA	0.2200	4627.4	32.00	Rv2754c, T
IAd	175	PNATETRIVVTGNRYR	ATETRIVVVT	0.2191	4671.9	32.00	Rv2754c, T
IAd	217	QLAAVAPAVFADFEV	AAVAPAVFA	0.2180	4724.9	32.00	Rv2754c, T
IAd	138	ARATYSELLAKLEAK	SELLAKLEA	0.2167	4792.5	32.00	Rv2754c, T
IAd	139	RATYSELLAKLEAKF	SELLAKLEA	0.2142	4924.3	32.00	Rv2754c, T
IAd	107	YVPEKDSRVVPPGPM	DSRVVPPPG	0.2141	4929.6	32.00	Rv2754c, T
IAd	121	MEDDADLRHILTEAA	LRHILTEAA	0.2139	4941.2	32.00	Rv2754c, T
IAd	98	FSYSQLSQRYVPEKD	YSQLSQRYV	0.2128	4998.6	32.00	Rv2754c, T
IAd	122	EDDADLRHILTEAAD	LRHILTEAA	0.2105	5129.1	32.00	Rv2754c, T
IAd	97	HFSYSQLSQRYVPEK	YSQLSQRYV	0.2050	5440.0	32.00	Rv2754c, T
IAd	178	TETRIVVTGNRYRAWR	TETRIVVTG	0.1986	5830.7	32.00	Rv2754c, T
IAd	96	RHFSYSQLSQRYVPE	YSQLSQRYV	0.1947	6082.3	32.00	Rv2754c, T
IAd	150	EAKFADQPNAILRRK	QPNAILRRK	0.1896	6429.7	32.00	Rv2754c, T
IAd	235	ADGTEVATSPLATEA	TEVATSPLA	0.1867	6631.4	32.00	Rv2754c, T
IAd	108	VPEKDSRVVPPPGME	DSRVVPPPG	0.1859	6692.2	32.00	Rv2754c, T
IAd	95	RHFYSYSQLSQRYVP	YSQLSQRYV	0.1858	6693.8	32.00	Rv2754c, T
IAd	219	AAVAPAVFADFEVTT	AAVAPAVFA	0.1794	7181.4	32.00	Rv2754c, T
IAd	218	LAAPAVFADFEVTT	AAVAPAVFA	0.1785	7243.9	50.00	Rv2754c, T
IAd	99	SYSQLSQRYVPEKDS	YSQLSQRYV	0.1772	7348.3	50.00	Rv2754c, T
IAd	106	RYVPEKDSRVVPPG	DSRVVPPPG	0.1769	7375.4	50.00	Rv2754c, T
IAd	184	VTGNYRAWRHFIAMR	YRAWRHFIA	0.1763	7423.3	50.00	Rv2754c, T
IAd	109	PEKDSRVVPPPGMED	DSRVVPPPG	0.1671	8203.6	50.00	Rv2754c, T
IAd	145	LLAKLEAKFADQPNA	LAKLEAKFA	0.1665	8248.7	50.00	Rv2754c, T
IAd	179	ETRIVVTGNRYRAWRH	IVVTGNRYRA	0.1663	8267.4	50.00	Rv2754c, T
IAd	110	EKDSRVVPPPGMEDD	DSRVVPPPG	0.1647	8417.1	50.00	Rv2754c, T
IAd	100	YSQLSQRYVPEKDSR	YSQLSQRYV	0.1639	8490.7	50.00	Rv2754c, T
IAd	68	HFSVLEHASVSFYIT	HASVSFYIT	0.1620	8665.9	50.00	Rv2754c, T
IAd	70	SVLEHASVSFYITGI	HASVSFYIT	0.1619	8673.7	50.00	Rv2754c, T
IAd	7	RVQLIAKTDFLAPPD	LIAKTDFLA	0.1614	8720.7	50.00	Rv2754c, T
IAd	69	FSVLEHASVSFYITG	HASVSFYIT	0.1612	8742.9	50.00	Rv2754c, T
IAd	234	LADGTEVATSPLATE	TEVATSPLA	0.1607	8785.5	50.00	Rv2754c, T
IAd	173	LPNATETRIVVTGN	ATETRIVVVT	0.1604	8811.4	50.00	Rv2754c, T
IAd	10	LIAKTDFLAPPDPWP	IAKTDFLAP	0.1604	8812.2	50.00	Rv2754c, T
IAd	146	LAKLEAKFADQPNAI	LAKLEAKFA	0.1600	8855.8	50.00	Rv2754c, T
IAd	9	QLIAKTDFLAPPDVP	LIAKTDFLA	0.1583	9021.0	50.00	Rv2754c, T
IAd	220	AVAPAVFADFEVTTL	AVAPAVFAD	0.1562	9221.4	50.00	Rv2754c, T
IAd	170	ARAVLPNATETRIVV	ARAVLPNAT	0.1547	9376.8	50.00	Rv2754c, T
IAd	84	ISRSCTHELIRHRHF	ISRSCTHEL	0.1542	9428.7	50.00	Rv2754c, T
IAd	119	PGMEDDADLRHILTE	MEDDADLRH	0.1542	9430.0	50.00	Rv2754c, T
IAd	49	PNPKTATNAGYLRHI	PNPKTATNA	0.1539	9457.5	50.00	Rv2754c, T
IAd	221	VAPAVFADFEVTTLA	ADFEVTTLA	0.1525	9599.2	50.00	Rv2754c, T
IAd	151	AKFADQPNAILRRKQ	QPNAILRRK	0.1508	9782.5	50.00	Rv2754c, T
IAd	8	VQLIAKTDFLAPPDVP	LIAKTDFLA	0.1506	9800.5	50.00	Rv2754c, T
IAd	154	ADQPNAILRRKQARQ	QPNAILRRK	0.1499	9877.7	50.00	Rv2754c, T
IAd	66	VGHFSVLEHASVSFY	GHFSVLEHA	0.1495	9915.2	50.00	Rv2754c, T
IAd	67	GHFSVLEHASVSFYI	GHFSVLEHA	0.1495	9917.7	50.00	Rv2754c, T
IAd	117	VPPGMEDDADLRHIL	MEDDADLRH	0.1492	9953.2	50.00	Rv2754c, T
IAd	118	PPGMEDDADLRHILT	MEDDADLRH	0.1490	9969.4	50.00	Rv2754c, T
IAd	32	PALVEFAGRACYQSW	PALVEFAGR	0.1489	9980.8	50.00	Rv2754c, T
IAd	116	VPPGMEDDADLRHI	MEDDADLRH	0.1457	10337.5	50.00	Rv2754c, T
IAd	152	KFADQPNAILRRKQA	QPNAILRRK	0.1431	10627.2	50.00	Rv2754c, T
IAd	180	TRIVVTGNRYRAWRH	IVVTGNRYRA	0.1427	10671.6	50.00	Rv2754c, T
IAd	94	RHRHFSYSQLSQRYV	FSYSQLSQR	0.1423	10727.6	50.00	Rv2754c, T
IAd	71	VLEHASVSFYITGIS	HASVSFYIT	0.1419	10771.9	50.00	Rv2754c, T
IAd	65	DVGHFSVLEHASVSF	GHFSVLEHA	0.1413	10838.1	50.00	Rv2754c, T
IAd	37	FAGRACYQSWKPNP	AGRACYQSW	0.1394	11066.3	50.00	Rv2754c, T
IAd	83	GISRSCTHELIRHRH	ISRSCTHEL	0.1393	11079.2	50.00	Rv2754c, T
IAd	11	IAKTDFLAPPDVPWT	IAKTDFLAP	0.1391	11098.4	50.00	Rv2754c, T
IAd	182	IVVTGNRYRAWRHFI	YRAWRHFIA	0.1386	11155.4	50.00	Rv2754c, T
IAd	153	FADQPNAILRRKQAR	QPNAILRRK	0.1386	11158.3	50.00	Rv2754c, T
IAd	183	VVTGNRYRAWRHFIAM	YRAWRHFIA	0.1374	11311.0	50.00	Rv2754c, T
IAd	50	NPKTATNAGYLRHII	TATNAGYLR	0.1372	11329.0	50.00	Rv2754c, T
IAd	233	TLADGTEVATSPLAT	ADGTEVATS	0.1356	11533.3	50.00	Rv2754c, T

IAd	73	EHASVSFYITGISRS	HASVSFYIT	0.1344	11676.7	50.00	Rv2754c, T
IAd	72	LEHASVSFYITGISR	HASVSFYIT	0.1344	11678.3	50.00	Rv2754c, T
IAd	27	DADGGPALVEFAGRA	GPALVEFAG	0.1324	11941.2	50.00	Rv2754c, T
IAd	28	ADGGPALVEFAGRAC	GPALVEFAG	0.1316	12040.6	50.00	Rv2754c, T
IAd	36	EFAGRACYQSWSKPN	AGRACYQSW	0.1316	12045.1	50.00	Rv2754c, T
IAd	223	PAVFADFEVTTLADG	AVFADFEVT	0.1298	12269.9	50.00	Rv2754c, T
IAd	51	PKTATNAGYLRHIID	KTATNAGYL	0.1293	12339.5	50.00	Rv2754c, T
IAd	48	KPNPKTATNAGYLRH	KTATNAGYL	0.1287	12416.2	50.00	Rv2754c, T
IAd	171	RAVLPNATETRIVVTT	ATETRIVVTT	0.1286	12430.3	50.00	Rv2754c, T
IAd	52	KTATNAGYLRHIIDV	KTATNAGYL	0.1277	12559.4	50.00	Rv2754c, T
IAd	149	LEAKFADQPNAILRR	DQPNAILRR	0.1267	12694.1	50.00	Rv2754c, T
IAd	172	AVLPNATETRIVVTTG	ATETRIVVTT	0.1266	12712.4	50.00	Rv2754c, T
IAd	35	VEFAGRACYQSWSKP	AGRACYQSW	0.1265	12723.5	50.00	Rv2754c, T
IAd	111	KDSRVVPPGMEDDA	DSRVVPPG	0.1257	12828.0	50.00	Rv2754c, T
IAd	85	SRSCTHELIRHRHFS	CHELIRHR	0.1256	12848.7	50.00	Rv2754c, T
IAd	64	IDVGHFVLEHASVS	GHFVLEHA	0.1245	13002.3	50.00	Rv2754c, T
IAd	222	APAVFADFEVTTLAD	ADFEVTTLA	0.1230	13218.6	50.00	Rv2754c, T
IAd	38	AGRACYQSWSKPNPK	AGRACYQSW	0.1219	13374.1	50.00	Rv2754c, T
IAd	29	DGGPALVEFAGRACY	GPALVEFAG	0.1212	13480.0	50.00	Rv2754c, T
IAd	62	HIIDVGHFVLEHAS	GHFVLEHA	0.1208	13536.6	50.00	Rv2754c, T
IAd	63	IIDVGHFVLEHASV	GHFVLEHA	0.1205	13579.5	50.00	Rv2754c, T
IAd	105	QRYVPEKDSRVVPP	VPEKDSRVV	0.1202	13612.2	50.00	Rv2754c, T
IAd	86	SCTHELIRHRHFSY	CHELIRHR	0.1194	13739.6	50.00	Rv2754c, T
IAd	12	AKTDFLAPPDVPWTT	AKTDFLAPP	0.1189	13813.5	50.00	Rv2754c, T
IAd	31	GPALVEFAGRACYQS	PALVEFAGR	0.1188	13825.8	50.00	Rv2754c, T
IAd	224	AVFADFEVTTLADGT	FADFEVTTL	0.1174	14034.8	50.00	Rv2754c, T
IAd	15	DFLAPPDVPWTTDAD	FLAPPDVPW	0.1170	14097.1	50.00	Rv2754c, T
IAd	232	TTLADGTEVATSPLA	TEVATSPLA	0.1165	14168.3	50.00	Rv2754c, T
IAd	30	GGPALVEFAGRACYQ	GPALVEFAG	0.1163	14201.3	50.00	Rv2754c, T
IAd	120	GMEDDADLRHILTEA	MEDDADLRH	0.1160	14254.1	50.00	Rv2754c, T
IAd	74	HASVSFYITGISRSC	HASVSFYIT	0.1140	14562.0	50.00	Rv2754c, T
IAd	87	SCTHELIRHRHFSYS	CHELIRHR	0.1137	14611.9	50.00	Rv2754c, T
IAd	115	VVVPPGMEDDADLRH	MEDDADLRH	0.1106	15105.2	50.00	Rv2754c, T
IAd	112	DSRVVPPGMEDDAD	DSRVVPPG	0.1106	15116.0	50.00	Rv2754c, T
IAd	33	ALVEFAGRACYQSW	ALVEFAGRA	0.1103	15158.3	50.00	Rv2754c, T
IAd	101	SQLSQRYVPEKDSRV	QLSQRYVPE	0.1103	15158.5	50.00	Rv2754c, T
IAd	34	LVEFAGRACYQSWSK	FAGRACYQS	0.1102	15178.8	50.00	Rv2754c, T
IAd	89	THELIRHRHFSYSQL	HRHFSYSQL	0.1100	15205.3	50.00	Rv2754c, T
IAd	78	SFYITGISRSCTHEL	ISRSCTHEL	0.1094	15299.8	50.00	Rv2754c, T
IAd	13	KTDFLAPPDVPWTTD	FLAPPDVPW	0.1094	15309.9	50.00	Rv2754c, T
IAd	40	RACYQSWSKPNPKTA	WSKPNPKTA	0.1089	15397.5	50.00	Rv2754c, T
IAd	181	RIVVTGNRAWRHFI	IVVTGNRA	0.1059	15900.8	50.00	Rv2754c, T
IAd	14	TDFLAPPDVPWTTDA	FLAPPDVPW	0.1057	15932.2	50.00	Rv2754c, T
IAd	16	FLAPPDVPWTTDADG	LAPPDVPWT	0.1027	16454.2	50.00	Rv2754c, T
IAd	26	TDADGGPALVEFAGR	GPALVEFAG	0.1024	16506.3	50.00	Rv2754c, T
IAd	104	SQRYVPEKDSRVVPP	VPEKDSRVV	0.0990	17129.5	50.00	Rv2754c, T
IAd	79	FYITGISRSCTHELI	FYITGISRS	0.0984	17251.5	50.00	Rv2754c, T
IAd	25	TTDADGGPALVEFAG	GPALVEFAG	0.0982	17279.5	50.00	Rv2754c, T
IAd	54	ATNAGYLRHIIDVGH	LRHIIDVGH	0.0981	17296.7	50.00	Rv2754c, T
IAd	148	KLEAKFADQPNAILR	AKFADQPNA	0.0970	17512.9	50.00	Rv2754c, T
IAd	88	CHELIRHRHFSYSQ	CHELIRHR	0.0969	17520.1	50.00	Rv2754c, T
IAd	39	GRACYQSWSKPNPKT	YQSWSKPNP	0.0959	17715.9	50.00	Rv2754c, T
IAd	93	IRHRHFSYSQLSQR	FSYSQLSQR	0.0948	17921.4	50.00	Rv2754c, T
IAd	231	VTTLADGTEVATSPL	GTEVATSPL	0.0920	18475.6	50.00	Rv2754c, T
IAd	53	TATNAGYLRHIIDVG	ATNAGYLRH	0.0909	18699.9	50.00	Rv2754c, T
IAd	41	ACYQSWSKPNPKTAT	WSKPNPKTA	0.0900	18875.1	50.00	Rv2754c, T
IAd	147	AKLEAKFADQPNAIL	AKLEAKFAD	0.0882	19254.4	50.00	Rv2754c, T
IAd	82	TGISRSCTHELIRHR	ISRSCTHEL	0.0876	19386.9	50.00	Rv2754c, T
IAd	102	QLSQRYVPEKDSRVV	LSQRYVPEK	0.0872	19467.9	50.00	Rv2754c, T
IAd	229	FEVTTLADGTEVATS	FEVTTLADG	0.0858	19754.1	50.00	Rv2754c, T
IAd	226	FADFEVTTLADGTEV	FADFEVTTL	0.0847	19998.2	50.00	Rv2754c, T
IAd	103	LSQRYVPEKDSRVVV	VPEKDSRVV	0.0836	20241.1	50.00	Rv2754c, T
IAd	225	VFADFEVTTLADGTE	FADFEVTTL	0.0820	20583.9	50.00	Rv2754c, T
IAd	81	ITGISRSCTHELIRH	ISRSCTHEL	0.0815	20692.4	50.00	Rv2754c, T
IAd	43	YQSWSKPNPKTATNA	WSKPNPKTA	0.0807	20874.8	50.00	Rv2754c, T
IAd	17	LAPPDVPWTTDADGG	APPDVPWTT	0.0792	21232.9	50.00	Rv2754c, T
IAd	47	SKPNPKTATNAGYLR	TATNAGYLR	0.0766	21825.2	50.00	Rv2754c, T
IAd	80	YITGISRSCTHELIR	ISRSCTHEL	0.0765	21843.4	50.00	Rv2754c, T
IAd	228	DFEVTTLADGTEVAT	FEVTTLADG	0.0746	22315.9	50.00	Rv2754c, T
IAd	92	LIRHRHFSYSQLSQR	FSYSQLSQR	0.0718	22990.1	50.00	Rv2754c, T
IAd	42	CYQSWSKPNPKTATN	WSKPNPKTA	0.0692	23658.6	50.00	Rv2754c, T
IAd	44	QSWSKPNPKTATNAG	WSKPNPKTA	0.0690	23691.9	50.00	Rv2754c, T
IAd	75	ASVSFYITGISRSCT	FYITGISRS	0.0689	23737.6	50.00	Rv2754c, T
IAd	227	ADFEVTTLADGTEVA	FEVTTLADG	0.0675	24077.5	50.00	Rv2754c, T
IAd	76	SVSFYITGISRSCTH	FYITGISRS	0.0672	24156.3	50.00	Rv2754c, T
IAd	45	SWSKPNPKTATNAGY	WSKPNPKTA	0.0662	24428.1	50.00	Rv2754c, T
IAd	22	VPWTTDADGGPALVE	TTDADGGPA	0.0646	24851.4	50.00	Rv2754c, T
IAd	21	DVPWTTDADGGPALV	TTDADGGPA	0.0639	25042.5	50.00	Rv2754c, T
IAd	46	WSKPNPKTATNAGYL	WSKPNPKTA	0.0637	25105.4	50.00	Rv2754c, T
IAd	230	EVTTLADGTEVATSP	ADGTEVATS	0.0621	25546.9	50.00	Rv2754c, T
IAd	24	WTTDADGGPALVEFA	GGPALVEFA	0.0608	25900.3	50.00	Rv2754c, T
IAd	18	APPDVPWTTDADGGP	APPDVPWTT	0.0602	26071.3	50.00	Rv2754c, T
IAd	90	HELIRHRHFSYSQLS	HRHFSYSQL	0.0601	26087.1	50.00	Rv2754c, T
IAd	20	PDVPWTTDADGGPAL	TTDADGGPA	0.0599	26143.0	50.00	Rv2754c, T
IAd	91	ELIRHRHFSYSQLSQ	HRHFSYSQL	0.0585	26549.8	50.00	Rv2754c, T

IAd	114	RVVVPPGMEDDADLR	GMEDDADLR	0.0581	26675.9	50.00	Rv2754c, T
IAd	113	SRVVVPPGMEDDADL	SRVVVPPGM	0.0572	26930.3	50.00	Rv2754c, T
IAd	19	PPDVPWTTDADGGPA	TTDADGGPA	0.0545	27718.7	50.00	Rv2754c, T
IAd	77	VSFYITGISRSCTHE	FYITGISRS	0.0501	29087.2	50.00	Rv2754c, T
IAd	23	PWTTDADGGPALVEF	TTDADGGPA	0.0445	30892.1	50.00	Rv2754c, T

Allele: IAd. Number of high binders 0. Number of weak binders 17. Number of peptides 236

Allele	pos	peptide	core	1-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
IAs	146	LAKLEAKFADQPNAI	KFADQPNAI	0.4956	234.5	WB	0.15	Rv2754c, T
IAs	108	VPEKDSRVVPPGME	RVVVP GME	0.4950	236.2	WB	0.15	Rv2754c, T
IAs	147	AKLEAKFADQPNAIL	KFADQPNAI	0.4798	278.2	WB	0.20	Rv2754c, T
IAs	109	PEKDSRVVPPGMED	RVVVP GME	0.4770	286.9	WB	0.20	Rv2754c, T
IAs	148	KLEAKFADQPNAILR	KFADQPNAI	0.4635	332.0	WB	0.30	Rv2754c, T
IAs	110	EKDSRVVPPGMEDD	RVVVP GME	0.4589	348.7	WB	0.30	Rv2754c, T
IAs	149	LEAKFADQPNAILRR	KFADQPNAI	0.4429	415.0	WB	0.30	Rv2754c, T
IAs	111	KDSRVVPPGMEDDA	RVVVP GME	0.4304	474.8	WB	0.40	Rv2754c, T
IAs	112	DSRVVPPGMEDDAD	RVVVP GME	0.3689	923.2		1.00	Rv2754c, T
IAs	9	QLIAKTDFLAPPDVP	DFLAPPDVP	0.3540	1085.3		2.00	Rv2754c, T
IAs	151	AKFADQPNAILRRKQ	KFADQPNAI	0.3514	1116.1		2.00	Rv2754c, T
IAs	113	SRVVVPPGMEDDADL	RVVVP GME	0.3467	1174.7		2.00	Rv2754c, T
IAs	150	EAKFADQPNAILRRK	KFADQPNAI	0.3412	1247.1		2.00	Rv2754c, T
IAs	10	LIAKTDFLAPPDVPW	DFLAPPDVP	0.3395	1270.0		2.00	Rv2754c, T
IAs	107	YVPEKDSRVVPPGM	SRVVVPPGM	0.3339	1348.5		2.00	Rv2754c, T
IAs	38	AGRACYQSWSKPNPK	QSWSKPNPK	0.3326	1367.9		2.00	Rv2754c, T
IAs	11	IAKTDFLAPPDVPWT	DFLAPPDVP	0.3302	1403.3		2.00	Rv2754c, T
IAs	145	LLAKLEAKFADQPN	AKFADQPN	0.3248	1488.0		2.00	Rv2754c, T
IAs	39	GRACYQSWSKPNPKT	QSWSKPNPK	0.3204	1561.9		2.00	Rv2754c, T
IAs	12	AKTDFLAPPDVPWTT	DFLAPPDVP	0.3144	1665.4		4.00	Rv2754c, T
IAs	40	RACYQSWSKPNPKTA	QSWSKPNPK	0.3013	1919.0		4.00	Rv2754c, T
IAs	41	ACYQSWSKPNPKTAT	QSWSKPNPK	0.2938	2082.0		4.00	Rv2754c, T
IAs	43	YQSWSKPNPKTATNA	QSWSKPNPK	0.2930	2100.3		4.00	Rv2754c, T
IAs	42	CYQSWSKPNPKTATN	QSWSKPNPK	0.2839	2316.6		4.00	Rv2754c, T
IAs	167	RQAARAVLPNATETR	RQAARAVLP	0.2834	2330.1		4.00	Rv2754c, T
IAs	166	AQAARAVLPNATET	RQAARAVLP	0.2780	2468.7		4.00	Rv2754c, T
IAs	165	QAARAVLPNATE	RQAARAVLP	0.2764	2512.4		4.00	Rv2754c, T
IAs	164	KQAARAVLPNAT	RQAARAVLP	0.2690	2723.0		4.00	Rv2754c, T
IAs	163	RQAARAVLPN	RQAARAVLP	0.2685	2736.8		4.00	Rv2754c, T
IAs	8	VQLIAKTDFLAPPDV	KTDFLAPPD	0.2668	2787.1		4.00	Rv2754c, T
IAs	114	RVVVP GME	RVVVP GME	0.2644	2860.8		8.00	Rv2754c, T
IAs	106	RYVPEKDSRVVPPG	KDSRVVPP	0.2559	3135.9		8.00	Rv2754c, T
IAs	212	IECLRQLAAVAPAVF	LAAVAPAVF	0.2494	3364.8		8.00	Rv2754c, T
IAs	213	ECLRQLAAVAPAVFA	LAAVAPAVF	0.2408	3694.1		8.00	Rv2754c, T
IAs	44	QSWSKPNPKTATNAG	QSWSKPNPK	0.2398	3735.8		8.00	Rv2754c, T
IAs	215	LRQLAAVAPAVFADF	RQLAAVAPA	0.2393	3756.0		8.00	Rv2754c, T
IAs	152	KFADQPNAILRRKQA	KFADQPNAI	0.2377	3820.6		8.00	Rv2754c, T
IAs	214	CLRQLAAVAPAVFAD	RQLAAVAPA	0.2375	3828.1		8.00	Rv2754c, T
IAs	13	KTDFLAPPDVPWTTD	DFLAPPDVP	0.2374	3832.6		8.00	Rv2754c, T
IAs	216	RQLAAVAPAVFADF	RQLAAVAPA	0.2324	4043.6		8.00	Rv2754c, T
IAs	162	RRQAARAVLPN	RQAARAVLP	0.2254	4363.1		8.00	Rv2754c, T
IAs	7	RVQLIAKTDFLAPPD	QLIAKTDFL	0.2200	4627.8		8.00	Rv2754c, T
IAs	105	QRYVPEKDSRVVPP	KDSRVVPP	0.2145	4910.7		8.00	Rv2754c, T
IAs	210	LAIECLRQLAAVAPA	RQLAAVAPA	0.2061	5377.4		16.00	Rv2754c, T
IAs	14	TDFLAPPDVPWTTDA	DFLAPPDVP	0.2036	5526.7		16.00	Rv2754c, T
IAs	161	LRRQAARAVLPN	RQAARAVLP	0.2009	5686.5		16.00	Rv2754c, T
IAs	211	AIECLRQLAAVAPAV	RQLAAVAPA	0.1917	6283.8		16.00	Rv2754c, T
IAs	15	DFLAPPDVPWTTDAD	DFLAPPDVP	0.1857	6701.9		16.00	Rv2754c, T
IAs	168	QAARAVLPNATETRI	AARAVLPNA	0.1831	6894.7		16.00	Rv2754c, T
IAs	144	ELLAKLEAKFADQPN	LEAKFADQP	0.1796	7159.2		16.00	Rv2754c, T
IAs	143	SELLAKLEAKFADQP	LEAKFADQP	0.1720	7779.5		16.00	Rv2754c, T
IAs	6	LRVQLIAKTDFLAPP	QLIAKTDFL	0.1698	7962.6		16.00	Rv2754c, T
IAs	233	TLADGTEVATSPLAT	TEVATSPLA	0.1686	8067.8		16.00	Rv2754c, T
IAs	235	ADGTEVATSPLATEA	TEVATSPLA	0.1638	8493.1		16.00	Rv2754c, T
IAs	234	LADGTEVATSPLATE	TEVATSPLA	0.1635	8526.5		16.00	Rv2754c, T
IAs	175	NATETRIVVTGNYR	RIVVTGNYR	0.1596	8892.2		32.00	Rv2754c, T
IAs	169	AARAVLPNATETRIV	AARAVLPNA	0.1586	8989.6		32.00	Rv2754c, T
IAs	46	WSKPNPKTATNAGYLR	KTATNAGYL	0.1585	9001.6		32.00	Rv2754c, T
IAs	47	SKPNPKTATNAGYLR	KTATNAGYL	0.1562	9227.0		32.00	Rv2754c, T
IAs	232	TTLADGTEVATSPLA	TEVATSPLA	0.1546	9386.5		32.00	Rv2754c, T
IAs	217	QLAAVAPAVFADFEV	LAAVAPAVF	0.1516	9691.1		32.00	Rv2754c, T
IAs	48	KPNPKTATNAGYLRH	KTATNAGYL	0.1477	10117.5		32.00	Rv2754c, T
IAs	176	NATETRIVVTGNYRA	RIVVTGNYR	0.1476	10121.7		32.00	Rv2754c, T
IAs	204	DVEIRRLAIECLRQL	LAIECLRQL	0.1433	10610.5		32.00	Rv2754c, T
IAs	3	ATPLRVQLIAKTDFL	QLIAKTDFL	0.1411	10860.9		32.00	Rv2754c, T
IAs	177	APETRIVVTGNYRAW	RIVVTGNYR	0.1378	11262.3		32.00	Rv2754c, T
IAs	100	YSQLSQRYVPEKDSR	RYVPEKDSR	0.1372	11329.0		32.00	Rv2754c, T
IAs	49	PNPKTATNAGYLRHI	KTATNAGYL	0.1358	11509.0		32.00	Rv2754c, T
IAs	205	VEIRRLAIECLRQLA	LAIECLRQL	0.1314	12068.5		32.00	Rv2754c, T
IAs	231	VTTLADGTEVATSPL	DGTEVATSPL	0.1294	12331.5		32.00	Rv2754c, T
IAs	192	RHFIAMRASEHADVE	RASEHADVE	0.1289	12394.1		32.00	Rv2754c, T
IAs	101	SQLSQRYVPEKDSRV	RYVPEKDSR	0.1281	12509.6		32.00	Rv2754c, T

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IAs	178	TETRIVVVTGNYRAWR	RIVVTGNYR	0.1268	12679.4	32.00	Rv2754c, T
IAs	50	NPKTATNAGYLRHII	KTATNAGYL	0.1264	12729.4	32.00	Rv2754c, T
IAs	4	APLRVQLIAKTDFLA	QLIAKTDFL	0.1261	12778.1	32.00	Rv2754c, T
IAs	202	HADVEIRRLAIECLR	RRLAIECLR	0.1258	12814.8	32.00	Rv2754c, T
IAs	206	EIRRLAIECLRQLAA	RRLAIECLR	0.1233	13174.7	32.00	Rv2754c, T
IAs	158	NAILRRKQARQAARA	KQARQAARA	0.1224	13294.5	32.00	Rv2754c, T
IAs	52	KTATNAGYLRHII DV	KTATNAGYL	0.1215	13426.3	32.00	Rv2754c, T
IAs	207	IRRLAIECLRQLAAV	RRLAIECLR	0.1215	13429.3	32.00	Rv2754c, T
IAs	208	RRLAIECLRQLAAVA	RRLAIECLR	0.1196	13704.0	32.00	Rv2754c, T
IAs	51	PKTATNAGYLRHII D	KTATNAGYL	0.1194	13744.2	32.00	Rv2754c, T
IAs	55	TNAGYLRHII DVGHF	RHII DVGHF	0.1182	13910.4	32.00	Rv2754c, T
IAs	218	LA AVAPAVFADFEVT	LA AVAPAVF	0.1155	14336.1	32.00	Rv2754c, T
IAs	203	ADVEIRRLAIECLRQ	RRLAIECLR	0.1152	14380.7	32.00	Rv2754c, T
IAs	102	QLSQRVYVEKDSRVV	RYVPEKDSR	0.1148	14431.8	32.00	Rv2754c, T
IAs	159	AILRRKQARQAARAV	KQARQAARA	0.1144	14498.4	32.00	Rv2754c, T
IAs	37	FAGRACYQSWSKPNP	ACYQSWSKP	0.1126	14792.9	32.00	Rv2754c, T
IAs	160	ILRRKQARQAARAVL	KQARQAARA	0.1084	15478.0	50.00	Rv2754c, T
IAs	209	RLAIECLRQLAAVAP	LAIECLRQL	0.1070	15714.7	50.00	Rv2754c, T
IAs	179	ETRIVVVTGNYRAWRH	RIVVTGNYR	0.1043	16170.1	50.00	Rv2754c, T
IAs	76	SVSFYITGISRSCSTH	TGISRSCSTH	0.1036	16294.1	50.00	Rv2754c, T
IAs	5	PLRVQLIAKTDFLAP	QLIAKTDFL	0.1025	16486.7	50.00	Rv2754c, T
IAs	103	LSQRVYVEKDSRVVV	RYVPEKDSR	0.1024	16514.2	50.00	Rv2754c, T
IAs	180	TRIVVTGNYRAWRHFI	RIVVTGNYR	0.1020	16587.2	50.00	Rv2754c, T
IAs	56	NAGYLRHII DVGHF S	RHII DVGHF	0.1006	16836.9	50.00	Rv2754c, T
IAs	104	SQRVYVEKDSRVVVP	RYVPEKDSR	0.0984	17238.8	50.00	Rv2754c, T
IAs	79	FYITGISRSCSTHEL I	TGISRSCSTH	0.0981	17295.8	50.00	Rv2754c, T
IAs	132	TEAADAARATYSELL	ARATYSELL	0.0948	17934.2	50.00	Rv2754c, T
IAs	181	RIVVTGNYRAWRHFI	RIVVTGNYR	0.0947	17940.4	50.00	Rv2754c, T
IAs	197	MRASEHADVEIRRLA	RASEHADVE	0.0940	18077.4	50.00	Rv2754c, T
IAs	80	YITGISRSCSTHELIR	TGISRSCSTH	0.0925	18385.7	50.00	Rv2754c, T
IAs	77	VSFYITGISRSCSTHE	TGISRSCSTH	0.0923	18416.5	50.00	Rv2754c, T
IAs	156	QPNAILRRKQARQAA	QPNAILRRK	0.0920	18471.2	50.00	Rv2754c, T
IAs	193	HFIAMRASEHADVEI	RASEHADVE	0.0915	18583.9	50.00	Rv2754c, T
IAs	96	RHFSYSQLSQRVYVE	RHFSYSQLS	0.0906	18757.2	50.00	Rv2754c, T
IAs	198	RASEHADVEIRRLAI	RASEHADVE	0.0902	18841.4	50.00	Rv2754c, T
IAs	81	ITGISRSCSTHELIRH	TGISRSCSTH	0.0901	18864.5	50.00	Rv2754c, T
IAs	82	TGISRSCSTHELIRHR	TGISRSCSTH	0.0897	18942.0	50.00	Rv2754c, T
IAs	1	AETAPLRVQLIAKTD	APLRVQLIA	0.0896	18965.2	50.00	Rv2754c, T
IAs	191	RHFIFIAMRASEHADV	RHFIFIAMRAS	0.0894	19001.7	50.00	Rv2754c, T
IAs	127	LRHILTEAADAARAT	EAADAARAT	0.0883	19237.1	50.00	Rv2754c, T
IAs	155	DQPNAILRRKQARQA	QPNAILRRK	0.0871	19478.2	50.00	Rv2754c, T
IAs	98	FSYSQLSQRVYVEKD	QLSQRVYVE	0.0859	19742.6	50.00	Rv2754c, T
IAs	154	ADQPNAILRRKQARQ	AILRRKQAR	0.0856	19803.1	50.00	Rv2754c, T
IAs	131	LTEAADAARATYSEL	EAADAARAT	0.0855	19834.0	50.00	Rv2754c, T
IAs	153	FADQPNAILRRKQAR	AILRRKQAR	0.0852	19898.0	50.00	Rv2754c, T
IAs	2	ETAPLRVQLIAKTDF	APLRVQLIA	0.0852	19898.5	50.00	Rv2754c, T
IAs	78	SFYITGISRSCSTHEL	TGISRSCSTH	0.0851	19915.5	50.00	Rv2754c, T
IAs	90	HELIRHRHFSYSQLS	RHFSYSQLS	0.0847	19987.2	50.00	Rv2754c, T
IAs	189	RAWRHFIAMRASEHA	RHFIFIAMRAS	0.0837	20214.2	50.00	Rv2754c, T
IAs	194	FIAMRASEHADVEIRR	RASEHADVE	0.0836	20235.2	50.00	Rv2754c, T
IAs	36	EFAGRACYQSWSKPN	EFAGRACYQ	0.0830	20361.7	50.00	Rv2754c, T
IAs	190	AWRHFIAMRASEHAD	RHFIFIAMRAS	0.0823	20525.8	50.00	Rv2754c, T
IAs	95	HRHFSYSQLSQRVVP	RHFSYSQLS	0.0821	20567.9	50.00	Rv2754c, T
IAs	0	VAETAPLRVQLIAKT	APLRVQLIA	0.0818	20625.1	50.00	Rv2754c, T
IAs	188	YRAWRHFIAMRASEH	RHFIFIAMRAS	0.0811	20799.3	50.00	Rv2754c, T
IAs	57	AGYLRHII DVGHF SV	RHII DVGHF	0.0810	20817.0	50.00	Rv2754c, T
IAs	186	GNIRAWRHFIAMRAS	RHFIFIAMRAS	0.0798	21081.3	50.00	Rv2754c, T
IAs	61	RHII DVGHF SVLEHA	RHII DVGHF	0.0795	21150.8	50.00	Rv2754c, T
IAs	128	RHILTEAADAARATY	RHILTEAAD	0.0786	21356.6	50.00	Rv2754c, T
IAs	93	IRHRHFSYSQLSQR	RHFSYSQLS	0.0784	21407.3	50.00	Rv2754c, T
IAs	129	HILTEAADAARATYS	EAADAARAT	0.0782	21453.0	50.00	Rv2754c, T
IAs	35	VEFAGRACYQSWSKP	ACYQSWSKP	0.0776	21593.8	50.00	Rv2754c, T
IAs	133	EAADAARATYSELLA	ADAARATYS	0.0773	21664.5	50.00	Rv2754c, T
IAs	195	IAMRASEHADVEIRR	RASEHADVE	0.0771	21713.6	50.00	Rv2754c, T
IAs	126	DLRHILTEAADAARA	RHILTEAAD	0.0767	21801.1	50.00	Rv2754c, T
IAs	99	SYSQLSQRVYVEPKDS	QLSQRVYVE	0.0766	21823.1	50.00	Rv2754c, T
IAs	196	AMRASEHADVEIRRL	RASEHADVE	0.0762	21928.4	50.00	Rv2754c, T
IAs	221	VAPAVFADFEVTTLA	APAVFADFE	0.0761	21938.6	50.00	Rv2754c, T
IAs	199	ASEHADVEIRRLAIE	VEIRRLAIE	0.0761	21956.0	50.00	Rv2754c, T
IAs	222	APAVFADFEVTTLAD	APAVFADFE	0.0759	21985.7	50.00	Rv2754c, T
IAs	187	NYRAWRHFIAMRASE	RHFIFIAMRAS	0.0758	22017.1	50.00	Rv2754c, T
IAs	92	LIRHRHFSYSQLSQR	RHFSYSQLS	0.0753	22139.6	50.00	Rv2754c, T
IAs	30	GGPALVEFAGRACYQ	EFAGRACYQ	0.0747	22291.8	50.00	Rv2754c, T
IAs	91	ELIRHRHFSYSQLSQ	RHFSYSQLS	0.0745	22328.0	50.00	Rv2754c, T
IAs	94	RHRHFSYSQLSQRVY	RHFSYSQLS	0.0743	22376.6	50.00	Rv2754c, T
IAs	60	LRHII DVGHF SVLEH	RHII DVGHF	0.0742	22410.5	50.00	Rv2754c, T
IAs	97	HFSYSQLSQRVYVEPK	QLSQRVYVE	0.0735	22570.2	50.00	Rv2754c, T
IAs	59	YLRHII DVGHF SVLE	RHII DVGHF	0.0728	22734.6	50.00	Rv2754c, T
IAs	200	SEHADVEIRRLAIEC	VEIRRLAIE	0.0722	22900.0	50.00	Rv2754c, T
IAs	58	GYLRHII DVGHF SVL	RHII DVGHF	0.0722	22900.3	50.00	Rv2754c, T
IAs	130	ILTEAADAARATYSE	EAADAARAT	0.0718	22993.1	50.00	Rv2754c, T
IAs	134	ADAARATYSELLAK	ADAARATYS	0.0718	22994.6	50.00	Rv2754c, T
IAs	135	ADAARATYSELLAKL	ADAARATYS	0.0713	23110.1	50.00	Rv2754c, T
IAs	170	ARAVLPNATETRIVV	ARAVLPNAT	0.0712	23134.1	50.00	Rv2754c, T
IAs	84	ISRSCSTHELIRHRHF	SRSCTHELI	0.0709	23213.4	50.00	Rv2754c, T

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IAs	124	DADLRHILTEAADAA	RHILTEAAD	0.0682	23897.1	50.00	Rv2754c, T
IAs	219	AAVAPAVFADFEVTT	APAVFADFE	0.0674	24119.7	50.00	Rv2754c, T
IAs	34	LHEFAGRACYQWSK	EFAGRACYQ	0.0670	24222.2	50.00	Rv2754c, T
IAs	220	AVAPAVFADFEVTTL	APAVFADFE	0.0662	24433.6	50.00	Rv2754c, T
IAs	125	ADLRHILTEAADAA	RHILTEAAD	0.0662	24437.0	50.00	Rv2754c, T
IAs	157	PNAILRRKQARQAAR	RKQARQAAR	0.0656	24578.6	50.00	Rv2754c, T
IAs	85	SRSCHELIRHRHFS	SRSCHELIR	0.0650	24741.9	50.00	Rv2754c, T
IAs	33	ALVEFAGRACYQSW	EFAGRACYQ	0.0647	24815.4	50.00	Rv2754c, T
IAs	137	AARATYSELLAKLEA	AARATYSEL	0.0636	25138.3	50.00	Rv2754c, T
IAs	123	DDADLRHILTEADA	RHILTEAAD	0.0631	25262.1	50.00	Rv2754c, T
IAs	201	EHADVEIRRLAIECL	HADVEIRRL	0.0628	25346.2	50.00	Rv2754c, T
IAs	17	LAPPDVPWTTDADGG	LAPPDVPWT	0.0617	25656.3	50.00	Rv2754c, T
IAs	122	EDDADLRHILTEAAD	RHILTEAAD	0.0615	25693.2	50.00	Rv2754c, T
IAs	174	LPNATETRIVVTGNY	TRIVVTGNY	0.0605	25986.5	50.00	Rv2754c, T
IAs	67	GHFSVLEHASVSFYI	GHFSVLEHA	0.0599	26162.8	50.00	Rv2754c, T
IAs	136	DAARATYSELLAKLE	ARATYSELL	0.0590	26404.0	50.00	Rv2754c, T
IAs	31	GPALVEFAGRACYQS	EFAGRACYQ	0.0586	26525.4	50.00	Rv2754c, T
IAs	16	FLAPPDVPWTTDADG	LAPPDVPWT	0.0584	26590.6	50.00	Rv2754c, T
IAs	20	PDPVWTTDADGGPAL	TTDADGGPA	0.0576	26814.5	50.00	Rv2754c, T
IAs	24	WTTDADGGPALVEFA	TTDADGGPA	0.0572	26941.1	50.00	Rv2754c, T
IAs	19	PPDVPWTTDADGGPA	TTDADGGPA	0.0569	27012.6	50.00	Rv2754c, T
IAs	32	PALVEFAGRACYQSW	EFAGRACYQ	0.0550	27584.7	50.00	Rv2754c, T
IAs	25	TTDADGGPALVEFAG	TTDADGGPA	0.0549	27606.2	50.00	Rv2754c, T
IAs	66	VGHFSVLEHASVSFY	SVLEHASVS	0.0545	27737.6	50.00	Rv2754c, T
IAs	64	IDVGHFSVLEHASVS	SVLEHASVS	0.0534	28046.6	50.00	Rv2754c, T
IAs	23	PWTTDADGGPALVEF	TTDADGGPA	0.0532	28105.5	50.00	Rv2754c, T
IAs	116	VVPPGMEDDADLRHI	PPGMEDDAD	0.0527	28275.1	50.00	Rv2754c, T
IAs	83	GISRSCTHELIRHRH	RSCTHELIR	0.0524	28361.6	50.00	Rv2754c, T
IAs	73	EHASVSFYITGISRS	FYITGISRS	0.0522	28422.4	50.00	Rv2754c, T
IAs	65	DVGHFSVLEHASVSF	SVLEHASVS	0.0521	28463.0	50.00	Rv2754c, T
IAs	74	HASVSFYITGISRSC	FYITGISRS	0.0517	28569.7	50.00	Rv2754c, T
IAs	22	VPWTTDADGGPALVE	TTDADGGPA	0.0517	28584.3	50.00	Rv2754c, T
IAs	72	LEHASVSFYITGISR	VSFYITGIS	0.0516	28616.5	50.00	Rv2754c, T
IAs	21	DVPWTTDADGGPALV	TTDADGGPA	0.0513	28687.4	50.00	Rv2754c, T
IAs	171	RAVLPNATETRIVVT	RAVLPNATE	0.0511	28761.7	50.00	Rv2754c, T
IAs	115	VVPPGMEDDADLRH	PPGMEDDAD	0.0508	28872.7	50.00	Rv2754c, T
IAs	27	DADGGPALVEFAGRA	ALVEFAGRA	0.0506	28935.3	50.00	Rv2754c, T
IAs	71	VLEHASVSFYITGIS	VSFYITGIS	0.0504	28986.4	50.00	Rv2754c, T
IAs	230	EVTTLADGTEVATSP	DGTEVATSP	0.0501	29064.2	50.00	Rv2754c, T
IAs	53	TATNAGYLRHIIDVG	NAGYLRHII	0.0498	29178.0	50.00	Rv2754c, T
IAs	138	ARATYSELLAKLEAK	ELLAKLEAK	0.0498	29179.6	50.00	Rv2754c, T
IAs	29	DGGPALVEFAGRACY	ALVEFAGRA	0.0493	29341.0	50.00	Rv2754c, T
IAs	226	PADFVTTLADGTEV	TTLADGTEV	0.0491	29406.2	50.00	Rv2754c, T
IAs	227	ADFEVTTLADGTEVA	TTLADGTEV	0.0490	29419.5	50.00	Rv2754c, T
IAs	28	ADGGPALVEFAGRAC	ALVEFAGRA	0.0488	29493.8	50.00	Rv2754c, T
IAs	68	HFSVLEHASVSFYIT	SVLEHASVS	0.0476	29884.4	50.00	Rv2754c, T
IAs	183	VVTGNYRAWRHFIAM	RAWRHFIAM	0.0458	30462.9	50.00	Rv2754c, T
IAs	70	SVLEHASVSFYITGI	LEHASVSFY	0.0453	30618.9	50.00	Rv2754c, T
IAs	45	SWSKPNPKTATNAGY	KPNPKTATN	0.0449	30749.7	50.00	Rv2754c, T
IAs	142	YSELLAKLEAKFADQ	ELLAKLEAK	0.0449	30755.0	50.00	Rv2754c, T
IAs	54	ATNAGYLRHIIDVGH	NAGYLRHII	0.0439	31088.2	50.00	Rv2754c, T
IAs	139	RATYSELLAKLEAKF	ELLAKLEAK	0.0435	31242.7	50.00	Rv2754c, T
IAs	173	VLPNATETRIVVTGN	PNATETRIV	0.0433	31306.6	50.00	Rv2754c, T
IAs	229	FEVTTLADGTEVATS	TTLADGTEV	0.0431	31367.0	50.00	Rv2754c, T
IAs	75	ASVSFYITGIRSCT	ASVSFYITG	0.0429	31420.3	50.00	Rv2754c, T
IAs	185	TGNYRAWRHFIAMRA	RAWRHFIAM	0.0427	31515.3	50.00	Rv2754c, T
IAs	172	AVLPNATETRIVVTG	PNATETRIV	0.0422	31675.6	50.00	Rv2754c, T
IAs	69	FSVLEHASVSFYITG	LEHASVSFY	0.0421	31717.1	50.00	Rv2754c, T
IAs	141	TYSELLAKLEAKFAD	ELLAKLEAK	0.0420	31743.2	50.00	Rv2754c, T
IAs	18	APPDVPWTTDADGGP	APPDVPWTT	0.0412	32032.0	50.00	Rv2754c, T
IAs	184	VTGNYRAWRHFIAMR	VTGNYRAWR	0.0411	32039.6	50.00	Rv2754c, T
IAs	224	AVFADFEVTTLADGT	EVTTLADGT	0.0411	32049.3	50.00	Rv2754c, T
IAs	228	ADFEVTTLADGTEVAT	TTLADGTEV	0.0407	32191.1	50.00	Rv2754c, T
IAs	62	HIIDVGHFSVLEHAS	GHFSVLEHA	0.0406	32208.5	50.00	Rv2754c, T
IAs	140	ATYSELLAKLEAKFA	ELLAKLEAK	0.0392	32714.3	50.00	Rv2754c, T
IAs	63	IIDVGHFSVLEHASV	GHFSVLEHA	0.0392	32715.3	50.00	Rv2754c, T
IAs	225	VFADFEVTTLADGTE	ADFEVTTLA	0.0392	32719.3	50.00	Rv2754c, T
IAs	26	TDADGGPALVEFAGR	GGPALVEFA	0.0383	33026.9	50.00	Rv2754c, T
IAs	182	IVVTGNYRAWRHFI	GNYRAWRH	0.0363	33774.6	50.00	Rv2754c, T
IAs	86	RSCTHELIRHRHFSY	HELIRHRHF	0.0354	34091.8	50.00	Rv2754c, T
IAs	89	THELIRHRHFSYSQL	HELIRHRHF	0.0353	34139.8	50.00	Rv2754c, T
IAs	223	PAVFADFEVTTLADG	ADFEVTTLA	0.0337	34709.3	50.00	Rv2754c, T
IAs	87	SCTHELIRHRHFSYS	HELIRHRHF	0.0267	37454.8	50.00	Rv2754c, T
IAs	88	CHELIRHRHFSYSQ	HELIRHRHF	0.0246	38296.5	50.00	Rv2754c, T
IAs	117	VPPGMEDDADLRHIL	VPPGMEDDA	0.0245	38356.2	50.00	Rv2754c, T
IAs	121	MEDDADLRHILTEAA	LRHILTEAA	0.0222	39307.4	50.00	Rv2754c, T
IAs	118	PPGMEDDADLRHILT	PPGMEDDAD	0.0200	40280.4	50.00	Rv2754c, T
IAs	119	PGMEDDADLRHILTE	ADLRHILTE	0.0168	41702.2	50.00	Rv2754c, T
IAs	120	GMEDDADLRHILTEA	ADLRHILTE	0.0157	42186.0	50.00	Rv2754c, T

Allele: IAs. Number of high binders 0. Number of weak binders 8. Number of peptides 236

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