



# 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	94	YGSFVRTVSLPVGAD	FVRTVSLPV	0.8756	3.8	SB	0.80	Sequence	
DRB1_0101	93	AYGSFVRTVSLPVG	FVRTVSLPV	0.8752	3.9	SB	0.80	Sequence	
DRB1_0101	92	FAYGSFVRTVSLPVG	FVRTVSLPV	0.8606	4.5	SB	2.00	Sequence	
DRB1_0101	95	GSFVRTVSLPVGAD	FVRTVSLPV	0.8594	4.6	SB	2.00	Sequence	
DRB1_0101	17	FSELFAAFPSFAGLR	LFAAFPSFA	0.8577	4.7	SB	2.00	Sequence	
DRB1_0101	91	EFAYGSFVRTVSLPV	FVRTVSLPV	0.8469	5.2	SB	4.00	Sequence	
DRB1_0101	96	SFVRTVSLPVGAD	FVRTVSLPV	0.8391	5.7	SB	4.00	Sequence	
DRB1_0101	18	SELFAAFPSFAGLRP	FAAFPSFAG	0.8384	5.7	SB	4.00	Sequence	
DRB1_0101	16	EFSELFAAFPSFAGL	LFAAFPSFA	0.8294	6.3	SB	4.00	Sequence	
DRB1_0101	97	FVRTVSLPVGAD	FVRTVSLPV	0.8046	8.3	SB	8.00	Sequence	
DRB1_0101	19	ELFAAFPSFAGLRPT	FAAFPSFAG	0.8006	8.6	SB	8.00	Sequence	
DRB1_0101	15	PEFSELFAAFPSFAG	LFAAFPSFA	0.7810	10.7	SB	8.00	Sequence	
DRB1_0101	14	FPEFSELFAAFPSFA	FSELFAAFPS	0.7764	11.2	SB	16.00	Sequence	
DRB1_0101	24	FPSFAGLRPTFDTRL	FAGLRPTFD	0.7761	11.3	SB	16.00	Sequence	
DRB1_0101	20	LFAAFPSFAGLRPTF	FAAFPSFAG	0.7701	12.0	SB	16.00	Sequence	
DRB1_0101	89	GRSEFAYGSFVRTVSL	FAYGSFVRT	0.7688	12.2	SB	16.00	Sequence	
DRB1_0101	88	GRSEFAYGSFVRTVS	FAYGSFVRT	0.7268	19.2	SB	16.00	Sequence	
DRB1_0101	25	PSFAGLRPTFDTRLM	FAGLRPTFD	0.7207	20.5	SB	16.00	Sequence	
DRB1_0101	23	AFPSFAGLRPTFDTR	FAGLRPTFD	0.7088	23.4	SB	32.00	Sequence	
DRB1_0101	90	SEFAYGSFVRTVSLP	FAYGSFVRT	0.7023	25.1	SB	32.00	Sequence	
DRB1_0101	13	LFPEFSELFAAFPSF	FSELFAAFPS	0.6998	25.7	SB	32.00	Sequence	
DRB1_0101	27	FAGLRPTFDTRLMLR	LRPTFDTRL	0.6974	26.4	SB	32.00	Sequence	
DRB1_0101	21	FAAFPSFAGLRPTFD	FAAFPSFAG	0.6971	26.5	SB	32.00	Sequence	
DRB1_0101	26	SFAGLRPTFDTRLMR	FAGLRPTFD	0.6964	26.7	SB	32.00	Sequence	
DRB1_0101	87	DGRSEFAYGSFVRTV	FAYGSFVRT	0.6899	28.6	SB	32.00	Sequence	
DRB1_0101	64	DVDIMVRDGQLTIKA	IMVRDGQLT	0.6528	42.8	SB	32.00	Sequence	
DRB1_0101	22	AAFPSFAGLRPTFDT	FAGLRPTFD	0.6434	47.4	SB	32.00	Sequence	
DRB1_0101	114	ATYDKGILTVSVAVS	DKGILTVSV	0.6377	50.4	WB	32.00	Sequence	
DRB1_0101	65	VDIMVRDGQLTIKAE	IMVRDGQLT	0.6251	57.8	WB	32.00	Sequence	
DRB1_0101	116	YDKGILTVSVAVSEG	GILTVSVAV	0.6188	61.8	WB	32.00	Sequence	
DRB1_0101	113	KATYDKGILTVSVAV	DKGILTVSV	0.6091	68.6	WB	32.00	Sequence	
DRB1_0101	12	SLFPEFSELFAAFPS	FSELFAAFPS	0.6090	68.8	WB	32.00	Sequence	
DRB1_0101	115	TYDKGILTVSVAVSE	DKGILTVSV	0.6058	71.2	WB	32.00	Sequence	
DRB1_0101	117	DKGILTVSVAVSEGK	ILTVSVAVS	0.6042	72.4	WB	32.00	Sequence	
DRB1_0101	70	RDGQLTIKAERTEQK	QLTIKAERT	0.5977	77.7	WB	50.00	Sequence	
DRB1_0101	86	FDGRSEFAYGSFVRT	FAYGSFVRT	0.5809	93.2	WB	50.00	Sequence	
DRB1_0101	118	KGILTVSVAVSEGK	ILTVSVAVS	0.5763	97.9	WB	50.00	Sequence	
DRB1_0101	28	AGLRPTFDTRLMLR	LRPTFDTRL	0.5714	103.3	WB	50.00	Sequence	
DRB1_0101	11	RSLFPEFSELFAAFPS	LFPEFSELF	0.5706	104.2	WB	50.00	Sequence	
DRB1_0101	63	KDVDIMVRDGQLTIK	IMVRDGQLT	0.5632	112.9	WB	50.00	Sequence	
DRB1_0101	10	PRSLFPEFSELFAAF	LFPEFSELF	0.5505	129.5	WB	50.00	Sequence	
DRB1_0101	66	DIMVRDGQLTIKAER	IMVRDGQLT	0.5467	135.0	WB	50.00	Sequence	
DRB1_0101	67	IMVRDGQLTIKAERT	IMVRDGQLT	0.5404	144.4	WB	50.00	Sequence	
DRB1_0101	7	QRHPRSLFPEFSELF	PRSLFPEFS	0.5368	150.2	WB	50.00	Sequence	
DRB1_0101	112	IKATYDKGILTVSVA	YDKGILTVS	0.5338	155.2	WB	50.00	Sequence	
DRB1_0101	69	VRDGQLTIKAERTEQ	QLTIKAERT	0.5178	184.5	WB	50.00	Sequence	
DRB1_0101	119	GILTVSVAVSEGKPT	ILTVSVAVS	0.5133	193.7	WB	50.00	Sequence	
DRB1_0101	29	GLRPTFDTRLMLRLE	LRPTFDTRL	0.5026	217.5	WB	50.00	Sequence	
DRB1_0101	9	HPRSLFPEFSELF	LFPEFSELF	0.5000	223.6	WB	50.00	Sequence	
DRB1_0101	111	DIKATYDKGILTVSV	YDKGILTVS	0.4925	242.6	WB	50.00	Sequence	
DRB1_0101	71	DGQLTIKAERTEQKD	QLTIKAERT	0.4888	252.5	WB	50.00	Sequence	
DRB1_0101	8	HPRSLFPEFSELF	PRSLFPEFS	0.4841	265.7	WB	50.00	Sequence	
DRB1_0101	62	KDVDIMVRDGQLTI	IMVRDGQLT	0.4811	274.2	WB	50.00	Sequence	
DRB1_0101	85	DFDGRSEFAYGSFVR	GRSEFAYGS	0.4720	302.8	WB	50.00	Sequence	
DRB1_0101	30	LRPTFDTRLMLRLE	LRPTFDTRL	0.4611	340.7	WB	50.00	Sequence	
DRB1_0101	72	QQLTIKAERTEQKDF	QLTIKAERT	0.4608	341.7	WB	50.00	Sequence	
DRB1_0101	68	MVRDGQLTIKAERTE	QLTIKAERT	0.4594	347.0	WB	50.00	Sequence	
DRB1_0101	120	ILTVSVAVSEGKPT	ILTVSVAVS	0.4531	371.5	WB	50.00	Sequence	

DRB1_0101	6	VQRHPRSLFPEFSEL	PRSLFPEFS	0.4177	544.8	50.00	Sequence
DRB1_0101	110	DDIKATYDKGILTVS	IKATYDKGI	0.4097	594.1	50.00	Sequence
DRB1_0101	0	MATTLPVQRHPRSLF	TLPVQRHPR	0.4012	651.6	50.00	Sequence
DRB1_0101	31	RPTFDTRLMLRLEDEM	FDTRLMLRLE	0.3961	688.3	50.00	Sequence
DRB1_0101	73	QLTIKAERTEQKDFD	QLTIKAERT	0.3904	731.8	50.00	Sequence
DRB1_0101	61	PKDQVDIMVRDQGLT	IMVRDQGLT	0.3810	810.6	50.00	Sequence
DRB1_0101	109	EDDIKATYDKGILTV	IKATYDKGI	0.3800	819.6	50.00	Sequence
DRB1_0101	1	ATTLPVQRHPRSLFP	LPVQRHPR	0.3739	875.5	50.00	Sequence
DRB1_0101	84	KDFDGRSEFAYGSFV	GRSEFAYGS	0.3734	880.1	50.00	Sequence
DRB1_0101	45	MKEGRYEVRAELPGV	RYEVRAELP	0.3640	973.5	50.00	Sequence
DRB1_0101	32	PFDTRLMLRLEDEM	FDTRLMLRLE	0.3621	994.0	50.00	Sequence
DRB1_0101	46	KEGRYEVRAELPGVD	RYEVRAELP	0.3557	1065.5	50.00	Sequence
DRB1_0101	33	TFDTRLMLRLEDEMKE	FDTRLMLRLE	0.3490	1145.3	50.00	Sequence
DRB1_0101	36	TRLMLRLEDEMKEGRY	MRLEDEMKE	0.3452	1193.8	50.00	Sequence
DRB1_0101	2	TTLPVQRHPRSLFPE	PVQRHPRSL	0.3381	1288.3	50.00	Sequence
DRB1_0101	83	QKDFDGRSEFAYGSF	FDGRSEFAY	0.3354	1327.0	50.00	Sequence
DRB1_0101	35	DTRLMLRLEDEMKEGR	LMRLEDEMKE	0.3266	1459.9	50.00	Sequence
DRB1_0101	122	TVSVAVSEGKPTTEKH	VAVSEGKPT	0.3221	1533.1	50.00	Sequence
DRB1_0101	34	FDTRLMLRLEDEMKEG	LMRLEDEMKE	0.3178	1605.9	50.00	Sequence
DRB1_0101	108	DEDDIKATYDKGILT	IKATYDKGI	0.3128	1694.0	50.00	Sequence
DRB1_0101	121	LTVSVAVSEGKPTTEK	VAVSEGKPT	0.3021	1903.5	50.00	Sequence
DRB1_0101	47	EGRYEVRAELPGVDP	RYEVRAELP	0.3008	1930.4	50.00	Sequence
DRB1_0101	123	VSVAVSEGKPTTEKHI	VAVSEGKPT	0.3005	1935.3	50.00	Sequence
DRB1_0101	5	PVQRHPRSLFPEFSE	PRSLFPEFS	0.2947	2061.7	50.00	Sequence
DRB1_0101	98	VRTVSLPVGADED	VRTVSLPVG	0.2942	2072.8	50.00	Sequence
DRB1_0101	37	LMRLEDEMKEGRY	MRLEDEMKE	0.2919	2123.9	50.00	Sequence
DRB1_0101	4	LPVQRHPRSLFPEFS	PRSLFPEFS	0.2907	2152.8	50.00	Sequence
DRB1_0101	3	TLPVQRHPRSLFPEF	PVQRHPRSL	0.2891	2190.3	50.00	Sequence
DRB1_0101	124	SVAVSEGKPTTEKHQI	VAVSEGKPT	0.2852	2285.0	50.00	Sequence
DRB1_0101	44	EMKEGRYEVRAELPG	RYEVRAELP	0.2812	2386.1	50.00	Sequence
DRB1_0101	48	GRYEVRAELPGVDPD	RYEVRAELP	0.2805	2404.1	50.00	Sequence
DRB1_0101	107	ADEDDIKATYDKGIL	IKATYDKGI	0.2780	2468.9	50.00	Sequence
DRB1_0101	49	RYEVRAELPGVDPDK	VRAELPGVD	0.2761	2520.6	50.00	Sequence
DRB1_0101	82	EQKDFDGRSEFAYGS	FDGRSEFAY	0.2729	2611.0	50.00	Sequence
DRB1_0101	125	VAVSEGKPTTEKHQI	VAVSEGKPT	0.2702	2686.7	50.00	Sequence
DRB1_0101	128	SEGKPTTEKHQIRST	KPTEKHQI	0.2607	2979.7	50.00	Sequence
DRB1_0101	106	GADEDDIKATYDKGI	IKATYDKGI	0.2459	3495.7	50.00	Sequence
DRB1_0101	129	EGKPTTEKHQIRSTN	KPTEKHQI	0.2404	3709.7	50.00	Sequence
DRB1_0101	38	LMRLEDEMKEGRYEV	LMRLEDEMKE	0.2389	3770.0	50.00	Sequence
DRB1_0101	43	DEMKEGRYEVRAELP	RYEVRAELP	0.2370	3847.3	50.00	Sequence
DRB1_0101	56	LPGVDPDKDQVDIMVR	VDPDKDQVDI	0.2334	4000.7	50.00	Sequence
DRB1_0101	81	TEQKDFDGRSEFAYG	EQKDFDGRS	0.2304	4133.1	50.00	Sequence
DRB1_0101	80	RTEQKDFDGRSEFAY	EQKDFDGRS	0.2291	4190.6	50.00	Sequence
DRB1_0101	42	EDEMKEGRYEVRAEL	MKEGRYEV	0.2246	4403.1	50.00	Sequence
DRB1_0101	50	YEVRAELPGVDPDKD	VRAELPGVD	0.2240	4428.0	50.00	Sequence
DRB1_0101	127	VSEGKPTTEKHQIRS	KPTEKHQI	0.2162	4819.1	50.00	Sequence
DRB1_0101	60	DPDKDQVDIMVRDQGL	DIMVRDQGL	0.2137	4950.7	50.00	Sequence
DRB1_0101	55	ELPGVDPDKDQVDIMV	VDPDKDQVDI	0.2134	4970.7	50.00	Sequence
DRB1_0101	57	PGVDPDKDQVDIMVRD	VDPDKDQVDI	0.2129	4996.1	50.00	Sequence
DRB1_0101	99	RTVSLPVGADED	TVSLPVGAD	0.2119	5047.8	50.00	Sequence
DRB1_0101	79	ERTEQKDFDGRSEFA	EQKDFDGRS	0.2089	5214.9	50.00	Sequence
DRB1_0101	58	GVDPDKDQVDIMVRD	VDPDKDQVDI	0.2043	5479.7	50.00	Sequence
DRB1_0101	41	LEDEMKEGRYEVRAE	EMKEGRYEV	0.2039	5505.5	50.00	Sequence
DRB1_0101	54	AELPGVDPDKDQVDIM	VDPDKDQVDI	0.2036	5522.1	50.00	Sequence
DRB1_0101	59	VDPDKDQVDIMVRDQ	VDPDKDQVDI	0.2020	5617.6	50.00	Sequence
DRB1_0101	53	RAELPGVDPDKDQVDI	VDPDKDQVDI	0.1987	5826.6	50.00	Sequence
DRB1_0101	76	IKAERTEQKDFDGRS	EQKDFDGRS	0.1980	5870.8	50.00	Sequence
DRB1_0101	40	RLEDEMKEGRYEVRA	EMKEGRYEV	0.1959	6002.7	50.00	Sequence
DRB1_0101	126	AVSEGKPTTEKHQIR	KPTEKHQI	0.1955	6029.1	50.00	Sequence
DRB1_0101	39	MRLEDEMKEGRYEV	MRLEDEMKE	0.1939	6137.3	50.00	Sequence
DRB1_0101	78	AERTEQKDFDGRSEF	EQKDFDGRS	0.1887	6487.8	50.00	Sequence
DRB1_0101	77	KAERTEQKDFDGRSE	EQKDFDGRS	0.1877	6560.7	50.00	Sequence
DRB1_0101	74	LTIKAERTEQKDFDG	IKAERTEQK	0.1853	6733.7	50.00	Sequence
DRB1_0101	51	EVRAELPGVDPDKDV	VRAELPGVD	0.1841	6818.8	50.00	Sequence
DRB1_0101	100	TVSLPVGADED	TVSLPVGAD	0.1829	6912.5	50.00	Sequence
DRB1_0101	52	VRAELPGVDPDKDQVD	VRAELPGVD	0.1689	8038.5	50.00	Sequence
DRB1_0101	101	VSLPVGADED	VGADEDDIK	0.1644	8439.3	50.00	Sequence
DRB1_0101	102	SLPVGADED	VGADEDDIK	0.1635	8522.4	50.00	Sequence
DRB1_0101	75	TIKAERTEQKDFDGR	IKAERTEQK	0.1611	8752.9	50.00	Sequence
DRB1_0101	103	LPVGADED	VGADEDDIK	0.1524	9610.2	50.00	Sequence
DRB1_0101	105	VGADEDDIKATYDKG	VGADEDDIK	0.1408	10900.8	50.00	Sequence
DRB1_0101	104	PVGADED	VGADEDDIK	0.1397	11033.8	50.00	Sequence

Allele: DRB1\_0101. Number of high binders 27. Number of weak binders 31. Number of peptides 130

Allele	pos	peptide	core	1-log50k(aff)	affinity(nM)	Bind	Level	%Random	Identity
DRB1_0301	29	GLRPTFDTRLMLRED	GLRPTFDTR	0.7001	25.7	SB	0.80	Sequence	
DRB1_0301	65	VDIMVRDQGQLTIKAE	VDIMVRDQG	0.6986	26.1	SB	0.80	Sequence	
DRB1_0301	64	DVDIMVRDQGQLTIKA	VDIMVRDQG	0.6892	28.9	SB	0.80	Sequence	
DRB1_0301	28	AGLRPTFDTRLMLRLE	GLRPTFDTR	0.6824	31.1	SB	1.00	Sequence	
DRB1_0301	27	FAGLRPTFDTRLMLRL	GLRPTFDTR	0.6611	39.1	SB	2.00	Sequence	
DRB1_0301	63	KDVDIMVRDQGQLTIK	VDIMVRDQG	0.6587	40.1	SB	2.00	Sequence	
DRB1_0301	26	SFAGLRPTFDTRLMLR	GLRPTFDTR	0.6165	63.4	WB	2.00	Sequence	
DRB1_0301	62	DKDVDIMVRDQGQLTI	VDIMVRDQG	0.6033	73.2	WB	4.00	Sequence	
DRB1_0301	30	LRPTFDTRLMLRLEDE	RPTFDTRLM	0.5793	94.9	WB	4.00	Sequence	
DRB1_0301	66	DIMVRDQGQLTIKAER	DIMVRDQGL	0.5533	125.5	WB	4.00	Sequence	
DRB1_0301	61	PDKDVDIMVRDQGQLT	VDIMVRDQG	0.5211	178.0	WB	8.00	Sequence	
DRB1_0301	31	RPTFDTRLMLRLEDEM	PTFDTRLMR	0.5180	184.0	WB	8.00	Sequence	
DRB1_0301	36	TRLMLRLEDEMKEGRY	RLMLRLEDEM	0.4895	250.5	WB	8.00	Sequence	
DRB1_0301	56	LPGVDPDKDVDIMVR	LPGVDPDKD	0.4868	258.0	WB	8.00	Sequence	
DRB1_0301	37	RLMLRLEDEMKEGRYE	RLMLRLEDEM	0.4781	283.4	WB	16.00	Sequence	
DRB1_0301	25	PSFAGLRPTFDTRLM	LRPTFDTRL	0.4644	328.6	WB	16.00	Sequence	
DRB1_0301	55	ELPGVDPDKDVDIMV	LPGVDPDKD	0.4560	359.8	WB	16.00	Sequence	
DRB1_0301	35	DTRLMLRLEDEMKEGR	RLMLRLEDEM	0.4552	363.1	WB	16.00	Sequence	
DRB1_0301	67	IMVRDQGQLTIKAERT	IMVRDQGLT	0.4534	370.2	WB	16.00	Sequence	
DRB1_0301	60	DPDKDVDIMVRDQGL	PDKDVDIMV	0.4510	379.9	WB	16.00	Sequence	
DRB1_0301	32	PTFDTRLMLRLEDEM	PTFDTRLMR	0.4502	383.4	WB	16.00	Sequence	
DRB1_0301	59	VDPDKDVDIMVRDQG	DPDKDVDIM	0.4302	475.9	WB	16.00	Sequence	
DRB1_0301	24	FPSFAGLRPTFDTRL	LRPTFDTRL	0.4163	553.2		16.00	Sequence	
DRB1_0301	58	GVPDKDVDIMVRD	DPDKDVDIM	0.4139	567.7		16.00	Sequence	
DRB1_0301	0	MATTLPVQRHPRSLF	MATTLPVQR	0.4033	636.6		16.00	Sequence	
DRB1_0301	34	FTRLMLRLEDEMKEG	RLMLRLEDEM	0.4004	657.2		16.00	Sequence	
DRB1_0301	54	AELPGVDPDKDVDIM	LPGVDPDKD	0.3934	708.5		32.00	Sequence	
DRB1_0301	57	PGVDPDKDVDIMVRD	DPDKDVDIM	0.3853	773.1		32.00	Sequence	
DRB1_0301	68	MVRDQGLTIKAERTE	MVRDQGLTI	0.3749	865.9		32.00	Sequence	
DRB1_0301	72	GQLTIKAERTEQKDF	QLTIKAERT	0.3700	912.3		32.00	Sequence	
DRB1_0301	33	TFDTRLMLRLEDEMKE	LMRLEDEM	0.3692	920.3		32.00	Sequence	
DRB1_0301	53	RAELPGVDPDKDVDI	LPGVDPDKD	0.3549	1074.6		32.00	Sequence	
DRB1_0301	71	DGQLTIKAERTEQKD	QLTIKAERT	0.3506	1126.5		32.00	Sequence	
DRB1_0301	38	LMRLEDEMKEGRYEV	LMRLEDEM	0.3456	1188.1		32.00	Sequence	
DRB1_0301	118	KGILTVSVAVSEGK	ILTVSVAVS	0.3393	1271.9		32.00	Sequence	
DRB1_0301	102	SLPVGAEDEDDIKATY	SLPVGAEDE	0.3382	1287.3		32.00	Sequence	
DRB1_0301	70	RDGQLTIKAERTEQK	QLTIKAERT	0.3269	1454.5		32.00	Sequence	
DRB1_0301	73	QLTIKAERTEQKDFD	QLTIKAERT	0.3250	1484.6		32.00	Sequence	
DRB1_0301	23	AFPSFAGLRPTFDTR	FPSFAGLRP	0.3225	1525.4		32.00	Sequence	
DRB1_0301	101	VSLPVGAEDEDDIKAT	SLPVGAEDE	0.3192	1581.8		32.00	Sequence	
DRB1_0301	117	DKGILTVSVAVSEGK	ILTVSVAVS	0.3174	1613.0		32.00	Sequence	
DRB1_0301	111	DIKATYDKGILTVSV	DIKATYDKG	0.3115	1718.5		32.00	Sequence	
DRB1_0301	45	MKEGRYEVRAELPGV	MKEGRYEV	0.3108	1731.9		32.00	Sequence	
DRB1_0301	119	GILTVSVAVSEGKPT	ILTVSVAVS	0.3095	1756.3		32.00	Sequence	
DRB1_0301	3	TLPVQRHPRSLFPEF	TLPVQRHPR	0.3011	1923.9		32.00	Sequence	
DRB1_0301	20	LFAAFPSPFAGLRPTF	LFAAFPSPA	0.2985	1978.2		50.00	Sequence	
DRB1_0301	100	TVSLPVGAEDEDDIKA	SLPVGAEDE	0.2891	2190.4		50.00	Sequence	
DRB1_0301	110	DDIKATYDKGILTVS	DIKATYDKG	0.2866	2251.0		50.00	Sequence	
DRB1_0301	116	YDKGILTVSVAVSEG	KGILTVSVA	0.2851	2288.4		50.00	Sequence	
DRB1_0301	120	ILTVSVAVSEGKPT	ILTVSVAVS	0.2849	2291.5		50.00	Sequence	
DRB1_0301	2	TTLPVQRHPRSLFPE	TLPVQRHPR	0.2839	2318.1		50.00	Sequence	
DRB1_0301	123	VSVAVSEGKPTKHI	VSVAVSEGK	0.2830	2340.0		50.00	Sequence	
DRB1_0301	10	PRSLFPEFSELFAAF	PRSLFPEFS	0.2824	2355.6		50.00	Sequence	
DRB1_0301	44	EMKEGRYEVRAELPG	MKEGRYEV	0.2811	2387.7		50.00	Sequence	
DRB1_0301	69	VRDQGLTIKAERTEQ	GQLTIKAER	0.2811	2388.3		50.00	Sequence	
DRB1_0301	46	KEGRYEVRAELPGVD	RYEVRAELP	0.2798	2423.4		50.00	Sequence	
DRB1_0301	52	VRAELPGVDPDKDVD	LPGVDPDKD	0.2784	2459.3		50.00	Sequence	
DRB1_0301	109	EDDIKATYDKGILTV	DIKATYDKG	0.2758	2530.0		50.00	Sequence	
DRB1_0301	1	ATTLPVQRHPRSLF	TLPVQRHPR	0.2685	2735.8		50.00	Sequence	
DRB1_0301	115	TYDKGILTVSVAVSE	KGILTVSVA	0.2658	2818.7		50.00	Sequence	
DRB1_0301	22	AAFPSFAGLRPTFD	FPSFAGLRP	0.2649	2846.7		50.00	Sequence	
DRB1_0301	12	SLFPEFSELFAAFPS	FPEFSELFA	0.2630	2904.8		50.00	Sequence	
DRB1_0301	14	FPEFSELFAAFPSFA	FPEFSELFA	0.2624	2924.2		50.00	Sequence	
DRB1_0301	114	ATYDKGILTVSVAVS	KGILTVSVA	0.2612	2960.7		50.00	Sequence	
DRB1_0301	92	FAYGSFVRTVSLPVG	FAYGSFVRT	0.2610	2967.5		50.00	Sequence	
DRB1_0301	48	GRYEVRAELPGVDP	RYEVRAELP	0.2603	2992.3		50.00	Sequence	
DRB1_0301	13	LFPEFSELFAAFPSF	FPEFSELFA	0.2593	3022.1		50.00	Sequence	
DRB1_0301	17	FSELFAAFPSFAGLR	FSELFAAFP	0.2585	3051.1		50.00	Sequence	
DRB1_0301	47	EGRYEVRAELPGVD	RYEVRAELP	0.2565	3115.4		50.00	Sequence	
DRB1_0301	99	RTVSLPVGAEDEDDI	SLPVGAEDE	0.2562	3125.1		50.00	Sequence	
DRB1_0301	122	VSVAVSEGKPTKHI	VSVAVSEGK	0.2558	3141.8		50.00	Sequence	
DRB1_0301	43	DEMKEGRYEVRAELP	MKEGRYEV	0.2547	3178.4		50.00	Sequence	
DRB1_0301	112	IKATYDKGILTVSVA	IKATYDKGI	0.2528	3244.3		50.00	Sequence	
DRB1_0301	9	HPRSLFPEFSELFAA	PRSLFPEFS	0.2516	3287.0		50.00	Sequence	

DRB1_0301	121	LTVSVAVSEGKPT	VSVAVSEGK	0.2487	3392.7	50.00	Sequence
DRB1_0301	11	RSLFPEFSELF	FPEFSELF	0.2461	3487.4	50.00	Sequence
DRB1_0301	91	EYAGSFVTVSLPV	FAYGSFVRT	0.2458	3498.5	50.00	Sequence
DRB1_0301	19	ELFAAFPSFAGLRPT	LFAAFPSFA	0.2445	3547.1	50.00	Sequence
DRB1_0301	51	EVRAELPGVDPDKDV	LPGVDPDKD	0.2413	3674.1	50.00	Sequence
DRB1_0301	103	LPVGADEDDIKATYD	VGAEDEDDIK	0.2412	3678.6	50.00	Sequence
DRB1_0301	94	YGSFVTVSLPVGAD	GSFVTVSL	0.2399	3730.4	50.00	Sequence
DRB1_0301	104	VGAEDEDDIKATYDK	VGAEDEDDIK	0.2369	3850.8	50.00	Sequence
DRB1_0301	49	RYEVRAELPGVDPDK	RYEVRAELP	0.2363	3878.0	50.00	Sequence
DRB1_0301	21	FAAFPSFAGLRPTFD	FPSFAGLRP	0.2359	3893.4	50.00	Sequence
DRB1_0301	95	GSFVTVSLPVGAD	FVTVSLPV	0.2336	3993.6	50.00	Sequence
DRB1_0301	15	PEFSELF	FSELF	0.2329	4021.7	50.00	Sequence
DRB1_0301	108	DEDDIKATYDKGILT	DIKATYDKG	0.2321	4057.9	50.00	Sequence
DRB1_0301	93	AYGSFVTVSLPVG	GSFVTVSL	0.2300	4151.7	50.00	Sequence
DRB1_0301	113	KATYDKGILTVSVAV	ATYDKGILT	0.2269	4293.9	50.00	Sequence
DRB1_0301	90	SEFAYGSFVTVSLP	FAYGSFVRT	0.2256	4351.6	50.00	Sequence
DRB1_0301	16	EFSELFAAFPSFAGL	FSELFAAFP	0.2235	4453.6	50.00	Sequence
DRB1_0301	105	VGAEDEDDIKATYDKG	VGAEDEDDIK	0.2212	4567.8	50.00	Sequence
DRB1_0301	89	RSEFAYGSFVTVSL	FAYGSFVRT	0.2209	4578.9	50.00	Sequence
DRB1_0301	81	TEQKDFDGRSEFAYG	TEQKDFDGR	0.2118	5052.5	50.00	Sequence
DRB1_0301	18	SELFAAFPSFAGLRP	LFAAFPSFA	0.2065	5354.9	50.00	Sequence
DRB1_0301	39	MRLEDEMKEGRYEV	MRLEDEMKE	0.2038	5509.4	50.00	Sequence
DRB1_0301	4	LPVQRHPRSLFPEFS	LPVQRHPRS	0.2017	5641.2	50.00	Sequence
DRB1_0301	8	RHPRSLFPEFSELF	PRSLFPEFS	0.1990	5807.6	50.00	Sequence
DRB1_0301	42	EDEMKEGRYEVRAEL	MKEGRYEV	0.1979	5873.5	50.00	Sequence
DRB1_0301	124	SVAVSEGKPTKHIQ	SVAVSEGKP	0.1977	5885.3	50.00	Sequence
DRB1_0301	80	RTEQKDFDGRSEFAY	TEQKDFDGR	0.1925	6232.3	50.00	Sequence
DRB1_0301	88	GRSEFAYGSFVTVS	FAYGSFVRT	0.1913	6312.4	50.00	Sequence
DRB1_0301	96	SFVTVSLPVGAD	FVTVSLPV	0.1806	7088.0	50.00	Sequence
DRB1_0301	97	FVTVSLPVGAD	FVTVSLPV	0.1805	7095.5	50.00	Sequence
DRB1_0301	83	QKDFDGRSEFAYGSF	KDFDGRSEF	0.1769	7377.9	50.00	Sequence
DRB1_0301	50	YEVRAELPGVDPDKD	LPGVDPDKD	0.1765	7403.7	50.00	Sequence
DRB1_0301	82	EQKDFDGRSEFAYGS	KDFDGRSEF	0.1759	7456.8	50.00	Sequence
DRB1_0301	98	VTVSLPVGAD	SLPVGAD	0.1746	7563.4	50.00	Sequence
DRB1_0301	7	QRHPRSLFPEFSELF	PRSLFPEFS	0.1695	7989.0	50.00	Sequence
DRB1_0301	84	KDFDGRSEFAYGSFV	KDFDGRSEF	0.1586	8992.4	50.00	Sequence
DRB1_0301	86	FDGRSEFAYGSFVRT	RSEFAYGSF	0.1572	9129.8	50.00	Sequence
DRB1_0301	87	DGRSEFAYGSFVRT	FAYGSFVRT	0.1532	9525.8	50.00	Sequence
DRB1_0301	79	ERTEQKDFDGRSEFA	TEQKDFDGR	0.1499	9873.8	50.00	Sequence
DRB1_0301	107	ADEDDIKATYDKGIL	DIKATYDKG	0.1477	10112.4	50.00	Sequence
DRB1_0301	106	GADEDDIKATYDKGI	GADEDDIKA	0.1464	10258.4	50.00	Sequence
DRB1_0301	125	VAVSEGKPTKHIQI	VAVSEGKPT	0.1452	10392.8	50.00	Sequence
DRB1_0301	74	LTIKAERTEQKDFDG	IKAERTEQK	0.1417	10789.8	50.00	Sequence
DRB1_0301	41	LEDEMKEGRYEVRAE	MKEGRYEV	0.1405	10933.4	50.00	Sequence
DRB1_0301	5	PVQRHPRSLFPEFSE	PVQRHPRSL	0.1389	11118.7	50.00	Sequence
DRB1_0301	6	VQRHPRSLFPEFSEL	PRSLFPEFS	0.1312	12090.9	50.00	Sequence
DRB1_0301	85	DFDGRSEFAYGSFVR	DFDGRSEFA	0.1288	12410.1	50.00	Sequence
DRB1_0301	78	AERTEQKDFDGRSEF	TEQKDFDGR	0.1250	12933.1	50.00	Sequence
DRB1_0301	40	RLEDEMKEGRYEVRA	LEDEMKEGR	0.1187	13838.7	50.00	Sequence
DRB1_0301	129	EKGKPTKHIQIRSTN	KPTKHIQI	0.1168	14131.1	50.00	Sequence
DRB1_0301	126	AVSEGKPTKHIQIR	VSEGKPTK	0.1149	14418.9	50.00	Sequence
DRB1_0301	76	IKAERTEQKDFDGRS	IKAERTEQK	0.1091	15355.4	50.00	Sequence
DRB1_0301	75	TIKAERTEQKDFDGR	IKAERTEQK	0.1055	15966.0	50.00	Sequence
DRB1_0301	127	VSEGKPTKHIQIRSI	VSEGKPTK	0.1029	16421.9	50.00	Sequence
DRB1_0301	128	SEGKPTKHIQIRST	KPTKHIQI	0.0881	19271.9	50.00	Sequence
DRB1_0301	77	KAERTEQKDFDGRSE	TEQKDFDGR	0.0719	22973.2	50.00	Sequence

Allele: DRB1\_0301. Number of high binders 6. Number of weak binders 16. Number of peptides 130

Allele	pos	peptide	core	1-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
DRB1_0401	94	YGSFVTVSLPVGAD	GSFVTVSL	0.6761	33.3	SB	4.00	Sequence
DRB1_0401	91	EYAGSFVTVSLPV	GSFVTVSL	0.6665	36.9	SB	4.00	Sequence
DRB1_0401	93	AYGSFVTVSLPVG	GSFVTVSL	0.6622	38.7	SB	4.00	Sequence
DRB1_0401	95	GSFVTVSLPVGAD	GSFVTVSL	0.6606	39.3	SB	4.00	Sequence
DRB1_0401	92	FAYGSFVTVSLPV	GSFVTVSL	0.6481	45.1	SB	4.00	Sequence
DRB1_0401	16	EFSELFAAFPSFAGL	ELFAAFPSF	0.6186	62.0	WB	8.00	Sequence
DRB1_0401	15	PEFSELF	SELFAAFPS	0.6107	67.5	WB	8.00	Sequence
DRB1_0401	90	SEFAYGSFVTVSLP	GSFVTVSL	0.5926	82.1	WB	8.00	Sequence
DRB1_0401	17	FSELFAAFPSFAGLR	SELFAAFPS	0.5900	84.5	WB	8.00	Sequence
DRB1_0401	36	TRLMRLEDEMKEGRY	LMRLEDEMK	0.5817	92.3	WB	8.00	Sequence
DRB1_0401	14	FPEFSELF	SELFAAFPS	0.5730	101.5	WB	8.00	Sequence
DRB1_0401	35	DTRLMRLEDEMKEGR	LMRLEDEMK	0.5719	102.7	WB	8.00	Sequence
DRB1_0401	89	RSEFAYGSFVTVSL	GSFVTVSL	0.5489	131.7	WB	16.00	Sequence

DRB1_0401	37	RLMRLEDEMKEGRYE	LMRLEDEMK	0.5431	140.3	WB	16.00	Sequence
DRB1_0401	34	FDTRLMRLEDEMKEG	RLMRLEDEM	0.5286	164.1	WB	16.00	Sequence
DRB1_0401	18	SELFAAFPSFAGLRP	SELFAAFPS	0.5205	179.1	WB	16.00	Sequence
DRB1_0401	96	SFVRTVSLPVGADED	FVRTVSLPV	0.5090	202.9	WB	16.00	Sequence
DRB1_0401	13	LFPEFSELFAAFPSF	SELFAAFPS	0.5078	205.6	WB	16.00	Sequence
DRB1_0401	33	TFDTRLMRLEDEMKE	RLMRLEDEM	0.4937	239.3	WB	16.00	Sequence
DRB1_0401	67	IMVRDGQLTIKAERT	MVRDGQLTI	0.4892	251.2	WB	16.00	Sequence
DRB1_0401	11	RSLFPEFSELFAAFP	RSLFPEFSE	0.4831	268.5	WB	32.00	Sequence
DRB1_0401	32	PTFDTRLMRLEDEM	RLMRLEDEM	0.4730	299.4	WB	32.00	Sequence
DRB1_0401	118	KGILTVSVAVSEGKP	GILTVSVAV	0.4678	316.9	WB	32.00	Sequence
DRB1_0401	97	FVRTVSLPVGADED	FVRTVSLPV	0.4623	336.2	WB	32.00	Sequence
DRB1_0401	66	DIMVRDGQLTIKAER	IMVRDGQLT	0.4615	339.2	WB	32.00	Sequence
DRB1_0401	12	SILFPEFSELFAAFPS	PEFSELFAA	0.4554	362.4	WB	32.00	Sequence
DRB1_0401	117	DKGILTVSVAVSEGK	GILTVSVAV	0.4445	407.7	WB	32.00	Sequence
DRB1_0401	65	VDIMVRDGQLTIKAE	IMVRDGQLT	0.4361	446.6	WB	32.00	Sequence
DRB1_0401	68	MVRDGQLTIKAERTE	MVRDGQLTI	0.4344	454.8	WB	32.00	Sequence
DRB1_0401	119	GILTVSVAVSEGKPT	ILTVSVAVS	0.4309	472.2	WB	32.00	Sequence
DRB1_0401	10	PRSLFPEFSELFAAF	RSLFPEFSE	0.4276	489.3	WB	32.00	Sequence
DRB1_0401	8	RHPRSLFPEFSELFA	RSLFPEFSE	0.4194	534.8		32.00	Sequence
DRB1_0401	116	YDKGILTVSVAVSEG	GILTVSVAV	0.4033	636.4		32.00	Sequence
DRB1_0401	64	DVDIMVRDGQLTIKA	IMVRDGQLT	0.4029	639.5		32.00	Sequence
DRB1_0401	88	GRSEFAYGSFVRTVS	FAYGSFVRT	0.3984	671.0		32.00	Sequence
DRB1_0401	9	HPRSLFPEFSELFAA	RSLFPEFSE	0.3948	697.8		32.00	Sequence
DRB1_0401	114	ATYDKGILTVSVAVS	ATYDKGILT	0.3943	702.0		32.00	Sequence
DRB1_0401	48	GRYEVRAELPGVDPD	YEVRAELPG	0.3920	719.5		32.00	Sequence
DRB1_0401	19	ELFAAFPSFAGLRPT	FAAFPSFAG	0.3918	721.2		32.00	Sequence
DRB1_0401	38	LMRLEDEMKEGRYEV	LMRLEDEMK	0.3887	745.8		32.00	Sequence
DRB1_0401	70	RDGQLTIKAERTEQK	QLTIKAERT	0.3876	754.2		32.00	Sequence
DRB1_0401	49	RYEVRAELPGVDPDK	YEVRAELPG	0.3876	754.5		32.00	Sequence
DRB1_0401	47	EGRYEVRAELPGVDP	RYEVRAELP	0.3835	788.4		50.00	Sequence
DRB1_0401	7	QRHPRSLFPEFSELF	RSLFPEFSE	0.3759	856.2		50.00	Sequence
DRB1_0401	31	RPTFDTRLMRLEDEM	RLMRLEDEM	0.3736	878.2		50.00	Sequence
DRB1_0401	46	KEGRYEVRAELPGVD	RYEVRAELP	0.3659	954.5		50.00	Sequence
DRB1_0401	113	KATYDKGILTVSVAV	ATYDKGILT	0.3629	985.9		50.00	Sequence
DRB1_0401	120	ILTVSVAVSEGKPT	ILTVSVAVS	0.3610	1006.2		50.00	Sequence
DRB1_0401	69	VRDGQLTIKAERTEQ	RDGQLTIKA	0.3582	1036.9		50.00	Sequence
DRB1_0401	115	TYDKGILTVSVAVSE	GILTVSVAV	0.3573	1047.3		50.00	Sequence
DRB1_0401	87	DGRSEFAYGSFVRTV	FAYGSFVRT	0.3458	1186.0		50.00	Sequence
DRB1_0401	86	FDGRSEFAYGSFVRT	FAYGSFVRT	0.3387	1280.3		50.00	Sequence
DRB1_0401	6	VQRHPRSLFPEFSEL	RSLFPEFSE	0.3381	1289.6		50.00	Sequence
DRB1_0401	45	MKEGRYEVRAELPGV	RYEVRAELP	0.3288	1425.5		50.00	Sequence
DRB1_0401	112	IKATYDKGILTVSVA	ATYDKGILT	0.3231	1515.9		50.00	Sequence
DRB1_0401	72	QLTIKAERTEQKDF	QLTIKAERT	0.3220	1533.8		50.00	Sequence
DRB1_0401	25	PSFAGLRPTFDTRLM	FAGLRPTFD	0.3178	1606.4		50.00	Sequence
DRB1_0401	71	DGQLTIKAERTEQKD	QLTIKAERT	0.3155	1645.3		50.00	Sequence
DRB1_0401	73	QLTIKAERTEQKDFD	QLTIKAERT	0.3109	1730.3		50.00	Sequence
DRB1_0401	63	KDVIDIMVRDGQLTIK	IMVRDGQLT	0.3105	1738.3		50.00	Sequence
DRB1_0401	5	PVQRHPRSLFPEFSE	RHPRSLFPE	0.3102	1742.7		50.00	Sequence
DRB1_0401	121	LTVSVAVSEGKPT	LTVSVAVSE	0.3090	1765.9		50.00	Sequence
DRB1_0401	111	DIKATYDKGILTVSV	ATYDKGILT	0.2995	1958.1		50.00	Sequence
DRB1_0401	0	MATTLPVQRHPRSLF	MATTLPVQR	0.2971	2008.7		50.00	Sequence
DRB1_0401	44	EMKEGRYEVRAELPG	RYEVRAELP	0.2940	2077.7		50.00	Sequence
DRB1_0401	24	FPSFAGLRPTFDTRL	PSFAGLRPT	0.2914	2137.5		50.00	Sequence
DRB1_0401	30	LRPTFDTRLMRLEDE	PTFDTRLMR	0.2888	2196.3		50.00	Sequence
DRB1_0401	26	SFAGLRPTFDTRLMR	FAGLRPTFD	0.2843	2306.0		50.00	Sequence
DRB1_0401	50	YEVRAELPGVDPDKD	YEVRAELPG	0.2777	2477.2		50.00	Sequence
DRB1_0401	98	VRTVSLPVGADED	RTVSLPVGA	0.2761	2521.7		50.00	Sequence
DRB1_0401	62	DKDVIDIMVRDGQLTI	IMVRDGQLT	0.2758	2528.7		50.00	Sequence
DRB1_0401	29	GLRPTFDTRLMRLED	PTFDTRLMR	0.2726	2619.5		50.00	Sequence
DRB1_0401	27	FAGLRPTFDTRLMRL	FAGLRPTFD	0.2702	2688.2		50.00	Sequence
DRB1_0401	85	FDGRSEFAYGSFVR	FDGRSEFAY	0.2562	3125.6		50.00	Sequence
DRB1_0401	23	AFPSFAGLRPTFDTR	PSFAGLRPT	0.2550	3169.0		50.00	Sequence
DRB1_0401	28	AGLRPTFDTRLMRLE	PTFDTRLMR	0.2526	3249.4		50.00	Sequence
DRB1_0401	110	DDIKATYDKGILTVS	ATYDKGILT	0.2517	3281.2		50.00	Sequence
DRB1_0401	3	TLPVQRHPRSLFPEF	QRHPRSLFP	0.2444	3553.2		50.00	Sequence
DRB1_0401	4	LPVQRHPRSLFPEFS	QRHPRSLFP	0.2411	3681.2		50.00	Sequence
DRB1_0401	21	FAAFPSFAGLRPTFD	FAAFPSFAG	0.2361	3887.1		50.00	Sequence
DRB1_0401	43	DEMKEGRYEVRAELP	RYEVRAELP	0.2348	3939.5		50.00	Sequence
DRB1_0401	1	ATTLPVQRHPRSLFP	TLPVQRHPR	0.2292	4187.7		50.00	Sequence
DRB1_0401	2	TTLPVQRHPRSLFPE	LPVQRHPRS	0.2290	4198.1		50.00	Sequence
DRB1_0401	99	RTVSLPVGADED	RTVSLPVGA	0.2267	4303.8		50.00	Sequence
DRB1_0401	20	LFAAFPSFAGLRPTF	FAAFPSFAG	0.2262	4326.4		50.00	Sequence
DRB1_0401	22	AAFPSFAGLRPTFD	FPSFAGLRP	0.2230	4480.1		50.00	Sequence
DRB1_0401	84	KDFDGRSEFAYGSFV	FDGRSEFAY	0.2181	4723.5		50.00	Sequence
DRB1_0401	74	LTIKAERTEQKDFDG	LTIKAERTE	0.2172	4767.8		50.00	Sequence
DRB1_0401	129	EKGKTEKHIQIRSTN	TEKHIQIRS	0.2146	4902.8		50.00	Sequence
DRB1_0401	83	QKDFDGRSEFAYGSF	FDGRSEFAY	0.2035	5529.2		50.00	Sequence

DRB1_0401	61	PKDKVDIMVRDQGLT	IMVRDQGLT	0.1997	5764.7	50.00	Sequence
DRB1_0401	123	VSVAVSEGKPTTEKHI	VSVAVSEGK	0.1951	6055.8	50.00	Sequence
DRB1_0401	122	TVSVAVSEGKPTTEKH	VSVAVSEGK	0.1942	6116.7	50.00	Sequence
DRB1_0401	109	EDDIKATYDKGILTV	ATYDKGILT	0.1866	6642.0	50.00	Sequence
DRB1_0401	51	EVRAELPGVDPDKDV	RAELPGVDP	0.1858	6698.8	50.00	Sequence
DRB1_0401	128	SEGKPTTEKHQIRST	EKHQIRST	0.1830	6905.2	50.00	Sequence
DRB1_0401	82	EQKDFDGRSEFAYGS	DFDGRSEFA	0.1804	7099.6	50.00	Sequence
DRB1_0401	39	MRLEDEMKEGRYEVRA	MRLEDEMKE	0.1675	8163.2	50.00	Sequence
DRB1_0401	124	SVAVSEGKPTTEKHQI	VAVSEGKPT	0.1662	8278.3	50.00	Sequence
DRB1_0401	80	RTEQKDFDGRSEFAY	FDGRSEFAY	0.1610	8760.9	50.00	Sequence
DRB1_0401	52	VRaelPGVDPDKDVD	RAELPGVDP	0.1602	8834.5	50.00	Sequence
DRB1_0401	75	TIKAERTEQKDFDGR	IKAERTEQK	0.1597	8885.0	50.00	Sequence
DRB1_0401	81	TEQKDFDGRSEFAYG	FDGRSEFAY	0.1580	9047.7	50.00	Sequence
DRB1_0401	125	VAVSEGKPTTEKHQI	SEGKPTTEKH	0.1567	9172.9	50.00	Sequence
DRB1_0401	76	IKAERTEQKDFDGRS	IKAERTEQK	0.1558	9265.2	50.00	Sequence
DRB1_0401	53	RAELPGVDPDKDVDI	RAELPGVDP	0.1553	9315.9	50.00	Sequence
DRB1_0401	108	DEDDIKATYDKGILT	ATYDKGILT	0.1443	10490.0	50.00	Sequence
DRB1_0401	127	VSEGKPTTEKHQIRS	SEGKPTTEKH	0.1351	11591.9	50.00	Sequence
DRB1_0401	42	EDEMKEGRYEVRAEL	KEGRYEVRA	0.1293	12344.8	50.00	Sequence
DRB1_0401	104	PVGADEDDIKATYDK	PVGADEDDI	0.1284	12467.0	50.00	Sequence
DRB1_0401	103	LPVGADEDDIKATYD	GADEDDIKA	0.1263	12743.3	50.00	Sequence
DRB1_0401	60	DPDKVDIMVRDQGL	DKVDIMVR	0.1177	13989.8	50.00	Sequence
DRB1_0401	102	SLPVGADEDDIKATY	PVGADEDDI	0.1164	14191.7	50.00	Sequence
DRB1_0401	79	ERTEQKDFDGRSEFA	RTEQKDFDG	0.1140	14560.8	50.00	Sequence
DRB1_0401	126	AVSEGKPTTEKHQIR	SEGKPTTEKH	0.1137	14611.9	50.00	Sequence
DRB1_0401	41	LEDEMKEGRYEVRAE	KEGRYEVRA	0.1084	15472.5	50.00	Sequence
DRB1_0401	101	VSLPVGADEDDIKAT	PVGADEDDI	0.1012	16721.1	50.00	Sequence
DRB1_0401	77	KAERTEQKDFDGRSE	RTEQKDFDG	0.0999	16963.5	50.00	Sequence
DRB1_0401	100	TVSLPVGADEDDIKA	TVSLPVGAD	0.0984	17242.0	50.00	Sequence
DRB1_0401	78	AERTEQKDFDGRSEF	RTEQKDFDG	0.0967	17566.2	50.00	Sequence
DRB1_0401	105	VGADEDDIKATYDKG	GADEDDIKA	0.0965	17607.9	50.00	Sequence
DRB1_0401	59	VDPKVDIMVRDQG	DKVDIMVR	0.0964	17626.0	50.00	Sequence
DRB1_0401	40	RLEDEMKEGRYEVRA	KEGRYEVRA	0.0924	18405.0	50.00	Sequence
DRB1_0401	106	GADEDDIKATYDKGI	GADEDDIKA	0.0878	19339.2	50.00	Sequence
DRB1_0401	58	GVDPDKVDIMVRDG	DKVDIMVR	0.0739	22474.6	50.00	Sequence
DRB1_0401	57	PGVDPDKVDIMVRD	DKVDIMVR	0.0681	23918.6	50.00	Sequence
DRB1_0401	55	ELPGVDPDKVDIMV	LPGVDPDKD	0.0640	25017.8	50.00	Sequence
DRB1_0401	56	LPGVDPDKVDIMVR	PGVDPDKDV	0.0630	25291.9	50.00	Sequence
DRB1_0401	107	ADEDDIKATYDKGIL	DDIKATYDK	0.0586	26530.3	50.00	Sequence
DRB1_0401	54	AELPGVDPDKVDIM	LPGVDPDKD	0.0573	26904.6	50.00	Sequence

Allele: DRB1\_0401. Number of high binders 5. Number of weak binders 26. Number of peptides 130

Allele	pos	peptide	core	l-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
DRB1_0404	94	YGSFVRTVSLPVGAD	FVRTVSLPV	0.7343	17.7	SB	2.00	Sequence
DRB1_0404	95	GSFVRTVSLPVGADE	FVRTVSLPV	0.7314	18.3	SB	2.00	Sequence
DRB1_0404	93	AYGSFVRTVSLPVGA	FVRTVSLPV	0.7109	22.8	SB	4.00	Sequence
DRB1_0404	18	SELFAAFPSFAGLRP	ELFAAFPSF	0.6939	27.5	SB	4.00	Sequence
DRB1_0404	96	SFVRTVSLPVGADED	FVRTVSLPV	0.6935	27.5	SB	4.00	Sequence
DRB1_0404	19	ELFAAFPSFAGLRPT	ELFAAFPSF	0.6898	28.7	SB	4.00	Sequence
DRB1_0404	17	FSELFAAFPSFAGLR	ELFAAFPSF	0.6765	33.1	SB	4.00	Sequence
DRB1_0404	92	FAYGSFVRTVSLPVG	FVRTVSLPV	0.6678	36.4	SB	8.00	Sequence
DRB1_0404	16	EFSELFAAFPSFAGL	ELFAAFPSF	0.6583	40.3	SB	8.00	Sequence
DRB1_0404	15	PEFSELFAAFPSFAG	ELFAAFPSF	0.6293	55.2	WB	8.00	Sequence
DRB1_0404	91	EFAYGSFVRTVSLPV	FVRTVSLPV	0.5982	77.3	WB	16.00	Sequence
DRB1_0404	97	FVRTVSLPVGADEDD	FVRTVSLPV	0.5921	82.5	WB	16.00	Sequence
DRB1_0404	14	FPEFSELFAAFPSFA	ELFAAFPSF	0.5381	148.0	WB	16.00	Sequence
DRB1_0404	21	FAAFPSFAGLRPTFD	AAFPSFAGL	0.5284	164.4	WB	16.00	Sequence
DRB1_0404	20	LFAAFPSFAGLRPTF	FAAFPSFAG	0.5278	165.5	WB	16.00	Sequence
DRB1_0404	22	AAFPSFAGLRPTFTD	SFAGLRPTF	0.5211	177.9	WB	32.00	Sequence
DRB1_0404	25	PSFAGLRPTFTDTRL	SFAGLRPTF	0.5201	180.0	WB	32.00	Sequence
DRB1_0404	24	PFSFAGLRPTFTDTRL	SFAGLRPTF	0.5184	183.2	WB	32.00	Sequence
DRB1_0404	23	AFPSFAGLRPTFTDR	SFAGLRPTF	0.5098	201.2	WB	32.00	Sequence
DRB1_0404	35	DTRLMLRLEDEMKEGR	RLMRLEDEM	0.5078	205.6	WB	32.00	Sequence
DRB1_0404	118	KGILTVSVAVSEGK	GILTVSVAV	0.5074	206.5	WB	32.00	Sequence
DRB1_0404	36	TRLMRLEDEMKEGRY	RLMRLEDEM	0.5071	207.0	WB	32.00	Sequence
DRB1_0404	117	DKGILTVSVAVSEGK	GILTVSVAV	0.5018	219.4	WB	32.00	Sequence
DRB1_0404	26	SFAGLRPTFTDTRLMR	SFAGLRPTF	0.4972	230.6	WB	32.00	Sequence
DRB1_0404	13	LFPEFSELFAAFPSF	ELFAAFPSF	0.4950	236.0	WB	32.00	Sequence
DRB1_0404	116	YDKGILTVSVAVSEG	GILTVSVAV	0.4816	272.7	WB	32.00	Sequence
DRB1_0404	34	FDTRLMRLEDEMKEG	RLMRLEDEM	0.4782	283.2	WB	32.00	Sequence
DRB1_0404	119	GILTVSVAVSEGKPT	GILTVSVAV	0.4454	403.7	WB	32.00	Sequence
DRB1_0404	66	DIMVRDQGLTIKAER	IMVRDQGLT	0.4453	404.1	WB	32.00	Sequence

DRB1_0404	90	SEFAYGSFVRTVSLP	SFVRTVSLP	0.4423	417.5	WB	32.00	Sequence
DRB1_0404	115	TYDKGILTVSVAVSE	GILTVSVAV	0.4414	421.7	WB	32.00	Sequence
DRB1_0404	65	VDIMVRDQGTLTIKAE	IMVRDQGTL	0.4410	423.4	WB	32.00	Sequence
DRB1_0404	37	RLMRLEDEMKEGRYE	RLMRLEDEM	0.4374	440.1	WB	32.00	Sequence
DRB1_0404	64	DVDIMVRDQGTLTIKA	DIMVRDQGQ	0.4222	518.9		32.00	Sequence
DRB1_0404	33	TFDTRLMLRLEDEMKE	RLMRLEDEM	0.4173	547.4		32.00	Sequence
DRB1_0404	12	SLFPEFSELFAAFP	EFSELFAAF	0.4136	569.2		32.00	Sequence
DRB1_0404	11	RSLFPEFSELFAAFP	SLFPEFSEL	0.3950	696.5		50.00	Sequence
DRB1_0404	114	ATYDKGILTVSVAVS	GILTVSVAV	0.3909	727.6		50.00	Sequence
DRB1_0404	9	HPRSLFPEFSELF	HPRSLFPEF	0.3903	732.6		50.00	Sequence
DRB1_0404	63	KDVDIMVRDQGTLTIK	DIMVRDQGQ	0.3817	803.8		50.00	Sequence
DRB1_0404	10	PRSLFPEFSELF	SLFPEFSEL	0.3779	838.3		50.00	Sequence
DRB1_0404	120	ILTVSVAVSEGKPT	LTVSVAVSE	0.3773	843.5		50.00	Sequence
DRB1_0404	8	RHPRSLFPEFSELF	HPRSLFPEF	0.3638	975.9		50.00	Sequence
DRB1_0404	27	FAGLRPTFDTRLMLRL	GLRPTFDTR	0.3550	1073.5		50.00	Sequence
DRB1_0404	113	KATYDKGILTVSVAV	GILTVSVAV	0.3518	1111.0		50.00	Sequence
DRB1_0404	32	PTFDTRLMLRLEDEM	RLMRLEDEM	0.3513	1117.4		50.00	Sequence
DRB1_0404	67	IMVRDQGTLTIKAERT	IMVRDQGTL	0.3379	1291.7		50.00	Sequence
DRB1_0404	7	QRHPRSLFPEFSELF	HPRSLFPEF	0.3365	1312.1		50.00	Sequence
DRB1_0404	62	DKDVDIMVRDQGTLTI	DIMVRDQGQ	0.3228	1520.4		50.00	Sequence
DRB1_0404	89	RSEFAYGSFVRTVSL	GSFVRTVSL	0.3169	1620.7		50.00	Sequence
DRB1_0404	6	VQRHPRSLFPEFSEL	HPRSLFPEF	0.3140	1672.2		50.00	Sequence
DRB1_0404	51	EVRAELPGVDPDKDV	EVRAELPGV	0.3130	1691.9		50.00	Sequence
DRB1_0404	49	RYEVRAELPGVDPDK	EVRAELPGV	0.3103	1741.7		50.00	Sequence
DRB1_0404	98	VRTVSLPVGADDDI	RTVSLPVGA	0.3097	1752.8		50.00	Sequence
DRB1_0404	50	YEVRAELPGVDPDKD	EVRAELPGV	0.3067	1811.4		50.00	Sequence
DRB1_0404	121	LTVSVAVSEGKPT	LTVSVAVSE	0.3060	1824.9		50.00	Sequence
DRB1_0404	48	GRYEVRAELPGVDPD	EVRAELPGV	0.2940	2078.0		50.00	Sequence
DRB1_0404	112	IKATYDKGILTVSVA	KGILTVSVA	0.2845	2302.2		50.00	Sequence
DRB1_0404	28	AGLRPTFDTRLMLRLE	LRPTFDTRL	0.2767	2506.0		50.00	Sequence
DRB1_0404	31	RPTFDTRLMLRLEDEM	RLMRLEDEM	0.2708	2669.7		50.00	Sequence
DRB1_0404	5	PVQRHPRSLFPEFSE	HPRSLFPEF	0.2679	2755.7		50.00	Sequence
DRB1_0404	4	LPVQRHPRSLFPEFS	HPRSLFPEF	0.2668	2787.9		50.00	Sequence
DRB1_0404	61	PKDVDIMVRDQGTLTI	DIMVRDQGQ	0.2625	2922.0		50.00	Sequence
DRB1_0404	3	TLPVQRHPRSLFPEF	LPVQRHPRS	0.2607	2979.7		50.00	Sequence
DRB1_0404	47	EGRYEVRAELPGVDP	EVRAELPGV	0.2580	3067.9		50.00	Sequence
DRB1_0404	0	MATTLPVQRHPRSLF	MATTLPVQR	0.2546	3182.2		50.00	Sequence
DRB1_0404	88	GRSEFAYGSFVRTVS	FAYGSFVRT	0.2519	3277.0		50.00	Sequence
DRB1_0404	29	GLRPTFDTRLMLRLE	LRPTFDTRL	0.2511	3303.7		50.00	Sequence
DRB1_0404	99	RTVSLPVGADDDIK	RTVSLPVGA	0.2510	3306.1		50.00	Sequence
DRB1_0404	129	EKGKTEKHQIRSTN	KHIQIRSTN	0.2339	3979.4		50.00	Sequence
DRB1_0404	68	MVRDQGTLTIKAERTE	MVRDQGTLTI	0.2266	4305.5		50.00	Sequence
DRB1_0404	111	DIKATYDKGILTVSV	KATYDKGIL	0.2201	4621.5		50.00	Sequence
DRB1_0404	87	DGRSEFAYGSFVRTV	FAYGSFVRT	0.2193	4661.4		50.00	Sequence
DRB1_0404	46	KEGRYEVRAELPGVD	EVRAELPGV	0.2156	4852.9		50.00	Sequence
DRB1_0404	2	TLPVQRHPRSLFPE	TLPVQRHPR	0.2111	5092.9		50.00	Sequence
DRB1_0404	30	LRPTFDTRLMLRLEDE	LRPTFDTRL	0.2097	5172.0		50.00	Sequence
DRB1_0404	38	LMRLEDEMKEGRYE	LMRLEDEM	0.2073	5308.2		50.00	Sequence
DRB1_0404	110	DDIKATYDKGILTVS	DIKATYDKG	0.1970	5934.6		50.00	Sequence
DRB1_0404	1	ATTLPVQRHPRSLFP	TLPVQRHPR	0.1944	6100.4		50.00	Sequence
DRB1_0404	86	FDGRSEFAYGSFVRT	FAYGSFVRT	0.1858	6694.5		50.00	Sequence
DRB1_0404	60	DPDKDVDIMVRDQGQ	DIMVRDQGQ	0.1736	7639.5		50.00	Sequence
DRB1_0404	109	EDDIKATYDKGILTV	DIKATYDKG	0.1725	7732.0		50.00	Sequence
DRB1_0404	45	MKEGRYEVRAELPGV	EVRAELPGV	0.1684	8081.1		50.00	Sequence
DRB1_0404	53	RAELPGVDPDKDVID	ELPGVDPDK	0.1669	8220.7		50.00	Sequence
DRB1_0404	52	VRAELPGVDPDKDVD	ELPGVDPDK	0.1655	8338.5		50.00	Sequence
DRB1_0404	73	QLTIKAERTEQKDFD	LTIKAERTE	0.1622	8646.4		50.00	Sequence
DRB1_0404	72	GQLTIKAERTEQKDF	LTIKAERTE	0.1584	9011.7		50.00	Sequence
DRB1_0404	74	LTIKAERTEQKDFDG	LTIKAERTE	0.1551	9340.4		50.00	Sequence
DRB1_0404	100	TVSLPVGADDDIKA	TVSLPVGAD	0.1518	9670.9		50.00	Sequence
DRB1_0404	71	DGQLTIKAERTEQKD	LTIKAERTE	0.1511	9744.2		50.00	Sequence
DRB1_0404	108	DEDDIKATYDKGILT	DIKATYDKG	0.1434	10597.7		50.00	Sequence
DRB1_0404	122	TVSVAVSEGKPT	TVSVAVSEG	0.1402	10973.8		50.00	Sequence
DRB1_0404	54	AELPGVDPDKDVID	ELPGVDPDK	0.1391	11096.7		50.00	Sequence
DRB1_0404	70	RDGQLTIKAERTEQK	LTIKAERTE	0.1367	11395.5		50.00	Sequence
DRB1_0404	69	VRDQGTLTIKAERTEQ	LTIKAERTE	0.1254	12873.2		50.00	Sequence
DRB1_0404	123	VSVAVSEGKPT	VAVSEGKPT	0.1250	12935.7		50.00	Sequence
DRB1_0404	125	VAVSEGKPT	VAVSEGKPT	0.1223	13314.6		50.00	Sequence
DRB1_0404	124	SVAVSEGKPT	VAVSEGKPT	0.1220	13357.7		50.00	Sequence
DRB1_0404	55	ELPGVDPDKDVID	ELPGVDPDK	0.1216	13419.7		50.00	Sequence
DRB1_0404	107	AEDDIKATYDKGIL	DIKATYDKG	0.1180	13945.2		50.00	Sequence
DRB1_0404	85	DFDGRSEFAYGSFVR	SEFAYGSFV	0.1136	14628.0		50.00	Sequence
DRB1_0404	75	TIKAERTEQKDFDGR	TIKAERTEQ	0.1093	15332.3		50.00	Sequence
DRB1_0404	101	VSLPVGADDDIKAT	PVGADDDI	0.1047	16113.3		50.00	Sequence
DRB1_0404	84	KDFDGRSEFAYGSFV	RSEFAYGSF	0.0999	16972.8		50.00	Sequence
DRB1_0404	44	EMKEGRYEVRAELPG	EMKEGRYEV	0.0969	17515.0		50.00	Sequence
DRB1_0404	102	SLPVGADDDIKATY	PVGADDDI	0.0952	17845.7		50.00	Sequence

DRB1_0404	56	LPGVDPDKDVIDMVR	LPGVDPDKD	0.0923	18424.9	50.00	Sequence
DRB1_0404	76	IKAERTEQKDFDGRS	IKAERTEQK	0.0862	19682.4	50.00	Sequence
DRB1_0404	43	DEMKEGRYEVRAELP	EMKEGRYEV	0.0857	19775.5	50.00	Sequence
DRB1_0404	126	AVSEGKPTKHKIQIR	AVSEGKPTK	0.0819	20618.2	50.00	Sequence
DRB1_0404	106	GADEDDIKATYDKGI	DIKATYDKG	0.0794	21171.4	50.00	Sequence
DRB1_0404	128	SEGKPTKHKIQIRST	EKHIQIRST	0.0775	21624.2	50.00	Sequence
DRB1_0404	57	PGVDPDKDVIDMVRD	PGVDPDKDV	0.0744	22343.2	50.00	Sequence
DRB1_0404	103	LPVGADEDDIKATYD	PVGADEDDI	0.0722	22896.6	50.00	Sequence
DRB1_0404	39	MRLEDEMKEGRYEV	MRLEDEMKE	0.0716	23036.0	50.00	Sequence
DRB1_0404	59	VDPKDVIDMVRDQG	DKDVIDMVR	0.0706	23295.4	50.00	Sequence
DRB1_0404	42	EDEMKEGRYEVRAEL	MKEGRYEV	0.0662	24420.4	50.00	Sequence
DRB1_0404	58	GVDPDKDVIDMVRD	DKDVIDMVR	0.0635	25146.8	50.00	Sequence
DRB1_0404	83	QKDFDGRSEFAYGSF	KDFDGRSEF	0.0633	25209.7	50.00	Sequence
DRB1_0404	104	PVGADEDDIKATYDK	PVGADEDDI	0.0623	25484.8	50.00	Sequence
DRB1_0404	77	KAERTEQKDFDGRSE	KAERTEQKD	0.0569	27028.1	50.00	Sequence
DRB1_0404	41	LEDEMKEGRYEVRAE	EMKEGRYEV	0.0567	27072.0	50.00	Sequence
DRB1_0404	105	VGADEDDIKATYDKG	DIKATYDKG	0.0561	27239.4	50.00	Sequence
DRB1_0404	127	VSEGKPTKHKIQIRS	SEGKPTKHK	0.0551	27553.6	50.00	Sequence
DRB1_0404	40	RLDEMKEGRYEVRA	EMKEGRYEV	0.0551	27558.4	50.00	Sequence
DRB1_0404	78	AERTEQKDFDGRSEF	AERTEQKDF	0.0517	28577.2	50.00	Sequence
DRB1_0404	82	EQKDFDGRSEFAYGS	KDFDGRSEF	0.0506	28906.2	50.00	Sequence
DRB1_0404	80	RTEQKDFDGRSEFAY	TEQKDFDGR	0.0491	29390.9	50.00	Sequence
DRB1_0404	81	TEQKDFDGRSEFAYG	TEQKDFDGR	0.0485	29592.3	50.00	Sequence
DRB1_0404	79	ERTEQKDFDGRSEFA	TEQKDFDGR	0.0481	29727.0	50.00	Sequence

Allele: DRB1\_0404. Number of high binders 9. Number of weak binders 24. Number of peptides 130

Allele	pos	peptide	core	l-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
DRB1_0405	94	YGSFVRTVSLPVGAD	FVRTVSLPV	0.7508	14.8	SB	0.80	Sequence
DRB1_0405	93	AYGSFVRTVSLPVGA	FVRTVSLPV	0.7407	16.5	SB	2.00	Sequence
DRB1_0405	95	GSFVRTVSLPVGAD	FVRTVSLPV	0.7393	16.8	SB	2.00	Sequence
DRB1_0405	92	FAYGSFVRTVSLPVG	FVRTVSLPV	0.7348	17.6	SB	2.00	Sequence
DRB1_0405	96	SFVRTVSLPVGAD	FVRTVSLPV	0.7120	22.6	SB	2.00	Sequence
DRB1_0405	91	EFAYGSFVRTVSLPV	FVRTVSLPV	0.7068	23.9	SB	4.00	Sequence
DRB1_0405	97	FVRTVSLPVGAD	FVRTVSLPV	0.6164	63.4	WB	16.00	Sequence
DRB1_0405	116	YDKGILTVSVAVSEG	GILTVSVAV	0.6087	69.0	WB	16.00	Sequence
DRB1_0405	117	DKGILTVSVAVSEGK	GILTVSVAV	0.6054	71.5	WB	16.00	Sequence
DRB1_0405	115	TYDKGILTVSVAVSE	GILTVSVAV	0.5987	76.8	WB	16.00	Sequence
DRB1_0405	15	PEFSELFAAFPSFAG	LFAAFPSFA	0.5775	96.6	WB	16.00	Sequence
DRB1_0405	14	FPEFSELFAAFPSFA	FSELFAAFP	0.5727	101.8	WB	16.00	Sequence
DRB1_0405	118	KGILTVSVAVSEGKP	GILTVSVAV	0.5713	103.4	WB	16.00	Sequence
DRB1_0405	16	EFSELFAAFPSFAGL	ELFAAFPSF	0.5614	115.0	WB	32.00	Sequence
DRB1_0405	17	FSELFAAFPSFAGLR	ELFAAFPSF	0.5598	117.1	WB	32.00	Sequence
DRB1_0405	114	ATYDKGILTVSVAVS	GILTVSVAV	0.5565	121.4	WB	32.00	Sequence
DRB1_0405	18	SELFAAFPSFAGLRP	LFAAFPSFA	0.5513	128.3	WB	32.00	Sequence
DRB1_0405	12	SLFPEFSELFAAFPS	PEFSELFAA	0.5405	144.3	WB	32.00	Sequence
DRB1_0405	24	FPSFAGLRPTFDTRL	FAGLRPTFD	0.5378	148.6	WB	32.00	Sequence
DRB1_0405	13	LFPEFSELFAAFPSF	FSELFAAFP	0.5333	156.0	WB	32.00	Sequence
DRB1_0405	19	ELFAAFPSFAGLRPT	LFAAFPSFA	0.5309	160.1	WB	32.00	Sequence
DRB1_0405	25	PSFAGLRPTFDTRLM	FAGLRPTFD	0.5308	160.2	WB	32.00	Sequence
DRB1_0405	35	DTRLMRLEDEMKEGR	LMRLEDEM	0.5274	166.2	WB	32.00	Sequence
DRB1_0405	90	SEFAYGSFVRTVSLP	FAYGSFVRT	0.5273	166.4	WB	32.00	Sequence
DRB1_0405	34	FDTRLMRLEDEMKEG	LMRLEDEM	0.5202	179.7	WB	32.00	Sequence
DRB1_0405	23	AFPFSFAGLRPTFDTR	FAGLRPTFD	0.5161	187.8	WB	32.00	Sequence
DRB1_0405	36	TRLMRLEDEMKEGRY	LMRLEDEM	0.5150	190.2	WB	32.00	Sequence
DRB1_0405	119	GILTVSVAVSEGKPT	GILTVSVAV	0.5106	199.3	WB	32.00	Sequence
DRB1_0405	113	KATYDKGILTVSVAV	GILTVSVAV	0.4995	224.8	WB	32.00	Sequence
DRB1_0405	33	TFDTRLMRLEDEMKE	LMRLEDEM	0.4983	227.7	WB	32.00	Sequence
DRB1_0405	11	RSLFPEFSELFAAFP	FPEFSELFA	0.4965	232.3	WB	32.00	Sequence
DRB1_0405	26	SFAGLRPTFDTRLMR	FAGLRPTFD	0.4910	246.4	WB	32.00	Sequence
DRB1_0405	37	RLMRLEDEMKEGRYE	RLMRLEDEM	0.4812	274.1	WB	32.00	Sequence
DRB1_0405	22	AAFPSFAGLRPTFD	FAGLRPTFD	0.4775	285.1	WB	32.00	Sequence
DRB1_0405	66	DIMVRDQQLTIKAER	MVRDQQLTI	0.4773	286.0	WB	32.00	Sequence
DRB1_0405	20	LFAAFPSFAGLRPTF	LFAAFPSFA	0.4758	290.7	WB	50.00	Sequence
DRB1_0405	32	PTFDTRLMRLEDEM	TRLMRLEDE	0.4696	310.7	WB	50.00	Sequence
DRB1_0405	65	VDIMVRDQQLTIKAE	MVRDQQLTI	0.4672	319.0	WB	50.00	Sequence
DRB1_0405	21	FAAFPSFAGLRPTFD	FAGLRPTFD	0.4582	351.5	WB	50.00	Sequence
DRB1_0405	27	FAGLRPTFDTRLML	FAGLRPTFD	0.4577	353.5	WB	50.00	Sequence
DRB1_0405	111	DIKATYDKGILTVSV	ATYDKGILT	0.4495	386.1	WB	50.00	Sequence
DRB1_0405	9	HPRSLFPEFSELFAA	FPEFSELFA	0.4491	387.7	WB	50.00	Sequence
DRB1_0405	112	IKATYDKGILTVSVA	ATYDKGILT	0.4480	392.6	WB	50.00	Sequence
DRB1_0405	64	DVIDMVRDQQLTIKA	MVRDQQLTI	0.4461	400.7	WB	50.00	Sequence
DRB1_0405	89	RSEFAYGSFVRTVSL	FAYGSFVRT	0.4443	408.6	WB	50.00	Sequence



DRB1_0405	67	IMVRDGQLTIKAERT	MVRDGQLTI	0.4393	431.4	WB	50.00	Sequence
DRB1_0405	10	PRSLFPEFSELFAAF	FPEFSELFA	0.4381	437.0	WB	50.00	Sequence
DRB1_0405	31	RPTFDTRLMLRLEDEM	FDTRLMLRLE	0.4292	480.9	WB	50.00	Sequence
DRB1_0405	63	KDVIDMVRDGQLTIK	DIMVRDGQL	0.4239	509.3		50.00	Sequence
DRB1_0405	68	MVRDGQLTIKAERTE	MVRDGQLTI	0.4228	515.7		50.00	Sequence
DRB1_0405	8	RHPRSLFPEFSELFA	FPEFSELFA	0.4136	569.2		50.00	Sequence
DRB1_0405	110	DDIKATYDKGILTYS	DIKATYDKG	0.4133	571.5		50.00	Sequence
DRB1_0405	30	LRPTFDTRLMLRLEDE	FDTRLMLRLE	0.4108	586.9		50.00	Sequence
DRB1_0405	38	LMRLEDEMKEGRYEV	MRLEDEMKE	0.4056	621.0		50.00	Sequence
DRB1_0405	88	GRSEFAYGSFVRTVS	FAYGSFVRT	0.4021	644.7		50.00	Sequence
DRB1_0405	86	FDGRSEFAYGSFVRT	FAYGSFVRT	0.3990	667.0		50.00	Sequence
DRB1_0405	71	DGQLTIKAERTEQKD	LTIKAERTE	0.3904	731.8		50.00	Sequence
DRB1_0405	109	EDDIKATYDKGILTV	IKATYDKGI	0.3888	744.5		50.00	Sequence
DRB1_0405	120	ILTVSVAVSEGKPT	ILTVSVAVS	0.3864	764.6		50.00	Sequence
DRB1_0405	28	AGLRPTFDTRLMLRLE	GLRPTFDTR	0.3833	790.5		50.00	Sequence
DRB1_0405	62	DKDVDIMVRDGQLTI	DIMVRDGQL	0.3821	800.6		50.00	Sequence
DRB1_0405	87	DGRSEFAYGSFVRTV	FAYGSFVRT	0.3812	808.5		50.00	Sequence
DRB1_0405	29	GLRPTFDTRLMLRLED	GLRPTFDTR	0.3789	829.1		50.00	Sequence
DRB1_0405	72	GQLTIKAERTEQKDF	LTIKAERTE	0.3745	869.4		50.00	Sequence
DRB1_0405	70	RDGQLTIKAERTEQK	LTIKAERTE	0.3698	914.3		50.00	Sequence
DRB1_0405	7	QRHPRSLFPEFSELF	HPRSLFPEF	0.3607	1009.6		50.00	Sequence
DRB1_0405	48	GRYEVRAELPGVDPD	GRYEVRAEL	0.3604	1012.1		50.00	Sequence
DRB1_0405	84	KDFDGRSEFAYGSFV	FDGRSEFAY	0.3584	1035.3		50.00	Sequence
DRB1_0405	47	EGRYEVRAELPGVDP	GRYEVRAEL	0.3563	1059.1		50.00	Sequence
DRB1_0405	69	VRDGQLTIKAERTEQ	DGQLTIKAE	0.3559	1063.2		50.00	Sequence
DRB1_0405	6	VQRHPRSLFPEFSEL	HPRSLFPEF	0.3530	1097.3		50.00	Sequence
DRB1_0405	85	DFDGRSEFAYGSFVR	FDGRSEFAY	0.3520	1108.6		50.00	Sequence
DRB1_0405	98	VRTVSLPVGADDDI	VRTVSLPVG	0.3486	1150.1		50.00	Sequence
DRB1_0405	46	KEGRYEVRAELPGVD	GRYEVRAEL	0.3432	1219.9		50.00	Sequence
DRB1_0405	61	PKDVDIMVRDGQLT	DIMVRDGQL	0.3430	1221.9		50.00	Sequence
DRB1_0405	83	QKDFDGRSEFAYGSF	FDGRSEFAY	0.3410	1249.5		50.00	Sequence
DRB1_0405	73	QLTIKAERTEQKDFD	LTIKAERTE	0.3335	1354.4		50.00	Sequence
DRB1_0405	5	PVQRHPRSLFPEFSE	HPRSLFPEF	0.3334	1355.6		50.00	Sequence
DRB1_0405	108	DEDDIKATYDKGILT	IKATYDKGI	0.3314	1386.1		50.00	Sequence
DRB1_0405	60	DPKDVDIMVRDGQL	DIMVRDGQL	0.3247	1489.8		50.00	Sequence
DRB1_0405	74	LTIKAERTEQKDFDG	LTIKAERTE	0.3174	1612.6		50.00	Sequence
DRB1_0405	82	EQKDFDGRSEFAYGS	FDGRSEFAY	0.3153	1650.2		50.00	Sequence
DRB1_0405	129	EGKPTKHIQIRSTN	EKHIQIRST	0.3136	1679.7		50.00	Sequence
DRB1_0405	49	RYEVRAELPGVDPDK	EVRAELPGV	0.3081	1783.9		50.00	Sequence
DRB1_0405	51	EVRAELPGVDPDKDV	EVRAELPGV	0.3074	1796.5		50.00	Sequence
DRB1_0405	50	YEVRAELPGVDPDKD	RAELPGVDP	0.3011	1923.8		50.00	Sequence
DRB1_0405	45	MKEGRYEVRAELPGV	GRYEVRAEL	0.2990	1966.8		50.00	Sequence
DRB1_0405	39	MRLEDEMKEGRYEV	MRLEDEMKE	0.2925	2111.8		50.00	Sequence
DRB1_0405	128	SEGKPTKHIQIRST	EKHIQIRST	0.2924	2114.2		50.00	Sequence
DRB1_0405	4	LPVQRHPRSLFPEFS	PVQRHPRSL	0.2661	2808.1		50.00	Sequence
DRB1_0405	53	RAELPGVDPDKDVID	RAELPGVDP	0.2644	2861.5		50.00	Sequence
DRB1_0405	107	AEDDIKATYDKGIL	IKATYDKGI	0.2570	3098.6		50.00	Sequence
DRB1_0405	52	VRAELPGVDPDKD	RAELPGVDP	0.2556	3148.1		50.00	Sequence
DRB1_0405	44	EMKEGRYEVRAELPG	GRYEVRAEL	0.2548	3175.2		50.00	Sequence
DRB1_0405	99	RTVSLPVGADDDIK	TVSLPVGAD	0.2545	3185.6		50.00	Sequence
DRB1_0405	121	LTVSVAVSEGKPTK	LTVSVAVSE	0.2536	3216.6		50.00	Sequence
DRB1_0405	55	ELPGVDPDKDVIDMV	LPGVDPDKD	0.2512	3301.3		50.00	Sequence
DRB1_0405	56	LPGVDPDKDVIDMVR	LPGVDPDKD	0.2480	3415.7		50.00	Sequence
DRB1_0405	54	AELPGVDPDKDVIDM	LPGVDPDKD	0.2466	3468.7		50.00	Sequence
DRB1_0405	43	DEMKEGRYEVRAELP	GRYEVRAEL	0.2443	3557.1		50.00	Sequence
DRB1_0405	57	PGVDPDKDVIDMVRD	PDKDVDIMV	0.2407	3697.7		50.00	Sequence
DRB1_0405	106	GAEDDDIKATYDKGI	IKATYDKGI	0.2392	3757.1		50.00	Sequence
DRB1_0405	3	TLPVQRHPRSLFPEF	PVQRHPRSL	0.2389	3772.1		50.00	Sequence
DRB1_0405	58	GVDPDKDVIDMVRDG	PDKDVDIMV	0.2375	3826.2		50.00	Sequence
DRB1_0405	59	VDPDKDVIDMVRDGG	PDKDVDIMV	0.2328	4027.5		50.00	Sequence
DRB1_0405	81	TEQKDFDGRSEFAYG	FDGRSEFAY	0.2320	4064.6		50.00	Sequence
DRB1_0405	42	EDEMKEGRYEVRAEL	GRYEVRAEL	0.2099	5159.9		50.00	Sequence
DRB1_0405	2	TTLPVQRHPRSLFPE	PVQRHPRSL	0.2090	5209.9		50.00	Sequence
DRB1_0405	0	MATTLPVQRHPRSLF	MATTLPVQR	0.2039	5507.6		50.00	Sequence
DRB1_0405	100	TVSLPVGADDDIKA	TVSLPVGAD	0.2038	5511.2		50.00	Sequence
DRB1_0405	1	ATTLPVQRHPRSLFP	PVQRHPRSL	0.1972	5917.1		50.00	Sequence
DRB1_0405	80	RTEQKDFDGRSEFAY	FDGRSEFAY	0.1869	6620.7		50.00	Sequence
DRB1_0405	126	AVSEGKPTKHIQIR	AVSEGKPT	0.1763	7425.5		50.00	Sequence
DRB1_0405	127	VSEGKPTKHIQIRS	EGKPTKHI	0.1734	7662.3		50.00	Sequence
DRB1_0405	75	TIKAERTEQKDFDGR	IKAERTEQK	0.1721	7768.4		50.00	Sequence
DRB1_0405	40	RLEDEMKEGRYEVRA	DEMKEGRYE	0.1691	8021.7		50.00	Sequence
DRB1_0405	105	VGAEDDDIKATYDKG	DIKATYDKG	0.1661	8288.0		50.00	Sequence
DRB1_0405	76	IKAERTEQKDFDGRS	KAERTEQKD	0.1655	8345.0		50.00	Sequence
DRB1_0405	125	VAVSEGKPTKHIQI	SEGKPTKHI	0.1649	8400.1		50.00	Sequence
DRB1_0405	41	LEDEMKEGRYEVRAE	DEMKEGRYE	0.1610	8759.4		50.00	Sequence
DRB1_0405	124	SVAVSEGKPTKHIQ	VAVSEGKPT	0.1592	8932.4		50.00	Sequence
DRB1_0405	77	KAERTEQKDFDGRSE	KAERTEQKD	0.1511	9745.2		50.00	Sequence

DRB1_0405	122	TVSVAVSEGKPTTEKH	VAVSEGKPT	0.1497	9902.8	50.00	Sequence
DRB1_0405	103	LPVGADEDDIKATYD	GADEDDIKA	0.1494	9927.7	50.00	Sequence
DRB1_0405	123	VSVAVSEGKPTTEKHI	VAVSEGKPT	0.1454	10369.3	50.00	Sequence
DRB1_0405	104	PVGADEDDIKATYDK	GADEDDIKA	0.1436	10572.3	50.00	Sequence
DRB1_0405	101	VSLPVGAEDEDDIKAT	LPVGADEDD	0.1425	10696.0	50.00	Sequence
DRB1_0405	102	SLPVGADEDDIKATY	LPVGADEDD	0.1319	11994.7	50.00	Sequence
DRB1_0405	79	ERTEQKDFDGRSEFA	EQKDFDGRS	0.1182	13913.6	50.00	Sequence
DRB1_0405	78	AERTEQKDFDGRSEF	EQKDFDGRS	0.1099	15223.2	50.00	Sequence

Allele: DRB1\_0405. Number of high binders 6. Number of weak binders 42. Number of peptides 130

Allele	pos	peptide	core	1-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
DRB1_0701	91	EFAYGSFVRTVSLPV	FVRTVSLPV	0.9655	1.5	SB	0.01	Sequence
DRB1_0701	92	FAYGSFVRTVSLPVG	FVRTVSLPV	0.9629	1.5	SB	0.01	Sequence
DRB1_0701	93	AYGSFVRTVSLPVGA	FVRTVSLPV	0.9599	1.5	SB	0.01	Sequence
DRB1_0701	94	YGSFVRTVSLPVGAD	FVRTVSLPV	0.9546	1.6	SB	0.05	Sequence
DRB1_0701	95	GSFVRTVSLPVGAE	FVRTVSLPV	0.9498	1.7	SB	0.05	Sequence
DRB1_0701	96	SFVRTVSLPVGAEDE	FVRTVSLPV	0.9406	1.9	SB	0.10	Sequence
DRB1_0701	97	FVRTVSLPVGAEDE	FVRTVSLPV	0.9332	2.1	SB	0.10	Sequence
DRB1_0701	24	FPSFAGLRPTFDTRL	LRPTFDTRL	0.8102	7.8	SB	4.00	Sequence
DRB1_0701	25	PSFAGLRPTFDTRL	LRPTFDTRL	0.8086	7.9	SB	4.00	Sequence
DRB1_0701	27	FAGLRPTFDTRLML	LRPTFDTRL	0.7949	9.2	SB	4.00	Sequence
DRB1_0701	26	SFAGLRPTFDTRLMR	LRPTFDTRL	0.7936	9.3	SB	4.00	Sequence
DRB1_0701	89	RSEFAYGSFVRTVSL	GSFVRTVSL	0.7776	11.1	SB	4.00	Sequence
DRB1_0701	28	AGLRPTFDTRLMLR	LRPTFDTRL	0.7613	13.2	SB	8.00	Sequence
DRB1_0701	90	SEFAYGSFVRTVSLP	GSFVRTVSL	0.7410	16.5	SB	8.00	Sequence
DRB1_0701	62	DKDVDIMVRDGQLTI	MVRDGQLTI	0.7410	16.5	SB	8.00	Sequence
DRB1_0701	29	GLRPTFDTRLMLRLE	LRPTFDTRL	0.7324	18.1	SB	8.00	Sequence
DRB1_0701	63	KDVDIMVRDGQLTIK	MVRDGQLTI	0.7071	23.8	SB	8.00	Sequence
DRB1_0701	106	GADEDDIKATYDKGI	IKATYDKGI	0.7048	24.4	SB	16.00	Sequence
DRB1_0701	107	ADEDDIKATYDKGIL	IKATYDKGI	0.6998	25.7	SB	16.00	Sequence
DRB1_0701	108	DEDDIKATYDKGILT	IKATYDKGI	0.6997	25.8	SB	16.00	Sequence
DRB1_0701	30	LRPTFDTRLMLRLE	LRPTFDTRL	0.6982	26.2	SB	16.00	Sequence
DRB1_0701	109	EDDIKATYDKGILTV	IKATYDKGI	0.6702	35.5	SB	16.00	Sequence
DRB1_0701	64	DVDIMVRDGQLTIKA	MVRDGQLTI	0.6674	36.6	SB	16.00	Sequence
DRB1_0701	1	ATTLPVQRHPRSLFP	VQRHPRSLF	0.6647	37.6	SB	16.00	Sequence
DRB1_0701	110	DDIKATYDKGILTIVS	IKATYDKGI	0.6507	43.8	SB	16.00	Sequence
DRB1_0701	111	DIKATYDKGILTIVSA	IKATYDKGI	0.6262	57.1	WB	16.00	Sequence
DRB1_0701	65	VDIMVRDGQLTIKAE	MVRDGQLTI	0.6197	61.2	WB	16.00	Sequence
DRB1_0701	0	MATTLPVQRHPRSLF	VQRHPRSLF	0.6194	61.5	WB	16.00	Sequence
DRB1_0701	113	KATYDKGILTIVSVAV	GILTIVSVAV	0.6172	62.9	WB	16.00	Sequence
DRB1_0701	2	TTLPVQRHPRSLFPE	VQRHPRSLF	0.6163	63.5	WB	16.00	Sequence
DRB1_0701	114	ATYDKGILTIVSVAVS	GILTIVSVAV	0.6124	66.3	WB	16.00	Sequence
DRB1_0701	115	TYDKGILTIVSVAVSE	GILTIVSVAV	0.6099	68.1	WB	16.00	Sequence
DRB1_0701	112	IKATYDKGILTIVSVA	IKATYDKGI	0.5990	76.6	WB	32.00	Sequence
DRB1_0701	67	IMVRDGQLTIKAERT	MVRDGQLTI	0.5936	81.2	WB	32.00	Sequence
DRB1_0701	66	DMVRDGQLTIKAER	MVRDGQLTI	0.5928	81.9	WB	32.00	Sequence
DRB1_0701	3	TLPVQRHPRSLFPEF	VQRHPRSLF	0.5751	99.2	WB	32.00	Sequence
DRB1_0701	68	MVRDGQLTIKAERTE	MVRDGQLTI	0.5635	112.5	WB	32.00	Sequence
DRB1_0701	116	YDKGILTIVSVAVSEG	GILTIVSVAV	0.5632	112.8	WB	32.00	Sequence
DRB1_0701	4	LPVQRHPRSLFPEFS	VQRHPRSLF	0.5366	150.6	WB	32.00	Sequence
DRB1_0701	117	DKGILTIVSVAVSEGG	GILTIVSVAV	0.5285	164.4	WB	32.00	Sequence
DRB1_0701	5	PVQRHPRSLFPEFSE	VQRHPRSLF	0.4985	227.2	WB	32.00	Sequence
DRB1_0701	7	QRHPRSLFPEFSELS	LFPEFSELF	0.4944	237.5	WB	32.00	Sequence
DRB1_0701	118	KGILTIVSVAVSEGKP	GILTIVSVAV	0.4869	257.7	WB	32.00	Sequence
DRB1_0701	11	RSLFPEFSELSFAAF	LFPEFSELF	0.4530	372.0	WB	50.00	Sequence
DRB1_0701	8	RHPRSLFPEFSELSFA	LFPEFSELF	0.4529	372.4	WB	50.00	Sequence
DRB1_0701	119	GILTIVSVAVSEGKPT	GILTIVSVAV	0.4527	372.9	WB	50.00	Sequence
DRB1_0701	6	VQRHPRSLFPEFSEL	VQRHPRSLF	0.4331	461.1	WB	50.00	Sequence
DRB1_0701	9	HPRSLFPEFSELSFAA	LFPEFSELF	0.4205	528.5	WB	50.00	Sequence
DRB1_0701	12	SLFPEFSELSFAAFPS	LFPEFSELF	0.4142	565.5	WB	50.00	Sequence
DRB1_0701	61	PKDVDIMVRDGQLT	IMVRDGQLT	0.4090	598.5	WB	50.00	Sequence
DRB1_0701	87	DGRSEFAYGSFVRTV	AYGSFVRTV	0.4082	603.7	WB	50.00	Sequence
DRB1_0701	10	PRSLFPEFSELSFAAF	LFPEFSELF	0.3871	758.3	WB	50.00	Sequence
DRB1_0701	13	LFPEFSELSFAAFPSF	LFPEFSELF	0.3791	826.7	WB	50.00	Sequence
DRB1_0701	88	GRSEFAYGSFVRTVS	AYGSFVRTV	0.3786	832.1	WB	50.00	Sequence
DRB1_0701	15	PEFSELSFAAFPSFAG	FAAFPSFAG	0.3759	856.7	WB	50.00	Sequence
DRB1_0701	21	FAAFPSFAGLRPTFD	FAGLRPTFD	0.3543	1081.5	WB	50.00	Sequence
DRB1_0701	16	EFSELSFAAFPSFAGL	FAAFPSFAG	0.3505	1127.0	WB	50.00	Sequence
DRB1_0701	14	FPEFSELSFAAFPSFA	LFAAFPSFA	0.3452	1194.2	WB	50.00	Sequence
DRB1_0701	17	FSELSFAAFPSFAGLR	AFPSFAGLR	0.3412	1246.8	WB	50.00	Sequence
DRB1_0701	60	DPDKDVDIMVRDGQL	DIMVRDGQL	0.3188	1587.8	WB	50.00	Sequence
DRB1_0701	22	AAFPSFAGLRPTFDT	FAGLRPTFD	0.3171	1617.9	WB	50.00	Sequence

DRB1_0701	31	RPTFDTRLMLRLEDEM	TFDTRLMLRL	0.3144	1666.5	50.00	Sequence
DRB1_0701	32	PTFDTRLMLRLEDEM	TFDTRLMLRL	0.2967	2017.8	50.00	Sequence
DRB1_0701	23	AFPSFAGLRPTFDTR	FAGLRPTFD	0.2923	2114.8	50.00	Sequence
DRB1_0701	18	SELFAAFPSFAGLRP	FAAFPSFAG	0.2856	2274.7	50.00	Sequence
DRB1_0701	84	KDFDGRSEFAYGSFV	SEFAYGSFV	0.2791	2440.9	50.00	Sequence
DRB1_0701	33	TFDTRLMLRLEDEMKE	TFDTRLMLRL	0.2710	2664.8	50.00	Sequence
DRB1_0701	19	ELFAAFPSFAGLRPT	AFPSFAGLR	0.2577	3074.9	50.00	Sequence
DRB1_0701	85	DFDGRSEFAYGSFVR	SEFAYGSFV	0.2545	3184.6	50.00	Sequence
DRB1_0701	120	ILTVSVAVSEGKPTPE	LTVSVAVSE	0.2543	3193.2	50.00	Sequence
DRB1_0701	86	FDGRSEFAYGSFVRT	SEFAYGSFV	0.2510	3307.9	50.00	Sequence
DRB1_0701	20	LFAAFPSFAGLRPTF	FAAFPSFAG	0.2304	4134.0	50.00	Sequence
DRB1_0701	69	VRDQLTIKAERTEQ	QLTIKAERT	0.2091	5203.8	50.00	Sequence
DRB1_0701	121	LTVSVAVSEGKPTPEK	LTVSVAVSE	0.1988	5818.3	50.00	Sequence
DRB1_0701	70	RDGQLTIKAERTEQK	QLTIKAERT	0.1889	6477.5	50.00	Sequence
DRB1_0701	72	GQLTIKAERTEQKDF	AERTEQKDF	0.1767	7392.1	50.00	Sequence
DRB1_0701	43	DEMKEGRYEVRAELP	RYEVRAELP	0.1746	7559.8	50.00	Sequence
DRB1_0701	38	LMRLEDEMKEGRYEV	EMKEGRYEV	0.1659	8307.6	50.00	Sequence
DRB1_0701	71	DGQLTIKAERTEQKD	QLTIKAERT	0.1605	8804.2	50.00	Sequence
DRB1_0701	73	QLTIKAERTEQKDFD	AERTEQKDF	0.1555	9298.4	50.00	Sequence
DRB1_0701	98	VRTVSLPVGADEDDI	PVGADEDDI	0.1528	9574.5	50.00	Sequence
DRB1_0701	80	RTQKDFDGRSEFAY	FDGRSEFAY	0.1474	10151.7	50.00	Sequence
DRB1_0701	44	EMKEGRYEVRAELPG	RYEVRAELP	0.1459	10314.0	50.00	Sequence
DRB1_0701	39	MRLEDEMKEGRYEV	EMKEGRYEV	0.1400	10996.6	50.00	Sequence
DRB1_0701	42	EDEMKEGRYEVRAEL	GRYEVRAEL	0.1397	11032.0	50.00	Sequence
DRB1_0701	123	VSVAVSEGKPTTEKHI	EGKPTTEKHI	0.1393	11072.2	50.00	Sequence
DRB1_0701	45	MKEGRYEVRAELPGV	RYEVRAELP	0.1380	11232.9	50.00	Sequence
DRB1_0701	46	KEGRYEVRAELPGVD	EVRAELPGV	0.1347	11635.7	50.00	Sequence
DRB1_0701	122	TVSVAVSEGKPTTEKH	VSEGKPTTEK	0.1343	11696.6	50.00	Sequence
DRB1_0701	53	RAELPGVDPDKDVDI	VDPDKDVDI	0.1327	11898.0	50.00	Sequence
DRB1_0701	82	EQKDFDGRSEFAYGS	FDGRSEFAY	0.1231	13204.4	50.00	Sequence
DRB1_0701	81	TEQKDFDGRSEFAYG	FDGRSEFAY	0.1214	13437.2	50.00	Sequence
DRB1_0701	125	VAVSEGKPTTEKHIIQI	EGKPTTEKHI	0.1178	13981.5	50.00	Sequence
DRB1_0701	54	AELPGVDPDKDVIM	VDPDKDVIM	0.1161	14229.6	50.00	Sequence
DRB1_0701	124	SVAVSEGKPTTEKHIIQ	EGKPTTEKHI	0.1154	14346.5	50.00	Sequence
DRB1_0701	40	RLEDEMKEGRYEVRA	EMKEGRYEV	0.1139	14576.4	50.00	Sequence
DRB1_0701	74	LTIKAERTEQKDFDGD	AERTEQKDF	0.1115	14966.8	50.00	Sequence
DRB1_0701	55	ELPGVDPDKDVIMV	VDPDKDVIM	0.1100	15215.6	50.00	Sequence
DRB1_0701	47	EGRYEVRAELPGVDP	VRAELPGVD	0.1094	15303.6	50.00	Sequence
DRB1_0701	83	QKDFDGRSEFAYGSF	FDGRSEFAY	0.1073	15662.6	50.00	Sequence
DRB1_0701	99	RTVSLPVGADEDDEIK	PVGADEDDEI	0.1031	16382.6	50.00	Sequence
DRB1_0701	126	AVSEGKPTTEKHIIQIR	EGKPTTEKHI	0.0999	16962.2	50.00	Sequence
DRB1_0701	75	TIKAERTEQKDFDGR	AERTEQKDF	0.0967	17565.5	50.00	Sequence
DRB1_0701	48	GRYEVRAELPGVDPD	VRAELPGVD	0.0939	18101.6	50.00	Sequence
DRB1_0701	56	LPGVDPDKDVIMVR	VDPDKDVIM	0.0926	18366.6	50.00	Sequence
DRB1_0701	76	IKAERTEQKDFDGRS	AERTEQKDF	0.0917	18537.1	50.00	Sequence
DRB1_0701	127	VSEGKPTTEKHIIQIRS	EGKPTTEKHI	0.0900	18882.0	50.00	Sequence
DRB1_0701	100	TVSLPVGADEDDEIKA	PVGADEDDEI	0.0897	18935.0	50.00	Sequence
DRB1_0701	41	LEDEMKEGRYEVRAE	EMKEGRYEV	0.0894	18996.2	50.00	Sequence
DRB1_0701	57	PGVDPDKDVIMVRD	VDPDKDVIM	0.0815	20708.8	50.00	Sequence
DRB1_0701	128	SEGKPTTEKHIIQIRST	EGKPTTEKHI	0.0809	20844.3	50.00	Sequence
DRB1_0701	58	GVDPDKDVIMVRD	VDPDKDVIM	0.0763	21896.4	50.00	Sequence
DRB1_0701	49	RYEVRAELPGVDPDK	VRAELPGVD	0.0762	21922.0	50.00	Sequence
DRB1_0701	103	LPVGADEDDEIKATYD	PVGADEDDEI	0.0754	22104.7	50.00	Sequence
DRB1_0701	34	FDTRLMLRLEDEMKEG	RLMRLEDEM	0.0754	22124.5	50.00	Sequence
DRB1_0701	101	VSLPVGADEDDEIKAT	PVGADEDDEI	0.0740	22442.3	50.00	Sequence
DRB1_0701	129	EGKPTTEKHIIQIRSTN	EGKPTTEKHI	0.0725	22828.8	50.00	Sequence
DRB1_0701	77	KAERTEQKDFDGRSE	AERTEQKDF	0.0720	22942.2	50.00	Sequence
DRB1_0701	104	PVGADEDDEIKATYDK	PVGADEDDEI	0.0712	23143.4	50.00	Sequence
DRB1_0701	102	SLPVGADEDDEIKATY	PVGADEDDEI	0.0702	23383.8	50.00	Sequence
DRB1_0701	50	YEVRAELPGVDPDKD	EVRAELPGV	0.0696	23538.1	50.00	Sequence
DRB1_0701	59	VDPDKDVIMVRDQG	VDPDKDVIM	0.0686	23798.3	50.00	Sequence
DRB1_0701	78	AERTEQKDFDGRSEF	AERTEQKDF	0.0684	23847.8	50.00	Sequence
DRB1_0701	51	EVRAELPGVDPDKDV	VRAELPGVD	0.0647	24826.1	50.00	Sequence
DRB1_0701	35	DTRLMLRLEDEMKEGR	RLMRLEDEM	0.0607	25922.8	50.00	Sequence
DRB1_0701	36	TRLMLRLEDEMKEGRY	RLMRLEDEM	0.0580	26695.3	50.00	Sequence
DRB1_0701	52	VRAELPGVDPDKDV	VRAELPGVD	0.0552	27511.3	50.00	Sequence
DRB1_0701	37	RLMRLEDEMKEGRYE	RLMRLEDEM	0.0533	28078.8	50.00	Sequence
DRB1_0701	105	VGADEDDEIKATYDKG	EDDIKATYD	0.0409	32127.4	50.00	Sequence
DRB1_0701	79	ERTEQKDFDGRSEFA	KDFDGRSEF	0.0402	32363.3	50.00	Sequence

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 Allele: DRB1\_0701. Number of high binders 25. Number of weak binders 22. Number of peptides 130  
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Allele	pos	peptide	core	1-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
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DRB1_0802	93	AYGSFVRTVSLPVGGA	YGSFVRTVS	0.6436	47.3	SB	2.00	Sequence
DRB1_0802	92	FAYGSFVRTVSLPVG	YGSFVRTVS	0.6294	55.2	WB	2.00	Sequence
DRB1_0802	91	EFAYGSFVRTVSLPV	YGSFVRTVS	0.5945	80.5	WB	4.00	Sequence
DRB1_0802	94	YGSFVRTVSLPVGAD	YGSFVRTVS	0.5692	105.8	WB	4.00	Sequence
DRB1_0802	90	SEFAYGSFVRTVSLP	YGSFVRTVS	0.5187	182.6	WB	8.00	Sequence
DRB1_0802	95	GSFVRTVSLPVGAD	FVRTVSLPV	0.5118	196.9	WB	8.00	Sequence
DRB1_0802	89	RSEFAYGSFVRTVSL	YGSFVRTVS	0.4865	258.8	WB	8.00	Sequence
DRB1_0802	24	FPSFAGLRPTFDTRL	FPSFAGLRP	0.4582	351.3	WB	16.00	Sequence
DRB1_0802	96	SFVRTVSLPVGAD	FVRTVSLPV	0.4520	375.7	WB	16.00	Sequence
DRB1_0802	23	AFPSFAGLRPTFDTR	FPSFAGLRP	0.4410	423.3	WB	16.00	Sequence
DRB1_0802	88	GRSEFAYGSFVRTVS	YGSFVRTVS	0.4382	436.3	WB	16.00	Sequence
DRB1_0802	20	LFAAFPSFAGLRPTF	FPSFAGLRP	0.4333	460.2	WB	16.00	Sequence
DRB1_0802	2	TTLPVQRHPRSLFPE	LPVQRHPRS	0.4221	519.5		16.00	Sequence
DRB1_0802	21	FAAFPSFAGLRPTFD	FPSFAGLRP	0.4204	529.0		16.00	Sequence
DRB1_0802	97	FVRTVSLPVGAD	FVRTVSLPV	0.4172	547.6		16.00	Sequence
DRB1_0802	1	ATLTPVQRHPRSLFP	LPVQRHPRS	0.4157	556.6		16.00	Sequence
DRB1_0802	22	AAFPSFAGLRPTFD	FPSFAGLRP	0.4113	583.8		16.00	Sequence
DRB1_0802	19	ELFAAFPSFAGLRPT	FPSFAGLRP	0.3988	668.6		32.00	Sequence
DRB1_0802	3	TLPVQRHPRSLFPEF	LPVQRHPRS	0.3965	685.4		32.00	Sequence
DRB1_0802	48	GRYEVRAELPGVDP	RYEVRAELP	0.3965	685.5		32.00	Sequence
DRB1_0802	0	MATLTPVQRHPRSLF	LPVQRHPRS	0.3899	735.8		32.00	Sequence
DRB1_0802	47	EGRYEVRAELPGVDP	RYEVRAELP	0.3815	805.6		32.00	Sequence
DRB1_0802	46	KEGRYEVRAELPGVD	RYEVRAELP	0.3797	821.9		32.00	Sequence
DRB1_0802	25	PSFAGLRPTFDTRLM	PSFAGLRPT	0.3765	850.6		32.00	Sequence
DRB1_0802	4	LPVQRHPRSLFPEFS	LPVQRHPRS	0.3765	850.7		32.00	Sequence
DRB1_0802	49	RYEVRAELPGVDPDK	RYEVRAELP	0.3612	1004.0		32.00	Sequence
DRB1_0802	67	IMVRDGQLTIKAERT	IMVRDGQLT	0.3609	1006.7		32.00	Sequence
DRB1_0802	31	RPTFDTRLMLRLEDEM	FDTRLMLRLE	0.3550	1073.2		32.00	Sequence
DRB1_0802	45	MKEGRYEVRAELPGV	RYEVRAELP	0.3463	1179.6		32.00	Sequence
DRB1_0802	70	RDGQLTIKAERTEQK	GQLTIKAER	0.3403	1258.9		32.00	Sequence
DRB1_0802	32	PTFDTRLMLRLEDEM	FDTRLMLRLE	0.3401	1261.6		32.00	Sequence
DRB1_0802	66	DIMVRDGQLTIKAER	IMVRDGQLT	0.3362	1315.8		32.00	Sequence
DRB1_0802	72	GQLTIKAERTEQKDF	GQLTIKAER	0.3342	1344.2		32.00	Sequence
DRB1_0802	33	TDTRLMLRLEDEMKE	FDTRLMLRLE	0.3301	1405.4		32.00	Sequence
DRB1_0802	87	DGRSEFAYGSFVRTV	AYGSFVRTV	0.3256	1476.0		32.00	Sequence
DRB1_0802	30	LRPTFDTRLMLRLEDE	FDTRLMLRLE	0.3248	1488.3		32.00	Sequence
DRB1_0802	44	EMKEGRYEVRAELPG	RYEVRAELP	0.3225	1526.6		32.00	Sequence
DRB1_0802	18	SELFAAFPSFAGLRP	FPSFAGLRP	0.3139	1674.3		50.00	Sequence
DRB1_0802	68	MVRDGQLTIKAERTE	GQLTIKAER	0.3135	1681.9		50.00	Sequence
DRB1_0802	71	DGQLTIKAERTEQKD	GQLTIKAER	0.3128	1695.4		50.00	Sequence
DRB1_0802	65	VDIMVRDGQLTIKAE	IMVRDGQLT	0.3120	1710.4		50.00	Sequence
DRB1_0802	69	VRDGQLTIKAERTEQ	GQLTIKAER	0.3089	1767.5		50.00	Sequence
DRB1_0802	29	GLRPTFDTRLMLRLE	FDTRLMLRLE	0.3083	1780.1		50.00	Sequence
DRB1_0802	64	DVDIMVRDGQLTIKA	IMVRDGQLT	0.3046	1851.6		50.00	Sequence
DRB1_0802	17	FSELFAAFPSFAGLR	FSELFAAFP	0.2934	2090.5		50.00	Sequence
DRB1_0802	119	GILTVSVAVSEGKPT	GILTVSVAV	0.2919	2124.9		50.00	Sequence
DRB1_0802	114	ATYDKGILTVSVAVS	GILTVSVAV	0.2899	2172.1		50.00	Sequence
DRB1_0802	115	TYDKGILTVSVAVSE	GILTVSVAV	0.2881	2214.3		50.00	Sequence
DRB1_0802	118	KGILTVSVAVSEGKP	GILTVSVAV	0.2866	2250.5		50.00	Sequence
DRB1_0802	28	AGLRPTFDTRLMLRLE	RPTFDTRLM	0.2856	2275.5		50.00	Sequence
DRB1_0802	34	FDTRLMLRLEDEMKE	FDTRLMLRLE	0.2850	2289.4		50.00	Sequence
DRB1_0802	63	KDVIDIMVRDGQLTIK	IMVRDGQLT	0.2775	2482.8		50.00	Sequence
DRB1_0802	16	EFSELFAAFPSFAGL	FSELFAAFP	0.2709	2667.4		50.00	Sequence
DRB1_0802	43	DEMKEGRYEVRAELP	RYEVRAELP	0.2705	2679.5		50.00	Sequence
DRB1_0802	26	SFAGLRPTFDTRLMR	RPTFDTRLM	0.2680	2751.4		50.00	Sequence
DRB1_0802	5	PVQRHPRSLFPEFSE	PVQRHPRSL	0.2663	2801.6		50.00	Sequence
DRB1_0802	15	PEFSELFAAFPSFAG	FSELFAAFP	0.2648	2849.0		50.00	Sequence
DRB1_0802	62	DKDVDIMVRDGQLTI	IMVRDGQLT	0.2632	2899.2		50.00	Sequence
DRB1_0802	116	YDKGILTVSVAVSEG	GILTVSVAV	0.2626	2917.1		50.00	Sequence
DRB1_0802	117	DKGILTVSVAVSEGK	GILTVSVAV	0.2578	3074.4		50.00	Sequence
DRB1_0802	113	KATYDKGILTVSVAV	GILTVSVAV	0.2560	3132.9		50.00	Sequence
DRB1_0802	27	FAGLRPTFDTRLMLR	RPTFDTRLM	0.2415	3667.0		50.00	Sequence
DRB1_0802	98	VRTVSLPVGAD	VRTVSLPVG	0.2367	3861.5		50.00	Sequence
DRB1_0802	13	LFPEFSELFAAFPSF	FSELFAAFP	0.2359	3893.2		50.00	Sequence
DRB1_0802	73	QLTIKAERTEQKDFD	QLTIKAERT	0.2355	3912.3		50.00	Sequence
DRB1_0802	86	FDGRSEFAYGSFVRT	EFAYGSFVR	0.2349	3935.7		50.00	Sequence
DRB1_0802	7	QRHPRSLFPEFSELF	QRHPRSLFP	0.2343	3963.2		50.00	Sequence
DRB1_0802	120	ILTVSVAVSEGKPT	ILTVSVAVS	0.2340	3974.2		50.00	Sequence
DRB1_0802	14	FPEFSELFAAFPSFA	FSELFAAFP	0.2339	3978.3		50.00	Sequence
DRB1_0802	129	EKGKPTKHKIIRSTN	GKPTKHKIQ	0.2285	4221.7		50.00	Sequence
DRB1_0802	85	DFDGRSEFAYGSFVR	FDGRSEFAY	0.2282	4233.7		50.00	Sequence
DRB1_0802	12	SLFPEFSELFAAFPS	FSELFAAFP	0.2266	4308.9		50.00	Sequence
DRB1_0802	50	YEVRAELPGVDPDKD	YEVRAELPG	0.2259	4337.9		50.00	Sequence
DRB1_0802	6	VQRHPRSLFPEFSEL	QRHPRSLFP	0.2247	4398.2		50.00	Sequence
DRB1_0802	8	RHPRSLFPEFSELFA	HPRSLFPEF	0.2203	4610.9		50.00	Sequence
DRB1_0802	11	RSLFPEFSELFAAFP	FSELFAAFP	0.2184	4705.1		50.00	Sequence
DRB1_0802	61	PKDVDIMVRDGQLT	IMVRDGQLT	0.2164	4811.0		50.00	Sequence

DRB1_0802	112	IKATYDKGILTVSVA	KATYDKGIL	0.2151	4878.2	50.00	Sequence
DRB1_0802	9	HRSLFPEFSELF	FPEFSELF	0.2149	4889.6	50.00	Sequence
DRB1_0802	128	SEKPTTEKHIQIRST	GKPTTEKHIQ	0.2119	5051.7	50.00	Sequence
DRB1_0802	84	KDFDGRSEFAYGSFV	DFDGRSEFA	0.2104	5130.0	50.00	Sequence
DRB1_0802	121	LTVSVAVSEGKPTTEK	TVSVAVSEG	0.1958	6008.4	50.00	Sequence
DRB1_0802	10	PRSLFPEFSELF	LFPEFSELF	0.1954	6034.9	50.00	Sequence
DRB1_0802	83	QKDFDGRSEFAYGSF	DFDGRSEFA	0.1933	6174.8	50.00	Sequence
DRB1_0802	42	EDEMKEGRYEVRAEL	GRYEVRAEL	0.1928	6208.5	50.00	Sequence
DRB1_0802	111	DIKATYDKGILTVSV	KATYDKGIL	0.1913	6311.8	50.00	Sequence
DRB1_0802	37	RLMRLEDEMKEGRYE	RLMRLEDEM	0.1886	6497.8	50.00	Sequence
DRB1_0802	110	DDIKATYDKGILTVS	KATYDKGIL	0.1860	6680.6	50.00	Sequence
DRB1_0802	125	VAVSEGKPTTEKHIQI	VAVSEGKPT	0.1843	6806.8	50.00	Sequence
DRB1_0802	82	EQKDFDGRSEFAYGS	DFDGRSEFA	0.1822	6963.3	50.00	Sequence
DRB1_0802	124	SVAVSEGKPTTEKHIQ	GKPTTEKHIQ	0.1803	7111.5	50.00	Sequence
DRB1_0802	127	VSEGKPTTEKHIQIRS	GKPTTEKHIQ	0.1790	7209.0	50.00	Sequence
DRB1_0802	122	TVSVAVSEGKPTTEKH	TVSVAVSEG	0.1790	7210.8	50.00	Sequence
DRB1_0802	126	AVSEGKPTTEKHIQIR	GKPTTEKHIQ	0.1737	7631.6	50.00	Sequence
DRB1_0802	36	TRLMRLEDEMKEGRY	RLMRLEDEM	0.1710	7857.5	50.00	Sequence
DRB1_0802	35	DTRLMRLEDEMKEGR	RLMRLEDEM	0.1629	8577.4	50.00	Sequence
DRB1_0802	74	LTIKAERTEQKDFD	LTIKAERTE	0.1614	8724.8	50.00	Sequence
DRB1_0802	109	EDDIKATYDKGILTV	KATYDKGIL	0.1484	10035.0	50.00	Sequence
DRB1_0802	123	VSVAVSEGKPTTEKHI	VSVAVSEGK	0.1452	10386.0	50.00	Sequence
DRB1_0802	81	TEQKDFDGRSEFAYG	FDGRSEFAY	0.1386	11165.0	50.00	Sequence
DRB1_0802	80	RTQKDFDGRSEFAY	FDGRSEFAY	0.1315	12054.8	50.00	Sequence
DRB1_0802	99	RTVSLPVGADDDIK	RTVSLPVG	0.1307	12155.6	50.00	Sequence
DRB1_0802	40	RLDEDEMKEGRYEVRA	KEGRYEVRA	0.1303	12210.6	50.00	Sequence
DRB1_0802	51	EVRAELPGVDPDKDV	RAELPGVDP	0.1222	13333.5	50.00	Sequence
DRB1_0802	108	DEDDIKATYDKGILT	KATYDKGIL	0.1219	13365.3	50.00	Sequence
DRB1_0802	41	LEDEMKEGRYEVRAE	KEGRYEVRA	0.1209	13519.9	50.00	Sequence
DRB1_0802	38	LMRLEDEMKEGRYEV	RLEDEMKEG	0.1199	13658.1	50.00	Sequence
DRB1_0802	75	TIKAERTEQKDFDGR	TIKAERTEQ	0.1193	13749.1	50.00	Sequence
DRB1_0802	107	ADEDDIKATYDKGIL	KATYDKGIL	0.1162	14227.3	50.00	Sequence
DRB1_0802	39	MRLEDEMKEGRYEV	RLEDEMKEG	0.1110	15044.9	50.00	Sequence
DRB1_0802	60	DPDKDVDIMVRDQGL	VDIMVRDQG	0.1094	15303.3	50.00	Sequence
DRB1_0802	76	IKARTEQKDFDGRS	IKARTEQK	0.0999	16957.6	50.00	Sequence
DRB1_0802	52	VRAELPGVDPDKDVD	RAELPGVDP	0.0995	17039.8	50.00	Sequence
DRB1_0802	106	GADEDDIKATYDKGI	IKATYDKGI	0.0933	18211.7	50.00	Sequence
DRB1_0802	59	VDPDKDVDIMVRDQG	VDIMVRDQG	0.0884	19214.0	50.00	Sequence
DRB1_0802	79	ERTEQKDFDGRSEFA	DFDGRSEFA	0.0814	20722.9	50.00	Sequence
DRB1_0802	58	GVDPPDKDVDIMVRD	GVDPPDKVD	0.0725	22809.0	50.00	Sequence
DRB1_0802	56	LPGVDPDKDVDIMVR	DKDVDIMVR	0.0720	22938.2	50.00	Sequence
DRB1_0802	57	PGVDPDKDVDIMVR	DKDVDIMVR	0.0715	23077.6	50.00	Sequence
DRB1_0802	53	RAELPGVDPDKDVDI	RAELPGVDP	0.0705	23327.4	50.00	Sequence
DRB1_0802	78	AERTEQKDFDGRSEF	QKDFDGRSE	0.0655	24616.7	50.00	Sequence
DRB1_0802	77	KAERTEQKDFDGRSE	KAERTEQK	0.0653	24677.8	50.00	Sequence
DRB1_0802	105	VGADEDDIKATYDKG	DIKATYDKG	0.0607	25915.5	50.00	Sequence
DRB1_0802	55	ELPGVDPDKDVDIMV	GVDPPDKVD	0.0471	30044.2	50.00	Sequence
DRB1_0802	104	PVGADEDDIKATYDK	GADEDDIKA	0.0460	30409.9	50.00	Sequence
DRB1_0802	100	TVSLPVGADDDIKAT	TVSLPVGAD	0.0448	30787.6	50.00	Sequence
DRB1_0802	101	VSLPVGADDDIKAT	GADEDDIKA	0.0431	31374.4	50.00	Sequence
DRB1_0802	54	AELPGVDPDKDVDIM	GVDPPDKVD	0.0415	31917.1	50.00	Sequence
DRB1_0802	103	LPVGADEDDIKATYD	GADEDDIKA	0.0359	33911.2	50.00	Sequence
DRB1_0802	102	SLPVGADDDIKATY	GADEDDIKA	0.0354	34104.3	50.00	Sequence

Allele: DRB1\_0802. Number of high binders 1. Number of weak binders 11. Number of peptides 130

Allele	pos	peptide	core	l-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
DRB1_0901	94	YGSFVRTVSLPVGAD	FVRTVSLPV	0.6748	33.7	SB	0.80	Sequence
DRB1_0901	91	EFAYGSFVRTVSLPV	FVRTVSLPV	0.6720	34.8	SB	1.00	Sequence
DRB1_0901	92	FAYGSFVRTVSLPVG	FVRTVSLPV	0.6707	35.3	SB	1.00	Sequence
DRB1_0901	93	AYGSFVRTVSLPVG	SFVRTVSLP	0.6589	40.1	SB	2.00	Sequence
DRB1_0901	95	GSFVRTVSLPVGAD	SFVRTVSLP	0.6568	41.0	SB	2.00	Sequence
DRB1_0901	96	SFVRTVSLPVGAD	FVRTVSLPV	0.5937	81.1	WB	4.00	Sequence
DRB1_0901	90	SEFAYGSFVRTVSLP	FAYGSFVRT	0.5772	97.0	WB	8.00	Sequence
DRB1_0901	89	RSEFAYGSFVRTVSL	FAYGSFVRT	0.5422	141.7	WB	16.00	Sequence
DRB1_0901	13	LFPEFSELF	FPEFSELF	0.5346	153.8	WB	16.00	Sequence
DRB1_0901	14	FPEFSELF	FPEFSELF	0.5331	156.3	WB	16.00	Sequence
DRB1_0901	12	SLFPEFSELF	FPEFSELF	0.5204	179.4	WB	16.00	Sequence
DRB1_0901	119	GILTVSVAVSEGKPT	LTVSVAVSE	0.5092	202.5	WB	16.00	Sequence
DRB1_0901	16	EFSELFAAFPSPF	ELFAAFPSP	0.5087	203.5	WB	16.00	Sequence
DRB1_0901	6	VQRHPRSLFPEFSEL	VQRHPRSLF	0.5068	207.8	WB	16.00	Sequence
DRB1_0901	118	KGILTVSVAVSEGKPT	ILTVSVAVS	0.5057	210.3	WB	16.00	Sequence
DRB1_0901	11	RSLFPEFSELF	FPEFSELF	0.5052	211.3	WB	16.00	Sequence

DRB1_0901	120	ILTVSVAVSEGKPT	LTVSVAVSE	0.4957	234.3	WB	16.00	Sequence
DRB1_0901	15	PEFSELFAAFPSFAG	ELFAAFPSF	0.4941	238.5	WB	16.00	Sequence
DRB1_0901	117	DKGILTVSVAVSEK	ILTVSVAVS	0.4924	242.9	WB	32.00	Sequence
DRB1_0901	88	GRSEFAYGFSVRTV	FAYGFSVRT	0.4866	258.5	WB	32.00	Sequence
DRB1_0901	5	PVQRHPRSLFPEFSE	VQRHPRSLF	0.4842	265.4	WB	32.00	Sequence
DRB1_0901	97	FVRTVSLPVGADDD	FVRTVSLPV	0.4840	265.9	WB	32.00	Sequence
DRB1_0901	17	FSELFAAFPSFAGLR	ELFAAFPSF	0.4840	266.0	WB	32.00	Sequence
DRB1_0901	4	LPVQRHPRSLFPEFS	VQRHPRSLF	0.4805	276.1	WB	32.00	Sequence
DRB1_0901	48	GRYEVRAELPGVDPD	RYEVRAELP	0.4755	291.4	WB	32.00	Sequence
DRB1_0901	116	YDKGILTVSVAVSEG	KGILTVSVA	0.4698	309.9	WB	32.00	Sequence
DRB1_0901	3	TLPVQRHPRSLFPEF	VQRHPRSLF	0.4680	316.0	WB	32.00	Sequence
DRB1_0901	9	HPRSLFPEFSELFAA	FPEFSELFA	0.4635	331.9	WB	32.00	Sequence
DRB1_0901	115	TYDKGILTVSVAVSE	KGILTVSVA	0.4604	343.4	WB	32.00	Sequence
DRB1_0901	8	RHPRSLFPEFSELFA	FPEFSELFA	0.4575	354.2	WB	32.00	Sequence
DRB1_0901	10	PRSLFPEFSELFAAF	FPEFSELFA	0.4506	381.6	WB	32.00	Sequence
DRB1_0901	47	EGRYEVRAELPGVDP	GRYEVRAEL	0.4412	422.5	WB	32.00	Sequence
DRB1_0901	18	SELFAAFPSFAGLRP	ELFAAFPSF	0.4402	427.2	WB	32.00	Sequence
DRB1_0901	87	DGRSEFAYGFSVRTV	FAYGFSVRT	0.4401	427.4	WB	32.00	Sequence
DRB1_0901	121	LTVSVAVSEGKPTK	LTVSVAVSE	0.4386	434.6	WB	32.00	Sequence
DRB1_0901	2	TTLPVQRHPRSLFPE	VQRHPRSLF	0.4375	439.9	WB	32.00	Sequence
DRB1_0901	46	KEGRYEVRAELPGVD	RYEVRAELP	0.4251	503.0		50.00	Sequence
DRB1_0901	49	RYEVRAELPGVDPDK	RYEVRAELP	0.4239	509.3		50.00	Sequence
DRB1_0901	86	FDGRSEFAYGFSVRT	EFAYGFSVR	0.4077	607.3		50.00	Sequence
DRB1_0901	50	YEVRAELPGVDPDKD	VRAELPGVD	0.4033	637.0		50.00	Sequence
DRB1_0901	1	ATTLPVQRHPRSLFP	VQRHPRSLF	0.4019	646.3		50.00	Sequence
DRB1_0901	112	IKATYDKGILTVSVA	IKATYDKGI	0.3959	689.7		50.00	Sequence
DRB1_0901	7	QRHPRSLFPEFSELF	HPRSLFPEF	0.3898	736.6		50.00	Sequence
DRB1_0901	52	VRAELPGVDPDKDVD	VRAELPGVD	0.3892	741.9		50.00	Sequence
DRB1_0901	114	ATYDKGILTVSVAVS	KGILTVSVA	0.3882	749.9		50.00	Sequence
DRB1_0901	51	EVRAELPGVDPDKDV	VRAELPGVD	0.3832	790.9		50.00	Sequence
DRB1_0901	19	ELFAAFPSFAGLRPT	ELFAAFPSF	0.3826	796.4		50.00	Sequence
DRB1_0901	111	DIKATYDKGILTVSV	IKATYDKGI	0.3801	818.7		50.00	Sequence
DRB1_0901	45	MKEGRYEVRAELPGV	GRYEVRAEL	0.3747	867.9		50.00	Sequence
DRB1_0901	110	DDIKATYDKGILTVS	IKATYDKGI	0.3650	963.4		50.00	Sequence
DRB1_0901	63	KDVIDMVRDGLTIK	DIMVRDGL	0.3640	973.8		50.00	Sequence
DRB1_0901	113	KATYDKGILTVSVAV	YDKGILTVS	0.3636	978.4		50.00	Sequence
DRB1_0901	0	MATTLPVQRHPRSLF	VQRHPRSLF	0.3544	1080.2		50.00	Sequence
DRB1_0901	109	EDDIKATYDKGILTV	IKATYDKGI	0.3513	1117.4		50.00	Sequence
DRB1_0901	66	DIMVRDGLTIKAER	DIMVRDGL	0.3505	1127.3		50.00	Sequence
DRB1_0901	44	EMKEGRYEVRAELPG	GRYEVRAEL	0.3428	1224.7		50.00	Sequence
DRB1_0901	65	VDIMVRDGLTIKAE	DIMVRDGL	0.3424	1230.5		50.00	Sequence
DRB1_0901	64	DVDIMVRDGLTIKA	DIMVRDGL	0.3413	1245.2		50.00	Sequence
DRB1_0901	98	VRTVSLPVGADDDDI	TVSLPVGAD	0.3373	1300.1		50.00	Sequence
DRB1_0901	62	DKDVDIMVRDGLTI	IMVRDGLT	0.3368	1307.8		50.00	Sequence
DRB1_0901	108	DEDDIKATYDKGILT	IKATYDKGI	0.3346	1338.9		50.00	Sequence
DRB1_0901	85	DFDGRSEFAYGFSVR	EFAYGFSVR	0.3231	1515.8		50.00	Sequence
DRB1_0901	68	MVRDGLTIKAERTE	MVRDGLTI	0.3190	1584.2		50.00	Sequence
DRB1_0901	107	ADEDDIKATYDKGIL	IKATYDKGI	0.3128	1695.1		50.00	Sequence
DRB1_0901	53	RAELPGVDPDKDVDI	RAELPGVDP	0.3097	1752.7		50.00	Sequence
DRB1_0901	34	FDTRLMLRLEDEMKEG	FDTRLMRLE	0.3079	1787.1		50.00	Sequence
DRB1_0901	123	ISVAVSEGKPTKERT	VAVSEGKPT	0.3077	1791.3		50.00	Sequence
DRB1_0901	67	IMVRDGLTIKAERT	IMVRDGLT	0.3075	1795.1		50.00	Sequence
DRB1_0901	125	VAVSEGKPTKHIQI	VAVSEGKPT	0.3073	1798.7		50.00	Sequence
DRB1_0901	28	AGLRPTFDTRLMRLE	LRPTFDTRL	0.3061	1822.1		50.00	Sequence
DRB1_0901	124	SVAVSEGKPTKHIQ	VAVSEGKPT	0.3046	1851.2		50.00	Sequence
DRB1_0901	122	TVSVAVSEGKPTKHI	TVSVAVSEG	0.3020	1905.8		50.00	Sequence
DRB1_0901	33	FDTRLMLRLEDEMKE	FDTRLMRLE	0.2987	1975.2		50.00	Sequence
DRB1_0901	27	FAGLRPTFDTRLML	AGLRPTFD	0.2970	2010.9		50.00	Sequence
DRB1_0901	99	RTVSLPVGADDDDIK	TVSLPVGAD	0.2945	2066.2		50.00	Sequence
DRB1_0901	61	PDKDVDIMVRDGLT	IMVRDGLT	0.2912	2142.1		50.00	Sequence
DRB1_0901	26	SFAGLRPTFDTRLMR	AGLRPTFD	0.2910	2146.4		50.00	Sequence
DRB1_0901	72	GQLTIKAERTEQKDF	LTIKAERTE	0.2892	2188.8		50.00	Sequence
DRB1_0901	25	PSFAGLRPTFDTRLM	LRPTFDTRL	0.2852	2284.5		50.00	Sequence
DRB1_0901	43	DEMKEGRYEVRAELP	GRYEVRAEL	0.2767	2505.0		50.00	Sequence
DRB1_0901	22	AFFPSFAGLRPTFD	AFPFSFAGLR	0.2763	2516.4		50.00	Sequence
DRB1_0901	73	QLTIKAERTEQKDFD	QLTIKAERT	0.2761	2520.5		50.00	Sequence
DRB1_0901	129	EGKPTKHIQIRSTN	EGKPTKHI	0.2758	2530.3		50.00	Sequence
DRB1_0901	24	FPSFAGLRPTFDTRL	FPSFAGLRP	0.2751	2549.0		50.00	Sequence
DRB1_0901	21	FAAFPSFAGLRPTFD	FAAFPSFAG	0.2744	2567.4		50.00	Sequence
DRB1_0901	32	PTFDTRLMLRLEDEM	FDTRLMRLE	0.2729	2611.2		50.00	Sequence
DRB1_0901	29	GLRPTFDTRLMRLED	LRPTFDTRL	0.2713	2655.7		50.00	Sequence
DRB1_0901	30	LRPTFDTRLMRLEDE	LRPTFDTRL	0.2707	2673.4		50.00	Sequence
DRB1_0901	35	DTRLMLRLEDEMKEGR	RLMRLEDEM	0.2671	2779.7		50.00	Sequence
DRB1_0901	71	DGQLTIKAERTEQKD	LTIKAERTE	0.2670	2781.7		50.00	Sequence
DRB1_0901	23	AFPFSFAGLRPTFDTR	FPSFAGLRP	0.2662	2805.7		50.00	Sequence
DRB1_0901	100	TVSLPVGADDDDIKA	TVSLPVGAD	0.2661	2808.5		50.00	Sequence
DRB1_0901	69	VRDGLTIKAERTEQ	VRDGLTIK	0.2631	2902.9		50.00	Sequence

DRB1_0901	36	TRLMRLEDEMKEGRY	RLMRLEDEM	0.2629	2906.9	50.00	Sequence
DRB1_0901	20	LFAAFPSFAGLRPTF	FAAFPSFAG	0.2618	2942.3	50.00	Sequence
DRB1_0901	54	AELPGVDPDKDVDIM	LPGVDPDKD	0.2572	3094.5	50.00	Sequence
DRB1_0901	31	RPTFFDTRLMRLEDEM	FDTRLMRLE	0.2530	3235.3	50.00	Sequence
DRB1_0901	126	AVSEGKPTKEKHQIR	VSEGKPTKEK	0.2474	3440.1	50.00	Sequence
DRB1_0901	84	KDFDGRSEFAYGSFV	SEFAYGSFV	0.2469	3457.0	50.00	Sequence
DRB1_0901	74	LTIKAERTEQKDFDG	LTIKAERTE	0.2459	3493.7	50.00	Sequence
DRB1_0901	70	RDGQLTIKAERTEQK	QLTIKAERT	0.2435	3587.7	50.00	Sequence
DRB1_0901	37	RLMRLEDEMKEGRYE	LMRLEDEMK	0.2368	3855.6	50.00	Sequence
DRB1_0901	42	EDEMKEGRYEVRAEL	GRYEVRAEL	0.2352	3925.3	50.00	Sequence
DRB1_0901	106	GADEDDIKATYDKGI	IKATYDKGI	0.2327	4032.9	50.00	Sequence
DRB1_0901	38	LMRLEDEMKEGRYEV	MRLEDEMKE	0.2284	4222.3	50.00	Sequence
DRB1_0901	127	VSEGKPTKEKHQIRS	VSEGKPTKEK	0.2221	4521.9	50.00	Sequence
DRB1_0901	60	DPDKDVDIMVRDGQL	DIMVRDGQL	0.2194	4658.5	50.00	Sequence
DRB1_0901	128	SEGKPTKEKHQIRST	EGKPTKEKH	0.2147	4901.5	50.00	Sequence
DRB1_0901	83	QKDFDGRSEFAYGSF	RSEFAYGSF	0.2141	4929.6	50.00	Sequence
DRB1_0901	55	ELPGVDPDKDVDIMV	LPGVDPDKD	0.2111	5094.4	50.00	Sequence
DRB1_0901	39	MRLEDEMKEGRYEV	MRLEDEMKE	0.1968	5943.3	50.00	Sequence
DRB1_0901	82	EQKDFDGRSEFAYGS	DFDGRSEFA	0.1948	6077.4	50.00	Sequence
DRB1_0901	101	VSLPVGAEDDIKAT	SLPVGADED	0.1946	6088.1	50.00	Sequence
DRB1_0901	56	LPVDPDKDVDIMVR	GVDPKDKVD	0.1933	6174.4	50.00	Sequence
DRB1_0901	81	TEQKDFDGRSEFAYG	DFDGRSEFA	0.1879	6549.3	50.00	Sequence
DRB1_0901	41	LEDEMKEGRYEVRAE	MKEGRYEV	0.1746	7560.1	50.00	Sequence
DRB1_0901	102	SLPVGAEDEDDIKAT	SLPVGADED	0.1687	8054.3	50.00	Sequence
DRB1_0901	75	TIKAERTEQKDFDGR	KAERTEQKD	0.1643	8449.9	50.00	Sequence
DRB1_0901	79	ERTEQKDFDGRSEFA	DFDGRSEFA	0.1575	9099.1	50.00	Sequence
DRB1_0901	57	PGVDPDKDVDIMVRD	PGVDPDKDV	0.1570	9141.2	50.00	Sequence
DRB1_0901	80	RTEQKDFDGRSEFAY	DFDGRSEFA	0.1565	9199.5	50.00	Sequence
DRB1_0901	58	GVDPKDKDVDIMVRD	GVDPKDKVD	0.1521	9639.1	50.00	Sequence
DRB1_0901	59	VDPDKDVDIMVRDQ	KDVDIMVRD	0.1484	10032.7	50.00	Sequence
DRB1_0901	40	RLEDEMKEGRYEVRA	MKEGRYEV	0.1449	10422.0	50.00	Sequence
DRB1_0901	76	IKAERTEQKDFDGRS	IKAERTEQK	0.1419	10773.7	50.00	Sequence
DRB1_0901	77	KAERTEQKDFDGRSE	KAERTEQKD	0.1375	11293.5	50.00	Sequence
DRB1_0901	103	LPVGAEDEDDIKATYD	LPVGAEDEDD	0.1339	11745.9	50.00	Sequence
DRB1_0901	78	AERTEQKDFDGRSEF	ERTEQKDFD	0.1290	12382.5	50.00	Sequence
DRB1_0901	105	VGADEDDIKATYDKG	DIKATYDKG	0.1027	16461.9	50.00	Sequence
DRB1_0901	104	PVGAEDEDDIKATYDK	EDDIKATYD	0.0942	18034.4	50.00	Sequence

Allele: DRB1\_0901. Number of high binders 5. Number of weak binders 31. Number of peptides 130

Allele	pos	peptide	core	1-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
DRB1_1101	92	FAYGSFVRTVSLPVG	FVRTVSLPV	0.5878	86.5	WB	8.00	Sequence
DRB1_1101	91	EFAYGSFVRTVSLPV	FVRTVSLPV	0.5848	89.3	WB	8.00	Sequence
DRB1_1101	93	AYGSFVRTVSLPVGA	FVRTVSLPV	0.5697	105.2	WB	8.00	Sequence
DRB1_1101	94	YGSFVRTVSLPVGAD	FVRTVSLPV	0.5692	105.8	WB	8.00	Sequence
DRB1_1101	95	GSFVRTVSLPVGADE	FVRTVSLPV	0.5248	170.9	WB	16.00	Sequence
DRB1_1101	90	SEFAYGSFVRTVSLP	FAYGSFVRT	0.4868	258.0	WB	16.00	Sequence
DRB1_1101	0	MATTLPVQRHPRSLF	LPVQRHPRS	0.4758	290.6	WB	16.00	Sequence
DRB1_1101	1	ATTLPVQRHPRSLFP	LPVQRHPRS	0.4742	295.5	WB	16.00	Sequence
DRB1_1101	96	SFVRTVSLPVGADED	FVRTVSLPV	0.4691	312.3	WB	32.00	Sequence
DRB1_1101	2	TTLPVQRHPRSLFPE	LPVQRHPRS	0.4595	346.7	WB	32.00	Sequence
DRB1_1101	89	RSEFAYGSFVRTVSL	FAYGSFVRT	0.4549	364.2	WB	32.00	Sequence
DRB1_1101	32	PTFDTRLMRLEDEM	DTRLMRLED	0.4507	381.3	WB	32.00	Sequence
DRB1_1101	3	TLPVQRHPRSLFPEF	LPVQRHPRS	0.4365	444.5	WB	32.00	Sequence
DRB1_1101	33	TFDTRLMRLEDEMKE	DTRLMRLED	0.4331	461.1	WB	32.00	Sequence
DRB1_1101	31	RPTFDTRLMRLEDEM	DTRLMRLED	0.4250	503.5		32.00	Sequence
DRB1_1101	23	AFPSFAGLRPTFDTR	SFAGLRPTF	0.4100	592.1		32.00	Sequence
DRB1_1101	97	FVRTVSLPVGAEDEDD	FVRTVSLPV	0.4084	602.1		32.00	Sequence
DRB1_1101	24	FPSFAGLRPTFDTRL	SFAGLRPTF	0.4060	618.4		32.00	Sequence
DRB1_1101	4	LPVQRHPRSLFPEFS	LPVQRHPRS	0.3875	754.9		32.00	Sequence
DRB1_1101	88	GRSEFAYGSFVRTVS	FAYGSFVRT	0.3837	786.9		32.00	Sequence
DRB1_1101	30	LRPTFDTRLMRLEDE	DTRLMRLED	0.3819	802.4		32.00	Sequence
DRB1_1101	21	FAAFPSFAGLRPTFD	FAAFPSFAG	0.3795	823.4		32.00	Sequence
DRB1_1101	20	LFAAFPSFAGLRPTF	FAAFPSFAG	0.3790	828.2		32.00	Sequence
DRB1_1101	22	AAFPSFAGLRPTFD	SFAGLRPTF	0.3680	933.2		32.00	Sequence
DRB1_1101	34	FDTRLMRLEDEMKEG	DTRLMRLED	0.3615	1000.5		32.00	Sequence
DRB1_1101	25	PSFAGLRPTFDTRLM	SFAGLRPTF	0.3566	1054.7		32.00	Sequence
DRB1_1101	116	YDKGILTVSVAVSEG	ILTVSVAVS	0.3449	1197.4		50.00	Sequence
DRB1_1101	117	DKGILTVSVAVSEGK	ILTVSVAVS	0.3411	1247.9		50.00	Sequence
DRB1_1101	29	GLRPTFDTRLMRLED	FDTRLMRLE	0.3368	1306.7		50.00	Sequence
DRB1_1101	19	ELFAAFPSFAGLRPT	FAAFPSFAG	0.3305	1399.8		50.00	Sequence
DRB1_1101	64	DVDIMVRDQQLTIKA	IMVRDQQLT	0.3304	1400.4		50.00	Sequence
DRB1_1101	118	KGILTVSVAVSEGKP	ILTVSVAVS	0.3274	1447.2		50.00	Sequence

DRB1_1101	65	VDIMVRDGQLTIKAE	IMVRDGQLT	0.3234	1510.6	50.00	Sequence
DRB1_1101	16	EFSELFAAFPFSFAGL	FSELFAAFP	0.3227	1522.7	50.00	Sequence
DRB1_1101	17	FSELFAAFPFSFAGLR	LFAAFPFSFA	0.3225	1525.6	50.00	Sequence
DRB1_1101	115	TYDKGILTVSVAVSE	ILTVSVAVS	0.3211	1549.9	50.00	Sequence
DRB1_1101	71	DGQLTIKAERTEQKD	QLTIKAERT	0.3174	1612.0	50.00	Sequence
DRB1_1101	26	SFAGLRPTFDTRLMR	SFAGLRPTF	0.3174	1612.3	50.00	Sequence
DRB1_1101	70	RDGQLTIKAERTEQK	QLTIKAERT	0.3172	1616.4	50.00	Sequence
DRB1_1101	72	QQLTIKAERTEQKDF	QLTIKAERT	0.3168	1623.6	50.00	Sequence
DRB1_1101	18	SELFAAFPFSFAGLRP	FAAFPFSFAG	0.3136	1680.6	50.00	Sequence
DRB1_1101	114	ATYDKGILTVSVAVS	YDKGILTVS	0.3117	1715.7	50.00	Sequence
DRB1_1101	13	LFPEFSELFAAFPFSF	FSELFAAFP	0.3095	1757.0	50.00	Sequence
DRB1_1101	14	FPEFSELFAAFPFSFA	FSELFAAFP	0.3092	1761.6	50.00	Sequence
DRB1_1101	119	GILTVSVAVSEGKPT	ILTVSVAVS	0.3088	1769.0	50.00	Sequence
DRB1_1101	15	PEFSELFAAFPFSFAG	FSELFAAFP	0.3061	1822.5	50.00	Sequence
DRB1_1101	63	KDVIDMVRDGQLTIK	IMVRDGQLT	0.3007	1932.7	50.00	Sequence
DRB1_1101	87	DGRSEFAYGFSFVRT	FAYGFSVRT	0.2923	2116.5	50.00	Sequence
DRB1_1101	11	RSLFPEFSELFAAFP	FPEFSELFA	0.2911	2143.8	50.00	Sequence
DRB1_1101	113	KATYDKGILTVSVAV	YDKGILTVS	0.2896	2177.6	50.00	Sequence
DRB1_1101	28	AGLRPTFDTRLMRLE	TFDTRLMRL	0.2879	2217.8	50.00	Sequence
DRB1_1101	12	SLFPEFSELFAAFPFS	FPEFSELFA	0.2840	2314.3	50.00	Sequence
DRB1_1101	112	IKATYDKGILTVSVA	YDKGILTVS	0.2703	2683.2	50.00	Sequence
DRB1_1101	10	PRSLFPEFSELFAAFP	FPEFSELFA	0.2692	2717.2	50.00	Sequence
DRB1_1101	62	DKDVDIMVRDGQLTI	IMVRDGQLT	0.2689	2726.6	50.00	Sequence
DRB1_1101	66	DIMVRDGQLTIKAER	IMVRDGQLT	0.2659	2815.1	50.00	Sequence
DRB1_1101	5	PVQRHPRSLFPEFSE	VQRHPRSLF	0.2656	2823.6	50.00	Sequence
DRB1_1101	47	EGRYEVRAELPGVDP	YEVRAELPG	0.2642	2869.0	50.00	Sequence
DRB1_1101	69	VRDGQLTIKAERTEQ	QLTIKAERT	0.2633	2896.5	50.00	Sequence
DRB1_1101	120	ILTVSVAVSEGKPT	ILTVSVAVS	0.2627	2915.0	50.00	Sequence
DRB1_1101	48	GRYEVRAELPGVDPD	YEVRAELPG	0.2621	2934.9	50.00	Sequence
DRB1_1101	73	QLTIKAERTEQKDFD	QLTIKAERT	0.2614	2955.2	50.00	Sequence
DRB1_1101	67	IMVRDGQLTIKAERT	IMVRDGQLT	0.2520	3270.8	50.00	Sequence
DRB1_1101	46	KEGRYEVRAELPGVD	RYEVRAELP	0.2445	3548.2	50.00	Sequence
DRB1_1101	49	RYEVRAELPGVDPDK	YEVRAELPG	0.2437	3580.4	50.00	Sequence
DRB1_1101	111	DIKATYDKGILTVSV	ATYDKGILT	0.2432	3597.0	50.00	Sequence
DRB1_1101	35	DTRLMRLEDEMKEGR	DTRLMRLED	0.2387	3779.3	50.00	Sequence
DRB1_1101	9	HPRSLFPEFSELFAA	FPEFSELFA	0.2385	3787.9	50.00	Sequence
DRB1_1101	86	FDGRSEFAYGFSVRT	FAYGFSVRT	0.2347	3946.6	50.00	Sequence
DRB1_1101	27	FAGLRPTFDTRLMRL	FAGLRPTFD	0.2269	4293.2	50.00	Sequence
DRB1_1101	6	VQRHPRSLFPEFSEL	VQRHPRSLF	0.2212	4566.2	50.00	Sequence
DRB1_1101	68	MVRDGQLTIKAERTE	QLTIKAERT	0.2205	4600.5	50.00	Sequence
DRB1_1101	8	RHPRSLFPEFSELFA	RSLFPEFSE	0.2142	4927.7	50.00	Sequence
DRB1_1101	45	MKEGRYEVRAELPGV	RYEVRAELP	0.2051	5433.4	50.00	Sequence
DRB1_1101	61	PKDVDIMVRDGQLT	IMVRDGQLT	0.1954	6035.9	50.00	Sequence
DRB1_1101	110	DDIKATYDKGILTVS	ATYDKGILT	0.1953	6045.7	50.00	Sequence
DRB1_1101	50	YEVRAELPGVDPDKD	YEVRAELPG	0.1785	7244.5	50.00	Sequence
DRB1_1101	129	EKGKTEKHIQIRSTN	TEKHIQIRS	0.1653	8357.8	50.00	Sequence
DRB1_1101	36	TRLMRLEDEMKEGRY	LMRLEDEMK	0.1609	8769.5	50.00	Sequence
DRB1_1101	7	QRHPRSLFPEFSELF	RSLFPEFSE	0.1581	9034.4	50.00	Sequence
DRB1_1101	44	EMKEGRYEVRAELPG	RYEVRAELP	0.1578	9065.5	50.00	Sequence
DRB1_1101	98	VRTVSLPVGADDDI	RTVSLPVGA	0.1572	9125.3	50.00	Sequence
DRB1_1101	121	LTVSVAVSEGKPTFK	LTVSVAVSE	0.1543	9420.5	50.00	Sequence
DRB1_1101	74	LTIKAERTEQKDFDG	IKAERTEQK	0.1380	11235.4	50.00	Sequence
DRB1_1101	37	RLMRLEDEMKEGRYE	LMRLEDEMK	0.1355	11538.2	50.00	Sequence
DRB1_1101	122	TVSVAVSEGKPTKEH	VAVSEGKPT	0.1323	11947.0	50.00	Sequence
DRB1_1101	123	VSVAVSEGKPTKEKH	VAVSEGKPT	0.1322	11958.5	50.00	Sequence
DRB1_1101	83	QKDFDGRSEFAYGSF	FDGRSEFAY	0.1298	12269.1	50.00	Sequence
DRB1_1101	109	EDDIKATYDKGILTV	ATYDKGILT	0.1250	12924.3	50.00	Sequence
DRB1_1101	82	EQKDFDGRSEFAYGS	FDGRSEFAY	0.1210	13508.5	50.00	Sequence
DRB1_1101	60	DPDKDVDIMVRDGQL	VDIMVRDGQ	0.1157	14291.8	50.00	Sequence
DRB1_1101	38	LMRLEDEMKEGRYEV	LMRLEDEMK	0.1120	14881.5	50.00	Sequence
DRB1_1101	84	KDFDGRSEFAYGSFV	FDGRSEFAY	0.1120	14885.9	50.00	Sequence
DRB1_1101	124	SVAVSEGKPTKEHIQ	VAVSEGKPT	0.1064	15813.7	50.00	Sequence
DRB1_1101	75	TIKAERTEQKDFDGR	IKAERTEQK	0.1064	15816.2	50.00	Sequence
DRB1_1101	125	VAVSEGKPTKEKHQI	VAVSEGKPT	0.1053	16000.7	50.00	Sequence
DRB1_1101	128	SEKPTKEKHQIRST	TEKHQIRS	0.1052	16024.5	50.00	Sequence
DRB1_1101	81	TEQKDFDGRSEFAYG	FDGRSEFAY	0.1038	16257.3	50.00	Sequence
DRB1_1101	85	DFDGRSEFAYGFSVR	FDGRSEFAY	0.1030	16397.4	50.00	Sequence
DRB1_1101	43	DEMKEGRYEVRAELP	RYEVRAELP	0.0976	17399.0	50.00	Sequence
DRB1_1101	80	RTEQKDFDGRSEFAY	FDGRSEFAY	0.0940	18078.2	50.00	Sequence
DRB1_1101	99	RTVSLPVGADDDIK	RTVSLPVGA	0.0915	18570.2	50.00	Sequence
DRB1_1101	39	MRLEDEMKEGRYEV	MRLEDEMKE	0.0914	18601.0	50.00	Sequence
DRB1_1101	59	VDPKDVDIMVRDGQ	DKDVDIMVR	0.0881	19277.3	50.00	Sequence
DRB1_1101	40	RLEDEMKEGRYEVRA	EMKEGRYEV	0.0848	19969.9	50.00	Sequence
DRB1_1101	108	DEDDIKATYDKGILT	ATYDKGILT	0.0822	20541.4	50.00	Sequence
DRB1_1101	127	VSEGKPTKEKHQIRS	TEKHQIRS	0.0807	20877.7	50.00	Sequence
DRB1_1101	41	LEDEMKEGRYEVRAE	EMKEGRYEV	0.0807	20885.2	50.00	Sequence
DRB1_1101	76	IKAERTEQKDFDGRS	IKAERTEQK	0.0802	21001.4	50.00	Sequence



DRB1_1101	42	EDEMKEGRYEVRAEL	MKEGRYEV	0.0753	22136.0	50.00	Sequence
DRB1_1101	51	EVRAELPGVDPDKDV	RAELPGVDP	0.0741	22422.7	50.00	Sequence
DRB1_1101	126	AVSEGKPTKEKHIQIR	AVSEGKPT	0.0653	24664.2	50.00	Sequence
DRB1_1101	58	GVDPDKDVIDIMVRD	DKDVIDIMV	0.0547	27677.6	50.00	Sequence
DRB1_1101	52	VRAELPGVDPDKD	RAELPGVDP	0.0484	29628.8	50.00	Sequence
DRB1_1101	57	PGVDPDKDVIDIMVR	DKDVIDIMV	0.0414	31963.8	50.00	Sequence
DRB1_1101	53	RAELPGVDPDKD	RAELPGVDP	0.0410	32099.6	50.00	Sequence
DRB1_1101	77	KAERTEQKDFDGRSE	RTEQKDFD	0.0381	33110.6	50.00	Sequence
DRB1_1101	56	LPGVDPDKDVIDIMV	DKDVIDIMV	0.0350	34248.9	50.00	Sequence
DRB1_1101	107	ADEDDIKATYDKGIL	IKATYDKGI	0.0348	34319.0	50.00	Sequence
DRB1_1101	78	AERTEQKDFDGRSEF	AERTEQKDF	0.0288	36618.5	50.00	Sequence
DRB1_1101	106	GADEDDIKATYDKGI	IKATYDKGI	0.0278	37010.5	50.00	Sequence
DRB1_1101	79	ERTEQKDFDGRSEFA	KDFDGRSEF	0.0275	37136.0	50.00	Sequence
DRB1_1101	100	TVSLPVGAEDEDDIKA	TVSLPVGAD	0.0209	39893.1	50.00	Sequence
DRB1_1101	105	VGADEDDIKATYDKG	DEDDIKATY	0.0207	39954.4	50.00	Sequence
DRB1_1101	55	ELPGVDPDKDVIDIMV	LPGVDPDKD	0.0179	41174.5	50.00	Sequence
DRB1_1101	101	VSLPVGAEDEDDIKAT	VSLPVGAD	0.0136	43162.5	50.00	Sequence
DRB1_1101	54	AELPGVDPDKDVIDIM	LPGVDPDKD	0.0134	43260.7	50.00	Sequence
DRB1_1101	104	PVGAEDEDDIKATYDK	DEDDIKATY	0.0118	44021.3	50.00	Sequence
DRB1_1101	102	SLPVGAEDEDDIKATY	DEDDIKATY	0.0100	44855.5	50.00	Sequence
DRB1_1101	103	LPVGAEDEDDIKATYD	DEDDIKATY	0.0099	44941.0	50.00	Sequence

Allele: DRB1\_1101. Number of high binders 0. Number of weak binders 14. Number of peptides 130

Allele	pos	peptide	core	l-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
DRB1_1302	114	ATYDKGILTVSVAVS	GILTVSVAV	0.5512	128.5	WB	8.00	Sequence
DRB1_1302	115	TYDKGILTVSVAVSE	GILTVSVAV	0.5377	148.7	WB	8.00	Sequence
DRB1_1302	113	KATYDKGILTVSVAV	GILTVSVAV	0.5263	168.2	WB	16.00	Sequence
DRB1_1302	116	YDKGILTVSVAVSEG	GILTVSVAV	0.5222	175.9	WB	16.00	Sequence
DRB1_1302	117	DKGILTVSVAVSEGK	GILTVSVAV	0.5014	220.3	WB	16.00	Sequence
DRB1_1302	118	KGILTVSVAVSEGKP	GILTVSVAV	0.4667	320.6	WB	16.00	Sequence
DRB1_1302	62	DKDVIDIMVRDQGLTI	MVRDQGLTI	0.4597	345.7	WB	16.00	Sequence
DRB1_1302	92	FAYGSFVRTVSLPVG	GSFVRTVSL	0.4451	405.2	WB	16.00	Sequence
DRB1_1302	63	KDVIDIMVRDQGLTIK	MVRDQGLTI	0.4385	434.9	WB	32.00	Sequence
DRB1_1302	91	EFAYGSFVRTVSLPV	GSFVRTVSL	0.4353	450.5	WB	32.00	Sequence
DRB1_1302	67	IMVRDQGLTIKAERT	QLTIKAERT	0.4313	470.0	WB	32.00	Sequence
DRB1_1302	93	AYGSFVRTVSLPVG	GSFVRTVSL	0.4282	486.2	WB	32.00	Sequence
DRB1_1302	119	GILTVSVAVSEGKPT	GILTVSVAV	0.4250	503.5		32.00	Sequence
DRB1_1302	64	DVIDIMVRDQGLTIKA	MVRDQGLTI	0.4205	528.4		32.00	Sequence
DRB1_1302	94	YGSFVRTVSLPVGAD	GSFVRTVSL	0.4090	598.4		32.00	Sequence
DRB1_1302	65	VDIMVRDQGLTIKAE	MVRDQGLTI	0.4004	657.0		32.00	Sequence
DRB1_1302	68	MVRDQGLTIKAERTE	MVRDQGLTI	0.3954	693.7		32.00	Sequence
DRB1_1302	66	DIMVRDQGLTIKAER	MVRDQGLTI	0.3899	736.3		32.00	Sequence
DRB1_1302	95	GSFVRTVSLPVGAD	GSFVRTVSL	0.3756	859.0		32.00	Sequence
DRB1_1302	1	ATLPLVQRHPRSLF	QRHPRSLF	0.3626	988.5		32.00	Sequence
DRB1_1302	89	RSEFAYGSFVRTVSL	GSFVRTVSL	0.3588	1029.9		32.00	Sequence
DRB1_1302	2	TFLPVQRHPRSLF	QRHPRSLF	0.3527	1100.4		32.00	Sequence
DRB1_1302	90	SFAYGSFVRTVSLPV	GSFVRTVSL	0.3444	1204.7		32.00	Sequence
DRB1_1302	112	IKATYDKGILTVSVA	DKGILTVSV	0.3440	1209.4		32.00	Sequence
DRB1_1302	3	TLPVQRHPRSLFPEF	QRHPRSLF	0.3416	1240.9		32.00	Sequence
DRB1_1302	25	PSFAGLRPTFDTRL	LRPTFDTRL	0.3313	1388.1		32.00	Sequence
DRB1_1302	4	LPVQRHPRSLFPEFS	QRHPRSLF	0.3277	1442.5		50.00	Sequence
DRB1_1302	61	PKDVIDIMVRDQGLT	DIMVRDQGL	0.3200	1568.4		50.00	Sequence
DRB1_1302	5	PVQRHPRSLFPEFSE	VQRHPRSLF	0.3151	1653.0		50.00	Sequence
DRB1_1302	26	SFAGLRPTFDTRLMR	LRPTFDTRL	0.3144	1666.3		50.00	Sequence
DRB1_1302	111	DIKATYDKGILTVSV	DKGILTVSV	0.3143	1668.0		50.00	Sequence
DRB1_1302	27	FAGLRPTFDTRLML	LRPTFDTRL	0.3077	1791.2		50.00	Sequence
DRB1_1302	24	FPSFAGLRPTFDTRL	LRPTFDTRL	0.2994	1959.4		50.00	Sequence
DRB1_1302	60	DPDKDVIDIMVRDQGL	DIMVRDQGL	0.2927	2107.0		50.00	Sequence
DRB1_1302	28	AGLRPTFDTRLMLR	LRPTFDTRL	0.2896	2178.5		50.00	Sequence
DRB1_1302	0	MATLPLVQRHPRSLF	VQRHPRSLF	0.2802	2412.4		50.00	Sequence
DRB1_1302	29	GLRPTFDTRLMLRLE	LRPTFDTRL	0.2683	2742.6		50.00	Sequence
DRB1_1302	109	EDDIKATYDKGILTV	IKATYDKGI	0.2681	2750.4		50.00	Sequence
DRB1_1302	69	VRDQGLTIKAERTEQ	QLTIKAERT	0.2680	2753.1		50.00	Sequence
DRB1_1302	6	VQRHPRSLFPEFSEL	QRHPRSLF	0.2644	2861.9		50.00	Sequence
DRB1_1302	120	ILTVSVAVSEGKPT	ILTVSVAVS	0.2643	2865.4		50.00	Sequence
DRB1_1302	110	DDIKATYDKGILTVS	IKATYDKGI	0.2606	2980.2		50.00	Sequence
DRB1_1302	30	LRPTFDTRLMLRLE	LRPTFDTRL	0.2457	3503.0		50.00	Sequence
DRB1_1302	96	SFVRTVSLPVGAD	FVRTVSLPV	0.2426	3623.0		50.00	Sequence
DRB1_1302	70	RDGQLTIKAERTEQ	QLTIKAERT	0.2350	3934.5		50.00	Sequence
DRB1_1302	108	DEDDIKATYDKGILT	IKATYDKGI	0.2215	4550.3		50.00	Sequence
DRB1_1302	97	FVRTVSLPVGAD	FVRTVSLPV	0.2198	4638.4		50.00	Sequence
DRB1_1302	7	QRHPRSLFPEFSELF	LFPEFSELF	0.2167	4795.0		50.00	Sequence

DRB1_1302	71	DGQLTIKAERTEQKD	QLTIKAERT	0.2162	4819.4	50.00	Sequence
DRB1_1302	107	ADEDDIKATYDKGIL	IKATYDKGI	0.2152	4872.0	50.00	Sequence
DRB1_1302	72	QLTIKAERTEQKDF	QLTIKAERT	0.2039	5506.5	50.00	Sequence
DRB1_1302	73	QLTIIKAERTEQKDFD	QLTIKAERT	0.1879	6549.8	50.00	Sequence
DRB1_1302	129	EGKPTEKHIQIRSTN	KPTEKHIQI	0.1873	6586.2	50.00	Sequence
DRB1_1302	86	FDGRSEFAYGSFVRT	SEFAYGSFV	0.1838	6841.9	50.00	Sequence
DRB1_1302	87	DGRSEFAYGSFVRT	SEFAYGSFV	0.1812	7042.8	50.00	Sequence
DRB1_1302	125	VAVSEGKPTKHIQI	KPTEKHIQI	0.1806	7082.6	50.00	Sequence
DRB1_1302	126	AVSEGKPTKHIQIR	KPTEKHIQI	0.1720	7772.5	50.00	Sequence
DRB1_1302	88	GRSEFAYGSFVRTVS	SEFAYGSFV	0.1681	8109.7	50.00	Sequence
DRB1_1302	127	VSEGKPTKHIQIRS	KPTEKHIQI	0.1681	8110.5	50.00	Sequence
DRB1_1302	128	SEKPTKHIQIRST	KPTEKHIQI	0.1667	8233.9	50.00	Sequence
DRB1_1302	85	DFDGRSEFAYGSFVR	SEFAYGSFV	0.1640	8482.1	50.00	Sequence
DRB1_1302	11	RSLFPEFSELFAAFP	LFPEFSELF	0.1599	8860.9	50.00	Sequence
DRB1_1302	106	GADEDDIKATYDKGI	IKATYDKGI	0.1580	9045.8	50.00	Sequence
DRB1_1302	10	PRSLFPEFSELFAAF	LFPEFSELF	0.1521	9639.4	50.00	Sequence
DRB1_1302	12	SLFPEFSELFAAFPS	LFPEFSELF	0.1488	9996.2	50.00	Sequence
DRB1_1302	8	RHRSLFPEFSELFA	LFPEFSELF	0.1486	10019.9	50.00	Sequence
DRB1_1302	9	HPRSLFPEFSELFAA	LFPEFSELF	0.1483	10046.4	50.00	Sequence
DRB1_1302	121	LTVSVAVSEGKPTK	VAVSEGKPT	0.1433	10603.2	50.00	Sequence
DRB1_1302	14	PEFSELFAAFPSFA	LFAAFPSFA	0.1430	10637.4	50.00	Sequence
DRB1_1302	13	LFPEFSELFAAFPSF	LFPEFSELF	0.1413	10842.9	50.00	Sequence
DRB1_1302	16	EFSELFAAFPSFAGL	LFAAFPSFA	0.1382	11211.6	50.00	Sequence
DRB1_1302	46	KEGRYEVRAELPGVD	RYEVRAELP	0.1374	11309.4	50.00	Sequence
DRB1_1302	15	PEFSELFAAFPSFAG	LFAAFPSFA	0.1372	11331.2	50.00	Sequence
DRB1_1302	45	MKEGRYEVRAELPGV	RYEVRAELP	0.1369	11370.0	50.00	Sequence
DRB1_1302	47	EGRYEVRAELPGVDP	RYEVRAELP	0.1342	11701.7	50.00	Sequence
DRB1_1302	43	DEMKEGRYEVRAELP	GRYEVRAEL	0.1315	12050.7	50.00	Sequence
DRB1_1302	44	EMKEGRYEVRAELPG	GRYEVRAEL	0.1292	12354.1	50.00	Sequence
DRB1_1302	31	RPTFDTRLMLREDEM	TFDTRLMLR	0.1242	13045.2	50.00	Sequence
DRB1_1302	122	TVSVAVSEGKPTK	VAVSEGKPT	0.1237	13110.7	50.00	Sequence
DRB1_1302	17	FSELFAAFPSFAGLR	LFAAFPSFA	0.1233	13176.3	50.00	Sequence
DRB1_1302	48	GRYEVRAELPGVDPD	RYEVRAELP	0.1230	13212.4	50.00	Sequence
DRB1_1302	84	KDFDGRSEFAYGSFV	SEFAYGSFV	0.1187	13834.9	50.00	Sequence
DRB1_1302	124	SVAVSEGKPTKHIQ	VAVSEGKPT	0.1172	14063.6	50.00	Sequence
DRB1_1302	18	SELFAAFPSFAGLRP	LFAAFPSFA	0.1105	15134.0	50.00	Sequence
DRB1_1302	123	VSVAVSEGKPTKHI	VAVSEGKPT	0.1076	15607.5	50.00	Sequence
DRB1_1302	19	ELFAAFPSFAGLRPT	LFAAFPSFA	0.1034	16332.0	50.00	Sequence
DRB1_1302	98	VRTVSLPVGADDDI	VRTVSLPVG	0.1032	16366.5	50.00	Sequence
DRB1_1302	20	LFAAFPSFAGLRPTF	LFAAFPSFA	0.1020	16590.1	50.00	Sequence
DRB1_1302	42	EDEMKEGRYEVRAEL	GRYEVRAEL	0.1011	16747.9	50.00	Sequence
DRB1_1302	33	TFDTRLMLREDEMKE	TFDTRLMLR	0.0960	17695.7	50.00	Sequence
DRB1_1302	32	PTFDTRLMLREDEM	TFDTRLMLR	0.0944	18004.4	50.00	Sequence
DRB1_1302	57	PGVDPDKDVIDIMVRD	VDPDKDVDI	0.0944	18012.0	50.00	Sequence
DRB1_1302	58	GVDPKDKVDIMVRDG	VDPDKDVDI	0.0931	18266.5	50.00	Sequence
DRB1_1302	49	RYEVRAELPGVDPDK	EVRAELPGV	0.0916	18553.7	50.00	Sequence
DRB1_1302	56	LPGVDPDKDVIDIMVR	VDPDKDVDI	0.0910	18680.4	50.00	Sequence
DRB1_1302	59	VDPDKDVIDIMVRDQG	VDPDKDVDI	0.0877	19355.3	50.00	Sequence
DRB1_1302	50	YEVRAELPGVDPDKD	EVRAELPGV	0.0721	22922.8	50.00	Sequence
DRB1_1302	39	MRLEDEMKEGRYEV	MKEGRYEV	0.0717	23005.8	50.00	Sequence
DRB1_1302	53	RAELPGVDPDKDVDI	VDPDKDVDI	0.0711	23176.2	50.00	Sequence
DRB1_1302	40	LEDEMKEGRYEVRA	MKEGRYEV	0.0691	23670.4	50.00	Sequence
DRB1_1302	83	QKDFDGRSEFAYGSF	RSEFAYGSF	0.0687	23773.3	50.00	Sequence
DRB1_1302	51	EVRAELPGVDPDKDV	EVRAELPGV	0.0665	24361.0	50.00	Sequence
DRB1_1302	55	ELPGVDPDKDVIDIM	VDPDKDVDI	0.0660	24473.5	50.00	Sequence
DRB1_1302	54	AELPGVDPDKDVIDIM	VDPDKDVDI	0.0633	25195.5	50.00	Sequence
DRB1_1302	41	LEDEMKEGRYEVRAE	MKEGRYEV	0.0614	25736.9	50.00	Sequence
DRB1_1302	21	FAAFPSFAGLRPTFD	SFAGLRPTF	0.0614	25739.1	50.00	Sequence
DRB1_1302	99	RTVSLPVGADDDIK	RTVSLPVG	0.0612	25786.0	50.00	Sequence
DRB1_1302	22	AAFPSFAGLRPTFDT	SFAGLRPTF	0.0552	27520.9	50.00	Sequence
DRB1_1302	79	ERTEQKDFDGRSEFA	DFDGRSEFA	0.0549	27620.5	50.00	Sequence
DRB1_1302	80	RTEQKDFDGRSEFAY	DFDGRSEFA	0.0532	28116.5	50.00	Sequence
DRB1_1302	52	VRAELPGVDPDKDVD	VRAELPGVD	0.0520	28476.5	50.00	Sequence
DRB1_1302	82	EQKDFDGRSEFAYGS	DFDGRSEFA	0.0511	28753.6	50.00	Sequence
DRB1_1302	38	LMRLEDEMKEGRYEV	EMKEGRYEV	0.0505	28961.6	50.00	Sequence
DRB1_1302	81	TEQKDFDGRSEFAYG	DFDGRSEFA	0.0486	29537.9	50.00	Sequence
DRB1_1302	23	AFPSFAGLRPTFDTR	SFAGLRPTF	0.0467	30168.7	50.00	Sequence
DRB1_1302	36	TRLMLREDEMKEGRY	EDEMKEGRY	0.0466	30207.2	50.00	Sequence
DRB1_1302	34	FDTRLMLREDEMKEG	MRLEDEMKE	0.0440	31044.5	50.00	Sequence
DRB1_1302	37	RLMLREDEMKEGRYE	EDEMKEGRY	0.0426	31544.6	50.00	Sequence
DRB1_1302	76	IKAERTEQKDFDGRS	IKAERTEQK	0.0398	32505.1	50.00	Sequence
DRB1_1302	74	LTIIKAERTEQKDFDG	IKAERTEQK	0.0397	32539.5	50.00	Sequence
DRB1_1302	35	DTRLMLREDEMKEGR	MRLEDEMKE	0.0383	33036.9	50.00	Sequence
DRB1_1302	75	TIKAERTEQKDFDGR	IKAERTEQK	0.0361	33830.2	50.00	Sequence
DRB1_1302	100	TVSLPVGADDDIKA	TVSLPVGAD	0.0345	34435.1	50.00	Sequence
DRB1_1302	105	VGADEDDIKATYDKG	DEDDIKATY	0.0329	35023.5	50.00	Sequence
DRB1_1302	78	AERTEQKDFDGRSEF	EQKDFDGRS	0.0326	35150.3	50.00	Sequence

DRB1_1302	104	PVGADEDDIKATYDK	DEDDIKATY	0.0325	35183.8	50.00	Sequence
DRB1_1302	103	LPVGADEDDIKATYD	DEDDIKATY	0.0324	35229.1	50.00	Sequence
DRB1_1302	101	VSLPVGAEDEDDIKAT	VSLPVGAE	0.0312	35691.1	50.00	Sequence
DRB1_1302	102	SLPVGAEDEDDIKATY	DEDDIKATY	0.0308	35817.6	50.00	Sequence
DRB1_1302	77	KAERTEQKDFDGRSE	EQKDFDGRS	0.0277	37062.6	50.00	Sequence

Allele: DRB1\_1302. Number of high binders 0. Number of weak binders 12. Number of peptides 130

Allele	pos	peptide	core	l-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
DRB1_1501	91	EFAYGSFVRTVSLPV	EFAYGSFVR	0.5004	222.5	WB	16.00	Sequence
DRB1_1501	93	AYGSFVRTVSLPVGA	FVRTVSLPV	0.5003	222.9	WB	16.00	Sequence
DRB1_1501	90	SEFAYGSFVRTVSLP	AYGSFVRTV	0.4939	238.8	WB	16.00	Sequence
DRB1_1501	92	FAYGSFVRTVSLPVG	FVRTVSLPV	0.4831	268.4	WB	32.00	Sequence
DRB1_1501	87	DGRSEFAYGSFVRTV	EFAYGSFVR	0.4693	311.7	WB	32.00	Sequence
DRB1_1501	94	YGSFVRTVSLPVGAD	FVRTVSLPV	0.4651	326.1	WB	32.00	Sequence
DRB1_1501	17	FSELFAAFPSFAGLR	ELFAAFPSF	0.4615	339.0	WB	32.00	Sequence
DRB1_1501	89	RSEFAYGSFVRTVSL	EFAYGSFVR	0.4614	339.5	WB	32.00	Sequence
DRB1_1501	18	SELFAAFPSFAGLRP	ELFAAFPSF	0.4593	347.4	WB	32.00	Sequence
DRB1_1501	95	GSFVRTVSLPVGADE	FVRTVSLPV	0.4569	356.5	WB	32.00	Sequence
DRB1_1501	88	GRSEFAYGSFVRTVS	EFAYGSFVR	0.4554	362.3	WB	32.00	Sequence
DRB1_1501	15	PEFSELFAAFPSFAG	ELFAAFPSF	0.4409	423.8	WB	32.00	Sequence
DRB1_1501	16	EFSELFAAFPSFAGL	ELFAAFPSF	0.4407	424.8	WB	32.00	Sequence
DRB1_1501	14	FPEFSELFAAFPSFA	EFSELFAAF	0.4200	531.2		32.00	Sequence
DRB1_1501	96	SFVRTVSLPVGADED	FVRTVSLPV	0.4164	552.3		32.00	Sequence
DRB1_1501	86	FDGRSEFAYGSFVRT	EFAYGSFVR	0.4138	568.3		32.00	Sequence
DRB1_1501	13	LFPEFSELFAAFPSF	EFSELFAAF	0.4121	579.1		32.00	Sequence
DRB1_1501	19	ELFAAFPSFAGLRPT	ELFAAFPSF	0.4035	635.2		32.00	Sequence
DRB1_1501	85	DFDGRSEFAYGSFVR	EFAYGSFVR	0.4004	656.5		32.00	Sequence
DRB1_1501	64	DVDIMVRDGGQLTIK	IMVRDGGQLT	0.3896	738.1		32.00	Sequence
DRB1_1501	63	KDVIDMVRDGGQLTIK	IMVRDGGQLT	0.3825	796.9		50.00	Sequence
DRB1_1501	65	VDIMVRDGGQLTIKAE	IMVRDGGQLT	0.3786	831.9		50.00	Sequence
DRB1_1501	66	DIMVRDGGQLTIKAER	MVRDGGQLTI	0.3692	920.4		50.00	Sequence
DRB1_1501	12	SLFPEFSELFAAFPS	EFSELFAAF	0.3587	1031.8		50.00	Sequence
DRB1_1501	62	DKDVIDMVRDGGQLTI	IMVRDGGQLT	0.3499	1135.0		50.00	Sequence
DRB1_1501	10	PRSLFPEFSELFAAF	EFSELFAAF	0.3404	1256.7		50.00	Sequence
DRB1_1501	67	IMVRDGGQLTIKAERT	MVRDGGQLTI	0.3368	1307.3		50.00	Sequence
DRB1_1501	11	RSLFPEFSELFAAF	EFSELFAAF	0.3339	1348.6		50.00	Sequence
DRB1_1501	22	AAFPSFAGLRPTFDTR	AFPSFAGLR	0.3244	1495.7		50.00	Sequence
DRB1_1501	23	AFPSFAGLRPTFDTR	AFPSFAGLR	0.3209	1553.3		50.00	Sequence
DRB1_1501	20	LFAAFPSFAGLRPTF	AFPSFAGLR	0.3194	1578.4		50.00	Sequence
DRB1_1501	21	FAAFPSFAGLRPTFD	AFPSFAGLR	0.3175	1611.0		50.00	Sequence
DRB1_1501	97	FVRTVSLPVGADEDD	FVRTVSLPV	0.3110	1727.5		50.00	Sequence
DRB1_1501	25	PSFAGLRPTFDTRLM	SFAGLRPTF	0.3102	1743.8		50.00	Sequence
DRB1_1501	68	MVRDGGQLTIKAERTE	MVRDGGQLTI	0.3046	1852.3		50.00	Sequence
DRB1_1501	26	SFAGLRPTFDTRLMR	GLRPTFDTR	0.2964	2023.5		50.00	Sequence
DRB1_1501	24	FPSFAGLRPTFDTRL	SFAGLRPTF	0.2898	2173.8		50.00	Sequence
DRB1_1501	27	FAGLRPTFDTRLMLR	GLRPTFDTR	0.2727	2614.4		50.00	Sequence
DRB1_1501	9	HPRSLFPEFSELF	LFPEFSELF	0.2689	2724.6		50.00	Sequence
DRB1_1501	61	PKDVIDMVRDGGQLT	IMVRDGGQLT	0.2577	3077.6		50.00	Sequence
DRB1_1501	28	AGLRPTFDTRLMRLE	GLRPTFDTR	0.2538	3207.6		50.00	Sequence
DRB1_1501	116	YDKGILTVSVAVSEG	GILTVSVAV	0.2524	3258.7		50.00	Sequence
DRB1_1501	117	RHGILTVSVAVSEGK	GILTVSVAV	0.2509	3312.8		50.00	Sequence
DRB1_1501	8	KHPRSLFPEFSELF	LFPEFSELF	0.2442	3558.4		50.00	Sequence
DRB1_1501	115	TYDKGILTVSVAVSE	GILTVSVAV	0.2424	3628.9		50.00	Sequence
DRB1_1501	118	KGILTVSVAVSEGKP	GILTVSVAV	0.2362	3881.5		50.00	Sequence
DRB1_1501	29	GLRPTFDTRLMRLED	GLRPTFDTR	0.2340	3976.5		50.00	Sequence
DRB1_1501	114	ATYDKGILTVSVAVS	GILTVSVAV	0.2328	4029.1		50.00	Sequence
DRB1_1501	7	QRHPRSLFPEFSELF	LFPEFSELF	0.2187	4689.4		50.00	Sequence
DRB1_1501	84	KDFDGRSEFAYGSFV	DFDGRSEFA	0.2176	4749.8		50.00	Sequence
DRB1_1501	113	KATYDKGILTVSVAV	GILTVSVAV	0.2098	5165.9		50.00	Sequence
DRB1_1501	119	GILTVSVAVSEGKPT	GILTVSVAV	0.2046	5466.4		50.00	Sequence
DRB1_1501	69	VRDGGQLTIKAERTEQ	QLTIKAERT	0.1945	6092.4		50.00	Sequence
DRB1_1501	44	EMKEGRYEVRAELPG	EMKEGRYEV	0.1933	6178.7		50.00	Sequence
DRB1_1501	3	TLPVQRHPRSLFPEF	VQRHPRSLF	0.1899	6406.2		50.00	Sequence
DRB1_1501	45	MKEGRYEVRAELPGV	MKEGRYEV	0.1883	6515.3		50.00	Sequence
DRB1_1501	33	FDTRLMRLEDEMKE	LMRLEDEM	0.1873	6591.6		50.00	Sequence
DRB1_1501	43	DEMKEGRYEVRAELP	MKEGRYEV	0.1854	6726.7		50.00	Sequence
DRB1_1501	6	VQRHPRSLFPEFSEL	VQRHPRSLF	0.1851	6751.2		50.00	Sequence
DRB1_1501	72	GQLTIKAERTEQKDF	QLTIKAERT	0.1840	6832.3		50.00	Sequence
DRB1_1501	34	FDTRLMRLEDEMKEG	LMRLEDEM	0.1818	6994.8		50.00	Sequence
DRB1_1501	35	DTRLMRLEDEMKEGR	LMRLEDEM	0.1817	7001.0		50.00	Sequence
DRB1_1501	70	RDGQLTIKAERTEQK	QLTIKAERT	0.1817	7001.3		50.00	Sequence
DRB1_1501	36	TRLMRLEDEMKEGRY	LMRLEDEM	0.1812	7038.6		50.00	Sequence

DRB1_1501	32	PTFDTRLMRLEDEMK	LMRLEDEMK	0.1791	7203.7	50.00	Sequence
DRB1_1501	71	DGQLTIKAERTEQKD	TIKAERTEQ	0.1779	7292.3	50.00	Sequence
DRB1_1501	5	PVQRHPRSLFPEFSE	VQRHPRSLF	0.1751	7521.5	50.00	Sequence
DRB1_1501	37	RLMRLEDEMKEGRYE	LMRLEDEMK	0.1747	7549.8	50.00	Sequence
DRB1_1501	1	ATTLPVQRHPRSLFP	TLPVQRHPR	0.1745	7565.2	50.00	Sequence
DRB1_1501	83	QKDFDGRSEFAYGSF	DFDGRSEFA	0.1745	7571.7	50.00	Sequence
DRB1_1501	4	LPVQRHPRSLFPEFS	VQRHPRSLF	0.1733	7663.4	50.00	Sequence
DRB1_1501	46	KEGRYEVRAELPGVD	KEGRYEVRA	0.1722	7759.0	50.00	Sequence
DRB1_1501	2	TTLPVQRHPRSLFPE	VQRHPRSLF	0.1704	7909.8	50.00	Sequence
DRB1_1501	129	EGKPTEKHIQIRSTN	TEKHIQIRS	0.1693	8010.2	50.00	Sequence
DRB1_1501	0	MATTLPVQRHPRSLF	TLPVQRHPR	0.1680	8120.2	50.00	Sequence
DRB1_1501	82	EQKDFDGRSEFAYGS	DFDGRSEFA	0.1672	8188.3	50.00	Sequence
DRB1_1501	81	TEQKDFDGRSEFAYG	DFDGRSEFA	0.1670	8203.9	50.00	Sequence
DRB1_1501	42	EDEMKEGRYEVRAEL	MKEGRYEV	0.1643	8453.7	50.00	Sequence
DRB1_1501	111	DIKATYDKGILTVSV	DIKATYDKG	0.1622	8646.2	50.00	Sequence
DRB1_1501	60	DPDKDVDIMVRDQGL	DIMVRDQGL	0.1616	8699.8	50.00	Sequence
DRB1_1501	112	IKATYDKGILTVSVA	DKGILTVSV	0.1606	8794.1	50.00	Sequence
DRB1_1501	73	QLTIKAERTEQKDFD	QLTIKAERT	0.1595	8897.1	50.00	Sequence
DRB1_1501	110	DDIKATYDKGILTVS	DIKATYDKG	0.1586	8984.9	50.00	Sequence
DRB1_1501	47	EGRYEVRAELPGVDP	EVRAELPGV	0.1548	9368.2	50.00	Sequence
DRB1_1501	109	EDDIKATYDKGILTV	DIKATYDKG	0.1540	9446.7	50.00	Sequence
DRB1_1501	98	VRTVSLPVGAEDEDDI	VRTVSLPVG	0.1479	10094.3	50.00	Sequence
DRB1_1501	48	GRYEVRAELPGVDPD	EVRAELPGV	0.1471	10175.6	50.00	Sequence
DRB1_1501	80	RTFQKDFDGRSEFAY	DFDGRSEFA	0.1457	10330.4	50.00	Sequence
DRB1_1501	41	LEDEMKEGRYEVRAE	MKEGRYEV	0.1436	10573.6	50.00	Sequence
DRB1_1501	30	LRPTFDTRLMLRLEDE	TFDTRLMLR	0.1432	10617.0	50.00	Sequence
DRB1_1501	31	RPTFDTRLMLRLEDEM	TFDTRLMLR	0.1343	11690.1	50.00	Sequence
DRB1_1501	108	DEDDIKATYDKGILT	DIKATYDKG	0.1335	11798.6	50.00	Sequence
DRB1_1501	40	RLDEMKEGRYEVRAE	MKEGRYEV	0.1324	11932.1	50.00	Sequence
DRB1_1501	74	LTIKAERTEQKDFDG	TIKAERTEQ	0.1245	13003.9	50.00	Sequence
DRB1_1501	128	SEGKPTEKHIQIRST	TEKHIQIRS	0.1233	13163.1	50.00	Sequence
DRB1_1501	79	ERTEQKDFDGRSEFA	EQKDFDGRS	0.1225	13287.8	50.00	Sequence
DRB1_1501	49	RYEVRAELPGVDPDK	EVRAELPGV	0.1193	13754.9	50.00	Sequence
DRB1_1501	38	LMRLEDEMKEGRYEV	LMRLEDEMK	0.1179	13964.3	50.00	Sequence
DRB1_1501	59	VDPDKDVDIMVRDQG	DVDIMVRDG	0.1123	14836.7	50.00	Sequence
DRB1_1501	120	ILTVSVAVSEGKPT	ILTVSVAVS	0.1121	14869.6	50.00	Sequence
DRB1_1501	107	ADEDDIKATYDKGIL	DIKATYDKG	0.1117	14930.1	50.00	Sequence
DRB1_1501	39	MRLEDEMKEGRYEV	MKEGRYEV	0.1089	15385.1	50.00	Sequence
DRB1_1501	127	VSEGKPTEKHIQIRS	TEKHIQIRS	0.1084	15473.6	50.00	Sequence
DRB1_1501	58	GVDPPDKDVDIMVRD	GVDPPDKDVD	0.1055	15961.5	50.00	Sequence
DRB1_1501	75	TIKAERTEQKDFDGR	TIKAERTEQ	0.1043	16180.2	50.00	Sequence
DRB1_1501	78	AERTEQKDFDGRSEF	EQKDFDGRS	0.0960	17686.6	50.00	Sequence
DRB1_1501	122	TVSVAVSEGKPTTEKH	TVSVAVSEG	0.0952	17846.3	50.00	Sequence
DRB1_1501	121	LTVSVAVSEGKPTTEK	VAVSEGKPT	0.0889	19105.2	50.00	Sequence
DRB1_1501	57	PGVDPDKDVDIMVRD	GVDPPDKDVD	0.0887	19144.3	50.00	Sequence
DRB1_1501	51	EVRAELPGVDPDKDV	EVRAELPGV	0.0875	19390.5	50.00	Sequence
DRB1_1501	106	GADEDDIKATYDKGI	DIKATYDKG	0.0871	19476.5	50.00	Sequence
DRB1_1501	56	LPVDPDKDVDIMVR	GVDPPDKDVD	0.0837	20222.3	50.00	Sequence
DRB1_1501	53	RAELPGVDPDKDVDI	RAELPGVDP	0.0823	20522.1	50.00	Sequence
DRB1_1501	123	VSVAVSEGKPTTEKHI	VAVSEGKPT	0.0818	20634.7	50.00	Sequence
DRB1_1501	54	AELPGVDPDKDVDIM	GVDPPDKDVD	0.0816	20687.9	50.00	Sequence
DRB1_1501	55	ELPGVDPDKDVDIMV	GVDPPDKDVD	0.0796	21127.7	50.00	Sequence
DRB1_1501	126	AVSEGKPTTEKHIQIR	AVSEGKPT	0.0788	21323.8	50.00	Sequence
DRB1_1501	124	SVAVSEGKPTTEKHIQ	VAVSEGKPT	0.0781	21484.8	50.00	Sequence
DRB1_1501	76	IKARTEQKDFDGRS	IKARTEQK	0.0779	21532.5	50.00	Sequence
DRB1_1501	50	YEVRAELPGVDPDKD	EVRAELPGV	0.0775	21628.0	50.00	Sequence
DRB1_1501	52	VRAELPGVDPDKDVD	RAELPGVDP	0.0713	23120.6	50.00	Sequence
DRB1_1501	77	KARTEQKDFDGRSE	EQKDFDGRS	0.0708	23237.5	50.00	Sequence
DRB1_1501	105	VGADEDDIKATYDKG	DIKATYDKG	0.0703	23371.9	50.00	Sequence
DRB1_1501	125	VAVSEGKPTTEKHIQI	VAVSEGKPT	0.0698	23491.8	50.00	Sequence
DRB1_1501	99	RTVSLPVGAEDEDDIK	RTVSLPVG	0.0697	23508.8	50.00	Sequence
DRB1_1501	104	PVGAEDEDDIKATYDK	DEDDIKATY	0.0406	32214.1	50.00	Sequence
DRB1_1501	102	SLPVGAEDEDDIKATY	DEDDIKATY	0.0394	32648.9	50.00	Sequence
DRB1_1501	103	LPVGAEDEDDIKATYD	DEDDIKATY	0.0391	32748.3	50.00	Sequence
DRB1_1501	100	TVSLPVGAEDEDDIKA	TVSLPVGAD	0.0376	33302.5	50.00	Sequence
DRB1_1501	101	VSLPVGAEDEDDIKAT	PVGAEDEDDI	0.0345	34423.9	50.00	Sequence

Allele: DRB1\_1501. Number of high binders 0. Number of weak binders 13. Number of peptides 130

Allele	pos	peptide	core	1-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
DRB3_0101	0	MATTLPVQRHPRSLF	VQRHPRSLF	0.3746	868.5	16.00	16.00	Sequence
DRB3_0101	57	PGVDPDKDVDIMVRD	VDPDKDVDI	0.3722	891.4	16.00	16.00	Sequence
DRB3_0101	80	RTFQKDFDGRSEFAY	FDGRSEFAY	0.3707	906.0	16.00	16.00	Sequence

DRB3_0101	1	ATTLPVQRHPRSLFP	VQRHPRSLF	0.3704	908.9	16.00	Sequence
DRB3_0101	55	ELPGVDPDKDVIDMV	VDPDKDVIDI	0.3691	922.1	16.00	Sequence
DRB3_0101	56	LPGVDPDKDVIDIMVR	VDPDKDVIDI	0.3651	962.5	16.00	Sequence
DRB3_0101	2	TTLPVQRHPRSLFPE	VQRHPRSLF	0.3613	1002.8	16.00	Sequence
DRB3_0101	81	TEQKDFDGRSEFAYG	FDGRSEFAY	0.3602	1014.4	16.00	Sequence
DRB3_0101	58	GVPDPDKDVIDIMVRDG	VDPDKDVIDI	0.3582	1037.6	16.00	Sequence
DRB3_0101	3	TLPVQRHPRSLFPEF	VQRHPRSLF	0.3562	1059.8	16.00	Sequence
DRB3_0101	6	VQRHPRSLFPEFSEL	VQRHPRSLF	0.3530	1097.2	16.00	Sequence
DRB3_0101	82	EQKDFDGRSEFAYGS	FDGRSEFAY	0.3514	1116.1	16.00	Sequence
DRB3_0101	59	VDPDKDVIDIMVRDGQ	VDPDKDVIDI	0.3513	1117.9	16.00	Sequence
DRB3_0101	62	DKDVIDIMVRDGQLTI	MVRDGQLTI	0.3465	1177.4	16.00	Sequence
DRB3_0101	4	LPVQRHPRSLFPEFS	VQRHPRSLF	0.3462	1180.3	16.00	Sequence
DRB3_0101	83	QKDFDGRSEFAYGSF	FDGRSEFAY	0.3451	1194.7	16.00	Sequence
DRB3_0101	84	KDFDGRSEFAYGSFV	FDGRSEFAY	0.3447	1199.6	16.00	Sequence
DRB3_0101	63	KVDIMVRDGQLTIK	MVRDGQLTI	0.3324	1370.3	16.00	Sequence
DRB3_0101	5	PVQRHPRSLFPEFSE	VQRHPRSLF	0.3320	1377.5	16.00	Sequence
DRB3_0101	85	DFDGRSEFAYGSFVR	FDGRSEFAY	0.3252	1482.7	16.00	Sequence
DRB3_0101	91	EFAYGSFVRTVSLPV	FVRTVSLPV	0.3248	1488.3	16.00	Sequence
DRB3_0101	54	AELPGVDPDKDVIDIM	VDPDKDVIDI	0.3140	1672.5	16.00	Sequence
DRB3_0101	86	FDGRSEFAYGSFVRT	FDGRSEFAY	0.3108	1731.6	16.00	Sequence
DRB3_0101	53	RAELPGVDPDKDVIDI	VDPDKDVIDI	0.3095	1756.6	16.00	Sequence
DRB3_0101	92	FAYGSFVRTVSLPVG	FVRTVSLPV	0.2983	1983.7	16.00	Sequence
DRB3_0101	64	DVDIMVRDGQLTIKA	MVRDGQLTI	0.2982	1985.5	16.00	Sequence
DRB3_0101	7	QRHPRSLFPEFSELF	LFPEFSELF	0.2911	2142.3	32.00	Sequence
DRB3_0101	8	HPRSLFPEFSELFA	LFPEFSELF	0.2822	2360.1	32.00	Sequence
DRB3_0101	9	RHPRSLFPEFSELFAA	LFPEFSELF	0.2782	2463.4	32.00	Sequence
DRB3_0101	65	VDIMVRDGQLTIKAE	MVRDGQLTI	0.2776	2480.9	32.00	Sequence
DRB3_0101	10	PRSLFPEFSELFAAF	LFPEFSELF	0.2751	2548.3	32.00	Sequence
DRB3_0101	93	AYGSFVRTVSLPVG	FVRTVSLPV	0.2732	2601.2	32.00	Sequence
DRB3_0101	61	PDKDVIDIMVRDGQLT	PDKDVIDIMV	0.2684	2738.6	32.00	Sequence
DRB3_0101	11	RSLFPEFSELFAAFP	LFPEFSELF	0.2663	2801.8	32.00	Sequence
DRB3_0101	66	DIMVRDGQLTIKAER	MVRDGQLTI	0.2514	3293.3	32.00	Sequence
DRB3_0101	12	SFPPEFSELFAAFPS	LFPEFSELF	0.2498	3350.9	32.00	Sequence
DRB3_0101	94	YGSFVRTVSLPVGAD	FVRTVSLPV	0.2488	3387.1	32.00	Sequence
DRB3_0101	60	DPDKDVIDIMVRDGQL	PDKDVIDIMV	0.2432	3600.7	32.00	Sequence
DRB3_0101	67	IMVRDGQLTIKAERT	MVRDGQLTI	0.2323	4048.0	32.00	Sequence
DRB3_0101	95	GSFVRTVSLPVGAD	FVRTVSLPV	0.2308	4113.9	32.00	Sequence
DRB3_0101	13	LFPEFSELFAAFPSF	LFPEFSELF	0.2244	4411.1	32.00	Sequence
DRB3_0101	96	SFVRTVSLPVGAD	FVRTVSLPV	0.2138	4947.3	32.00	Sequence
DRB3_0101	68	MVRDGQLTIKAERTE	MVRDGQLTI	0.1964	5973.9	50.00	Sequence
DRB3_0101	110	DDIKATYDKGILTVS	ATYDKGILT	0.1945	6097.3	50.00	Sequence
DRB3_0101	97	FVRTVSLPVGAD	FVRTVSLPV	0.1824	6948.2	50.00	Sequence
DRB3_0101	111	DIKATYDKGILTVSV	ATYDKGILT	0.1811	7043.1	50.00	Sequence
DRB3_0101	113	KATYDKGILTVSVAV	GILTVSVAV	0.1746	7559.1	50.00	Sequence
DRB3_0101	78	AERTEQKDFDGRSEF	KDFDGRSEF	0.1707	7888.1	50.00	Sequence
DRB3_0101	79	ERTEQKDFDGRSEFA	KDFDGRSEF	0.1704	7908.2	50.00	Sequence
DRB3_0101	28	AGLRPTFDTRLMRLE	FDTRLMRLE	0.1688	8047.2	50.00	Sequence
DRB3_0101	108	DEDDIKATYDKGILT	ATYDKGILT	0.1682	8098.2	50.00	Sequence
DRB3_0101	102	SLPVGADDDIKATY	VGADEDDIK	0.1673	8181.7	50.00	Sequence
DRB3_0101	112	IKATYDKGILTVSVA	ATYDKGILT	0.1666	8242.0	50.00	Sequence
DRB3_0101	114	ATYDKGILTVSVAVS	GILTVSVAV	0.1664	8264.5	50.00	Sequence
DRB3_0101	103	LPVGADDDIKATYD	VGADEDDIK	0.1644	8438.8	50.00	Sequence
DRB3_0101	51	EVRAELPGVDPDKDV	PGVDPDKDV	0.1631	8558.1	50.00	Sequence
DRB3_0101	52	VRAELPGVDPDKDVD	PGVDPDKDV	0.1619	8674.8	50.00	Sequence
DRB3_0101	104	VGADEDDIKATYDK	VGADEDDIK	0.1618	8679.7	50.00	Sequence
DRB3_0101	101	VSLPVGADDDIKAT	VGADEDDIK	0.1612	8739.1	50.00	Sequence
DRB3_0101	109	EDDIKATYDKGILTV	ATYDKGILT	0.1604	8812.5	50.00	Sequence
DRB3_0101	29	GLRPTFDTRLMRLE	FDTRLMRLE	0.1556	9288.8	50.00	Sequence
DRB3_0101	107	ADEDDIKATYDKGIL	IKATYDKGI	0.1531	9538.1	50.00	Sequence
DRB3_0101	105	VGADEDDIKATYDKG	VGADEDDIK	0.1522	9636.8	50.00	Sequence
DRB3_0101	106	GADEDDIKATYDKGI	IKATYDKGI	0.1465	10242.0	50.00	Sequence
DRB3_0101	87	DGRSEFAYGSFVRTV	AYGSFVRTV	0.1465	10246.8	50.00	Sequence
DRB3_0101	115	TYDKGILTVSVAVSE	GILTVSVAV	0.1435	10590.2	50.00	Sequence
DRB3_0101	34	FDTRLMRLEDEMKEG	MRLEDEMKE	0.1430	10636.6	50.00	Sequence
DRB3_0101	33	TFDTRLMRLEDEMKE	MRLEDEMKE	0.1427	10673.6	50.00	Sequence
DRB3_0101	30	LRPTFDTRLMRLEDE	FDTRLMRLE	0.1413	10835.2	50.00	Sequence
DRB3_0101	99	RTVSLPVGADDDIK	VGADEDDIK	0.1407	10907.5	50.00	Sequence
DRB3_0101	90	SEFAYGSFVRTVSLP	AYGSFVRTV	0.1401	10983.1	50.00	Sequence
DRB3_0101	100	TVSLPVGADDDIKA	VGADEDDIK	0.1400	10993.8	50.00	Sequence
DRB3_0101	88	GRSEFAYGSFVRTVS	AYGSFVRTV	0.1369	11370.0	50.00	Sequence
DRB3_0101	38	LMRLEDEMKEGRYEV	EMKEGRYEV	0.1354	11554.0	50.00	Sequence
DRB3_0101	32	PTFDTRLMRLEDEM	FDTRLMRLE	0.1344	11675.3	50.00	Sequence
DRB3_0101	26	SFAGLRPTFDTRLMR	LRPTFDTRL	0.1325	11924.9	50.00	Sequence
DRB3_0101	31	RPTFDTRLMRLEDEM	FDTRLMRLE	0.1311	12097.8	50.00	Sequence
DRB3_0101	27	FAGLRPTFDTRLMR	LRPTFDTRL	0.1305	12188.1	50.00	Sequence
DRB3_0101	22	AAFPSFAGLRPTFD	FAGLRPTFD	0.1286	12436.2	50.00	Sequence
DRB3_0101	89	RSEFAYGSFVRTVSL	AYGSFVRTV	0.1280	12514.5	50.00	Sequence

DRB3_0101	116	YDKGILTVSVAVSEG	GILTVSVAV	0.1272	12620.5	50.00	Sequence
DRB3_0101	46	KEGRYEVRAELPGVD	VRAELPGVD	0.1243	13024.8	50.00	Sequence
DRB3_0101	21	FAAFPSFAGLRPTFD	FAGLRPTFD	0.1231	13201.7	50.00	Sequence
DRB3_0101	35	DTRLRMRLEDEMKEGR	MRLEDEMKE	0.1217	13395.2	50.00	Sequence
DRB3_0101	25	PSFAGLRPTFDTRL	LRPTFDTRL	0.1206	13553.9	50.00	Sequence
DRB3_0101	24	FPSFAGLRPTFDTRL	FAGLRPTFD	0.1188	13824.5	50.00	Sequence
DRB3_0101	36	TRLMRLEDEMKEGRY	MRLEDEMKE	0.1173	14056.9	50.00	Sequence
DRB3_0101	47	EGRYEVRAELPGVDP	VRAELPGVD	0.1169	14115.7	50.00	Sequence
DRB3_0101	37	RLMRLEDEMKEGRY	MRLEDEMKE	0.1150	14408.1	50.00	Sequence
DRB3_0101	16	EFSELFAAFPSFAGL	LFAAFPSFA	0.1149	14418.4	50.00	Sequence
DRB3_0101	48	GRYEVRAELPGVDPD	VRAELPGVD	0.1137	14606.4	50.00	Sequence
DRB3_0101	23	AFPSFAGLRPTFDTR	FAGLRPTFD	0.1135	14648.6	50.00	Sequence
DRB3_0101	15	PEFSELFAAFPSFAG	LFAAFPSFA	0.1116	14941.7	50.00	Sequence
DRB3_0101	14	FPEFSELFAAFPSFA	LFAAFPSFA	0.1095	15298.2	50.00	Sequence
DRB3_0101	117	DKGILTVSVAVSEGK	GILTVSVAV	0.1033	16357.3	50.00	Sequence
DRB3_0101	44	EMKEGRYEVRAELPG	EMKEGRYEV	0.1029	16426.8	50.00	Sequence
DRB3_0101	17	FSLELFAAFPSFAGLR	FAAFPSFAG	0.1018	16613.5	50.00	Sequence
DRB3_0101	43	DEMKEGRYEVRAELP	EMKEGRYEV	0.1000	16950.1	50.00	Sequence
DRB3_0101	39	MRLEDEMKEGRYEV	EMKEGRYEV	0.0960	17704.9	50.00	Sequence
DRB3_0101	118	KGILTVSVAVSEGK	GILTVSVAV	0.0954	17807.1	50.00	Sequence
DRB3_0101	42	EDEMKEGRYEVRAEL	EMKEGRYEV	0.0954	17813.5	50.00	Sequence
DRB3_0101	119	GILTVSVAVSEGKPT	GILTVSVAV	0.0930	18281.5	50.00	Sequence
DRB3_0101	45	MKEGRYEVRAELPGV	GRYEVRAEL	0.0926	18363.6	50.00	Sequence
DRB3_0101	19	ELFAAFPSFAGLRPT	LFAAFPSFA	0.0913	18625.9	50.00	Sequence
DRB3_0101	49	RYEVRAELPGVDPDK	VRAELPGVD	0.0910	18680.4	50.00	Sequence
DRB3_0101	20	LFAAFPSFAGLRPTF	LFAAFPSFA	0.0897	18935.8	50.00	Sequence
DRB3_0101	18	SELFAAFPSFAGLRP	LFAAFPSFA	0.0886	19169.4	50.00	Sequence
DRB3_0101	40	RLDEMKEGRYEVRA	EMKEGRYEV	0.0784	21408.9	50.00	Sequence
DRB3_0101	50	YEVRAELPGVDPDKD	VRAELPGVD	0.0739	22478.8	50.00	Sequence
DRB3_0101	41	LEDEMKEGRYEVRAE	EMKEGRYEV	0.0659	24507.5	50.00	Sequence
DRB3_0101	76	IKAERTEQKDFDGRS	EQKDFDGRS	0.0631	25252.3	50.00	Sequence
DRB3_0101	120	ILTVSVAVSEGKPT	ILTVSVAVS	0.0626	25398.9	50.00	Sequence
DRB3_0101	98	VRTVSLPVGADDDI	PVGADDDI	0.0620	25572.3	50.00	Sequence
DRB3_0101	72	GQLTIKAERTEQKDF	IKAERTEQK	0.0608	25905.9	50.00	Sequence
DRB3_0101	73	QLTIKAERTEQKDFD	IKAERTEQK	0.0607	25932.6	50.00	Sequence
DRB3_0101	70	RDGQLTIKAERTEQK	IKAERTEQK	0.0536	27993.9	50.00	Sequence
DRB3_0101	74	LTIKAERTEQKDFDG	IKAERTEQK	0.0530	28174.7	50.00	Sequence
DRB3_0101	75	TIKAERTEQKDFDGR	IKAERTEQK	0.0518	28539.8	50.00	Sequence
DRB3_0101	77	KAERTEQKDFDGRSE	EQKDFDGRS	0.0514	28686.5	50.00	Sequence
DRB3_0101	71	DGQLTIKAERTEQKD	IKAERTEQK	0.0503	29008.3	50.00	Sequence
DRB3_0101	121	LTVSVAVSEGKPT	LTVSVAVSE	0.0489	29447.9	50.00	Sequence
DRB3_0101	122	TVSVAVSEGKPT	VAVSEGKPT	0.0369	33543.3	50.00	Sequence
DRB3_0101	125	VAVSEGKPTKHIQI	VAVSEGKPT	0.0366	33657.8	50.00	Sequence
DRB3_0101	124	SVAVSEGKPTKHIQ	VAVSEGKPT	0.0297	36256.6	50.00	Sequence
DRB3_0101	69	VRDGQLTIKAERTEQ	RDGQLTIKA	0.0295	36354.0	50.00	Sequence
DRB3_0101	123	VSVAVSEGKPT	VAVSEGKPT	0.0294	36376.5	50.00	Sequence
DRB3_0101	129	EGKPTKHIQIRST	EKHIQIRST	0.0290	36535.0	50.00	Sequence
DRB3_0101	128	SEKPTKHIQIRST	EKHIQIRST	0.0285	36747.1	50.00	Sequence
DRB3_0101	126	AVSEGKPTKHIQIR	GKPTKHIQ	0.0283	36826.3	50.00	Sequence
DRB3_0101	127	VSEGKPTKHIQIRS	GKPTKHIQ	0.0263	37612.8	50.00	Sequence

Allele: DRB3\_0101. Number of high binders 0. Number of weak binders 0. Number of peptides 130

Allele	pos	peptide	core	1-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
DRB4_0101	63	KVDIMVRDQGQLTIK	VDIMVRDQG	0.5981	77.4	WB	8.00	Sequence
DRB4_0101	64	DVDIMVRDQGQLTIKA	VDIMVRDQG	0.5800	94.1	WB	8.00	Sequence
DRB4_0101	62	DKDVDIMVRDQGQLTI	VDIMVRDQG	0.5759	98.4	WB	8.00	Sequence
DRB4_0101	35	DTRLRMRLEDEMKEGR	RLMRLEDEM	0.5714	103.2	WB	8.00	Sequence
DRB4_0101	36	TRLMRLEDEMKEGRY	RLMRLEDEM	0.5694	105.5	WB	16.00	Sequence
DRB4_0101	34	FDTRLRMRLEDEMKEG	RLMRLEDEM	0.5690	106.0	WB	16.00	Sequence
DRB4_0101	65	VDIMVRDQGQLTIKAE	VDIMVRDQG	0.5597	117.2	WB	16.00	Sequence
DRB4_0101	33	TFDTRLRMRLEDEMKE	RLMRLEDEM	0.5594	117.6	WB	16.00	Sequence
DRB4_0101	1	ATTLPVQRHPRSLFP	ATTLPVQRH	0.5454	136.8	WB	16.00	Sequence
DRB4_0101	61	PKDKVDIMVRDQGQLT	VDIMVRDQG	0.5422	141.6	WB	16.00	Sequence
DRB4_0101	32	PTFDTRLRMRLEDEMT	TRLMRLEDE	0.5382	147.9	WB	16.00	Sequence
DRB4_0101	0	MATTLPVQRHPRSLF	ATTLPVQRH	0.5310	160.0	WB	16.00	Sequence
DRB4_0101	60	DPDKVDIMVRDQGQL	VDIMVRDQG	0.5196	180.8	WB	16.00	Sequence
DRB4_0101	66	DIMVRDQGQLTIKAER	IMVRDQQLT	0.5025	217.6	WB	16.00	Sequence
DRB4_0101	2	TTLPVQRHPRSLFPE	LPVQRHPRS	0.4992	225.6	WB	16.00	Sequence
DRB4_0101	31	RPTFDTRLRMRLEDEM	RLMRLEDEM	0.4937	239.3	WB	32.00	Sequence
DRB4_0101	116	YDKGILTVSVAVSEG	KGILTVSVA	0.4884	253.5	WB	32.00	Sequence
DRB4_0101	117	DKGILTVSVAVSEGK	KGILTVSVA	0.4883	253.8	WB	32.00	Sequence
DRB4_0101	115	TYDKGILTVSVAVSE	GILTVSVAV	0.4836	267.1	WB	32.00	Sequence

DRB4_0101	114	ATYDKGILTVSVAVS	KGILTVSVA	0.4818	272.3	WB	32.00	Sequence
DRB4_0101	37	RLMRLEDEMKEGRYE	RLMRLEDEM	0.4693	311.7	WB	32.00	Sequence
DRB4_0101	118	KGILTVSVAVSEGKP	GILTVSVAV	0.4676	317.5	WB	32.00	Sequence
DRB4_0101	113	KATYDKGILTVSVAV	KGILTVSVA	0.4477	393.7	WB	32.00	Sequence
DRB4_0101	59	VDPDKDVDIMVRDGG	VDIMVRDGG	0.4436	411.5	WB	32.00	Sequence
DRB4_0101	67	IMVRDQGQLTIKAERT	IMVRDQGQLT	0.4326	463.8	WB	32.00	Sequence
DRB4_0101	3	TLPVQRHPRSLFPEF	LPVQRHPRS	0.4273	491.0	WB	32.00	Sequence
DRB4_0101	4	LPVQRHPRSLFPEFS	LPVQRHPRS	0.4253	501.8		32.00	Sequence
DRB4_0101	30	LRPTFDTRLMRLEDE	TRLMRLEDE	0.4181	542.3		32.00	Sequence
DRB4_0101	95	GSFVRTVSLPVGAD	GSFVRTVSL	0.4170	548.8		32.00	Sequence
DRB4_0101	94	YGSFVRTVSLPVGAD	GSFVRTVSL	0.4093	596.4		32.00	Sequence
DRB4_0101	93	AYGSFVRTVSLPVG	GSFVRTVSL	0.4059	619.1		32.00	Sequence
DRB4_0101	92	FAYGSFVRTVSLPVG	GSFVRTVSL	0.3881	750.2		50.00	Sequence
DRB4_0101	119	GILTVSVAVSEGKPT	GILTVSVAV	0.3723	890.2		50.00	Sequence
DRB4_0101	96	SFVRTVSLPVGAD	VRTVSLPVG	0.3577	1042.6		50.00	Sequence
DRB4_0101	28	AGLRPTFDTRLMRLE	AGLRPTFD	0.3525	1102.8		50.00	Sequence
DRB4_0101	29	GLRPTFDTRLMRLED	LRPTFDTRL	0.3440	1209.6		50.00	Sequence
DRB4_0101	91	EFAYGSFVRTVSLPV	GSFVRTVSL	0.3430	1222.3		50.00	Sequence
DRB4_0101	97	FVRTVSLPVGAD	VRTVSLPVG	0.3349	1333.7		50.00	Sequence
DRB4_0101	27	FAGLRPTFDTRLMR	AGLRPTFD	0.3289	1424.2		50.00	Sequence
DRB4_0101	48	GRYEVRAELPGVDP	GRYEVRAEL	0.3272	1449.8		50.00	Sequence
DRB4_0101	47	EGRYEVRAELPGVDP	GRYEVRAEL	0.3230	1517.1		50.00	Sequence
DRB4_0101	112	IKATYDKGILTVSVA	KGILTVSVA	0.3214	1544.6		50.00	Sequence
DRB4_0101	26	SFAGLRPTFDTRLMR	RPTFDTRL	0.3188	1589.1		50.00	Sequence
DRB4_0101	25	PSFAGLRPTFDTRL	AGLRPTFD	0.3165	1628.0		50.00	Sequence
DRB4_0101	129	EGKPTKHKIQRSTN	KHKIQRSTN	0.3139	1674.7		50.00	Sequence
DRB4_0101	46	KEGRYEVRAELPGVD	GRYEVRAEL	0.3116	1717.3		50.00	Sequence
DRB4_0101	24	FPSFAGLRPTFDTRL	FPSFAGLRP	0.3113	1722.6		50.00	Sequence
DRB4_0101	68	MVRDQGQLTIKAERTE	MVRDQGLTI	0.3099	1748.4		50.00	Sequence
DRB4_0101	90	SEFAYGSFVRTVSLP	GSFVRTVSL	0.3061	1822.7		50.00	Sequence
DRB4_0101	49	RYEVRAELPGVDPDK	RYEVRAELP	0.3007	1931.0		50.00	Sequence
DRB4_0101	50	YEVRAELPGVDPDKD	LPGVDPDKD	0.2963	2026.7		50.00	Sequence
DRB4_0101	38	LMRLEDEMKEGRYEV	LMRLEDEM	0.2953	2049.0		50.00	Sequence
DRB4_0101	58	GVDPKDVDIMVRD	KDVDIMVRD	0.2914	2137.2		50.00	Sequence
DRB4_0101	89	RSEFAYGSFVRTVSL	GSFVRTVSL	0.2890	2193.3		50.00	Sequence
DRB4_0101	5	PVQRHPRSLFPEFSE	PVQRHPRSL	0.2887	2198.9		50.00	Sequence
DRB4_0101	45	MKEGRYEVRAELPGV	GRYEVRAEL	0.2879	2219.0		50.00	Sequence
DRB4_0101	23	AFPSFAGLRPTFDTR	FPSFAGLRP	0.2802	2412.2		50.00	Sequence
DRB4_0101	6	VQRHPRSLFPEFSEL	VQRHPRSLF	0.2787	2451.9		50.00	Sequence
DRB4_0101	98	VRTVSLPVGAD	VRTVSLPVG	0.2778	2474.6		50.00	Sequence
DRB4_0101	8	RHPRSLFPEFSELFA	FPEFSELFA	0.2758	2529.2		50.00	Sequence
DRB4_0101	9	HPRSLFPEFSELFAA	FPEFSELFA	0.2686	2735.4		50.00	Sequence
DRB4_0101	7	QRHPRSLFPEFSELF	RSLFPEFSE	0.2651	2839.1		50.00	Sequence
DRB4_0101	69	VRDQGQLTIKAERTEQ	VRDQGQLTIK	0.2638	2880.1		50.00	Sequence
DRB4_0101	44	EMKEGRYEVRAELPG	GRYEVRAEL	0.2586	3045.7		50.00	Sequence
DRB4_0101	22	AAFPSFAGLRPTFD	FPSFAGLRP	0.2581	3062.3		50.00	Sequence
DRB4_0101	51	EVRAELPGVDPDKDV	LPGVDPDKD	0.2572	3092.7		50.00	Sequence
DRB4_0101	10	PRSLFPEFSELFAAF	FPEFSELFA	0.2490	3380.4		50.00	Sequence
DRB4_0101	55	ELPGVDPDKDVDIMV	LPGVDPDKD	0.2475	3437.2		50.00	Sequence
DRB4_0101	120	ILTVSVAVSEGKPT	ILTVSVAVS	0.2448	3536.4		50.00	Sequence
DRB4_0101	70	RDGQLTIKAERTEQK	QLTIKAERT	0.2433	3596.5		50.00	Sequence
DRB4_0101	72	QLTIKAERTEQKDF	QLTIKAERT	0.2412	3679.1		50.00	Sequence
DRB4_0101	54	AELPGVDPDKDVDIM	LPGVDPDKD	0.2393	3752.8		50.00	Sequence
DRB4_0101	56	LPGVDPDKDVDIMVR	LPGVDPDKD	0.2377	3817.6		50.00	Sequence
DRB4_0101	53	RAELPGVDPDKDVDI	LPGVDPDKD	0.2366	3867.2		50.00	Sequence
DRB4_0101	13	LFPEFSELFAAFPSF	FPEFSELFA	0.2329	4024.8		50.00	Sequence
DRB4_0101	71	DGQLTIKAERTEQKD	GQLTIKAER	0.2280	4242.1		50.00	Sequence
DRB4_0101	39	MRLEDEMKEGRYEV	MRLEDEMKE	0.2268	4298.7		50.00	Sequence
DRB4_0101	52	VRAELPGVDPDKDVD	LPGVDPDKD	0.2265	4311.5		50.00	Sequence
DRB4_0101	11	RSLFPEFSELFAAF	FPEFSELFA	0.2248	4392.3		50.00	Sequence
DRB4_0101	14	FPEFSELFAAFPSFA	FPEFSELFA	0.2246	4401.1		50.00	Sequence
DRB4_0101	43	DEMKEGRYEVRAELP	GRYEVRAEL	0.2235	4456.0		50.00	Sequence
DRB4_0101	128	SEGKPTKHKIQRST	EKHKIQRST	0.2214	4554.3		50.00	Sequence
DRB4_0101	57	PGVDPDKDVDIMVRD	DKDVDIMVR	0.2187	4691.8		50.00	Sequence
DRB4_0101	21	FAAFPSFAGLRPTFD	FPSFAGLRP	0.2173	4764.4		50.00	Sequence
DRB4_0101	12	SLFPEFSELFAAFPS	FPEFSELFA	0.2163	4817.4		50.00	Sequence
DRB4_0101	15	PEFSELFAAFPSFAG	FSELFAAFP	0.2063	5364.5		50.00	Sequence
DRB4_0101	73	QLTIKAERTEQKDFD	QLTIKAERT	0.2063	5365.0		50.00	Sequence
DRB4_0101	86	FDGRSEFAYGSFVRT	FAYGSFVRT	0.2027	5578.9		50.00	Sequence
DRB4_0101	99	RTVSLPVGAD	RTVSLPVG	0.1982	5858.9		50.00	Sequence
DRB4_0101	20	LFAAFPSFAGLRPTF	FPSFAGLRP	0.1969	5941.5		50.00	Sequence
DRB4_0101	42	EDEMKEGRYEVRAEL	GRYEVRAEL	0.1954	6036.7		50.00	Sequence
DRB4_0101	87	DGRSEFAYGSFVRTV	FAYGSFVRT	0.1951	6058.1		50.00	Sequence
DRB4_0101	18	SELFAAFPSFAGLRP	SELFAAFPS	0.1943	6105.9		50.00	Sequence
DRB4_0101	16	EFSELFAAFPSFAGL	FSELFAAFP	0.1922	6250.7		50.00	Sequence
DRB4_0101	88	GRSEFAYGSFVRTVS	FAYGSFVRT	0.1914	6303.6		50.00	Sequence
DRB4_0101	19	ELFAAFPSFAGLRPT	FPSFAGLRP	0.1894	6444.8		50.00	Sequence

DRB4_0101	111	DIKATYDKGILTVSV	DKGILTVSV	0.1862	6666.2	50.00	Sequence
DRB4_0101	17	FSELFAAFPSFAGLR	SELFAAFPS	0.1861	6675.8	50.00	Sequence
DRB4_0101	121	LTVSVAVSEGKPTK	LTVSVAVSE	0.1822	6965.5	50.00	Sequence
DRB4_0101	108	DEDDIKATYDKGILT	DDIKATYDK	0.1732	7673.2	50.00	Sequence
DRB4_0101	109	EDDIKATYDKGILTV	DDIKATYDK	0.1730	7693.2	50.00	Sequence
DRB4_0101	123	VSVAVSEGKPTKHI	VSVAVSEGK	0.1687	8054.5	50.00	Sequence
DRB4_0101	122	TVSVAVSEGKPTKHI	VSVAVSEGK	0.1686	8065.7	50.00	Sequence
DRB4_0101	110	DDIKATYDKGILTVS	DDIKATYDK	0.1658	8316.6	50.00	Sequence
DRB4_0101	127	VSEGKPTKHIQIRS	KPTKHIQI	0.1628	8585.4	50.00	Sequence
DRB4_0101	74	LTIKAERTEQKDFDG	LTIKAERTE	0.1571	9138.1	50.00	Sequence
DRB4_0101	101	VSLPVGAEDEDDIK	LPVGADEDD	0.1567	9176.4	50.00	Sequence
DRB4_0101	40	RLEDEMKEGRYEVRA	EMKEGRYEV	0.1565	9197.4	50.00	Sequence
DRB4_0101	41	LEDEMKEGRYEVRAE	EMKEGRYEV	0.1553	9318.6	50.00	Sequence
DRB4_0101	100	TVSVPVGADEDDIKA	LPVGADEDD	0.1528	9573.9	50.00	Sequence
DRB4_0101	75	TIKAERTEQKDFDGR	IKAERTEQK	0.1483	10047.4	50.00	Sequence
DRB4_0101	107	ADEDDIKATYDKGIL	DDIKATYDK	0.1472	10171.9	50.00	Sequence
DRB4_0101	126	AVSEGKPTKHIQIR	KPTKHIQI	0.1468	10208.9	50.00	Sequence
DRB4_0101	76	IKAERTEQKDFDGRS	IKAERTEQK	0.1445	10471.1	50.00	Sequence
DRB4_0101	106	GADEDDIKATYDKGI	DDIKATYDK	0.1397	11025.5	50.00	Sequence
DRB4_0101	125	VAVSEGKPTKHIQI	KPTKHIQI	0.1394	11061.3	50.00	Sequence
DRB4_0101	102	SLPVGAEDEDDIKATY	LPVGADEDD	0.1383	11202.5	50.00	Sequence
DRB4_0101	85	DFDGRSEFAYGSFVR	RSEFAYGSF	0.1346	11649.3	50.00	Sequence
DRB4_0101	84	KDFDGRSEFAYGSFV	KDFDGRSEF	0.1308	12140.0	50.00	Sequence
DRB4_0101	105	VGADEDDIKATYDKG	DDIKATYDK	0.1274	12595.4	50.00	Sequence
DRB4_0101	78	AERTEQKDFDGRSEF	AERTEQKDF	0.1271	12643.8	50.00	Sequence
DRB4_0101	77	KAERTEQKDFDGRSE	KAERTEQKDF	0.1262	12761.7	50.00	Sequence
DRB4_0101	124	SVAVSEGKPTKHIQ	VAVSEGKPT	0.1251	12912.0	50.00	Sequence
DRB4_0101	83	QKDFDGRSEFAYGSF	KDFDGRSEF	0.1238	13103.5	50.00	Sequence
DRB4_0101	103	LPVGADEDDIKATYD	LPVGADEDD	0.1194	13732.9	50.00	Sequence
DRB4_0101	104	PVGADEDDIKATYDK	DDIKATYDK	0.1173	14049.9	50.00	Sequence
DRB4_0101	79	ERTEQKDFDGRSEFA	KDFDGRSEF	0.1000	16942.7	50.00	Sequence
DRB4_0101	80	RTQKDFDGRSEFAY	KDFDGRSEF	0.0991	17106.7	50.00	Sequence
DRB4_0101	82	EQKDFDGRSEFAYGS	KDFDGRSEF	0.0965	17604.5	50.00	Sequence
DRB4_0101	81	TEQKDFDGRSEFAYG	KDFDGRSEF	0.0901	18861.2	50.00	Sequence

Allele: DRB4\_0101. Number of high binders 0. Number of weak binders 26. Number of peptides 130

Allele	pos	peptide	core	l-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
DRB5_0101	91	EFAYGFSFVRTVSLPV	FVRTVSLPV	0.6539	42.3	SB	8.00	Sequence
DRB5_0101	92	FAYGSFVRTVSLPVG	FVRTVSLPV	0.6371	50.7	WB	8.00	Sequence
DRB5_0101	93	AYGSFVRTVSLPVGA	FVRTVSLPV	0.5985	77.1	WB	16.00	Sequence
DRB5_0101	23	AFPSFAGLRPTFDTR	FAGLRPTFD	0.5696	105.3	WB	16.00	Sequence
DRB5_0101	21	FAAFPSFAGLRPTFD	AFPSFAGLR	0.5606	116.1	WB	16.00	Sequence
DRB5_0101	94	YGSFVRTVSLPVGAD	FVRTVSLPV	0.5470	134.5	WB	16.00	Sequence
DRB5_0101	22	AAFPSFAGLRPTFDT	AFPSFAGLR	0.5456	136.5	WB	16.00	Sequence
DRB5_0101	19	ELFAAFPSFAGLRPT	AFPSFAGLR	0.5382	147.9	WB	16.00	Sequence
DRB5_0101	0	MATTLPVQRHPRSLF	MATTLPVQR	0.5283	164.6	WB	16.00	Sequence
DRB5_0101	18	SELFAAFPSFAGLRP	AFPSFAGLR	0.5229	174.6	WB	16.00	Sequence
DRB5_0101	95	GSFVRTVSLPVGAD	FVRTVSLPV	0.5227	174.9	WB	16.00	Sequence
DRB5_0101	24	FPSFAGLRPTFDTRL	FAGLRPTFD	0.5132	193.9	WB	32.00	Sequence
DRB5_0101	27	FAGLRPTFDTRLML	FAGLRPTFD	0.5130	194.3	WB	32.00	Sequence
DRB5_0101	20	LFAAFPSFAGLRPTF	AFPSFAGLR	0.5011	221.0	WB	32.00	Sequence
DRB5_0101	17	FSELFAAFPSFAGLR	AFPSFAGLR	0.5001	223.5	WB	32.00	Sequence
DRB5_0101	90	SEFAYGSFVRTVSLP	FAYGSFVRT	0.4956	234.6	WB	32.00	Sequence
DRB5_0101	89	RSEFAYGSFVRTVSL	FAYGSFVRT	0.4882	254.1	WB	32.00	Sequence
DRB5_0101	25	PSFAGLRPTFDTRLM	FAGLRPTFD	0.4860	260.1	WB	32.00	Sequence
DRB5_0101	26	SFAGLRPTFDTRLMR	FAGLRPTFD	0.4841	265.6	WB	32.00	Sequence
DRB5_0101	16	EFSELFAAFPSFAGL	FSELFAAFPS	0.4750	293.0	WB	32.00	Sequence
DRB5_0101	88	GRSEFAYGSFVRTVS	FAYGSFVRT	0.4719	303.0	WB	32.00	Sequence
DRB5_0101	15	PEFSELFAAFPSFAG	FSELFAAFPS	0.4670	319.6	WB	32.00	Sequence
DRB5_0101	87	DGRSEFAYGSFVRTV	FAYGSFVRT	0.4590	348.4	WB	32.00	Sequence
DRB5_0101	28	AGLRPTFDTRLMRLE	LRPTFDTRL	0.4517	376.9	WB	32.00	Sequence
DRB5_0101	11	RSLFPEFSELFAAFPS	FSELFAAFPS	0.4461	400.8	WB	32.00	Sequence
DRB5_0101	29	GLRPTFDTRLMRLED	LRPTFDTRL	0.4433	412.9	WB	32.00	Sequence
DRB5_0101	96	SFVRTVSLPVGAD	FVRTVSLPV	0.4416	420.6	WB	32.00	Sequence
DRB5_0101	86	FDGRSEFAYGSFVRT	FAYGSFVRT	0.4399	428.4	WB	32.00	Sequence
DRB5_0101	14	FPEFSELFAAFPSFA	FSELFAAFPS	0.4310	471.9	WB	32.00	Sequence
DRB5_0101	30	LRPTFDTRLMRLEDE	TFDTRLMR	0.4115	582.5		50.00	Sequence
DRB5_0101	70	RDGQLTIKAERTEQK	GQLTIKAER	0.4066	614.2		50.00	Sequence
DRB5_0101	10	PRSLFPEFSELFAAF	LFPEFSELF	0.4061	617.5		50.00	Sequence
DRB5_0101	13	LFPEFSELFAAFPSF	FSELFAAFPS	0.4041	631.2		50.00	Sequence
DRB5_0101	2	TTLPVQRHPRSLFPE	LPVQRHPRS	0.4036	634.4		50.00	Sequence
DRB5_0101	1	ATTLPVQRHPRSLFP	LPVQRHPRS	0.3990	666.6		50.00	Sequence



DRB5_0101	3	TLPVQRHPRSLFPEF	LPVQRHPRS	0.3875	755.1	50.00	Sequence
DRB5_0101	12	SLFPEFSELFAAFP	FSELFAAFP	0.3871	758.4	50.00	Sequence
DRB5_0101	32	PTFDTRLMRLEDEM	TFDTRLMRL	0.3856	770.8	50.00	Sequence
DRB5_0101	97	FVRTVSLPVGADDD	FVRTVSLPV	0.3854	773.0	50.00	Sequence
DRB5_0101	72	GQLTIKAERTEQKDF	GQLTIKAER	0.3763	852.2	50.00	Sequence
DRB5_0101	69	VRDQQLTIKAERTEQ	GQLTIKAER	0.3743	871.0	50.00	Sequence
DRB5_0101	33	TFDTRLMRLEDEMKE	TFDTRLMRL	0.3683	929.7	50.00	Sequence
DRB5_0101	9	HPRSLFPEFSELF	LFPEFSELF	0.3668	944.6	50.00	Sequence
DRB5_0101	71	DGQLTIKAERTEQKD	GQLTIKAER	0.3667	945.6	50.00	Sequence
DRB5_0101	31	RPTFDTRLMRLEDEM	TFDTRLMRL	0.3613	1002.7	50.00	Sequence
DRB5_0101	8	RHPRSLFPEFSELF	LFPEFSELF	0.3494	1140.1	50.00	Sequence
DRB5_0101	36	TRLMRLEDEMKEGRY	LMRLEDEMK	0.3489	1147.2	50.00	Sequence
DRB5_0101	4	LPVQRHPRSLFPEFS	LPVQRHPRS	0.3458	1185.5	50.00	Sequence
DRB5_0101	35	DTRLMRLEDEMKEGR	LMRLEDEMK	0.3451	1195.1	50.00	Sequence
DRB5_0101	7	QRHPRSLFPEFSELF	LFPEFSELF	0.3444	1204.6	50.00	Sequence
DRB5_0101	68	MVRDQQLTIKAERTE	GQLTIKAER	0.3425	1229.2	50.00	Sequence
DRB5_0101	67	IMVRDQQLTIKAERT	GQLTIKAER	0.3404	1257.1	50.00	Sequence
DRB5_0101	37	RLMRLEDEMKEGRYE	LMRLEDEMK	0.3344	1342.3	50.00	Sequence
DRB5_0101	85	DFDGRSEFAYGSFVR	EFAYGSFVR	0.3298	1410.2	50.00	Sequence
DRB5_0101	6	VQRHPRSLFPEFSEL	QRHPRSLFP	0.3162	1633.7	50.00	Sequence
DRB5_0101	34	FTRLMRLEDEMKEG	LMRLEDEMK	0.3160	1637.7	50.00	Sequence
DRB5_0101	66	DIMVRDQQLTIKAER	IMVRDQQLT	0.3059	1825.7	50.00	Sequence
DRB5_0101	5	PVQRHPRSLFPEFSE	QRHPRSLFP	0.2992	1963.8	50.00	Sequence
DRB5_0101	73	QLTIKAERTEQKDFD	IKARTEQK	0.2899	2172.3	50.00	Sequence
DRB5_0101	64	DVDIMVRDQQLTIKA	IMVRDQQLT	0.2753	2543.6	50.00	Sequence
DRB5_0101	65	VIMVRDQQLTIKAE	IMVRDQQLT	0.2744	2566.9	50.00	Sequence
DRB5_0101	47	EGRYEVRAELPGVDP	YEVRAELPG	0.2724	2623.7	50.00	Sequence
DRB5_0101	38	LMRLEDEMKEGRYEV	LMRLEDEMK	0.2716	2647.8	50.00	Sequence
DRB5_0101	46	KEGRYEVRAELPGVD	GRYEVRAEL	0.2712	2659.3	50.00	Sequence
DRB5_0101	48	GRYEVRAELPGVDPD	YEVRAELPG	0.2698	2698.7	50.00	Sequence
DRB5_0101	74	LTIKARTEQKDFDGD	IKARTEQK	0.2690	2723.5	50.00	Sequence
DRB5_0101	119	GILTVSVAVSEGKPT	GILTVSVAV	0.2681	2748.4	50.00	Sequence
DRB5_0101	121	LTVSVAVSEGKPTKE	LTVSVAVSE	0.2616	2948.8	50.00	Sequence
DRB5_0101	117	DGILTVSVAVSEGK	GILTVSVAV	0.2589	3036.5	50.00	Sequence
DRB5_0101	118	KGILTVSVAVSEGKP	GILTVSVAV	0.2581	3062.7	50.00	Sequence
DRB5_0101	122	TVSVAVSEGKPTKEH	VSVAVSEGK	0.2547	3177.1	50.00	Sequence
DRB5_0101	115	TYDKGILTVSVAVSE	GILTVSVAV	0.2544	3189.8	50.00	Sequence
DRB5_0101	120	ILTVSVAVSEGKPT	LTVSVAVSE	0.2540	3200.8	50.00	Sequence
DRB5_0101	116	YDKGILTVSVAVSEG	GILTVSVAV	0.2501	3340.6	50.00	Sequence
DRB5_0101	123	VSVAVSEGKPTKEKHI	VSVAVSEGK	0.2458	3498.6	50.00	Sequence
DRB5_0101	49	RYEVRAELPGVDPDK	YEVRAELPG	0.2415	3667.7	50.00	Sequence
DRB5_0101	63	KDVDIMVRDQQLTIK	IMVRDQQLT	0.2409	3689.2	50.00	Sequence
DRB5_0101	39	MRLEDEMKEGRYEV	MRLEDEMKE	0.2363	3878.3	50.00	Sequence
DRB5_0101	45	MKEGRYEVRAELPGV	GRYEVRAEL	0.2312	4098.1	50.00	Sequence
DRB5_0101	114	ATYDKGILTVSVAVS	GILTVSVAV	0.2311	4103.0	50.00	Sequence
DRB5_0101	75	TIKARTEQKDFDGR	IKARTEQK	0.2304	4131.5	50.00	Sequence
DRB5_0101	62	KDVDIMVRDQQLTI	IMVRDQQLT	0.2298	4158.7	50.00	Sequence
DRB5_0101	124	SVAVSEGKPTKEKHIQ	VAVSEGKPT	0.2297	4164.7	50.00	Sequence
DRB5_0101	50	YEVRAELPGVDPDKD	YEVRAELPG	0.2294	4179.8	50.00	Sequence
DRB5_0101	113	KATYDKGILTVSVAV	GILTVSVAV	0.2283	4230.2	50.00	Sequence
DRB5_0101	111	DIKATYDKGILTVSV	IKATYDKGI	0.2263	4320.6	50.00	Sequence
DRB5_0101	84	KDFDGRSEFAYGSFV	FDGRSEFAY	0.2250	4380.9	50.00	Sequence
DRB5_0101	125	VAVSEGKPTKEKHIQI	VAVSEGKPT	0.2217	4540.9	50.00	Sequence
DRB5_0101	110	DDIKATYDKGILTVS	IKATYDKGI	0.2133	4973.8	50.00	Sequence
DRB5_0101	112	IKATYDKGILTVSV	IKATYDKGI	0.2117	5062.6	50.00	Sequence
DRB5_0101	109	EDDIKATYDKGILTV	IKATYDKGI	0.2077	5284.3	50.00	Sequence
DRB5_0101	129	EGKPTKEKHIQIRST	EKHIQIRST	0.2028	5572.3	50.00	Sequence
DRB5_0101	128	SEGKPTKEKHIQIRST	EKHIQIRST	0.1979	5873.7	50.00	Sequence
DRB5_0101	61	PKDVDIMVRDQQLT	IMVRDQQLT	0.1976	5896.5	50.00	Sequence
DRB5_0101	83	QKDFDGRSEFAYGSF	FDGRSEFAY	0.1957	6020.1	50.00	Sequence
DRB5_0101	44	EMKEGRYEVRAELPG	GRYEVRAEL	0.1942	6118.6	50.00	Sequence
DRB5_0101	40	RLEDEMKEGRYEVRA	LEDEMKEGR	0.1931	6186.1	50.00	Sequence
DRB5_0101	98	VRTVSLPVGADDDI	RTVSLPVGA	0.1891	6463.0	50.00	Sequence
DRB5_0101	126	AVSEGKPTKEKHIQIR	GKPTKEKHIQ	0.1860	6679.4	50.00	Sequence
DRB5_0101	76	IKARTEQKDFDGRS	IKARTEQK	0.1803	7107.4	50.00	Sequence
DRB5_0101	127	VSEGKPTKEKHIQIRS	GKPTKEKHIQ	0.1768	7379.2	50.00	Sequence
DRB5_0101	108	DEDDIKATYDKGILT	IKATYDKGI	0.1713	7832.6	50.00	Sequence
DRB5_0101	82	EQKDFDGRSEFAYGS	FDGRSEFAY	0.1708	7877.1	50.00	Sequence
DRB5_0101	43	DEMKEGRYEVRAELP	GRYEVRAEL	0.1704	7911.7	50.00	Sequence
DRB5_0101	41	LEDEMKEGRYEVRAE	LEDEMKEGR	0.1673	8180.5	50.00	Sequence
DRB5_0101	42	EDEMKEGRYEVRAEL	GRYEVRAEL	0.1577	9074.9	50.00	Sequence
DRB5_0101	51	EVRAELPGVDPDKDV	VRAELPGVD	0.1481	10074.9	50.00	Sequence
DRB5_0101	99	RTVSLPVGADDDIK	RTVSLPVGA	0.1452	10388.5	50.00	Sequence
DRB5_0101	107	ADEDDIKATYDKGIL	IKATYDKGI	0.1387	11145.7	50.00	Sequence
DRB5_0101	81	TEQKDFDGRSEFAYG	FDGRSEFAY	0.1277	12561.1	50.00	Sequence
DRB5_0101	52	VRAELPGVDPDKDVD	VRAELPGVD	0.1229	13231.2	50.00	Sequence
DRB5_0101	106	GADEDDIKATYDKGI	IKATYDKGI	0.1168	14137.0	50.00	Sequence

DRB5_0101	60	DPDKDVDIMVRDGQL	DKDVDIMVR	0.1134	14660.7	50.00	Sequence
DRB5_0101	80	RTEQKDFDGRSEFAY	FDGRSEFAY	0.1041	16214.1	50.00	Sequence
DRB5_0101	77	KAERTEQKDFDGRSE	AERTEQKDF	0.0922	18448.1	50.00	Sequence
DRB5_0101	59	VDPDKDVDIMVRDGG	DKDVDIMVR	0.0878	19331.2	50.00	Sequence
DRB5_0101	79	ERTEQKDFDGRSEFA	ERTEQKDFD	0.0848	19976.8	50.00	Sequence
DRB5_0101	78	AERTEQKDFDGRSEF	AERTEQKDF	0.0842	20105.4	50.00	Sequence
DRB5_0101	56	LPGVDPDKDVDIMVR	DKDVDIMVR	0.0770	21723.7	50.00	Sequence
DRB5_0101	53	RÄELPGVDPDKVDI	LPGVDPDKD	0.0702	23388.3	50.00	Sequence
DRB5_0101	58	GVPDPDKDVDIMVRD	DKDVDIMVR	0.0691	23666.0	50.00	Sequence
DRB5_0101	55	ELPGVDPDKDVDIMV	LPGVDPDKD	0.0609	25875.7	50.00	Sequence
DRB5_0101	57	PGVDPDKDVDIMVRD	DKDVDIMVR	0.0604	26020.8	50.00	Sequence
DRB5_0101	54	AELPGVDPDKDVDIM	LPGVDPDKD	0.0587	26484.4	50.00	Sequence
DRB5_0101	105	VGÄEDDDIKATYDKG	DDIKATYDK	0.0516	28603.2	50.00	Sequence
DRB5_0101	104	PVGÄEDDDIKATYDK	DDIKATYDK	0.0407	32205.1	50.00	Sequence
DRB5_0101	100	TVSLPVGÄEDDDIKA	VSLPVGÄE	0.0373	33412.9	50.00	Sequence
DRB5_0101	103	LPVGÄEDDDIKATYD	DEDDIKATY	0.0340	34603.5	50.00	Sequence
DRB5_0101	101	VSLPVGÄEDDDIKAT	VSLPVGÄE	0.0334	34843.6	50.00	Sequence
DRB5_0101	102	SLPVGÄEDDDIKATY	SLPVGÄED	0.0320	35351.7	50.00	Sequence

Allele: DRB5\_0101. Number of high binders 1. Number of weak binders 28. Number of peptides 130

Allele	pos	peptide	core	l-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
IAb	17	FSELFAAFPSFAGLR	LFAAFPSFA	0.5794	94.7	WB	2.00	Sequence
IAb	18	SELFAAFPSFAGLRP	LFAAFPSFA	0.5775	96.7	WB	2.00	Sequence
IAb	20	LFAAFPSFAGLRPTF	LFAAFPSFA	0.5765	97.7	WB	2.00	Sequence
IAb	19	ELFAAFPSFAGLRPT	LFAAFPSFA	0.5697	105.2	WB	4.00	Sequence
IAb	16	EFSELFAAFPSFAGL	LFAAFPSFA	0.5640	111.9	WB	4.00	Sequence
IAb	24	FPSFAGLRPTFDTRL	FAGLRPTFD	0.5575	120.0	WB	4.00	Sequence
IAb	15	PEFSELFAAFPSFAG	LFAAFPSFA	0.5547	123.7	WB	4.00	Sequence
IAb	23	AFPSFAGLRPTFDTR	PSFAGLRPT	0.5435	139.6	WB	4.00	Sequence
IAb	22	AAFPSFAGLRPTFDT	PSFAGLRPT	0.5307	160.4	WB	4.00	Sequence
IAb	21	FAAFPSFAGLRPTFD	PSFAGLRPT	0.5221	176.1	WB	4.00	Sequence
IAb	25	PSFAGLRPTFDTRLM	FAGLRPTFD	0.5164	187.2	WB	4.00	Sequence
IAb	14	FPEFSELFAAFPSFA	LFAAFPSFA	0.5053	211.1	WB	8.00	Sequence
IAb	91	EFAYGSFVRTVSLPV	FAYGSFVRT	0.4591	348.0	WB	8.00	Sequence
IAb	90	SEFAYGSFVRTVSLP	FAYGSFVRT	0.4570	356.1	WB	8.00	Sequence
IAb	89	RSEFAYGSFVRTVSL	FAYGSFVRT	0.4486	390.1	WB	8.00	Sequence
IAb	92	FAYGSFVRTVSLPVG	FAYGSFVRT	0.4127	574.9		16.00	Sequence
IAb	88	GRSEFAYGSFVRTVS	FAYGSFVRT	0.4080	604.9		16.00	Sequence
IAb	26	SFAGLRPTFDTRLMR	FAGLRPTFD	0.3873	756.6		16.00	Sequence
IAb	13	LFPEFSELFAAFPSF	FSELFAAFP	0.3841	783.7		16.00	Sequence
IAb	94	YGSFVRTVSLPVGAD	FVRTVSLPV	0.3741	873.2		16.00	Sequence
IAb	93	AYGSFVRTVSLPVG	FVRTVSLPV	0.3712	900.8		16.00	Sequence
IAb	87	DGRSEFAYGSFVRTV	FAYGSFVRT	0.3617	998.1		16.00	Sequence
IAb	27	FAGLRPTFDTRLMRL	FAGLRPTFD	0.3617	998.3		16.00	Sequence
IAb	95	GSFVRTVSLPVGÄE	FVRTVSLPV	0.3466	1175.9		16.00	Sequence
IAb	12	SLFPEFSELFAAFPS	SELFAAFPS	0.3425	1228.7		32.00	Sequence
IAb	96	SVFVRTVSLPVGÄED	FVRTVSLPV	0.3226	1525.0		32.00	Sequence
IAb	97	FVRTVSLPVGÄEDDD	FVRTVSLPV	0.3216	1541.5		32.00	Sequence
IAb	86	FDGRSEFAYGSFVRT	FAYGSFVRT	0.3206	1558.1		32.00	Sequence
IAb	98	VRTVSLPVGÄEDDDI	RTVSLPVG	0.2817	2374.1		32.00	Sequence
IAb	11	RSLFPEFSELFAAFP	PEFSELFAA	0.2777	2476.9		32.00	Sequence
IAb	4	LPVQRHPRSLFPEFS	PVQRHPRSL	0.2572	3093.3		32.00	Sequence
IAb	49	RYEVRAELPGVDPDK	YEVRAELPG	0.2490	3381.0		32.00	Sequence
IAb	50	YEVRAELPGVDPDK	YEVRAELPG	0.2468	3462.7		32.00	Sequence
IAb	48	GRYEVRAELPGVDPD	YEVRAELPG	0.2401	3723.8		50.00	Sequence
IAb	123	VSVAVSEGKPTTEKHI	VAVSEGKPT	0.2385	3787.6		50.00	Sequence
IAb	5	PVQRHPRSLFPEFSE	PVQRHPRSL	0.2385	3787.6		50.00	Sequence
IAb	113	KATYDKGILTVSVAV	ATYDKGILT	0.2365	3870.2		50.00	Sequence
IAb	124	SVAVSEGKPTTEKHIQ	VAVSEGKPT	0.2359	3896.1		50.00	Sequence
IAb	125	VAVSEGKPTTEKHIQI	VAVSEGKPT	0.2343	3964.2		50.00	Sequence
IAb	3	TLPVQRHPRSLFPEF	PVQRHPRSL	0.2334	4002.3		50.00	Sequence
IAb	47	EGRYEVRAELPGVDP	YEVRAELPG	0.2319	4066.2		50.00	Sequence
IAb	99	RTVSLPVGÄEDDDIK	RTVSLPVG	0.2313	4091.8		50.00	Sequence
IAb	114	ATYDKGILTVSVAVS	ATYDKGILT	0.2309	4112.6		50.00	Sequence
IAb	121	LTVSVAVSEGKPTTEK	VAVSEGKPT	0.2260	4333.8		50.00	Sequence
IAb	2	TTLPVQRHPRSLFPE	PVQRHPRSL	0.2259	4340.5		50.00	Sequence
IAb	122	TVSVAVSEGKPTTEKH	VAVSEGKPT	0.2230	4477.5		50.00	Sequence
IAb	10	PRSLFPEFSELFAAFP	PEFSELFAA	0.2215	4550.3		50.00	Sequence
IAb	112	IKATYDKGILTVSVA	ATYDKGILT	0.2208	4586.1		50.00	Sequence
IAb	120	ILTVSVAVSEGKPTTE	VAVSEGKPT	0.2124	5024.9		50.00	Sequence
IAb	1	ATTLPVQRHPRSLF	PVQRHPRSL	0.2101	5149.3		50.00	Sequence
IAb	85	DFDGRSEFAYGSFVR	SEFAYGSFV	0.2094	5187.5		50.00	Sequence

IAb	46	KEGRYEVRAELPGVD	YEVRAELPG	0.2068	5337.9	50.00	Sequence
IAb	111	DIKATYDKGILTVSV	ATYDKGILT	0.2053	5422.9	50.00	Sequence
IAb	119	GILTVSVAVSEGKPT	VAVSEGKPT	0.2027	5577.6	50.00	Sequence
IAb	118	KGILTVSVAVSEGKP	LTVSVAVSE	0.1989	5814.2	50.00	Sequence
IAb	28	AGLRPTFDTRLMRLE	AGLRPTFDT	0.1925	6227.2	50.00	Sequence
IAb	116	YDKGILTVSVAVSEG	YDKGILTVS	0.1919	6266.2	50.00	Sequence
IAb	117	DKGILTVSVAVSEGK	ILTVSVAVS	0.1918	6277.5	50.00	Sequence
IAb	8	RHPRSLFPEFSELF	RHPRSLFPE	0.1897	6419.9	50.00	Sequence
IAb	115	TYDKGILTVSVAVSE	GILTVSVAV	0.1891	6462.1	50.00	Sequence
IAb	9	HPRSLFPEFSELF	PEFSELF	0.1885	6505.6	50.00	Sequence
IAb	7	QRHPRSLFPEFSELF	RHPRSLFPE	0.1865	6647.7	50.00	Sequence
IAb	0	MATTLPVQRHPRSL	PVQRHPRSL	0.1842	6817.2	50.00	Sequence
IAb	110	DDIKATYDKGILTVS	ATYDKGILT	0.1825	6941.2	50.00	Sequence
IAb	6	VQRHPRSLFPEFSEL	RHPRSLFPE	0.1791	7198.1	50.00	Sequence
IAb	51	EVRAELPGVDPDKDV	VRAELPGVD	0.1683	8092.4	50.00	Sequence
IAb	45	MKEGRYEVRAELPGV	YEVRAELPG	0.1644	8441.4	50.00	Sequence
IAb	52	VRAELPGVDPDKD	VRAELPGVD	0.1617	8689.1	50.00	Sequence
IAb	84	KDFDGRSEFAYGSFV	SEFAYGSFV	0.1583	9021.3	50.00	Sequence
IAb	100	TVSLPVGAEDEDDIKA	TVSLPVGAD	0.1435	10583.4	50.00	Sequence
IAb	67	IMVRDQQLTIKAERT	IMVRDQQLT	0.1433	10602.0	50.00	Sequence
IAb	126	AVSEGKPEKHIQIR	AVSEGKPE	0.1319	11995.6	50.00	Sequence
IAb	30	LRPTFDTRLMRLEDE	LRPTFDTRL	0.1275	12578.4	50.00	Sequence
IAb	29	GLRPTFDTRLMRLED	LRPTFDTRL	0.1268	12682.0	50.00	Sequence
IAb	66	DIMVRDQQLTIKAER	IMVRDQQLT	0.1264	12737.1	50.00	Sequence
IAb	44	EMKEGRYEVRAELPG	YEVRAELPG	0.1227	13255.7	50.00	Sequence
IAb	65	VDIMVRDQQLTIKAE	IMVRDQQLT	0.1198	13684.6	50.00	Sequence
IAb	109	EDDIKATYDKGILTV	ATYDKGILT	0.1133	14676.2	50.00	Sequence
IAb	64	DVDIMVRDQQLTIKA	IMVRDQQLT	0.1043	16182.3	50.00	Sequence
IAb	68	MVRDQQLTIKAERTE	MVRDQQLTI	0.0999	16957.0	50.00	Sequence
IAb	101	VSLPVGAEDEDDIKAT	SLPVGAEDE	0.0962	17654.3	50.00	Sequence
IAb	53	RAELPGVDPDKDV	AELPGVDPD	0.0933	18215.4	50.00	Sequence
IAb	127	VSEGKPEKHIQIR	VSEGKPEK	0.0929	18294.2	50.00	Sequence
IAb	31	RPTFDTRLMRLEDEM	RPTFDTRL	0.0911	18662.1	50.00	Sequence
IAb	70	RDGQLTIKAERTEQK	QLTIKAERT	0.0906	18764.1	50.00	Sequence
IAb	71	DGQLTIKAERTEQKD	QLTIKAERT	0.0880	19298.2	50.00	Sequence
IAb	72	GQLTIKAERTEQKDF	QLTIKAERT	0.0874	19417.2	50.00	Sequence
IAb	73	QLTIKAERTEQKDFD	LTIKAEERTE	0.0852	19892.7	50.00	Sequence
IAb	69	VRDQQLTIKAERTEQ	QLTIKAERT	0.0842	20105.6	50.00	Sequence
IAb	83	QKDFDGRSEFAYGSF	FDGRSEFAY	0.0822	20538.5	50.00	Sequence
IAb	108	DEDDIKATYDKGILT	ATYDKGILT	0.0774	21630.3	50.00	Sequence
IAb	63	KVDIMVRDQQLTIK	MVRDQQLTI	0.0755	22089.4	50.00	Sequence
IAb	43	DEMKEGRYEVRAELP	RYEVRAELP	0.0750	22221.7	50.00	Sequence
IAb	102	SLPVGAEDEDDIKATY	SLPVGAEDE	0.0734	22589.2	50.00	Sequence
IAb	82	EQKDFDGRSEFAYGS	FDGRSEFAY	0.0698	23487.5	50.00	Sequence
IAb	54	AELPGVDPDKDV	AELPGVDPD	0.0686	23812.7	50.00	Sequence
IAb	128	SEGKPEKHIQIRST	SEGKPEKH	0.0665	24348.6	50.00	Sequence
IAb	74	LTIKAEERTEQKDFD	LTIKAEERTE	0.0652	24701.8	50.00	Sequence
IAb	81	TEQKDFDGRSEFAYG	FDGRSEFAY	0.0598	26181.5	50.00	Sequence
IAb	80	RTEQKDFDGRSEFAY	FDGRSEFAY	0.0580	26693.0	50.00	Sequence
IAb	62	DKDVIDIMVRDQQLTI	MVRDQQLTI	0.0580	26704.0	50.00	Sequence
IAb	55	ELPGVDPDKDV	LPGVDPDKD	0.0564	27149.4	50.00	Sequence
IAb	32	PTFDTRLMRLEDEM	FDTRLMRLE	0.0555	27435.8	50.00	Sequence
IAb	129	EKGKPEKHIQIRSTN	EKHIQIRST	0.0540	27889.6	50.00	Sequence
IAb	42	EDEMKEGRYEVRAEL	EGRYEVRAE	0.0494	29303.9	50.00	Sequence
IAb	56	LPGVDPDKDV	LPGVDPDKD	0.0469	30100.5	50.00	Sequence
IAb	107	ADEDDIKATYDKGIL	IKATYDKGI	0.0468	30124.0	50.00	Sequence
IAb	34	FDTRLMRLEDEMKEG	FDTRLMRLE	0.0394	32630.9	50.00	Sequence
IAb	33	TFDTRLMRLEDEMKE	FDTRLMRLE	0.0388	32874.7	50.00	Sequence
IAb	79	ERTEQKDFDGRSEFA	QKDFDGRSE	0.0338	34691.3	50.00	Sequence
IAb	36	TRLMRLEDEMKEGRY	TRLMRLEDE	0.0330	34994.0	50.00	Sequence
IAb	35	DTRLMRLEDEMKEGR	TRLMRLEDE	0.0320	35365.1	50.00	Sequence
IAb	75	TIKAERTEQKDFDGR	IKAEERTEQK	0.0314	35607.4	50.00	Sequence
IAb	61	PKDVIDIMVRDQQLTI	IMVRDQQLT	0.0305	35962.8	50.00	Sequence
IAb	106	GADEDDIKATYDKGI	IKATYDKGI	0.0286	36694.3	50.00	Sequence
IAb	41	LEDEMKEGRYEVRAE	EGRYEVRAE	0.0278	37019.3	50.00	Sequence
IAb	76	IKAEERTEQKDFDGRS	IKAEERTEQK	0.0275	37151.7	50.00	Sequence
IAb	37	RLMRLEDEMKEGRYE	LMRLEDEM	0.0257	37873.3	50.00	Sequence
IAb	38	LMRLEDEMKEGRYEV	MRLEDEMKE	0.0249	38200.1	50.00	Sequence
IAb	103	LPVGAEDEDDIKATYD	LPVGAEDEDD	0.0229	39019.3	50.00	Sequence
IAb	78	AERTEQKDFDGRSEF	KDFDGRSEF	0.0187	40859.8	50.00	Sequence
IAb	77	KAERTEQKDFDGRSE	QKDFDGRSE	0.0180	41140.2	50.00	Sequence
IAb	105	VGADEDDIKATYDKG	ADEDDIKAT	0.0162	41942.9	50.00	Sequence
IAb	39	MRLEDEMKEGRYEV	MRLEDEMKE	0.0161	41987.0	50.00	Sequence
IAb	40	RLEDEMKEGRYEVRA	KEGRYEVRA	0.0150	42506.2	50.00	Sequence
IAb	57	PGVDPDKDV	PGVDPDKDV	0.0146	42681.8	50.00	Sequence
IAb	104	PVGAEDEDDIKATYDK	ADEDDIKAT	0.0133	43309.8	50.00	Sequence
IAb	59	VDPDKDV	VDPDKDV	0.0129	43468.5	50.00	Sequence

IAb	60	DPDKDVIDIMVRDGQL	DIMVRDGQL	0.0121	43871.1	50.00	Sequence
IAb	58	GVDPKDQVDIMVRDG	VDPDKDVIDI	0.0109	44443.4	50.00	Sequence

Allele: IAb. Number of high binders 0. Number of weak binders 15. Number of peptides 130

Allele	pos	peptide	core	l-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
IAd	94	YGSFVRTVSLPVGAD	FVRTVSLPV	0.2736	2589.8	16.00	16.00	Sequence
IAd	96	SFVRTVSLPVGAD	FVRTVSLPV	0.2719	2639.4	16.00	16.00	Sequence
IAd	95	GSFVRTVSLPVGAD	VRTVSLPVG	0.2696	2704.7	16.00	16.00	Sequence
IAd	92	FAYGSFVRTVSLPVG	VRTVSLPVG	0.2670	2783.3	16.00	16.00	Sequence
IAd	93	AYGSFVRTVSLPVG	VRTVSLPVG	0.2644	2861.4	16.00	16.00	Sequence
IAd	47	EGRYEVRAELPGVDP	YEVRAELPG	0.2536	3217.3	16.00	16.00	Sequence
IAd	87	DGRSEFAYGSFVRTV	GRSEFAYGS	0.2455	3509.3	16.00	16.00	Sequence
IAd	46	KEGRYEVRAELPGVD	YEVRAELPG	0.2445	3547.4	16.00	16.00	Sequence
IAd	68	MVRDQQLTIKAERTE	RDGQLTIKA	0.2414	3670.2	32.00	32.00	Sequence
IAd	45	MKEGRYEVRAELPGV	YEVRAELPG	0.2408	3695.4	32.00	32.00	Sequence
IAd	86	FDGRSEFAYGSFVRT	GRSEFAYGS	0.2407	3698.2	32.00	32.00	Sequence
IAd	70	RDGQLTIKAERTEQK	RDGQLTIKA	0.2401	3720.1	32.00	32.00	Sequence
IAd	67	IMVRDQQLTIKAERT	RDGQLTIKA	0.2395	3745.1	32.00	32.00	Sequence
IAd	69	VRDQQLTIKAERTEQ	RDGQLTIKA	0.2377	3818.5	32.00	32.00	Sequence
IAd	97	FVRTVSLPVGAD	FVRTVSLPV	0.2369	3851.3	32.00	32.00	Sequence
IAd	116	YDKGILTVSVAVSEG	KGILTVSVA	0.2344	3959.0	32.00	32.00	Sequence
IAd	88	GRSEFAYGSFVRTVS	GRSEFAYGS	0.2323	4048.5	32.00	32.00	Sequence
IAd	114	ATYDKGILTVSVAVS	KGILTVSVA	0.2318	4073.1	32.00	32.00	Sequence
IAd	0	MATTLPVQRHPRSLF	ATTLPVQRH	0.2303	4139.0	32.00	32.00	Sequence
IAd	48	GRYEVRAELPGVDPD	EVRAELPGV	0.2278	4251.2	32.00	32.00	Sequence
IAd	112	IKATYDKGILTVSVA	KGILTVSVA	0.2243	4416.6	32.00	32.00	Sequence
IAd	115	TYDKGILTVSVAVSE	KGILTVSVA	0.2214	4556.8	32.00	32.00	Sequence
IAd	9	HPRSLFPEFSELFAA	PEFSELFAA	0.2158	4838.9	32.00	32.00	Sequence
IAd	117	DKGILTVSVAVSEGK	KGILTVSVA	0.2158	4842.0	32.00	32.00	Sequence
IAd	49	RYEVRAELPGVDPDK	YEVRAELPG	0.2156	4851.0	32.00	32.00	Sequence
IAd	19	ELFAAFPSFAGLRPT	PSFAGLRPT	0.2155	4859.1	32.00	32.00	Sequence
IAd	14	FPEFSELFAAFPSFA	PEFSELFAA	0.2148	4896.0	32.00	32.00	Sequence
IAd	113	KATYDKGILTVSVAV	KGILTVSVA	0.2088	5223.8	32.00	32.00	Sequence
IAd	66	DIMVRDQQLTIKAER	RDGQLTIKA	0.2079	5270.3	32.00	32.00	Sequence
IAd	13	LFPEFSELFAAFPSF	SELFAAFPS	0.2061	5378.3	32.00	32.00	Sequence
IAd	18	SELFAAFPSFAGLRP	SELFAAFPS	0.2026	5584.2	32.00	32.00	Sequence
IAd	50	YEVRAELPGVDPDKD	EVRAELPGV	0.2026	5586.8	32.00	32.00	Sequence
IAd	110	DDIKATYDKGILTVS	ATYDKGILT	0.2021	5615.6	32.00	32.00	Sequence
IAd	118	KGILTVSVAVSEGKP	KGILTVSVA	0.2001	5737.7	32.00	32.00	Sequence
IAd	20	LFAAFPSFAGLRPTF	PSFAGLRPT	0.1996	5771.5	32.00	32.00	Sequence
IAd	71	DGQLTIKAERTEQKD	QLTIKAERT	0.1995	5776.1	32.00	32.00	Sequence
IAd	111	DIKATYDKGILTVSV	ATYDKGILT	0.1984	5845.6	32.00	32.00	Sequence
IAd	12	SLFPEFSELFAAFPS	SELFAAFPS	0.1954	6037.2	32.00	32.00	Sequence
IAd	34	FDTRLMRLEDEMKEG	MRLEDEMKE	0.1948	6075.0	32.00	32.00	Sequence
IAd	15	PEFSELFAAFPSFAG	PEFSELFAA	0.1941	6124.7	32.00	32.00	Sequence
IAd	21	FAAFPSFAGLRPTFD	PSFAGLRPT	0.1937	6149.0	32.00	32.00	Sequence
IAd	128	SEGKPTKHIQIRST	EKHIQIRST	0.1918	6274.9	32.00	32.00	Sequence
IAd	89	RSEFAYGSFVRTVSL	FAYGSFVRT	0.1916	6287.3	32.00	32.00	Sequence
IAd	33	TFDTRLMRLEDEMKE	MRLEDEMKE	0.1914	6303.6	32.00	32.00	Sequence
IAd	35	DTRLMRLEDEMKEGR	MRLEDEMKE	0.1875	6573.3	32.00	32.00	Sequence
IAd	36	TRLMRLEDEMKEGRY	MRLEDEMKE	0.1870	6609.4	32.00	32.00	Sequence
IAd	65	VDIMVRDQQLTIKAE	RDGQLTIKA	0.1833	6881.6	32.00	32.00	Sequence
IAd	91	EFAYGSFVRTVSLPV	FAYGSFVRT	0.1802	7118.9	32.00	32.00	Sequence
IAd	22	AAFPSFAGLRPTFDT	PSFAGLRPT	0.1800	7129.3	32.00	32.00	Sequence
IAd	51	EVRAELPGVDPDKDV	EVRAELPGV	0.1735	7651.7	50.00	50.00	Sequence
IAd	85	DFDGRSEFAYGSFVR	GRSEFAYGS	0.1715	7816.2	50.00	50.00	Sequence
IAd	10	PRSLFPEFSELFAAF	PEFSELFAA	0.1714	7823.7	50.00	50.00	Sequence
IAd	39	MRLEDEMKEGRYEV	MRLEDEMKE	0.1706	7897.6	50.00	50.00	Sequence
IAd	37	RLMRLEDEMKEGRY	MRLEDEMKE	0.1693	8009.9	50.00	50.00	Sequence
IAd	64	DVDIMVRDQQLTIKA	RDGQLTIKA	0.1684	8086.3	50.00	50.00	Sequence
IAd	129	EKGKPTKHIQIRSTN	EKHIQIRST	0.1672	8190.1	50.00	50.00	Sequence
IAd	11	RSLFPEFSELFAAFP	PEFSELFAA	0.1665	8255.9	50.00	50.00	Sequence
IAd	83	QKDFDGRSEFAYGSF	GRSEFAYGS	0.1656	8336.7	50.00	50.00	Sequence
IAd	84	KDFDGRSEFAYGSFV	GRSEFAYGS	0.1652	8367.5	50.00	50.00	Sequence
IAd	44	EMKEGRYEVRAELPG	YEVRAELPG	0.1612	8738.9	50.00	50.00	Sequence
IAd	8	RHPRSLFPEFSELFA	RHPRSLFPE	0.1610	8757.7	50.00	50.00	Sequence
IAd	38	LMRLEDEMKEGRYEV	MRLEDEMKE	0.1605	8806.6	50.00	50.00	Sequence
IAd	98	VRTVSLPVGAD	RTVSLPVG	0.1601	8840.1	50.00	50.00	Sequence
IAd	109	EDDIKATYDKGILTV	KATYDKGIL	0.1574	9107.5	50.00	50.00	Sequence
IAd	72	GQLTIKAERTEQKDF	QLTIKAERT	0.1517	9684.7	50.00	50.00	Sequence
IAd	23	AFPSFAGLRPTFDTR	PSFAGLRPT	0.1458	10321.2	50.00	50.00	Sequence
IAd	17	FSELFAAFPSFAGLR	SELFAAFPS	0.1457	10335.1	50.00	50.00	Sequence

IAd	59	VDPDKDVDIMVRDGO	DKDVDIMVR	0.1419	10770.3	50.00	Sequence
IAd	58	GVDPDKDVDIMVRDG	DKDVDIMVR	0.1399	11008.4	50.00	Sequence
IAd	108	DEDDIKATYDKGILT	ATYDKGILT	0.1385	11175.8	50.00	Sequence
IAd	16	EFSELFAAFPSFAGL	SELFAAFPS	0.1364	11434.5	50.00	Sequence
IAd	57	PGVDPDKDVDIMVRD	DKDVDIMVR	0.1360	11483.3	50.00	Sequence
IAd	61	PKDVDIMVRDQQLT	DKDVDIMVR	0.1351	11592.9	50.00	Sequence
IAd	60	DPDKDVDIMVRDGO	DKDVDIMVR	0.1345	11670.6	50.00	Sequence
IAd	90	SEFAYGSFVRTVSLP	FAYGSFVRT	0.1331	11841.6	50.00	Sequence
IAd	24	FPSFAGLRPTFDTRL	PSFAGLRPT	0.1330	11857.8	50.00	Sequence
IAd	119	GILTVSVAVSEGKPT	ILTVSVAVS	0.1244	13007.7	50.00	Sequence
IAd	62	DKDVDIMVRDQQLTI	DKDVDIMVR	0.1232	13182.2	50.00	Sequence
IAd	56	LPGVDPDKDVDIMVR	DKDVDIMVR	0.1224	13292.0	50.00	Sequence
IAd	7	QRHPRSLFPEFSELF	PRSLFPEFS	0.1165	14169.3	50.00	Sequence
IAd	73	QLTIKAERTEQKDFD	QLTIKAERT	0.1161	14234.6	50.00	Sequence
IAd	107	ADEDDIKATYDKGIL	ADEDDIKAT	0.1157	14298.6	50.00	Sequence
IAd	5	PVQRHPRSLFPEFSE	RHPRSLFPE	0.1156	14320.8	50.00	Sequence
IAd	6	VQRHPRSLFPEFSEL	PRSLFPEFS	0.1133	14674.2	50.00	Sequence
IAd	4	LPVQRHPRSLFPEFS	RHPRSLFPE	0.1124	14810.9	50.00	Sequence
IAd	25	PSFAGLRPTFDTRLM	PSFAGLRPT	0.1107	15098.0	50.00	Sequence
IAd	1	ATTLPVQRHPRSLFP	ATTLPVQRH	0.1081	15519.7	50.00	Sequence
IAd	106	GADEDDIKATYDKGI	ADEDDIKAT	0.1060	15882.9	50.00	Sequence
IAd	40	RLEDEMKEGRYEVRA	MKEGRYEV	0.1050	16045.7	50.00	Sequence
IAd	42	EDEMKEGRYEVRAEL	MKEGRYEV	0.1046	16114.9	50.00	Sequence
IAd	43	DEMKEGRYEVRAELP	MKEGRYEV	0.1027	16458.5	50.00	Sequence
IAd	3	TLPVQRHPRSLFPEF	RHPRSLFPE	0.1017	16638.1	50.00	Sequence
IAd	120	ILTVSVAVSEGKPT	ILTVSVAVS	0.1006	16838.2	50.00	Sequence
IAd	52	VRAELPGVDPDKDVD	RAELPGVDP	0.0993	17070.8	50.00	Sequence
IAd	99	RTVSLPVGAEDEDDIK	RTVSLPVGA	0.0985	17232.6	50.00	Sequence
IAd	41	LEDEMKEGRYEVRAE	MKEGRYEV	0.0952	17847.3	50.00	Sequence
IAd	53	RAELPGVDPDKDVDI	RAELPGVDP	0.0931	18262.8	50.00	Sequence
IAd	30	LRPTFDTRLMRLEDE	RPTFDTRLM	0.0922	18428.7	50.00	Sequence
IAd	122	TVSVAVSEGKPTKEH	TVSVAVSEG	0.0918	18509.6	50.00	Sequence
IAd	31	RPTFDTRLMRLEDEM	PTFDTRLMR	0.0914	18600.0	50.00	Sequence
IAd	101	VSLPVGAEDEDDIKAT	ADEDDIKAT	0.0895	18986.1	50.00	Sequence
IAd	76	IKAERTEQKDFDGRS	IKAERTEQK	0.0870	19503.1	50.00	Sequence
IAd	121	LTVSVAVSEGKPTKEK	TVSVAVSEG	0.0868	19539.4	50.00	Sequence
IAd	27	FAGLRPTFDTRLMR	PTFDTRLMR	0.0856	19796.5	50.00	Sequence
IAd	82	EQKDFDGRSEFAYGS	GRSEFAYGS	0.0850	19939.9	50.00	Sequence
IAd	105	VGADEDDIKATYDKG	ADEDDIKAT	0.0847	19986.5	50.00	Sequence
IAd	125	VAVSEGKPTKHIQI	VAVSEGKPT	0.0846	20014.9	50.00	Sequence
IAd	127	VSEGKPTKHIQIRS	TEKHIQIRS	0.0843	20088.0	50.00	Sequence
IAd	63	KDVDIMVRDQQLTIK	IMVRDQQLT	0.0836	20238.1	50.00	Sequence
IAd	100	TVSLPVGAEDEDDIKA	GADEDDIKA	0.0834	20287.2	50.00	Sequence
IAd	28	AGLRPTFDTRLMRLE	PTFDTRLMR	0.0832	20313.7	50.00	Sequence
IAd	75	TIKAERTEQKDFDGR	IKAERTEQK	0.0821	20576.1	50.00	Sequence
IAd	32	PTFDTRLMRLEDEM	TFDTRLMR	0.0820	20600.2	50.00	Sequence
IAd	102	SLPVGAEDEDDIKATY	ADEDDIKAT	0.0794	21188.8	50.00	Sequence
IAd	29	GLRPTFDTRLMRLED	PTFDTRLMR	0.0785	21386.2	50.00	Sequence
IAd	104	PVGAEDEDDIKATYDK	ADEDDIKAT	0.0774	21643.7	50.00	Sequence
IAd	103	LPVGAEDEDDIKATYD	ADEDDIKAT	0.0762	21934.6	50.00	Sequence
IAd	55	ALPGVDPDKDVDIMV	PKDVDIMV	0.0758	22023.3	50.00	Sequence
IAd	78	ERTEQKDFDGRSEF	TEQKDFDGR	0.0747	22286.7	50.00	Sequence
IAd	26	SFAGLRPTFDTRLMR	RPTFDTRLM	0.0746	22299.5	50.00	Sequence
IAd	123	VSVAVSEGKPTKHI	VAVSEGKPT	0.0739	22467.1	50.00	Sequence
IAd	124	SVAVSEGKPTKHIQ	VAVSEGKPT	0.0736	22541.1	50.00	Sequence
IAd	74	LTIKAERTEQKDFDGR	IKAERTEQK	0.0703	23376.4	50.00	Sequence
IAd	54	AELPGVDPDKDVDIM	AELPGVDP	0.0690	23709.9	50.00	Sequence
IAd	126	AVSEGKPTKHIQIR	KPTKHIQI	0.0682	23897.1	50.00	Sequence
IAd	77	KAERTEQKDFDGRSE	TEQKDFDGR	0.0655	24620.7	50.00	Sequence
IAd	80	RTEQKDFDGRSEFAY	TEQKDFDGR	0.0566	27099.2	50.00	Sequence
IAd	2	TTLPVQRHPRSLFPE	RHPRSLFPE	0.0543	27778.1	50.00	Sequence
IAd	81	TEQKDFDGRSEFAYG	TEQKDFDGR	0.0511	28763.3	50.00	Sequence
IAd	79	ERTEQKDFDGRSEFA	TEQKDFDGR	0.0507	28878.0	50.00	Sequence

Allele: IAd. Number of high binders 0. Number of weak binders 0. Number of peptides 130

Allele	pos	peptide	core	1-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
IAs	93	AYGSFVRTVSLPVGA	RTVSLPVGA	0.2356	3908.0	8.00	8.00	Sequence
IAs	90	SEFAYGSFVRTVSLP	SFVRTVSLP	0.2163	4815.7	8.00	8.00	Sequence
IAs	91	EFAYGSFVRTVSLPV	SFVRTVSLP	0.2045	5468.9	16.00	16.00	Sequence
IAs	92	FAYGSFVRTVSLPVG	SFVRTVSLP	0.2038	5510.8	16.00	16.00	Sequence
IAs	95	GSFVRTVSLPVGADE	SFVRTVSLP	0.2017	5638.4	16.00	16.00	Sequence
IAs	94	YGSFVRTVSLPVGAD	SFVRTVSLP	0.2013	5660.5	16.00	16.00	Sequence

IAs	48	GRYEVRAELPGVDPD	RYEVRAELP	0.1917	6280.2	16.00	Sequence
IAs	49	RYEVRAELPGVDPDK	RYEVRAELP	0.1906	6360.9	16.00	Sequence
IAs	46	KEGRYEVRAELPGVD	VRAELPGVD	0.1902	6382.8	16.00	Sequence
IAs	96	SFVRTVSLPVGADED	SFVRTVSLP	0.1896	6428.1	16.00	Sequence
IAs	47	EGRYEVRAELPGVDP	VRAELPGVD	0.1859	6690.7	16.00	Sequence
IAs	31	RPTFDTRLMLRLEDEM	RLMRLEDEM	0.1817	6999.4	16.00	Sequence
IAs	32	PTFDTRLMLRLEDEM	RLMRLEDEM	0.1679	8131.8	16.00	Sequence
IAs	112	IKATYDKGILLTVSVA	KGILLTVSVA	0.1665	8254.9	16.00	Sequence
IAs	119	GILLTVSVAVSEGKPT	VAVSEGKPT	0.1594	8910.8	32.00	Sequence
IAs	33	TFDTRLMLRLEDEMKE	RLMRLEDEM	0.1581	9037.1	32.00	Sequence
IAs	118	KGILLTVSVAVSEGKP	KGILLTVSVA	0.1571	9131.9	32.00	Sequence
IAs	51	EVRAELPGVDPDKDV	VRAELPGVD	0.1556	9281.1	32.00	Sequence
IAs	50	YEVRAELPGVDPDKD	VRAELPGVD	0.1541	9436.4	32.00	Sequence
IAs	113	KATYDKGILLTVSVAV	KGILLTVSVA	0.1538	9463.7	32.00	Sequence
IAs	34	FDTRLMLRLEDEMKEG	RLMRLEDEM	0.1517	9684.4	32.00	Sequence
IAs	45	MKEGRYEVRAELPGV	RYEVRAELP	0.1517	9689.2	32.00	Sequence
IAs	122	TVSVAVSEGKPKTEKH	VAVSEGKPT	0.1502	9839.2	32.00	Sequence
IAs	120	ILTVSVAVSEGKPT	VAVSEGKPT	0.1498	9887.8	32.00	Sequence
IAs	2	TTLPVQRHPRSLFPE	TTLPVQRHP	0.1487	10008.8	32.00	Sequence
IAs	124	SVAVSEGKPKTEKHIQ	SVAVSEGKP	0.1434	10600.3	32.00	Sequence
IAs	43	DEMKEGRYEVRAELP	RYEVRAELP	0.1432	10617.4	32.00	Sequence
IAs	121	LTVSVAVSEGKPKTEK	VAVSEGKPT	0.1427	10679.9	32.00	Sequence
IAs	114	ATYDKGILLTVSVAVS	KGILLTVSVA	0.1409	10885.9	32.00	Sequence
IAs	123	VSVAVSEGKPKTEKHI	SVAVSEGKP	0.1389	11122.8	32.00	Sequence
IAs	44	EMKEGRYEVRAELPG	RYEVRAELP	0.1381	11224.8	32.00	Sequence
IAs	116	YDKGILLTVSVAVSEG	KGILLTVSVA	0.1368	11374.4	32.00	Sequence
IAs	129	EGKPKTEKHIQIRSTN	KHIQIRSTN	0.1359	11492.3	32.00	Sequence
IAs	125	VAVSEGKPKTEKHIQI	VAVSEGKPT	0.1350	11605.9	32.00	Sequence
IAs	36	TRLMRLEDEMKEGRY	RLMRLEDEM	0.1342	11704.8	32.00	Sequence
IAs	52	VRAELPGVDPDKD	VRAELPGVD	0.1328	11885.4	32.00	Sequence
IAs	115	TYDKGILLTVSVAVSE	KGILLTVSVA	0.1321	11977.4	32.00	Sequence
IAs	98	VRTVSLPVGADED	RTVSLPVGA	0.1314	12064.6	32.00	Sequence
IAs	35	DTRLMLRLEDEMKEGR	RLMRLEDEM	0.1309	12131.6	32.00	Sequence
IAs	99	RTVSLPVGADED	RTVSLPVGA	0.1297	12291.3	32.00	Sequence
IAs	117	DKGILLTVSVAVSEGK	KGILLTVSVA	0.1254	12872.4	32.00	Sequence
IAs	97	FVRTVSLPVGADED	RTVSLPVGA	0.1229	13226.3	32.00	Sequence
IAs	17	FSELFAAFPSFAGLR	ELFAAFPSF	0.1168	14124.0	32.00	Sequence
IAs	0	MATTLPVQRHPRSLF	TTLPVQRHP	0.1158	14281.5	32.00	Sequence
IAs	1	ATTLPVQRHPRSLFP	TTLPVQRHP	0.1134	14663.5	32.00	Sequence
IAs	3	TLPVQRHPRSLFPEF	LPVQRHPRS	0.1123	14832.8	32.00	Sequence
IAs	16	EFSELFAAFPSFAGL	FSELFAAFP	0.1088	15406.3	50.00	Sequence
IAs	14	FPEFSELFAAFPSFA	SELFAAFPS	0.1057	15935.4	50.00	Sequence
IAs	126	AVSEGKPKTEKHIQIR	KPKTEKHIQI	0.1028	16434.8	50.00	Sequence
IAs	15	PEFSELFAAFPSFAG	SELFAAFPS	0.0995	17037.8	50.00	Sequence
IAs	37	RLMRLEDEMKEGRYE	RLMRLEDEM	0.0987	17177.2	50.00	Sequence
IAs	4	LPVQRHPRSLFPEFS	LPVQRHPRS	0.0935	18187.8	50.00	Sequence
IAs	18	SELFAAFPSFAGLRP	LFAAFPSFA	0.0934	18204.0	50.00	Sequence
IAs	89	RSEFAYGSFVRTVSL	AYGSFVRTV	0.0934	18204.6	50.00	Sequence
IAs	7	QRHPRSLFPEFSELF	SLFPEFSEL	0.0906	18766.5	50.00	Sequence
IAs	100	TVSLPVGADED	VGADED	0.0905	18772.0	50.00	Sequence
IAs	13	LFPEFSELFAAFPSF	SELFAAFPS	0.0895	18983.0	50.00	Sequence
IAs	70	RDGQLTIKAERTEQK	LTIKAERTE	0.0892	19039.0	50.00	Sequence
IAs	54	AELPGVDPDKD	AELPGVDPD	0.0890	19096.7	50.00	Sequence
IAs	19	ELFAAFPSFAGLRPT	PSFAGLRPT	0.0887	19142.2	50.00	Sequence
IAs	30	LRPTFDTRLMLRLEDE	FDTRLMLRLE	0.0881	19283.2	50.00	Sequence
IAs	53	RAELPGVDPDKD	AELPGVDPD	0.0865	19613.6	50.00	Sequence
IAs	127	VSEGKPKTEKHIQIRS	KPKTEKHIQI	0.0865	19616.9	50.00	Sequence
IAs	69	VRDGQLTIKAERTEQ	LTIKAERTE	0.0861	19692.7	50.00	Sequence
IAs	25	PSFAGLRPTFDTRLM	RPTFDTRLM	0.0852	19895.0	50.00	Sequence
IAs	20	LFAAFPSFAGLRPTF	LFAAFPSFA	0.0847	19990.4	50.00	Sequence
IAs	68	MVRDGQLTIKAERTE	LTIKAERTE	0.0841	20124.5	50.00	Sequence
IAs	128	SEGKPKTEKHIQIRST	KPKTEKHIQI	0.0832	20323.9	50.00	Sequence
IAs	71	DGQLTIKAERTEQKD	LTIKAERTE	0.0828	20414.7	50.00	Sequence
IAs	101	VSLPVGADED	VGADED	0.0820	20581.4	50.00	Sequence
IAs	22	AAFPSFAGLRPTFD	AAFPSFAGL	0.0816	20670.9	50.00	Sequence
IAs	57	PGVDPDKD	KD	0.0776	21603.0	50.00	Sequence
IAs	21	FAAFPSFAGLRPTFD	PSFAGLRPT	0.0775	21610.9	50.00	Sequence
IAs	6	VQRHPRSLFPEFSEL	RHPRSLFPE	0.0768	21770.0	50.00	Sequence
IAs	8	RHPRSLFPEFSELFA	RHPRSLFPE	0.0761	21936.9	50.00	Sequence
IAs	102	SLPVGADED	VGADED	0.0761	21948.8	50.00	Sequence
IAs	104	PVGADED	VGADED	0.0752	22158.1	50.00	Sequence
IAs	12	SLFPEFSELFAAFPS	SELFAAFPS	0.0745	22342.0	50.00	Sequence
IAs	56	LPGVDPDKD	LPGVDPDKD	0.0736	22553.3	50.00	Sequence
IAs	73	QLTIKAERTEQKDFD	IKAERTEQK	0.0719	22969.5	50.00	Sequence
IAs	23	AFPSFAGLRPTFDTR	PSFAGLRPT	0.0717	23007.3	50.00	Sequence
IAs	103	LPVGADED	VGADED	0.0716	23039.7	50.00	Sequence
IAs	72	GQLTIKAERTEQKDF	IKAERTEQK	0.0715	23075.1	50.00	Sequence

IAs	5	PVQRHPRSLFPEFSE	RHPRSLFPE	0.0711	23177.7	50.00	Sequence
IAs	58	GVDPDKVDIMVRDG	KDVDIMVRD	0.0684	23860.4	50.00	Sequence
IAs	74	LTIKAERTEQKDFDG	IKAERTEQK	0.0664	24367.3	50.00	Sequence
IAs	107	ADEDDIKATYDKGIL	KATYDKGIL	0.0658	24541.2	50.00	Sequence
IAs	61	PDKDVIDMVRDQGLT	KDVIDMVRD	0.0657	24565.9	50.00	Sequence
IAs	62	DKDVIDMVRDQGLTI	KDVIDMVRD	0.0648	24792.3	50.00	Sequence
IAs	67	IMVRDQGLTIKAERT	QLTIKAERT	0.0647	24841.4	50.00	Sequence
IAs	111	DIKATYDKGILTVSV	KATYDKGIL	0.0641	24991.9	50.00	Sequence
IAs	55	ELPGVDPDKDVIDIMV	LPGVDPDKD	0.0635	25156.8	50.00	Sequence
IAs	59	VDPDKDVIDMVRDQG	KDVIDMVRD	0.0625	25439.3	50.00	Sequence
IAs	108	DEDDIKATYDKGILT	KATYDKGIL	0.0609	25864.5	50.00	Sequence
IAs	24	FPSFAGLRPTFDTRL	PSFAGLRPT	0.0606	25952.2	50.00	Sequence
IAs	26	SFAGLRPTFDTRLMR	RPTFDTRLM	0.0585	26551.8	50.00	Sequence
IAs	60	DPDKDVIDMVRDQGL	KDVIDMVRD	0.0584	26591.8	50.00	Sequence
IAs	63	KVDIMVRDQGLTIK	KDVIDMVRD	0.0579	26717.5	50.00	Sequence
IAs	109	EDDIKATYDKGILTV	KATYDKGIL	0.0556	27402.3	50.00	Sequence
IAs	27	FAGLRPTFDTRLML	RPTFDTRLM	0.0545	27725.6	50.00	Sequence
IAs	75	TIKAERTEQKDFDGR	IKAERTEQK	0.0544	27766.1	50.00	Sequence
IAs	42	EDEMKEGRYEVRAEL	DEMKEGRYE	0.0537	27974.2	50.00	Sequence
IAs	28	AGLRPTFDTRLMLR	RPTFDTRLM	0.0531	28162.5	50.00	Sequence
IAs	29	GLRPTFDTRLMLRLE	RPTFDTRLM	0.0521	28455.9	50.00	Sequence
IAs	110	DDIKATYDKGILTVS	KATYDKGIL	0.0514	28679.1	50.00	Sequence
IAs	105	VGADEDDIKATYDKG	VGADEDDIK	0.0513	28713.2	50.00	Sequence
IAs	87	DGRSEFAYGSFVRTV	AYGSFVRTV	0.0478	29805.9	50.00	Sequence
IAs	66	DIMVRDQGLTIKAER	IMVRDQGLT	0.0475	29916.8	50.00	Sequence
IAs	76	IKAERTEQKDFDGRS	IKAERTEQK	0.0474	29948.5	50.00	Sequence
IAs	11	RSLFPEFSELFAAFP	FSELFAAFP	0.0447	30834.3	50.00	Sequence
IAs	9	HPRSLFPEFSELFAA	HPRSLFPEF	0.0443	30961.7	50.00	Sequence
IAs	88	GRSEFAYGSFVRTVS	AYGSFVRTV	0.0437	31169.7	50.00	Sequence
IAs	65	VDIMVRDQGLTIKAE	IMVRDQGLT	0.0421	31708.9	50.00	Sequence
IAs	64	DVDIMVRDQGLTIKA	IMVRDQGLT	0.0407	32186.6	50.00	Sequence
IAs	78	AERTEQKDFDGRSEF	KDFDGRSEF	0.0378	33233.7	50.00	Sequence
IAs	10	PRSLFPEFSELFAAF	SLFPEFSEL	0.0366	33660.0	50.00	Sequence
IAs	79	ERTEQKDFDGRSEFA	ERTEQKDFD	0.0348	34299.4	50.00	Sequence
IAs	38	LMRLEDEMKEGRYEV	RLEDEMKEG	0.0338	34677.0	50.00	Sequence
IAs	77	KAERTEQKDFDGRSE	KAERTEQKD	0.0336	34766.0	50.00	Sequence
IAs	39	MRLEDEMKEGRYEV	DEMKEGRYE	0.0327	35090.3	50.00	Sequence
IAs	84	KDFDGRSEFAYGSFV	KDFDGRSEF	0.0311	35724.7	50.00	Sequence
IAs	40	RLEDEMKEGRYEVRA	MKEGRYEV	0.0310	35765.7	50.00	Sequence
IAs	85	DFDGRSEFAYGSFVR	SEFAYGSFV	0.0304	35972.5	50.00	Sequence
IAs	41	LEDEMKEGRYEVRAE	MKEGRYEV	0.0301	36095.0	50.00	Sequence
IAs	86	FDGRSEFAYGSFVRT	SEFAYGSFV	0.0301	36097.7	50.00	Sequence
IAs	83	QKDFDGRSEFAYGSF	KDFDGRSEF	0.0289	36559.1	50.00	Sequence
IAs	80	RTEQKDFDGRSEFAY	KDFDGRSEF	0.0274	37190.7	50.00	Sequence
IAs	81	TEQKDFDGRSEFAYG	KDFDGRSEF	0.0266	37492.5	50.00	Sequence
IAs	82	EQKDFDGRSEFAYGS	KDFDGRSEF	0.0255	37958.2	50.00	Sequence
IAs	106	GADEDDIKATYDKGI	DDIKATYDK	0.0202	40166.8	50.00	Sequence

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 Allele: IAs. Number of high binders 0. Number of weak binders 0. Number of peptides 130  
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