



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	89	TAAFASAAAIAVGLG	FASAAAIAV	0.8899	3.3	SB	0.20	Sequence	
DRB1_0101	88	RTAAFASAAAIAVGL	FASAAAIAV	0.8844	3.5	SB	0.40	Sequence	
DRB1_0101	90	AAFASAAAIAVGLGA	FASAAAIAV	0.8782	3.7	SB	0.80	Sequence	
DRB1_0101	87	WRTAAFASAAAIAVG	FASAAAIAV	0.8708	4.0	SB	1.00	Sequence	
DRB1_0101	91	AFASAAAIAVGLGAF	FASAAAIAV	0.8615	4.5	SB	2.00	Sequence	
DRB1_0101	86	RWRTAAFASAAAIAV	FASAAAIAV	0.8610	4.5	SB	2.00	Sequence	
DRB1_0101	92	FASAAAIAVGLGAFG	FASAAAIAV	0.8360	5.9	SB	4.00	Sequence	
DRB1_0101	195	TATLTDLGASTALAF	LTDLGASTA	0.8130	7.6	SB	8.00	Sequence	
DRB1_0101	85	SRWRTAAFASAAAIA	WRTAAFASA	0.8068	8.1	SB	8.00	Sequence	
DRB1_0101	84	QSRWRTAAFASAAAIA	WRTAAFASA	0.8008	8.6	SB	8.00	Sequence	
DRB1_0101	6	FELLELATPYALNAV	LELATPYAL	0.7999	8.7	SB	8.00	Sequence	
DRB1_0101	5	DFELLELATPYALNA	LELATPYAL	0.7989	8.8	SB	8.00	Sequence	
DRB1_0101	168	YQMWLLGGAKGPRSA	WLLGGAKGP	0.7984	8.9	SB	8.00	Sequence	
DRB1_0101	28	IDRRVAAAAPSPVAAA	RVAAAAPSPV	0.7970	9.0	SB	8.00	Sequence	
DRB1_0101	29	DRRVAAAAPSPVAAAF	VAAAAPSPVA	0.7969	9.0	SB	8.00	Sequence	
DRB1_0101	196	ATLTDLGASTALAF	LTDLGASTA	0.7856	10.2	SB	8.00	Sequence	
DRB1_0101	30	RRVAAAAPSPVAAAFN	VAAAAPSPVA	0.7850	10.2	SB	8.00	Sequence	
DRB1_0101	150	NTGLLMNNAVPPSR	LLVMNNVAP	0.7824	10.5	SB	8.00	Sequence	
DRB1_0101	50	VRETMAVVSAAATTA	TMAVVSAAAT	0.7756	11.3	SB	16.00	Sequence	
DRB1_0101	4	TFELLELATPYALN	LELATPYAL	0.7698	12.1	SB	16.00	Sequence	
DRB1_0101	167	VYQMWLLGGAKGPRS	MWLLGGAKG	0.7692	12.2	SB	16.00	Sequence	
DRB1_0101	51	RETMAVVSAAATTAEP	MAVVSAAAT	0.7651	12.7	SB	16.00	Sequence	
DRB1_0101	49	AVRETMAVVSAAATTA	TMAVVSAAAT	0.7583	13.7	SB	16.00	Sequence	
DRB1_0101	3	HTDFELLELATPYAL	LELATPYAL	0.7577	13.8	SB	16.00	Sequence	
DRB1_0101	7	LELELATPYALNAVS	LELATPYAL	0.7557	14.1	SB	16.00	Sequence	
DRB1_0101	169	QMWLLGGAKGPRSA	WLLGGAKGP	0.7521	14.6	SB	16.00	Sequence	
DRB1_0101	151	TGLLMNNAVPPSRG	LLVMNNVAP	0.7514	14.7	SB	16.00	Sequence	
DRB1_0101	197	TLTDLGASTALAF	LTDLGASTA	0.7450	15.8	SB	16.00	Sequence	
DRB1_0101	194	TATLTDLGASTALAF	LTDLGASTA	0.7420	16.3	SB	16.00	Sequence	
DRB1_0101	130	RTVSRPLGAGTATVV	SRPLGAGTA	0.7419	16.3	SB	16.00	Sequence	
DRB1_0101	83	RQSRWRTAAFASAAA	WRTAAFASA	0.7402	16.6	SB	16.00	Sequence	
DRB1_0101	170	MWLLGGAKGPRSA	LGGAKGPRS	0.7397	16.7	SB	16.00	Sequence	
DRB1_0101	142	TVVFSRDRNTGLLVM	FSRDRNTGL	0.7386	16.9	SB	16.00	Sequence	
DRB1_0101	27	DIDRRVAAAAPSPVAA	RVAAAAPSPV	0.7382	17.0	SB	16.00	Sequence	
DRB1_0101	133	SRPLGAGTATVVFSR	LGAGTATVV	0.7330	18.0	SB	16.00	Sequence	
DRB1_0101	149	RNTGLLMNNAVPPS	LLVMNNVAP	0.7260	19.4	SB	16.00	Sequence	
DRB1_0101	48	RAVRETMAVVSAAAT	TMAVVSAAAT	0.7241	19.8	SB	16.00	Sequence	
DRB1_0101	47	VRAVRETMAVVSAAAT	VRETMAVVS	0.7227	20.1	SB	16.00	Sequence	
DRB1_0101	152	GLLMNNAVPPSRGT	VMNNVAPPS	0.7207	20.5	SB	16.00	Sequence	
DRB1_0101	164	RGTVYQMWLLGGAKG	VYQMWLLGG	0.7185	21.0	SB	16.00	Sequence	
DRB1_0101	8	LLELATPYALNAVSD	LELATPYAL	0.7181	21.1	SB	16.00	Sequence	
DRB1_0101	166	TVYQMWLLGGAKGPR	MWLLGGAKG	0.7132	22.3	SB	16.00	Sequence	
DRB1_0101	132	VSRPLGAGTATVVFS	LGAGTATVV	0.7098	23.1	SB	32.00	Sequence	
DRB1_0101	31	RVAAAAPSPVAAAFND	VAAAAPSPVA	0.7086	23.4	SB	32.00	Sequence	
DRB1_0101	44	NDEVRAVRETMAVVS	VRAVRETMA	0.7038	24.6	SB	32.00	Sequence	
DRB1_0101	143	VVFSRDRNTGLLVM	FSRDRNTGL	0.7027	24.9	SB	32.00	Sequence	
DRB1_0101	95	AAIAVGLGAFGLGV	IAVGLGAFG	0.7002	25.6	SB	32.00	Sequence	
DRB1_0101	131	TVSRPLGAGTATVV	LGAGTATVV	0.6960	26.8	SB	32.00	Sequence	
DRB1_0101	46	EVRAVRETMAVVSAA	VRETMAVVS	0.6847	30.3	SB	32.00	Sequence	
DRB1_0101	198	LTDLGASTALAF	LTDLGASTA	0.6837	30.6	SB	32.00	Sequence	
DRB1_0101	52	ETMAVVSAAATTAEP	MAVVSAAAT	0.6833	30.8	SB	32.00	Sequence	
DRB1_0101	82	RQSRWRTAAFASAAA	WRTAAFASA	0.6815	31.4	SB	32.00	Sequence	
DRB1_0101	134	RPLGAGTATVVFSRD	LGAGTATVV	0.6791	32.2	SB	32.00	Sequence	
DRB1_0101	129	VRTVSRPLGAGTATV	SRPLGAGTA	0.6754	33.5	SB	32.00	Sequence	
DRB1_0101	96	AAIAVGLGAFGLGVL	AVGLGAFGL	0.6753	33.6	SB	32.00	Sequence	
DRB1_0101	165	GTVYQMWLLGGAKGP	VYQMWLLGG	0.6742	34.0	SB	32.00	Sequence	
DRB1_0101	144	VFSRDRNTGLLVMN	FSRDRNTGL	0.6725	34.6	SB	32.00	Sequence	
DRB1_0101	153	LLVMNNAVPPSRGT	VMNNVAPPS	0.6694	35.8	SB	32.00	Sequence	

DRB1_0101	26	ADIDRRVAAAPSPVA	RVAAAPSPV	0.6684	36.1	SB	32.00	Sequence
DRB1_0101	45	DEVRAVRETMVAVSA	VRVRETMA	0.6680	36.3	SB	32.00	Sequence
DRB1_0101	58	SAATTAEPHAHLRTA	TTAEPHAHL	0.6654	37.4	SB	32.00	Sequence
DRB1_0101	120	AEQVLTAPDVRTVSR	VLTAPDVRT	0.6622	38.7	SB	32.00	Sequence
DRB1_0101	193	STTATLTDLGASTAL	LTDLGASTA	0.6590	40.0	SB	32.00	Sequence
DRB1_0101	148	DRNTGLLVMNNVAPP	LLVMNNVAP	0.6551	41.8	SB	32.00	Sequence
DRB1_0101	141	ATVVFSSRDRTGLLV	FSRDRTGGL	0.6539	42.3	SB	32.00	Sequence
DRB1_0101	97	AIAVGLGAFGLGVLV	AVGLGAFGL	0.6533	42.6	SB	32.00	Sequence
DRB1_0101	98	IAVGLGAFGLGVLTR	GLGAFGLGV	0.6532	42.6	SB	32.00	Sequence
DRB1_0101	9	LELATPYALNAVSDD	LELATPYAL	0.6532	42.6	SB	32.00	Sequence
DRB1_0101	171	WLLGGAKGPRSAGTM	LGGAKGPRS	0.6529	42.8	SB	32.00	Sequence
DRB1_0101	147	RDRNTGLLVMNNVAP	LLVMNNVAP	0.6528	42.8	SB	32.00	Sequence
DRB1_0101	163	SRGTVYQMWLLGGAK	VYQMWLLGG	0.6516	43.4	SB	32.00	Sequence
DRB1_0101	93	ASAAAIAVGLGAFGL	SAAAIAVGL	0.6455	46.3	SB	32.00	Sequence
DRB1_0101	43	FNDEVRAVRETMVAV	VRVRETMA	0.6353	51.7	WB	32.00	Sequence
DRB1_0101	118	TVAEQVLTAPDVRTV	EQVLTAPDV	0.6334	52.8	WB	32.00	Sequence
DRB1_0101	94	SAAAIAVGLGAFGLG	AVGLGAFGL	0.6322	53.5	WB	32.00	Sequence
DRB1_0101	53	TMAVVSAAATTAEP	MAVVSAAAT	0.6312	54.1	WB	32.00	Sequence
DRB1_0101	99	AVGLGAFGLGVLTRP	GLGAFGLGV	0.6206	60.7	WB	32.00	Sequence
DRB1_0101	119	VAEQVLTAPDVRTVS	VLTAPDVRT	0.6199	61.1	WB	32.00	Sequence
DRB1_0101	2	EHTDFELLELATPYA	FELLELATP	0.6162	63.6	WB	32.00	Sequence
DRB1_0101	184	TMGTAAVTPSTTATL	TAAVTPSTT	0.6153	64.2	WB	32.00	Sequence
DRB1_0101	145	FSRDRNTGLLVMNNV	FSRDRNTGL	0.6078	69.6	WB	32.00	Sequence
DRB1_0101	121	EQVLTAPDVRTVSRP	VLTAPDVRT	0.6003	75.5	WB	50.00	Sequence
DRB1_0101	162	PSRGTVYQMWLLGGA	VYQMWLLGG	0.6002	75.6	WB	50.00	Sequence
DRB1_0101	135	PLGAGTATVVFSSRDR	LGAGTATVV	0.5994	76.3	WB	50.00	Sequence
DRB1_0101	100	VGLGAFGLGVLTRPS	GAFGLGVLV	0.5986	76.9	WB	50.00	Sequence
DRB1_0101	140	TATVVFSSRDRTGGL	FSRDRTGGL	0.5956	79.4	WB	50.00	Sequence
DRB1_0101	125	TAPDVRTVSRPLGAG	DVRTVSRPL	0.5933	81.5	WB	50.00	Sequence
DRB1_0101	81	VRQSRWRRTAAFASA	WRRTAAFASA	0.5860	88.2	WB	50.00	Sequence
DRB1_0101	59	AATTAEPHAHLRTAI	TTAEPHAHL	0.5832	90.9	WB	50.00	Sequence
DRB1_0101	199	TDLGASTALAFVTEP	DLGASTALA	0.5818	92.3	WB	50.00	Sequence
DRB1_0101	154	LVMNNVAPPSRGTVY	NNVAPPSPRG	0.5809	93.2	WB	50.00	Sequence
DRB1_0101	128	DVRTVSRPLGAGTAT	SRPLGAGTA	0.5665	108.9	WB	50.00	Sequence
DRB1_0101	57	VSAATTAEPHAHLRT	TTAEPHAHL	0.5664	109.0	WB	50.00	Sequence
DRB1_0101	101	GLGAFGLGVLTRPSP	GLGAFGLGV	0.5597	117.2	WB	50.00	Sequence
DRB1_0101	32	VAAAPSPVAAAFNDE	VAAAPSPVA	0.5570	120.7	WB	50.00	Sequence
DRB1_0101	146	SRDRNTGLLVMNNVA	GLLVMNNVA	0.5565	121.4	WB	50.00	Sequence
DRB1_0101	122	QVLTAPDVRTVSRPL	VLTAPDVRT	0.5549	123.4	WB	50.00	Sequence
DRB1_0101	200	DLGASTALAFVTEPG	ASTALAFVTV	0.5517	127.8	WB	50.00	Sequence
DRB1_0101	68	HLRTAILDATKPEVR	TAILDATKP	0.5478	133.4	WB	50.00	Sequence
DRB1_0101	180	RSAGTMGTAAVTPST	GTMGTAAVT	0.5453	136.9	WB	50.00	Sequence
DRB1_0101	78	KPEVRRQRWRRTAAF	VRRQRWRRT	0.5409	143.6	WB	50.00	Sequence
DRB1_0101	136	LGAGTATVVFSSRDRN	LGAGTATVV	0.5405	144.3	WB	50.00	Sequence
DRB1_0101	124	LTAPDVRTVSRPLGA	DVRTVSRPL	0.5403	144.5	WB	50.00	Sequence
DRB1_0101	161	PPSRGTVYQMWLLGG	VYQMWLLGG	0.5401	144.9	WB	50.00	Sequence
DRB1_0101	182	AGTMGTAAVTPSTTA	MGTAAVTPS	0.5388	146.9	WB	50.00	Sequence
DRB1_0101	181	SAGTMGTAAVTPSTT	TMGTAAVTP	0.5381	148.1	WB	50.00	Sequence
DRB1_0101	107	LGVLTRPSPPTVAE	LTRPSPPTT	0.5373	149.3	WB	50.00	Sequence
DRB1_0101	192	PSTTATLTDLGASTA	LTDLGASTA	0.5371	149.7	WB	50.00	Sequence
DRB1_0101	185	MGTAAVTPSTTATLT	TAAVTPSTT	0.5347	153.7	WB	50.00	Sequence
DRB1_0101	108	GVLTRPSPPTVAEQ	TRPSPPTTV	0.5331	156.4	WB	50.00	Sequence
DRB1_0101	126	APDVRTVSRPLGAGT	DVRTVSRPL	0.5329	156.7	WB	50.00	Sequence
DRB1_0101	172	LLGGAKGPRSAGTMG	LGGAKGPRS	0.5312	159.5	WB	50.00	Sequence
DRB1_0101	25	RADIDRRVAAAPSPV	RVAAAPSPV	0.5298	162.0	WB	50.00	Sequence
DRB1_0101	42	AFNDEVRAVRETMVAV	VRVRETMA	0.5192	181.7	WB	50.00	Sequence
DRB1_0101	117	PTVAEQVLTAPDVRT	EQVLTAPDV	0.5170	186.0	WB	50.00	Sequence
DRB1_0101	206	ALAFVTEPGTGSPQP	FTVEPGTGS	0.5148	190.5	WB	50.00	Sequence
DRB1_0101	127	PDVRTVSRPLGAGTA	SRPLGAGTA	0.5147	190.7	WB	50.00	Sequence
DRB1_0101	179	PRSAGTMGTAAVTPS	AGTMGTAAV	0.5140	192.1	WB	50.00	Sequence
DRB1_0101	205	TALAFVTEPGTGSPQ	FTVEPGTGS	0.5131	194.0	WB	50.00	Sequence
DRB1_0101	201	LGASTALAFVTEPGT	ASTALAFVTV	0.5123	195.7	WB	50.00	Sequence
DRB1_0101	102	LGAFGLGVLTRPSP	GAFGLGVLV	0.5111	198.3	WB	50.00	Sequence
DRB1_0101	60	ATTAEPPAHLRTAIL	TTAEPPAHL	0.5102	200.2	WB	50.00	Sequence
DRB1_0101	155	VNMNVAPPSPRGTVYQ	NVAPPSPRG	0.5095	201.7	WB	50.00	Sequence
DRB1_0101	106	GLGVLTRPSPPTVAE	LTRPSPPTT	0.5071	207.1	WB	50.00	Sequence
DRB1_0101	54	MAVVSAAATTAEP	MAVVSAAAT	0.5070	207.3	WB	50.00	Sequence
DRB1_0101	123	VLTAPDVRTVSRPLG	VLTAPDVRT	0.5068	207.8	WB	50.00	Sequence
DRB1_0101	1	TEHTDFELLELATPY	FELLELATP	0.5043	213.5	WB	50.00	Sequence
DRB1_0101	183	GTMGTAAVTPSTTAT	TAAVTPSTT	0.5000	223.6	WB	50.00	Sequence
DRB1_0101	63	AEPHAHLRTAILDAT	PAHLRTAIL	0.4959	233.7	WB	50.00	Sequence
DRB1_0101	177	KGPRSAGTMGTAAVT	SAGTMGTAA	0.4940	238.6	WB	50.00	Sequence
DRB1_0101	178	GPRSAGTMGTAAVTP	SAGTMGTAA	0.4911	246.1	WB	50.00	Sequence
DRB1_0101	203	ASTALAFVTEPGTGS	FTVEPGTGS	0.4895	250.6	WB	50.00	Sequence
DRB1_0101	159	VAPPSRGTVYQMWLL	PSRGTVYQM	0.4889	252.1	WB	50.00	Sequence
DRB1_0101	69	LRTAILDATKPEVRR	TAILDATKP	0.4800	277.7	WB	50.00	Sequence
DRB1_0101	160	APPSRGTVYQMWLLG	SRGTVYQMW	0.4787	281.6	WB	50.00	Sequence

DRB1_0101	64	EPPAHLRTAILDATK	PAHLRTAIL	0.4759	290.2	WB	50.00	Sequence
DRB1_0101	204	STALAFFTVEPGTGSP	FTVEPGTGS	0.4709	306.3	WB	50.00	Sequence
DRB1_0101	176	AKGFRSAGTMGTAAV	PRSAGTMGT	0.4669	319.8	WB	50.00	Sequence
DRB1_0101	56	VVSAATTAEPHAHLR	TTAEPHAHL	0.4646	327.9	WB	50.00	Sequence
DRB1_0101	139	GTATVVFSRDRNTGL	FSRDRNTGL	0.4627	334.9	WB	50.00	Sequence
DRB1_0101	187	TAAVTPSTTATLTDL	VTPSTTATL	0.4625	335.6	WB	50.00	Sequence
DRB1_0101	109	VLTRPSPPTVAEQV	TRPSPPTV	0.4615	339.2	WB	50.00	Sequence
DRB1_0101	67	AHLRTAILDATKPEV	TAILDATKP	0.4598	345.4	WB	50.00	Sequence
DRB1_0101	65	PPAHLRTAILDATKP	PAHLRTAIL	0.4590	348.3	WB	50.00	Sequence
DRB1_0101	11	LATPYALNAVSDDER	PYALNAVSD	0.4582	351.3	WB	50.00	Sequence
DRB1_0101	79	PEVRRQSRWRATAFA	VRRQSRWRT	0.4568	356.7	WB	50.00	Sequence
DRB1_0101	207	LAFTVEPGTGSPQPT	FTVEPGTGS	0.4560	359.9	WB	50.00	Sequence
DRB1_0101	103	GAFGLGVLTRPSPPP	AFGLGVLTR	0.4549	364.4	WB	50.00	Sequence
DRB1_0101	217	SPQPTGTILAEPLG	TGTILAEPL	0.4534	370.3	WB	50.00	Sequence
DRB1_0101	66	PAHLRTAILDATKPE	PAHLRTAIL	0.4507	381.2	WB	50.00	Sequence
DRB1_0101	0	MTEHTDFELLELELAP	HTDFELLEL	0.4458	401.9	WB	50.00	Sequence
DRB1_0101	105	FGLGVLTRPSPPTV	LTRPSPPTV	0.4445	407.5	WB	50.00	Sequence
DRB1_0101	71	TAILDATKPEVRRQS	LDATKPEVR	0.4402	427.0	WB	50.00	Sequence
DRB1_0101	70	RTAILDATKPEVRRQ	TAILDATKP	0.4386	434.3	WB	50.00	Sequence
DRB1_0101	202	GASTALAFFTVEPGTG	ASTALAFTV	0.4377	438.8	WB	50.00	Sequence
DRB1_0101	116	PPTVAEQVLTAPDVR	EQVLTAPDV	0.4363	445.6	WB	50.00	Sequence
DRB1_0101	61	TTAEPHAHLRTAILD	TTAEPHAHL	0.4351	451.5	WB	50.00	Sequence
DRB1_0101	158	NVAPPSRGTVYQMWL	PSRGTVYQM	0.4334	459.5	WB	50.00	Sequence
DRB1_0101	186	GTAAVTPSTTATLTD	TAAVTPSTT	0.4306	473.7	WB	50.00	Sequence
DRB1_0101	156	MNNVAPPSRGTVYQM	NVAPPSRGT	0.4296	479.2	WB	50.00	Sequence
DRB1_0101	173	LGGAKGPRRSAGTMGT	LGGAKGPRS	0.4267	494.2	WB	50.00	Sequence
DRB1_0101	77	TKPEVRRQSRWRATA	VRRQSRWRT	0.4267	494.4	WB	50.00	Sequence
DRB1_0101	62	TAEPHAHLRTAILDA	PAHLRTAIL	0.4266	494.7	WB	50.00	Sequence
DRB1_0101	80	EVRRQSRWRATAAFAS	VRRQSRWRT	0.4253	502.0	WB	50.00	Sequence
DRB1_0101	115	PPPTVAEQVLTAPDV	TVAEQVLTA	0.4207	527.2	WB	50.00	Sequence
DRB1_0101	10	ELATPYALNAVSDDE	PYALNAVSD	0.4185	540.2	WB	50.00	Sequence
DRB1_0101	41	AAFNDEVRAVRETMA	VRAVRETMA	0.4160	555.2	WB	50.00	Sequence
DRB1_0101	104	AFGLGVLTRPSPPPPT	AFGLGVLTR	0.4103	590.4	WB	50.00	Sequence
DRB1_0101	216	GSPQPTGTILAEPL	TGTILAEPL	0.4040	631.6	WB	50.00	Sequence
DRB1_0101	188	AAVTPSTTATLTDLG	VTPSTTATL	0.4014	649.9	WB	50.00	Sequence
DRB1_0101	157	NNVAPPSRGTVYQMW	SRGTVYQMW	0.3991	666.2	WB	50.00	Sequence
DRB1_0101	36	PSPVAAAFNDEVRAV	VAAAFNDEV	0.3986	670.0	WB	50.00	Sequence
DRB1_0101	208	AFTVEPGTGSPQPTG	FTVEPGTGS	0.3876	754.3	WB	50.00	Sequence
DRB1_0101	110	LTRPSPPTVVAEQVL	TRPSPPTV	0.3797	822.1	WB	50.00	Sequence
DRB1_0101	12	ATPYALNAVSDDERA	PYALNAVSD	0.3743	871.1	WB	50.00	Sequence
DRB1_0101	55	AVVSAATTAEPHAHL	TTAEPHAHL	0.3701	912.3	WB	50.00	Sequence
DRB1_0101	191	TPSTTATLTDLGAST	TATLTDLGA	0.3687	925.3	WB	50.00	Sequence
DRB1_0101	37	SPVAAAFNDEVRAVR	VAAAFNDEV	0.3636	978.3	WB	50.00	Sequence
DRB1_0101	24	ERADIDRRVAAAPSP	DRRVAAAPS	0.3589	1029.7	WB	50.00	Sequence
DRB1_0101	138	AGTATVVFSRDRNTG	VVFSRDRNT	0.3565	1056.8	WB	50.00	Sequence
DRB1_0101	23	DERADIDRRVAAAPSP	DRRVAAAPS	0.3553	1069.7	WB	50.00	Sequence
DRB1_0101	175	GAKGPRRSAGTMGTA	PRSAGTMGT	0.3522	1107.1	WB	50.00	Sequence
DRB1_0101	209	FTVEPGTGSPQPTGT	FTVEPGTGS	0.3511	1119.6	WB	50.00	Sequence
DRB1_0101	137	GAGTATVVFSRDRNT	VVFSRDRNT	0.3492	1143.3	WB	50.00	Sequence
DRB1_0101	189	AVTPSTTATLTDLGA	TPSTTATLT	0.3471	1169.2	WB	50.00	Sequence
DRB1_0101	72	AILDATKPEVRRQSR	LDATKPEVR	0.3460	1183.5	WB	50.00	Sequence
DRB1_0101	190	VTPSTTATLTDLGAS	TATLTDLGA	0.3425	1228.7	WB	50.00	Sequence
DRB1_0101	76	ATKPEVRRQSRWRATA	VRRQSRWRT	0.3379	1291.5	WB	50.00	Sequence
DRB1_0101	112	RSPSPPTVVAEQVLTA	TVAEQVLTA	0.3316	1383.5	WB	50.00	Sequence
DRB1_0101	113	PSPPPTVVAEQVLTAP	TVAEQVLTA	0.3259	1470.3	WB	50.00	Sequence
DRB1_0101	114	SPPPTVVAEQVLTAPD	TVAEQVLTA	0.3230	1517.2	WB	50.00	Sequence
DRB1_0101	38	PVAAAFNDEVRAVRE	VAAAFNDEV	0.3177	1606.6	WB	50.00	Sequence
DRB1_0101	13	TPYALNAVSDDERAD	PYALNAVSD	0.3168	1623.3	WB	50.00	Sequence
DRB1_0101	35	APSPVAAAFNDEVRA	VAAAFNDEV	0.3147	1660.6	WB	50.00	Sequence
DRB1_0101	39	VAAAFNDEVRAVRET	VAAAFNDEV	0.3111	1725.7	WB	50.00	Sequence
DRB1_0101	215	TGSPQPTGTILAEPL	PQPTGTILA	0.3035	1873.9	WB	50.00	Sequence
DRB1_0101	214	GTGSPQPTGTILAEPL	PQPTGTILA	0.2970	2011.2	WB	50.00	Sequence
DRB1_0101	174	GGAKGPRRSAGTMGTA	PRSAGTMGT	0.2966	2019.3	WB	50.00	Sequence
DRB1_0101	40	AAAFNDEVRAVRETM	FNDEVRAVR	0.2940	2078.0	WB	50.00	Sequence
DRB1_0101	33	AAAPSPVAAAFNDEV	AAAPSPVAA	0.2930	2100.7	WB	50.00	Sequence
DRB1_0101	14	PYALNAVSDDERADI	PYALNAVSD	0.2870	2239.4	WB	50.00	Sequence
DRB1_0101	34	AAPSPVAAAFNDEVRA	VAAAFNDEV	0.2819	2368.8	WB	50.00	Sequence
DRB1_0101	73	ILDATKPEVRRQSRWR	LDATKPEVR	0.2815	2377.5	WB	50.00	Sequence
DRB1_0101	210	TVEPGTGSPQPTGTI	PGTGSPQPT	0.2803	2408.7	WB	50.00	Sequence
DRB1_0101	111	TRPSPPTVVAEQVLT	TRPSPPTV	0.2803	2408.7	WB	50.00	Sequence
DRB1_0101	75	DATKPEVRRQSRWRATA	VRRQSRWRT	0.2672	2774.9	WB	50.00	Sequence
DRB1_0101	15	YALNAVSDDERADID	NAVSDDERA	0.2544	3187.1	WB	50.00	Sequence
DRB1_0101	211	VEPGTGSPQPTGTIL	PGTGSPQPT	0.2399	3728.4	WB	50.00	Sequence
DRB1_0101	212	EPGTGSPQPTGTILA	TGSPQPTGT	0.2282	4232.6	WB	50.00	Sequence
DRB1_0101	213	PGTGSPQPTGTILAE	SPQPTGTIL	0.2262	4324.1	WB	50.00	Sequence
DRB1_0101	74	LDATKPEVRRQSRWR	LDATKPEVR	0.2242	4422.3	WB	50.00	Sequence
DRB1_0101	22	DDERADIDRRVAAAP	IDRRVAAAP	0.2216	4544.9	WB	50.00	Sequence

DRB1_0101	16	ALNAVSDDERADIDR	NAVSDDERA	0.2213	4560.4	50.00	Sequence
DRB1_0101	21	SDDERADIDRRVAAA	ERADIDRRV	0.2144	4916.0	50.00	Sequence
DRB1_0101	17	LNAVSDDERADIDRR	NAVSDDERA	0.2070	5325.2	50.00	Sequence
DRB1_0101	18	NAVSDDERADIDRRV	NAVSDDERA	0.2023	5602.3	50.00	Sequence
DRB1_0101	20	VSDDERADIDRRVAA	ERADIDRRV	0.1902	6385.7	50.00	Sequence
DRB1_0101	19	AVSDDERADIDRRVA	ERADIDRRV	0.1763	7420.6	50.00	Sequence

Allele: DRB1_0101. Number of high binders 72. Number of weak binders 91. Number of peptides 218

Allele	pos	peptide	core	1-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
DRB1_0301	141	ATVVFSRDRNTGLLV	TVVFSRDRN	0.6844	30.4	SB	0.80	Sequence
DRB1_0301	140	TATVVFSRDRNTGLL	TVVFSRDRN	0.6628	38.4	SB	2.00	Sequence
DRB1_0301	142	TVVFSRDRNTGLLVM	TVVFSRDRN	0.6581	40.4	SB	2.00	Sequence
DRB1_0301	139	GTATVVFSRDRNTGL	TVVFSRDRN	0.6173	62.9	WB	2.00	Sequence
DRB1_0301	138	AGTATVVFSRDRNTG	TVVFSRDRN	0.5183	183.4	WB	8.00	Sequence
DRB1_0301	122	QVLTAPDVRTVSRPL	QVLTAPDVR	0.5099	200.8	WB	8.00	Sequence
DRB1_0301	39	VAAAFNDEVRAVRET	VAAAFNDEV	0.4880	254.6	WB	8.00	Sequence
DRB1_0301	121	EQVLTAPDVRTVSRP	QVLTAPDVR	0.4835	267.3	WB	8.00	Sequence
DRB1_0301	197	LTDLGASTALAFTV	LTDLGASTA	0.4717	303.7	WB	16.00	Sequence
DRB1_0301	38	PVAAAFNDEVRAVRE	VAAAFNDEV	0.4617	338.5	WB	16.00	Sequence
DRB1_0301	196	ATLTDLGASTALAFT	LTDLGASTA	0.4612	340.4	WB	16.00	Sequence
DRB1_0301	16	ALNAVSDDERADIDR	LNAVSDDER	0.4607	342.1	WB	16.00	Sequence
DRB1_0301	120	AEQVLTAPDVRTVSR	QVLTAPDVR	0.4595	346.6	WB	16.00	Sequence
DRB1_0301	69	LRTAILDATKPEVRR	LRTAILDAT	0.4580	352.2	WB	16.00	Sequence
DRB1_0301	17	LNAVSDDERADIDRR	LNAVSDDER	0.4552	363.2	WB	16.00	Sequence
DRB1_0301	195	TATLTDLGASTALAF	LTDLGASTA	0.4526	373.3	WB	16.00	Sequence
DRB1_0301	15	YALNAVSDDERADID	LNAVSDDER	0.4424	417.1	WB	16.00	Sequence
DRB1_0301	152	GLLVMMNVAPP SRGT	LLVMNNVAP	0.4421	418.3	WB	16.00	Sequence
DRB1_0301	40	AAAFNDEVRAVRETM	AAAFNDEV	0.4402	426.9	WB	16.00	Sequence
DRB1_0301	143	VVFSRDRNTGLLVMN	VVFSRDRNT	0.4400	428.1	WB	16.00	Sequence
DRB1_0301	198	LTDLGASTALAFTVE	LTDLGASTA	0.4350	452.0	WB	16.00	Sequence
DRB1_0301	194	TTATLTDLGASTALA	LTDLGASTA	0.4345	454.1	WB	16.00	Sequence
DRB1_0301	68	HLRTAILDATKPEVR	LRTAILDAT	0.4276	489.4	WB	16.00	Sequence
DRB1_0301	37	SPVAAAFNDEVRAV	VAAAFNDEV	0.4262	496.9	WB	16.00	Sequence
DRB1_0301	23	DERADIDRRVAAAPS	DERADIDRR	0.4258	498.9	WB	16.00	Sequence
DRB1_0301	137	GAGTATVVFSRDRNT	VVFSRDRNT	0.4258	499.0	WB	16.00	Sequence
DRB1_0301	151	TGLLVMMNVAPP SRG	LLVMNNVAP	0.4230	514.6	WB	16.00	Sequence
DRB1_0301	14	PYALNAVSDDERADI	LNAVSDDER	0.4229	514.8	WB	16.00	Sequence
DRB1_0301	119	VAEQVLTAPDVRTVS	QVLTAPDVR	0.4202	530.2	WB	16.00	Sequence
DRB1_0301	70	RTAILDATKPEVRRQ	RTAILDATK	0.4183	541.3	WB	16.00	Sequence
DRB1_0301	153	LLVMNNVAPP SRGTV	LLVMNNVAP	0.4102	590.8	WB	16.00	Sequence
DRB1_0301	22	DDERADIDRRVAAAP	DERADIDRR	0.4091	598.2	WB	16.00	Sequence
DRB1_0301	21	SDDERADIDRRVAAA	DERADIDRR	0.4008	654.0	WB	16.00	Sequence
DRB1_0301	150	NTGLLVMMNVAPP SR	LLVMNNVAP	0.3938	705.3	WB	32.00	Sequence
DRB1_0301	71	TAILDATKPEVRRQS	LDATKPEVR	0.3862	766.0	WB	32.00	Sequence
DRB1_0301	123	VLTPADVRTVSRPLG	APDVRTVSR	0.3770	846.3	WB	32.00	Sequence
DRB1_0301	13	TPYALNAVSDDERAD	LNAVSDDER	0.3758	857.0	WB	32.00	Sequence
DRB1_0301	24	ERADIDRRVAAAPSR	RADIDRRVA	0.3749	865.8	WB	32.00	Sequence
DRB1_0301	41	AAFNDEVRAVRETMA	AAFNDEVRA	0.3749	866.1	WB	32.00	Sequence
DRB1_0301	20	VSDDERADIDRRVAA	DERADIDRR	0.3727	886.4	WB	32.00	Sequence
DRB1_0301	193	STTATLTDLGASTAL	LTDLGASTA	0.3706	906.8	WB	32.00	Sequence
DRB1_0301	118	TVAEQVLTAPDVRTV	QVLTAPDVR	0.3631	983.8	WB	32.00	Sequence
DRB1_0301	67	AHLRTAILDATKPEV	LRTAILDAT	0.3607	1009.3	WB	32.00	Sequence
DRB1_0301	43	FNDEVRAVRETMAVV	NDEVRAVRE	0.3581	1038.6	WB	32.00	Sequence
DRB1_0301	47	VRAVRETMAVVSAA	VRAVRETMA	0.3553	1069.7	WB	32.00	Sequence
DRB1_0301	124	LTAPDVRTVSRPLGA	APDVRTVSR	0.3540	1085.5	WB	32.00	Sequence
DRB1_0301	125	TAPDVRTVSRPLGAG	APDVRTVSR	0.3519	1110.7	WB	32.00	Sequence
DRB1_0301	44	NDEVRAVRETMAVVS	NDEVRAVRE	0.3483	1154.3	WB	32.00	Sequence
DRB1_0301	126	APDVRTVSRPLGAGT	APDVRTVSR	0.3482	1155.1	WB	32.00	Sequence
DRB1_0301	72	AILDATKPEVRRQSR	LDATKPEVR	0.3478	1160.3	WB	32.00	Sequence
DRB1_0301	46	EVRAVRETMAVVSAA	VRAVRETMA	0.3476	1162.5	WB	32.00	Sequence
DRB1_0301	144	VFSRDRNTGLLVMNN	VFSRDRNTG	0.3390	1276.1	WB	32.00	Sequence
DRB1_0301	73	ILDATKPEVRRQSRW	LDATKPEVR	0.3387	1281.3	WB	32.00	Sequence
DRB1_0301	25	RADIDRRVAAAPSPV	ADIDRRVAA	0.3346	1339.0	WB	32.00	Sequence
DRB1_0301	36	PSPVAAAFNDEVRAV	VAAAFNDEV	0.3306	1398.5	WB	32.00	Sequence
DRB1_0301	42	AFNDEVRAVRETMAV	NDEVRAVRE	0.3302	1404.7	WB	32.00	Sequence
DRB1_0301	45	DEVRAVRETMAVVS	VRAVRETMA	0.3270	1453.6	WB	32.00	Sequence
DRB1_0301	149	RNTGLLVMMNVAPP S	GLLVMMNV	0.3210	1550.7	WB	32.00	Sequence
DRB1_0301	12	ATPYALNAVSDDERA	LNAVSDDER	0.3205	1559.0	WB	32.00	Sequence
DRB1_0301	170	MWLLGGAKGPR	LLGGAKGPR	0.3197	1573.4	WB	32.00	Sequence
DRB1_0301	6	FELLELATPYALNAV	FELLELATP	0.3120	1709.6	WB	32.00	Sequence
DRB1_0301	66	PAHLRTAILDATKPE	LRTAILDAT	0.3081	1783.0	WB	32.00	Sequence
DRB1_0301	5	DFELLELATPYALNA	FELLELATP	0.3062	1821.0	WB	32.00	Sequence

DRB1_0301	169	QMWLLGGAKGPRSAG	LLGGAKGPR	0.3062	1821.1	32.00	Sequence
DRB1_0301	117	PTVAEQVLTAPDVRT	QVLTAPDVRT	0.3035	1874.9	32.00	Sequence
DRB1_0301	192	PSTATLTLDLGASTA	TTATLTLDLG	0.3034	1875.9	32.00	Sequence
DRB1_0301	74	LDATKPEVRRQSRWR	LDATKPEVR	0.2938	2081.7	50.00	Sequence
DRB1_0301	187	TAAVTPSTTATLTDL	TAAVTPSTT	0.2884	2207.7	50.00	Sequence
DRB1_0301	19	AVSDDERADIDRRVA	DERADIDRR	0.2869	2242.5	50.00	Sequence
DRB1_0301	7	LLELATPYALNAVS	LLELATPYA	0.2847	2297.5	50.00	Sequence
DRB1_0301	4	TDFELLELATPYALN	LLELATPYA	0.2836	2324.0	50.00	Sequence
DRB1_0301	48	RAVRETMAVVSAAAT	VRETMAVVS	0.2818	2369.2	50.00	Sequence
DRB1_0301	18	NAVSDDERADIDRRV	NAVSDDERA	0.2801	2415.3	50.00	Sequence
DRB1_0301	168	YQMWLLGGAKGPRSA	LLGGAKGPR	0.2733	2598.1	50.00	Sequence
DRB1_0301	50	VRETMAVVSAAATTA	VRETMAVVS	0.2728	2612.7	50.00	Sequence
DRB1_0301	148	DRNTGLLLVMNNVAPP	LLVMNNVAP	0.2699	2695.8	50.00	Sequence
DRB1_0301	54	MAVVSAAATTAEP	MAVVSAAAT	0.2694	2711.8	50.00	Sequence
DRB1_0301	8	LLELATPYALNAVS	LLELATPYA	0.2692	2717.7	50.00	Sequence
DRB1_0301	191	TPSTTATLTLDLGAST	TLTDLGAST	0.2636	2885.3	50.00	Sequence
DRB1_0301	145	FSRDRNTGLLLVMNNV	FSRDRNTGL	0.2633	2895.6	50.00	Sequence
DRB1_0301	171	WLLGGAKGPRSAGTM	LLGGAKGPR	0.2617	2945.5	50.00	Sequence
DRB1_0301	186	GTAAVTPSTTATLTD	TAAVTPSTT	0.2596	3014.6	50.00	Sequence
DRB1_0301	136	LGAGTATVVF	TVVFSRDRN	0.2581	3061.6	50.00	Sequence
DRB1_0301	154	LVMNNVAPP	PSRGT	0.2568	3106.6	50.00	Sequence
DRB1_0301	26	ADIDRRVAAAPSPVA	ADIDRRVAA	0.2491	3377.6	50.00	Sequence
DRB1_0301	199	TDLGASTALAF	TVEP	0.2460	3492.2	50.00	Sequence
DRB1_0301	11	LATPYALNAVSDDER	LNAVSDDER	0.2458	3500.3	50.00	Sequence
DRB1_0301	3	HTDFELLELATPYAL	FELLELATP	0.2443	3555.6	50.00	Sequence
DRB1_0301	65	PPAHLRTAILLDATK	LRTAILLDAT	0.2426	3624.0	50.00	Sequence
DRB1_0301	53	TMAVVSAAATTAEP	MAVVSAAAT	0.2425	3625.4	50.00	Sequence
DRB1_0301	56	VVSAATTAEP	PAHLR	0.2408	3692.2	50.00	Sequence
DRB1_0301	167	VYQMWLLGGAKGPRS	LLGGAKGPR	0.2400	3724.4	50.00	Sequence
DRB1_0301	57	VSAATTAEP	PAHLRT	0.2391	3764.1	50.00	Sequence
DRB1_0301	105	FGLGVLTRSP	PPPTV	0.2383	3793.0	50.00	Sequence
DRB1_0301	104	AFGLGVLTRSP	PPPT	0.2375	3829.8	50.00	Sequence
DRB1_0301	172	LLGGAKGPRSAG	TMG	0.2367	3860.1	50.00	Sequence
DRB1_0301	49	AVRETMAVVSAAAT	TAE	0.2365	3871.2	50.00	Sequence
DRB1_0301	55	AVVSAATTAEP	PAHL	0.2353	3918.2	50.00	Sequence
DRB1_0301	127	PDVRTVSRPLGAG	TAE	0.2349	3938.8	50.00	Sequence
DRB1_0301	185	MGTAAVTPSTTATLT	TAAVTPSTT	0.2348	3939.9	50.00	Sequence
DRB1_0301	106	GLGVLTRSP	PPPTVA	0.2278	4251.0	50.00	Sequence
DRB1_0301	52	ETMAVVSAAATTAEP	P	0.2251	4378.6	50.00	Sequence
DRB1_0301	35	APSPVAAAFNDEV	R	0.2246	4401.0	50.00	Sequence
DRB1_0301	116	PPTVAEQVLTAPDV	R	0.2240	4429.5	50.00	Sequence
DRB1_0301	58	SAATTAEP	PAHLRTA	0.2231	4473.9	50.00	Sequence
DRB1_0301	147	RDRNTGLLLVMNNV	APP	0.2225	4503.5	50.00	Sequence
DRB1_0301	1	TEHTDFELLELATPY		0.2199	4630.8	50.00	Sequence
DRB1_0301	103	GAFGLGVLTRSP	PPPP	0.2161	4827.5	50.00	Sequence
DRB1_0301	51	RETMAVVSAAATTAEP		0.2157	4846.5	50.00	Sequence
DRB1_0301	107	LGVLTRSP	PPPTVAE	0.2114	5078.1	50.00	Sequence
DRB1_0301	184	TMGTAAVTPSTTATL	TAAVTPSTT	0.2069	5331.5	50.00	Sequence
DRB1_0301	0	MTEHTDFELLELATP		0.2066	5347.8	50.00	Sequence
DRB1_0301	102	LGAFGLGVLTRSP	PP	0.2059	5388.7	50.00	Sequence
DRB1_0301	133	SRPLGAGTATV	VFSR	0.1998	5758.2	50.00	Sequence
DRB1_0301	128	DVRTVSRPLGAG	TAT	0.1908	6341.8	50.00	Sequence
DRB1_0301	2	EHTDFELLELATPYA		0.1896	6426.1	50.00	Sequence
DRB1_0301	64	EPPAHLRTAILLDATK		0.1885	6507.3	50.00	Sequence
DRB1_0301	27	DIDRRVAAAPSPVAA		0.1879	6546.0	50.00	Sequence
DRB1_0301	155	VMNNVAPP	SRGT	0.1878	6556.0	50.00	Sequence
DRB1_0301	166	TVYQMWLLGGAKGPR		0.1860	6686.2	50.00	Sequence
DRB1_0301	146	SRDRNTGLLLVMNNV	A	0.1826	6933.3	50.00	Sequence
DRB1_0301	132	VSRPLGAGTATV	VVFS	0.1817	6997.6	50.00	Sequence
DRB1_0301	78	KPEVRRQSRWR	TAAF	0.1802	7116.5	50.00	Sequence
DRB1_0301	115	PPPTVAEQVLTAPDV		0.1793	7185.0	50.00	Sequence
DRB1_0301	135	PLGAGTATV	VFSRDR	0.1791	7204.7	50.00	Sequence
DRB1_0301	134	RPLGAGTATV	VFSRD	0.1785	7243.9	50.00	Sequence
DRB1_0301	108	GVLTRSP	PPPTVAEQ	0.1772	7349.2	50.00	Sequence
DRB1_0301	9	LELATPYALNAVSD	D	0.1761	7435.2	50.00	Sequence
DRB1_0301	101	GLGAFGLGVLTRSP		0.1748	7545.4	50.00	Sequence
DRB1_0301	190	VTPSTTATLTLDLGAS		0.1722	7755.8	50.00	Sequence
DRB1_0301	200	DLGASTALAF	TVEPG	0.1715	7815.1	50.00	Sequence
DRB1_0301	88	RTAAFASAAAIAVGL		0.1662	8282.7	50.00	Sequence
DRB1_0301	28	IDRRVAAAPSPVAAA		0.1659	8303.0	50.00	Sequence
DRB1_0301	77	TKPEVRRQSRWR	TAA	0.1615	8708.0	50.00	Sequence
DRB1_0301	87	WRTAAFASAAAIAVG		0.1613	8727.6	50.00	Sequence
DRB1_0301	206	ALAF	TVEPGT	0.1601	8845.9	50.00	Sequence
DRB1_0301	114	SPPTVAEQVLTAPD		0.1596	8895.4	50.00	Sequence
DRB1_0301	204	STALAF	TVEPGT	0.1592	8932.6	50.00	Sequence
DRB1_0301	75	DATKPEVRRQSRWR	T	0.1550	9344.4	50.00	Sequence
DRB1_0301	86	RWRTAAFASAAAIAV		0.1534	9505.8	50.00	Sequence

DRB1_0301	205	TALAFTVEPGTGSPO	LAFTVEPGT	0.1495	9915.5	50.00	Sequence
DRB1_0301	131	TVSRPLGAGTATVVF	SRPLGAGTA	0.1493	9937.6	50.00	Sequence
DRB1_0301	10	ELATPYALNAVSDDE	TPYALNAV	0.1488	9990.2	50.00	Sequence
DRB1_0301	201	LGASTALAFVTEPGT	LGASTALAF	0.1488	9992.1	50.00	Sequence
DRB1_0301	189	AVTPSTTATLTLDLGA	VTPSTTATL	0.1486	10014.1	50.00	Sequence
DRB1_0301	156	MNNVAPPSRGTVYQM	MNNVAPPSR	0.1485	10023.1	50.00	Sequence
DRB1_0301	89	TAAFASAAAIAVGLG	TAAFASAAA	0.1460	10305.1	50.00	Sequence
DRB1_0301	207	LAFTVEPGTGSPPQT	LAFTVEPGT	0.1449	10424.0	50.00	Sequence
DRB1_0301	217	SPQPTGTILAEPLG	TGTILAEPL	0.1447	10442.6	50.00	Sequence
DRB1_0301	100	VGLGAFGLGVLTRPS	LGAFGLGVL	0.1427	10680.8	50.00	Sequence
DRB1_0301	29	DRRVAAAPSPVAAAF	DRRVAAAPS	0.1426	10692.2	50.00	Sequence
DRB1_0301	76	ATKPEVRRQSRWRTA	KPEVRRQSR	0.1424	10708.3	50.00	Sequence
DRB1_0301	188	AAVTPSTTATLTLDLG	VTPSTTATL	0.1399	11002.5	50.00	Sequence
DRB1_0301	113	PSPPTVAEQVLTAP	PPPTVAEQV	0.1399	11006.8	50.00	Sequence
DRB1_0301	183	GTMGTAAVTPSTTAT	TAAVTPSTT	0.1379	11250.2	50.00	Sequence
DRB1_0301	63	AEPHAHLRTAILDAT	LRTAILDAT	0.1359	11495.9	50.00	Sequence
DRB1_0301	203	ASTALAFVTEPGTGS	LAFTVEPGT	0.1292	12362.0	50.00	Sequence
DRB1_0301	90	AAFASAAAIAVGLGA	AFASAAAIA	0.1277	12554.5	50.00	Sequence
DRB1_0301	85	SRWRTAAFASAAAIA	WRTAAFASA	0.1249	12944.7	50.00	Sequence
DRB1_0301	34	AAPSPVAAAFNDEV	VAAAFNDEV	0.1229	13226.7	50.00	Sequence
DRB1_0301	130	RTVSRPLGAGTATVV	RTVSRPLGA	0.1226	13273.8	50.00	Sequence
DRB1_0301	30	RRVAAAPSPVAAAFN	RVAAPSPV	0.1218	13391.2	50.00	Sequence
DRB1_0301	81	VRRQSRWRTAAFASA	RRQSRWRTA	0.1202	13614.1	50.00	Sequence
DRB1_0301	31	RVAAAPSPVAAAFND	RVAAAPSPV	0.1146	14466.2	50.00	Sequence
DRB1_0301	112	RPSPPPTVAEQVLT	PPPTVAEQV	0.1129	14731.3	50.00	Sequence
DRB1_0301	129	VRTVSRPLGAGTATV	VRTVSRPLG	0.1117	14930.4	50.00	Sequence
DRB1_0301	99	AVGLGAFGLGVLTRP	LGAFGLGVL	0.1094	15313.7	50.00	Sequence
DRB1_0301	80	EVRQSRWRTAAFAS	RRQSRWRTA	0.1076	15607.3	50.00	Sequence
DRB1_0301	161	PPSRGTVYQMWLLGG	PSRGTVYQM	0.1072	15674.0	50.00	Sequence
DRB1_0301	182	AGTMGTAAVTPSTTA	TAAVTPSTT	0.1051	16033.8	50.00	Sequence
DRB1_0301	82	RRQSRWRTAAFASAA	RRQSRWRTA	0.1035	16319.1	50.00	Sequence
DRB1_0301	159	VAPPSRGTVYQMWLL	PSRGTVYQM	0.1028	16443.0	50.00	Sequence
DRB1_0301	216	GSPQPTGTILAEPL	TGTILAEPL	0.1017	16638.1	50.00	Sequence
DRB1_0301	79	PEVRRQSRWRTAAFA	RRQSRWRTA	0.1014	16689.7	50.00	Sequence
DRB1_0301	202	GASTALAFVTEPGTG	LAFTVEPGT	0.1003	16897.9	50.00	Sequence
DRB1_0301	59	AATTAEPHAHLRTAI	AATTAEPPI	0.0996	17020.6	50.00	Sequence
DRB1_0301	162	PSRGTVYQMWLLGGA	PSRGTVYQM	0.0994	17061.0	50.00	Sequence
DRB1_0301	160	APPSRGTVYQMWLLG	PSRGTVYQM	0.0991	17118.9	50.00	Sequence
DRB1_0301	180	RSAGTMGTAAVTPST	RSAGTMGTA	0.0948	17928.0	50.00	Sequence
DRB1_0301	98	IAVGLGAFGLGVLTR	AVGLGAFGL	0.0914	18590.1	50.00	Sequence
DRB1_0301	179	PRSAAGTMGTAAVTPS	RSAGTMGTA	0.0912	18633.8	50.00	Sequence
DRB1_0301	91	AFASAAAIAVGLGAF	FASAAAIAV	0.0890	19078.3	50.00	Sequence
DRB1_0301	84	QSRWRTAAFASAAAIA	WRTAAFASA	0.0884	19220.9	50.00	Sequence
DRB1_0301	181	SAGTMGTAAVTPSTT	SAGTMGTAA	0.0883	19234.6	50.00	Sequence
DRB1_0301	173	LGGAKGPRSAGTMGT	LGGAKGPRS	0.0848	19980.0	50.00	Sequence
DRB1_0301	158	NVAPPSRGTVYQMWL	VAPPSRGTV	0.0813	20737.9	50.00	Sequence
DRB1_0301	109	VLTRPSPPTVAEQV	VLTRPSPPP	0.0756	22071.5	50.00	Sequence
DRB1_0301	157	NNVAPPSRGTVYQMW	NNVAPPSRG	0.0753	22131.5	50.00	Sequence
DRB1_0301	83	RQSRWRTAAFASAAA	WRTAAFASA	0.0747	22270.6	50.00	Sequence
DRB1_0301	62	TAEPHAHLRTAILDA	PAHLRTAIL	0.0741	22426.0	50.00	Sequence
DRB1_0301	32	VAAAPSPVAAAFNDE	VAAAPSPVA	0.0693	23610.5	50.00	Sequence
DRB1_0301	215	TGSPQPTGTILAEPL	TGTILAEPL	0.0686	23790.8	50.00	Sequence
DRB1_0301	163	SRGTVYQMWLLGGAK	SRGTVYQMW	0.0685	23839.5	50.00	Sequence
DRB1_0301	97	IAVGLGAFGLGVLTR	IAVGLGAFG	0.0679	23975.6	50.00	Sequence
DRB1_0301	178	GPRSAAGTMGTAAVTP	RSAGTMGTA	0.0679	23979.7	50.00	Sequence
DRB1_0301	60	ATTAEPHAHLRTAIL	ATTAEPPI	0.0679	23995.8	50.00	Sequence
DRB1_0301	111	TRPSPPTVAEQVLT	PPPTVAEQV	0.0648	24796.9	50.00	Sequence
DRB1_0301	33	AAAPSPVAAAFNDEV	VAAAFNDEV	0.0645	24883.1	50.00	Sequence
DRB1_0301	110	LTRPSPPTVAEQVLT	LTRPSPPP	0.0643	24926.5	50.00	Sequence
DRB1_0301	92	FASAAAIAVGLGAFG	FASAAAIAV	0.0641	24996.8	50.00	Sequence
DRB1_0301	61	TTAEPHAHLRTAILD	PAHLRTAIL	0.0628	25349.2	50.00	Sequence
DRB1_0301	165	GTVYQMWLLGGAKGP	QMWLLGGAK	0.0620	25554.3	50.00	Sequence
DRB1_0301	177	KGPRSAGTMGTAAVT	RSAGTMGTA	0.0617	25646.0	50.00	Sequence
DRB1_0301	96	AAIAVGLGAFGLGVL	IAVGLGAFG	0.0576	26802.7	50.00	Sequence
DRB1_0301	164	RGTVYQMWLLGGAKG	QMWLLGGAK	0.0571	26965.3	50.00	Sequence
DRB1_0301	212	EPGTGSPQPTGTILA	EPGTGSPQP	0.0559	27315.0	50.00	Sequence
DRB1_0301	176	AKGPRSAGTMGTAAV	PRSAGTMGT	0.0556	27389.6	50.00	Sequence
DRB1_0301	208	AFTVEPGTGSPPQPTG	AFTVEPGTG	0.0548	27638.7	50.00	Sequence
DRB1_0301	209	FTVEPGTGSPPQPTG	EPGTGSPQP	0.0543	27776.6	50.00	Sequence
DRB1_0301	211	VEPGTGSPPQPTGTIL	EPGTGSPQP	0.0535	28037.8	50.00	Sequence
DRB1_0301	213	PGTGSPQPTGTILAE	PGTGSPQPT	0.0530	28182.0	50.00	Sequence
DRB1_0301	214	GTGSPQPTGTILAE	TGSPQPTGT	0.0510	28805.3	50.00	Sequence
DRB1_0301	210	TVEPGTGSPPQPTGTI	EPGTGSPQP	0.0493	29335.6	50.00	Sequence
DRB1_0301	95	AAIAVGLGAFGLGVL	AAIAVGLGA	0.0475	29896.7	50.00	Sequence
DRB1_0301	94	SAAAIAVGLGAFGLG	SAAAIAVGL	0.0454	30608.9	50.00	Sequence
DRB1_0301	175	GAKGPRSAGTMGTAA	AKGPRSAGT	0.0450	30713.8	50.00	Sequence
DRB1_0301	174	GGAKGPRSAGTMGTA	GGAKGPRSA	0.0408	32166.1	50.00	Sequence

Allele	pos	peptide	core	l-log50k(aff)	affinity(nM)	Bind	Level	%Random	Identity
DRB1_0301	93	ASAAAIIVGLGAFGL	SAAAIIVGL	0.0374	33362.7	50.00	Sequence		

Allele: DRB1_0301. Number of high binders 3. Number of weak binders 23. Number of peptides 218									

Allele	pos	peptide	core	l-log50k(aff)	affinity(nM)	Bind	Level	%Random	Identity
DRB1_0401	151	TGLLVMNNAVPPSRG	LLVMNNVAP	0.8219	6.9	SB	0.10	Sequence	
DRB1_0401	150	NTGLLVMNNAVPPSR	LLVMNNVAP	0.8198	7.0	SB	0.10	Sequence	
DRB1_0401	152	GLLVMNNAVPPSRGT	LLVMNNVAP	0.8161	7.3	SB	0.10	Sequence	
DRB1_0401	149	RNTGLLVMNNAVPPS	LLVMNNVAP	0.7879	9.9	SB	0.30	Sequence	
DRB1_0401	153	LLVMNNVAPPSPRGTV	LLVMNNVAP	0.7347	17.7	SB	1.00	Sequence	
DRB1_0401	148	DRNTGLLVMNNAVAPP	LLVMNNVAP	0.7311	18.3	SB	1.00	Sequence	
DRB1_0401	147	RDRNTGLLVMNNAVAP	LLVMNNVAP	0.6849	30.2	SB	2.00	Sequence	
DRB1_0401	48	RAVRETMVVSAATT	RAVRETMVAV	0.6697	35.6	SB	4.00	Sequence	
DRB1_0401	5	DFELLELATPYALNA	FELLELATP	0.6619	38.8	SB	4.00	Sequence	
DRB1_0401	4	TDFELLELATPYALN	FELLELATP	0.6544	42.1	SB	4.00	Sequence	
DRB1_0401	51	RETMAVVSAAATTAEP	MAVVSAAAT	0.6446	46.8	SB	4.00	Sequence	
DRB1_0401	3	HTDFELLELATPYAL	FELLELATP	0.6400	49.2	SB	4.00	Sequence	
DRB1_0401	6	FELLELATPYALNAV	FELLELATP	0.6376	50.5	WB	4.00	Sequence	
DRB1_0401	50	VRETMAVVSAAATTAE	MAVVSAAAT	0.6266	56.8	WB	8.00	Sequence	
DRB1_0401	47	VRAVRETMVVSAAT	RAVRETMVAV	0.6209	60.4	WB	8.00	Sequence	
DRB1_0401	46	EVRAVRETMVVSAAT	RAVRETMVAV	0.5972	78.1	WB	8.00	Sequence	
DRB1_0401	2	EHTDFELLELATPYA	FELLELATP	0.5896	84.9	WB	8.00	Sequence	
DRB1_0401	49	AVRETMVVSAATTA	RETMAVVSAA	0.5885	85.9	WB	8.00	Sequence	
DRB1_0401	53	TMAVVSAAATTAEP	MAVVSAAAT	0.5835	90.6	WB	8.00	Sequence	
DRB1_0401	52	ETMAVVSAAATTAEP	MAVVSAAAT	0.5829	91.2	WB	8.00	Sequence	
DRB1_0401	45	DEVRAVRETMVVSA	RAVRETMVAV	0.5690	106.0	WB	16.00	Sequence	
DRB1_0401	54	MAVVSAAATTAEP	MAVVSAAAT	0.5496	130.7	WB	16.00	Sequence	
DRB1_0401	142	TVVFSRDRNTGLLVM	VVFSRDRNT	0.5377	148.7	WB	16.00	Sequence	
DRB1_0401	83	RQSRWRTAAFASAAA	QSRWRTAAF	0.5268	167.3	WB	16.00	Sequence	
DRB1_0401	84	QSRWRTAAFASAAA	RWRTAAFAS	0.5261	168.7	WB	16.00	Sequence	
DRB1_0401	143	VVFSRDRNTGLLVMN	FSRDRNTGL	0.5241	172.3	WB	16.00	Sequence	
DRB1_0401	85	SRWRTAAFASAAAIA	RWRTAAFAS	0.5167	186.6	WB	16.00	Sequence	
DRB1_0401	82	RRQSRWRTAAFASAA	QSRWRTAAF	0.5122	195.9	WB	16.00	Sequence	
DRB1_0401	1	TEHTDFELLELATPY	FELLELATP	0.5095	201.9	WB	16.00	Sequence	
DRB1_0401	141	ATVVFSRDRNTGLLV	VVFSRDRNT	0.5045	213.0	WB	16.00	Sequence	
DRB1_0401	86	RWRTAAFASAAAIAV	WRTAAFASA	0.5009	221.4	WB	16.00	Sequence	
DRB1_0401	29	DRVAAAPSPVAAAF	RRVAAAPSP	0.5000	223.7	WB	16.00	Sequence	
DRB1_0401	28	IDRRVAAAPSPVAAA	RRVAAAPSP	0.4991	225.9	WB	16.00	Sequence	
DRB1_0401	103	GAFGLGVLTRPSPPP	AFGLGVLTR	0.4958	234.0	WB	16.00	Sequence	
DRB1_0401	81	VRRQSRWRTAAFASA	QSRWRTAAF	0.4926	242.3	WB	16.00	Sequence	
DRB1_0401	44	NDEVRAVRETMVV	RAVRETMVAV	0.4870	257.3	WB	32.00	Sequence	
DRB1_0401	30	RRVAAAPSPVAAAFN	RRVAAAPSP	0.4832	268.2	WB	32.00	Sequence	
DRB1_0401	7	ELLELATPYALNAV	LLELATPYA	0.4803	276.7	WB	32.00	Sequence	
DRB1_0401	145	FSRDRNTGLLVMNNV	FSRDRNTGL	0.4701	309.0	WB	32.00	Sequence	
DRB1_0401	87	WRTAAFASAAAIAVG	WRTAAFASA	0.4671	319.2	WB	32.00	Sequence	
DRB1_0401	140	TATVVFSRDRNTGLL	VVFSRDRNT	0.4648	327.4	WB	32.00	Sequence	
DRB1_0401	102	LGAFGLGVLTRPSP	AFGLGVLTR	0.4633	332.4	WB	32.00	Sequence	
DRB1_0401	27	DIDRRVAAAPSPVAA	RRVAAAPSP	0.4579	352.7	WB	32.00	Sequence	
DRB1_0401	146	SRDRNTGLLVMNNVA	GLLVMNNVA	0.4574	354.5	WB	32.00	Sequence	
DRB1_0401	144	VFSRDRNTGLLVMNN	FSRDRNTGL	0.4528	372.7	WB	32.00	Sequence	
DRB1_0401	104	AFGLGVLTRPSPPP	LGVLTRPSP	0.4523	374.8	WB	32.00	Sequence	
DRB1_0401	206	LAFTVEPGTGSPQP	LAFTVEPGT	0.4495	386.2	WB	32.00	Sequence	
DRB1_0401	207	LAFTVEPGTGSPQPT	LAFTVEPGT	0.4490	388.4	WB	32.00	Sequence	
DRB1_0401	205	TALFTVEPGTGSPQ	LAFTVEPGT	0.4380	437.2	WB	32.00	Sequence	
DRB1_0401	101	GLGAFGLGVLTRPSP	AFGLGVLTR	0.4248	504.3	32.00	Sequence		
DRB1_0401	43	FNDEVRAVRETMVV	RAVRETMVAV	0.4224	517.6	32.00	Sequence		
DRB1_0401	8	LLELATPYALNAVSD	LLELATPYAL	0.4194	534.7	32.00	Sequence		
DRB1_0401	182	AGTMGTAAVTPSTTA	TMGTAAVTP	0.4142	566.0	32.00	Sequence		
DRB1_0401	183	GTMGTAAVTPSTTAT	TMGTAAVTP	0.4140	566.7	32.00	Sequence		
DRB1_0401	0	MTEHTDFELLELATP	FELLELATP	0.4133	571.2	32.00	Sequence		
DRB1_0401	139	GTATVVFSRDRNTGL	VVFSRDRNT	0.4126	575.9	32.00	Sequence		
DRB1_0401	66	PAHLRTAILDATKPE	LRTAILDAT	0.4106	588.1	32.00	Sequence		
DRB1_0401	88	RTAAFASAAAIAVGL	TAAFASAAA	0.4097	593.8	32.00	Sequence		
DRB1_0401	195	TATLTDLGASTALAF	ATLTDLGAS	0.4084	602.2	32.00	Sequence		
DRB1_0401	204	STALFTVEPGTGSP	LAFTVEPGT	0.4065	615.0	32.00	Sequence		
DRB1_0401	89	TAAFASAAAIAVGLG	TAAFASAAA	0.4042	630.2	32.00	Sequence		
DRB1_0401	179	PRSAGTMGTAAVTPS	RSAGTMGTA	0.3963	686.5	32.00	Sequence		
DRB1_0401	80	EVRRQSRWRTAAFAS	QSRWRTAAF	0.3961	687.9	32.00	Sequence		
DRB1_0401	180	RSAGTMGTAAVTPST	RSAGTMGTA	0.3947	698.7	32.00	Sequence		
DRB1_0401	194	TTATLTDLGASTALA	TATLTDLGA	0.3928	713.5	32.00	Sequence		
DRB1_0401	130	RTVSRPLGAGTATVV	RTVSRPLGA	0.3881	750.5	32.00	Sequence		
DRB1_0401	181	SAGTMGTAAVTPSTT	TMGTAAVTP	0.3862	766.3	50.00	Sequence		
DRB1_0401	105	FGGLGVLTRPSPPP	LGVLTRPSP	0.3841	783.3	50.00	Sequence		

DRB1_0401	26	ADIDRRVAAAPSPVA	RRVAAAPSP	0.3828	794.5	50.00	Sequence
DRB1_0401	65	PPAHLRTAILDATKP	HLRTAILDA	0.3780	837.2	50.00	Sequence
DRB1_0401	67	AHLRTAILDATKPEV	LRTAILDAT	0.3779	838.3	50.00	Sequence
DRB1_0401	68	HLRTAILDATKPEVR	LRTAILDAT	0.3706	906.4	50.00	Sequence
DRB1_0401	178	GPRSAGTMGTAAVTP	RSAGTMGTA	0.3701	911.7	50.00	Sequence
DRB1_0401	42	AFNDEVRAVRETMAV	RAVRETMAV	0.3687	926.1	50.00	Sequence
DRB1_0401	117	TVAEQVLTAPDVRT	TVAEQVLTA	0.3650	963.7	50.00	Sequence
DRB1_0401	118	TVAEQVLTAPDVRTV	TVAEQVLTA	0.3635	978.9	50.00	Sequence
DRB1_0401	9	LELATPYALNAVSD	LELATPYAL	0.3617	998.5	50.00	Sequence
DRB1_0401	184	TMGTAAVTPSTTATL	TMGTAAVTP	0.3576	1044.2	50.00	Sequence
DRB1_0401	165	GTVYQMWLLGGAKGP	YQMWLLGGA	0.3570	1050.8	50.00	Sequence
DRB1_0401	129	VRTVSRPLGAGTATV	RTVSRPLGA	0.3556	1066.2	50.00	Sequence
DRB1_0401	203	ASTALAFSTVEPGTGS	LAFTVEPGT	0.3509	1122.7	50.00	Sequence
DRB1_0401	106	GLGVLTRPSPPTVA	LGVLTRPSP	0.3501	1131.6	50.00	Sequence
DRB1_0401	193	STTATLTDLGASTAL	TATLTDLGA	0.3483	1153.8	50.00	Sequence
DRB1_0401	100	VGLGAFGLGVLTRPS	AFGLGVLTR	0.3481	1156.6	50.00	Sequence
DRB1_0401	121	EQVLTAPDVRTVSRP	VLTAPDVRT	0.3477	1161.7	50.00	Sequence
DRB1_0401	177	KGPRSAGTMGTAAVT	PRSAGTMGT	0.3469	1172.1	50.00	Sequence
DRB1_0401	196	ATLTDLGASTALAFST	TLTDLGAST	0.3439	1211.1	50.00	Sequence
DRB1_0401	90	AAFASAAAIAVGLGA	FASAAAIAV	0.3431	1220.8	50.00	Sequence
DRB1_0401	164	RGTVYQMWLLGGAKG	TVYQMWLLG	0.3427	1226.9	50.00	Sequence
DRB1_0401	128	DVRTVSRPLGAGTAT	RTVSRPLGA	0.3410	1249.8	50.00	Sequence
DRB1_0401	208	AFTVEPGTGSPQPTG	FTVEPGTGS	0.3370	1304.8	50.00	Sequence
DRB1_0401	122	QVLTAPDVRTVSRPL	VLTAPDVRT	0.3352	1330.6	50.00	Sequence
DRB1_0401	166	TVYQMWLLGGAKGPR	YQMWLLGGA	0.3340	1348.0	50.00	Sequence
DRB1_0401	120	AEQVLTAPDVRTVSR	VLTAPDVRT	0.3323	1372.8	50.00	Sequence
DRB1_0401	168	YQMWLLGGAKGPRSA	YQMWLLGGA	0.3291	1420.1	50.00	Sequence
DRB1_0401	11	LATPYALNAVSDDER	PYALNAVSD	0.3252	1481.3	50.00	Sequence
DRB1_0401	163	SRGTVYQMWLLGGAK	TVYQMWLLG	0.3252	1482.1	50.00	Sequence
DRB1_0401	69	LRTAILDATKPEVRR	LRTAILDAT	0.3246	1491.2	50.00	Sequence
DRB1_0401	127	PDVRTVSRPLGAGTA	RTVSRPLGA	0.3235	1509.3	50.00	Sequence
DRB1_0401	116	PPTVAEQVLTAPDVR	TVAEQVLTA	0.3228	1521.9	50.00	Sequence
DRB1_0401	64	EPPAHLRTAILDATK	PAHLRTAIL	0.3203	1562.4	50.00	Sequence
DRB1_0401	10	ELATPYALNAVSDDE	TPYALNAVSD	0.3192	1581.5	50.00	Sequence
DRB1_0401	192	PSTTATLTDLGASTA	TATLTDLGA	0.3190	1584.9	50.00	Sequence
DRB1_0401	138	AGTATVVF SRDRNTG	VVFSRDRNT	0.3140	1672.8	50.00	Sequence
DRB1_0401	12	ATPYALNAVSDDERA	PYALNAVSD	0.3133	1685.2	50.00	Sequence
DRB1_0401	167	VYQMWLLGGAKGPR	YQMWLLGGA	0.3116	1716.4	50.00	Sequence
DRB1_0401	79	PEVRRQSRWRTAFA	QSRWRTAFA	0.3115	1718.1	50.00	Sequence
DRB1_0401	134	RPLGAGTATVVF SRD	PLGAGTATV	0.3082	1781.2	50.00	Sequence
DRB1_0401	25	RADIDRRVAAAPSPV	RRVAAAPSP	0.3066	1812.4	50.00	Sequence
DRB1_0401	107	LGVLTRPSPPTVAE	LGVLTRPSP	0.3028	1888.0	50.00	Sequence
DRB1_0401	119	VAEQVLTAPDVRTVS	VLTAPDVRT	0.3027	1890.5	50.00	Sequence
DRB1_0401	209	FTVEPGTGSPQPTGT	FTVEPGTGS	0.3023	1899.2	50.00	Sequence
DRB1_0401	197	TLTDLGASTALAFSTV	TLTDLGAST	0.3006	1933.5	50.00	Sequence
DRB1_0401	133	SRPLGAGTATVVF SR	PLGAGTATV	0.2986	1976.7	50.00	Sequence
DRB1_0401	31	RVAAPSPVAAAFND	RVAAPSPV	0.2980	1989.8	50.00	Sequence
DRB1_0401	123	VLTAPDVRTVSRPLG	VLTAPDVRT	0.2977	1996.2	50.00	Sequence
DRB1_0401	115	PPPTVAEQVLTAPDV	TVAEQVLTA	0.2969	2012.2	50.00	Sequence
DRB1_0401	13	TPYALNAVSDDERAD	PYALNAVSD	0.2903	2163.0	50.00	Sequence
DRB1_0401	99	AVGLGAFGLGVLTRP	AFGLGVLTR	0.2888	2197.1	50.00	Sequence
DRB1_0401	91	AFASAAAIAVGLGAF	FASAAAIAV	0.2865	2253.4	50.00	Sequence
DRB1_0401	176	AKGPRSAGTMGTAAV	PRSAGTMGT	0.2862	2260.6	50.00	Sequence
DRB1_0401	169	QMWLLGGAKGPR SAG	QMWLLGGAK	0.2849	2293.1	50.00	Sequence
DRB1_0401	202	GASTALAFSTVEPGTG	TALAFSTVEP	0.2846	2300.5	50.00	Sequence
DRB1_0401	162	PSRGTVYQMWLLGGA	TVYQMWLLG	0.2845	2301.1	50.00	Sequence
DRB1_0401	137	GAGTATVVF SRDRNT	VVFSRDRNT	0.2820	2365.2	50.00	Sequence
DRB1_0401	171	WLLGGAKGPR SAGTM	WLLGGAKGP	0.2753	2541.7	50.00	Sequence
DRB1_0401	63	AEP AHLRTAILDAT	PAHLRTAIL	0.2734	2594.6	50.00	Sequence
DRB1_0401	170	MWLLGGAKGPR SAGT	LLGGAKGPR	0.2732	2600.8	50.00	Sequence
DRB1_0401	201	LGASTALAFSTVEPGT	LGASTALAF	0.2703	2683.4	50.00	Sequence
DRB1_0401	132	VSRPLGAGTATVVF S	PLGAGTATV	0.2663	2804.3	50.00	Sequence
DRB1_0401	126	APDVRTVSRPLGAGT	RTVSRPLGA	0.2650	2843.8	50.00	Sequence
DRB1_0401	200	DLGASTALAFSTVEPG	DLGASTALA	0.2600	3000.6	50.00	Sequence
DRB1_0401	199	TDLGASTALAFSTVEP	DLGASTALA	0.2559	3137.1	50.00	Sequence
DRB1_0401	198	LTDLGASTALAFSTVE	LTDLGASTA	0.2555	3150.1	50.00	Sequence
DRB1_0401	55	AVVSAATTAEP PAHL	VSAATTAEP	0.2550	3166.9	50.00	Sequence
DRB1_0401	131	TVSRPLGAGTATVVF	RPLGAGTAT	0.2534	3222.9	50.00	Sequence
DRB1_0401	78	KPEVRRQSRWRTAFA	QSRWRTAFA	0.2518	3279.4	50.00	Sequence
DRB1_0401	185	MGTAAVTPSTTATLT	GTAAVTPST	0.2468	3462.6	50.00	Sequence
DRB1_0401	135	PLGAGTATVVF SRDR	PLGAGTATV	0.2467	3463.5	50.00	Sequence
DRB1_0401	154	LVMNNVAPP SRGTVY	LVMNNVAPP	0.2463	3481.6	50.00	Sequence
DRB1_0401	14	PYALNAVSDDERADI	PYALNAVSD	0.2460	3490.4	50.00	Sequence
DRB1_0401	191	TPSTTATLTDLGAST	TATLTDLGA	0.2460	3491.3	50.00	Sequence
DRB1_0401	41	AAFNDEVRAVRETMA	AAFNDEVRA	0.2443	3556.7	50.00	Sequence
DRB1_0401	172	LLGGAKGPR SAGTMG	LLGGAKGPR	0.2424	3631.4	50.00	Sequence
DRB1_0401	92	FASAAAIAVGLGAFG	FASAAAIAV	0.2362	3882.5	50.00	Sequence

DRB1_0401	175	GAKGPRSAGTMGTAA	PRSAGTMGT	0.2354	3915.6	50.00	Sequence
DRB1_0401	70	RTAILDATKPEVRRQ	TAILDATKP	0.2337	3989.1	50.00	Sequence
DRB1_0401	161	PPSRGTVYQMWLLGG	GTVYQMWLL	0.2264	4316.9	50.00	Sequence
DRB1_0401	114	SPPTVAEQVLTAPD	TVAEQVLTA	0.2256	4355.7	50.00	Sequence
DRB1_0401	98	IAVGLGAFGLGVLTR	AFGLGVLTR	0.2239	4435.2	50.00	Sequence
DRB1_0401	125	TAPDVRTVSRPLGAG	RTVSRPLGA	0.2232	4468.1	50.00	Sequence
DRB1_0401	186	GTAAVTPSTTATLTD	AAVTPSTTA	0.2164	4808.4	50.00	Sequence
DRB1_0401	136	LGAGTATVVFSDRDN	TVVFSRDRN	0.2098	5163.3	50.00	Sequence
DRB1_0401	62	TAEPHAHLRTAILDA	PAHLRTAIL	0.2093	5191.9	50.00	Sequence
DRB1_0401	24	ERADIDRRVAAAPSP	RRVAAAPSP	0.2076	5290.3	50.00	Sequence
DRB1_0401	190	VTPSTTATLTDLGA	TATLTDLGA	0.1988	5816.5	50.00	Sequence
DRB1_0401	188	AAVTPSTTATLTDLG	AAVTPSTTA	0.1960	5995.8	50.00	Sequence
DRB1_0401	187	TAAVTPSTTATLTDL	AAVTPSTTA	0.1957	6016.8	50.00	Sequence
DRB1_0401	71	TAILDATKPEVRRQS	TAILDATKP	0.1956	6023.4	50.00	Sequence
DRB1_0401	97	AIAVGLGAFGLGVL	AIAVGLGAF	0.1951	6054.5	50.00	Sequence
DRB1_0401	173	LGGAKGPRSAGTMGT	LGGAKGPRS	0.1940	6126.2	50.00	Sequence
DRB1_0401	124	LTAPDVRTVSRPLGA	RTVSRPLGA	0.1929	6199.1	50.00	Sequence
DRB1_0401	56	VVSAATTAEPHAHLR	VSAATTAEP	0.1926	6223.5	50.00	Sequence
DRB1_0401	96	AAIAVGLGAFGLGVL	AAIAVGLGA	0.1917	6285.9	50.00	Sequence
DRB1_0401	40	AAAFNDEVRAVRETM	AAFNDEVRA	0.1908	6344.7	50.00	Sequence
DRB1_0401	174	GGAKGPRSAGTMGT	PRSAGTMGT	0.1906	6359.6	50.00	Sequence
DRB1_0401	160	APPSRGTVYQMWLLG	GTVYQMWLL	0.1867	6633.6	50.00	Sequence
DRB1_0401	189	AVTPSTTATLTDLGA	PSTTATLTD	0.1834	6875.1	50.00	Sequence
DRB1_0401	95	AAAIAVGLGAFGLGV	AAIAVGLGA	0.1823	6954.8	50.00	Sequence
DRB1_0401	77	TKPEVRRQSRWRATA	VRRQSRWRT	0.1791	7203.8	50.00	Sequence
DRB1_0401	94	SAAAIAVGLGAFGLG	AAIAVGLGA	0.1775	7325.4	50.00	Sequence
DRB1_0401	108	GVLTRPSPPTVAEQ	VLTRPSPPP	0.1731	7686.1	50.00	Sequence
DRB1_0401	113	PSPPPTVAEQVLTAP	TVAEQVLTA	0.1671	8196.6	50.00	Sequence
DRB1_0401	93	ASAAAIAVGLGAFGL	AAIAVGLGA	0.1641	8469.5	50.00	Sequence
DRB1_0401	61	TTAEPHAHLRTAILD	TTAEPHAHL	0.1582	9030.6	50.00	Sequence
DRB1_0401	109	VLTRPSPPPPTVAEQV	VLTRPSPPP	0.1581	9040.3	50.00	Sequence
DRB1_0401	39	VAAAFNDEVRAVRET	AAFNDEVRA	0.1504	9823.5	50.00	Sequence
DRB1_0401	217	SPQPTGTILAEPLG	GTILAEPL	0.1420	10753.9	50.00	Sequence
DRB1_0401	112	RSPFPPTVAEQVLT	TVAEQVLTA	0.1403	10962.3	50.00	Sequence
DRB1_0401	57	VSAATTAEPHAHLRT	VSAATTAEP	0.1401	10984.4	50.00	Sequence
DRB1_0401	32	VAAAPSPVAAAFNDE	VAAAPSPVA	0.1393	11074.5	50.00	Sequence
DRB1_0401	38	PVAAAFNDEVRAVRE	AAFNDEVRA	0.1354	11555.4	50.00	Sequence
DRB1_0401	76	ATKPEVRRQSRWRATA	VRRQSRWRT	0.1330	11860.6	50.00	Sequence
DRB1_0401	216	GSPQPTGTILAEPL	GTILAEPL	0.1302	12223.3	50.00	Sequence
DRB1_0401	23	DERADIDRRVAAAPS	IDRRVAAAP	0.1275	12584.0	50.00	Sequence
DRB1_0401	15	YALNAVSDDERADID	YALNAVSD	0.1236	13129.9	50.00	Sequence
DRB1_0401	37	SPVAAAFNDEVRAVR	AAFNDEVRA	0.1229	13229.3	50.00	Sequence
DRB1_0401	159	VAPPSRGTVYQMWLL	GTVYQMWLL	0.1207	13552.2	50.00	Sequence
DRB1_0401	215	TGSPQPTGTILAEPL	PQPTGTILA	0.1163	14206.7	50.00	Sequence
DRB1_0401	60	ATTAEPHAHLRTAIL	PAHLRTAIL	0.1125	14807.8	50.00	Sequence
DRB1_0401	213	PGTGSPQPTGTILAE	GTGSPQPTG	0.1116	14940.7	50.00	Sequence
DRB1_0401	75	DATKPEVRRQSRWRATA	VRRQSRWRT	0.1099	15229.8	50.00	Sequence
DRB1_0401	212	EPGTGSPQPTGTILA	PGTGSPQPT	0.1076	15600.6	50.00	Sequence
DRB1_0401	214	GTGSPQPTGTILAE	GTGSPQPTG	0.1061	15860.3	50.00	Sequence
DRB1_0401	22	DERADIDRRVAAAP	RADIDRRVA	0.1059	15900.8	50.00	Sequence
DRB1_0401	155	VMNNVAPPSPRGTVYQ	VMNNVAPPS	0.1036	16306.1	50.00	Sequence
DRB1_0401	16	ALNAVSDDERADIDR	LNAVSDDER	0.0993	17070.8	50.00	Sequence
DRB1_0401	211	VEPGTGSPQPTGTIL	GTGSPQPTG	0.0984	17242.5	50.00	Sequence
DRB1_0401	36	PSPVAAAFNDEVRAV	VAAAFNDEV	0.0969	17515.7	50.00	Sequence
DRB1_0401	17	LNAVSDDERADIDRR	LNAVSDDER	0.0964	17619.5	50.00	Sequence
DRB1_0401	74	LDATKPEVRRQSRWR	LDATKPEVR	0.0901	18858.8	50.00	Sequence
DRB1_0401	210	TVEPPTGSPQPTGTI	PGTGSPQPT	0.0885	19201.2	50.00	Sequence
DRB1_0401	35	APSPVAAAFNDEVRA	AAFNDEVRA	0.0844	20065.8	50.00	Sequence
DRB1_0401	111	TRPSPPTVAEQVLT	TRPSPPTV	0.0841	20136.1	50.00	Sequence
DRB1_0401	58	SAATTAEPHAHLRTA	TTAEPHAHL	0.0818	20637.6	50.00	Sequence
DRB1_0401	73	ILDATKPEVRRQSRW	LDATKPEVR	0.0807	20875.2	50.00	Sequence
DRB1_0401	158	NVAPPSRGTVYQMWL	PSRGTVYQM	0.0805	20927.3	50.00	Sequence
DRB1_0401	72	AILDATKPEVRRQSR	LDATKPEVR	0.0800	21049.4	50.00	Sequence
DRB1_0401	21	SDDERADIDRRVAAA	DERADIDRR	0.0798	21097.3	50.00	Sequence
DRB1_0401	110	LTRPSPPTVAEQVLT	LTRPSPPT	0.0770	21734.0	50.00	Sequence
DRB1_0401	59	AATTAEPHAHLRTAI	TTAEPHAHL	0.0769	21762.7	50.00	Sequence
DRB1_0401	157	NNVAPPSPRGTVYQMW	NNVAPPSPRG	0.0714	23081.6	50.00	Sequence
DRB1_0401	156	MNNVAPPSPRGTVYQ	MNNVAPPSPR	0.0701	23410.1	50.00	Sequence
DRB1_0401	33	AAAPSPVAAAFNDEV	AAAPSPVAA	0.0661	24463.2	50.00	Sequence
DRB1_0401	20	VSDDERADIDRRVAA	DERADIDRR	0.0637	25105.2	50.00	Sequence
DRB1_0401	34	AAPSPVAAAFNDEV	SPVAAAFND	0.0630	25285.9	50.00	Sequence
DRB1_0401	18	NAVSDDERADIDRRV	NAVSDDERA	0.0620	25573.4	50.00	Sequence
DRB1_0401	19	AVSDDERADIDRRVA	DERADIDRR	0.0567	27085.7	50.00	Sequence

Allele: DRB1_0401. Number of high binders 12. Number of weak binders 37. Number of peptides 218

Allele	pos	peptide	core	l-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
DRB1_0404	150	NTGLLVMMNNVAPPSR	LLVMNNVAP	0.7543	14.3	SB	1.00	Sequence
DRB1_0404	151	TGLLVMMNNVAPPSSRG	LLVMNNVAP	0.7536	14.4	SB	1.00	Sequence
DRB1_0404	149	RNTGLLVMMNNVAPPS	LLVMNNVAP	0.7322	18.1	SB	2.00	Sequence
DRB1_0404	152	GLLVMMNNVAPPSSRG	LLVMNNVAP	0.6976	26.4	SB	4.00	Sequence
DRB1_0404	148	DRNTGLLVMMNNVAPP	LLVMNNVAP	0.6907	28.4	SB	4.00	Sequence
DRB1_0404	153	LLVMMNNVAPPSSRGTV	LLVMNNVAP	0.6344	52.2	WB	8.00	Sequence
DRB1_0404	6	FELLELATPYALNAV	ELLELATPY	0.6340	52.4	WB	8.00	Sequence
DRB1_0404	5	DFELLELATPYALNA	ELLELATPY	0.6314	53.9	WB	8.00	Sequence
DRB1_0404	147	RDRNTGLLVMMNNVAP	LLVMNNVAP	0.6308	54.3	WB	8.00	Sequence
DRB1_0404	4	TDFELLELATPYALN	ELLELATPY	0.6119	66.7	WB	8.00	Sequence
DRB1_0404	7	ELLELATPYALNAVS	ELLELATPY	0.5944	80.5	WB	16.00	Sequence
DRB1_0404	166	TVYQMWLLGGAKGPR	TVYQMWLLG	0.5908	83.7	WB	16.00	Sequence
DRB1_0404	165	GTVYQMWLLGGAKGP	TVYQMWLLG	0.5851	89.1	WB	16.00	Sequence
DRB1_0404	164	RGTVYQMWLLGGAKG	TVYQMWLLG	0.5736	100.9	WB	16.00	Sequence
DRB1_0404	52	ETMAVVSAAATTAEP	MAVVSAAAT	0.5716	103.0	WB	16.00	Sequence
DRB1_0404	3	HTDFELLELATPYAL	ELLELATPY	0.5685	106.5	WB	16.00	Sequence
DRB1_0404	51	RETMAVVSAAATTAEP	MAVVSAAAT	0.5685	106.6	WB	16.00	Sequence
DRB1_0404	53	TMAVVSAAATTAEP	MAVVSAAAT	0.5544	124.1	WB	16.00	Sequence
DRB1_0404	50	VRETMAVVSAAATTAEP	TMAVVSAAAT	0.5448	137.7	WB	16.00	Sequence
DRB1_0404	163	SRGTVYQMWLLGGAK	TVYQMWLLG	0.5239	172.6	WB	32.00	Sequence
DRB1_0404	49	AVRETMAVVSAAATTAEP	ETMAVVSAAAT	0.5188	182.5	WB	32.00	Sequence
DRB1_0404	2	EHTDFELLELATPYA	ELLELATPY	0.5149	190.3	WB	32.00	Sequence
DRB1_0404	46	EVRAVRETMAVVSAAAT	EVRAVRETM	0.5138	192.5	WB	32.00	Sequence
DRB1_0404	167	VYQMWLLGGAKGPR	YQMWLLGGA	0.4974	229.9	WB	32.00	Sequence
DRB1_0404	45	DEVRAVRETMAVVSAAAT	EVRAVRETM	0.4962	232.9	WB	32.00	Sequence
DRB1_0404	54	MAVVSAAATTAEP	AVVSAAATTA	0.4955	234.8	WB	32.00	Sequence
DRB1_0404	168	YQMWLLGGAKGPR	YQMWLLGGA	0.4856	261.2	WB	32.00	Sequence
DRB1_0404	48	RAVRETMAVVSAAAT	AVRETMAVV	0.4827	269.6	WB	32.00	Sequence
DRB1_0404	146	SRDRNTGLLVMMNNVA	TGLLVMMNNV	0.4766	288.0	WB	32.00	Sequence
DRB1_0404	44	NDEVRAVRETMAVVSAAAT	EVRAVRETM	0.4606	342.5	WB	32.00	Sequence
DRB1_0404	47	VRAVRETMAVVSAAAT	AVRETMAVV	0.4496	385.8	WB	32.00	Sequence
DRB1_0404	162	PSRGTVYQMWLLGGA	TVYQMWLLG	0.4469	397.0	WB	32.00	Sequence
DRB1_0404	8	LLELATPYALNAVSD	LELATPYAL	0.4437	411.0	WB	32.00	Sequence
DRB1_0404	67	AHLRTAILDATKPEV	LRTAILDAT	0.4427	415.8	WB	32.00	Sequence
DRB1_0404	66	PAHLRTAILDATKPE	LRTAILDAT	0.4367	443.4	WB	32.00	Sequence
DRB1_0404	68	HLRTAILDATKPEV	HLRTAILDA	0.4325	464.2	WB	32.00	Sequence
DRB1_0404	1	TEHTDFELLELATPY	ELLELATPY	0.4270	492.8	WB	32.00	Sequence
DRB1_0404	43	FNDEVRAVRETMAVVSAAAT	EVRAVRETM	0.4260	497.9	WB	32.00	Sequence
DRB1_0404	29	DRRVAAAPSPVAAAF	RVAAAPSPV	0.4216	522.5	WB	32.00	Sequence
DRB1_0404	86	RWRTAAFASAAAI	WRTAAFASA	0.4129	574.0	WB	32.00	Sequence
DRB1_0404	65	PPAHLRTAILDATKPE	HLRTAILDA	0.4104	589.8	WB	32.00	Sequence
DRB1_0404	30	RRVAAAPSPVAAAFN	RVAAAPSPV	0.4080	604.8	WB	32.00	Sequence
DRB1_0404	142	TVVFSRDRNTGLLV	VVFSRDRNT	0.4071	611.1	WB	32.00	Sequence
DRB1_0404	141	ATVVFSRDRNTGLLV	VVFSRDRNT	0.4048	626.2	WB	50.00	Sequence
DRB1_0404	28	IDRRVAAAPSPVAAA	RVAAAPSPV	0.4045	628.4	WB	50.00	Sequence
DRB1_0404	143	VVFSRDRNTGLLV	VVFSRDRNT	0.4029	639.6	WB	50.00	Sequence
DRB1_0404	85	SRWRTAAFASAAAI	RTAAFASAA	0.4024	642.5	WB	50.00	Sequence
DRB1_0404	55	AVVSAAATTAEP	AVVSAAATTA	0.4016	648.1	WB	50.00	Sequence
DRB1_0404	87	WRTAAFASAAAI	AAFASAAAI	0.4010	652.6	WB	50.00	Sequence
DRB1_0404	9	LELATPYALNAVSD	LELATPYAL	0.3957	691.0	WB	50.00	Sequence
DRB1_0404	205	TALAFVTEPGTGSPQ	TALAFVTEP	0.3951	695.9	WB	50.00	Sequence
DRB1_0404	154	LVMNNVAPPSSRGTV	LVMNNVAPP	0.3939	704.8	WB	50.00	Sequence
DRB1_0404	193	STTATLTDLGASTAL	STTATLTDL	0.3919	720.1	WB	50.00	Sequence
DRB1_0404	169	QMWLLGGAKGPR	QMWLLGGAK	0.3846	779.0	WB	50.00	Sequence
DRB1_0404	161	PPSRGTVYQMWLLG	TVYQMWLLG	0.3805	814.5	WB	50.00	Sequence
DRB1_0404	192	PSTTATLTDLGASTA	STTATLTDL	0.3800	819.2	WB	50.00	Sequence
DRB1_0404	69	LRTAILDATKPEVRR	LRTAILDAT	0.3787	830.7	WB	50.00	Sequence
DRB1_0404	204	STALAFVTEPGTGSP	TALAFVTEP	0.3782	835.1	WB	50.00	Sequence
DRB1_0404	84	QSRWRTAAFASAAAI	WRTAAFASA	0.3763	853.0	WB	50.00	Sequence
DRB1_0404	140	TATVVFSRDRNTGLL	VVFSRDRNT	0.3763	853.0	WB	50.00	Sequence
DRB1_0404	118	TVAEQVLTAPDVRTV	QVLTAPDVR	0.3741	873.2	WB	50.00	Sequence
DRB1_0404	97	AIAVGLGAFGLVLT	AIAVGLGAF	0.3727	886.4	WB	50.00	Sequence
DRB1_0404	42	AFNDEVRAVRETMAV	EVRAVRETM	0.3716	897.3	WB	50.00	Sequence
DRB1_0404	96	AAIAVGLGAFGLVLT	AIAVGLGAF	0.3676	936.4	WB	50.00	Sequence
DRB1_0404	194	TTATLTDLGASTALA	TLTDLGAST	0.3666	947.0	WB	50.00	Sequence
DRB1_0404	64	EPPAHLRTAILDATK	HLRTAILDA	0.3609	1006.9	WB	50.00	Sequence
DRB1_0404	27	DIDRRVAAAPSPVAA	RRVAAAPSP	0.3605	1011.4	WB	50.00	Sequence
DRB1_0404	119	VAEQVLTAPDVRTV	QVLTAPDVR	0.3592	1026.3	WB	50.00	Sequence
DRB1_0404	117	PTVAEQVLTAPDVRTV	TVAEQVLT	0.3575	1045.2	WB	50.00	Sequence
DRB1_0404	95	AAAIAVGLGAFGLV	AIAVGLGAF	0.3557	1065.6	WB	50.00	Sequence
DRB1_0404	104	AFGLVLTTRPSPPT	LGVLTRPSP	0.3548	1075.9	WB	50.00	Sequence
DRB1_0404	203	ASTALAFVTEPGTGS	TALAFVTEP	0.3541	1083.6	WB	50.00	Sequence
DRB1_0404	191	TPSTTATLTDLGAST	STTATLTDL	0.3541	1083.7	WB	50.00	Sequence

DRB1_0404	195	TATLTDLGASTALAF	TLTDLGAST	0.3508	1123.2	50.00	Sequence
DRB1_0404	145	FSRDRNTGLLVMMNV	TGLLVMMNV	0.3497	1136.6	50.00	Sequence
DRB1_0404	106	GLGVLTRPSPPTVA	LGVLTRPSP	0.3495	1139.8	50.00	Sequence
DRB1_0404	105	FGLGVLTRPSPPTV	LGVLTRPSP	0.3474	1165.3	50.00	Sequence
DRB1_0404	88	RTAAFASAAAIAVGL	AAFASAAAI	0.3469	1172.1	50.00	Sequence
DRB1_0404	94	SAAAIAVGLGAFGLG	AIAVGLGAF	0.3415	1242.7	50.00	Sequence
DRB1_0404	120	AEQVLTAPDVRTVSR	QVLTAPDVR	0.3411	1247.7	50.00	Sequence
DRB1_0404	107	LGVLTRPSPPTVAE	LGVLTRPSP	0.3383	1285.8	50.00	Sequence
DRB1_0404	11	LATPYALNAVSDDER	TPYALNAVS	0.3338	1349.7	50.00	Sequence
DRB1_0404	10	ELATPYALNAVSDDE	TPYALNAVS	0.3322	1374.2	50.00	Sequence
DRB1_0404	116	PPTVAEQVLTAPDVR	TVAEQVLTA	0.3319	1378.3	50.00	Sequence
DRB1_0404	83	RQSRWRRTAAFASAAA	WRTAAFASA	0.3316	1382.4	50.00	Sequence
DRB1_0404	196	ATLTDLGASTALAF	TLTDLGAST	0.3308	1394.3	50.00	Sequence
DRB1_0404	183	GTMGTAAVTPSTTAT	TMGTAAVTP	0.3267	1457.7	50.00	Sequence
DRB1_0404	89	TAAFASAAAIAVGLG	AAFASAAAI	0.3261	1467.0	50.00	Sequence
DRB1_0404	190	VTPSTTATLTDLGAS	VTPSTTATL	0.3261	1467.2	50.00	Sequence
DRB1_0404	182	AGTMGTAAVTPSTTA	TMGTAAVTP	0.3260	1469.0	50.00	Sequence
DRB1_0404	103	GAFGLGVLTRPSPPP	LGVLTRPSP	0.3256	1475.1	50.00	Sequence
DRB1_0404	184	TMGTAAVTPSTTATL	TMGTAAVTP	0.3256	1476.2	50.00	Sequence
DRB1_0404	128	DVRTVSRPLGAGTAT	DVRTVSRPL	0.3225	1526.0	50.00	Sequence
DRB1_0404	202	GASTALAFVTEPGTG	TALAFVTEP	0.3209	1552.8	50.00	Sequence
DRB1_0404	139	GTATVVFSDRNTGL	VVFSDRNT	0.3199	1569.1	50.00	Sequence
DRB1_0404	197	TLTDLGASTALAF	TLTDLGAST	0.3194	1578.5	50.00	Sequence
DRB1_0404	127	PDVRTVSRPLGAGTA	DVRTVSRPL	0.3191	1583.1	50.00	Sequence
DRB1_0404	181	SAGTMGTAAVTPSTT	TMGTAAVTP	0.3148	1659.1	50.00	Sequence
DRB1_0404	63	AEPFAHLRTAILDAT	HLRTAILDA	0.3147	1660.3	50.00	Sequence
DRB1_0404	31	RVAAAPSPVAAAFND	RVAAAPSPV	0.3134	1683.2	50.00	Sequence
DRB1_0404	126	APDVRTVSRPLGAGT	DVRTVSRPL	0.3133	1685.3	50.00	Sequence
DRB1_0404	121	EQVLTAPDVRTVSRP	QVLTAPDVR	0.3113	1722.4	50.00	Sequence
DRB1_0404	41	AAFNDDEVRAVRETMA	EVRAVRETM	0.3080	1784.3	50.00	Sequence
DRB1_0404	189	AVTPSTTATLTDLGA	VTPSTTATL	0.3080	1784.5	50.00	Sequence
DRB1_0404	12	ATPYALNAVSDDERA	TPYALNAVS	0.3035	1874.8	50.00	Sequence
DRB1_0404	90	AAFASAAAIAVGLGA	AAFASAAAI	0.3026	1893.3	50.00	Sequence
DRB1_0404	187	TAAVTPSTTATLTDL	VTPSTTATL	0.3004	1937.6	50.00	Sequence
DRB1_0404	26	ADIDRRVAAAPSPVA	RRVAAAPSP	0.3001	1944.4	50.00	Sequence
DRB1_0404	144	VFSRDRNTGLLVMMN	VFSRDRNTG	0.2978	1993.6	50.00	Sequence
DRB1_0404	206	ALAFVTEPGTGSPQP	LAFTVEPGT	0.2941	2074.5	50.00	Sequence
DRB1_0404	125	TAPDVRTVSRPLGAG	DVRTVSRPL	0.2937	2083.3	50.00	Sequence
DRB1_0404	93	ASAAAIAVGLGAFGL	AIAVGLGAF	0.2937	2083.3	50.00	Sequence
DRB1_0404	82	RRQSRWRRTAAFASAA	WRTAAFASA	0.2923	2116.4	50.00	Sequence
DRB1_0404	115	PPPTVAEQVLTAPDV	TVAEQVLTA	0.2886	2203.1	50.00	Sequence
DRB1_0404	188	AAVTPSTTATLTDLG	VTPSTTATL	0.2883	2210.3	50.00	Sequence
DRB1_0404	102	LGAFGLGVLTRPSP	LGVLTRPSP	0.2851	2287.9	50.00	Sequence
DRB1_0404	92	FASAAAIAVGLGAFG	FASAAAIAV	0.2845	2301.9	50.00	Sequence
DRB1_0404	185	MGTAAVTPSTTATLT	MGTAAVTPS	0.2842	2308.9	50.00	Sequence
DRB1_0404	160	APPSRGTVYQMWLLG	TVYQMWLLG	0.2836	2325.4	50.00	Sequence
DRB1_0404	70	RTAILDATKPEVRRQ	TAILDATKP	0.2825	2352.0	50.00	Sequence
DRB1_0404	217	SPQPTGTILAEPLG	TILAEPLG	0.2819	2367.5	50.00	Sequence
DRB1_0404	186	GTAAVTPSTTATLTD	VTPSTTATL	0.2798	2422.1	50.00	Sequence
DRB1_0404	201	LGASTALAFVTEPGT	TALAFVTEP	0.2781	2466.8	50.00	Sequence
DRB1_0404	180	RSAGTMGTAAVTPST	TMGTAAVTP	0.2764	2512.4	50.00	Sequence
DRB1_0404	98	IAVGLGAFGLGVLTR	IAVGLGAFG	0.2760	2523.7	50.00	Sequence
DRB1_0404	199	TDLGASTALAFVTEP	TDLGASTAL	0.2758	2528.8	50.00	Sequence
DRB1_0404	0	MTEHTDFELLELATP	FELLELATP	0.2751	2548.9	50.00	Sequence
DRB1_0404	122	QVLTAPDVRTVSRPL	QVLTAPDVR	0.2702	2686.0	50.00	Sequence
DRB1_0404	207	LAFTVEPGTGSPQPT	LAFTVEPGT	0.2698	2699.7	50.00	Sequence
DRB1_0404	124	LTAPDVRTVSRPLGA	DVRTVSRPL	0.2661	2808.7	50.00	Sequence
DRB1_0404	138	AGTATVVFSDRNTG	VVFSDRNT	0.2637	2882.6	50.00	Sequence
DRB1_0404	129	VRTVSRPLGAGTATV	TVSRPLGAG	0.2596	3012.6	50.00	Sequence
DRB1_0404	62	TAEPFAHLRTAILDA	HLRTAILDA	0.2579	3068.1	50.00	Sequence
DRB1_0404	198	LTDLGASTALAF	TDLGASTAL	0.2564	3120.7	50.00	Sequence
DRB1_0404	108	GVLTRPSPPTVAEQ	GVLTRPSP	0.2559	3135.9	50.00	Sequence
DRB1_0404	101	GLGAFGLGVLTRPSP	AFGLGVLTR	0.2533	3225.6	50.00	Sequence
DRB1_0404	81	VRRQSRWRRTAAFASA	QSRWRRTAAF	0.2529	3240.8	50.00	Sequence
DRB1_0404	200	DLGASTALAFVTEPG	TALAFVTEP	0.2522	3263.6	50.00	Sequence
DRB1_0404	130	RTVSRPLGAGTATVV	TVSRPLGAG	0.2511	3303.4	50.00	Sequence
DRB1_0404	179	PRSAGTMGTAAVTPS	TMGTAAVTP	0.2475	3436.3	50.00	Sequence
DRB1_0404	132	VSRPLGAGTATVVF	PLGAGTATV	0.2469	3457.6	50.00	Sequence
DRB1_0404	133	SRPLGAGTATVVF	PLGAGTATV	0.2463	3482.0	50.00	Sequence
DRB1_0404	13	TPYALNAVSDDERAD	TPYALNAVS	0.2425	3628.2	50.00	Sequence
DRB1_0404	91	AFASAAAIAVGLGAF	FASAAAIAV	0.2416	3660.6	50.00	Sequence
DRB1_0404	25	RADIDRRVAAAPSPV	RRVAAAPSP	0.2406	3700.7	50.00	Sequence
DRB1_0404	123	VLTAPDVRTVSRPLG	DVRTVSRPL	0.2390	3766.4	50.00	Sequence
DRB1_0404	208	AFTVEPGTGSPQPTG	FTVEPGTGS	0.2384	3792.3	50.00	Sequence
DRB1_0404	71	TAILDATKPEVRRQS	TAILDATKP	0.2376	3823.1	50.00	Sequence
DRB1_0404	134	RPLGAGTATVVF	PLGAGTATV	0.2361	3885.6	50.00	Sequence
DRB1_0404	131	TVSRPLGAGTATVV	PLGAGTATV	0.2347	3944.0	50.00	Sequence

DRB1_0404	56	VVSAATTAEPHAHLR	VVSAATTAE	0.2328	4027.2	50.00	Sequence
DRB1_0404	114	SPPTVAEQVLTAPD	TVAEQVLTA	0.2303	4140.1	50.00	Sequence
DRB1_0404	170	MWLLGGAKGPRRSAGT	WLLGGAKGP	0.2273	4272.6	50.00	Sequence
DRB1_0404	178	GPRRSAGTMGTAAVTP	SAGTMGTAA	0.2204	4607.5	50.00	Sequence
DRB1_0404	109	VLTRPSPPTVAEQV	VLTRPSPPP	0.2183	4711.4	50.00	Sequence
DRB1_0404	135	PLGAGTATVVFSDRDR	PLGAGTATV	0.2151	4878.2	50.00	Sequence
DRB1_0404	209	FTVEPGTGSPOPTGT	FTVEPGTGS	0.2044	5476.8	50.00	Sequence
DRB1_0404	40	AAAFNDEVRAVRETM	EVRAVRETM	0.2033	5539.6	50.00	Sequence
DRB1_0404	14	PYALNAVSDDERADI	YALNAVSD	0.1983	5853.0	50.00	Sequence
DRB1_0404	100	VGLGAFGLGVLTRPS	AFGLGVLTR	0.1979	5876.7	50.00	Sequence
DRB1_0404	36	PSPVAAAFNDEVRAV	PVAAAFNDE	0.1937	6148.8	50.00	Sequence
DRB1_0404	99	AVGLGAFGLGVLTRP	AFGLGVLTR	0.1920	6265.3	50.00	Sequence
DRB1_0404	137	GAGTATVVFSDRDRNT	VVFSDRDRNT	0.1896	6428.9	50.00	Sequence
DRB1_0404	37	SPVAAAFNDEVRAVR	PVAAAFNDE	0.1855	6722.3	50.00	Sequence
DRB1_0404	35	APSPVAAAFNDEVRA	PVAAAFNDE	0.1837	6854.4	50.00	Sequence
DRB1_0404	155	VMNNVAPP SRGT VYQ	VMNNVAPPS	0.1791	7200.5	50.00	Sequence
DRB1_0404	171	WLLGGAKGPRRSAGTM	WLLGGAKGP	0.1768	7380.9	50.00	Sequence
DRB1_0404	80	EVRRQSRWR TAA FAS	RQSRWR TAA	0.1764	7414.9	50.00	Sequence
DRB1_0404	113	PSPPPTVAEQVLTAP	TVAEQVLTA	0.1744	7577.0	50.00	Sequence
DRB1_0404	38	PVAAAFNDEVRAVRE	PVAAAFNDE	0.1721	7763.9	50.00	Sequence
DRB1_0404	34	AAAPSPVAAAFNDEV	PVAAAFNDE	0.1674	8172.1	50.00	Sequence
DRB1_0404	32	VAAAPSPVAAAFNDE	VAAAPSPVA	0.1657	8325.3	50.00	Sequence
DRB1_0404	24	ERADIDRRVAAAPSP	RRVAAAPSP	0.1654	8350.2	50.00	Sequence
DRB1_0404	177	KGPRRSAGTMGTAAVT	SAGTMGTAA	0.1645	8432.9	50.00	Sequence
DRB1_0404	15	YALNAVSDDERADID	YALNAVSD	0.1637	8510.8	50.00	Sequence
DRB1_0404	110	LTRPSPPTVAEQVLT	TRPSPPTV	0.1626	8604.7	50.00	Sequence
DRB1_0404	61	TTAEPHAHLR TAILD	PAHLR TAIL	0.1610	8755.3	50.00	Sequence
DRB1_0404	33	AAAPSPVAAAFNDEV	PVAAAFNDE	0.1479	10090.6	50.00	Sequence
DRB1_0404	176	AKGPRRSAGTMGTAAV	SAGTMGTAA	0.1450	10415.1	50.00	Sequence
DRB1_0404	39	VAAAFNDEVRAVRETT	VAAAFNDEV	0.1434	10594.8	50.00	Sequence
DRB1_0404	79	PEVRRQSRWR TAAFA	RRQSRWR TAA	0.1419	10774.2	50.00	Sequence
DRB1_0404	216	GSPOPTGTILAE LPL	SPQPTGTIL	0.1387	11150.8	50.00	Sequence
DRB1_0404	112	RPSPPPTVAEQVLT	TVAEQVLTA	0.1342	11700.6	50.00	Sequence
DRB1_0404	111	TRPSPPTVAEQVLT	TRPSPPTV	0.1319	12000.9	50.00	Sequence
DRB1_0404	60	ATTAEPHAHLR TAIL	PAHLR TAIL	0.1317	12031.1	50.00	Sequence
DRB1_0404	159	VAPPSRGT VYQ MWLL	RGT VYQ MWL	0.1289	12389.2	50.00	Sequence
DRB1_0404	72	ILDATKPEVRRQSR	ILDATKPEV	0.1247	12965.7	50.00	Sequence
DRB1_0404	215	TGSPQPTGTILAE L	PQPTGTILA	0.1196	13711.7	50.00	Sequence
DRB1_0404	210	TVEPGTGSPOPTGTI	TVEPGTGS	0.1192	13770.0	50.00	Sequence
DRB1_0404	175	GAKGPRRSAGTMGTAA	KGPRRSAGTM	0.1182	13921.4	50.00	Sequence
DRB1_0404	214	GTGSPQPTGTILAE L	SPQPTGTIL	0.1175	14027.1	50.00	Sequence
DRB1_0404	57	VSAATTAEPHAHLRT	VSAATTAEP	0.1157	14304.2	50.00	Sequence
DRB1_0404	78	KPEVRRQSRWR TAAF	QSRWR TAAF	0.1133	14673.8	50.00	Sequence
DRB1_0404	136	LGAGTATVVFSDRDRN	TVVFSDRDRN	0.1132	14684.8	50.00	Sequence
DRB1_0404	172	LLGGAKGPRRSAGTMG	LLGGAKGPR	0.1111	15035.8	50.00	Sequence
DRB1_0404	156	MNNVAPPSRGT VYQM	VAPPSRGT V	0.1093	15320.7	50.00	Sequence
DRB1_0404	174	GGAKGPRRSAGTMGT	KGPRRSAGTM	0.1070	15706.1	50.00	Sequence
DRB1_0404	158	NVAPPSRGT VYQ MWL	VAPPSRGT V	0.1068	15735.7	50.00	Sequence
DRB1_0404	212	EPGTGSPQPTGTILA	SPQPTGTIL	0.1060	15882.1	50.00	Sequence
DRB1_0404	213	PTGSPQPTGTILAE	SPQPTGTIL	0.1046	16120.0	50.00	Sequence
DRB1_0404	157	NNVAPPSRGT VYQ MW	VAPPSRGT V	0.1044	16155.9	50.00	Sequence
DRB1_0404	23	DERADIDRRVAAAPS	DIDRRVAAA	0.1036	16292.7	50.00	Sequence
DRB1_0404	16	ALNAVSDDERADIDR	ALNAVSDDE	0.0972	17464.8	50.00	Sequence
DRB1_0404	211	VEPGTGSPOPTGTIL	EPGTGSPQP	0.0972	17465.6	50.00	Sequence
DRB1_0404	77	TKPEVRRQSRWR TAA	RRQSRWR TAA	0.0971	17491.7	50.00	Sequence
DRB1_0404	173	LGGAKGPRRSAGTMGT	KGPRRSAGTM	0.0950	17891.7	50.00	Sequence
DRB1_0404	73	ILDATKPEVRRQSRW	ILDATKPEV	0.0935	18179.6	50.00	Sequence
DRB1_0404	59	AATTAEPHAHLR TAI	ATTAEPHAH	0.0931	18264.7	50.00	Sequence
DRB1_0404	58	SAATTAEPHAHLR T	SAATTAEPH	0.0917	18532.3	50.00	Sequence
DRB1_0404	76	ATKPEVRRQSRWR T	RRQSRWR T	0.0772	21688.4	50.00	Sequence
DRB1_0404	22	DDERADIDRRVAAAP	DIDRRVAAA	0.0744	22355.1	50.00	Sequence
DRB1_0404	75	DATKPEVRRQSRWR T	KPEVRRQSR	0.0658	24532.1	50.00	Sequence
DRB1_0404	17	LNAVSDDERADIDRR	NAVSDDERA	0.0651	24719.7	50.00	Sequence
DRB1_0404	74	LDATKPEVRRQSRWR	TKPEVRRQS	0.0627	25358.8	50.00	Sequence
DRB1_0404	21	SDDERADIDRRVAAA	DIDRRVAAA	0.0593	26313.6	50.00	Sequence
DRB1_0404	18	NAVSDDERADIDRRV	NAVSDDERA	0.0524	28374.1	50.00	Sequence
DRB1_0404	19	AVSDDERADIDRRVA	AVSDDERAD	0.0377	33246.3	50.00	Sequence
DRB1_0404	20	VSDDERADIDRRVAA	DERADIDRR	0.0337	34733.7	50.00	Sequence

Allele: DRB1_0404. Number of high binders 5. Number of weak binders 33. Number of peptides 218

Allele	pos	peptide	core 1-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity	
DRB1_0405	150	NTGLLVMMNNVAPPSR	GLLVMMNVA	0.6776	32.7	SB	4.00	Sequence

DRB1_0405	149	RNTGLLVMMNNVAPPS	GLLVMMNNVA	0.6726	34.5	SB	8.00	Sequence
DRB1_0405	151	TGLLVMMNNVAPPSRG	GLLVMMNNVA	0.6696	35.7	SB	8.00	Sequence
DRB1_0405	152	GLLVMMNNVAPPSRGT	GLLVMMNNVA	0.6579	40.5	SB	8.00	Sequence
DRB1_0405	148	DRNTGGLLVMMNNVAPP	TGLLVMMNNV	0.6472	45.5	SB	8.00	Sequence
DRB1_0405	5	DFELLELELATPYALNA	FELLELELATP	0.6374	50.6	WB	8.00	Sequence
DRB1_0405	4	TDFELLELELATPYALN	FELLELELATP	0.6360	51.3	WB	8.00	Sequence
DRB1_0405	3	HTDFELLELELATPYAL	FELLELELATP	0.6271	56.5	WB	8.00	Sequence
DRB1_0405	6	FELLELELATPYALNAV	LLELELATPYA	0.6166	63.3	WB	16.00	Sequence
DRB1_0405	2	EHTDFELLELELATPYA	FELLELELATP	0.6098	68.2	WB	16.00	Sequence
DRB1_0405	147	RDRNTGGLLVMMNNVAP	GLLVMMNNVA	0.5946	80.4	WB	16.00	Sequence
DRB1_0405	153	LLVMNNVAPPSRGTV	LLVMNNVAP	0.5641	111.8	WB	16.00	Sequence
DRB1_0405	146	SRDRNTGGLLVMMNNVA	GLLVMMNNVA	0.5529	126.1	WB	32.00	Sequence
DRB1_0405	48	RAVRETMVVSAATT	MAVVSAAAT	0.5523	127.0	WB	32.00	Sequence
DRB1_0405	102	LGAFGLGVLTRPSP	FGLGVLTRP	0.5511	128.6	WB	32.00	Sequence
DRB1_0405	103	GAFGLGVLTRPSP	LGVLTRPSP	0.5490	131.6	WB	32.00	Sequence
DRB1_0405	104	AFGLGVLTRPSPPT	LGVLTRPSP	0.5488	131.8	WB	32.00	Sequence
DRB1_0405	142	TVVFSRDRNTGGLLV	VVFSRDRNT	0.5454	136.9	WB	32.00	Sequence
DRB1_0405	105	FGLGVLTRPSPPTV	LGVLTRPSP	0.5418	142.3	WB	32.00	Sequence
DRB1_0405	143	VVFSRDRNTGGLLV	VVFSRDRNT	0.5350	153.1	WB	32.00	Sequence
DRB1_0405	141	ATVVFSRDRNTGGLV	VVFSRDRNT	0.5345	154.0	WB	32.00	Sequence
DRB1_0405	7	ELLELELATPYALNAV	LLELELATPYA	0.5176	184.9	WB	32.00	Sequence
DRB1_0405	140	TATVVFSRDRNTGGL	VVFSRDRNT	0.5164	187.3	WB	32.00	Sequence
DRB1_0405	49	AVRETMVVSAATTA	MAVVSAAAT	0.5156	188.8	WB	32.00	Sequence
DRB1_0405	47	VRAVRETMVVSAAT	AVRETMVV	0.5137	192.8	WB	32.00	Sequence
DRB1_0405	1	TEHTDFELLELELATP	FELLELELATP	0.5130	194.2	WB	32.00	Sequence
DRB1_0405	101	GLGAFGLGVLTRPSP	GLGVLTRPS	0.5124	195.5	WB	32.00	Sequence
DRB1_0405	106	GLGVLTRPSPPTVA	LGVLTRPSP	0.4995	224.7	WB	32.00	Sequence
DRB1_0405	46	EVRAVRETMVVSA	AVRETMVV	0.4988	226.6	WB	32.00	Sequence
DRB1_0405	8	LLELELATPYALNAV	LLELELATPYA	0.4975	229.8	WB	32.00	Sequence
DRB1_0405	154	LVMNNVAPPSRGTV	LVMNNVAPP	0.4865	258.7	WB	32.00	Sequence
DRB1_0405	139	GTATVVFSRDRNTGL	VVFSRDRNT	0.4850	263.1	WB	32.00	Sequence
DRB1_0405	65	PPAHLRTAILDATKP	AHLRTAILD	0.4847	263.9	WB	32.00	Sequence
DRB1_0405	145	FSRDRNTGGLLVMM	FSRDRNTGL	0.4802	277.2	WB	32.00	Sequence
DRB1_0405	0	MTEHTDFELLELELATP	FELLELELATP	0.4786	281.8	WB	32.00	Sequence
DRB1_0405	45	DEVRAVRETMVVSA	AVRETMVV	0.4770	286.8	WB	32.00	Sequence
DRB1_0405	64	EPPAHLRTAILDATK	AHLRTAILD	0.4766	288.0	WB	32.00	Sequence
DRB1_0405	165	GTVYQMWLLGGAKGP	YQMWLLGGA	0.4723	301.9	WB	50.00	Sequence
DRB1_0405	50	VRETMVVSAATTA	MAVVSAAAT	0.4711	305.8	WB	50.00	Sequence
DRB1_0405	164	RGTVYQMWLLGGAKG	YQMWLLGGA	0.4705	307.7	WB	50.00	Sequence
DRB1_0405	51	RETMVVSAATTAEP	MAVVSAAAT	0.4628	334.3	WB	50.00	Sequence
DRB1_0405	66	PAHLRTAILDATKPE	AHLRTAILD	0.4593	347.2	WB	50.00	Sequence
DRB1_0405	100	VGLGAFGLGVLTRPS	GLGVLTRPS	0.4585	350.5	WB	50.00	Sequence
DRB1_0405	12	ATPYALNAVSDDERA	YALNAVSD	0.4570	356.2	WB	50.00	Sequence
DRB1_0405	163	SRGTVYQMWLLGGAK	YQMWLLGGA	0.4542	367.2	WB	50.00	Sequence
DRB1_0405	144	VFSRDRNTGGLLVMM	FSRDRNTGL	0.4511	379.6	WB	50.00	Sequence
DRB1_0405	166	TVYQMWLLGGAKGPR	YQMWLLGGA	0.4460	401.2	WB	50.00	Sequence
DRB1_0405	44	NDEVRAVRETMVV	AVRETMVV	0.4445	407.5	WB	50.00	Sequence
DRB1_0405	63	AEPHAHLRTAILDAT	PAHLRTAIL	0.4418	419.6	WB	50.00	Sequence
DRB1_0405	107	LGVLTRPSPPTVAE	LGVLTRPSP	0.4370	442.2	WB	50.00	Sequence
DRB1_0405	11	LATPYALNAVSDDER	YALNAVSD	0.4347	453.2	WB	50.00	Sequence
DRB1_0405	117	PTVAEQVLTAPDVRT	EQVLTAPDV	0.4342	455.9	WB	50.00	Sequence
DRB1_0405	9	LELATPYALNAVSD	YALNAVSD	0.4321	466.4	WB	50.00	Sequence
DRB1_0405	162	PSRGTVYQMWLLGGA	YQMWLLGGA	0.4315	469.4	WB	50.00	Sequence
DRB1_0405	52	ETMAVVSAATTAEP	MAVVSAAAT	0.4313	470.1	WB	50.00	Sequence
DRB1_0405	13	TPYALNAVSDDERAD	YALNAVSD	0.4283	485.8	WB	50.00	Sequence
DRB1_0405	10	ELATPYALNAVSD	YALNAVSD	0.4280	487.5	WB	50.00	Sequence
DRB1_0405	116	PPTVAEQVLTAPDVR	EQVLTAPDV	0.4257	499.5	WB	50.00	Sequence
DRB1_0405	167	VYQMWLLGGAKGPRS	YQMWLLGGA	0.4244	506.6		50.00	Sequence
DRB1_0405	67	AHLRTAILDATKPEV	HLRTAILDA	0.4207	527.3		50.00	Sequence
DRB1_0405	118	TVAEQVLTAPDVRTV	EQVLTAPDV	0.4205	528.4		50.00	Sequence
DRB1_0405	168	YQMWLLGGAKGPRSA	YQMWLLGGA	0.4112	584.3		50.00	Sequence
DRB1_0405	87	WRTAAFASAAAIAVG	AAFASAAAI	0.4085	601.6		50.00	Sequence
DRB1_0405	14	PYALNAVSDDERADI	YALNAVSD	0.4070	611.3		50.00	Sequence
DRB1_0405	86	RWRTAAFASAAAIAV	AAFASAAAI	0.4016	648.6		50.00	Sequence
DRB1_0405	115	PPPTVAEQVLTAPDV	TVAEQVLT	0.4013	650.8		50.00	Sequence
DRB1_0405	206	ALAFVTEPGTGSPQP	FTVEPGTGS	0.4002	658.0		50.00	Sequence
DRB1_0405	53	TMAVVSAATTAEPPA	MAVVSAAAT	0.3981	673.6		50.00	Sequence
DRB1_0405	43	FNDEVRAVRETMVV	AVRETMVV	0.3972	679.9		50.00	Sequence
DRB1_0405	205	TALAFVTEPGTGSPQ	LAFTVEPGT	0.3972	679.9		50.00	Sequence
DRB1_0405	204	STALAFVTEPGTGSP	LAFTVEPGT	0.3954	693.4		50.00	Sequence
DRB1_0405	28	IDRRVAAAPSPVAAA	RRVAAAPSP	0.3923	717.1		50.00	Sequence
DRB1_0405	88	RTAAFASAAAIAVGL	AAFASAAAI	0.3896	738.1		50.00	Sequence
DRB1_0405	62	TAEPHAHLRTAILDA	AHLRTAILD	0.3866	762.7		50.00	Sequence
DRB1_0405	119	VAEQVLTAPDVRTVS	EQVLTAPDV	0.3847	778.3		50.00	Sequence
DRB1_0405	29	DRRVAAAPSPVAAAF	RRVAAAPSP	0.3846	779.5		50.00	Sequence
DRB1_0405	27	DIDRRVAAAPSPVAA	RRVAAAPSP	0.3835	788.8		50.00	Sequence
DRB1_0405	89	TAAFASAAAIAVGLG	FASAAAIAV	0.3782	835.7		50.00	Sequence

DRB1_0405	15	YALNAVSDDERADID	YALNAVSDD	0.3752	863.1	50.00	Sequence
DRB1_0405	30	RRVAAAPSPVAAAFN	RRVAAAPSP	0.3681	931.8	50.00	Sequence
DRB1_0405	203	ASTALAFVVEPGTGS	LAFTVEPGT	0.3672	940.5	50.00	Sequence
DRB1_0405	108	GVLTRPSPPTVAEQ	GVLTRPSP	0.3665	947.5	50.00	Sequence
DRB1_0405	182	AGTMGTAAVTPSTTA	GTMGTAAVT	0.3645	969.0	50.00	Sequence
DRB1_0405	180	RSAGTMGTAAVTPST	GTMGTAAVT	0.3629	985.9	50.00	Sequence
DRB1_0405	181	SAGTMGTAAVTPSTT	GTMGTAAVT	0.3601	1016.1	50.00	Sequence
DRB1_0405	26	ADIDRRVAAAPSPVA	RRVAAAPSP	0.3592	1025.5	50.00	Sequence
DRB1_0405	120	AEQVLTAPDVRTVSR	EQVLTAPDV	0.3580	1039.7	50.00	Sequence
DRB1_0405	84	QSRWRTAAFASAAAI	WRTAAFASA	0.3570	1050.3	50.00	Sequence
DRB1_0405	99	AVGLGAFGLGVLTRP	FGLGVLTRP	0.3565	1056.7	50.00	Sequence
DRB1_0405	85	SRWRTAAFASAAAI	WRTAAFASA	0.3537	1089.2	50.00	Sequence
DRB1_0405	194	TTATLTDLGASTALA	ATLTDLGAS	0.3518	1111.5	50.00	Sequence
DRB1_0405	138	AGTATVVF SRDRNTG	VVFSRDRNT	0.3466	1175.2	50.00	Sequence
DRB1_0405	90	AAFASAAAIAVGLGA	FASAAAIAV	0.3446	1201.9	50.00	Sequence
DRB1_0405	191	TPSTTATLTDLGAST	TTATLTDLG	0.3432	1219.6	50.00	Sequence
DRB1_0405	161	PPSRGTVYQMWLLGG	GTVYQMWLL	0.3411	1247.5	50.00	Sequence
DRB1_0405	192	PSTTATLTDLGASTA	TTATLTDLG	0.3397	1267.4	50.00	Sequence
DRB1_0405	179	PRSAGTMGTAAVTPS	GTMGTAAVT	0.3394	1270.7	50.00	Sequence
DRB1_0405	183	GTMGTAAVTPSTTAT	GTMGTAAVT	0.3383	1285.8	50.00	Sequence
DRB1_0405	54	MAVVSAATTAEPPIA	MAVVSAATT	0.3380	1291.1	50.00	Sequence
DRB1_0405	207	LAFTVEPGTGSPQPT	FTVEPGTGS	0.3361	1317.0	50.00	Sequence
DRB1_0405	68	HLRTAILDATKPEVR	HLRTAILDA	0.3338	1350.1	50.00	Sequence
DRB1_0405	193	STTATLTDLGASTAL	ATLTDLGAS	0.3332	1359.1	50.00	Sequence
DRB1_0405	190	VTPSTTATLTDLGAS	TTATLTDLG	0.3329	1363.9	50.00	Sequence
DRB1_0405	196	ATLTDLGASTALAF	DLGASTALA	0.3321	1375.6	50.00	Sequence
DRB1_0405	25	RADIDRRVAAAPSPV	RRVAAAPSP	0.3289	1424.5	50.00	Sequence
DRB1_0405	195	TATLTDLGASTALAF	ATLTDLGAS	0.3276	1444.6	50.00	Sequence
DRB1_0405	42	AFNDEVRAVRETM	EVRAVRETM	0.3259	1470.8	50.00	Sequence
DRB1_0405	114	SPPTVAEQVLTAPD	TVAEQVLT	0.3253	1479.8	50.00	Sequence
DRB1_0405	137	GAGTATVVF SRDRNT	VVFSRDRNT	0.3246	1491.9	50.00	Sequence
DRB1_0405	178	GPRSRAGTMGTAAVTP	GTMGTAAVT	0.3245	1492.6	50.00	Sequence
DRB1_0405	83	RQSRWRTAAFASAAA	RWRRTAAFAS	0.3233	1513.5	50.00	Sequence
DRB1_0405	121	EQVLTAPDVRTVSRP	EQVLTAPDV	0.3221	1532.0	50.00	Sequence
DRB1_0405	160	APP SRGTVYQMWLLG	GTVYQMWLL	0.3131	1689.4	50.00	Sequence
DRB1_0405	61	TTAEPPIHLRTAILD	AHLRTAILD	0.3130	1691.8	50.00	Sequence
DRB1_0405	98	IAVGLGAFGLGVLTR	GLGAFGLGV	0.3098	1750.1	50.00	Sequence
DRB1_0405	177	KGPRSRAGTMGTAAVT	GTMGTAAVT	0.3087	1771.3	50.00	Sequence
DRB1_0405	209	FTVEPGTGSPQPTGT	EPGTGSPQP	0.3078	1788.8	50.00	Sequence
DRB1_0405	97	AI VGLGAFGLGVLT	GLGAFGLGV	0.3054	1836.4	50.00	Sequence
DRB1_0405	82	RRQSRWRTAAFASAA	SRWRRTAFA	0.3052	1840.3	50.00	Sequence
DRB1_0405	208	AFTVEPGTGSPQPTG	FTVEPGTGS	0.3038	1867.3	50.00	Sequence
DRB1_0405	31	RVAAPSPVAAAFND	VAAAPSPVA	0.2999	1948.8	50.00	Sequence
DRB1_0405	202	GASTALAFVVEPGTG	LAFTVEPGT	0.2930	2099.7	50.00	Sequence
DRB1_0405	186	GTAAVTPSTTATLTD	TAAVTPSTT	0.2875	2228.1	50.00	Sequence
DRB1_0405	189	AVTPSTTATLTDLGA	VTPSTTATL	0.2864	2255.9	50.00	Sequence
DRB1_0405	187	TAAVTPSTTATLTDL	TAAVTPSTT	0.2859	2268.5	50.00	Sequence
DRB1_0405	217	SPQPTGTILAELPLG	GTILAELPL	0.2834	2330.8	50.00	Sequence
DRB1_0405	96	AAIAVGLGAFGLGVL	IAVGLGAFG	0.2829	2341.4	50.00	Sequence
DRB1_0405	81	VRRQSRWRTAAFASAA	QSRWRRTAAF	0.2826	2351.0	50.00	Sequence
DRB1_0405	159	VAPPSRGTVYQMWLL	GTVYQMWLL	0.2792	2437.8	50.00	Sequence
DRB1_0405	41	AAFNDEVRAVRETM	EVRAVRETM	0.2784	2459.5	50.00	Sequence
DRB1_0405	188	AAVTPSTTATLTDLGA	VTPSTTATL	0.2778	2474.7	50.00	Sequence
DRB1_0405	122	QVLTAPDVRTVSRPL	DVRTVSRPL	0.2735	2591.9	50.00	Sequence
DRB1_0405	184	TMGTAAVTPSTTATL	GTAAVTPST	0.2732	2601.1	50.00	Sequence
DRB1_0405	95	AAAIAVGLGAFGLGV	IAVGLGAFG	0.2726	2618.5	50.00	Sequence
DRB1_0405	197	TLTDLGASTALAF	DLGASTALA	0.2717	2643.3	50.00	Sequence
DRB1_0405	185	MGTAAVTPSTTATLT	GTAAVTPST	0.2661	2810.3	50.00	Sequence
DRB1_0405	109	VLTRPSPPTVAEQV	LTRPSPPT	0.2655	2827.0	50.00	Sequence
DRB1_0405	212	EPGTGSPQPTGTILA	EPGTGSPQP	0.2631	2903.0	50.00	Sequence
DRB1_0405	123	VLTAPDVRTVSRPLG	DVRTVSRPL	0.2628	2910.0	50.00	Sequence
DRB1_0405	216	GSPQPTGTILAELPL	GTILAELPL	0.2627	2913.1	50.00	Sequence
DRB1_0405	201	LGASTALAFVVEPGT	LAFTVEPGT	0.2627	2914.1	50.00	Sequence
DRB1_0405	211	VEPGTGSPQPTGTIL	EPGTGSPQP	0.2591	3030.3	50.00	Sequence
DRB1_0405	127	PDVRTVSRPLGAGTA	DVRTVSRPL	0.2578	3073.4	50.00	Sequence
DRB1_0405	176	AKGPRSRAGTMGTA	GPRSRAGTMG	0.2563	3122.0	50.00	Sequence
DRB1_0405	198	LTDLGASTALAFVVE	DLGASTALA	0.2561	3129.9	50.00	Sequence
DRB1_0405	124	LTAPDVRTVSRPLGA	DVRTVSRPL	0.2541	3197.6	50.00	Sequence
DRB1_0405	91	AFASAAAIAVGLGAF	FASAAAIAV	0.2540	3202.7	50.00	Sequence
DRB1_0405	210	TVEPGTGSPQPTGTI	EPGTGSPQP	0.2509	3311.3	50.00	Sequence
DRB1_0405	128	DVRTVSRPLGAGTAT	DVRTVSRPL	0.2488	3386.8	50.00	Sequence
DRB1_0405	126	ADVVRTVSRPLGAGT	DVRTVSRPL	0.2488	3388.0	50.00	Sequence
DRB1_0405	125	TAPDVRTVSRPLGAG	DVRTVSRPL	0.2485	3397.4	50.00	Sequence
DRB1_0405	199	TDLGASTALAFVVEP	DLGASTALA	0.2462	3483.6	50.00	Sequence
DRB1_0405	175	GAKGPRSRAGTMGTAA	GPRSRAGTMG	0.2452	3520.9	50.00	Sequence
DRB1_0405	24	ERADIDRRVAAAPSP	RRVAAAPSP	0.2445	3548.5	50.00	Sequence
DRB1_0405	134	RPLGAGTATVVF SRD	LGAGTATVV	0.2433	3595.2	50.00	Sequence

DRB1_0405	133	SRPLGAGTATVVFSSR	LGAGTATVV	0.2424	3631.8	50.00	Sequence
DRB1_0405	69	LRTAILDATKPEVRR	LRTAILDAT	0.2416	3660.8	50.00	Sequence
DRB1_0405	155	VMNNVAPPSSRGTVYQ	VMNNVAPPS	0.2409	3690.0	50.00	Sequence
DRB1_0405	173	LGGAAGPRGAGTMGT	KGPRGAGTM	0.2402	3717.9	50.00	Sequence
DRB1_0405	135	PLGAGTATVVFSSRDR	LGAGTATVV	0.2399	3729.1	50.00	Sequence
DRB1_0405	110	LTRPSPPTVAEQVL	LTRPSPPT	0.2370	3847.8	50.00	Sequence
DRB1_0405	80	EVRQRSRWRTAFAA	QSRWRTAFA	0.2366	3864.7	50.00	Sequence
DRB1_0405	40	AAAFNDEVRAVRETM	FNDEVRAVR	0.2356	3905.8	50.00	Sequence
DRB1_0405	136	LGAGTATVVFSSRDRN	LGAGTATVV	0.2312	4097.1	50.00	Sequence
DRB1_0405	174	GGAKGPRGAGTMGTA	GPRGAGTMG	0.2305	4128.1	50.00	Sequence
DRB1_0405	36	PSPVAAAFNDEVRAV	VAAAFNDEV	0.2285	4217.5	50.00	Sequence
DRB1_0405	169	QMWLLGGAKGPRGAG	QMWLLGGAK	0.2277	4258.2	50.00	Sequence
DRB1_0405	132	VSRPLGAGTATVVFSS	LGAGTATVV	0.2256	4355.3	50.00	Sequence
DRB1_0405	35	APSPVAAAFNDEVRA	SPVAAAFND	0.2230	4475.7	50.00	Sequence
DRB1_0405	92	FASAAAIAVGLGAFG	FASAAAIAV	0.2225	4502.0	50.00	Sequence
DRB1_0405	200	DLGASTALAFSTVEPG	DLGASTALA	0.2195	4648.6	50.00	Sequence
DRB1_0405	34	AAAPSPVAAAFNDEV	SPVAAAFND	0.2178	4737.3	50.00	Sequence
DRB1_0405	213	PGTGSPQPTGTILAE	GTGSPQPTG	0.2166	4796.8	50.00	Sequence
DRB1_0405	39	VAAAFNDEVRAVRET	AAFNDEVRA	0.2154	4859.9	50.00	Sequence
DRB1_0405	55	AVVSAATTAEPHAHL	AVVSAATTA	0.2152	4871.8	50.00	Sequence
DRB1_0405	172	LLGGAKGPRGAGTMG	LGGAKGPRS	0.2145	4909.6	50.00	Sequence
DRB1_0405	215	TGSPQPTGTILAEPL	SPQPTGTIL	0.2141	4933.2	50.00	Sequence
DRB1_0405	37	SPVAAAFNDEVRAVR	SPVAAAFND	0.2139	4942.2	50.00	Sequence
DRB1_0405	32	VAAAPSPVAAAFNDE	VAAAPSPVA	0.2127	5006.9	50.00	Sequence
DRB1_0405	131	TVSRPLGAGTATVVF	LGAGTATVV	0.2125	5019.4	50.00	Sequence
DRB1_0405	60	ATTAEPHAHLRTAIL	PAHLRTAIL	0.2119	5051.2	50.00	Sequence
DRB1_0405	113	PSPPTVAEQVLTAP	TVAEQVLT	0.2114	5075.0	50.00	Sequence
DRB1_0405	214	GTGSPQPTGTILAE	SPQPTGTIL	0.2101	5150.5	50.00	Sequence
DRB1_0405	171	WLLGGAKGPRGAGTM	WLLGGAKGP	0.2078	5281.4	50.00	Sequence
DRB1_0405	33	AAAPSPVAAAFNDEV	SPVAAAFND	0.2069	5331.8	50.00	Sequence
DRB1_0405	70	RTAILDATKPEVRRQ	ILDATKPEV	0.2043	5480.3	50.00	Sequence
DRB1_0405	94	SAAAIAVGLGAFGLG	IAVGLGAFG	0.2043	5482.7	50.00	Sequence
DRB1_0405	79	PEVRRQSRWRTAFA	QSRWRTAFA	0.2027	5575.6	50.00	Sequence
DRB1_0405	170	MWLLGGAKGPRGAGT	WLLGGAKGP	0.2004	5721.3	50.00	Sequence
DRB1_0405	38	PVAAAFNDEVRAVRE	AAFNDEVRA	0.2003	5723.1	50.00	Sequence
DRB1_0405	158	NVAPPSSRGTVYQMWL	RGTVYQMWL	0.1970	5931.8	50.00	Sequence
DRB1_0405	71	TAILDATKPEVRRQS	ILDATKPEV	0.1959	6007.0	50.00	Sequence
DRB1_0405	23	DERADIDRRVAAAPS	DRRVAAAPS	0.1945	6094.4	50.00	Sequence
DRB1_0405	130	RTVSRPLGAGTATVV	LGAGTATVV	0.1852	6738.8	50.00	Sequence
DRB1_0405	111	TRPSPPTVAEQVLT	TRPSPPTV	0.1814	7023.0	50.00	Sequence
DRB1_0405	129	VRTVSRPLGAGTATV	VRTVSRPLG	0.1807	7078.7	50.00	Sequence
DRB1_0405	112	RPSPPPTVAEQVLT	TVAEQVLT	0.1779	7298.4	50.00	Sequence
DRB1_0405	93	ASAAAIAVGLGAFGL	IAVGLGAFG	0.1753	7507.0	50.00	Sequence
DRB1_0405	72	AILDATKPEVRRQSR	ILDATKPEV	0.1736	7644.5	50.00	Sequence
DRB1_0405	156	MNNVAPPSSRGTVYQM	PSRGTVYQM	0.1607	8786.0	50.00	Sequence
DRB1_0405	78	KPEVRRQSRWRTAFA	QSRWRTAFA	0.1579	9055.4	50.00	Sequence
DRB1_0405	157	NNVAPPSSRGTVYQM	PSRGTVYQM	0.1555	9291.9	50.00	Sequence
DRB1_0405	16	ALNAVSDDERADIDR	ALNAVSDDE	0.1548	9369.4	50.00	Sequence
DRB1_0405	56	VVSAATTAEPHAHLR	VVSAATTAE	0.1497	9893.5	50.00	Sequence
DRB1_0405	73	ILDATKPEVRRQSRW	ILDATKPEV	0.1316	12032.6	50.00	Sequence
DRB1_0405	77	TKPEVRRQSRWRTA	EVRRQSRWR	0.1303	12212.2	50.00	Sequence
DRB1_0405	17	LNAVSDDERADIDRR	NAVSDDERA	0.1273	12615.9	50.00	Sequence
DRB1_0405	57	VSAATTAEPHAHLRT	VSAATTAEP	0.1227	13249.9	50.00	Sequence
DRB1_0405	18	NAVSDDERADIDRRV	NAVSDDERA	0.1174	14042.9	50.00	Sequence
DRB1_0405	59	AATTAEPHAHLRTAI	AATTAEP	0.1171	14088.4	50.00	Sequence
DRB1_0405	58	SAATTAEPHAHLRTA	SAATTAEP	0.1166	14153.0	50.00	Sequence
DRB1_0405	76	ATKPEVRRQSRWRTA	EVRRQSRWR	0.1100	15200.3	50.00	Sequence
DRB1_0405	22	DDERADIDRRVAAAP	ERADIDRRV	0.1066	15771.3	50.00	Sequence
DRB1_0405	19	AVSDDERADIDRRVA	ERADIDRRV	0.1025	16492.2	50.00	Sequence
DRB1_0405	75	DATKPEVRRQSRWR	EVRRQSRWR	0.0970	17501.3	50.00	Sequence
DRB1_0405	21	SDDERADIDRRVAAA	ERADIDRRV	0.0946	17959.8	50.00	Sequence
DRB1_0405	20	VSDDERADIDRRVAA	ERADIDRRV	0.0904	18799.5	50.00	Sequence
DRB1_0405	74	LDATKPEVRRQSRWR	EVRRQSRWR	0.0818	20623.8	50.00	Sequence

Allele: DRB1_0405. Number of high binders 5. Number of weak binders 53. Number of peptides 218

Allele	pos	peptide	core	1-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
DRB1_0701	86	RWRTAFAFASAAAIAV	FASAAAIAV	0.9032	2.9	SB	0.40	Sequence
DRB1_0701	87	WRTAFAFASAAAIAVG	FASAAAIAV	0.8930	3.2	SB	0.80	Sequence
DRB1_0701	88	RTAAFAFASAAAIAVGL	FASAAAIAV	0.8867	3.4	SB	0.80	Sequence
DRB1_0701	89	TAAFAFASAAAIAVGLG	FASAAAIAV	0.8625	4.4	SB	2.00	Sequence
DRB1_0701	90	AAFASAAAIAVGLGA	FASAAAIAV	0.8528	4.9	SB	2.00	Sequence
DRB1_0701	91	AFASAAAIAVGLGAF	FASAAAIAV	0.8379	5.8	SB	2.00	Sequence

DRB1_0701	92	FASAAAAIAVGLGAFG	FASAAAAIAV	0.8174	7.2	SB	4.00	Sequence
DRB1_0701	122	QVLTAPDVRTVSRPL	DVRTVSRPL	0.7636	12.9	SB	8.00	Sequence
DRB1_0701	140	TATVVFSDRDRNTGLL	FSRDRNTGL	0.7555	14.1	SB	8.00	Sequence
DRB1_0701	139	GTATVVFSDRDRNTGL	FSRDRNTGL	0.7448	15.8	SB	8.00	Sequence
DRB1_0701	141	ATVVFSDRDRNTGLLV	FSRDRNTGL	0.7448	15.8	SB	8.00	Sequence
DRB1_0701	26	ADIDRRVAAAPSPVA	RVAAAPSPV	0.7446	15.9	SB	8.00	Sequence
DRB1_0701	184	MGTAAVTPSTTATL	VTPSTTATL	0.7336	17.9	SB	8.00	Sequence
DRB1_0701	123	VLTAAPDVRTVSRPLG	DVRTVSRPL	0.7273	19.1	SB	8.00	Sequence
DRB1_0701	27	DIDRRVAAAPSPVAA	RVAAAPSPV	0.7144	22.0	SB	8.00	Sequence
DRB1_0701	142	TVVFSDRDRNTGLLVM	FSRDRNTGL	0.7087	23.4	SB	8.00	Sequence
DRB1_0701	185	MGTAAVTPSTTATLT	VTPSTTATL	0.7074	23.7	SB	8.00	Sequence
DRB1_0701	3	HTDFELLELELATPYAL	LELATPYAL	0.7019	25.2	SB	16.00	Sequence
DRB1_0701	28	IDRRVAAAPSPVAAA	RVAAAPSPV	0.6792	32.2	SB	16.00	Sequence
DRB1_0701	143	VVFSDRDRNTGLLVMN	FSRDRNTGL	0.6756	33.4	SB	16.00	Sequence
DRB1_0701	118	TVAEQVLTAPDVRTV	VLTAAPDVRT	0.6753	33.6	SB	16.00	Sequence
DRB1_0701	25	RADIDRRVAAAPSPV	RVAAAPSPV	0.6704	35.4	SB	16.00	Sequence
DRB1_0701	186	GTAAPVTPSTTATLTD	VTPSTTATL	0.6680	36.3	SB	16.00	Sequence
DRB1_0701	4	TDFELLELELATPYALN	LELATPYAL	0.6654	37.4	SB	16.00	Sequence
DRB1_0701	29	DRRVAAAPSPVAAAF	RVAAAPSPV	0.6549	41.8	SB	16.00	Sequence
DRB1_0701	124	LTAPDVRTVSRPLGA	DVRTVSRPL	0.6507	43.8	SB	16.00	Sequence
DRB1_0701	119	VAEQVLTAPDVRTVS	VLTAAPDVRT	0.6497	44.3	SB	16.00	Sequence
DRB1_0701	187	TAAVTPSTTATLTDL	VTPSTTATL	0.6363	51.2	WB	16.00	Sequence
DRB1_0701	30	RRVAAAPSPVAAAFN	RVAAAPSPV	0.6351	51.8	WB	16.00	Sequence
DRB1_0701	144	VFSRDRNTGLLVMNN	FSRDRNTGL	0.6348	52.0	WB	16.00	Sequence
DRB1_0701	117	PTVAEQVLTAPDVRT	VLTAAPDVRT	0.6314	54.0	WB	16.00	Sequence
DRB1_0701	5	DFELLELELATPYALNA	LELATPYAL	0.6288	55.5	WB	16.00	Sequence
DRB1_0701	197	TLTDLGASTALAF TV	ASTALAF TV	0.6206	60.7	WB	16.00	Sequence
DRB1_0701	120	AEQVLTAPDVRTVSR	VLTAAPDVRT	0.6107	67.5	WB	16.00	Sequence
DRB1_0701	137	GAGTATVVFSDRDRNT	VVFSDRDRNT	0.6091	68.7	WB	16.00	Sequence
DRB1_0701	188	AAVTPSTTATLTDLGA	VTPSTTATL	0.6069	70.3	WB	16.00	Sequence
DRB1_0701	50	VRETMAVSAATTAE	VVSAATTAE	0.6048	72.0	WB	16.00	Sequence
DRB1_0701	145	FSRDRNTGLLVMNNV	FSRDRNTGL	0.6024	73.8	WB	16.00	Sequence
DRB1_0701	6	FELLELELATPYALNAV	LELATPYAL	0.5931	81.6	WB	32.00	Sequence
DRB1_0701	31	RVAAAPSPVAAAFND	RVAAAPSPV	0.5927	82.0	WB	32.00	Sequence
DRB1_0701	198	LTDLGASTALAF TVE	ASTALAF TV	0.5778	96.3	WB	32.00	Sequence
DRB1_0701	48	RAVRETMAVSAATT	MAVSAATT	0.5766	97.6	WB	32.00	Sequence
DRB1_0701	105	FGLGLVLRPSPPPTV	TRPSPPTV	0.5749	99.4	WB	32.00	Sequence
DRB1_0701	121	EQVLTAPDVRTVSRP	VLTAAPDVRT	0.5749	99.5	WB	32.00	Sequence
DRB1_0701	189	AVTPSTTATLTDLGA	VTPSTTATL	0.5672	108.1	WB	32.00	Sequence
DRB1_0701	49	AVRETMAVSAATTA	MAVSAATT	0.5646	111.2	WB	32.00	Sequence
DRB1_0701	55	AVVSAATTAEP PAHL	TTAEP PAHL	0.5644	111.4	WB	32.00	Sequence
DRB1_0701	125	TAPDVRTVSRPLGAG	DVRTVSRPL	0.5613	115.2	WB	32.00	Sequence
DRB1_0701	138	AGTATVVFSDRDRNTG	VVFSDRDRNT	0.5541	124.5	WB	32.00	Sequence
DRB1_0701	68	HLRTAILDATKPEVR	ILDATKPEV	0.5529	126.2	WB	32.00	Sequence
DRB1_0701	51	RETMAVSAATTAEP	VVSAATTAE	0.5492	131.4	WB	32.00	Sequence
DRB1_0701	7	ELLELELATPYALNAV	LELATPYAL	0.5475	133.8	WB	32.00	Sequence
DRB1_0701	106	GLGLVLRPSPPPTVA	TRPSPPTV	0.5352	152.8	WB	32.00	Sequence
DRB1_0701	199	TDLGASTALAF TVEP	ASTALAF TV	0.5351	153.0	WB	32.00	Sequence
DRB1_0701	190	VTPSTTATLTDLGA	VTPSTTATL	0.5327	156.9	WB	32.00	Sequence
DRB1_0701	126	APDVRTVSRPLGAGT	DVRTVSRPL	0.5283	164.5	WB	32.00	Sequence
DRB1_0701	195	TATLTDLGASTALAF	LGASTALAF	0.5278	165.5	WB	32.00	Sequence
DRB1_0701	131	TVSRPLGAGTATVVF	LGAGTATVV	0.5217	176.8	WB	32.00	Sequence
DRB1_0701	44	NDEVRAVRETMAVVS	VRETMAVVS	0.5200	180.1	WB	32.00	Sequence
DRB1_0701	43	FNDEVRAVRETMAVV	AVRETMAVV	0.5193	181.4	WB	32.00	Sequence
DRB1_0701	130	RTVSRPLGAGTATVV	LGAGTATVV	0.5147	190.7	WB	32.00	Sequence
DRB1_0701	8	LLELATPYALNAVSD	LELATPYAL	0.5123	195.7	WB	32.00	Sequence
DRB1_0701	56	VVSAATTAEP PAHLR	TTAEP PAHL	0.5097	201.4	WB	32.00	Sequence
DRB1_0701	69	LRTAILDATKPEVRR	ILDATKPEV	0.5061	209.3	WB	32.00	Sequence
DRB1_0701	196	ATLTDLGASTALAF T	LGASTALAF	0.5029	216.7	WB	32.00	Sequence
DRB1_0701	67	AHLRTAILDATKPEV	ILDATKPEV	0.5023	218.0	WB	32.00	Sequence
DRB1_0701	127	PDVRTVSRPLGAGTA	DVRTVSRPL	0.4925	242.5	WB	32.00	Sequence
DRB1_0701	52	ETMAVSAATTAEP P	VVSAATTAE	0.4924	242.8	WB	32.00	Sequence
DRB1_0701	107	LGVLTRPSPPPTVAE	TRPSPPTV	0.4875	256.1	WB	32.00	Sequence
DRB1_0701	41	AAFNDEVRAVRETMA	VRAVRETMA	0.4859	260.4	WB	32.00	Sequence
DRB1_0701	200	DLGASTALAF TVEPG	ASTALAF TV	0.4848	263.6	WB	32.00	Sequence
DRB1_0701	132	VSRPLGAGTATVVF	LGAGTATVV	0.4796	278.9	WB	32.00	Sequence
DRB1_0701	42	AFNDEVRAVRETMAV	VRAVRETMA	0.4737	297.1	WB	32.00	Sequence
DRB1_0701	45	DEVRAVRETMAVVS	VRETMAVVS	0.4735	297.9	WB	32.00	Sequence
DRB1_0701	104	AFGLGLVLRPSPPPT	LTRPSPPTV	0.4706	307.4	WB	32.00	Sequence
DRB1_0701	128	DVRTVSRPLGAGTAT	DVRTVSRPL	0.4621	336.9	WB	32.00	Sequence
DRB1_0701	84	QSRWRTAAFASAAAI	AAFASAAAI	0.4617	338.3	WB	32.00	Sequence
DRB1_0701	201	LGASTALAF TVEPGT	LGASTALAF	0.4586	350.1	WB	32.00	Sequence
DRB1_0701	53	TMAVSAATTAEP PA	MAVSAATT	0.4536	369.5	WB	50.00	Sequence
DRB1_0701	70	RTAILDATKPEVRRQ	ILDATKPEV	0.4497	385.3	WB	50.00	Sequence
DRB1_0701	133	SRPLGAGTATVVF	LGAGTATVV	0.4447	406.7	WB	50.00	Sequence
DRB1_0701	9	LELATPYALNAVSD	LELATPYAL	0.4432	413.4	WB	50.00	Sequence
DRB1_0701	60	ATAEP PAHLRTAIL	PAHLRTAIL	0.4417	420.0	WB	50.00	Sequence

DRB1_0701	108	GVLTRPSPPTVAEQ	TRPSPPTV	0.4387	434.0	WB	50.00	Sequence
DRB1_0701	85	SRWRTAAFASAAAIA	AAFASAAAI	0.4383	436.0	WB	50.00	Sequence
DRB1_0701	33	AAAPSPVAAAFNDEV	VAAAFNDEV	0.4359	447.4	WB	50.00	Sequence
DRB1_0701	46	EVRAVRETMVVSA	VRETMVVSA	0.4308	472.5	WB	50.00	Sequence
DRB1_0701	135	PLGAGTATVVFSDR	LGAGTATVV	0.4277	488.8	WB	50.00	Sequence
DRB1_0701	103	GAFGLGVLTRPSPPP	VLTRPSPPP	0.4262	496.8	WB	50.00	Sequence
DRB1_0701	47	VRAVRETMVVSAAT	TMAVVSAAAT	0.4236	510.9		50.00	Sequence
DRB1_0701	54	MAVVSAAATAEPPAH	MAVVSAAAT	0.4187	538.9		50.00	Sequence
DRB1_0701	134	RPLGAGTATVVFSDR	LGAGTATVV	0.4116	581.7		50.00	Sequence
DRB1_0701	71	TAILDATKPEVRRQS	ILDATKPEV	0.4028	639.7		50.00	Sequence
DRB1_0701	109	VLTRPSPPTVAEQV	TRPSPPTV	0.4013	650.3		50.00	Sequence
DRB1_0701	57	VSAATTAEPHAHLRT	TTAEPHAHL	0.4003	657.4		50.00	Sequence
DRB1_0701	61	TTAEPHAHLRTAILD	PAHLRTAIL	0.3961	688.1		50.00	Sequence
DRB1_0701	32	VAAAPSPVAAAFNDE	VAAAPSPVA	0.3877	753.6		50.00	Sequence
DRB1_0701	34	AAAPSPVAAAFNDEV	VAAAFNDEV	0.3863	765.0		50.00	Sequence
DRB1_0701	129	VRTVSRPLGAGTATV	PLGAGTATV	0.3801	817.8		50.00	Sequence
DRB1_0701	96	AAIAVGLGAFGLGVL	GLGAFGLGV	0.3789	829.2		50.00	Sequence
DRB1_0701	182	AGTMGTAAVTPSTTA	AAVTPSTTA	0.3774	842.7		50.00	Sequence
DRB1_0701	95	AAAIAGVGLGAFGLGV	GLGAFGLGV	0.3754	861.4		50.00	Sequence
DRB1_0701	72	AILDATKPEVRRQSR	ILDATKPEV	0.3733	880.9		50.00	Sequence
DRB1_0701	216	GSPOQTGTILAEPL	GTILAEPL	0.3585	1034.2		50.00	Sequence
DRB1_0701	136	LGAGTATVVFSDRDN	LGAGTATVV	0.3549	1074.8		50.00	Sequence
DRB1_0701	146	SRDRNTGLLVMNVA	GLLVMNVA	0.3537	1088.7		50.00	Sequence
DRB1_0701	203	ASTALAFVTEPGTGS	ASTALAFV	0.3517	1112.2		50.00	Sequence
DRB1_0701	73	ILDATKPEVRRQSRW	ILDATKPEV	0.3496	1138.3		50.00	Sequence
DRB1_0701	40	AAAFNDEVRAVRETM	EVRAVRETM	0.3439	1211.2		50.00	Sequence
DRB1_0701	97	AAIAVGLGAFGLGVL	GLGAFGLGV	0.3417	1239.8		50.00	Sequence
DRB1_0701	183	GTMGTAAVTPSTTAT	AAVTPSTTA	0.3407	1253.6		50.00	Sequence
DRB1_0701	58	SAATTAEPHAHLRTA	TTAEPHAHL	0.3405	1255.8		50.00	Sequence
DRB1_0701	35	APSPVAAAFNDEVRA	VAAAFNDEV	0.3357	1322.9		50.00	Sequence
DRB1_0701	202	GASTALAFVTEPGTG	ASTALAFV	0.3171	1618.2		50.00	Sequence
DRB1_0701	193	STTATLTDLGASTAL	TDLGASTAL	0.3117	1714.3		50.00	Sequence
DRB1_0701	59	AATTAEPHAHLRTAI	TTAEPHAHL	0.3103	1740.6		50.00	Sequence
DRB1_0701	62	TAEPHAHLRTAILDA	PAHLRTAIL	0.3031	1882.7		50.00	Sequence
DRB1_0701	217	SPQPTGTILAEPLG	GTILAEPL	0.3025	1894.7		50.00	Sequence
DRB1_0701	110	LTRPSPPTVAEQVL	TRPSPPTV	0.3013	1919.9		50.00	Sequence
DRB1_0701	194	TTATLTDLGASTALA	TDLGASTAL	0.3010	1925.2		50.00	Sequence
DRB1_0701	102	LGAFGLGVLTRPSP	GVLTRPSP	0.2980	1989.1		50.00	Sequence
DRB1_0701	178	GPRASAGTMGTAAVTP	TMGTAAVTP	0.2977	1995.4		50.00	Sequence
DRB1_0701	98	IAVGLGAFGLGVLTR	GLGAFGLGV	0.2971	2009.2		50.00	Sequence
DRB1_0701	37	SPVAAAFNDEVRAVR	VAAAFNDEV	0.2913	2138.3		50.00	Sequence
DRB1_0701	36	PSPVAAAFNDEVRAV	VAAAFNDEV	0.2913	2139.5		50.00	Sequence
DRB1_0701	159	VAPPSRGTVYQMWLL	RGTVYQMWL	0.2904	2158.8		50.00	Sequence
DRB1_0701	93	ASAAAIAVGLGAFGL	AVGLGAFGL	0.2833	2331.9		50.00	Sequence
DRB1_0701	99	AVGLGAFGLGVLTRP	GLGAFGLGV	0.2813	2384.4		50.00	Sequence
DRB1_0701	111	TRPSPPTVAEQVLT	TRPSPPTV	0.2801	2414.0		50.00	Sequence
DRB1_0701	147	RDRNTGLLVMNVA	GLLVMNVA	0.2800	2415.6		50.00	Sequence
DRB1_0701	75	DATKPEVRRQSRWRT	VRRQSRWRT	0.2793	2435.6		50.00	Sequence
DRB1_0701	179	PRASAGTMGTAAVTP	TMGTAAVTP	0.2768	2501.6		50.00	Sequence
DRB1_0701	100	VGLGAFGLGVLTRPS	GLGAFGLGV	0.2718	2639.7		50.00	Sequence
DRB1_0701	38	PVAAAFNDEVRAVR	VAAAFNDEV	0.2625	2919.3		50.00	Sequence
DRB1_0701	0	MTEHTDFELLELATP	MTEHTDFEL	0.2599	3003.5		50.00	Sequence
DRB1_0701	158	NVAPPSRGTVYQMWL	RGTVYQMWL	0.2571	3095.6		50.00	Sequence
DRB1_0701	63	AEPHAHLRTAILDAT	PAHLRTAIL	0.2464	3478.2		50.00	Sequence
DRB1_0701	181	SAGTMGTAAVTPSTT	TAAVTPSTT	0.2463	3479.9		50.00	Sequence
DRB1_0701	101	GLGAFGLGVLTRPSP	GLGAFGLGV	0.2456	3505.1		50.00	Sequence
DRB1_0701	39	VAAAFNDEVRAVRET	VAAAFNDEV	0.2443	3557.7		50.00	Sequence
DRB1_0701	76	ATKPEVRRQSRWRTA	VRRQSRWRT	0.2398	3733.5		50.00	Sequence
DRB1_0701	94	SAAAIAVGLGAFGLG	AVGLGAFGL	0.2344	3960.5		50.00	Sequence
DRB1_0701	160	APPSRGTVYQMWLLG	GTVYQMWLL	0.2319	4068.7		50.00	Sequence
DRB1_0701	177	KGPRASAGTMGTAAVT	GTMGTAAVT	0.2288	4205.0		50.00	Sequence
DRB1_0701	79	PEVRRQSRWRTAFA	VRRQSRWRT	0.2235	4456.4		50.00	Sequence
DRB1_0701	11	LATPYALNAVSDDER	LNAVSDDER	0.2232	4468.4		50.00	Sequence
DRB1_0701	2	EHTDFELLELATPYA	LLELATPYA	0.2204	4606.8		50.00	Sequence
DRB1_0701	180	RSAGTMGTAAVTPST	TMGTAAVTP	0.2203	4609.1		50.00	Sequence
DRB1_0701	82	RRQSRWRTAAFASAA	RTAAFASAA	0.2144	4912.5		50.00	Sequence
DRB1_0701	80	EVRRQSRWRTAAFAS	SRWRTAFA	0.2127	5008.3		50.00	Sequence
DRB1_0701	192	PSTTATLTDLGASTA	LTDLGASTA	0.2126	5010.1		50.00	Sequence
DRB1_0701	173	LGGAKGPRASAGTMGT	PRASAGTMGT	0.2122	5035.4		50.00	Sequence
DRB1_0701	153	LLVMNNVAPPVSRGT	VAPPVSRGT	0.2110	5099.7		50.00	Sequence
DRB1_0701	74	LDATKPEVRRQSRWR	EVRRQSRWR	0.2109	5102.3		50.00	Sequence
DRB1_0701	64	EPPHAHLRTAILDATK	PAHLRTAIL	0.2094	5186.7		50.00	Sequence
DRB1_0701	150	NTGLLVMNNVAPPVSR	MNVAPPVSR	0.2094	5188.1		50.00	Sequence
DRB1_0701	81	VRRQSRWRTAAFASA	VRRQSRWRT	0.2089	5216.9		50.00	Sequence
DRB1_0701	12	ATPYALNAVSDDERA	LNAVSDDER	0.2050	5443.6		50.00	Sequence
DRB1_0701	116	PPTVAEQVLTAPDVR	QVLTAPDVR	0.2037	5520.2		50.00	Sequence
DRB1_0701	148	DRNTGLLVMNNVAPP	GLLVMNVA	0.2004	5717.9		50.00	Sequence

DRB1_0701	77	TKPEVRRQSRWRATA	VRRQSRWRT	0.1975	5903.0	50.00	Sequence
DRB1_0701	204	STALAFTVEPGTGSP	FTVEPGTGS	0.1974	5908.5	50.00	Sequence
DRB1_0701	210	TVEPGTGSPQPTGTI	GSPQPTGTI	0.1954	6036.3	50.00	Sequence
DRB1_0701	161	PPSRGTVYQMWLLGG	RGTVYQMWL	0.1845	6792.3	50.00	Sequence
DRB1_0701	211	VEPGTGSPQPTGTIL	GSPQPTGTI	0.1836	6857.6	50.00	Sequence
DRB1_0701	83	RQSRWRATAAFASAAA	RTAAFASAA	0.1834	6874.5	50.00	Sequence
DRB1_0701	13	TPYALNAVSDDERAD	LNAVSDDER	0.1828	6915.4	50.00	Sequence
DRB1_0701	174	GGAKGPRASAGTMGT	PRASAGTMGT	0.1819	6986.9	50.00	Sequence
DRB1_0701	154	LVMNNVAPPSPRGTVY	VAPPSPRGTV	0.1792	7190.1	50.00	Sequence
DRB1_0701	65	PPAHLRTAILDATKPK	PAHLRTAIL	0.1784	7256.4	50.00	Sequence
DRB1_0701	14	PYALNAVSDDERADI	LNAVSDDER	0.1770	7368.6	50.00	Sequence
DRB1_0701	152	GLLVMNNVAPPSPRG	MNNVAPPSPR	0.1745	7566.8	50.00	Sequence
DRB1_0701	78	KPEVRRQSRWRATAAF	VRRQSRWRT	0.1744	7579.6	50.00	Sequence
DRB1_0701	151	TGLLVMNNVAPPSPRG	MNNVAPPSPR	0.1735	7647.3	50.00	Sequence
DRB1_0701	156	MNNVAPPSPRGTVYQM	PSRGTVYQM	0.1732	7677.8	50.00	Sequence
DRB1_0701	149	RNTGLLVMNNVAPPSP	GLLVMNNVA	0.1688	8049.3	50.00	Sequence
DRB1_0701	15	YALNAVSDDERADID	LNAVSDDER	0.1681	8108.6	50.00	Sequence
DRB1_0701	162	PSRGTVYQMWLLGGA	RGTVYQMWL	0.1659	8304.2	50.00	Sequence
DRB1_0701	212	EPGTGSPQPTGTILA	GSPQPTGTI	0.1641	8469.4	50.00	Sequence
DRB1_0701	205	TALAFTVEPGTGSPQ	FTVEPGTGS	0.1635	8520.7	50.00	Sequence
DRB1_0701	66	PAHLRTAILDATKPE	PAHLRTAIL	0.1588	8967.2	50.00	Sequence
DRB1_0701	165	GTVYQMWLLGGAKGP	WLLGGAKGP	0.1582	9026.9	50.00	Sequence
DRB1_0701	16	ALNAVSDDERADIDR	LNAVSDDER	0.1570	9147.7	50.00	Sequence
DRB1_0701	167	VYQMWLLGGAKGPR	LGGAKGPR	0.1565	9199.4	50.00	Sequence
DRB1_0701	175	GAKGPRASAGTMGTAA	PRASAGTMGT	0.1565	9200.1	50.00	Sequence
DRB1_0701	157	MNNVAPPSPRGTVYQM	VAPPSPRGTV	0.1544	9411.7	50.00	Sequence
DRB1_0701	115	PPPTVAEQVLTAPDV	EQVLTAPDV	0.1510	9761.3	50.00	Sequence
DRB1_0701	24	ERADIDRRVAAAPSP	RRVAAAPSP	0.1509	9767.2	50.00	Sequence
DRB1_0701	155	VMNNVAPPSPRGTVYQ	VAPPSPRGTV	0.1482	10060.7	50.00	Sequence
DRB1_0701	214	GTGSPQPTGTILAE	GSPQPTGTI	0.1472	10171.7	50.00	Sequence
DRB1_0701	166	TVYQMWLLGGAKGPR	WLLGGAKGP	0.1465	10240.8	50.00	Sequence
DRB1_0701	17	LNAVSDDERADIDRR	LNAVSDDER	0.1457	10336.2	50.00	Sequence
DRB1_0701	176	AKGPRASAGTMGTA	PRASAGTMGT	0.1406	10916.5	50.00	Sequence
DRB1_0701	168	YQMWLLGGAKGPRSA	LGGAKGPR	0.1396	11038.2	50.00	Sequence
DRB1_0701	163	SRGTVYQMWLLGGAK	RGTVYQMWL	0.1374	11301.2	50.00	Sequence
DRB1_0701	112	RPSPPPTVAEQVLT	PTVAEQVLT	0.1370	11357.1	50.00	Sequence
DRB1_0701	213	PGTGSPQPTGTILAE	GSPQPTGTI	0.1364	11435.3	50.00	Sequence
DRB1_0701	208	AFTVEPGTGSPQPTG	GTGSPQPTG	0.1344	11685.6	50.00	Sequence
DRB1_0701	164	RGTVYQMWLLGGAKG	RGTVYQMWL	0.1310	12122.8	50.00	Sequence
DRB1_0701	171	WLLGGAKGPRASAGTM	AKGPRASAGT	0.1310	12123.7	50.00	Sequence
DRB1_0701	206	ALAFTVEPGTGSPQP	FTVEPGTGS	0.1304	12192.9	50.00	Sequence
DRB1_0701	170	MWLLGGAKGPRASAGT	AKGPRASAGT	0.1264	12742.5	50.00	Sequence
DRB1_0701	215	TGSPQPTGTILAE	GSPQPTGTI	0.1246	12979.2	50.00	Sequence
DRB1_0701	169	QMWLLGGAKGPRASAG	LGGAKGPR	0.1189	13808.2	50.00	Sequence
DRB1_0701	207	LAFTVEPGTGSPQPT	FTVEPGTGS	0.1187	13849.0	50.00	Sequence
DRB1_0701	209	FTVEPGTGSPQPTGT	GTGSPQPTG	0.1165	14181.1	50.00	Sequence
DRB1_0701	1	TEHTDFELLELATPY	ELLELATPY	0.1080	15546.3	50.00	Sequence
DRB1_0701	191	TPSTTATLTDLGAST	TTATLTDL	0.1077	15589.1	50.00	Sequence
DRB1_0701	23	DERADIDRRVAAAPS	DRRVAAAPS	0.1076	15603.9	50.00	Sequence
DRB1_0701	172	LLGGAKGPRASAGTM	AKGPRASAGT	0.1065	15789.4	50.00	Sequence
DRB1_0701	113	PSPPPTVAEQVLTAP	PTVAEQVLT	0.1002	16917.3	50.00	Sequence
DRB1_0701	10	ELATPYALNAVSDDE	LATPYALNA	0.0891	19064.9	50.00	Sequence
DRB1_0701	114	SPPTVAEQVLTAPD	PTVAEQVLT	0.0814	20714.6	50.00	Sequence
DRB1_0701	22	DDERADIDRRVAAAP	IDRRVAAAP	0.0804	20944.5	50.00	Sequence
DRB1_0701	18	NAVSDDERADIDRRV	ERADIDRRV	0.0746	22305.8	50.00	Sequence
DRB1_0701	19	AVSDDERADIDRRVA	ERADIDRRV	0.0697	23523.8	50.00	Sequence
DRB1_0701	20	VSDDERADIDRRVAA	ERADIDRRV	0.0612	25778.5	50.00	Sequence
DRB1_0701	21	SDDERADIDRRVAAA	ERADIDRRV	0.0546	27706.1	50.00	Sequence

Allele: DRB1_0701. Number of high binders 27. Number of weak binders 62. Number of peptides 218

Allele	pos	peptide	core	l-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
DRB1_0802	80	EVRQRSRWRATAAFAS	RRQRWRATA	0.7024	25.0	SB	0.40	Sequence
DRB1_0802	79	PEVRRQSRWRATAAFA	EVRQRSRWR	0.6710	35.1	SB	0.80	Sequence
DRB1_0802	78	KPEVRRQSRWRATAAF	EVRQRSRWR	0.6521	43.1	SB	1.00	Sequence
DRB1_0802	81	VRRQSRWRATAAFASA	RRQRWRATA	0.6427	47.7	SB	2.00	Sequence
DRB1_0802	82	RRQRWRATAAFASAAA	RRQRWRATA	0.6424	47.9	SB	2.00	Sequence
DRB1_0802	77	TKPEVRRQSRWRATA	EVRQRSRWR	0.6258	57.3	WB	2.00	Sequence
DRB1_0802	76	ATKPEVRRQSRWRATA	EVRQRSRWR	0.5784	95.8	WB	4.00	Sequence
DRB1_0802	105	FGLGVLTRPSPPTV	GLGVLTRPS	0.5758	98.5	WB	4.00	Sequence
DRB1_0802	104	AFGLGVLTRPSPPT	GLGVLTRPS	0.5646	111.1	WB	4.00	Sequence
DRB1_0802	106	GLGVLTRPSPPTVA	GLGVLTRPS	0.5600	116.8	WB	4.00	Sequence
DRB1_0802	83	RQSRWRATAAFASAAA	RQSRWRATA	0.5370	149.8	WB	8.00	Sequence

DRB1_0802	103	GAFGLGVLTRPSPPP	GLGVLTRPS	0.5218	176.5	WB	8.00	Sequence
DRB1_0802	128	DVRTVSRPLGAGTAT	VRTVSRPLG	0.4994	225.1	WB	8.00	Sequence
DRB1_0802	127	PDVRTVSRPLGAGTA	VRTVSRPLG	0.4984	227.5	WB	8.00	Sequence
DRB1_0802	102	LGAFGLGVLTRPSP	GLGVLTRPS	0.4804	276.3	WB	16.00	Sequence
DRB1_0802	75	DATKPEVRRQSRWRT	EVRQRSRWR	0.4777	284.7	WB	16.00	Sequence
DRB1_0802	126	APDVRTVSRPLGAGT	VRTVSRPLG	0.4746	294.2	WB	16.00	Sequence
DRB1_0802	129	VRTVSRPLGAGTATV	VRTVSRPLG	0.4703	308.3	WB	16.00	Sequence
DRB1_0802	164	RGTVYQMWLLGGAKG	RGTVYQMWL	0.4563	358.7	WB	16.00	Sequence
DRB1_0802	165	GTVYQMWLLGGAKGP	GTVYQMWLL	0.4477	393.8	WB	16.00	Sequence
DRB1_0802	163	SRGTVYQMWLLGGAK	RGTVYQMWL	0.4471	396.3	WB	16.00	Sequence
DRB1_0802	85	SRWRTAAFASAAAIA	RWRTAAFAS	0.4453	404.2	WB	16.00	Sequence
DRB1_0802	101	GLGAFGLGVLTRPSP	GLGVLTRPS	0.4426	416.2	WB	16.00	Sequence
DRB1_0802	84	QSRWRTAAFASAAAI	WRTAAFASA	0.4348	452.9	WB	16.00	Sequence
DRB1_0802	86	RWRTAAFASAAAIIV	WRTAAFASA	0.4332	460.8	WB	16.00	Sequence
DRB1_0802	125	TAPDVRTVSRPLGAG	VRTVSRPLG	0.4247	505.2		16.00	Sequence
DRB1_0802	169	QMWLLGGAKGPRSA	MWLLGGAKG	0.4238	509.8		16.00	Sequence
DRB1_0802	162	PSRGTVYQMWLLGGA	GTVYQMWLL	0.4185	539.8		16.00	Sequence
DRB1_0802	166	TVYQMWLLGGAKGPR	TVYQMWLLG	0.4125	576.4		16.00	Sequence
DRB1_0802	170	MWLLGGAKGPRSA	MWLLGGAKG	0.4110	585.9		16.00	Sequence
DRB1_0802	161	PPSRGTVYQMWLLG	RGTVYQMWL	0.4034	635.6		32.00	Sequence
DRB1_0802	107	LGVLTRPSPPTVAE	LGVLTRPSP	0.4027	641.1		32.00	Sequence
DRB1_0802	124	LTAPDVRTVSRPLGA	VRTVSRPLG	0.4021	645.3		32.00	Sequence
DRB1_0802	168	YQMWLLGGAKGPRSA	MWLLGGAKG	0.3982	672.9		32.00	Sequence
DRB1_0802	87	WRTAAFASAAAIAVG	WRTAAFASA	0.3893	741.1		32.00	Sequence
DRB1_0802	171	WLLGGAKGPRSA	WLLGGAKG	0.3831	792.3		32.00	Sequence
DRB1_0802	25	RADIDRRVAAAPSPV	RADIDRRVA	0.3792	826.6		32.00	Sequence
DRB1_0802	123	VTAPDVRTVSRPLG	VRTVSRPLG	0.3726	887.1		32.00	Sequence
DRB1_0802	160	APPSRGTVYQMWLLG	RGTVYQMWL	0.3712	901.0		32.00	Sequence
DRB1_0802	167	VYQMWLLGGAKGPR	MWLLGGAKG	0.3706	907.1		32.00	Sequence
DRB1_0802	42	FNDEVRAVRETMVAV	FNDEVRAVR	0.3654	959.6		32.00	Sequence
DRB1_0802	24	ERADIDRRVAAAPSP	RADIDRRVA	0.3501	1132.6		32.00	Sequence
DRB1_0802	74	LDATKPEVRRQSRWR	EVRQRSRWR	0.3478	1161.0		32.00	Sequence
DRB1_0802	41	AAFNDEVRAVRETM	EVRAVRETM	0.3451	1194.9		32.00	Sequence
DRB1_0802	28	IDRRVAAAPSPVAAA	RRVAAAPSP	0.3406	1254.4		32.00	Sequence
DRB1_0802	27	DIDRRVAAAPSPVAA	IDRRVAAAP	0.3345	1340.0		32.00	Sequence
DRB1_0802	26	ADIDRRVAAAPSPVA	IDRRVAAAP	0.3322	1374.2		32.00	Sequence
DRB1_0802	159	VAPPSRGTVYQMWLL	RGTVYQMWL	0.3264	1463.2		32.00	Sequence
DRB1_0802	172	LLGGAKGPRSA	LGGAKGPR	0.3226	1524.5		32.00	Sequence
DRB1_0802	43	FNDEVRAVRETMVAV	EVRAVRETM	0.3216	1541.6		32.00	Sequence
DRB1_0802	100	VGLGAFGLGVLTRPS	GLGVLTRPS	0.3205	1559.1		32.00	Sequence
DRB1_0802	40	AAAFNDEVRAVRETM	FNDEVRAVR	0.3200	1568.5		32.00	Sequence
DRB1_0802	88	RTAAFASAAAIAVGL	RTAAFASAA	0.3168	1622.5		50.00	Sequence
DRB1_0802	152	GLLVMNNAVPPSRGT	LLVMNNVAP	0.3165	1628.0		50.00	Sequence
DRB1_0802	153	LLVMNNNAVPPSRGT	LLVMNNVAP	0.3088	1770.4		50.00	Sequence
DRB1_0802	45	DEVRAVRETMVAVSA	EVRAVRETM	0.3067	1810.1		50.00	Sequence
DRB1_0802	108	GVLTRPSPPTVAEQ	VLTRPSPPP	0.3053	1838.7		50.00	Sequence
DRB1_0802	141	ATVVFSRDRNTGLLV	VFSRDRNTG	0.3041	1862.3		50.00	Sequence
DRB1_0802	46	EVRAVRETMVAVSAA	EVRAVRETM	0.2901	2166.3		50.00	Sequence
DRB1_0802	151	TGLLVMNNAVPPSRG	GLLVMNNA	0.2858	2269.4		50.00	Sequence
DRB1_0802	173	LGGAKGPRSA	LGGAKGPR	0.2852	2285.6		50.00	Sequence
DRB1_0802	23	DERADIDRRVAAAPS	RADIDRRVA	0.2849	2292.6		50.00	Sequence
DRB1_0802	44	NDEVRAVRETMVAVS	EVRAVRETM	0.2849	2293.0		50.00	Sequence
DRB1_0802	142	TVVFSRDRNTGLLVM	VFSRDRNTG	0.2800	2416.3		50.00	Sequence
DRB1_0802	29	DRRVAAAPSPVAAAF	RRVAAAPSP	0.2731	2603.0		50.00	Sequence
DRB1_0802	109	VLTRPSPPTVAEQV	VLTRPSPPP	0.2701	2689.7		50.00	Sequence
DRB1_0802	174	GGAKGPRSA	GGAKGPR	0.2657	2820.2		50.00	Sequence
DRB1_0802	140	TATVVFSRDRNTGLL	VFSRDRNTG	0.2646	2855.9		50.00	Sequence
DRB1_0802	143	VVFSRDRNTGLLVMN	VFSRDRNTG	0.2638	2880.7		50.00	Sequence
DRB1_0802	6	FELLELATPYALNAV	LLELATPYA	0.2608	2974.1		50.00	Sequence
DRB1_0802	130	RTVSRPLGAGTATVV	RTVSRPLGA	0.2605	2985.1		50.00	Sequence
DRB1_0802	158	NVAPPSRGTVYQMWL	RGTVYQMWL	0.2604	2987.9		50.00	Sequence
DRB1_0802	150	NTGLLVMNNAVPPSR	GLLVMNNA	0.2582	3059.8		50.00	Sequence
DRB1_0802	154	LMNNVAPPSPSRGT	VMNNVAPP	0.2579	3070.0		50.00	Sequence
DRB1_0802	30	RRVAAAPSPVAAAFN	RRVAAAPSP	0.2544	3189.7		50.00	Sequence
DRB1_0802	5	DFELLELATPYALNA	LLELATPYA	0.2501	3341.5		50.00	Sequence
DRB1_0802	22	DERADIDRRVAAAP	IDRRVAAAP	0.2466	3470.2		50.00	Sequence
DRB1_0802	139	GTATVVFSRDRNTGL	ATVVFSRDR	0.2457	3502.6		50.00	Sequence
DRB1_0802	53	TMAVVSAAATAEPPA	MAVVSAAAT	0.2456	3506.8		50.00	Sequence
DRB1_0802	54	MAVVSAAATAEPPAH	MAVVSAAAT	0.2428	3615.4		50.00	Sequence
DRB1_0802	144	VFSRDRNTGLLVMN	VFSRDRNTG	0.2427	3620.1		50.00	Sequence
DRB1_0802	65	PPAHLRTAILDATKP	LRTAILDAT	0.2387	3779.2		50.00	Sequence
DRB1_0802	131	TVSRPLGAGTATVVF	VSRPLGAGT	0.2375	3826.4		50.00	Sequence
DRB1_0802	155	VMNNVAPPSPSRGT	VMNNVAPP	0.2372	3841.1		50.00	Sequence
DRB1_0802	73	ILDATKPEVRRQSRW	ILDATKPEV	0.2367	3860.5		50.00	Sequence
DRB1_0802	39	VAAAFNDEVRAVRET	FNDEVRAVR	0.2362	3883.8		50.00	Sequence
DRB1_0802	48	RAVRETMVAVSAAAT	RAVRETMAV	0.2342	3966.0		50.00	Sequence
DRB1_0802	7	ELLELATPYALNAVS	LLELATPYA	0.2342	3968.6		50.00	Sequence

DRB1_0802	4	TDFELLELATPYALN	LLELATPYA	0.2337	3990.7	50.00	Sequence
DRB1_0802	47	VRAVRETMVAVSAAT	VRAVRETM	0.2335	3998.8	50.00	Sequence
DRB1_0802	8	LLELATPYALNAVSD	LLELATPYA	0.2296	4171.4	50.00	Sequence
DRB1_0802	51	RETMVAVSAATTAEP	TMVAVSAAT	0.2290	4198.0	50.00	Sequence
DRB1_0802	91	AFASAAAIAVGLGAF	FASAAAIAV	0.2290	4198.5	50.00	Sequence
DRB1_0802	89	TAAFASAAAIAVGLG	AFASAAAIA	0.2287	4210.0	50.00	Sequence
DRB1_0802	149	RNTGLLVMMNVAPPS	GLLVMMNVA	0.2276	4262.3	50.00	Sequence
DRB1_0802	64	EPPAHLRRTAILDATK	LRTAILDAT	0.2262	4325.9	50.00	Sequence
DRB1_0802	3	HTDFELLELATPYAL	LLELATPYA	0.2260	4335.7	50.00	Sequence
DRB1_0802	138	AGTATVVFSRDRNTG	VFSRDRNTG	0.2257	4348.6	50.00	Sequence
DRB1_0802	68	HLRRTAILDATKPEVR	HLRRTAILDA	0.2250	4383.1	50.00	Sequence
DRB1_0802	52	ETMAVVSAAATTAEP	MAVVSAAAT	0.2249	4386.2	50.00	Sequence
DRB1_0802	49	AVRETMVAVSAATTA	MAVVSAAAT	0.2246	4400.3	50.00	Sequence
DRB1_0802	90	AAFASAAAIAVGLGA	AFASAAAIA	0.2230	4476.1	50.00	Sequence
DRB1_0802	122	QVLTAPDVRTVSRPL	DVRTVSRPL	0.2208	4584.1	50.00	Sequence
DRB1_0802	67	AHLRRTAILDATKPEV	HLRRTAILDA	0.2200	4627.1	50.00	Sequence
DRB1_0802	66	PAHLRRTAILDATKPE	HLRRTAILDA	0.2195	4649.5	50.00	Sequence
DRB1_0802	50	VRETMVAVSAATTAE	MAVVSAAAT	0.2193	4662.7	50.00	Sequence
DRB1_0802	183	GTMGTAAVTPSTTAT	GTMGTAAVT	0.2190	4675.9	50.00	Sequence
DRB1_0802	132	VSRPLGAGTATVVFS	VSRPLGAGT	0.2187	4692.0	50.00	Sequence
DRB1_0802	182	AGTMGTAAVTPSTTA	GTMGTAAVT	0.2161	4823.9	50.00	Sequence
DRB1_0802	178	GPRSAGTMGTAAVTP	GPRSAGTMG	0.2158	4838.4	50.00	Sequence
DRB1_0802	177	KGPRSAGTMGTAAVT	GPRSAGTMG	0.2153	4869.8	50.00	Sequence
DRB1_0802	38	PVAAAFNDEVRAVRE	FNDEVRAVR	0.2086	5233.5	50.00	Sequence
DRB1_0802	55	AVVSAATTAEPHAHL	AVVSAATTA	0.2083	5248.5	50.00	Sequence
DRB1_0802	181	SAGTMGTAAVTPSTT	GTMGTAAVT	0.2051	5434.3	50.00	Sequence
DRB1_0802	63	AEPHAHLRRTAILDAT	PPAHLRRTAI	0.2040	5501.9	50.00	Sequence
DRB1_0802	97	IAVGLGAFGLGVLT	IAVGLGAFG	0.2025	5590.6	50.00	Sequence
DRB1_0802	135	PLGAGTATVVFSRDR	GTATVVFSR	0.2017	5636.0	50.00	Sequence
DRB1_0802	157	NNVAPPSRGTIVYQW	PPSRGTIVYQ	0.2015	5651.8	50.00	Sequence
DRB1_0802	175	GAKGPRSAGTMGTAA	GPRSAGTMG	0.1999	5751.5	50.00	Sequence
DRB1_0802	98	IAVGLGAFGLGVLTR	IAVGLGAFG	0.1988	5816.8	50.00	Sequence
DRB1_0802	37	SPVAAAFNDEVRAVR	FNDEVRAVR	0.1987	5824.3	50.00	Sequence
DRB1_0802	148	DRNTGLLVMMNVAPP	GLLVMMNVA	0.1985	5837.5	50.00	Sequence
DRB1_0802	180	RSAGTMGTAAVTPST	GTMGTAAVT	0.1977	5890.6	50.00	Sequence
DRB1_0802	92	FASAAAIAVGLGAFG	FASAAAIAV	0.1975	5903.1	50.00	Sequence
DRB1_0802	217	SPQPTGTILAEPLG	GTILAEPL	0.1962	5982.9	50.00	Sequence
DRB1_0802	147	RDRNTGLLVMMNVAP	GLLVMMNVA	0.1942	6118.7	50.00	Sequence
DRB1_0802	134	RPLGAGTATVVFSRD	PLGAGTATV	0.1935	6159.9	50.00	Sequence
DRB1_0802	2	EHTDFELLELATPYA	LLELATPYA	0.1912	6316.1	50.00	Sequence
DRB1_0802	137	GAGTATVVFSRDRNT	ATVVFSRDR	0.1911	6323.9	50.00	Sequence
DRB1_0802	72	AILDATKPEVRRQSR	ILDATKPEV	0.1899	6407.8	50.00	Sequence
DRB1_0802	133	SRLGAGTATVVFSR	PLGAGTATV	0.1883	6521.1	50.00	Sequence
DRB1_0802	205	TALAFTVEPGTGSPQ	ALAFTEVEPG	0.1881	6533.1	50.00	Sequence
DRB1_0802	176	AKGPRSAGTMGTAAV	GPRSAGTMG	0.1879	6547.1	50.00	Sequence
DRB1_0802	156	MNNVAPPSRGTIVYQ	MNNVAPPSR	0.1845	6795.8	50.00	Sequence
DRB1_0802	99	AVGLGAFGLGVLTRP	GAFGLGVLT	0.1806	7085.5	50.00	Sequence
DRB1_0802	71	TAILDATKPEVRRQS	ILDATKPEV	0.1802	7118.6	50.00	Sequence
DRB1_0802	70	RTAILDATKPEVRRQ	ILDATKPEV	0.1802	7118.7	50.00	Sequence
DRB1_0802	204	STALAFTVEPGTGSP	TALAFTVEP	0.1779	7293.0	50.00	Sequence
DRB1_0802	96	AAIAVGLGAFGLGVL	IAVGLGAFG	0.1765	7409.8	50.00	Sequence
DRB1_0802	21	SDDERADIDRRVAA	RADIDRRVA	0.1751	7517.4	50.00	Sequence
DRB1_0802	203	ASTALAFTVEPGTGS	ASTALAFTV	0.1749	7534.2	50.00	Sequence
DRB1_0802	146	SRDRNTGLLVMMNVA	GLLVMMNVA	0.1747	7549.7	50.00	Sequence
DRB1_0802	117	PTVAEQVLTAPDVRT	PTVAEQVLT	0.1738	7629.5	50.00	Sequence
DRB1_0802	184	TMGTAAVTPSTTATL	GTAAVTPST	0.1737	7631.3	50.00	Sequence
DRB1_0802	179	PRSAGTMGTAAVTPS	GTMGTAAVT	0.1713	7834.1	50.00	Sequence
DRB1_0802	31	RVAAAPSPVAAAFND	RVAAAPSPV	0.1713	7838.2	50.00	Sequence
DRB1_0802	202	GASTALAFTVEPGTG	GASTALAFT	0.1700	7948.9	50.00	Sequence
DRB1_0802	69	LRTAILDATKPEVRR	ILDATKPEV	0.1689	8042.6	50.00	Sequence
DRB1_0802	121	EQVLTAPDVRTVSRP	LTAPDVRTV	0.1672	8186.1	50.00	Sequence
DRB1_0802	185	MGTAAVTPSTTATLT	GTAAVTPST	0.1663	8272.1	50.00	Sequence
DRB1_0802	95	AAAIAVGLGAFGLGV	IAVGLGAFG	0.1642	8460.0	50.00	Sequence
DRB1_0802	136	LGAGTATVVFSRDRN	ATVVFSRDR	0.1637	8509.0	50.00	Sequence
DRB1_0802	206	ALAFTEVEPGTGSPQ	ALAFTEVEPG	0.1603	8828.4	50.00	Sequence
DRB1_0802	118	TVAEQVLTAPDVRTV	TVAEQVLT	0.1594	8912.8	50.00	Sequence
DRB1_0802	201	LGASTALAFTVEPGT	GASTALAFT	0.1579	9055.5	50.00	Sequence
DRB1_0802	57	VSAATTAEPHAHLRT	VSAATTAEP	0.1567	9178.5	50.00	Sequence
DRB1_0802	119	VAEQVLTAPDVRTVS	VAEQVLTAP	0.1565	9199.8	50.00	Sequence
DRB1_0802	216	GSPQPTGTILAEPL	GTILAEPL	0.1561	9235.6	50.00	Sequence
DRB1_0802	56	VVSAATTAEPHAHLR	VVSAATTAE	0.1559	9252.6	50.00	Sequence
DRB1_0802	62	TAEPHAHLRRTAILDA	HLRRTAILDA	0.1544	9409.3	50.00	Sequence
DRB1_0802	20	VSDDERADIDRRVAA	RADIDRRVA	0.1539	9458.7	50.00	Sequence
DRB1_0802	200	DLGASTALAFTVEPG	GASTALAFT	0.1513	9729.8	50.00	Sequence
DRB1_0802	120	AEQVLTAPDVRTVSR	LTAPDVRTV	0.1495	9918.2	50.00	Sequence
DRB1_0802	145	FSRDRNTGLLVMMNV	RDRNTGLLV	0.1483	10051.7	50.00	Sequence
DRB1_0802	197	TLTDLGASTALAFTV	GASTALAFT	0.1472	10167.0	50.00	Sequence

DRB1_0802	186	GTAAVTPSTTATLTD	GTAAVTPST	0.1469	10206.8	50.00	Sequence
DRB1_0802	198	LTDLGASTALAFVTE	GASTALAF	0.1434	10592.9	50.00	Sequence
DRB1_0802	93	ASAAAIAVGLGAFGL	IAVGLGAFG	0.1392	11089.8	50.00	Sequence
DRB1_0802	94	SAAAIAVGLGAFGLG	IAVGLGAFG	0.1382	11214.0	50.00	Sequence
DRB1_0802	116	PPTVAEQVLTAPDVR	PPTVAEQVL	0.1362	11453.0	50.00	Sequence
DRB1_0802	32	VAAAPSPVAAAFNDE	VAAAPSPVA	0.1357	11514.5	50.00	Sequence
DRB1_0802	19	AVSDDERADIDRRVA	RADIDRRVA	0.1352	11573.6	50.00	Sequence
DRB1_0802	199	TDLGASTALAFVTEP	GASTALAF	0.1310	12123.0	50.00	Sequence
DRB1_0802	209	FTVEPGTGSPPQPTGT	FTVEPGTGS	0.1306	12167.3	50.00	Sequence
DRB1_0802	9	LELATPYALNAVSD	LELATPYAL	0.1267	12696.5	50.00	Sequence
DRB1_0802	214	GTGSPQPTGTILAE	GTGSPQPTG	0.1249	12950.0	50.00	Sequence
DRB1_0802	212	EPGTGSPQPTGTILA	GTGSPQPTG	0.1244	13014.8	50.00	Sequence
DRB1_0802	1	TEHTDFELLELATPY	FELLELATP	0.1220	13351.8	50.00	Sequence
DRB1_0802	208	AFTVEPGTGSPPQPTG	FTVEPGTGS	0.1203	13601.9	50.00	Sequence
DRB1_0802	110	LTRPSPPTVAEQVL	LTRPSPPT	0.1199	13669.3	50.00	Sequence
DRB1_0802	36	PSPVAAAFNDEVRAV	AFNDEVRAV	0.1173	14047.3	50.00	Sequence
DRB1_0802	196	ATLTDLGASTALAF	LTDLGASTA	0.1167	14144.0	50.00	Sequence
DRB1_0802	11	LATPYALNAVSDDER	LATPYALNA	0.1165	14178.0	50.00	Sequence
DRB1_0802	194	TTATLTDLGASTALA	TTATLTDLG	0.1143	14524.1	50.00	Sequence
DRB1_0802	210	VTEPGTGSPPQPTGTI	GTGSPQPTG	0.1136	14623.3	50.00	Sequence
DRB1_0802	211	VEPGTGSPPQPTGTIL	GTGSPQPTG	0.1134	14654.6	50.00	Sequence
DRB1_0802	115	PPPTVAEQVLTAPDV	PPTVAEQVL	0.1125	14801.9	50.00	Sequence
DRB1_0802	213	PGTGSPPQPTGTILAE	GTGSPQPTG	0.1124	14824.8	50.00	Sequence
DRB1_0802	0	MTEHTDFELLELATP	FELLELATP	0.1113	15003.1	50.00	Sequence
DRB1_0802	10	ELATPYALNAVSDDE	TPYALNAVS	0.1105	15118.5	50.00	Sequence
DRB1_0802	61	TTAEPHAHLRRTAILD	PAHLRRTAIL	0.1099	15223.7	50.00	Sequence
DRB1_0802	188	AAVTPSTTATLTDLG	AVTPSTTAT	0.1072	15681.4	50.00	Sequence
DRB1_0802	193	STTATLTDLGASTAL	TTATLTDLG	0.1062	15852.7	50.00	Sequence
DRB1_0802	207	LAFTVEPGTGSPPQPT	FTVEPGTGS	0.1058	15913.6	50.00	Sequence
DRB1_0802	192	PSTTATLTDLGASTA	TTATLTDLG	0.1023	16526.0	50.00	Sequence
DRB1_0802	60	ATTAEPHAHLRRTAIL	PAHLRRTAIL	0.1018	16613.1	50.00	Sequence
DRB1_0802	215	TGSPQPTGTILAE	TGTILAE	0.1006	16841.7	50.00	Sequence
DRB1_0802	189	AVTPSTTATLTDLGA	AVTPSTTAT	0.1000	16955.0	50.00	Sequence
DRB1_0802	59	AATTAEPHAHLRRTAI	AATTAEP	0.0983	17252.0	50.00	Sequence
DRB1_0802	12	ATPYALNAVSDDERA	TPYALNAVS	0.0969	17526.9	50.00	Sequence
DRB1_0802	114	SPPPTVAEQVLTAPD	PPTVAEQVL	0.0965	17603.3	50.00	Sequence
DRB1_0802	190	VTPSTTATLTDLGAS	TTATLTDLG	0.0947	17947.8	50.00	Sequence
DRB1_0802	113	PSPPTVAEQVLTAPD	PPTVAEQVL	0.0923	18423.5	50.00	Sequence
DRB1_0802	112	RPSPPPTVAEQVLTAT	PTVAEQVLT	0.0875	19396.6	50.00	Sequence
DRB1_0802	13	TPYALNAVSDDERAD	TPYALNAVS	0.0866	19594.7	50.00	Sequence
DRB1_0802	191	TPSTTATLTDLGAST	TTATLTDLG	0.0861	19706.1	50.00	Sequence
DRB1_0802	58	SAATTAEPHAHLRRTA	AATTAEP	0.0845	20047.8	50.00	Sequence
DRB1_0802	187	TAAVTPSTTATLTDL	AVTPSTTAT	0.0831	20342.8	50.00	Sequence
DRB1_0802	195	TATLTDLGASTALAF	LTDLGASTA	0.0805	20924.1	50.00	Sequence
DRB1_0802	111	TRPSPPTVAEQVLT	RPSPPPTVA	0.0792	21215.0	50.00	Sequence
DRB1_0802	34	AAAPSPVAAAFNDEV	AAAFNDEV	0.0759	22000.9	50.00	Sequence
DRB1_0802	35	APSPVAAAFNDEVRA	PSPVAAAFN	0.0722	22901.8	50.00	Sequence
DRB1_0802	33	AAAPSPVAAAFNDEV	AAAPSPVAA	0.0678	24007.8	50.00	Sequence
DRB1_0802	14	PYALNAVSDDERADI	PYALNAVSD	0.0487	29533.7	50.00	Sequence
DRB1_0802	17	LNAVSDDERADIDRR	LNAVSDDER	0.0477	29856.3	50.00	Sequence
DRB1_0802	16	ALNAVSDDERADIDR	LNAVSDDER	0.0470	30081.6	50.00	Sequence
DRB1_0802	15	YALNAVSDDERADID	LNAVSDDER	0.0468	30125.0	50.00	Sequence
DRB1_0802	18	NAVSDDERADIDRRV	ERADIDRRV	0.0431	31357.5	50.00	Sequence

Allele: DRB1_0802. Number of high binders 5. Number of weak binders 20. Number of peptides 218

Allele	pos	peptide	core	l-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
DRB1_0901	86	RWRTAAFASAAAIAV	WRTAAFASA	0.7135	22.2	SB	0.30	Sequence
DRB1_0901	87	WRTAAFASAAAIAVG	WRTAAFASA	0.7082	23.5	SB	0.40	Sequence
DRB1_0901	85	SRWRTAAFASAAAIA	WRTAAFASA	0.6850	30.2	SB	0.80	Sequence
DRB1_0901	89	TAAFASAAAIAVGLG	AFASAAAIA	0.6754	33.5	SB	0.80	Sequence
DRB1_0901	88	RTAAFASAAAIAVGL	AFASAAAIA	0.6530	42.7	SB	2.00	Sequence
DRB1_0901	90	AAFASAAAIAVGLGA	AFASAAAIA	0.6503	44.0	SB	2.00	Sequence
DRB1_0901	28	IDRRVAAAPSPVAAA	VAAAPSPVA	0.6343	52.3	WB	2.00	Sequence
DRB1_0901	27	DIDRRVAAAPSPVAA	DRRVAAAPS	0.6191	61.6	WB	4.00	Sequence
DRB1_0901	29	DRRVAAAPSPVAAAF	VAAAPSPVA	0.6184	62.1	WB	4.00	Sequence
DRB1_0901	84	QSRWRTAAFASAAAI	WRTAAFASA	0.6149	64.5	WB	4.00	Sequence
DRB1_0901	26	ADIDRRVAAAPSPVA	VAAAPSPVA	0.6068	70.4	WB	4.00	Sequence
DRB1_0901	91	AFASAAAIAVGLGAF	FASAAAIAV	0.6052	71.7	WB	4.00	Sequence
DRB1_0901	83	RQSRWRTAAFASAAA	WRTAAFASA	0.5992	76.4	WB	4.00	Sequence
DRB1_0901	30	RRVAAAPSPVAAAFN	VAAAPSPVA	0.5868	87.4	WB	8.00	Sequence
DRB1_0901	46	EVRAVRETMVVVSA	EVRAVRETM	0.5717	103.0	WB	8.00	Sequence
DRB1_0901	45	DEVRAVRETMVVVSA	EVRAVRETM	0.5715	103.1	WB	8.00	Sequence

DRB1_0901	171	WLLGGAKGPRSAGTM	WLLGGAKGP	0.5713	103.4	WB	8.00	Sequence
DRB1_0901	44	NDEVRAVRETMVAVS	DEVRAVRET	0.5663	109.1	WB	8.00	Sequence
DRB1_0901	109	VLTRPSPPTVAEQV	LTRPSPPT	0.5620	114.3	WB	8.00	Sequence
DRB1_0901	108	GVLTRPSPPTVAEQ	LTRPSPPT	0.5607	115.9	WB	8.00	Sequence
DRB1_0901	82	RRQSRWRTAAFASAA	WRTAAFASA	0.5569	120.8	WB	8.00	Sequence
DRB1_0901	47	VRAVRETMVAVSAAT	AVRETMAVV	0.5541	124.5	WB	8.00	Sequence
DRB1_0901	170	MWLLGGAKGPRSAGT	WLLGGAKGP	0.5497	130.6	WB	8.00	Sequence
DRB1_0901	48	RAVRETMVAVSAATT	AVRETMAVV	0.5475	133.8	WB	16.00	Sequence
DRB1_0901	169	QMWLLGGAKGPRSAG	WLLGGAKGP	0.5472	134.1	WB	16.00	Sequence
DRB1_0901	107	LGVLTRPSPPTVAE	LTRPSPPT	0.5357	152.0	WB	16.00	Sequence
DRB1_0901	31	RVAAAPSPVAAAFND	VAAAPSPVA	0.5353	152.7	WB	16.00	Sequence
DRB1_0901	168	YQMWLLGGAKGPRSA	LGGAKGPRS	0.5331	156.4	WB	16.00	Sequence
DRB1_0901	49	AVRETMVAVSAATTA	AVRETMAVV	0.5253	170.0	WB	16.00	Sequence
DRB1_0901	25	RADIDRRVAAAPSPV	RVAAAPSPV	0.5184	183.2	WB	16.00	Sequence
DRB1_0901	8	LLELATPYALNAVSD	ELATPYALN	0.5097	201.4	WB	16.00	Sequence
DRB1_0901	81	VRQSRWRTAAFASAA	WRTAAFASA	0.5084	204.1	WB	16.00	Sequence
DRB1_0901	9	LELATPYALNAVSD	ELATPYALN	0.5059	209.8	WB	16.00	Sequence
DRB1_0901	110	LTRPSPPTVAEQVL	LTRPSPPT	0.5027	217.3	WB	16.00	Sequence
DRB1_0901	106	GLGVLTRPSPPTVA	VLTRPSPPT	0.5025	217.7	WB	16.00	Sequence
DRB1_0901	32	VAAAPSPVAAAFNDE	VAAAPSPVA	0.5002	223.1	WB	16.00	Sequence
DRB1_0901	6	FELLELATPYALNAV	ELATPYALN	0.4915	245.1	WB	32.00	Sequence
DRB1_0901	92	FASAAAIAVGLGAFG	FASAAAIAV	0.4906	247.5	WB	32.00	Sequence
DRB1_0901	43	FNDEVRAVRETMVAV	EVRAVRETM	0.4900	249.1	WB	32.00	Sequence
DRB1_0901	7	ELELATPYALNAVSD	ELATPYALN	0.4889	252.2	WB	32.00	Sequence
DRB1_0901	182	AGTMGTAAVTPSTTA	AGTMGTAAV	0.4889	252.2	WB	32.00	Sequence
DRB1_0901	128	DVRTVSRPLGAGTAT	DVRTVSRPL	0.4870	257.3	WB	32.00	Sequence
DRB1_0901	100	VGLGAFGLGVLTRPS	VGLGAFGLG	0.4856	261.4	WB	32.00	Sequence
DRB1_0901	172	LLGGAKGPRSAGTMG	LLGGAKGPR	0.4851	262.6	WB	32.00	Sequence
DRB1_0901	177	KGPRSAGTMGTAAVT	AGTMGTAAV	0.4801	277.4	WB	32.00	Sequence
DRB1_0901	50	VRETMVAVSAATTA	VRETMAVVS	0.4792	279.9	WB	32.00	Sequence
DRB1_0901	167	VYQMWLLGGAKGPRS	LGGAKGPRS	0.4733	298.4	WB	32.00	Sequence
DRB1_0901	5	DFELLELATPYALNA	ELATPYALN	0.4725	301.2	WB	32.00	Sequence
DRB1_0901	181	SAGTMGTAAVTPSTT	AGTMGTAAV	0.4668	320.1	WB	32.00	Sequence
DRB1_0901	10	ELATPYALNAVSDDE	ELATPYALN	0.4657	324.1	WB	32.00	Sequence
DRB1_0901	185	MGTAAVTPSTTATLT	MGTAAVTPS	0.4655	324.9	WB	32.00	Sequence
DRB1_0901	99	AVGLGAFGLGVLTRP	VGLGAFGLG	0.4636	331.5	WB	32.00	Sequence
DRB1_0901	184	TMGTAAVTPSTTATL	MGTAAVTPS	0.4629	333.9	WB	32.00	Sequence
DRB1_0901	105	FGLGVLTRPSPPTV	LTRPSPPT	0.4608	341.6	WB	32.00	Sequence
DRB1_0901	127	PDVRTVSRPLGAGTA	DVRTVSRPL	0.4596	346.1	WB	32.00	Sequence
DRB1_0901	98	IAVGLGAFGLGVLTR	LGAFGLGVL	0.4585	350.2	WB	32.00	Sequence
DRB1_0901	180	RSAGTMGTAAVTPST	AGTMGTAAV	0.4575	354.2	WB	32.00	Sequence
DRB1_0901	4	TDFELLELATPYALN	LLELATPYA	0.4536	369.5	WB	32.00	Sequence
DRB1_0901	178	GPRSAGTMGTAAVTP	AGTMGTAAV	0.4469	397.1	WB	32.00	Sequence
DRB1_0901	134	RPLGAGTATVVFSRD	PLGAGTATV	0.4465	399.0	WB	32.00	Sequence
DRB1_0901	51	RETMVAVSAATTAEP	MAVVSAAAT	0.4438	410.9	WB	32.00	Sequence
DRB1_0901	176	AKGPRSAGTMGTAAV	AGTMGTAAV	0.4404	426.2	WB	32.00	Sequence
DRB1_0901	179	PRSAGTMGTAAVTPS	AGTMGTAAV	0.4402	426.9	WB	32.00	Sequence
DRB1_0901	42	AFNDEVRAVRETMAV	EVRAVRETM	0.4365	444.5	WB	32.00	Sequence
DRB1_0901	173	LGGAKGPRSAGTMGT	LGGAKGPRS	0.4359	447.2	WB	32.00	Sequence
DRB1_0901	12	ATPYALNAVSDDERA	ATPYALNAV	0.4329	462.2	WB	32.00	Sequence
DRB1_0901	133	SRPLGAGTATVVFSR	PLGAGTATV	0.4315	469.2	WB	32.00	Sequence
DRB1_0901	126	APDVRTVSRPLGAGT	DVRTVSRPL	0.4295	479.3	WB	32.00	Sequence
DRB1_0901	131	TVSRPLGAGTATVVF	LGAGTATVV	0.4292	481.2	WB	32.00	Sequence
DRB1_0901	183	GTMGTAAVTPSTTAT	MGTAAVTPS	0.4287	483.5	WB	32.00	Sequence
DRB1_0901	129	VRTVSRPLGAGTATV	TVSRPLGAG	0.4257	499.6	WB	50.00	Sequence
DRB1_0901	135	PLGAGTATVVFSRDR	LGAGTATVV	0.4252	502.4	WB	50.00	Sequence
DRB1_0901	111	TRPSPPTVAEQVLT	TRPSPPTV	0.4239	509.5	WB	50.00	Sequence
DRB1_0901	198	LTDLGASTALAFVTE	DLGASTALA	0.4238	510.1	WB	50.00	Sequence
DRB1_0901	130	RTVSRPLGAGTATVV	TVSRPLGAG	0.4232	513.3	WB	50.00	Sequence
DRB1_0901	187	TAAVTPSTTATLTDL	VTPSTTATL	0.4232	513.5	WB	50.00	Sequence
DRB1_0901	11	LATPYALNAVSDDER	ATPYALNAV	0.4227	516.3	WB	50.00	Sequence
DRB1_0901	154	LVMNNVAPPSRGTVY	VMNNVAPPS	0.4212	524.8	WB	50.00	Sequence
DRB1_0901	15	YALNAVSDDERADID	YALNAVSDD	0.4194	534.7	WB	50.00	Sequence
DRB1_0901	14	PYALNAVSDDERADI	YALNAVSDD	0.4182	541.6	WB	50.00	Sequence
DRB1_0901	97	AIAVGLGAFGLGVL	LGAFGLGVL	0.4182	541.9	WB	50.00	Sequence
DRB1_0901	132	VSRPLGAGTATVVFS	PLGAGTATV	0.4170	549.1	WB	50.00	Sequence
DRB1_0901	188	AAVTPSTTATLTDLG	VTPSTTATL	0.4153	558.9	WB	50.00	Sequence
DRB1_0901	165	GTVYQMWLLGGAKGP	GTVYQMWLL	0.4151	560.4	WB	50.00	Sequence
DRB1_0901	13	TPYALNAVSDDERAD	YALNAVSDD	0.4107	587.7	WB	50.00	Sequence
DRB1_0901	54	MAVVSAAATTAEP	MAVVSAAAT	0.4104	589.4	WB	50.00	Sequence
DRB1_0901	197	TLTDLGASTALAFVTV	DLGASTALA	0.4081	604.4	WB	50.00	Sequence
DRB1_0901	53	TMAVVSAAATTAEP	MAVVSAAAT	0.4073	609.7	WB	50.00	Sequence
DRB1_0901	102	LGAFGLGVLTRPSP	LGAFGLGVL	0.4040	632.0	WB	50.00	Sequence
DRB1_0901	186	GTAAVTPSTTATLTD	VTPSTTATL	0.4039	632.7	WB	50.00	Sequence
DRB1_0901	67	AHLRTAILDATKPEV	AHLRTAILD	0.4031	638.0	WB	50.00	Sequence
DRB1_0901	56	VVSAATTAEP	VVSAATTA	0.4026	641.8	WB	50.00	Sequence
DRB1_0901	199	TDLGASTALAFVTEP	DLGASTALA	0.4005	656.5	WB	50.00	Sequence

DRB1_0901	96	AAIAVGLGAFGLGVL	LGAFGLGVL	0.3961	688.3	50.00	Sequence
DRB1_0901	153	LLVMNNVAPP SRGTV	VMNNVAPPS	0.3954	693.7	50.00	Sequence
DRB1_0901	155	VMNNVAPP SRGTVYQ	VMNNVAPPS	0.3939	704.4	50.00	Sequence
DRB1_0901	125	TAPDVRTVSRPLGAG	DVRTVSRPL	0.3930	711.6	50.00	Sequence
DRB1_0901	101	GLGAFGLGVLTRPSP	LGAFGLGVL	0.3923	717.0	50.00	Sequence
DRB1_0901	104	AFGLGVLTRPSPPT	VLTRPSPPP	0.3922	717.8	50.00	Sequence
DRB1_0901	196	ATLTDLGASTALAF	DLGASTALA	0.3902	733.9	50.00	Sequence
DRB1_0901	34	AAPSPVAAAFNDEV	AAPSPVAAA	0.3886	746.6	50.00	Sequence
DRB1_0901	189	AVTPSTTATLTDLGA	VTPSTTATL	0.3875	755.6	50.00	Sequence
DRB1_0901	52	ETMAVVSAAATTAEP	MAVVSAAAT	0.3868	761.2	50.00	Sequence
DRB1_0901	41	AAFNDEVRAVRETMA	DEVRAVRET	0.3866	762.9	50.00	Sequence
DRB1_0901	24	ERADIDRRVAAAPSP	DRRVAAAPS	0.3863	765.0	50.00	Sequence
DRB1_0901	136	LGAGTATVVF SRDRN	LGAGTATVV	0.3856	771.1	50.00	Sequence
DRB1_0901	200	DLGASTALAF TVEPG	DLGASTALA	0.3846	779.5	50.00	Sequence
DRB1_0901	166	TVYQM WLLGGAKGPR	MWLLGGAKG	0.3818	803.1	50.00	Sequence
DRB1_0901	123	VL TAPDVRTVSRPLG	DVRTVSRPL	0.3806	813.6	50.00	Sequence
DRB1_0901	37	SPVAAAFNDEVRAVR	SPVAAAFND	0.3726	887.6	50.00	Sequence
DRB1_0901	190	VTPSTTATLTDLGAS	VTPSTTATL	0.3723	890.4	50.00	Sequence
DRB1_0901	33	AAAPSPVAAAFNDEV	AAPSPVAAA	0.3715	898.3	50.00	Sequence
DRB1_0901	122	QVLTAPDVRTVSRPL	DVRTVSRPL	0.3690	922.3	50.00	Sequence
DRB1_0901	80	EVRQR SRWR TAAFA	SRWR TAAFA	0.3634	980.7	50.00	Sequence
DRB1_0901	164	RGT VYQM WLLGGAKG	TVYQM WLLG	0.3629	985.7	50.00	Sequence
DRB1_0901	35	APSPVAAAFNDEVRA	SPVAAAFND	0.3619	996.6	50.00	Sequence
DRB1_0901	55	AVVSAATTAEP PAHL	AVVSAATTA	0.3594	1024.0	50.00	Sequence
DRB1_0901	152	GLLVMNNVAPP SRGT	VMNNVAPPS	0.3586	1032.9	50.00	Sequence
DRB1_0901	117	PTVAEQVLTAPDVRT	EQVLTAPDV	0.3575	1045.2	50.00	Sequence
DRB1_0901	66	PAHLRTAILDATKPE	AHLRTAILD	0.3527	1100.7	50.00	Sequence
DRB1_0901	36	PSPVAAAFNDEVRAV	SPVAAAFND	0.3504	1127.8	50.00	Sequence
DRB1_0901	119	VAEQVLTAPDVRTVS	EQVLTAPDV	0.3495	1139.8	50.00	Sequence
DRB1_0901	61	TTAEP PAHLRTAILD	TTAEP PAHL	0.3489	1146.3	50.00	Sequence
DRB1_0901	59	AATTAEP PAHLRTAI	AATTAEP PA	0.3489	1147.4	50.00	Sequence
DRB1_0901	195	TATLTDLGASTALAF	DLGASTALA	0.3478	1160.4	50.00	Sequence
DRB1_0901	118	TVAEQVLTAPDVRTV	EQVLTAPDV	0.3459	1184.4	50.00	Sequence
DRB1_0901	120	AEQVLTAPDVRTVSR	QVLTAPDVR	0.3456	1188.6	50.00	Sequence
DRB1_0901	217	SPQPTGTILAE LPLG	GTILAE LPL	0.3441	1208.1	50.00	Sequence
DRB1_0901	65	PPAHLRTAILDATKP	AHLRTAILD	0.3428	1225.6	50.00	Sequence
DRB1_0901	156	MNNVAPP SRGT VYQM	MNNVAPP SR	0.3420	1235.4	50.00	Sequence
DRB1_0901	71	TAILDATKPEVRRQS	ILDATKPEV	0.3413	1245.0	50.00	Sequence
DRB1_0901	72	AILDATKPEVRRQSR	ILDATKPEV	0.3404	1257.2	50.00	Sequence
DRB1_0901	121	EQVLTAPDVRTVSRP	QVLTAPDVR	0.3399	1264.5	50.00	Sequence
DRB1_0901	70	RTAILDATKPEVRRQ	ILDATKPEV	0.3374	1298.4	50.00	Sequence
DRB1_0901	124	LTAPDVRTVSRPLGA	DVRTVSRPL	0.3354	1327.2	50.00	Sequence
DRB1_0901	174	GGAKGPR SAGTMGT	KGPR SAGTM	0.3335	1354.6	50.00	Sequence
DRB1_0901	69	LRTAILDATKPEVRR	ILDATKPEV	0.3332	1359.3	50.00	Sequence
DRB1_0901	57	VSAATTAEP PAHLRT	VSAATTAEP	0.3324	1370.6	50.00	Sequence
DRB1_0901	58	SAATTAEP PAHLRT	AATTAEP PA	0.3318	1380.3	50.00	Sequence
DRB1_0901	116	PPTVAEQVLTAPDVR	EQVLTAPDV	0.3313	1387.2	50.00	Sequence
DRB1_0901	216	GSPQPTGTILAE LPL	GTILAE LPL	0.3298	1410.2	50.00	Sequence
DRB1_0901	175	GAKGPR SAGTMGTAA	KGPR SAGTM	0.3298	1410.6	50.00	Sequence
DRB1_0901	62	TAEP PAHLRTAILDA	AHLRTAILD	0.3289	1423.7	50.00	Sequence
DRB1_0901	3	HTDFELLE L ATPYA	LLE L ATPYA	0.3285	1429.8	50.00	Sequence
DRB1_0901	40	AAAFNDEVRAVRETM	EVRAVRETM	0.3250	1485.3	50.00	Sequence
DRB1_0901	94	SAAAIAVGLGAFGLG	VGLGAFGLG	0.3234	1510.9	50.00	Sequence
DRB1_0901	64	EPPAHLRTAILDATK	AHLRTAILD	0.3232	1515.0	50.00	Sequence
DRB1_0901	115	PPPTVAEQVLTAPDV	EQVLTAPDV	0.3230	1518.5	50.00	Sequence
DRB1_0901	151	TGLLVMNNVAPP SRG	VMNNVAPPS	0.3223	1529.7	50.00	Sequence
DRB1_0901	79	PEVRRQSRWR TAAFA	SRWR TAAFA	0.3213	1546.0	50.00	Sequence
DRB1_0901	163	SRGT VYQM WLLGGAK	RGT VYQM WL	0.3212	1548.2	50.00	Sequence
DRB1_0901	145	FSRDRNTGLLVMNNV	SRDRNTGLL	0.3206	1558.1	50.00	Sequence
DRB1_0901	73	ILDATKPEVRRQSRW	ILDATKPEV	0.3178	1604.7	50.00	Sequence
DRB1_0901	68	HLRTAILDATKPEVR	ILDATKPEV	0.3137	1679.1	50.00	Sequence
DRB1_0901	112	RPSPPPTVAEQVLT	RPSPPPTVA	0.3135	1681.4	50.00	Sequence
DRB1_0901	194	TTATLTDLGASTALA	DLGASTALA	0.3125	1700.6	50.00	Sequence
DRB1_0901	60	ATAEP PAHLRTAIL	TTAEP PAHL	0.3086	1774.4	50.00	Sequence
DRB1_0901	201	LGASTALAF TVEPGT	LGASTALAF	0.3085	1776.0	50.00	Sequence
DRB1_0901	38	PVAAAFNDEVRAVRE	VAAAFNDEV	0.3068	1807.9	50.00	Sequence
DRB1_0901	95	AAAIAVGLGAFGLGV	VGLGAFGLG	0.3060	1823.5	50.00	Sequence
DRB1_0901	2	EHTDFELLE L ATPYA	LLE L ATPYA	0.3029	1886.2	50.00	Sequence
DRB1_0901	162	PSRGT VYQM WLLGGA	TVYQM WLLG	0.3029	1886.5	50.00	Sequence
DRB1_0901	144	VFSRDRNTGLLVMNN	SRDRNTGLL	0.3025	1894.5	50.00	Sequence
DRB1_0901	103	GAFGLGVLTRPSPPP	VLTRPSPPP	0.2998	1951.1	50.00	Sequence
DRB1_0901	161	PPSRGT VYQM WLLGG	RGT VYQM WL	0.2996	1955.6	50.00	Sequence
DRB1_0901	146	SRDRNTGLLVMNNVA	SRDRNTGLL	0.2965	2021.7	50.00	Sequence
DRB1_0901	63	AEPPAHLRTAILDAT	AHLRTAILD	0.2955	2044.8	50.00	Sequence
DRB1_0901	39	VAAAFNDEVRAVRET	VAAAFNDEV	0.2934	2090.7	50.00	Sequence
DRB1_0901	143	VVFSRDRNTGLLVMN	SRDRNTGLL	0.2909	2147.5	50.00	Sequence
DRB1_0901	160	APP SRGT VYQM WLLG	RGT VYQM WL	0.2839	2317.5	50.00	Sequence

DRB1_0901	113	PSPPPTVAEQVLTAP	PPTVAEQVL	0.2829	2342.9	50.00	Sequence
DRB1_0901	23	DERADIDRRVAAAPS	DRRVAAAPS	0.2827	2348.0	50.00	Sequence
DRB1_0901	16	ALNAVSDDERADIDR	ALNAVSDDE	0.2823	2358.7	50.00	Sequence
DRB1_0901	157	NNVAPPSRGTVYQMW	NNVAPPSRG	0.2821	2362.6	50.00	Sequence
DRB1_0901	149	RNTGLLVMNNVAPPS	TGLLVMNNV	0.2810	2390.6	50.00	Sequence
DRB1_0901	137	GAGTATVVFSRDRNT	GAGTATVVF	0.2759	2525.5	50.00	Sequence
DRB1_0901	141	ATVVFSRDRNTGLLV	SRDRNTGLL	0.2734	2594.5	50.00	Sequence
DRB1_0901	114	SPPTVAEQVLTAPD	PPTVAEQVL	0.2723	2625.5	50.00	Sequence
DRB1_0901	140	TATVVFSRDRNTGLL	SRDRNTGLL	0.2701	2691.3	50.00	Sequence
DRB1_0901	215	TGSPQPTGTILAELE	GSPQPTGTI	0.2697	2700.6	50.00	Sequence
DRB1_0901	204	STALAFTEPPTGSP	STALAFTE	0.2689	2725.9	50.00	Sequence
DRB1_0901	142	TVVFSRDRNTGLLVM	SRDRNTGLL	0.2672	2776.8	50.00	Sequence
DRB1_0901	147	RDRNTGLLVMNNVAP	RNTGLLVMN	0.2640	2874.2	50.00	Sequence
DRB1_0901	93	ASAAAIAVGLGAFGL	ASAAAIAVG	0.2607	2978.5	50.00	Sequence
DRB1_0901	0	MTEHTDFELLELELATP	MTEHTDFEL	0.2601	2996.8	50.00	Sequence
DRB1_0901	150	NTGLLVMNNVAPPSR	VMNNVAPPS	0.2590	3032.9	50.00	Sequence
DRB1_0901	138	AGTATVVFSRDRNTG	AGTATVVFS	0.2584	3051.8	50.00	Sequence
DRB1_0901	214	GTGSPQPTGTILAELE	GSPQPTGTI	0.2572	3093.8	50.00	Sequence
DRB1_0901	159	VAPPSRGTVYQMWLL	VAPPSRGTV	0.2561	3128.9	50.00	Sequence
DRB1_0901	148	DRNTGLLVMNNVAP	DRNTGLLVM	0.2546	3181.4	50.00	Sequence
DRB1_0901	158	NVAPPSRGTVYQMWL	NVAPPSRGT	0.2537	3212.3	50.00	Sequence
DRB1_0901	205	TALAFTEPPTGSPQ	LAFTVEPPT	0.2514	3294.9	50.00	Sequence
DRB1_0901	203	ASTALAFTEPPTGSG	FTVEPPTGS	0.2509	3309.6	50.00	Sequence
DRB1_0901	78	KPEVRRQSRWRTAAF	QSRWRTAAF	0.2445	3549.7	50.00	Sequence
DRB1_0901	213	PGTGSPQPTGTILAE	GSPQPTGTI	0.2399	3728.4	50.00	Sequence
DRB1_0901	74	LDATKPEVRRQSRWR	DATKPEVRR	0.2379	3813.2	50.00	Sequence
DRB1_0901	193	STTATLTDLGASTAL	LTDLGASTA	0.2359	3893.9	50.00	Sequence
DRB1_0901	192	PSTTATLTDLGASTA	LTDLGASTA	0.2342	3966.2	50.00	Sequence
DRB1_0901	75	DATKPEVRRQSRWR	DATKPEVRR	0.2324	4046.5	50.00	Sequence
DRB1_0901	202	GASTALAFTEPPTG	GASTALAFTE	0.2317	4074.6	50.00	Sequence
DRB1_0901	139	GTATVVFSRDRNTGL	TATVVFSRD	0.2305	4128.2	50.00	Sequence
DRB1_0901	212	EPGTGSPQPTGTILA	GSPQPTGTI	0.2244	4409.0	50.00	Sequence
DRB1_0901	191	TPSTTATLTDLGAST	TPSTTATLT	0.2174	4759.6	50.00	Sequence
DRB1_0901	211	VEPPTGSPQPTGTIL	GSPQPTGTI	0.2170	4778.0	50.00	Sequence
DRB1_0901	210	TVEPPTGSPQPTGTI	TVEPPTGSP	0.2151	4875.9	50.00	Sequence
DRB1_0901	1	TEHTDFELLELELATPY	HTDFELLELE	0.2144	4917.4	50.00	Sequence
DRB1_0901	77	TKPEVRRQSRWRTA	EVRQRSRWR	0.2133	4971.9	50.00	Sequence
DRB1_0901	76	ATKPEVRRQSRWR	ATKPEVRRQ	0.2097	5172.4	50.00	Sequence
DRB1_0901	206	ALAFTEPPTGSPQP	LAFTVEPPT	0.2004	5717.4	50.00	Sequence
DRB1_0901	207	LAFTVEPPTGSPQPT	FTVEPPTGS	0.1973	5912.5	50.00	Sequence
DRB1_0901	209	FTVEPPTGSPQPTGT	FTVEPPTGS	0.1905	6367.7	50.00	Sequence
DRB1_0901	17	LNAVSDDERADIDRR	LNAVSDDER	0.1794	7177.2	50.00	Sequence
DRB1_0901	22	DDERADIDRRVAAAP	ERADIDRRV	0.1749	7532.2	50.00	Sequence
DRB1_0901	208	AFTVEPPTGSPQPTG	FTVEPPTGS	0.1688	8047.1	50.00	Sequence
DRB1_0901	18	NAVSDDERADIDRRV	NAVSDDERA	0.1405	10929.3	50.00	Sequence
DRB1_0901	21	SDDERADIDRRVAAA	ERADIDRRV	0.1381	11219.1	50.00	Sequence
DRB1_0901	20	VSDDERADIDRRVAA	DDERADIDR	0.1350	11606.7	50.00	Sequence
DRB1_0901	19	AVSDDERADIDRRVA	ERADIDRRV	0.1323	11947.5	50.00	Sequence

Allele: DRB1_0901. Number of high binders 6. Number of weak binders 65. Number of peptides 218

Allele	pos	peptide	core	1-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
DRB1_1101	104	AFGLGVLTRPSPPT	LGVLTRPSP	0.6178	62.5	WB	8.00	Sequence
DRB1_1101	126	APDVRTVSRPLGAGT	VRTVSRPLG	0.6035	72.9	WB	8.00	Sequence
DRB1_1101	127	PDVRTVSRPLGAGTA	VRTVSRPLG	0.5994	76.3	WB	8.00	Sequence
DRB1_1101	105	FGLGVLTRPSPPTV	LGVLTRPSP	0.5990	76.6	WB	8.00	Sequence
DRB1_1101	103	GAFGLGVLTRPSPPP	LGVLTRPSP	0.5989	76.7	WB	8.00	Sequence
DRB1_1101	128	DVRTVSRPLGAGTAT	VRTVSRPLG	0.5844	89.7	WB	8.00	Sequence
DRB1_1101	125	TAPDVRTVSRPLGAG	VRTVSRPLG	0.5655	110.0	WB	16.00	Sequence
DRB1_1101	102	LGAFGLGVLTRPSP	LGVLTRPSP	0.5510	128.7	WB	16.00	Sequence
DRB1_1101	150	NTGLLVMNNVAPPSR	LLVMNNVAP	0.5391	146.4	WB	16.00	Sequence
DRB1_1101	149	RNTGLLVMNNVAPPS	GLLMNNVVA	0.5317	158.8	WB	16.00	Sequence
DRB1_1101	151	TGLLVMNNVAPPSRG	LLVMNNVAP	0.5242	172.2	WB	16.00	Sequence
DRB1_1101	106	GLGVLTRPSPPTVA	LGVLTRPSP	0.5032	216.1	WB	16.00	Sequence
DRB1_1101	101	GLGAFGLGVLTRPSP	LGVLTRPSP	0.5027	217.2	WB	16.00	Sequence
DRB1_1101	152	GLLMNNVAPPSRGT	LLVMNNVAP	0.4978	229.0	WB	16.00	Sequence
DRB1_1101	124	LTAPDVRTVSRPLGA	VRTVSRPLG	0.4962	233.0	WB	16.00	Sequence
DRB1_1101	148	DRNTGLLVMNNVAP	GLLMNNVVA	0.4861	259.8	WB	16.00	Sequence
DRB1_1101	129	VRTVSRPLGAGTATV	VRTVSRPLG	0.4783	282.8	WB	16.00	Sequence
DRB1_1101	167	VYQMWLLGGAKGPRS	MWLLGGAKG	0.4680	316.3	WB	32.00	Sequence
DRB1_1101	147	RDRNTGLLVMNNVAP	NTGLLVMNN	0.4651	326.2	WB	32.00	Sequence
DRB1_1101	46	EVRAVRETMAVVSAA	VRAVRETMA	0.4640	330.2	WB	32.00	Sequence
DRB1_1101	88	RTAAAFASAAAIAVGL	FASAAAIAV	0.4632	333.1	WB	32.00	Sequence

DRB1_1101	89	TAAFASAAAIAVGLG	FASAAAIAV	0.4611	340.7	WB	32.00	Sequence
DRB1_1101	45	DEVRAVRETMVAVSA	VRAVRETM	0.4522	374.9	WB	32.00	Sequence
DRB1_1101	86	RWRTAAFASAAAIAV	RWRTAAFAS	0.4467	398.1	WB	32.00	Sequence
DRB1_1101	168	YQMWLLGGAKGPRSA	MWLLGGAKG	0.4430	414.2	WB	32.00	Sequence
DRB1_1101	141	ATVVFSRDRNTGLLV	VFSRDRNTG	0.4412	422.7	WB	32.00	Sequence
DRB1_1101	47	VRAVRETMVAVSAAT	AVRETMVAV	0.4384	435.5	WB	32.00	Sequence
DRB1_1101	87	WRTAAFASAAAIAV	FASAAAIAV	0.4384	435.7	WB	32.00	Sequence
DRB1_1101	44	NDEVRAVRETMVAVS	VRAVRETM	0.4376	439.1	WB	32.00	Sequence
DRB1_1101	166	TVYQMWLLGGAKGPR	VYQMWLLGG	0.4272	491.5	WB	32.00	Sequence
DRB1_1101	123	VLTPDVRTVSRPLG	VRTVSRPLG	0.4269	493.0	WB	32.00	Sequence
DRB1_1101	169	QMWLLGGAKGPRSA	MWLLGGAKG	0.4268	493.8	WB	32.00	Sequence
DRB1_1101	170	MWLLGGAKGPRSA	MWLLGGAKG	0.4209	526.0		32.00	Sequence
DRB1_1101	81	VRRQSRWRTAAFASA	VRRQSRWRT	0.4160	554.6		32.00	Sequence
DRB1_1101	142	TVVFSRDRNTGLLVM	VFSRDRNTG	0.4151	560.4		32.00	Sequence
DRB1_1101	51	RETMVAVSAATTAEP	MAVVAAT	0.4131	572.6		32.00	Sequence
DRB1_1101	82	RRQSRWRTAAFASAA	RWRTAAFAS	0.4130	573.2		32.00	Sequence
DRB1_1101	90	AAFASAAAIAVGLGA	FASAAAIAV	0.4110	585.7		32.00	Sequence
DRB1_1101	43	FNDEVRAVRETMVAV	EVRAVRETM	0.4089	599.0		32.00	Sequence
DRB1_1101	78	KPEVRRQSRWRTAAF	VRRQSRWRT	0.4089	599.4		32.00	Sequence
DRB1_1101	140	TATVVFSRDRNTGLL	VVFSRDRNT	0.4088	599.7		32.00	Sequence
DRB1_1101	85	SRWRTAAFASAAAIA	RWRTAAFAS	0.4036	634.5		32.00	Sequence
DRB1_1101	83	RQSRWRTAAFASAAA	RWRTAAFAS	0.3994	664.1		32.00	Sequence
DRB1_1101	84	QSRWRTAAFASAAAIA	RWRTAAFAS	0.3965	685.3		32.00	Sequence
DRB1_1101	52	ETMAVVAATTAEP	MAVVAAT	0.3959	689.7		32.00	Sequence
DRB1_1101	100	VGLGAFGLGVLTRPS	AFGLGVLTR	0.3948	698.0		32.00	Sequence
DRB1_1101	80	EVRQSRWRTAAFAS	VRRQSRWRT	0.3938	705.3		32.00	Sequence
DRB1_1101	48	RAVRETMVAVSAATT	AVRETMVAV	0.3896	738.7		32.00	Sequence
DRB1_1101	77	TKPEVRRQSRWRTA	VRRQSRWRT	0.3888	744.6		32.00	Sequence
DRB1_1101	50	VRETMVAVSAATTAE	MAVVAAT	0.3857	769.8		32.00	Sequence
DRB1_1101	165	GTVYQMWLLGGAKGP	VYQMWLLGG	0.3849	776.8		32.00	Sequence
DRB1_1101	5	DFELLELATPYALNA	FELLELATP	0.3822	800.1		32.00	Sequence
DRB1_1101	143	VVFSRDRNTGLLVMN	VVFSRDRNT	0.3803	816.5		32.00	Sequence
DRB1_1101	4	TDFELLELATPYALN	FELLELATP	0.3791	827.3		32.00	Sequence
DRB1_1101	42	AFNDEVRAVRETMAV	VRAVRETM	0.3771	845.4		32.00	Sequence
DRB1_1101	79	PEVRRQSRWRTAFA	VRRQSRWRT	0.3747	867.0		32.00	Sequence
DRB1_1101	49	AVRETMVAVSAATTA	MAVVAAT	0.3690	922.6		32.00	Sequence
DRB1_1101	146	SRDRNTGLLVMNNVA	NTGLLVMNN	0.3675	937.5		32.00	Sequence
DRB1_1101	53	TMAVVAATTAEP	MAVVAAT	0.3658	955.3		32.00	Sequence
DRB1_1101	3	HTDFELLELATPYAL	FELLELATP	0.3657	955.9		32.00	Sequence
DRB1_1101	107	LGVLTRPSPPTVAE	LGVLTRPSP	0.3608	1008.6		32.00	Sequence
DRB1_1101	91	AFASAAAIAVGLGAF	FASAAAIAV	0.3604	1012.4		32.00	Sequence
DRB1_1101	139	GTATVVFSRDRNTGL	VVFSRDRNT	0.3600	1017.1		32.00	Sequence
DRB1_1101	76	ATKPEVRRQSRWRTA	VRRQSRWRT	0.3599	1018.2		32.00	Sequence
DRB1_1101	41	AAFNDEVRAVRETM	FNDEVRAVR	0.3513	1117.8		50.00	Sequence
DRB1_1101	171	WLLGGAKGPRSA	LGGAKGPRS	0.3416	1241.3		50.00	Sequence
DRB1_1101	6	FELLELATPYALNAV	FELLELATP	0.3404	1257.1		50.00	Sequence
DRB1_1101	144	VFSRDRNTGLLVMNN	VFSRDRNTG	0.3383	1286.9		50.00	Sequence
DRB1_1101	164	RGTVYQMWLLGGAKG	VYQMWLLGG	0.3343	1343.4		50.00	Sequence
DRB1_1101	206	ALAFVTEPGTGSPQP	FTVEPGTGS	0.3273	1448.5		50.00	Sequence
DRB1_1101	40	AAAFNDEVRAVRETM	FNDEVRAVR	0.3243	1495.9		50.00	Sequence
DRB1_1101	2	EHTDFELLELATPYA	DFELLELAT	0.3216	1540.7		50.00	Sequence
DRB1_1101	54	MAVVAATTAEP	MAVVAAT	0.3216	1541.6		50.00	Sequence
DRB1_1101	205	TALAFVTEPGTGSPQ	LAFTVEPGT	0.3186	1592.1		50.00	Sequence
DRB1_1101	153	LLVMNNVAPP	LLVMNNVAP	0.3173	1613.9		50.00	Sequence
DRB1_1101	75	DATKPEVRRQSRWRT	VRRQSRWRT	0.3142	1669.7		50.00	Sequence
DRB1_1101	207	LAFTVEPGTGSPQPT	FTVEPGTGS	0.3101	1744.4		50.00	Sequence
DRB1_1101	196	ATLTDLGASTALAF	LTDLGASTA	0.3015	1915.9		50.00	Sequence
DRB1_1101	195	TATLTDLGASTALAF	LTDLGASTA	0.3009	1927.2		50.00	Sequence
DRB1_1101	197	TLTDLGASTALAF	LTDLGASTA	0.2980	1988.2		50.00	Sequence
DRB1_1101	99	AVGLGAFGLGVLTRP	AFGLGVLTR	0.2948	2060.2		50.00	Sequence
DRB1_1101	138	AGTATVVFSRDRNTG	VVFSRDRNT	0.2840	2314.7		50.00	Sequence
DRB1_1101	145	FSRDRNTGLLVMNNV	NTGLLVMNN	0.2833	2331.9		50.00	Sequence
DRB1_1101	198	LTDLGASTALAF	LTDLGASTA	0.2780	2469.2		50.00	Sequence
DRB1_1101	204	STALAFVTEPGTGSP	LAFTVEPGT	0.2779	2473.2		50.00	Sequence
DRB1_1101	163	SRGTVYQMWLLGGAK	VYQMWLLGG	0.2766	2506.5		50.00	Sequence
DRB1_1101	67	AHLRTAILDATKPEV	HLRTAILDA	0.2761	2522.2		50.00	Sequence
DRB1_1101	28	IDRRVAAAPSPVAAA	VAAAPSPVA	0.2731	2605.6		50.00	Sequence
DRB1_1101	39	VAAAFNDEVRAVRET	FNDEVRAVR	0.2726	2618.1		50.00	Sequence
DRB1_1101	68	HLRTAILDATKPEV	HLRTAILDA	0.2673	2772.9		50.00	Sequence
DRB1_1101	208	AFTVEPGTGSPQPTG	FTVEPGTGS	0.2628	2910.8		50.00	Sequence
DRB1_1101	29	DRRVAAAPSPVAAAF	VAAAPSPVA	0.2610	2968.4		50.00	Sequence
DRB1_1101	66	PAHLRTAILDATKPE	HLRTAILDA	0.2556	3147.9		50.00	Sequence
DRB1_1101	130	RTVSRPLGAGTATVV	RTVSRPLGA	0.2554	3153.6		50.00	Sequence
DRB1_1101	172	LLGGAKGPRSA	LGGAKGPRS	0.2552	3161.9		50.00	Sequence
DRB1_1101	65	PPAHLRTAILDATKP	HLRTAILDA	0.2489	3382.4		50.00	Sequence
DRB1_1101	194	TTATLTDLGASTALA	LTDLGASTA	0.2472	3448.2		50.00	Sequence
DRB1_1101	7	ELLELATPYALNAV	LLELATPYA	0.2455	3511.1		50.00	Sequence

DRB1_1101	27	DIDRRVAAAPSPVAA	RVAAAPSPV	0.2453	3518.4	50.00	Sequence
DRB1_1101	98	IAVGLGAFGLGVLTR	IAVGLGAFG	0.2452	3523.5	50.00	Sequence
DRB1_1101	122	QVLTAPDVRTVSRPL	VLTPADVRT	0.2448	3538.8	50.00	Sequence
DRB1_1101	1	TEHTDFELLELELATPY	FELLELELATP	0.2418	3654.0	50.00	Sequence
DRB1_1101	203	ASTALAFVTEPGTGS	LAFTVEPGT	0.2374	3833.9	50.00	Sequence
DRB1_1101	162	PSRGTVYQMWLLGGA	VYQMWLLGG	0.2349	3935.8	50.00	Sequence
DRB1_1101	30	RRVAAAPSPVAAAFN	VAAAPSPVA	0.2337	3989.9	50.00	Sequence
DRB1_1101	74	LDATKPEVRRQSRWR	TKPEVRRQS	0.2333	4005.0	50.00	Sequence
DRB1_1101	69	LRTAILDATKPEVRR	ILDATKPEV	0.2319	4066.1	50.00	Sequence
DRB1_1101	96	AAIAVGLGAFGLGVL	IAVGLGAFG	0.2291	4193.0	50.00	Sequence
DRB1_1101	95	AAIAVGLGAFGLGV	IAVGLGAFG	0.2279	4249.0	50.00	Sequence
DRB1_1101	26	ADIDRRVAAAPSPVA	IDRRVAAAP	0.2278	4250.2	50.00	Sequence
DRB1_1101	92	FASAAAIAVGLGAFG	FASAAAIAV	0.2258	4344.0	50.00	Sequence
DRB1_1101	38	PVAAAFNDEVRAVRE	FNDEVRAVR	0.2236	4447.8	50.00	Sequence
DRB1_1101	70	RTAILDATKPEVRRQ	ILDATKPEV	0.2232	4467.5	50.00	Sequence
DRB1_1101	25	RADIDRRVAAAPSPV	IDRRVAAAP	0.2218	4538.5	50.00	Sequence
DRB1_1101	64	EPPAHLRRTAILDATK	HLRRTAILDA	0.2174	4758.3	50.00	Sequence
DRB1_1101	97	AIAVGLGAFGLGVLT	IAVGLGAFG	0.2171	4771.1	50.00	Sequence
DRB1_1101	8	LLELATPYALNAVSD	LLELATPYA	0.2171	4775.5	50.00	Sequence
DRB1_1101	173	LGGAKGPRSAGTMGT	LGGAKGPRS	0.2163	4815.7	50.00	Sequence
DRB1_1101	73	ILDATKPEVRRQSRW	ILDATKPEV	0.2160	4830.5	50.00	Sequence
DRB1_1101	118	TVAEQVLTAPDVRTV	EQVLTAPDV	0.2128	4999.7	50.00	Sequence
DRB1_1101	71	TAILDATKPEVRRQS	ILDATKPEV	0.2098	5165.1	50.00	Sequence
DRB1_1101	119	VAEQVLTAPDVRTVS	VLTPADVRT	0.2093	5195.5	50.00	Sequence
DRB1_1101	120	AEQVLTAPDVRTVSR	VLTPADVRT	0.2083	5247.8	50.00	Sequence
DRB1_1101	94	SAAAIAVGLGAFGLG	AAIAVGLGA	0.2078	5276.1	50.00	Sequence
DRB1_1101	24	ERADIDRRVAAAPSP	RADIDRRVA	0.2074	5299.6	50.00	Sequence
DRB1_1101	202	GASTALAFVTEPGTG	ASTALAFTV	0.2006	5705.2	50.00	Sequence
DRB1_1101	201	LGASTALAFVTEPGT	ASTALAFTV	0.1978	5883.4	50.00	Sequence
DRB1_1101	72	ALLDATKPEVRRQSR	ILDATKPEV	0.1971	5926.5	50.00	Sequence
DRB1_1101	193	STTATLTDLGASTAL	LTDLGASTA	0.1971	5926.9	50.00	Sequence
DRB1_1101	117	PTVAEQVLTAPDVRT	AEQVLTAPD	0.1942	6112.5	50.00	Sequence
DRB1_1101	121	EQVLTAPDVRTVSRP	VLTPADVRT	0.1926	6224.2	50.00	Sequence
DRB1_1101	154	VMNNVAPPSPRGTVY	VMNNVAPPS	0.1922	6247.4	50.00	Sequence
DRB1_1101	200	DLGASTALAFVTEPG	ASTALAFTV	0.1900	6398.1	50.00	Sequence
DRB1_1101	199	TDLGASTALAFVTEP	ASTALAFTV	0.1884	6508.3	50.00	Sequence
DRB1_1101	63	AEPHAHLRRTAILDAT	HLRRTAILDA	0.1865	6643.3	50.00	Sequence
DRB1_1101	23	DERADIDRRVAAAPS	RADIDRRVA	0.1844	6796.1	50.00	Sequence
DRB1_1101	93	ASAAAIAVGLGAFGL	AAIAVGLGA	0.1803	7108.1	50.00	Sequence
DRB1_1101	22	DDERADIDRRVAAAP	RADIDRRVA	0.1792	7196.4	50.00	Sequence
DRB1_1101	0	MTEHTDFELLELELATP	DFELLELELAT	0.1769	7374.6	50.00	Sequence
DRB1_1101	31	RVAAAPSPVAAAFND	VAAAPSPVA	0.1764	7412.3	50.00	Sequence
DRB1_1101	155	VMNNVAPPSPRGTVYQ	VMNNVAPPS	0.1736	7642.2	50.00	Sequence
DRB1_1101	37	SPVAAAFNDEVRAVR	FNDEVRAVR	0.1726	7725.9	50.00	Sequence
DRB1_1101	161	PPSRGTVYQMWLLGG	VYQMWLLGG	0.1624	8627.0	50.00	Sequence
DRB1_1101	55	AVVSAATTAEPHAHL	AVVSAATTA	0.1615	8708.0	50.00	Sequence
DRB1_1101	131	TVSRPLGAGTATVVF	SRPLGAGTA	0.1571	9133.9	50.00	Sequence
DRB1_1101	137	GAGTATVVFSTRDRNT	VVFSTRDRNT	0.1565	9191.8	50.00	Sequence
DRB1_1101	177	KGPRSAGTMGTAAVT	RSAGTMGTA	0.1531	9544.6	50.00	Sequence
DRB1_1101	192	PSTTATLTDLGASTA	LTDLGASTA	0.1530	9547.8	50.00	Sequence
DRB1_1101	62	TAEPHAHLRRTAILDA	HLRRTAILDA	0.1493	9943.1	50.00	Sequence
DRB1_1101	21	SDDERADIDRRVAAA	RADIDRRVA	0.1467	10220.5	50.00	Sequence
DRB1_1101	175	GAKGPRSAGTMGTAA	GAKGPRSAG	0.1460	10307.2	50.00	Sequence
DRB1_1101	116	PPTVAEQVLTAPDVR	TVAEQVLTA	0.1441	10515.5	50.00	Sequence
DRB1_1101	156	MNNVAPPSPRGTVYQM	MNNVAPPSR	0.1436	10573.9	50.00	Sequence
DRB1_1101	209	FTVEPGTGSPQPTGT	FTVEPGTGS	0.1427	10673.4	50.00	Sequence
DRB1_1101	176	AKGPRSAGTMGTAAV	GPRSAGTMG	0.1419	10770.6	50.00	Sequence
DRB1_1101	178	GPRSAGTMGTAAVTP	RSAGTMGTA	0.1414	10826.0	50.00	Sequence
DRB1_1101	132	VSRPLGAGTATVVF	SRPLGAGTA	0.1378	11263.7	50.00	Sequence
DRB1_1101	9	LELATPYALNAVSD	TPYALNAVS	0.1352	11581.2	50.00	Sequence
DRB1_1101	174	GGAKGPRSAGTMGTA	GAKGPRSAG	0.1314	12065.6	50.00	Sequence
DRB1_1101	10	ELATPYALNAVSDDE	TPYALNAVS	0.1310	12116.4	50.00	Sequence
DRB1_1101	179	PRSAGTMGTAAVTPS	AGTMGTAAV	0.1249	12948.6	50.00	Sequence
DRB1_1101	157	NNVAPPSPRGTVYQMW	NNVAPPSPRG	0.1239	13086.5	50.00	Sequence
DRB1_1101	20	VSDDERADIDRRVAA	RADIDRRVA	0.1140	14564.4	50.00	Sequence
DRB1_1101	115	PPPTVAEQVLTAPDV	TVAEQVLTA	0.1132	14695.5	50.00	Sequence
DRB1_1101	180	RSAGTMGTAAVTPST	GTMGTAAVT	0.1058	15915.6	50.00	Sequence
DRB1_1101	108	GVLTRPSPPTVAEQ	VLTRPSPPP	0.1056	15950.3	50.00	Sequence
DRB1_1101	133	SRPLGAGTATVVF	SRPLGAGTA	0.1053	16007.3	50.00	Sequence
DRB1_1101	136	LGAGTATVVFSTRDRN	TVVFSTRDRN	0.1035	16317.5	50.00	Sequence
DRB1_1101	32	VAAAPSPVAAAFNDE	VAAAPSPVA	0.1011	16751.7	50.00	Sequence
DRB1_1101	160	APPSRGTVYQMWLLG	TVYQMWLLG	0.0990	17123.9	50.00	Sequence
DRB1_1101	158	NVAPPSPRGTVYQMWL	VAPPSPRGTV	0.0990	17130.6	50.00	Sequence
DRB1_1101	185	MGTAAVTPSTTATLT	AAVTPSTTA	0.0976	17387.7	50.00	Sequence
DRB1_1101	11	LATPYALNAVSDDER	TPYALNAVS	0.0962	17648.5	50.00	Sequence
DRB1_1101	186	GTAAVTPSTTATLTD	AAVTPSTTA	0.0960	17701.9	50.00	Sequence
DRB1_1101	61	TTAEPHAHLRRTAILD	PAHLRTAIL	0.0916	18563.0	50.00	Sequence

DRB1_1101	12	ATPYALNAVSDDERA	TPYALNAVS	0.0905	18770.8	50.00	Sequence
DRB1_1101	181	SAGTMGTAAVTPSTT	GTMGTAAVT	0.0899	18910.9	50.00	Sequence
DRB1_1101	36	PSPVAAAFNDEVRAV	AAFNDEVRA	0.0874	19431.5	50.00	Sequence
DRB1_1101	159	VAPPSRGTVYQMWLL	PSRGTVYQM	0.0873	19432.1	50.00	Sequence
DRB1_1101	182	AGTMGTAAVTPSTTA	MGTAAVTPS	0.0852	19898.9	50.00	Sequence
DRB1_1101	184	TMGTAAVTPSTTATL	AAVTPSTTA	0.0851	19902.8	50.00	Sequence
DRB1_1101	187	TAAVTPSTTATLTDL	AAVTPSTTA	0.0832	20317.7	50.00	Sequence
DRB1_1101	13	TPYALNAVSDDERAD	TPYALNAVS	0.0818	20634.1	50.00	Sequence
DRB1_1101	183	GTMGTAAVTPSTTAT	MGTAAVTPS	0.0799	21065.8	50.00	Sequence
DRB1_1101	56	VVSAATTAEPHAHLR	VSAATTAEP	0.0797	21107.8	50.00	Sequence
DRB1_1101	135	PLGAGTATVVFSDRDR	LGAGTATVV	0.0759	21999.0	50.00	Sequence
DRB1_1101	19	AVSDDERADIDRRVA	RADIDRRVA	0.0752	22156.9	50.00	Sequence
DRB1_1101	188	AAVTPSTTATLTDLG	AAVTPSTTA	0.0748	22253.0	50.00	Sequence
DRB1_1101	114	SPPPTVAEQVLTAPD	TVAEQVLT	0.0726	22799.2	50.00	Sequence
DRB1_1101	134	RPLGAGTATVVFSDR	LGAGTATVV	0.0697	23529.7	50.00	Sequence
DRB1_1101	191	TPSTTATLTDLGAST	TATLTDLGA	0.0657	24551.5	50.00	Sequence
DRB1_1101	109	VLTRPSPPTVAEQV	VLTRPSPPP	0.0654	24635.6	50.00	Sequence
DRB1_1101	217	SPQPTGTILAEPLG	GTILAEPL	0.0652	24706.1	50.00	Sequence
DRB1_1101	57	VSAATTAEPHAHLRT	VSAATTAEP	0.0618	25607.5	50.00	Sequence
DRB1_1101	60	ATTAEPHAHLRTAIL	PAHLRTAIL	0.0560	27291.4	50.00	Sequence
DRB1_1101	14	PYALNAVSDDERADI	PYALNAVSD	0.0543	27787.2	50.00	Sequence
DRB1_1101	189	AVTPSTTATLTDLGA	VTPSTTATL	0.0541	27847.7	50.00	Sequence
DRB1_1101	211	VEPGTGSPQPTGTIL	GTGSPQPTG	0.0511	28767.0	50.00	Sequence
DRB1_1101	216	GSPQPTGTILAEPL	GTILAEPL	0.0490	29423.0	50.00	Sequence
DRB1_1101	113	PSPPTVAEQVLTAP	PTVAEQVLT	0.0490	29424.6	50.00	Sequence
DRB1_1101	213	PGTGSPPQPTGTILAE	GTGSPQPTG	0.0484	29605.1	50.00	Sequence
DRB1_1101	212	EPGTGSPPQPTGTILA	GTGSPQPTG	0.0480	29759.9	50.00	Sequence
DRB1_1101	190	VTPSTTATLTDLGAS	TATLTDLGA	0.0456	30512.7	50.00	Sequence
DRB1_1101	35	APSPVAAAFNDEVRA	AAFNDEVRA	0.0444	30910.5	50.00	Sequence
DRB1_1101	15	YALNAVSDDERADID	YALNAVSD	0.0438	31122.9	50.00	Sequence
DRB1_1101	210	TVEPGTGSPPQPTGTI	GTGSPQPTG	0.0422	31666.4	50.00	Sequence
DRB1_1101	214	GTGSPQPTGTILAE	GTGSPQPTG	0.0364	33721.6	50.00	Sequence
DRB1_1101	215	TGSPQPTGTILAEPL	PQPTGTILA	0.0325	35175.4	50.00	Sequence
DRB1_1101	112	RPSPPPTVAEQVLT	PTVAEQVLT	0.0274	37166.6	50.00	Sequence
DRB1_1101	59	AATTAEPHAHLRTAI	AATTAEP	0.0266	37489.3	50.00	Sequence
DRB1_1101	18	NAVSDDERADIDRRV	VSDDERADI	0.0264	37587.2	50.00	Sequence
DRB1_1101	16	ALNAVSDDERADIDR	LNAVSDDER	0.0251	38110.5	50.00	Sequence
DRB1_1101	17	LNAVSDDERADIDRR	VSDDERADI	0.0251	38111.7	50.00	Sequence
DRB1_1101	58	SAATTAEPHAHLRTAI	AATTAEP	0.0246	38315.2	50.00	Sequence
DRB1_1101	34	AAPSPVAAAFNDEV	PSPVAAAFN	0.0243	38449.3	50.00	Sequence
DRB1_1101	33	AAAPSPVAAAFNDEV	PSPVAAAFN	0.0220	39391.7	50.00	Sequence
DRB1_1101	110	LTRPSPPTVAEQVLT	LTRPSPPT	0.0180	41138.0	50.00	Sequence
DRB1_1101	111	TRPSPPTVAEQVLT	PTVAEQVLT	0.0152	42417.1	50.00	Sequence

Allele: DRB1_1101. Number of high binders 0. Number of weak binders 32. Number of peptides 218

Allele	pos	peptide	core	l-log50k(aff)	affinity(nM)	Bind	Level	%Random	Identity
DRB1_1302	148	DRNTGLLVMNNAVAPP	LLVMNNVAP	0.6980	26.2	SB	2.00	2.00	Sequence
DRB1_1302	149	RNTGLLVMNNAVAPP	LLVMNNVAP	0.6805	31.7	SB	2.00	2.00	Sequence
DRB1_1302	147	RDRNTGLLVMNNAVAPP	LLVMNNVAP	0.6790	32.2	SB	2.00	2.00	Sequence
DRB1_1302	150	NTGLLVMNNAVAPP	LLVMNNVAP	0.6675	36.5	SB	2.00	2.00	Sequence
DRB1_1302	151	TGLLVMNNAVAPP	LLVMNNVAP	0.6479	45.2	SB	4.00	4.00	Sequence
DRB1_1302	50	VRETMAVVSAAATTAEP	MAVVSAAAT	0.6210	60.4	WB	4.00	4.00	Sequence
DRB1_1302	152	GLLVMNNAVAPP	LLVMNNVAP	0.6017	74.4	WB	8.00	8.00	Sequence
DRB1_1302	49	AVRETMAVVSAAATTAEP	MAVVSAAAT	0.5971	78.2	WB	8.00	8.00	Sequence
DRB1_1302	48	RAVRETMAVVSAAATTAEP	MAVVSAAAT	0.5925	82.2	WB	8.00	8.00	Sequence
DRB1_1302	51	RETMAVVSAAATTAEP	MAVVSAAAT	0.5914	83.2	WB	8.00	8.00	Sequence
DRB1_1302	153	LLVMNNNAVAPP	LLVMNNVAP	0.5864	87.8	WB	8.00	8.00	Sequence
DRB1_1302	52	ETMAVVSAAATTAEP	MAVVSAAAT	0.5496	130.7	WB	8.00	8.00	Sequence
DRB1_1302	53	TMAVVSAAATTAEP	MAVVSAAAT	0.5265	167.9	WB	16.00	16.00	Sequence
DRB1_1302	146	SRDRNTGLLVMNNAV	GLLVMNNA	0.5053	211.0	WB	16.00	16.00	Sequence
DRB1_1302	54	MAVVSAAATTAEP	MAVVSAAAT	0.5040	214.0	WB	16.00	16.00	Sequence
DRB1_1302	184	TMGTAAVTPSTTATL	VTPSTTATL	0.4973	230.3	WB	16.00	16.00	Sequence
DRB1_1302	185	MGTAAVTPSTTATLT	VTPSTTATL	0.4958	234.1	WB	16.00	16.00	Sequence
DRB1_1302	186	GTAAVTPSTTATLTD	VTPSTTATL	0.4762	289.1	WB	16.00	16.00	Sequence
DRB1_1302	45	DEVRAVRETMAVVSAAAT	RAVRETMAV	0.4689	312.9	WB	16.00	16.00	Sequence
DRB1_1302	131	TVSRPLGAGTATVVF	LGAGTATVV	0.4639	330.5	WB	16.00	16.00	Sequence
DRB1_1302	130	RTVSRPLGAGTATVV	LGAGTATVV	0.4628	334.6	WB	16.00	16.00	Sequence
DRB1_1302	145	FSRDRNTGLLVMNNAV	FSRDRNTGL	0.4612	340.1	WB	16.00	16.00	Sequence
DRB1_1302	132	VSRPLGAGTATVVF	LGAGTATVV	0.4573	354.8	WB	16.00	16.00	Sequence
DRB1_1302	47	VRVRETMAVVSAAAT	RAVRETMAV	0.4508	380.7	WB	16.00	16.00	Sequence
DRB1_1302	46	EVRAVRETMAVVSAAAT	RAVRETMAV	0.4507	381.2	WB	16.00	16.00	Sequence
DRB1_1302	86	RWRTAAFASAAAIAV	AAFASAAA	0.4479	393.0	WB	16.00	16.00	Sequence

DRB1_1302	187	TAAVTPSTTATLTDL	VTPSTTATL	0.4479	393.1	WB	16.00	Sequence
DRB1_1302	133	SRPLGAGTATVVFSSR	LGAGTATVV	0.4473	395.3	WB	16.00	Sequence
DRB1_1302	44	NDEVRAVRETMVVVS	RAVRETMVV	0.4426	416.2	WB	32.00	Sequence
DRB1_1302	87	WRTAAFASAAAIAVGL	AAFASAAAIA	0.4399	428.3	WB	32.00	Sequence
DRB1_1302	134	RPLGAGTATVVFSSRD	LGAGTATVV	0.4396	429.9	WB	32.00	Sequence
DRB1_1302	91	AFASAAAIAVGLGAF	AIIVGLGAF	0.4374	440.4	WB	32.00	Sequence
DRB1_1302	6	FELLELATPYALNAV	LELATPYAL	0.4366	443.8	WB	32.00	Sequence
DRB1_1302	88	RTAAFASAAAIAVGL	AAFASAAAIA	0.4357	448.6	WB	32.00	Sequence
DRB1_1302	142	TVVFSRDRNTGLLVM	FSRDRNTGL	0.4346	453.7	WB	32.00	Sequence
DRB1_1302	84	QSRWRTAAFASAAAIA	AAFASAAAIA	0.4332	460.6	WB	32.00	Sequence
DRB1_1302	92	FASAAAIAVGLGAFG	AIIVGLGAF	0.4325	463.9	WB	32.00	Sequence
DRB1_1302	143	VVFSRDRNTGLLVM	FSRDRNTGL	0.4286	484.4	WB	32.00	Sequence
DRB1_1302	89	TAAFASAAAIAVGLG	AAFASAAAIA	0.4238	509.8		32.00	Sequence
DRB1_1302	188	AAVTPSTTATLTDLG	VTPSTTATL	0.4187	538.9		32.00	Sequence
DRB1_1302	144	VFSRDRNTGLLVMNN	FSRDRNTGL	0.4178	543.9		32.00	Sequence
DRB1_1302	7	ELLELATPYALNAVS	LELATPYAL	0.4157	556.6		32.00	Sequence
DRB1_1302	90	AAFASAAAIAVGLGA	AAFASAAAIA	0.4055	621.3		32.00	Sequence
DRB1_1302	63	AEPHAHLRTAILDAT	PAHLRTAIL	0.4005	656.2		32.00	Sequence
DRB1_1302	26	ADIDRRVAAAPSPVA	RVAAAPSPV	0.3993	664.5		32.00	Sequence
DRB1_1302	135	PLGAGTATVVFSSRD	LGAGTATVV	0.3941	703.4		32.00	Sequence
DRB1_1302	141	ATVVFSSRDRNTGLLV	FSRDRNTGL	0.3940	704.0		32.00	Sequence
DRB1_1302	43	FNDEVRAVRETMVV	RAVRETMVV	0.3938	705.3		32.00	Sequence
DRB1_1302	27	DIDRRVAAAPSPVAA	RVAAAPSPV	0.3938	705.7		32.00	Sequence
DRB1_1302	5	DFELLELATPYALNA	LELATPYAL	0.3926	714.5		32.00	Sequence
DRB1_1302	8	LLELATPYALNAVSD	LELATPYAL	0.3896	738.4		32.00	Sequence
DRB1_1302	154	LVMNNVAPPSPRGTVY	LVMNNVAPP	0.3886	746.1		32.00	Sequence
DRB1_1302	189	AVTPSTTATLTDLGA	VTPSTTATL	0.3878	752.6		32.00	Sequence
DRB1_1302	85	SRWRTAAFASAAAIA	AAFASAAAIA	0.3871	758.2		32.00	Sequence
DRB1_1302	159	VAPPSRGTVYQMWLL	RGTVYQMWL	0.3865	763.2		32.00	Sequence
DRB1_1302	197	TLTDLGASTALAF	LGASTALAF	0.3863	764.9		32.00	Sequence
DRB1_1302	64	EPPAHLRTAILDATK	PAHLRTAIL	0.3851	775.3		32.00	Sequence
DRB1_1302	25	RADIDRRVAAAPSPV	RVAAAPSPV	0.3837	787.1		32.00	Sequence
DRB1_1302	195	TATLTDLGASTALAF	LGASTALAF	0.3823	798.9		32.00	Sequence
DRB1_1302	177	KGPRSAGTMGTAAVT	AGTMGTAAV	0.3741	872.9		32.00	Sequence
DRB1_1302	196	ATLTDLGASTALAF	LGASTALAF	0.3737	876.7		32.00	Sequence
DRB1_1302	61	TTAEPHAHLRTAILD	PAHLRTAIL	0.3729	884.5		32.00	Sequence
DRB1_1302	62	TAEPHAHLRTAILDA	PAHLRTAIL	0.3714	899.0		32.00	Sequence
DRB1_1302	28	IDRRVAAAPSPVAAA	RVAAAPSPV	0.3713	900.3		32.00	Sequence
DRB1_1302	29	DRRVAAAPSPVAAAF	RVAAAPSPV	0.3699	914.1		32.00	Sequence
DRB1_1302	176	AKGPRSAGTMGTAAV	AGTMGTAAV	0.3692	920.5		32.00	Sequence
DRB1_1302	9	LELATPYALNAVSD	LELATPYAL	0.3680	932.4		32.00	Sequence
DRB1_1302	198	LTDLGASTALAF	LGASTALAF	0.3679	933.9		32.00	Sequence
DRB1_1302	60	ATTAEPHAHLRTAIL	PAHLRTAIL	0.3672	941.1		32.00	Sequence
DRB1_1302	97	AIIVGLGAFGLGVLT	AIIVGLGAF	0.3623	991.6		32.00	Sequence
DRB1_1302	140	TATVVFSSRDRNTGLL	FSRDRNTGL	0.3601	1015.8		32.00	Sequence
DRB1_1302	65	PPAHLRTAILDATKP	PAHLRTAIL	0.3596	1020.9		32.00	Sequence
DRB1_1302	81	VRRQSRWRTAAFASA	QSRWRTAAF	0.3525	1102.7		32.00	Sequence
DRB1_1302	82	RQSRWRTAAFASAA	QSRWRTAAF	0.3519	1110.0		32.00	Sequence
DRB1_1302	190	VTPSTTATLTDLGAS	VTPSTTATL	0.3518	1111.5		32.00	Sequence
DRB1_1302	30	RRVAAAPSPVAAAFN	RVAAAPSPV	0.3514	1116.5		32.00	Sequence
DRB1_1302	78	KPEVRRQSRWRTAAF	QSRWRTAAF	0.3503	1129.3		32.00	Sequence
DRB1_1302	96	AAIAVGLGAFGLGV	AIIVGLGAF	0.3500	1132.9		32.00	Sequence
DRB1_1302	79	PEVRRQSRWRTAAFA	QSRWRTAAF	0.3497	1137.1		32.00	Sequence
DRB1_1302	93	ASAAAIAVGLGAFGL	AIIVGLGAF	0.3495	1139.8		32.00	Sequence
DRB1_1302	199	TDLGASTALAF	LGASTALAF	0.3486	1150.8		32.00	Sequence
DRB1_1302	160	APPSRGTVYQMWLLG	RGTVYQMWL	0.3479	1159.9		32.00	Sequence
DRB1_1302	83	QSRWRTAAFASAAA	QSRWRTAAF	0.3475	1164.5		32.00	Sequence
DRB1_1302	179	PRSAGTMGTAAVTPS	AGTMGTAAV	0.3411	1248.2		32.00	Sequence
DRB1_1302	80	EVRRQSRWRTAAFAS	QSRWRTAAF	0.3394	1271.6		32.00	Sequence
DRB1_1302	31	RVAAAPSPVAAAFND	RVAAAPSPV	0.3387	1281.2		32.00	Sequence
DRB1_1302	3	HTDFELLELATPYAL	LELATPYAL	0.3384	1284.8		32.00	Sequence
DRB1_1302	178	GPRSAGTMGTAAVTP	AGTMGTAAV	0.3372	1301.2		32.00	Sequence
DRB1_1302	161	PPSRGTVYQMWLLGG	RGTVYQMWL	0.3358	1322.1		32.00	Sequence
DRB1_1302	94	SAAAIAVGLGAFGLG	AIIVGLGAF	0.3338	1350.4		32.00	Sequence
DRB1_1302	66	PAHLRTAILDATKPE	PAHLRTAIL	0.3322	1373.2		32.00	Sequence
DRB1_1302	4	TDFELLELATPYALN	LELATPYAL	0.3304	1401.5		32.00	Sequence
DRB1_1302	136	LGAGTATVVFSSRDRN	LGAGTATVV	0.3295	1414.6		50.00	Sequence
DRB1_1302	180	RSAGTMGTAAVTPST	AGTMGTAAV	0.3208	1554.0		50.00	Sequence
DRB1_1302	95	AAAIAVGLGAFGLGV	AIIVGLGAF	0.3174	1612.0		50.00	Sequence
DRB1_1302	162	PSRGTVYQMWLLGGA	RGTVYQMWL	0.3160	1637.7		50.00	Sequence
DRB1_1302	118	TVAEQVLTAPDVRTV	VLTAPDVRT	0.3132	1687.0		50.00	Sequence
DRB1_1302	200	DLGASTALAF	LGASTALAF	0.3119	1710.7		50.00	Sequence
DRB1_1302	123	VLTAPDVRTVSRPLG	DVRTVSRPL	0.3056	1832.0		50.00	Sequence
DRB1_1302	42	AFNDEVRAVRETMVV	RAVRETMVV	0.3014	1916.8		50.00	Sequence
DRB1_1302	119	VAEQVLTAPDVRTVS	VLTAPDVRT	0.3008	1929.1		50.00	Sequence
DRB1_1302	158	NVAPPSRGTVYQMWL	RGTVYQMWL	0.2985	1979.5		50.00	Sequence
DRB1_1302	139	GTATVVFSSRDRNTGL	FSRDRNTGL	0.2981	1986.4		50.00	Sequence

DRB1_1302	163	SRGTVYQMWLLGGAK	RGTVYQMWL	0.2977	1995.3	50.00	Sequence
DRB1_1302	181	SAGTMGTAAVTPSTT	AGTMGTAAV	0.2964	2022.8	50.00	Sequence
DRB1_1302	129	VRTVSRPLGAGTATV	PLGAGTATV	0.2936	2086.0	50.00	Sequence
DRB1_1302	164	RGTVYQMWLLGGAKG	RGTVYQMWL	0.2901	2167.2	50.00	Sequence
DRB1_1302	182	AGTMGTAAVTPSTTA	AGTMGTAAV	0.2872	2235.4	50.00	Sequence
DRB1_1302	117	PTVAEQVLTAPDVRT	VLTAPDVRT	0.2857	2272.7	50.00	Sequence
DRB1_1302	120	AEQVLTAPDVRTVSR	VLTAPDVRT	0.2790	2442.1	50.00	Sequence
DRB1_1302	98	IAVGLGAFGLGVLTR	LGAFGLGVLT	0.2747	2559.2	50.00	Sequence
DRB1_1302	122	QVLTAPDVRTVSRPL	VLTAPDVRT	0.2744	2567.7	50.00	Sequence
DRB1_1302	126	APDVRTVSRPLGAGT	VSRPLGAGT	0.2683	2743.5	50.00	Sequence
DRB1_1302	194	TTATLTDLGASTALA	DLGASTALA	0.2616	2948.7	50.00	Sequence
DRB1_1302	124	LTAPDVRTVSRPLGA	DVRTVSRPL	0.2612	2963.4	50.00	Sequence
DRB1_1302	10	ELATPYALNAVSDDE	LATPYALNA	0.2565	3115.3	50.00	Sequence
DRB1_1302	121	EQVLTAPDVRTVSRP	VLTAPDVRT	0.2563	3123.0	50.00	Sequence
DRB1_1302	201	LGASTALAFVTEPPT	LGASTALAF	0.2553	3158.8	50.00	Sequence
DRB1_1302	127	PDVRTVSRPLGAGT	VSRPLGAGT	0.2533	3225.6	50.00	Sequence
DRB1_1302	55	AVVSAATTAEPHAHL	VVSAATTAE	0.2532	3228.6	50.00	Sequence
DRB1_1302	76	ATKPEVRRQSRWRTA	VRRQSRWRT	0.2494	3364.5	50.00	Sequence
DRB1_1302	128	DVRTVSRPLGAGTAT	VSRPLGAGT	0.2453	3518.5	50.00	Sequence
DRB1_1302	99	AVGLGAFGLGVLTRP	GLGAFGLGV	0.2453	3519.8	50.00	Sequence
DRB1_1302	68	HLRTAILDATKPEVR	ILDATKPEV	0.2416	3660.0	50.00	Sequence
DRB1_1302	77	TKPEVRRQSRWRATA	VRRQSRWRT	0.2410	3687.0	50.00	Sequence
DRB1_1302	67	AHLRTAILDATKPEV	ILDATKPEV	0.2394	3748.4	50.00	Sequence
DRB1_1302	213	PTGSPQPTGTILAE	GSPQPTGTI	0.2365	3871.2	50.00	Sequence
DRB1_1302	69	LRTAILDATKPEVRR	ILDATKPEV	0.2329	4022.5	50.00	Sequence
DRB1_1302	100	VGLGAFGLGVLTRPS	GLGAFGLGV	0.2287	4211.1	50.00	Sequence
DRB1_1302	156	MNNVAPPSRGTVYQM	PSRGTVYQM	0.2279	4247.3	50.00	Sequence
DRB1_1302	214	GTGSPQPTGTILAE	GSPQPTGTI	0.2263	4322.5	50.00	Sequence
DRB1_1302	11	LATPYALNAVSDDER	LATPYALNA	0.2249	4385.7	50.00	Sequence
DRB1_1302	183	GTMGTAAVTPSTTAT	AVTPSTTAT	0.2245	4407.9	50.00	Sequence
DRB1_1302	125	TAPDVRTVSRPLGAG	DVRTVSRPL	0.2238	4441.8	50.00	Sequence
DRB1_1302	212	EPGTGSPQPTGTILA	GSPQPTGTI	0.2225	4502.7	50.00	Sequence
DRB1_1302	216	GSPQPTGTILAEPL	GSPQPTGTI	0.2209	4582.0	50.00	Sequence
DRB1_1302	101	VLGAFGLGVLTRPSP	GLGAFGLGV	0.2173	4760.7	50.00	Sequence
DRB1_1302	211	VEPGTGSPQPTGTIL	GSPQPTGTI	0.2154	4861.6	50.00	Sequence
DRB1_1302	33	AAAPSPVAAAFNDEV	VAAAFNDEV	0.2143	4918.0	50.00	Sequence
DRB1_1302	165	GTVYQMWLLGGAKGP	GTVYQMWLL	0.2136	4958.0	50.00	Sequence
DRB1_1302	215	TGSPQPTGTILAEPL	GSPQPTGTI	0.2128	5001.1	50.00	Sequence
DRB1_1302	210	TVEPGTGSPQPTGTI	GSPQPTGTI	0.2120	5043.5	50.00	Sequence
DRB1_1302	75	DATKPEVRRQSRWRT	VRRQSRWRT	0.2111	5093.8	50.00	Sequence
DRB1_1302	157	NNVAPPSRGTVYQMW	PSRGTVYQM	0.2095	5180.8	50.00	Sequence
DRB1_1302	70	RTAILDATKPEVRRQ	ILDATKPEV	0.2048	5454.9	50.00	Sequence
DRB1_1302	155	MNNVAPPSRGTVYQ	APPSRGTVY	0.2036	5525.4	50.00	Sequence
DRB1_1302	34	AAPSPVAAAFNDEV	VAAAFNDEV	0.2012	5666.8	50.00	Sequence
DRB1_1302	36	PSPVAAAFNDEVRAV	VAAAFNDEV	0.1957	6019.6	50.00	Sequence
DRB1_1302	171	WLLGGAKGPRASAGTM	KGPRSAGTM	0.1938	6141.9	50.00	Sequence
DRB1_1302	167	YQMWLLGGAKGPRSA	MWLLGGAKG	0.1916	6291.2	50.00	Sequence
DRB1_1302	168	VYQMWLLGGAKGPRSA	MWLLGGAKG	0.1911	6326.8	50.00	Sequence
DRB1_1302	35	APSPVAAAFNDEVRA	VAAAFNDEV	0.1908	6342.5	50.00	Sequence
DRB1_1302	71	TAILDATKPEVRRQS	ILDATKPEV	0.1906	6359.1	50.00	Sequence
DRB1_1302	37	SPVAAAFNDEVRAVR	VAAAFNDEV	0.1894	6439.0	50.00	Sequence
DRB1_1302	193	STTATLTDLGASTAL	TDLGASTAL	0.1860	6681.5	50.00	Sequence
DRB1_1302	41	AAFNDEVRAVRETMA	VRAVRETMA	0.1860	6684.7	50.00	Sequence
DRB1_1302	56	VVSAATTAEPHAHLR	VVSAATTAE	0.1826	6930.5	50.00	Sequence
DRB1_1302	38	PVAAAFNDEVRAVRE	VAAAFNDEV	0.1808	7067.5	50.00	Sequence
DRB1_1302	174	GGAKGPRASAGTMGTA	KGPRSAGTM	0.1804	7101.1	50.00	Sequence
DRB1_1302	169	QMWLLGGAKGPRASAG	MWLLGGAKG	0.1788	7221.9	50.00	Sequence
DRB1_1302	39	VAAAFNDEVRAVRET	VAAAFNDEV	0.1773	7341.5	50.00	Sequence
DRB1_1302	175	GAKGPRASAGTMGTAA	KGPRSAGTM	0.1768	7384.7	50.00	Sequence
DRB1_1302	172	LLGGAKGPRASAGTMG	KGPRSAGTM	0.1745	7566.7	50.00	Sequence
DRB1_1302	102	LGAFGLGVLTRPSP	GAFGLGVLT	0.1738	7622.3	50.00	Sequence
DRB1_1302	166	TVYQMWLLGGAKGPR	MWLLGGAKG	0.1678	8139.5	50.00	Sequence
DRB1_1302	173	LGAKGPRASAGTMGT	KGPRSAGTM	0.1663	8272.5	50.00	Sequence
DRB1_1302	170	MWLLGGAKGPRASAGT	MWLLGGAKG	0.1657	8324.9	50.00	Sequence
DRB1_1302	73	ILDATKPEVRRQSRW	ILDATKPEV	0.1626	8603.9	50.00	Sequence
DRB1_1302	72	AILDATKPEVRRQSR	ILDATKPEV	0.1622	8647.5	50.00	Sequence
DRB1_1302	115	PPPTVAEQVLTAPDV	EQVLTAPDV	0.1620	8668.8	50.00	Sequence
DRB1_1302	2	EHTDFELLELATPYA	LLELATPYA	0.1613	8734.5	50.00	Sequence
DRB1_1302	116	PPTVAEQVLTAPDVR	EQVLTAPDV	0.1505	9810.9	50.00	Sequence
DRB1_1302	114	SPPTVAEQVLTAPD	PTVAEQVLT	0.1468	10214.8	50.00	Sequence
DRB1_1302	217	SPQPTGTILAEPLG	GTILAEPL	0.1463	10269.9	50.00	Sequence
DRB1_1302	106	GLGVLTRPSPPTVA	TRPSPPTV	0.1441	10512.7	50.00	Sequence
DRB1_1302	104	AFGLGVLTRPSPPTV	LTRPSPPTV	0.1413	10842.5	50.00	Sequence
DRB1_1302	105	FGLGVLTRPSPPTV	TRPSPPTV	0.1406	10923.7	50.00	Sequence
DRB1_1302	107	LGVLTRPSPPTVAE	TRPSPPTV	0.1385	11177.5	50.00	Sequence
DRB1_1302	103	GAFGLGVLTRPSP	GVLTRPSP	0.1372	11332.3	50.00	Sequence
DRB1_1302	32	VAAAPSPVAAAFNDE	VAAAPSPVA	0.1367	11397.6	50.00	Sequence

DRB1_1302	12	ATPYALNAVSDDERA	ATPYALNAV	0.1338	11757.8	50.00	Sequence
DRB1_1302	108	GVLTRPSPPTVAEQ	TRPSPPTV	0.1335	11794.9	50.00	Sequence
DRB1_1302	40	AAAFNDEVRAVRETM	EVRAVRETM	0.1283	12471.9	50.00	Sequence
DRB1_1302	192	PSTTATLTLDLGASTA	LTDLGA	0.1266	12704.8	50.00	Sequence
DRB1_1302	113	PSPPPTVAEQVLTAP	PTVAEQVLT	0.1261	12776.9	50.00	Sequence
DRB1_1302	137	GAGTATVVFVSRDRNT	GAGTATVVF	0.1260	12795.0	50.00	Sequence
DRB1_1302	202	GASTALAFVTEPGTG	ASTALAFV	0.1234	13158.9	50.00	Sequence
DRB1_1302	24	ERADIDRRVAAAPSP	DRRVAAAP	0.1218	13390.3	50.00	Sequence
DRB1_1302	111	TRPSPPTVAEQVLT	TRPSPPTV	0.1130	14721.5	50.00	Sequence
DRB1_1302	23	DERADIDRRVAAAP	DRRVAAAP	0.1125	14797.9	50.00	Sequence
DRB1_1302	112	RSPSPPTVAEQVLT	PTVAEQVLT	0.1122	14857.2	50.00	Sequence
DRB1_1302	109	VLTRPSPPTVAEQV	TRPSPPTV	0.1115	14967.9	50.00	Sequence
DRB1_1302	110	LTRPSPPTVAEQV	TRPSPPTV	0.1114	14987.4	50.00	Sequence
DRB1_1302	203	ASTALAFVTEPGTGS	ASTALAFV	0.1108	15071.8	50.00	Sequence
DRB1_1302	59	AATTAEPAPHLRTAI	TTAEPAPHL	0.1087	15416.1	50.00	Sequence
DRB1_1302	205	TALAFVTEPGTGSPQ	VEPGTGSPQ	0.1064	15813.7	50.00	Sequence
DRB1_1302	1	TEHTDFELLELATPY	ELLELATPY	0.1024	16508.3	50.00	Sequence
DRB1_1302	74	LDATEVRRQSRWR	PEVRRQSRW	0.1001	16929.6	50.00	Sequence
DRB1_1302	57	VSAATTAEPAPHLRT	TTAEPAPHL	0.0915	18570.6	50.00	Sequence
DRB1_1302	206	ALAFVTEPGTGSPQ	VEPGTGSPQ	0.0859	19748.1	50.00	Sequence
DRB1_1302	138	AGTATVVFVSRDRNTG	AGTATVVF	0.0858	19755.4	50.00	Sequence
DRB1_1302	22	DERADIDRRVAAAP	IDRRVAAAP	0.0853	19872.2	50.00	Sequence
DRB1_1302	207	LAFTVTEPGTGSPQ	VEPGTGSPQ	0.0798	21085.0	50.00	Sequence
DRB1_1302	58	SAATTAEPAPHLRT	TTAEPAPHL	0.0792	21216.8	50.00	Sequence
DRB1_1302	191	TPSTTATLTLDLGAST	TLTDLGAST	0.0773	21658.2	50.00	Sequence
DRB1_1302	208	AFTVTEPGTGSPQ	VEPGTGSPQ	0.0749	22244.1	50.00	Sequence
DRB1_1302	21	SDDERADIDRRVAAA	ADIDRRVAA	0.0724	22844.3	50.00	Sequence
DRB1_1302	204	STALAFVTEPGTGSP	TALAFVTEP	0.0716	23043.2	50.00	Sequence
DRB1_1302	209	FTVTEPGTGSPQPTGT	VEPGTGSPQ	0.0668	24262.1	50.00	Sequence
DRB1_1302	20	VSDDERADIDRRVAA	ADIDRRVAA	0.0530	28177.1	50.00	Sequence
DRB1_1302	14	PYALNAVSDDERADI	VSDDERADI	0.0486	29544.9	50.00	Sequence
DRB1_1302	19	AVSDDERADIDRRVA	VSDDERADI	0.0442	31005.9	50.00	Sequence
DRB1_1302	13	TPYALNAVSDDERAD	TPYALNAV	0.0440	31048.2	50.00	Sequence
DRB1_1302	18	NAVSDDERADIDRRV	VSDDERADI	0.0398	32498.0	50.00	Sequence
DRB1_1302	15	YALNAVSDDERADID	VSDDERADI	0.0386	32918.1	50.00	Sequence
DRB1_1302	0	MTEHTDFELLELATP	MTEHTDFEL	0.0352	34148.7	50.00	Sequence
DRB1_1302	16	ALNAVSDDERADIDR	VSDDERADI	0.0334	34824.8	50.00	Sequence
DRB1_1302	17	LNAVSDDERADIDRR	VSDDERADI	0.0279	36962.0	50.00	Sequence

Allele: DRB1_1302. Number of high binders 5. Number of weak binders 33. Number of peptides 218

Allele	pos	peptide	core	l-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
DRB1_1501	149	RNTGLLVMMNNVAPPS	GLLVMMNVA	0.6794	32.1	SB	2.00	Sequence
DRB1_1501	148	DRNTGLLVMMNNVAPP	GLLVMMNVA	0.6601	39.5	SB	4.00	Sequence
DRB1_1501	150	NTGLLVMMNNVAPPSR	GLLVMMNVA	0.6341	52.4	WB	4.00	Sequence
DRB1_1501	151	TGLLVMMNNVAPPSRG	GLLVMMNVA	0.6219	59.8	WB	8.00	Sequence
DRB1_1501	152	GLLVMMNNVAPPSRGT	GLLVMMNVA	0.5933	81.5	WB	8.00	Sequence
DRB1_1501	147	RDRNTGLLVMMNNVAP	LLVMMNNVAP	0.5878	86.4	WB	8.00	Sequence
DRB1_1501	4	TDFELLELATPYALN	ELLELATPY	0.5853	88.9	WB	8.00	Sequence
DRB1_1501	5	DFELLELATPYALNA	ELLELATPY	0.5734	101.0	WB	8.00	Sequence
DRB1_1501	3	HTDFELLELATPYAL	ELLELATPY	0.5712	103.5	WB	8.00	Sequence
DRB1_1501	80	EVRQRSRWRTAAFAS	EVRQRSRWR	0.5529	126.1	WB	16.00	Sequence
DRB1_1501	141	ATVVFVSRDRNTGLLV	VFSRDRNTG	0.5447	137.8	WB	16.00	Sequence
DRB1_1501	6	FELLELATPYALNAV	ELLELATPY	0.5440	138.9	WB	16.00	Sequence
DRB1_1501	79	PEVRRQSRWRTAFA	EVRQRSRWR	0.5338	155.1	WB	16.00	Sequence
DRB1_1501	98	IAVGLGAFGLGVLTR	GLGAFGLGV	0.5312	159.5	WB	16.00	Sequence
DRB1_1501	78	KPEVRRQSRWRTAFA	EVRQRSRWR	0.5276	166.0	WB	16.00	Sequence
DRB1_1501	100	VGLGAFGLGVLTRPS	AFGLGVLTR	0.5214	177.3	WB	16.00	Sequence
DRB1_1501	163	SRGTVYQMWLLGGAK	QMWLLGGAK	0.5190	182.1	WB	16.00	Sequence
DRB1_1501	2	EHTDFELLELATPYA	ELLELATPY	0.5124	195.6	WB	16.00	Sequence
DRB1_1501	7	ELLELATPYALNAV	ELLELATPY	0.5104	199.7	WB	16.00	Sequence
DRB1_1501	96	AAIAVGLGAFGLGVL	GLGAFGLGV	0.5102	200.2	WB	16.00	Sequence
DRB1_1501	140	TATVVFVSRDRNTGLL	TVVFSRDRN	0.5071	207.1	WB	16.00	Sequence
DRB1_1501	142	TVVFSRDRNTGLLVM	VFSRDRNTG	0.5070	207.2	WB	16.00	Sequence
DRB1_1501	164	RGTVYQMWLLGGAK	QMWLLGGAK	0.5048	212.2	WB	16.00	Sequence
DRB1_1501	97	AIHAVGLGAFGLGVL	GLGAFGLGV	0.4962	232.9	WB	16.00	Sequence
DRB1_1501	99	AVGLGAFGLGVLTRP	GLGAFGLGV	0.4902	248.7	WB	16.00	Sequence
DRB1_1501	139	GTATVVFVSRDRNTGL	TVVFSRDRN	0.4853	262.2	WB	32.00	Sequence
DRB1_1501	77	TKPEVRRQSRWRATA	EVRQRSRWR	0.4839	266.2	WB	32.00	Sequence
DRB1_1501	95	AAIAVGLGAFGLGV	IHAVGLGAFG	0.4830	268.9	WB	32.00	Sequence
DRB1_1501	101	GLGAFGLGVLTRPSP	AFGLGVLTR	0.4801	277.2	WB	32.00	Sequence
DRB1_1501	153	LLVMMNNVAPPSRGT	LLVMMNNVAP	0.4789	281.0	WB	32.00	Sequence
DRB1_1501	162	PSRGTVYQMWLLGGA	TVYQMWLLG	0.4639	330.6	WB	32.00	Sequence

DRB1_1501	165	GTVYQMWLLGGAKGP	QMWLLGGAK	0.4609	341.2	WB	32.00	Sequence
DRB1_1501	161	PPSRGTVYQMWLLGG	GTVYQMWLL	0.4571	355.7	WB	32.00	Sequence
DRB1_1501	76	ATKPEVRRQSRWRTA	EVRQRQRWR	0.4485	390.3	WB	32.00	Sequence
DRB1_1501	103	GAFGLGVLTRPSPPP	AFGLGVLTR	0.4471	396.2	WB	32.00	Sequence
DRB1_1501	81	VRRQSRWRTAAFASA	QSRWRTAAF	0.4434	412.6	WB	32.00	Sequence
DRB1_1501	104	AFGLGVLTRPSPPT	GLGVLTRPS	0.4362	445.7	WB	32.00	Sequence
DRB1_1501	146	SRDRNTGLLVMNVA	GLLVMNVA	0.4353	450.4	WB	32.00	Sequence
DRB1_1501	160	APPSRGTVYQMWLLG	GTVYQMWLL	0.4331	461.1	WB	32.00	Sequence
DRB1_1501	46	EVRAVRETMVVSA	AVRETMVV	0.4328	462.5	WB	32.00	Sequence
DRB1_1501	49	AVRETMVVSAATTA	TMAVVSAA	0.4324	464.7	WB	32.00	Sequence
DRB1_1501	166	TVYQMWLLGGAKGPR	QMWLLGGAK	0.4306	473.9	WB	32.00	Sequence
DRB1_1501	102	LGAFGLGVLTRPSP	AFGLGVLTR	0.4303	475.5	WB	32.00	Sequence
DRB1_1501	143	VVFSRDRNTGLLVN	VFSRDRNTG	0.4291	481.6	WB	32.00	Sequence
DRB1_1501	47	VRAVRETMVVSAAT	AVRETMVV	0.4268	493.9	WB	32.00	Sequence
DRB1_1501	1	TEHTDFELLELATPY	ELLELATPY	0.4244	506.4		32.00	Sequence
DRB1_1501	195	TATLTDLGASTALAF	TLTDLGAST	0.4224	517.6		32.00	Sequence
DRB1_1501	138	AGTATVVFSRDRNTG	TVVFSRDRN	0.4214	523.2		32.00	Sequence
DRB1_1501	86	RWRTAAFASAAIAV	RTAAFASAA	0.4197	533.1		32.00	Sequence
DRB1_1501	82	RRQSRWRTAAFASAA	QSRWRTAAF	0.4190	537.0		32.00	Sequence
DRB1_1501	196	ATLTDLGASTALAF	TLTDLGAST	0.4178	544.1		32.00	Sequence
DRB1_1501	48	RAVRETMVVSAATT	AVRETMVV	0.4173	547.1		32.00	Sequence
DRB1_1501	94	SAAAIAVGLGAFGLG	IAVGLGAFG	0.4167	550.7		32.00	Sequence
DRB1_1501	167	VYQMWLLGGAKGPRS	QMWLLGGAK	0.4163	553.3		32.00	Sequence
DRB1_1501	45	DEVRAVRETMVVSA	AVRETMVV	0.4140	567.1		32.00	Sequence
DRB1_1501	194	TTATLTDLGASTALA	TLTDLGAST	0.4112	584.4		32.00	Sequence
DRB1_1501	168	YQMWLLGGAKGPRSA	QMWLLGGAK	0.4088	599.6		32.00	Sequence
DRB1_1501	50	VRETMVVSAATTAE	TMAVVSAA	0.4075	608.3		32.00	Sequence
DRB1_1501	87	WRTAAFASAAIAVG	RTAAFASAA	0.4072	610.4		32.00	Sequence
DRB1_1501	85	SRWRTAAFASAAAIA	RTAAFASAA	0.4070	611.5		32.00	Sequence
DRB1_1501	75	DATKPEVRRQSRWRT	EVRQRQRWR	0.4035	635.4		32.00	Sequence
DRB1_1501	44	NDEVRAVRETMVV	AVRETMVV	0.4024	642.5		32.00	Sequence
DRB1_1501	84	QSRWRTAAFASAAI	RTAAFASAA	0.4003	657.8		32.00	Sequence
DRB1_1501	51	RETMVVSAATTAEP	TMAVVSAA	0.3958	690.6		32.00	Sequence
DRB1_1501	88	RTAAFASAAIAVGL	RTAAFASAA	0.3937	706.0		32.00	Sequence
DRB1_1501	105	FGLGVLTRPSPPTV	GLGVLTRPS	0.3900	735.0		32.00	Sequence
DRB1_1501	83	RQSRWRTAAFASAAA	QSRWRTAAF	0.3888	744.9		32.00	Sequence
DRB1_1501	197	TLTDLGASTALAF	TLTDLGAST	0.3844	780.6		50.00	Sequence
DRB1_1501	169	QMWLLGGAKGPRSAG	QMWLLGGAK	0.3841	783.3		50.00	Sequence
DRB1_1501	144	VFSRDRNTGLLVMN	VFSRDRNTG	0.3838	785.8		50.00	Sequence
DRB1_1501	43	FNDEVRAVRETMVV	AVRETMVV	0.3801	818.4		50.00	Sequence
DRB1_1501	193	STTATLTDLGASTAL	TLTDLGAST	0.3752	862.6		50.00	Sequence
DRB1_1501	52	ETMAVVSAAATTAEP	AVVSAATTA	0.3749	865.3		50.00	Sequence
DRB1_1501	130	RTVSRPLGAGTATV	VSRPLGAGT	0.3741	872.8		50.00	Sequence
DRB1_1501	129	VRTVSRPLGAGTATV	VSRPLGAGT	0.3689	924.1		50.00	Sequence
DRB1_1501	159	VAPPSRGTVYQMWLL	GTVYQMWLL	0.3647	967.1		50.00	Sequence
DRB1_1501	53	TMAVVSAAATTAEP	AVVSAATTA	0.3616	999.7		50.00	Sequence
DRB1_1501	131	TVSRPLGAGTATV	VSRPLGAGT	0.3587	1030.9		50.00	Sequence
DRB1_1501	106	GLGVLTRPSPPTVA	GLGVLTRPS	0.3551	1072.2		50.00	Sequence
DRB1_1501	128	DVRTVSRPLGAGTAT	DVRTVSRPL	0.3522	1107.0		50.00	Sequence
DRB1_1501	93	ASAAAIAVGLGAFGL	IAVGLGAFG	0.3451	1195.5		50.00	Sequence
DRB1_1501	154	LVMNNAVPPSRGTV	LVMNNAV	0.3448	1198.6		50.00	Sequence
DRB1_1501	25	RADIDRRVAAAPSPV	DIDRRVAAA	0.3406	1254.1		50.00	Sequence
DRB1_1501	137	GAGTATVVFSDRNT	TVVFSRDRN	0.3367	1308.1		50.00	Sequence
DRB1_1501	127	PDVRTVSRPLGAGTA	DVRTVSRPL	0.3319	1377.9		50.00	Sequence
DRB1_1501	192	PSTTATLTDLGASTA	TLTDLGAST	0.3298	1410.8		50.00	Sequence
DRB1_1501	132	VSRPLGAGTATV	PLGAGTATV	0.3283	1433.8		50.00	Sequence
DRB1_1501	24	ERADIDRRVAAAPSP	DIDRRVAAA	0.3210	1551.2		50.00	Sequence
DRB1_1501	26	ADIDRRVAAAPSPVA	DIDRRVAAA	0.3156	1645.1		50.00	Sequence
DRB1_1501	23	DERADIDRRVAAAPS	DIDRRVAAA	0.3139	1674.3		50.00	Sequence
DRB1_1501	27	DIDRRVAAAPSPVAA	DIDRRVAAA	0.3102	1742.5		50.00	Sequence
DRB1_1501	198	LTDLGASTALAF	DLGASTALA	0.3060	1824.3		50.00	Sequence
DRB1_1501	178	GPRASAGTMGTAAVTP	SAGTMGTAA	0.3037	1871.2		50.00	Sequence
DRB1_1501	74	LDATKPEVRRQSRWR	EVRQRQRWR	0.2969	2013.3		50.00	Sequence
DRB1_1501	22	DERADIDRRVAAAP	DIDRRVAAA	0.2955	2043.8		50.00	Sequence
DRB1_1501	179	PRASAGTMGTAAVTP	SAGTMGTAA	0.2940	2076.7		50.00	Sequence
DRB1_1501	118	TVAEQVLTAPDVRTV	AEQVLTAPD	0.2866	2251.2		50.00	Sequence
DRB1_1501	170	MWLLGGAKGPRASAGT	MWLLGGAKG	0.2854	2279.9		50.00	Sequence
DRB1_1501	145	FSRDRNTGLLVMN	RNTGLLVMN	0.2853	2282.3		50.00	Sequence
DRB1_1501	177	KGPRASAGTMGTAAVT	SAGTMGTAA	0.2848	2293.6		50.00	Sequence
DRB1_1501	63	AEPFAHLRTAILDAT	PAHLRTAIL	0.2837	2321.6		50.00	Sequence
DRB1_1501	200	DLGASTALAF	ALAF	0.2823	2358.0		50.00	Sequence
DRB1_1501	133	SRPLGAGTATV	PLGAGTATV	0.2809	2394.5		50.00	Sequence
DRB1_1501	126	APDVRTVSRPLGAGT	DVRTVSRPL	0.2798	2422.4		50.00	Sequence
DRB1_1501	117	PTVAEQVLTAPDVRT	AEQVLTAPD	0.2793	2435.7		50.00	Sequence
DRB1_1501	125	TAPDVRTVSRPLGAG	DVRTVSRPL	0.2778	2474.3		50.00	Sequence
DRB1_1501	180	RSAGTMGTAAVTPST	AGTMGTAAV	0.2768	2501.7		50.00	Sequence
DRB1_1501	65	PPAHLRTAILDATKP	PAHLRTAIL	0.2755	2537.8		50.00	Sequence

DRB1_1501	42	AFNDEVRAVRETM	EVRAVRETM	0.2745	2565.6	50.00	Sequence
DRB1_1501	89	TAAFASAAAIAVGLG	TAAFASAAA	0.2725	2622.1	50.00	Sequence
DRB1_1501	64	EPPAHLRTAILDATK	PAHLRTAIL	0.2719	2638.1	50.00	Sequence
DRB1_1501	119	VAEQVLTAPDVRTVS	VAEQVLTAP	0.2711	2660.2	50.00	Sequence
DRB1_1501	54	MAVVSAAATTAEP	AVVSAATTA	0.2709	2667.5	50.00	Sequence
DRB1_1501	62	TAEPHAHLRTAILDA	HLRTAILDA	0.2696	2705.5	50.00	Sequence
DRB1_1501	136	LGAGTATVVF	TVVFSRDRN	0.2679	2754.0	50.00	Sequence
DRB1_1501	116	PPTVAEQVLTAPDVR	VAEQVLTAP	0.2668	2787.4	50.00	Sequence
DRB1_1501	8	LLELATPYALNAVSD	ELATPYALN	0.2651	2839.9	50.00	Sequence
DRB1_1501	176	AKGPRSAGTMGTAAV	SAGTMGTAA	0.2649	2845.0	50.00	Sequence
DRB1_1501	123	VLTA	DVRTVSRPL	0.2649	2845.8	50.00	Sequence
DRB1_1501	124	LTAPDVRTVSRPLGA	DVRTVSRPL	0.2641	2872.1	50.00	Sequence
DRB1_1501	122	QVLTAPDVRTVSRPL	DVRTVSRPL	0.2619	2938.4	50.00	Sequence
DRB1_1501	184	TMGTA	AVTPSTTAT	0.2552	3159.9	50.00	Sequence
DRB1_1501	181	SAGTMGTA	AGTMGTA	0.2552	3161.0	50.00	Sequence
DRB1_1501	201	LGASTALAF	ALAF	0.2547	3178.6	50.00	Sequence
DRB1_1501	199	TDLGASTALAF	DLGASTALA	0.2512	3302.1	50.00	Sequence
DRB1_1501	66	PAHLRTAILDATKPE	PAHLRTAIL	0.2484	3403.3	50.00	Sequence
DRB1_1501	171	WLLGGAKGPRSAGTM	LLGGAKGPR	0.2483	3405.1	50.00	Sequence
DRB1_1501	135	PLGAGTATVVF	PLGAGTATV	0.2469	3459.3	50.00	Sequence
DRB1_1501	185	MGTAAVTPSTTATLT	AVTPSTTAT	0.2460	3492.6	50.00	Sequence
DRB1_1501	107	LGVLTRPS	VLTRPSPPP	0.2432	3598.7	50.00	Sequence
DRB1_1501	158	NVAPPSRGT	RGT	0.2398	3731.8	50.00	Sequence
DRB1_1501	203	ASTALAF	ALAF	0.2395	3746.1	50.00	Sequence
DRB1_1501	202	GASTALAF	ALAF	0.2369	3853.3	50.00	Sequence
DRB1_1501	92	FASAAAIAVGLGAFG	AI	0.2367	3860.5	50.00	Sequence
DRB1_1501	186	GTA	AVTPSTTAT	0.2362	3880.6	50.00	Sequence
DRB1_1501	68	HLRTAILDATKPEVR	HLRTAILDA	0.2349	3936.8	50.00	Sequence
DRB1_1501	134	RPLGAGTATVVF	PLGAGTATV	0.2347	3943.8	50.00	Sequence
DRB1_1501	21	SDDERADIDRRVAAA	DIDRRVAAA	0.2339	3981.4	50.00	Sequence
DRB1_1501	0	MTEHTDFELLE	DFELLELAT	0.2322	4053.3	50.00	Sequence
DRB1_1501	191	TPSTTATL	TLTDLGAST	0.2314	4087.2	50.00	Sequence
DRB1_1501	205	TALAF	ALAF	0.2285	4221.3	50.00	Sequence
DRB1_1501	115	PPPTVAEQVLTAPDV	AEQVLTAPD	0.2282	4233.4	50.00	Sequence
DRB1_1501	204	STALAF	ALAF	0.2251	4378.3	50.00	Sequence
DRB1_1501	187	TAAVTPSTTATLTDL	AVTPSTTAT	0.2245	4406.6	50.00	Sequence
DRB1_1501	28	IDRRVAAA	IDRRVAAA	0.2233	4463.6	50.00	Sequence
DRB1_1501	41	AAFNDEVRAVRETM	EVRAVRETM	0.2207	4590.8	50.00	Sequence
DRB1_1501	67	AHLRTAILDATKPEV	HLRTAILDA	0.2201	4623.2	50.00	Sequence
DRB1_1501	55	AVVSAATTAEP	AVVSAATTA	0.2195	4651.6	50.00	Sequence
DRB1_1501	188	AAVTPSTTATLTDLG	AVTPSTTAT	0.2194	4654.6	50.00	Sequence
DRB1_1501	183	GTMGTA	AVTPSTTAT	0.2184	4707.0	50.00	Sequence
DRB1_1501	182	AGTMGTA	TMGTA	0.2164	4809.3	50.00	Sequence
DRB1_1501	120	AEQVLTAPDVRTVSR	QVLTAPDVR	0.2153	4868.3	50.00	Sequence
DRB1_1501	172	LLGGAKGPRSAGTMG	LLGGAKGPR	0.2094	5190.7	50.00	Sequence
DRB1_1501	189	AVTPSTTATLTDLGA	AVTPSTTAT	0.2043	5481.0	50.00	Sequence
DRB1_1501	108	GVLTRPS	VLTRPSPPP	0.2040	5500.8	50.00	Sequence
DRB1_1501	114	SPPTVAEQVLTAPD	VAEQVLTAP	0.2019	5628.3	50.00	Sequence
DRB1_1501	61	TTAEPHAHLRTAILD	PAHLRTAIL	0.2007	5699.5	50.00	Sequence
DRB1_1501	175	GAKGPRSAGTMGTAA	SAGTMGTAA	0.2005	5715.4	50.00	Sequence
DRB1_1501	121	EQVLTAPDVRTVSRP	LTAPDVRTV	0.2001	5738.4	50.00	Sequence
DRB1_1501	90	AAFASAAAIAVGLGA	AAFASAAA	0.1998	5756.5	50.00	Sequence
DRB1_1501	9	LELATPYALNAVSD	ELATPYALN	0.1986	5828.1	50.00	Sequence
DRB1_1501	39	VAAAFNDEVRAVRET	VAAAFNDEV	0.1976	5894.8	50.00	Sequence
DRB1_1501	10	ELATPYALNAVSDDE	ELATPYALN	0.1912	6318.9	50.00	Sequence
DRB1_1501	40	AAAFNDEVRAVRETM	EVRAVRETM	0.1901	6396.3	50.00	Sequence
DRB1_1501	37	SPVAAAFNDEVRAVR	AFNDEVRAV	0.1900	6401.6	50.00	Sequence
DRB1_1501	38	PVAAAFNDEVRAVRE	VAAAFNDEV	0.1897	6420.7	50.00	Sequence
DRB1_1501	70	RTAILDATKPEVRRQ	RTAILDATK	0.1842	6812.1	50.00	Sequence
DRB1_1501	206	ALAF	ALAF	0.1835	6862.5	50.00	Sequence
DRB1_1501	60	ATTAEPHAHLRTAIL	PAHLRTAIL	0.1830	6904.8	50.00	Sequence
DRB1_1501	36	PSPVAAAFNDEVRAV	VAAAFNDEV	0.1789	7217.9	50.00	Sequence
DRB1_1501	69	LRTAILDATKPEVRR	RTAILDATK	0.1759	7454.4	50.00	Sequence
DRB1_1501	29	DRRVAAAPSPVAAAF	RRVAAAPSP	0.1727	7713.9	50.00	Sequence
DRB1_1501	91	AFASAAAIAVGLGAF	AI	0.1714	7827.9	50.00	Sequence
DRB1_1501	30	RRVAAAPSPVAAAFN	RRVAAAPSP	0.1680	8123.5	50.00	Sequence
DRB1_1501	217	SPQPTGTILAEPLG	TILAEPLG	0.1662	8279.8	50.00	Sequence
DRB1_1501	155	VMNNVAPPSRGT	VMNNVAPPS	0.1646	8422.6	50.00	Sequence
DRB1_1501	190	VTPSTTATLTDLGAS	TTATLTDLG	0.1645	8431.2	50.00	Sequence
DRB1_1501	113	VSPPTVAEQVLTAP	VAEQVLTAP	0.1605	8809.9	50.00	Sequence
DRB1_1501	157	NNVAPPSRGT	VAPPSRGT	0.1596	8895.7	50.00	Sequence
DRB1_1501	109	VLTRPS	VLTRPSPPP	0.1590	8950.7	50.00	Sequence
DRB1_1501	11	LATPYALNAVSDDER	LATPYALNA	0.1449	10428.0	50.00	Sequence
DRB1_1501	71	TAILDATKPEVRRQS	TAILDATKP	0.1394	11064.9	50.00	Sequence
DRB1_1501	35	APSPVAAAFNDEVRA	VAAAFNDEV	0.1325	11922.6	50.00	Sequence
DRB1_1501	156	MNNVAPPSRGT	VAPPSRGT	0.1296	12307.0	50.00	Sequence
DRB1_1501	173	LGAKGPRSAGTMGT	GAKGPRSAG	0.1226	13269.7	50.00	Sequence

DRB1_1501	207	LAFTVEPGTGSQPPT	AFTVEPGTG	0.1224	13292.7	50.00	Sequence
DRB1_1501	216	GSPQPTGTILAEPL	PTGTILAE	0.1191	13786.8	50.00	Sequence
DRB1_1501	12	ATPYALNAVSDDERA	ATPYALNAV	0.1182	13921.0	50.00	Sequence
DRB1_1501	31	RVAAAPSPVAAAFND	RVAAAPSPV	0.1179	13965.0	50.00	Sequence
DRB1_1501	174	GGAKGPRSAGTMGTA	AKGPRSAGT	0.1165	14173.6	50.00	Sequence
DRB1_1501	34	AAPSPVAAAFNDEVR	VAAAFNDEV	0.1165	14174.5	50.00	Sequence
DRB1_1501	214	GTGSPQPTGTILAE	PTGTILAE	0.1121	14867.1	50.00	Sequence
DRB1_1501	210	TVEPGTGSQPPTGTI	TVEPGTGSP	0.1099	15232.4	50.00	Sequence
DRB1_1501	208	AFTVEPGTGSQPPTG	TVEPGTGSP	0.1089	15396.5	50.00	Sequence
DRB1_1501	73	ILDATKPEVRRQSRW	ATKPEVRRQ	0.1061	15864.9	50.00	Sequence
DRB1_1501	215	TGSPQPTGTILAE	PTGTILAE	0.1059	15898.6	50.00	Sequence
DRB1_1501	72	ALLDATKPEVRRQSR	ILDATKPEV	0.1036	16297.8	50.00	Sequence
DRB1_1501	13	TPYALNAVSDDERAD	TPYALNAV	0.0975	17403.5	50.00	Sequence
DRB1_1501	209	FTVEPGTGSQPPTGT	TVEPGTGSP	0.0971	17492.6	50.00	Sequence
DRB1_1501	59	AATTAEPHAHLRTAI	PPAHLRTAI	0.0953	17822.4	50.00	Sequence
DRB1_1501	212	EPGTGSPQPTGTILA	GTGSPQPTG	0.0948	17933.2	50.00	Sequence
DRB1_1501	20	VSDDERADIDRRVAA	ADIDRRVAA	0.0924	18400.8	50.00	Sequence
DRB1_1501	213	PGTGSQPPTGTILAE	GTGSPQPTG	0.0915	18571.0	50.00	Sequence
DRB1_1501	112	RPSPPTVAEQVLT	TVAEQVLT	0.0895	18983.0	50.00	Sequence
DRB1_1501	33	AAAPSPVAAAFNDEV	VAAAFNDEV	0.0868	19554.6	50.00	Sequence
DRB1_1501	19	AVSDDERADIDRRVA	AVSDDERAD	0.0849	19960.4	50.00	Sequence
DRB1_1501	56	VVSAATTAEPHAHLR	VVSAATTA	0.0814	20715.9	50.00	Sequence
DRB1_1501	211	VEPGTGSQPPTGTIL	GTGSPQPTG	0.0798	21088.0	50.00	Sequence
DRB1_1501	32	VAAAPSPVAAAFNDE	AAPSPVAAA	0.0756	22076.7	50.00	Sequence
DRB1_1501	58	SAATTAEPHAHLRTA	ATTAEPHA	0.0652	24685.0	50.00	Sequence
DRB1_1501	18	NAVSDDERADIDRRV	ERADIDRRV	0.0646	24850.3	50.00	Sequence
DRB1_1501	17	LNAVSDDERADIDRR	DERADIDRR	0.0626	25400.2	50.00	Sequence
DRB1_1501	57	VSAATTAEPHAHLRT	ATTAEPHA	0.0580	26703.1	50.00	Sequence
DRB1_1501	16	ALNAVSDDERADIDR	AVSDDERAD	0.0542	27804.3	50.00	Sequence
DRB1_1501	14	PYALNAVSDDERADI	YALNAVSD	0.0505	28966.0	50.00	Sequence
DRB1_1501	15	YALNAVSDDERADID	YALNAVSD	0.0500	29103.6	50.00	Sequence
DRB1_1501	110	LTRSPPTVAEQVLT	LTRSPPT	0.0382	33056.2	50.00	Sequence
DRB1_1501	111	TRSPPTVAEQVLT	PTVAEQVLT	0.0313	35647.1	50.00	Sequence

Allele: DRB1_1501. Number of high binders 2. Number of weak binders 43. Number of peptides 218

Allele	pos	peptide	core	l-log50k(aff)	affinity(nM)	Bind	Level	%Random	Identity
DRB3_0101	141	ATVVFSDRNTGLLV	FSRDRNTGL	0.5826	91.5	WB	2.00	2.00	Sequence
DRB3_0101	140	TATVVFSDRNTGLL	FSRDRNTGL	0.5808	93.2	WB	2.00	2.00	Sequence
DRB3_0101	139	GTATVVFSDRNTGL	FSRDRNTGL	0.5802	93.8	WB	2.00	2.00	Sequence
DRB3_0101	142	TVVFSDRNTGLLVM	FSRDRNTGL	0.5650	110.6	WB	2.00	2.00	Sequence
DRB3_0101	143	VVFSDRNTGLLVMN	FSRDRNTGL	0.5277	165.7	WB	4.00	4.00	Sequence
DRB3_0101	144	VFSRDRNTGLLVMNN	FSRDRNTGL	0.5027	217.1	WB	4.00	4.00	Sequence
DRB3_0101	145	FSRDRNTGLLVMNNV	FSRDRNTGL	0.4285	484.7	WB	8.00	8.00	Sequence
DRB3_0101	86	RWRTAAFASAAAI	FASAAAI	0.4018	647.4		8.00	8.00	Sequence
DRB3_0101	87	WRTAAFASAAAI	FASAAAI	0.3783	834.0		16.00	16.00	Sequence
DRB3_0101	88	RTAAAFASAAI	FASAAAI	0.3664	949.4		16.00	16.00	Sequence
DRB3_0101	37	SPVAAAFNDEVRAV	AFNDEVRAV	0.3423	1231.6		16.00	16.00	Sequence
DRB3_0101	38	PVAAAFNDEVRAVRE	AFNDEVRAV	0.3363	1314.2		16.00	16.00	Sequence
DRB3_0101	3	HTDFELLELATPYAL	LELATPYAL	0.3352	1330.5		16.00	16.00	Sequence
DRB3_0101	89	TAAFASAAI	FASAAAI	0.3260	1469.1		16.00	16.00	Sequence
DRB3_0101	39	VAAAFNDEVRAVRET	AFNDEVRAV	0.3256	1475.5		16.00	16.00	Sequence
DRB3_0101	36	PSPVAAAFNDEVRAV	AFNDEVRAV	0.3232	1514.0		16.00	16.00	Sequence
DRB3_0101	4	TDFELLELATPYALN	LELATPYAL	0.3135	1682.6		16.00	16.00	Sequence
DRB3_0101	40	AAAFNDEVRAVRETM	AFNDEVRAV	0.3111	1726.5		16.00	16.00	Sequence
DRB3_0101	90	AAFASAAI	FASAAAI	0.3011	1924.1		16.00	16.00	Sequence
DRB3_0101	41	AAFNDEVRAVRETMA	AFNDEVRAV	0.2878	2220.7		32.00	32.00	Sequence
DRB3_0101	5	DFELLELATPYALNA	LELATPYAL	0.2870	2240.6		32.00	32.00	Sequence
DRB3_0101	9	LELATPYALNAVSD	LELATPYAL	0.2869	2241.9		32.00	32.00	Sequence
DRB3_0101	42	AFNDEVRAVRETMAV	AFNDEVRAV	0.2795	2430.9		32.00	32.00	Sequence
DRB3_0101	91	AFASAAI	FASAAAI	0.2782	2465.2		32.00	32.00	Sequence
DRB3_0101	6	FELLELATPYALNAV	LELATPYAL	0.2657	2822.1		32.00	32.00	Sequence
DRB3_0101	203	ASTALFTVEPGTGS	FTVEPGTGS	0.2561	3129.5		32.00	32.00	Sequence
DRB3_0101	7	ELLELATPYALNAV	LELATPYAL	0.2524	3259.5		32.00	32.00	Sequence
DRB3_0101	92	FASAAI	FASAAAI	0.2508	3314.7		32.00	32.00	Sequence
DRB3_0101	8	LLELATPYALNAVSD	LELATPYAL	0.2506	3322.1		32.00	32.00	Sequence
DRB3_0101	195	TATLTDLGASTALAF	LGASTALAF	0.2481	3413.0		32.00	32.00	Sequence
DRB3_0101	14	PYALNAVSDDERADI	VSDDERADI	0.2480	3418.0		32.00	32.00	Sequence
DRB3_0101	197	TLTDLGASTALAF	LGASTALAF	0.2450	3530.6		32.00	32.00	Sequence
DRB3_0101	20	VSDDERADIDRRVAA	ADIDRRVAA	0.2422	3638.8		32.00	32.00	Sequence
DRB3_0101	15	YALNAVSDDERADID	VSDDERADI	0.2413	3672.4		32.00	32.00	Sequence
DRB3_0101	196	ATLTDLGASTALAF	LGASTALAF	0.2402	3717.3		32.00	32.00	Sequence
DRB3_0101	204	STALFTVEPGTGS	FTVEPGTGS	0.2400	3724.3		32.00	32.00	Sequence

DRB3_0101	198	LTDLGASTALAF	LGASTALAF	0.2321	4057.3	32.00	Sequence
DRB3_0101	201	LGASTALAF	LGASTALAF	0.2292	4187.1	32.00	Sequence
DRB3_0101	200	DLGASTALAF	LGASTALAF	0.2258	4344.8	32.00	Sequence
DRB3_0101	199	TDLGASTALAF	LGASTALAF	0.2230	4477.7	32.00	Sequence
DRB3_0101	205	TALAF	FTVEPGTGS	0.2213	4561.8	32.00	Sequence
DRB3_0101	16	ALNAVSDDERAD	VSDDERADI	0.2159	4835.0	32.00	Sequence
DRB3_0101	18	NAVSDDERAD	VSDDERADI	0.2118	5053.8	32.00	Sequence
DRB3_0101	17	LNAVSDDERAD	VSDDERADI	0.2095	5184.6	32.00	Sequence
DRB3_0101	10	ELATPYALNAVSD	YALNAVSD	0.1980	5867.5	50.00	Sequence
DRB3_0101	19	AVSDDERAD	VSDDERADI	0.1964	5971.8	50.00	Sequence
DRB3_0101	206	ALAF	FTVEPGTGS	0.1960	5996.7	50.00	Sequence
DRB3_0101	11	LATPYALNAVSD	YALNAVSD	0.1885	6504.6	50.00	Sequence
DRB3_0101	21	SDDERAD	ADIDRRVAA	0.1836	6857.8	50.00	Sequence
DRB3_0101	13	TPYALNAVSD	YALNAVSD	0.1766	7397.9	50.00	Sequence
DRB3_0101	43	FNDEVRAVRETM	AVRETM	0.1755	7490.2	50.00	Sequence
DRB3_0101	12	ATPYALNAVSD	YALNAVSD	0.1706	7895.2	50.00	Sequence
DRB3_0101	207	LAF	FTVEPGTGS	0.1652	8370.9	50.00	Sequence
DRB3_0101	22	DDERAD	ADIDRRVAA	0.1636	8519.0	50.00	Sequence
DRB3_0101	23	DERAD	ADIDRRVAA	0.1529	9563.0	50.00	Sequence
DRB3_0101	25	RAD	ADIDRRVAA	0.1492	9953.8	50.00	Sequence
DRB3_0101	44	NDEVRAVRETM	AVRETM	0.1477	10118.7	50.00	Sequence
DRB3_0101	208	AFTVEPGTGS	FTVEPGTGS	0.1471	10177.6	50.00	Sequence
DRB3_0101	26	ADIDRRVAA	ADIDRRVAA	0.1420	10758.1	50.00	Sequence
DRB3_0101	24	ERAD	ADIDRRVAA	0.1408	10896.1	50.00	Sequence
DRB3_0101	146	SRDRNTGLLV	RDRNTGLLV	0.1376	11287.6	50.00	Sequence
DRB3_0101	45	DEVRAVRETM	AVRETM	0.1345	11672.5	50.00	Sequence
DRB3_0101	35	APSPVAAAFN	VAAAFN	0.1332	11836.3	50.00	Sequence
DRB3_0101	131	TVSRPLGAGT	LGAGT	0.1328	11884.7	50.00	Sequence
DRB3_0101	147	RDRNTGLLV	RDRNTGLLV	0.1325	11927.1	50.00	Sequence
DRB3_0101	136	LGAGT	LGAGT	0.1320	11986.7	50.00	Sequence
DRB3_0101	67	AHLR	ILDATKPEV	0.1304	12193.7	50.00	Sequence
DRB3_0101	68	HLR	ILDATKPEV	0.1274	12603.9	50.00	Sequence
DRB3_0101	130	RTVSRPLGAGT	LGAGT	0.1271	12639.7	50.00	Sequence
DRB3_0101	138	AGT	VVFSRDRNT	0.1268	12676.6	50.00	Sequence
DRB3_0101	63	AEP	LRTAILDAT	0.1264	12734.8	50.00	Sequence
DRB3_0101	0	MTEHTDFEL	MTEHTDFEL	0.1256	12842.9	50.00	Sequence
DRB3_0101	46	EVRAVRETM	AVRETM	0.1247	12970.2	50.00	Sequence
DRB3_0101	209	FTVEPGTGS	FTVEPGTGS	0.1244	13009.6	50.00	Sequence
DRB3_0101	137	GAGT	GAGT	0.1241	13057.5	50.00	Sequence
DRB3_0101	132	VSRPLGAGT	LGAGT	0.1239	13088.1	50.00	Sequence
DRB3_0101	34	AAPSPVAAAFN	VAAAFN	0.1235	13136.9	50.00	Sequence
DRB3_0101	1	TEHTDFEL	ELLELATPY	0.1234	13151.0	50.00	Sequence
DRB3_0101	33	AAAPSPVAAAFN	VAAAFN	0.1212	13466.3	50.00	Sequence
DRB3_0101	64	EPP	LRTAILDAT	0.1179	13957.5	50.00	Sequence
DRB3_0101	65	PP	LRTAILDAT	0.1176	14014.1	50.00	Sequence
DRB3_0101	47	VRAVRETM	AVRETM	0.1164	14184.3	50.00	Sequence
DRB3_0101	66	PAHLR	LRTAILDAT	0.1150	14415.0	50.00	Sequence
DRB3_0101	48	RAVRETM	AVRETM	0.1147	14458.9	50.00	Sequence
DRB3_0101	2	EHTDFEL	ELLELATPY	0.1142	14531.5	50.00	Sequence
DRB3_0101	133	SRPLGAGT	LGAGT	0.1133	14674.6	50.00	Sequence
DRB3_0101	105	FGLGVLTR	TRPSPPTV	0.1128	14747.4	50.00	Sequence
DRB3_0101	119	VAEQVLTAP	TAPDVRTVS	0.1117	14936.2	50.00	Sequence
DRB3_0101	151	TGLLV	MNNVAPPSR	0.1092	15336.3	50.00	Sequence
DRB3_0101	149	RNTGLLV	VMNNVAPPS	0.1091	15353.6	50.00	Sequence
DRB3_0101	134	RPLGAGT	LGAGT	0.1084	15480.0	50.00	Sequence
DRB3_0101	159	VAPPSRGTV	GTVYQMWLL	0.1081	15526.8	50.00	Sequence
DRB3_0101	135	PLGAGT	LGAGT	0.1069	15720.5	50.00	Sequence
DRB3_0101	69	LRTAILDAT	LRTAILDAT	0.1066	15779.1	50.00	Sequence
DRB3_0101	106	GLGVLTR	TRPSPPTV	0.1049	16076.2	50.00	Sequence
DRB3_0101	193	STTATL	TLTDLGAST	0.1049	16079.4	50.00	Sequence
DRB3_0101	150	NTGLLV	VMNNVAPPS	0.1048	16093.6	50.00	Sequence
DRB3_0101	49	AVRETM	AVRETM	0.1036	16299.9	50.00	Sequence
DRB3_0101	191	TPSTTATL	TLTDLGAST	0.1011	16744.1	50.00	Sequence
DRB3_0101	107	LGVLTR	TRPSPPTV	0.1010	16763.9	50.00	Sequence
DRB3_0101	120	AEQVLTAP	TAPDVRTVS	0.0992	17098.0	50.00	Sequence
DRB3_0101	202	GASTALAF	ASTALAF	0.0985	17217.2	50.00	Sequence
DRB3_0101	194	TTATL	TLTDLGAST	0.0968	17541.7	50.00	Sequence
DRB3_0101	192	PSTTATL	TLTDLGAST	0.0953	17828.7	50.00	Sequence
DRB3_0101	148	DRNTGLLV	TGLLV	0.0950	17888.2	50.00	Sequence
DRB3_0101	62	TAEP	HLR	0.0929	18294.0	50.00	Sequence
DRB3_0101	121	EQVLTAP	TAPDVRTVS	0.0926	18368.2	50.00	Sequence
DRB3_0101	160	APPSRGTV	GTVYQMWLL	0.0917	18547.9	50.00	Sequence
DRB3_0101	158	NVAPPSRGTV	RGTVYQMWL	0.0911	18663.5	50.00	Sequence
DRB3_0101	152	GLLV	MNNVAPPSR	0.0909	18706.7	50.00	Sequence
DRB3_0101	108	GVLTR	TRPSPPTV	0.0906	18760.7	50.00	Sequence
DRB3_0101	118	TVAEQVLTAP	EQVLTAPDV	0.0905	18789.3	50.00	Sequence
DRB3_0101	70	RTAILDAT	ILDATKPEV	0.0895	18979.9	50.00	Sequence

DRB3_0101	71	TAILDATKPEVRRQS	ILDATKPEV	0.0890	19085.8	50.00	Sequence
DRB3_0101	122	QVLTAPDVRTVSRPL	TAPDVRTVS	0.0876	19384.8	50.00	Sequence
DRB3_0101	109	VLTRPSPPTVAEQV	TRPSPPTV	0.0866	19598.1	50.00	Sequence
DRB3_0101	156	MNNVAPPSRGTVYQM	MNNVAPPSR	0.0853	19865.6	50.00	Sequence
DRB3_0101	162	PSRGTVYQMWLLGGA	GTVYQMWLL	0.0848	19985.4	50.00	Sequence
DRB3_0101	117	PTVAEQVLTAPDVRT	EQVLTAPDV	0.0843	20079.1	50.00	Sequence
DRB3_0101	153	LLVMNNVAPPSRGTV	MNNVAPPSR	0.0839	20177.7	50.00	Sequence
DRB3_0101	123	VLTPADVRTVSRPLG	TAPDVRTVS	0.0813	20754.5	50.00	Sequence
DRB3_0101	116	PPTVAEQVLTAPDVR	EQVLTAPDV	0.0799	21074.3	50.00	Sequence
DRB3_0101	110	LTRPSPPTVAEQVLT	TRPSPPTV	0.0793	21191.6	50.00	Sequence
DRB3_0101	111	TRPSPPTVAEQVLT	TRPSPPTV	0.0789	21281.9	50.00	Sequence
DRB3_0101	157	NNVAPPSRGTVYQMW	SRGTVYQMW	0.0779	21522.5	50.00	Sequence
DRB3_0101	124	LTAPDVRTVSRPLGA	TAPDVRTVS	0.0778	21541.3	50.00	Sequence
DRB3_0101	154	LVMNNVAPPSRGTVY	MNNVAPPSR	0.0762	21934.8	50.00	Sequence
DRB3_0101	72	AILDATKPEVRRQSR	ILDATKPEV	0.0755	22082.7	50.00	Sequence
DRB3_0101	161	PPSRGTVYQMWLLGG	GTVYQMWLL	0.0754	22110.7	50.00	Sequence
DRB3_0101	163	SRGTVYQMWLLGGAK	GTVYQMWLL	0.0747	22280.4	50.00	Sequence
DRB3_0101	115	PPPTVAEQVLTAPDV	EQVLTAPDV	0.0740	22452.0	50.00	Sequence
DRB3_0101	27	DIDRRVAAAPSPVAA	RVAAAPSPV	0.0734	22600.0	50.00	Sequence
DRB3_0101	99	AVGLGAFGLGVLTRP	FGLGVLTRP	0.0728	22754.6	50.00	Sequence
DRB3_0101	73	ILDATKPEVRRQSRW	ILDATKPEV	0.0709	23226.9	50.00	Sequence
DRB3_0101	61	TTAEPHAHLRTAILD	AHLRTAILD	0.0707	23277.7	50.00	Sequence
DRB3_0101	164	RGTVYQMWLLGGAKG	GTVYQMWLL	0.0683	23868.9	50.00	Sequence
DRB3_0101	95	AAAIIVGLGAFGLGV	GLGAFGLGV	0.0681	23927.6	50.00	Sequence
DRB3_0101	100	VGLGAFGLGVLTRPS	FGLGVLTRP	0.0675	24077.7	50.00	Sequence
DRB3_0101	84	QSRWRTAAFASAAAI	AAFASAAAI	0.0671	24190.0	50.00	Sequence
DRB3_0101	217	SPQPTGTILAEPLG	TILAEPLG	0.0664	24388.4	50.00	Sequence
DRB3_0101	155	VMNNVAPPSRGTVYQ	MNNVAPPSR	0.0664	24388.4	50.00	Sequence
DRB3_0101	85	SRWRTAAFASAAAI	AAFASAAAI	0.0654	24633.0	50.00	Sequence
DRB3_0101	125	TAPDVRTVSRPLGAG	TAPDVRTVS	0.0652	24687.1	50.00	Sequence
DRB3_0101	96	AAIIVGLGAFGLGVL	GLGAFGLGV	0.0650	24751.8	50.00	Sequence
DRB3_0101	81	VRRQSRWRTAAFASA	RWRTAAFAS	0.0649	24767.1	50.00	Sequence
DRB3_0101	75	DATKPEVRRQSRWRT	VRRQSRWRT	0.0637	25096.8	50.00	Sequence
DRB3_0101	98	IIVGLGAFGLGVLTR	GLGAFGLGV	0.0634	25190.3	50.00	Sequence
DRB3_0101	97	AIIVGLGAFGLGVL	GLGAFGLGV	0.0633	25211.3	50.00	Sequence
DRB3_0101	28	IDRRVAAAPSPVAAA	RVAAAPSPV	0.0630	25298.2	50.00	Sequence
DRB3_0101	80	EVRRQSRWRTAAFAS	RWRTAAFAS	0.0621	25533.3	50.00	Sequence
DRB3_0101	82	RRQSRWRTAAFASAA	RWRTAAFAS	0.0619	25586.2	50.00	Sequence
DRB3_0101	101	GLGAFGLGVLTRPSP	FGLGVLTRP	0.0612	25797.1	50.00	Sequence
DRB3_0101	76	ATKPEVRRQSRWRTA	VRRQSRWRT	0.0609	25860.0	50.00	Sequence
DRB3_0101	165	GTVYQMWLLGGAKGP	GTVYQMWLL	0.0601	26100.6	50.00	Sequence
DRB3_0101	29	DRRVAAAPSPVAAAF	RVAAAPSPV	0.0594	26300.5	50.00	Sequence
DRB3_0101	77	TKPEVRRQSRWRTA	VRRQSRWRT	0.0582	26648.0	50.00	Sequence
DRB3_0101	50	VRETMAVVSAAATTA	MAVVSAAAT	0.0580	26682.6	50.00	Sequence
DRB3_0101	83	RQSRWRTAAFASAAA	RWRTAAFAS	0.0569	27020.7	50.00	Sequence
DRB3_0101	184	TMGTAAVTPSTTATL	VTPSTTATL	0.0565	27120.0	50.00	Sequence
DRB3_0101	94	SAAAIIVGLGAFGLG	AIIVGLGAF	0.0557	27369.4	50.00	Sequence
DRB3_0101	60	ATAEPHAHLRTAIL	TAEPHAHLR	0.0545	27722.9	50.00	Sequence
DRB3_0101	216	GSPQPTGTILAEPL	GSPQPTGTI	0.0544	27762.8	50.00	Sequence
DRB3_0101	93	ASAAAIIVGLGAFGL	AIIVGLGAF	0.0543	27772.1	50.00	Sequence
DRB3_0101	214	GTGSPQPTGTILAE	GSPQPTGTI	0.0540	27863.3	50.00	Sequence
DRB3_0101	78	KPEVRRQSRWRTA	VRRQSRWRT	0.0538	27944.8	50.00	Sequence
DRB3_0101	215	TGSPQPTGTILAEPL	GSPQPTGTI	0.0535	28031.2	50.00	Sequence
DRB3_0101	79	PEVRRQSRWRTA	VRRQSRWRT	0.0533	28092.2	50.00	Sequence
DRB3_0101	102	LGAFGLGVLTRPSP	FGLGVLTRP	0.0530	28171.6	50.00	Sequence
DRB3_0101	185	MGTAAVTPSTTATLT	VTPSTTATL	0.0527	28273.0	50.00	Sequence
DRB3_0101	30	RRVAAAPSPVAAAFN	RVAAAPSPV	0.0525	28332.7	50.00	Sequence
DRB3_0101	187	TAAVTPSTTATLTDL	VTPSTTATL	0.0522	28418.1	50.00	Sequence
DRB3_0101	31	RVAAAPSPVAAAFND	RVAAAPSPV	0.0519	28518.5	50.00	Sequence
DRB3_0101	74	LDATKPEVRRQSRWR	LDATKPEVR	0.0517	28570.4	50.00	Sequence
DRB3_0101	188	AAVTPSTTATLTDLG	VTPSTTATL	0.0509	28822.8	50.00	Sequence
DRB3_0101	190	VTPSTTATLTDLGAS	VTPSTTATL	0.0509	28836.8	50.00	Sequence
DRB3_0101	186	GTAAVTPSTTATLTD	VTPSTTATL	0.0504	28974.4	50.00	Sequence
DRB3_0101	56	VVSAATTAEPHAHLR	TAEPHAHLR	0.0493	29344.2	50.00	Sequence
DRB3_0101	103	GAFGLGVLTRPSP	FGLGVLTRP	0.0488	29503.4	50.00	Sequence
DRB3_0101	189	AVTPSTTATLTDLGA	VTPSTTATL	0.0487	29507.9	50.00	Sequence
DRB3_0101	51	RETMAVVSAAATTA	MAVVSAAAT	0.0484	29608.3	50.00	Sequence
DRB3_0101	112	RPSPPPTVAEQVLT	TVAEQVLT	0.0482	29670.5	50.00	Sequence
DRB3_0101	212	EPGTGSPQPTGTILA	GSPQPTGTI	0.0470	30075.8	50.00	Sequence
DRB3_0101	113	PSPPTVAEQVLTAP	TVAEQVLT	0.0467	30155.0	50.00	Sequence
DRB3_0101	52	ETMAVVSAAATTA	MAVVSAAAT	0.0462	30341.9	50.00	Sequence
DRB3_0101	166	TVYQMWLLGGAKGPR	YQMWLLGGA	0.0461	30359.9	50.00	Sequence
DRB3_0101	167	VYQMWLLGGAKGPRS	YQMWLLGGA	0.0460	30403.6	50.00	Sequence
DRB3_0101	104	AFGLGVLTRPSP	FGLGVLTRP	0.0458	30448.1	50.00	Sequence
DRB3_0101	55	AVVSAATTAEPHAHL	TTAEPHAHL	0.0453	30628.8	50.00	Sequence
DRB3_0101	210	TVEPPTGSPQPTGTI	GSPQPTGTI	0.0450	30716.8	50.00	Sequence
DRB3_0101	57	VSAATTAEPHAHLRT	TAEPHAHLR	0.0448	30809.6	50.00	Sequence

DRB3_0101	54	MAVVSAAATTAEPPEAH	MAVVSAAAT	0.0447	30827.3	50.00	Sequence
DRB3_0101	211	VEPGTGSPQPTGTIL	GSPQPTGTI	0.0443	30944.3	50.00	Sequence
DRB3_0101	114	SPPPTVAEQVLTAPE	TVAEQVLTA	0.0443	30949.3	50.00	Sequence
DRB3_0101	53	TMAVVSAATTAEPPEA	MAVVSAAAT	0.0439	31101.0	50.00	Sequence
DRB3_0101	213	PGTGSPQPTGTILAE	GSPQPTGTI	0.0437	31146.1	50.00	Sequence
DRB3_0101	58	SAATTAEPPAHLRRTA	TAEPPAHLR	0.0432	31331.4	50.00	Sequence
DRB3_0101	168	YQMWLLGGAKGPRSA	YQMWLLGGA	0.0430	31381.9	50.00	Sequence
DRB3_0101	59	AATTAEPPAHLRTAI	TAEPPAHLR	0.0428	31468.3	50.00	Sequence
DRB3_0101	32	VAAAPSPVAAAFNDE	VAAAPSPVA	0.0422	31667.1	50.00	Sequence
DRB3_0101	180	RSAGTMGTAAVTPST	MGTAAVTPS	0.0413	31990.4	50.00	Sequence
DRB3_0101	126	APDVRTVSRPLGAGT	RTVSRPLGA	0.0409	32108.0	50.00	Sequence
DRB3_0101	179	PRSAGTMGTAAVTPS	MGTAAVTPS	0.0404	32308.0	50.00	Sequence
DRB3_0101	182	AGTMGTAAVTPSTTA	MGTAAVTPS	0.0388	32874.7	50.00	Sequence
DRB3_0101	181	SAGTMGTAAVTPSTT	MGTAAVTPS	0.0385	32969.4	50.00	Sequence
DRB3_0101	127	PDVRTVSRPLGAGTA	RTVSRPLGA	0.0381	33118.9	50.00	Sequence
DRB3_0101	183	GTMGTAAVTPSTTAT	MGTAAVTPS	0.0366	33638.6	50.00	Sequence
DRB3_0101	129	VRTVSRPLGAGTATV	PLGAGTATV	0.0334	34853.8	50.00	Sequence
DRB3_0101	128	DVRTVSRPLGAGTAT	RTVSRPLGA	0.0309	35780.4	50.00	Sequence
DRB3_0101	169	QMWLLGGAKGPRSA	LGGAKGPRS	0.0276	37077.8	50.00	Sequence
DRB3_0101	170	MWLLGGAKGPRSA	LGGAKGPRS	0.0255	37948.0	50.00	Sequence
DRB3_0101	177	KGPRSAAGTMGTA	GTMGTA	0.0228	39089.4	50.00	Sequence
DRB3_0101	178	GPRSAAGTMGTA	GTMGTA	0.0211	39789.2	50.00	Sequence
DRB3_0101	171	WLLGGAKGPRSA	LGGAKGPRS	0.0208	39944.1	50.00	Sequence
DRB3_0101	172	LLGGAKGPRSA	LGGAKGPRS	0.0190	40730.5	50.00	Sequence
DRB3_0101	173	LGGAKGPRSA	LGGAKGPRS	0.0186	40889.9	50.00	Sequence
DRB3_0101	176	AKGPRSAAGTMGTA	RSAGTMGTA	0.0182	41064.2	50.00	Sequence
DRB3_0101	175	GAKGPRSAAGTMGTA	RSAGTMGTA	0.0166	41773.5	50.00	Sequence
DRB3_0101	174	GGAKGPRSAAGTMGTA	RSAGTMGTA	0.0162	41949.3	50.00	Sequence

Allele: DRB3_0101. Number of high binders 0. Number of weak binders 7. Number of peptides 218

Allele	pos	peptide	core	1-log50k(aff)	affinity(nM)	Bind	Level	%Random	Identity
DRB4_0101	46	EVRAVRETMVVSA	VRAVRETM	0.5253	170.1	WB	16.00	16.00	Sequence
DRB4_0101	45	DEVRAVRETMVVSA	VRAVRETM	0.5180	184.0	WB	16.00	16.00	Sequence
DRB4_0101	47	VRAVRETMVVSAAT	VRAVRETM	0.4909	246.6	WB	32.00	32.00	Sequence
DRB4_0101	78	KPEVRRQSRWRTA	VRRQSRWR	0.4905	247.9	WB	32.00	32.00	Sequence
DRB4_0101	44	NDEVRAVRETMVV	VRAVRETM	0.4904	248.1	WB	32.00	32.00	Sequence
DRB4_0101	79	PEVRRQSRWRTA	VRRQSRWR	0.4860	260.2	WB	32.00	32.00	Sequence
DRB4_0101	43	FNDEVRAVRETM	VRAVRETM	0.4812	274.1	WB	32.00	32.00	Sequence
DRB4_0101	80	EVRRQSRWRTA	VRRQSRWR	0.4800	277.5	WB	32.00	32.00	Sequence
DRB4_0101	162	PSRGTVYQMWLLG	GTVYQMWLL	0.4759	290.2	WB	32.00	32.00	Sequence
DRB4_0101	81	VRRQSRWRTA	VRRQSRWR	0.4753	292.0	WB	32.00	32.00	Sequence
DRB4_0101	77	TKPEVRRQSRWR	VRRQSRWR	0.4738	296.9	WB	32.00	32.00	Sequence
DRB4_0101	163	SRGTVYQMWLLG	GTVYQMWLL	0.4723	301.8	WB	32.00	32.00	Sequence
DRB4_0101	42	AFNDEVRAVRETM	VRAVRETM	0.4691	312.3	WB	32.00	32.00	Sequence
DRB4_0101	148	DRNTGLLMNNAV	LLVMNNV	0.4547	364.9	WB	32.00	32.00	Sequence
DRB4_0101	76	ATKPEVRRQSRWR	VRRQSRWR	0.4543	366.5	WB	32.00	32.00	Sequence
DRB4_0101	48	RAVRETMVVSAAT	MAVVSAA	0.4525	374.0	WB	32.00	32.00	Sequence
DRB4_0101	161	PPSRGTVYQMWLL	GTVYQMWLL	0.4510	379.9	WB	32.00	32.00	Sequence
DRB4_0101	149	RNTGLLMNNAV	LLVMNNV	0.4457	402.5	WB	32.00	32.00	Sequence
DRB4_0101	147	RDRNTGLLMNNAV	TGLLMNNV	0.4407	424.9	WB	32.00	32.00	Sequence
DRB4_0101	160	APPSRGTVYQMWLL	GTVYQMWLL	0.4401	427.4	WB	32.00	32.00	Sequence
DRB4_0101	41	AAFNDEVRAVRETM	VRAVRETM	0.4398	428.8	WB	32.00	32.00	Sequence
DRB4_0101	164	RGTVYQMWLLG	GTVYQMWLL	0.4323	465.2	WB	32.00	32.00	Sequence
DRB4_0101	3	HTDFELLELATPY	ELLELATPY	0.4299	477.6	WB	32.00	32.00	Sequence
DRB4_0101	4	TDFELLELATPY	ELLELATPY	0.4250	503.1	WB	32.00	32.00	Sequence
DRB4_0101	49	AVRETMVVSAATTA	MAVVSAA	0.4215	522.8	WB	32.00	32.00	Sequence
DRB4_0101	75	DATKPEVRRQSRWR	VRRQSRWR	0.4193	535.4	WB	32.00	32.00	Sequence
DRB4_0101	150	NTGLLMNNAV	TGLLMNNV	0.4179	543.7	WB	32.00	32.00	Sequence
DRB4_0101	159	VAPPSRGTVYQMWLL	GTVYQMWLL	0.4173	547.3	WB	32.00	32.00	Sequence
DRB4_0101	50	VRETMVVSAATTA	MAVVSAA	0.4132	571.8	WB	32.00	32.00	Sequence
DRB4_0101	146	SRDRNTGLLMNNAV	GLLMNNVA	0.4131	572.7	WB	32.00	32.00	Sequence
DRB4_0101	151	TGLLMNNVAPP	TGLLMNNV	0.4117	581.5	WB	32.00	32.00	Sequence
DRB4_0101	5	DFELLELATPY	ELLELATPY	0.4031	637.8	WB	32.00	32.00	Sequence
DRB4_0101	126	APDVRTVSRPLGAGT	VRTVSRPLG	0.3989	667.4	WB	50.00	50.00	Sequence
DRB4_0101	165	GTVYQMWLLG	GTVYQMWLL	0.3985	670.5	WB	50.00	50.00	Sequence
DRB4_0101	51	RETMVVSAATTA	MAVVSAA	0.3972	680.2	WB	50.00	50.00	Sequence
DRB4_0101	127	PDVRTVSRPLGAGTA	VRTVSRPLG	0.3952	695.1	WB	50.00	50.00	Sequence
DRB4_0101	52	ETMAVVSAAATTA	MAVVSAA	0.3946	699.8	WB	50.00	50.00	Sequence
DRB4_0101	125	TAPDVRTVSRPLGAG	VRTVSRPLG	0.3927	714.2	WB	50.00	50.00	Sequence
DRB4_0101	65	PPAHLRRTAILD	AHLRRTAILD	0.3897	737.2	WB	50.00	50.00	Sequence
DRB4_0101	6	FELLELATPY	ELLELATPY	0.3897	737.9	WB	50.00	50.00	Sequence
DRB4_0101	7	ELLELATPY	ELLELATPY	0.3886	746.6	WB	50.00	50.00	Sequence

DRB4_0101	2	EHTDFELLELATPYA	ELLELATPY	0.3884	748.1	50.00	Sequence
DRB4_0101	128	DVRTVSRPLGAGTAT	VRTVSRPLG	0.3882	749.8	50.00	Sequence
DRB4_0101	64	EPPAHLRTAILDATK	AHLRTAILD	0.3840	784.6	50.00	Sequence
DRB4_0101	124	LTAPDVRTVSRPLGA	VRTVSRPLG	0.3821	801.0	50.00	Sequence
DRB4_0101	63	AEPFAHLRTAILDAT	LRTAILDAT	0.3817	804.4	50.00	Sequence
DRB4_0101	152	GLLVMNNAVPPSRGT	GLLVMNVA	0.3672	940.4	50.00	Sequence
DRB4_0101	1	TEHTDFELLELATPY	ELLELATPY	0.3640	974.0	50.00	Sequence
DRB4_0101	104	AFGLGVLTRPSPPT	LGVLTRPSP	0.3597	1020.9	50.00	Sequence
DRB4_0101	103	GAFGLGVLTRPSPPP	LGVLTRPSP	0.3571	1050.0	50.00	Sequence
DRB4_0101	123	VLTAPEVRTVSRPLG	VRTVSRPLG	0.3550	1073.3	50.00	Sequence
DRB4_0101	66	PAHLRTAILDATKPE	AHLRTAILD	0.3524	1104.2	50.00	Sequence
DRB4_0101	217	SPQPTGTILAEPLG	GTILAEPL	0.3521	1107.4	50.00	Sequence
DRB4_0101	53	TMAVVSAAATTAEP	MAVVSAAAT	0.3518	1112.0	50.00	Sequence
DRB4_0101	102	LGAFGLGVLTRPSP	LGVLTRPSP	0.3512	1119.2	50.00	Sequence
DRB4_0101	101	GLGAFGLGVLTRP	LGVLTRPSP	0.3490	1145.8	50.00	Sequence
DRB4_0101	145	FSRDRNTGLLVMN	TGLLVMN	0.3488	1148.1	50.00	Sequence
DRB4_0101	105	FGLGVLTRPSPPT	LGVLTRPSP	0.3460	1183.2	50.00	Sequence
DRB4_0101	106	GLGVLTRPSPPTVA	LGVLTRPSP	0.3458	1186.1	50.00	Sequence
DRB4_0101	143	VVFSRDRNTGLLV	VVFSRDRNT	0.3406	1254.3	50.00	Sequence
DRB4_0101	67	AHLRTAILDATKPE	AHLRTAILD	0.3389	1278.2	50.00	Sequence
DRB4_0101	141	ATVVFSRDRNTGL	ATVVFSRDR	0.3210	1551.3	50.00	Sequence
DRB4_0101	82	RRQSRWRTAAFAS	QSRWRTAAF	0.3204	1560.5	50.00	Sequence
DRB4_0101	129	VRTVSRPLGAGTAT	VRTVSRPLG	0.3164	1630.9	50.00	Sequence
DRB4_0101	140	TATVVFSRDRNTG	ATVVFSRDR	0.3121	1707.0	50.00	Sequence
DRB4_0101	142	TVVFSRDRNTGL	VVFSRDRNT	0.3099	1749.4	50.00	Sequence
DRB4_0101	158	NVAPPSRGTVYQ	SRGTVYQMW	0.3086	1773.2	50.00	Sequence
DRB4_0101	153	LLVMNNVAPP	LVMNNVAPP	0.3069	1807.5	50.00	Sequence
DRB4_0101	216	GSQPTGTILAEPL	GTILAEPL	0.3046	1851.6	50.00	Sequence
DRB4_0101	144	VFSRDRNTGLLV	RNTGLLV	0.3035	1874.9	50.00	Sequence
DRB4_0101	116	PPTVAEQVLTAP	PTVAEQVLT	0.3014	1917.6	50.00	Sequence
DRB4_0101	83	RQSRWRTAAFAS	SRWRTAafa	0.3002	1943.1	50.00	Sequence
DRB4_0101	74	LDATKPEVRRQSR	KPEVRRQSR	0.2991	1965.0	50.00	Sequence
DRB4_0101	139	GTATVVFSRDRNT	ATVVFSRDR	0.2974	2002.9	50.00	Sequence
DRB4_0101	100	VGLGAFGLGVLTR	VGLGAFGLG	0.2974	2003.2	50.00	Sequence
DRB4_0101	9	LELATPYALNAV	LELATPYAL	0.2967	2017.8	50.00	Sequence
DRB4_0101	115	PPPTVAEQVLTAP	EQVLTAPDV	0.2962	2028.1	50.00	Sequence
DRB4_0101	62	TAEPFAHLRTAIL	AHLRTAILD	0.2947	2062.1	50.00	Sequence
DRB4_0101	54	MAVVSAAATTAEP	MAVVSAAAT	0.2945	2065.6	50.00	Sequence
DRB4_0101	8	LLELATPYALNAV	LELATPYAL	0.2904	2159.3	50.00	Sequence
DRB4_0101	73	ILDATKPEVRRQ	KPEVRRQSR	0.2860	2264.9	50.00	Sequence
DRB4_0101	84	QSRWRTAAFAS	SRWRTAafa	0.2858	2271.1	50.00	Sequence
DRB4_0101	0	MTEHTDFELLELA	FELLELATP	0.2854	2279.9	50.00	Sequence
DRB4_0101	107	LGVLTRPSPPTVA	LGVLTRPSP	0.2838	2320.0	50.00	Sequence
DRB4_0101	72	ALLDATKPEVRRQ	KPEVRRQSR	0.2797	2425.1	50.00	Sequence
DRB4_0101	13	TPYALNAVSDDER	LNAVSDDER	0.2769	2499.2	50.00	Sequence
DRB4_0101	68	HLRTAILDATKPE	LRTAILDAT	0.2766	2508.3	50.00	Sequence
DRB4_0101	12	ATPYALNAVSDDER	LNAVSDDER	0.2743	2571.6	50.00	Sequence
DRB4_0101	138	AGTATVVFSRDR	ATVVFSRDR	0.2717	2644.9	50.00	Sequence
DRB4_0101	11	LATPYALNAVSDDER	TPYALNAV	0.2698	2698.2	50.00	Sequence
DRB4_0101	117	PTVAEQVLTAPDV	EQVLTAPDV	0.2682	2746.5	50.00	Sequence
DRB4_0101	98	IAVGLGAFGLGVL	IAVGLGAFG	0.2645	2857.4	50.00	Sequence
DRB4_0101	114	SPPTVAEQVLTAP	PTVAEQVLT	0.2603	2992.1	50.00	Sequence
DRB4_0101	96	AAIAVGLGAFGLG	AAIAVGLGA	0.2565	3116.6	50.00	Sequence
DRB4_0101	122	QVLTAPDVRTVSR	DVRTVSRPL	0.2538	3210.3	50.00	Sequence
DRB4_0101	99	AVGLGAFGLGVL	VGLGAFGLG	0.2535	3219.3	50.00	Sequence
DRB4_0101	69	LRTAILDATKPE	LRTAILDAT	0.2535	3219.9	50.00	Sequence
DRB4_0101	137	GAGTATVVFSRDR	ATVVFSRDR	0.2535	3220.5	50.00	Sequence
DRB4_0101	61	TTAEPFAHLRTAIL	AHLRTAILD	0.2533	3225.4	50.00	Sequence
DRB4_0101	97	AIAGVGLGAFGLG	VGLGAFGLG	0.2526	3252.6	50.00	Sequence
DRB4_0101	23	DERADIDRRVAA	IDRRVAAAP	0.2517	3282.7	50.00	Sequence
DRB4_0101	25	RADIDRRVAAAP	IDRRVAAAP	0.2509	3310.2	50.00	Sequence
DRB4_0101	157	NNVAPPSRGTVY	SRGTVYQMW	0.2508	3314.2	50.00	Sequence
DRB4_0101	113	PSPPPTVAEQVLT	PTVAEQVLT	0.2484	3403.0	50.00	Sequence
DRB4_0101	166	TVYQMWLLGGAK	TVYQMWLLG	0.2484	3403.2	50.00	Sequence
DRB4_0101	24	ERADIDRRVAA	IDRRVAAAP	0.2480	3418.3	50.00	Sequence
DRB4_0101	95	AAIAVGLGAFGLG	AAIAVGLGA	0.2450	3531.1	50.00	Sequence
DRB4_0101	40	AAAFNDEVRAVRE	EVRAVRETM	0.2415	3666.6	50.00	Sequence
DRB4_0101	14	PYALNAVSDDER	LNAVSDDER	0.2413	3674.9	50.00	Sequence
DRB4_0101	26	ADIDRRVAAAP	IDRRVAAAP	0.2366	3867.5	50.00	Sequence
DRB4_0101	85	SRWRTAAFAS	SRWRTAafa	0.2331	4013.1	50.00	Sequence
DRB4_0101	10	ELATPYALNAVSD	TPYALNAV	0.2331	4015.4	50.00	Sequence
DRB4_0101	27	DIRRVAAAP	IDRRVAAAP	0.2326	4035.6	50.00	Sequence
DRB4_0101	94	SAAIAVGLGAFGL	AAIAVGLGA	0.2297	4164.4	50.00	Sequence
DRB4_0101	15	YALNAVSDDER	LNAVSDDER	0.2268	4296.4	50.00	Sequence
DRB4_0101	136	LGAGTATVVFSR	ATVVFSRDR	0.2255	4358.4	50.00	Sequence
DRB4_0101	154	LVMNNVAPP	LVMNNVAPP	0.2216	4544.7	50.00	Sequence
DRB4_0101	205	TALAFTEVEPGT	LAFTVEPGT	0.2204	4605.7	50.00	Sequence

DRB4_0101	112	RPSPPPTVAEQVLTA	PPTVAEQVL	0.2186	4694.9	50.00	Sequence
DRB4_0101	28	IDRRVAAAAPSPVAAA	IDRRVAAAAP	0.2183	4711.2	50.00	Sequence
DRB4_0101	120	AEQVLTAPDVRTVSR	EQVLTAPDV	0.2178	4739.1	50.00	Sequence
DRB4_0101	130	RTVSRPLGAGTATVV	RTVSRPLGA	0.2169	4784.3	50.00	Sequence
DRB4_0101	203	ASTALAFVTEPGTGS	TALAFVTEP	0.2140	4935.0	50.00	Sequence
DRB4_0101	119	VAEQVLTAPDVRTVS	EQVLTAPDV	0.2135	4961.7	50.00	Sequence
DRB4_0101	156	MNNVAPPSRGTVYQM	MNNVAPPSR	0.2130	4990.8	50.00	Sequence
DRB4_0101	118	TVAEQVLTAPDVRTV	EQVLTAPDV	0.2121	5040.9	50.00	Sequence
DRB4_0101	204	STALAFVTEPGTGSP	TALAFVTEP	0.2115	5071.9	50.00	Sequence
DRB4_0101	22	DDERADIDRRVAAAAP	IDRRVAAAAP	0.2102	5145.0	50.00	Sequence
DRB4_0101	135	PLGAGTATVVFSTRDR	ATVVFSTRDR	0.2086	5234.3	50.00	Sequence
DRB4_0101	121	EQVLTAPDVRTVSRP	EQVLTAPDV	0.2056	5404.0	50.00	Sequence
DRB4_0101	197	LTDLGASTALAFVTV	LTDLGASTA	0.2050	5441.1	50.00	Sequence
DRB4_0101	201	LGASTALAFVTEPGT	ALAFVTEPG	0.2047	5461.6	50.00	Sequence
DRB4_0101	70	RTAILDATKPEVRRQ	TAILDATKP	0.2042	5486.7	50.00	Sequence
DRB4_0101	196	ATLTDLGASTALAFV	LTDLGASTA	0.2038	5510.1	50.00	Sequence
DRB4_0101	198	LTDLGASTALAFVTE	LTDLGASTA	0.2028	5572.3	50.00	Sequence
DRB4_0101	195	TATLTDLGASTALAF	LTDLGASTA	0.2000	5743.1	50.00	Sequence
DRB4_0101	60	ATTAEPPAHLRTAIL	PAHLRTAIL	0.1995	5775.6	50.00	Sequence
DRB4_0101	71	TAILDATKPEVRRQS	TAILDATKP	0.1972	5922.0	50.00	Sequence
DRB4_0101	202	GASTALAFVTEPGTG	LAFTVEPGT	0.1963	5975.7	50.00	Sequence
DRB4_0101	132	VSRPLGAGTATVVFS	RPLGAGTAT	0.1951	6055.2	50.00	Sequence
DRB4_0101	93	ASAAAIAVGLGAFGL	AAIAVGLGA	0.1948	6077.1	50.00	Sequence
DRB4_0101	16	ALNAVSDDERADIDR	LNAVSDDER	0.1942	6113.0	50.00	Sequence
DRB4_0101	111	TRPSPPTVAEQVLT	PPTVAEQVL	0.1942	6116.7	50.00	Sequence
DRB4_0101	206	ALAFVTEPGTGSPQP	LAFTVEPGT	0.1925	6228.9	50.00	Sequence
DRB4_0101	167	VYQMWLLGGAKGPRS	YQMWLLGGA	0.1925	6231.4	50.00	Sequence
DRB4_0101	131	TVSRPLGAGTATVVF	RPLGAGTAT	0.1917	6284.8	50.00	Sequence
DRB4_0101	194	TTATLTDLGASTALA	LTDLGASTA	0.1869	6618.0	50.00	Sequence
DRB4_0101	193	STTATLTDLGASTAL	LTDLGASTA	0.1850	6753.5	50.00	Sequence
DRB4_0101	92	FASAAAIAVGLGAFG	AAIAVGLGA	0.1848	6766.7	50.00	Sequence
DRB4_0101	155	VMNNVAPP SRGTVYQ	MNNVAPPSR	0.1847	6778.2	50.00	Sequence
DRB4_0101	133	SRPLGAGTATVVF SR	RPLGAGTAT	0.1806	7081.3	50.00	Sequence
DRB4_0101	168	YQMWLLGGAKGPRSA	YQMWLLGGA	0.1777	7309.3	50.00	Sequence
DRB4_0101	134	RPLGAGTATVVF SRD	RPLGAGTAT	0.1763	7425.0	50.00	Sequence
DRB4_0101	29	DRRVAAAAPSPVAAF	DRRVAAAAP	0.1743	7586.0	50.00	Sequence
DRB4_0101	192	PSTTATLTDLGASTA	LTDLGASTA	0.1739	7614.6	50.00	Sequence
DRB4_0101	17	LNAVSDDERADIDRR	LNAVSDDER	0.1732	7679.4	50.00	Sequence
DRB4_0101	200	DLGASTALAFVTEPG	LGASTALAF	0.1700	7943.4	50.00	Sequence
DRB4_0101	110	LTRPSPPTVAEQVLT	PPTVAEQVL	0.1685	8074.7	50.00	Sequence
DRB4_0101	59	AATTAEPPAHLRTAI	AEPPAHLRT	0.1608	8781.0	50.00	Sequence
DRB4_0101	35	APSPVAAA FNDEVRA	SPVAAA FNND	0.1607	8788.3	50.00	Sequence
DRB4_0101	21	SDDERADIDRRVAAA	RADIDRRVA	0.1595	8900.2	50.00	Sequence
DRB4_0101	207	LAFTVEPGTGSPQPT	LAFTVEPGT	0.1591	8936.3	50.00	Sequence
DRB4_0101	108	GVLTRPSPPTVAEQ	GVLTRPSP	0.1587	8978.5	50.00	Sequence
DRB4_0101	20	VSDDERADIDRRVAA	RADIDRRVA	0.1556	9283.0	50.00	Sequence
DRB4_0101	199	TDLGASTALAFVTEP	TDLGASTAL	0.1526	9589.0	50.00	Sequence
DRB4_0101	34	AAAPSPVAAA FNDEV	VAAA FNDEV	0.1518	9671.3	50.00	Sequence
DRB4_0101	37	SPVAAA FNDEVRAVR	SPVAAA FNND	0.1506	9805.5	50.00	Sequence
DRB4_0101	86	RWRTAAFASAAAIAV	WRTAAFASA	0.1484	10033.8	50.00	Sequence
DRB4_0101	36	PSPVAAA FNDEVRAV	SPVAAA FNND	0.1465	10244.0	50.00	Sequence
DRB4_0101	109	VLTRPSPPTVAEQV	VLTRPSP	0.1461	10285.4	50.00	Sequence
DRB4_0101	39	VAAA FNDEVRAVRET	DEVRAVRET	0.1461	10287.2	50.00	Sequence
DRB4_0101	215	TGSPQPTGTILAE L	TGTILAE L	0.1461	10290.7	50.00	Sequence
DRB4_0101	19	AVSDDERADIDRRVA	VSDDERADI	0.1440	10526.3	50.00	Sequence
DRB4_0101	91	AFASAAAIAVGLGAF	AAIAVGLGA	0.1437	10563.5	50.00	Sequence
DRB4_0101	182	AGTMGTA AVTPSTTA	MGTA AVTPS	0.1395	11048.2	50.00	Sequence
DRB4_0101	179	PR SAGTMGTA AVTPS	MGTA AVTPS	0.1381	11219.5	50.00	Sequence
DRB4_0101	180	RSAGTMGTA AVTPST	MGTA AVTPS	0.1373	11321.9	50.00	Sequence
DRB4_0101	170	MWLLGGAKGPR SAGT	WLLGGAKGP	0.1371	11348.5	50.00	Sequence
DRB4_0101	33	AAAPSPVAAA FNDEV	VAAA FNDEV	0.1369	11365.7	50.00	Sequence
DRB4_0101	181	SAGTMGTA AVTPSTT	MGTA AVTPS	0.1361	11465.5	50.00	Sequence
DRB4_0101	169	QMWLLGGAKGPR SAG	MWLLGGAKG	0.1360	11484.8	50.00	Sequence
DRB4_0101	183	GTMGTA AVTPSTTAT	MGTA AVTPS	0.1349	11621.4	50.00	Sequence
DRB4_0101	87	WR TAAFASAAAIAV	WRTAAFASA	0.1345	11672.5	50.00	Sequence
DRB4_0101	18	NAVSDDERADIDRRV	VSDDERADI	0.1341	11720.4	50.00	Sequence
DRB4_0101	30	RRVAAAAPSPVAAA FN	RRVAAAAPSP	0.1300	12253.5	50.00	Sequence
DRB4_0101	184	TMGTA AVTPSTTATM	MGTA AVTPS	0.1200	13641.5	50.00	Sequence
DRB4_0101	171	WLLGGAKGPR SAGTM	WLLGGAKGP	0.1182	13916.0	50.00	Sequence
DRB4_0101	38	PVAAA FNDEVRAVRE	FNDEVRAVR	0.1182	13924.7	50.00	Sequence
DRB4_0101	178	GPR SAGTMGTA AVTP	GTMGTA AVT	0.1158	14280.2	50.00	Sequence
DRB4_0101	31	RVAAAAPSPVAAA FNND	APSPVAAA FN	0.1150	14414.4	50.00	Sequence
DRB4_0101	32	VAAAAPSPVAAA FNND	APSPVAAA FN	0.1140	14566.1	50.00	Sequence
DRB4_0101	185	MGTA AVTPSTTATLT	MGTA AVTPS	0.1140	14567.1	50.00	Sequence
DRB4_0101	177	KGPR SAGTMGTA AVT	GTMGTA AVT	0.1138	14590.1	50.00	Sequence
DRB4_0101	214	GTGSPQPTGTILAE L	QPTGTILAE	0.1111	15030.7	50.00	Sequence
DRB4_0101	209	FTVEPGTGSPQPTGT	FTVEPGTGS	0.1096	15272.0	50.00	Sequence

DRB4_0101	55	AVVSAATTAEPHAHL	AVVSAATTA	0.1080	15535.0	50.00	Sequence
DRB4_0101	208	AFTVEPGTGSPQPTG	FTVEPGTGS	0.1074	15640.1	50.00	Sequence
DRB4_0101	187	TAAVTPSTTATLTDL	STTATLTDL	0.1057	15931.7	50.00	Sequence
DRB4_0101	210	TVEPGTGSPQPTGTI	PGTGSPQPT	0.1048	16094.3	50.00	Sequence
DRB4_0101	173	LGGAKGPRSAGTMGT	LGGAKGPRS	0.1039	16247.1	50.00	Sequence
DRB4_0101	90	AAFASAAAIAVGLGA	AAIAVGLGA	0.1028	16443.2	50.00	Sequence
DRB4_0101	212	EPGTGSPQPTGTILA	PGTGSPQPT	0.1019	16609.1	50.00	Sequence
DRB4_0101	213	PGTGSPQPTGTILAE	PGTGSPQPT	0.1009	16775.5	50.00	Sequence
DRB4_0101	58	SAATTAEPHAHLRTA	AEPHAHLRT	0.1009	16776.7	50.00	Sequence
DRB4_0101	190	VTPSTTATLTDLGAS	STTATLTDL	0.0984	17246.8	50.00	Sequence
DRB4_0101	211	VEPGTGSPQPTGTIL	EPGTGSPQP	0.0980	17310.6	50.00	Sequence
DRB4_0101	186	GTAAVTPSTTATLTD	TAAVTPSTT	0.0979	17336.6	50.00	Sequence
DRB4_0101	188	AAVTPSTTATLTDLG	STTATLTDL	0.0977	17379.1	50.00	Sequence
DRB4_0101	176	AKGPRSAGTMGTA AV	AGTMGTA AV	0.0973	17450.8	50.00	Sequence
DRB4_0101	189	AVTPSTTATLTDLGA	VTPSTTATL	0.0950	17890.0	50.00	Sequence
DRB4_0101	172	LLGGAKGPRSAGTMG	LGGAKGPRS	0.0920	18475.4	50.00	Sequence
DRB4_0101	191	TPSTTATLTDLGAST	STTATLTDL	0.0918	18513.8	50.00	Sequence
DRB4_0101	88	RTAAFASAAAIAVGL	AAFASAAAI	0.0879	19312.8	50.00	Sequence
DRB4_0101	174	GGAKGPRSAGTMGTA	PRSAGTMGT	0.0849	19945.9	50.00	Sequence
DRB4_0101	89	TAAFASAAAIAVGL	AAFASAAAI	0.0837	20217.7	50.00	Sequence
DRB4_0101	57	VSAATTAEPHAHLRT	AEPHAHLRT	0.0801	21008.2	50.00	Sequence
DRB4_0101	175	GAKGPRSAGTMGTAA	PRSAGTMGT	0.0797	21119.0	50.00	Sequence
DRB4_0101	56	VVSAATTAEPHAHLR	VSAATTAEP	0.0667	24297.3	50.00	Sequence

Allele: DRB4_0101. Number of high binders 0. Number of weak binders 23. Number of peptides 218

Allele	pos	peptide	core	l-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
DRB5_0101	169	QMWLLGGAKGPRSAG	WLLGGAKGP	0.6042	72.4	WB	16.00	Sequence
DRB5_0101	167	VYQMWLLGGAKGPRS	QMWLLGGAK	0.6011	74.9	WB	16.00	Sequence
DRB5_0101	168	YQMWLLGGAKGPRSA	MWLLGGAKG	0.5994	76.3	WB	16.00	Sequence
DRB5_0101	170	MWLLGGAKGPRSAGT	WLLGGAKGP	0.5780	96.2	WB	16.00	Sequence
DRB5_0101	166	TVYQMWLLGGAKGPR	QMWLLGGAK	0.5614	115.1	WB	16.00	Sequence
DRB5_0101	171	WLLGGAKGPRSAGTM	WLLGGAKGP	0.5090	202.8	WB	32.00	Sequence
DRB5_0101	165	GTVYQMWLLGGAKGP	QMWLLGGAK	0.5081	204.8	WB	32.00	Sequence
DRB5_0101	5	DFELLELATPYALNA	ELLELATPY	0.4816	272.8	WB	32.00	Sequence
DRB5_0101	48	RAVRETMAVVSAAAT	VRETMAVVS	0.4815	273.2	WB	32.00	Sequence
DRB5_0101	47	VRAVRETMAVVSAAAT	VRETMAVVS	0.4805	276.1	WB	32.00	Sequence
DRB5_0101	4	TDFELLELATPYALN	ELLELATPY	0.4801	277.2	WB	32.00	Sequence
DRB5_0101	46	EVRAVRETMAVVSAA	VRETMAVVS	0.4775	285.1	WB	32.00	Sequence
DRB5_0101	45	DEVRAVRETMAVVSAA	VRETMAVVS	0.4684	314.7	WB	32.00	Sequence
DRB5_0101	6	FELLELATPYALNAV	ELLELATPY	0.4682	315.5	WB	32.00	Sequence
DRB5_0101	164	RGTVYQMWLLGGAKG	QMWLLGGAK	0.4663	322.2	WB	32.00	Sequence
DRB5_0101	86	RWRTAAFASAAAIAV	FASAAAIAV	0.4578	352.9	WB	32.00	Sequence
DRB5_0101	80	EVRQRWRRTAAAFAS	VRRQSRWRT	0.4498	385.0	WB	32.00	Sequence
DRB5_0101	3	HTDFELLELATPYAL	FELLELATP	0.4482	391.6	WB	32.00	Sequence
DRB5_0101	44	NDEVRAVRETMAVVS	VRETMAVVS	0.4427	415.5	WB	32.00	Sequence
DRB5_0101	150	NTGLLMNNAVPPSR	GLLMNNAV	0.4354	449.6	WB	32.00	Sequence
DRB5_0101	149	RNTGLLMNNAVPPSR	GLLMNNAV	0.4346	453.9	WB	32.00	Sequence
DRB5_0101	49	AVRETMAVVSAAATTA	VRETMAVVS	0.4341	456.2	WB	32.00	Sequence
DRB5_0101	151	TGLLMNNAVPPSRG	MNNVAPPSP	0.4341	456.4	WB	32.00	Sequence
DRB5_0101	81	VRRQSRWRRTAAAFASA	VRRQSRWRT	0.4318	467.6	WB	32.00	Sequence
DRB5_0101	79	PEVRRQSRWRRTAAFA	VRRQSRWRT	0.4273	491.0	WB	32.00	Sequence
DRB5_0101	43	FNDEVRAVRETMAVV	FNDEVRAVR	0.4238	509.9		32.00	Sequence
DRB5_0101	85	SRWRTAAFASAAAIA	RWRTAAFAS	0.4215	522.7		32.00	Sequence
DRB5_0101	148	DRNTGLLMNNAVAPP	GLLMNNAV	0.4212	524.7		32.00	Sequence
DRB5_0101	84	QSRWRTAAFASAAAIA	SRWRTAAFAS	0.4203	529.8		32.00	Sequence
DRB5_0101	126	APDVRTVSRPLGAGT	RTVSRPLGA	0.4173	547.1		32.00	Sequence
DRB5_0101	89	TAAFASAAAIAVGLG	FASAAAIAV	0.4156	557.3		32.00	Sequence
DRB5_0101	104	AFGLGVLTRPSPPT	AFGLGVLTR	0.4145	563.8		32.00	Sequence
DRB5_0101	127	PDVRTVSRPLGAGTA	RTVSRPLGA	0.4142	565.8		32.00	Sequence
DRB5_0101	88	RTAAFASAAAIAVGL	FASAAAIAV	0.4128	574.6		32.00	Sequence
DRB5_0101	153	LLVMNNAVPPSRGTV	MNNVAPPSP	0.4127	575.0		32.00	Sequence
DRB5_0101	87	WRTAAFASAAAIAVG	FASAAAIAV	0.4124	576.8		32.00	Sequence
DRB5_0101	103	GAFGLGVLTRPSPPP	AFGLGVLTR	0.4108	587.2		50.00	Sequence
DRB5_0101	152	GLLMNNAVPPSRGT	MNNVAPPSP	0.4105	588.6		50.00	Sequence
DRB5_0101	83	RQSRWRRTAAAFASAA	RWRTAAFAS	0.4095	595.1		50.00	Sequence
DRB5_0101	163	SRGTVYQMWLLGGAK	QMWLLGGAK	0.4078	606.2		50.00	Sequence
DRB5_0101	147	RDRNTGLLMNNAVAP	LLVMNNAV	0.4072	610.5		50.00	Sequence
DRB5_0101	128	DVRTVSRPLGAGTAT	RTVSRPLGA	0.4066	614.6		50.00	Sequence
DRB5_0101	42	FNDEVRAVRETMAV	FNDEVRAVR	0.4041	630.8		50.00	Sequence
DRB5_0101	82	RRQSRWRRTAAAFASAA	SRWRTAAFAS	0.4035	635.1		50.00	Sequence
DRB5_0101	78	KPEVRRQSRWRRTAAF	VRRQSRWRT	0.4014	649.9		50.00	Sequence
DRB5_0101	90	AAFASAAAIAVGLGA	FASAAAIAV	0.4001	658.7		50.00	Sequence

DRB5_0101	102	LGAFGLGVLTRPSP	AFGLGVLTR	0.3988	668.7	50.00	Sequence
DRB5_0101	172	LLGGAKGPRSAGTMG	LLGGAKGPR	0.3963	686.5	50.00	Sequence
DRB5_0101	101	GLGAFGLGVLTRPSP	AFGLGVLTR	0.3942	702.6	50.00	Sequence
DRB5_0101	2	EHTDFELLELELATPYA	FELLELATP	0.3926	714.8	50.00	Sequence
DRB5_0101	129	VRTVSRPLGAGTATV	RTVSRPLGA	0.3888	744.6	50.00	Sequence
DRB5_0101	41	AAFNDEVRAVRETMA	FNDEVRAVR	0.3873	757.2	50.00	Sequence
DRB5_0101	77	TKPEVRRQSRWRTA	EVRRQSRWR	0.3848	777.9	50.00	Sequence
DRB5_0101	50	VRETMAVVAATTAE	VRETMAVVS	0.3846	779.1	50.00	Sequence
DRB5_0101	105	FGLGVLTRPSPPTV	GVLTRPSP	0.3830	793.2	50.00	Sequence
DRB5_0101	7	ELLELATPYALNAVS	LELATPYAL	0.3801	818.4	50.00	Sequence
DRB5_0101	154	LVMNNVAPSRGTV	MNNVAPPSR	0.3797	822.1	50.00	Sequence
DRB5_0101	100	VGLGAFGLGVLTRPS	AFGLGVLTR	0.3788	830.1	50.00	Sequence
DRB5_0101	125	TAPDVRTVSRPLGAG	DVRTVSRPL	0.3746	868.8	50.00	Sequence
DRB5_0101	91	AFASAAAI AVGLGAF	FASAAAI AV	0.3730	884.0	50.00	Sequence
DRB5_0101	76	ATKPEVRRQSRWRTA	EVRRQSRWR	0.3683	929.5	50.00	Sequence
DRB5_0101	40	AAAFNDEVRAVRETM	FNDEVRAVR	0.3631	983.8	50.00	Sequence
DRB5_0101	28	IDRRVAAAPSPVAAA	RRVAAAPSP	0.3612	1003.6	50.00	Sequence
DRB5_0101	27	DIDRRVAAAPSPVAA	RRVAAAPSP	0.3585	1034.1	50.00	Sequence
DRB5_0101	70	RTAILDATKPEVRRQ	LDATKPEVR	0.3584	1034.4	50.00	Sequence
DRB5_0101	139	GTATVVFSRDRNTGL	ATVVFSRDR	0.3577	1042.7	50.00	Sequence
DRB5_0101	120	AEQVLTAPDVRTVSR	VLTAPDVRT	0.3557	1066.0	50.00	Sequence
DRB5_0101	106	GLGVLTRPSPPTVA	GVLTRPSP	0.3460	1182.8	50.00	Sequence
DRB5_0101	124	LTAPDVRTVSRPLGA	VRTVSRPLG	0.3455	1189.8	50.00	Sequence
DRB5_0101	121	EQVLTAPDVRTVSRP	VLTAPDVRT	0.3431	1220.7	50.00	Sequence
DRB5_0101	141	ATVVFSRDRNTGLLV	ATVVFSRDR	0.3428	1224.5	50.00	Sequence
DRB5_0101	75	DATKPEVRRQSRWRT	EVRRQSRWR	0.3424	1229.9	50.00	Sequence
DRB5_0101	99	AVGLGAFGLGVLTRP	AFGLGVLTR	0.3420	1235.4	50.00	Sequence
DRB5_0101	155	VMNNVAPP SRGTVYQ	MNNVAPPSR	0.3420	1235.9	50.00	Sequence
DRB5_0101	29	DRRVAAAPSPVAAA	RVAAAPSPV	0.3409	1250.2	50.00	Sequence
DRB5_0101	122	QVLTAPDVRTVSRPL	VLTAPDVRT	0.3409	1250.6	50.00	Sequence
DRB5_0101	140	TATVVFSRDRNTGLL	TVVFSRDRN	0.3396	1268.7	50.00	Sequence
DRB5_0101	71	TAILDATKPEVRRQS	LDATKPEVR	0.3374	1299.0	50.00	Sequence
DRB5_0101	69	LRTAILDATKPEVRR	LDATKPEVR	0.3351	1331.0	50.00	Sequence
DRB5_0101	119	VAEQVLTAPDVRTVS	VLTAPDVRT	0.3345	1340.8	50.00	Sequence
DRB5_0101	74	LDATKPEVRRQSRWR	LDATKPEVR	0.3331	1360.3	50.00	Sequence
DRB5_0101	146	SRDRNTGLLVMMNVA	GLLVMMNVA	0.3314	1385.8	50.00	Sequence
DRB5_0101	8	LELATPYALNAVSD	LELATPYAL	0.3314	1386.0	50.00	Sequence
DRB5_0101	30	RRVAAAPSPVAAA	RVAAAPSPV	0.3314	1386.2	50.00	Sequence
DRB5_0101	26	ADIDRRVAAAPSPVA	RRVAAAPSP	0.3288	1425.0	50.00	Sequence
DRB5_0101	207	LAFTVEPGTGSPQPT	FTVEPGTGS	0.3287	1427.5	50.00	Sequence
DRB5_0101	206	ALAFTVEPGTGSPQP	FTVEPGTGS	0.3278	1441.6	50.00	Sequence
DRB5_0101	205	TALAFTVEPGTGSPQ	FTVEPGTGS	0.3270	1453.3	50.00	Sequence
DRB5_0101	1	TEHTDFELLELELATPY	FELLELATP	0.3263	1464.1	50.00	Sequence
DRB5_0101	123	VLTAPDVRTVSRPLG	VLTAPDVRT	0.3218	1538.4	50.00	Sequence
DRB5_0101	118	TVAEQVLTAPDVRTV	VLTAPDVRT	0.3195	1577.1	50.00	Sequence
DRB5_0101	138	AGTATVVFSRDRNTG	ATVVFSRDR	0.3170	1620.1	50.00	Sequence
DRB5_0101	39	VAAAFNDEVRAVRET	FNDEVRAVR	0.3169	1621.8	50.00	Sequence
DRB5_0101	130	RTVSRPLGAGTATVV	RTVSRPLGA	0.3089	1767.0	50.00	Sequence
DRB5_0101	142	TVVFSRDRNTGLLVM	VVFSRDRNT	0.3080	1785.3	50.00	Sequence
DRB5_0101	51	RETMAVVAATTAE	MAVVAATT	0.3078	1788.8	50.00	Sequence
DRB5_0101	72	AILDATKPEVRRQSR	LDATKPEVR	0.3076	1792.7	50.00	Sequence
DRB5_0101	197	LTDLGASTALAFSTV	DLGASTALA	0.3060	1823.8	50.00	Sequence
DRB5_0101	198	LTDLGASTALAFSTVE	LGASTALAF	0.3057	1829.7	50.00	Sequence
DRB5_0101	199	TDLGASTALAFSTVEP	LGASTALAF	0.3032	1880.9	50.00	Sequence
DRB5_0101	156	MNNVAPP SRGTVYQM	MNNVAPPSR	0.3031	1883.3	50.00	Sequence
DRB5_0101	162	PSRGTVYQMWLLGGA	TVYQMWLLG	0.3017	1910.3	50.00	Sequence
DRB5_0101	73	ILDATKPEVRRQSRW	LDATKPEVR	0.3016	1914.1	50.00	Sequence
DRB5_0101	68	HLRTAILDATKPEVR	LDATKPEVR	0.2995	1956.6	50.00	Sequence
DRB5_0101	204	STALAFSTVEPGTGSP	FTVEPGTGS	0.2992	1962.6	50.00	Sequence
DRB5_0101	92	FASAAAI AVGLGAFG	FASAAAI AV	0.2970	2010.7	50.00	Sequence
DRB5_0101	208	AFTVEPGTGSPQPTG	FTVEPGTGS	0.2969	2013.7	50.00	Sequence
DRB5_0101	137	GAGTATVVFSRDRNT	GTATVVFSR	0.2932	2095.7	50.00	Sequence
DRB5_0101	107	LGVLTRPSPPTVAE	GVLTRPSP	0.2912	2141.8	50.00	Sequence
DRB5_0101	9	LELATPYALNAVSD	LELATPYAL	0.2887	2200.1	50.00	Sequence
DRB5_0101	98	IAVGLGAFGLGVLTR	AFGLGVLTR	0.2878	2222.5	50.00	Sequence
DRB5_0101	200	DLGASTALAFSTVEPG	LGASTALAF	0.2834	2329.3	50.00	Sequence
DRB5_0101	117	PTVAEQVLTAPDVRT	VLTAPDVRT	0.2818	2371.2	50.00	Sequence
DRB5_0101	143	VVFSRDRNTGLLVMN	VVFSRDRNT	0.2804	2407.3	50.00	Sequence
DRB5_0101	38	PVAAAFNDEVRAVRE	FNDEVRAVR	0.2803	2408.0	50.00	Sequence
DRB5_0101	203	ASTALAFSTVEPGTGS	FTVEPGTGS	0.2801	2413.2	50.00	Sequence
DRB5_0101	25	RADIDRRVAAAPSPV	RRVAAAPSP	0.2771	2494.3	50.00	Sequence
DRB5_0101	161	PPSRGTVYQMWLLGG	TVYQMWLLG	0.2766	2506.5	50.00	Sequence
DRB5_0101	53	TMAVVAATTAEPPA	MAVVAATT	0.2756	2533.4	50.00	Sequence
DRB5_0101	52	ETMAVVAATTAEPP	MAVVAATT	0.2750	2550.7	50.00	Sequence
DRB5_0101	173	LGGAKGPRSAGTMGT	LGGAKGPRS	0.2734	2595.9	50.00	Sequence
DRB5_0101	37	SPVAAAFNDEVRAVR	FNDEVRAVR	0.2727	2616.0	50.00	Sequence
DRB5_0101	136	LGAGTATVVFSRDRN	GTATVVFSR	0.2709	2667.0	50.00	Sequence

DRB5_0101	67	AHLRTAILDATKPEV	AHLRTAILD	0.2706	2675.0	50.00	Sequence
DRB5_0101	196	ATLTDLGASTALAF	LGASTALAF	0.2637	2883.1	50.00	Sequence
DRB5_0101	145	FSRDRNTGLLVMMNV	FSRDRNTGL	0.2595	3017.5	50.00	Sequence
DRB5_0101	144	VFSRDRNTGLLVMMN	FSRDRNTGL	0.2592	3027.6	50.00	Sequence
DRB5_0101	54	MAVVSAAATTAEP	MAVVSAAAT	0.2577	3076.2	50.00	Sequence
DRB5_0101	31	RVAAAPSPVAAAFND	RVAAAPSPV	0.2531	3234.0	50.00	Sequence
DRB5_0101	66	PAHLRTAILDATKPE	AHLRTAILD	0.2502	3337.4	50.00	Sequence
DRB5_0101	0	MTEHTDFELLELATP	FELLELATP	0.2461	3489.0	50.00	Sequence
DRB5_0101	65	PPAHLRTAILDATKP	AHLRTAILD	0.2388	3773.3	50.00	Sequence
DRB5_0101	195	TATLTDLGASTALAF	LGASTALAF	0.2376	3821.9	50.00	Sequence
DRB5_0101	176	AKGPRSAGTMGTAAV	PRSAGTMGT	0.2372	3839.8	50.00	Sequence
DRB5_0101	135	PLGAGTATVVF	ATVVF	0.2355	3913.2	50.00	Sequence
DRB5_0101	108	GVLTRPSPPTVAEQ	GVLTRPSP	0.2324	4044.4	50.00	Sequence
DRB5_0101	64	EPPAHLRTAILDATK	AHLRTAILD	0.2277	4255.3	50.00	Sequence
DRB5_0101	160	APPSRGTVYQMWLLG	TVYQMWLLG	0.2273	4273.5	50.00	Sequence
DRB5_0101	97	IAVGLGAFGLGVL	IAVGLGAFG	0.2254	4364.4	50.00	Sequence
DRB5_0101	175	GAKGPRSAGTMGTAA	PRSAGTMGT	0.2245	4405.7	50.00	Sequence
DRB5_0101	96	AAIAVGLGAFGLGVL	IAVGLGAFG	0.2238	4441.6	50.00	Sequence
DRB5_0101	116	PPTVAEQVLTAPDVR	TVAEQVLT	0.2222	4517.3	50.00	Sequence
DRB5_0101	55	AVVSAATTAEP	AVVSAATTA	0.2222	4518.0	50.00	Sequence
DRB5_0101	201	LGASTALAF	LGASTALAF	0.2182	4719.4	50.00	Sequence
DRB5_0101	95	AAAIAVGLGAFGLGV	IAVGLGAFG	0.2118	5054.9	50.00	Sequence
DRB5_0101	177	KGPRSAGTMGTA	PRSAGTMGT	0.2114	5078.3	50.00	Sequence
DRB5_0101	202	GASTALAF	ASTALAF	0.2067	5343.9	50.00	Sequence
DRB5_0101	131	VSRPLGAGTATVVF	VSRPLGAGT	0.2061	5378.9	50.00	Sequence
DRB5_0101	174	GGAKGPRSAGTMGT	PRSAGTMGT	0.2055	5409.7	50.00	Sequence
DRB5_0101	178	GPRSAGTMGTA	PRSAGTMGT	0.2038	5510.9	50.00	Sequence
DRB5_0101	134	RPLGAGTATVVF	GTATVVF	0.2030	5563.0	50.00	Sequence
DRB5_0101	132	VSRPLGAGTATVVF	VSRPLGAGT	0.2028	5574.5	50.00	Sequence
DRB5_0101	209	FTVEPGTGS	FTVEPGTGS	0.2016	5644.5	50.00	Sequence
DRB5_0101	133	SRPLGAGTATVVF	GTATVVF	0.2016	5646.7	50.00	Sequence
DRB5_0101	24	ERADIDRRVAAAPSP	RRVAAAPSP	0.1945	6096.0	50.00	Sequence
DRB5_0101	184	TMGTAAVTPSTT	TMGTAAVTP	0.1929	6202.4	50.00	Sequence
DRB5_0101	63	AEP	AHLRTAILD	0.1919	6270.1	50.00	Sequence
DRB5_0101	56	VVSAATTAEP	VVSAATTAEP	0.1910	6332.2	50.00	Sequence
DRB5_0101	10	ELATPYALNAVSDDE	TPYALNAV	0.1863	6658.5	50.00	Sequence
DRB5_0101	194	TATLTDLGASTALA	DLGASTALA	0.1845	6790.9	50.00	Sequence
DRB5_0101	94	AAAAIAVGLGAFGLG	IAVGLGAFG	0.1793	7187.0	50.00	Sequence
DRB5_0101	187	TAAVTPSTTATLTDL	VTPSTTATL	0.1788	7221.7	50.00	Sequence
DRB5_0101	62	TAEP	AHLRTAILD	0.1742	7595.7	50.00	Sequence
DRB5_0101	179	PRSAGTMGTA	PRSAGTMGT	0.1732	7677.3	50.00	Sequence
DRB5_0101	93	ASAAAIAVGLGAFGL	IAVGLGAFG	0.1719	7787.9	50.00	Sequence
DRB5_0101	186	GTAAVTPSTTATLTD	VTPSTTATL	0.1704	7909.2	50.00	Sequence
DRB5_0101	185	MGTAAVTPSTTATLT	VTPSTTATL	0.1666	8247.0	50.00	Sequence
DRB5_0101	11	LATPYALNAVSDDER	TPYALNAV	0.1638	8496.2	50.00	Sequence
DRB5_0101	60	ATTAEPPAHLRTAIL	ATTAEPPAH	0.1638	8501.3	50.00	Sequence
DRB5_0101	61	TTAEPPAHLRTAILD	AHLRTAILD	0.1630	8568.1	50.00	Sequence
DRB5_0101	188	AAVTPSTTATLTDL	VTPSTTATL	0.1623	8633.9	50.00	Sequence
DRB5_0101	12	ATPYALNAVSDDERA	TPYALNAV	0.1619	8674.8	50.00	Sequence
DRB5_0101	180	RSAGTMGTA	TMGTAAVTP	0.1608	8777.4	50.00	Sequence
DRB5_0101	183	GTMGTA	TMGTAAVTP	0.1604	8814.2	50.00	Sequence
DRB5_0101	36	PSPVAAAFN	PSPVAAAFN	0.1553	9316.0	50.00	Sequence
DRB5_0101	109	VLTRPSPPTVAEQ	LTRPSPPT	0.1546	9383.1	50.00	Sequence
DRB5_0101	182	AGTMGTA	TMGTAAVTP	0.1523	9621.4	50.00	Sequence
DRB5_0101	181	SAGTMGTA	TMGTAAVTP	0.1495	9921.9	50.00	Sequence
DRB5_0101	13	TPYALNAVSDDERAD	YALNAVSD	0.1479	10094.5	50.00	Sequence
DRB5_0101	57	VSAATTAEP	ATTAEPPAH	0.1457	10334.1	50.00	Sequence
DRB5_0101	189	AVTPSTTATLTDLGA	VTPSTTATL	0.1454	10366.5	50.00	Sequence
DRB5_0101	58	SAATTAEP	ATTAEPPAH	0.1430	10642.7	50.00	Sequence
DRB5_0101	59	AATTAEP	ATTAEPPAH	0.1429	10647.7	50.00	Sequence
DRB5_0101	115	PPPTVAEQVLTAPDV	TVAEQVLT	0.1400	10995.2	50.00	Sequence
DRB5_0101	114	SPPPTVAEQVLTAPD	TVAEQVLT	0.1394	11065.5	50.00	Sequence
DRB5_0101	23	DERADIDRRVAAAPS	DERADIDRR	0.1383	11191.9	50.00	Sequence
DRB5_0101	35	APSPVAAAFNDEVRA	PSPVAAAFN	0.1380	11233.7	50.00	Sequence
DRB5_0101	113	PSPPTVAEQVLTAP	PTVAEQVLT	0.1353	11562.1	50.00	Sequence
DRB5_0101	159	VAPPSRGTVYQMWLL	GTVYQMWLL	0.1346	11652.3	50.00	Sequence
DRB5_0101	157	NNVAPPSRGTVYQMW	NNVAPPSRG	0.1338	11757.1	50.00	Sequence
DRB5_0101	217	SPQPTGTILAEPLG	GTILAEPL	0.1313	12084.3	50.00	Sequence
DRB5_0101	14	YPALNAVSDDERADI	LNAVSDDER	0.1284	12466.2	50.00	Sequence
DRB5_0101	193	STATLTDL	TLTDL	0.1245	13003.7	50.00	Sequence
DRB5_0101	34	AAPSPVAAAFNDEV	PSPVAAAFN	0.1218	13378.7	50.00	Sequence
DRB5_0101	112	RSPPPTVAEQVLT	PTVAEQVLT	0.1212	13466.1	50.00	Sequence
DRB5_0101	22	DDERADIDRRVAAAP	DERADIDRR	0.1189	13819.2	50.00	Sequence
DRB5_0101	32	VAAAPSPVAAAFN	PSPVAAAFN	0.1178	13970.6	50.00	Sequence
DRB5_0101	15	YALNAVSDDERADID	LNAVSDDER	0.1080	15543.4	50.00	Sequence
DRB5_0101	21	SDDERADIDRRVAAA	DERADIDRR	0.1064	15818.5	50.00	Sequence
DRB5_0101	190	VTPSTTATLTDL	VTPSTTATL	0.1062	15844.0	50.00	Sequence

DRB5_0101	192	PSTTATLTDLGASTA	TLTDLGAST	0.1050	16049.6	50.00	Sequence
DRB5_0101	33	AAAPSPVAAAFNDEV	PSPVAAAFN	0.1021	16563.7	50.00	Sequence
DRB5_0101	110	LTRPSPPPPTVAEQVL	LTRPSPPTT	0.0989	17140.6	50.00	Sequence
DRB5_0101	20	VSDDERADIDRRVAA	DERADIDRR	0.0982	17280.1	50.00	Sequence
DRB5_0101	19	AVSDDERADIDRRVA	DERADIDRR	0.0963	17640.3	50.00	Sequence
DRB5_0101	17	LNAVSDDERADIDRR	DERADIDRR	0.0920	18470.4	50.00	Sequence
DRB5_0101	18	NAVSDDERADIDRRV	DERADIDRR	0.0836	20244.2	50.00	Sequence
DRB5_0101	158	NVAPP SRGTVYQMWL	RGTVYQMWL	0.0807	20886.1	50.00	Sequence
DRB5_0101	191	TPSTTATLTDLGAST	TLTDLGAST	0.0779	21513.4	50.00	Sequence
DRB5_0101	211	VEPGTGSPQPTGTIL	GTGSPQPTG	0.0750	22214.3	50.00	Sequence
DRB5_0101	212	EPGTGSPQPTGTILA	GTGSPQPTG	0.0747	22274.2	50.00	Sequence
DRB5_0101	16	ALNAVSDDERADIDR	LNAVSDDER	0.0740	22458.6	50.00	Sequence
DRB5_0101	210	TVEPGTGSPQPTGTI	GTGSPQPTG	0.0738	22488.7	50.00	Sequence
DRB5_0101	216	GSPQPTGTILAELPL	GTILAELPL	0.0727	22772.3	50.00	Sequence
DRB5_0101	213	PTGSPQPTGTILAE	GTGSPQPTG	0.0714	23097.6	50.00	Sequence
DRB5_0101	214	GTGSPQPTGTILAEL	GTGSPQPTG	0.0702	23399.4	50.00	Sequence
DRB5_0101	111	TRPSPPPPTVAEQVLT	TRPSPPTV	0.0683	23889.9	50.00	Sequence
DRB5_0101	215	TGSPQPTGTILAELP	PTGTILAEL	0.0371	33480.2	50.00	Sequence

Allele: DRB5_0101. Number of high binders 0. Number of weak binders 25. Number of peptides 218

Allele	pos	peptide	core	l-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
IAb	87	WRTAAFASAAAIAVG	AAFASAAAI	0.8678	4.2	SB	0.01	Sequence
IAb	88	RTAAFASAAAIAVGL	AAFASAAAI	0.8648	4.3	SB	0.01	Sequence
IAb	86	RWRTAAFASAAAIAV	AAFASAAAI	0.8605	4.5	SB	0.01	Sequence
IAb	89	TAAFASAAAIAVGLG	AAFASAAAI	0.8566	4.7	SB	0.01	Sequence
IAb	85	SRWRTAAFASAAAIA	AAFASAAAI	0.8228	6.8	SB	0.05	Sequence
IAb	31	RVAAAPSPVAAAFND	RVAAAPSPV	0.7981	8.9	SB	0.05	Sequence
IAb	30	RRVAAAPSPVAAAFN	RVAAAPSPV	0.7949	9.2	SB	0.05	Sequence
IAb	90	AAFASAAAIAVGLGA	AAFASAAAI	0.7898	9.7	SB	0.05	Sequence
IAb	29	DRRVAAAPSPVAAAF	RVAAAPSPV	0.7829	10.5	SB	0.10	Sequence
IAb	84	QSRWRTAAFASAAAI	AAFASAAAI	0.7804	10.8	SB	0.10	Sequence
IAb	28	IDRRVAAAPSPVAAA	RVAAAPSPV	0.7698	12.1	SB	0.10	Sequence
IAb	27	DIDRRVAAAPSPVAA	RVAAAPSPV	0.7293	18.7	SB	0.20	Sequence
IAb	32	VAAAPSPVAAAFNDE	AAAPSPVAA	0.6894	28.8	SB	0.40	Sequence
IAb	83	RQSRWRTAAFASAAA	TAAFASAAA	0.6752	33.6	SB	0.80	Sequence
IAb	26	ADIDRRVAAAPSPVA	RVAAAPSPV	0.6315	53.9	WB	1.00	Sequence
IAb	8	LLELATPYALNAVSD	LELATPYAL	0.5939	81.0	WB	2.00	Sequence
IAb	91	AFASAAAIAVGLGAF	FASAAAIAV	0.5920	82.6	WB	2.00	Sequence
IAb	184	TMGTAAVTPSTTATL	TAAVTPSTT	0.5912	83.3	WB	2.00	Sequence
IAb	9	LELATPYALNAVSD	LELATPYAL	0.5894	85.0	WB	2.00	Sequence
IAb	185	MGTAAVTPSTTATLT	TAAVTPSTT	0.5860	88.2	WB	2.00	Sequence
IAb	33	AAAPSPVAAAFNDEV	AAAPSPVAA	0.5841	90.0	WB	2.00	Sequence
IAb	82	RRQSRWRTAAFASAA	RTAAFASAA	0.5838	90.3	WB	2.00	Sequence
IAb	7	ELLELATPYALNAVS	LELATPYAL	0.5809	93.2	WB	2.00	Sequence
IAb	132	VSRPLGAGTATVVFS	SRPLGAGTA	0.5798	94.3	WB	2.00	Sequence
IAb	6	FELLELATPYALNAV	LELATPYAL	0.5755	98.8	WB	2.00	Sequence
IAb	133	SRPLGAGTATVVFS	SRPLGAGTA	0.5752	99.1	WB	2.00	Sequence
IAb	55	AVVSAATTAEPHAHL	VVSAATTAE	0.5720	102.6	WB	4.00	Sequence
IAb	54	MAVVSAATTAEPHAH	VVSAATTAE	0.5714	103.3	WB	4.00	Sequence
IAb	183	GTMGTAAVTPSTTAT	TAAVTPSTT	0.5681	107.0	WB	4.00	Sequence
IAb	131	TVSRPLGAGTATVVF	SRPLGAGTA	0.5664	109.0	WB	4.00	Sequence
IAb	56	VVSAATTAEPHAHLR	VVSAATTAE	0.5591	118.0	WB	4.00	Sequence
IAb	182	AGTMGTAAVTPSTTA	TAAVTPSTT	0.5582	119.1	WB	4.00	Sequence
IAb	130	RTVSRPLGAGTATVV	SRPLGAGTA	0.5581	119.2	WB	4.00	Sequence
IAb	53	TMAVVSAATTAEPHA	VVSAATTAE	0.5574	120.1	WB	4.00	Sequence
IAb	108	GVLTRPSPPPPTVAEQ	TRPSPPTV	0.5504	129.6	WB	4.00	Sequence
IAb	186	GTAAVTPSTTATLTD	TAAVTPSTT	0.5488	131.9	WB	4.00	Sequence
IAb	25	RADIDRRVAAAPSPV	RVAAAPSPV	0.5471	134.3	WB	4.00	Sequence
IAb	107	LGVLTRPSPPPPTVAE	TRPSPPTV	0.5315	158.9	WB	4.00	Sequence
IAb	52	ETMAVVSAATTAEPH	AVVSAATTA	0.5309	160.1	WB	4.00	Sequence
IAb	181	SAGTMGTAAVTPSTT	MGTAAVTPS	0.5232	174.0	WB	4.00	Sequence
IAb	109	VLTRPSPPPPTVAEQV	TRPSPPTV	0.5230	174.4	WB	4.00	Sequence
IAb	187	TAAVTPSTTATLTDL	TAAVTPSTT	0.5229	174.5	WB	4.00	Sequence
IAb	129	VRTVSRPLGAGTATV	SRPLGAGTA	0.5226	175.2	WB	4.00	Sequence
IAb	57	VSAATTAEPHAHLRT	ATTAEPHAH	0.4987	226.8	WB	8.00	Sequence
IAb	106	GLGVLTRPSPPPPTVA	TRPSPPTV	0.4982	228.1	WB	8.00	Sequence
IAb	110	LTRPSPPPPTVAEQVL	TRPSPPTV	0.4969	231.4	WB	8.00	Sequence
IAb	51	RETMAVVSAATTAEP	MAVVSAATT	0.4941	238.4	WB	8.00	Sequence
IAb	11	LATPYALNAVSDDER	ATPYALNAV	0.4817	272.5	WB	8.00	Sequence
IAb	128	DVRTVSRPLGAGTAT	SRPLGAGTA	0.4740	296.2	WB	8.00	Sequence
IAb	10	ELATPYALNAVSDDE	ATPYALNAV	0.4736	297.5	WB	8.00	Sequence
IAb	58	SAATTAEPHAHLRTA	ATTAEPHAH	0.4732	298.8	WB	8.00	Sequence

IAb	5	DFELLELATPYALNA	LELATPYAL	0.4667	320.7	WB	8.00	Sequence
IAb	92	FASAAAAIAVGLGAFG	FASAAAAIAV	0.4589	348.9	WB	8.00	Sequence
IAb	180	RSAGTMGTAAVTPST	MGTAAVTPS	0.4588	349.0	WB	8.00	Sequence
IAb	134	RPLGAGTATVVFSD	RPLGAGTAT	0.4547	365.1	WB	8.00	Sequence
IAb	81	VRQRWRRTAAAFASA	SRWRTAAFAS	0.4509	380.2	WB	8.00	Sequence
IAb	59	AATTAEPPIHLRTAI	ATTAEPPIAH	0.4485	390.3	WB	8.00	Sequence
IAb	50	VRETMAVSAATTAE	MAVSAATT	0.4397	429.3	WB	8.00	Sequence
IAb	198	LTDLGASTALAFVTE	TDLGASTAL	0.4361	446.2	WB	8.00	Sequence
IAb	105	FGLGLVLRPSPPPTV	TRPSPPPTV	0.4293	480.3	WB	16.00	Sequence
IAb	174	GGAKGPRASAGTMGT	GGAKGPRSA	0.4280	487.1	WB	16.00	Sequence
IAb	34	AAPSPVAAAFNDEVR	AAPSPVAAA	0.4264	496.1	WB	16.00	Sequence
IAb	127	PDVRTVSRPLGAGTA	SRPLGAGTA	0.4251	502.9		16.00	Sequence
IAb	197	TLTDLGASTALAFV	TDLGASTAL	0.4229	515.0		16.00	Sequence
IAb	60	ATTAEPPIHLRTAIL	ATTAEPPIAH	0.4217	521.9		16.00	Sequence
IAb	171	WLLGGAKGPRASAGTM	GGAKGPRSA	0.4196	533.8		16.00	Sequence
IAb	199	TDLGASTALAFVTE	TDLGASTAL	0.4194	534.9		16.00	Sequence
IAb	111	TRPSPPPTVAEQVLT	TRPSPPPTV	0.4194	535.1		16.00	Sequence
IAb	188	AAVTPSTTATLTDLG	AAVTPSTTA	0.4176	545.2		16.00	Sequence
IAb	169	QMWLLGGAKGPRASAG	QMWLLGGAK	0.4153	559.0		16.00	Sequence
IAb	179	PRSAGTMGTAAVTPS	MGTAAVTPS	0.4143	565.5		16.00	Sequence
IAb	12	ATPYALNAVSDDERA	ATPYALNAV	0.4091	597.6		16.00	Sequence
IAb	173	LGGAKGPRASAGTMGT	GGAKGPRSA	0.4081	604.4		16.00	Sequence
IAb	168	YQMWLLGGAKGPRSA	WLLGGAKGP	0.3967	683.8		16.00	Sequence
IAb	196	ATLTDLGASTALAFV	TDLGASTAL	0.3909	727.7		16.00	Sequence
IAb	153	LLVMNNVAPPSPRGTV	LVMNNVAPP	0.3904	731.8		16.00	Sequence
IAb	4	TDFELLELATPYALN	LELATPYAL	0.3895	738.7		16.00	Sequence
IAb	172	LLGGAKGPRASAGTMG	GGAKGPRSA	0.3890	743.5		16.00	Sequence
IAb	177	KGPRASAGTMGTAAVT	KGPRASAGTM	0.3875	755.2		16.00	Sequence
IAb	49	AVRETMAVSAATTA	MAVSAATT	0.3800	819.3		16.00	Sequence
IAb	170	MWLLGGAKGPRASAGT	GGAKGPRSA	0.3767	849.1		16.00	Sequence
IAb	176	AKGPRASAGTMGTAAV	KGPRASAGTM	0.3738	875.7		16.00	Sequence
IAb	152	GLLVMNNVAPPSPRG	LVMNNVAPP	0.3689	923.5		16.00	Sequence
IAb	178	GPRASAGTMGTAAVTP	AGTMGTAAV	0.3638	976.0		16.00	Sequence
IAb	205	TALAFVTEPGTGSPQ	TALAFVTEP	0.3633	981.3		16.00	Sequence
IAb	3	HTDFELLELATPYAL	LELATPYAL	0.3618	997.6		16.00	Sequence
IAb	204	STALAFVTEPGTGSP	FTVEPGTGS	0.3569	1051.2		16.00	Sequence
IAb	200	DLGASTALAFVTEPG	DLGASTALA	0.3567	1053.9		16.00	Sequence
IAb	211	VEPGTGSPQPTGTIL	PGTGSPQPT	0.3525	1103.2		16.00	Sequence
IAb	175	GAKGPRASAGTMGTAA	KGPRASAGTM	0.3496	1138.6		16.00	Sequence
IAb	195	TATLTDLGASTALAF	TDLGASTAL	0.3485	1151.7		16.00	Sequence
IAb	210	TVEPGTGSPQPTGTI	PGTGSPQPT	0.3468	1172.9		16.00	Sequence
IAb	104	AFGLGLVLRPSPPPTV	LTRPSPPPTV	0.3460	1183.9		32.00	Sequence
IAb	203	ASTALAFVTEPGTGS	TALAFVTEP	0.3457	1187.4		32.00	Sequence
IAb	151	TGLLVMNNVAPPSPRG	LVMNNVAPP	0.3453	1192.4		32.00	Sequence
IAb	154	LVMNNVAPPSPRGTVY	LVMNNVAPP	0.3426	1228.2		32.00	Sequence
IAb	167	VYQMWLLGGAKGPRSA	QMWLLGGAK	0.3415	1241.9		32.00	Sequence
IAb	212	EPGTGSPQPTGTILA	PGTGSPQPT	0.3351	1332.1		32.00	Sequence
IAb	121	EQVLTAPDVRTVSRP	QVLTAPDVR	0.3330	1362.3		32.00	Sequence
IAb	80	EVRRQRWRRTAAAFAS	SRWRTAAFAS	0.3314	1386.1		32.00	Sequence
IAb	201	LGASTALAFVTEPGT	LGASTALAF	0.3293	1417.0		32.00	Sequence
IAb	48	RAVRETMAVSAATT	MAVSAATT	0.3292	1419.7		32.00	Sequence
IAb	209	FTVEPGTGSPQPTGT	PGTGSPQPT	0.3288	1425.4		32.00	Sequence
IAb	24	ERADIDRRVAAAPSP	RRVAAAPSP	0.3284	1431.2		32.00	Sequence
IAb	213	PGTGSPQPTGTILAE	PGTGSPQPT	0.3280	1438.0		32.00	Sequence
IAb	189	AVTPSTTATLTDLGA	AVTPSTTAT	0.3246	1491.1		32.00	Sequence
IAb	119	VAEQVLTAPDVRTVS	QVLTAPDVR	0.3239	1502.3		32.00	Sequence
IAb	120	AEQVLTAPDVRTVSR	QVLTAPDVR	0.3235	1509.1		32.00	Sequence
IAb	122	QVLTAPDVRTVSRPL	QVLTAPDVR	0.3113	1722.0		32.00	Sequence
IAb	208	AFTVEPGTGSPQPTG	PGTGSPQPT	0.3099	1749.6		32.00	Sequence
IAb	102	LGAFGLGLVLRPSPP	GAFGLGLVLT	0.3066	1811.6		32.00	Sequence
IAb	13	TPYALNAVSDDERAD	TPYALNAV	0.3059	1826.1		32.00	Sequence
IAb	103	GAFGLGLVLRPSPPP	GAFGLGLVLT	0.3045	1854.7		32.00	Sequence
IAb	207	LAFTVEPGTGSPQPT	VEPGTGSPQ	0.3038	1869.2		32.00	Sequence
IAb	47	VRVRETMAVSAATT	RAVRETMAV	0.3034	1875.4		32.00	Sequence
IAb	135	PLGAGTATVVFSDR	PLGAGTATV	0.3033	1877.8		32.00	Sequence
IAb	126	APDVRTVSRPLGAGT	RTVSRPLGA	0.3033	1878.6		32.00	Sequence
IAb	166	TVYQMWLLGGAKGPR	QMWLLGGAK	0.3030	1884.0		32.00	Sequence
IAb	206	ALAFVTEPGTGSPQP	FTVEPGTGS	0.3030	1884.7		32.00	Sequence
IAb	165	GTVYQMWLLGGAKGP	QMWLLGGAK	0.3023	1897.8		32.00	Sequence
IAb	202	GASTALAFVTEPGTG	TALAFVTEP	0.3022	1900.4		32.00	Sequence
IAb	118	TVAEQVLTAPDVRTV	QVLTAPDVR	0.3013	1918.9		32.00	Sequence
IAb	36	PSPVAAAFNDEVRVAV	PSPVAAAFN	0.2979	1991.2		32.00	Sequence
IAb	150	NTGLLVMNNVAPPSP	LVMNNVAPP	0.2960	2031.8		32.00	Sequence
IAb	35	APSPVAAAFNDEVRA	PSPVAAAFN	0.2886	2203.2		32.00	Sequence
IAb	71	TAILDATKPEVRRQS	AILDATKPE	0.2872	2234.9		32.00	Sequence
IAb	46	EVRAVRETMAVVSAA	RAVRETMAV	0.2848	2294.5		32.00	Sequence
IAb	112	RPSPPPTVAEQVLT	RPSPPPTVA	0.2841	2310.8		32.00	Sequence

IAb	61	TTAEPHAHLRTAILD	TTAEPHAHL	0.2800	2416.5	32.00	Sequence
IAb	100	VGLGAFGLGVLTRPS	GAFGLGVLT	0.2780	2469.0	32.00	Sequence
IAb	99	AVGLGAFGLGVLTRP	GAFGLGVLT	0.2761	2519.7	32.00	Sequence
IAb	70	RTAILDATKPEVRRQ	AILDATKPE	0.2757	2531.3	32.00	Sequence
IAb	101	GLGAFGLGVLTRPSP	GAFGLGVLT	0.2727	2614.1	32.00	Sequence
IAb	155	VMNNVAPPSRGTVYQ	MNNVAPPSR	0.2721	2631.7	32.00	Sequence
IAb	69	LRTAILDATKPEVRR	AILDATKPE	0.2701	2690.3	32.00	Sequence
IAb	194	TTATLTDLGASTALA	TDLGASTAL	0.2635	2889.1	32.00	Sequence
IAb	37	SPVAAAFNDEVRAVR	SPVAAAFND	0.2595	3018.3	32.00	Sequence
IAb	215	TGSPQPTGTILAELP	GSPQPTGTI	0.2540	3202.5	32.00	Sequence
IAb	79	PEVRRQSRWRTAafa	SRWRTAafa	0.2537	3210.9	32.00	Sequence
IAb	124	LTAPDVRTVSRPLGA	RTVSRPLGA	0.2519	3276.5	32.00	Sequence
IAb	214	GTGSPQPTGTILAEL	GSPQPTGTI	0.2513	3298.5	32.00	Sequence
IAb	68	HLRTAILDATKPEVR	AILDATKPE	0.2507	3319.2	32.00	Sequence
IAb	45	DEVRAVRETMAVVS	RAVRETMAV	0.2504	3327.7	32.00	Sequence
IAb	125	TAPDVRTVSRPLGAG	RTVSRPLGA	0.2502	3335.7	32.00	Sequence
IAb	72	AILDATKPEVRRQSR	AILDATKPE	0.2433	3596.1	50.00	Sequence
IAb	156	MNNVAPPSRGTVYQM	MNNVAPPSR	0.2412	3676.6	50.00	Sequence
IAb	190	VTPSTTATLTDLGAS	VTPSTTATL	0.2390	3764.8	50.00	Sequence
IAb	67	AHLRTAILDATKPEV	AILDATKPE	0.2389	3771.6	50.00	Sequence
IAb	117	PTVAEQVLTAPDVR	QVLTAPDVR	0.2338	3983.9	50.00	Sequence
IAb	149	RNTGLLVMNNVAPPS	LVMNNVAPP	0.2300	4150.5	50.00	Sequence
IAb	93	ASAAAIAVGLGAFGL	ASAAAIAVG	0.2271	4284.0	50.00	Sequence
IAb	66	PAHLRTAILDATKPE	LRTAILDAT	0.2232	4467.2	50.00	Sequence
IAb	164	RGTVYQMWLLGGAKG	YQMWLLGGA	0.2209	4581.5	50.00	Sequence
IAb	98	IAVGLGAFGLGVLTR	GAFGLGVLT	0.2207	4588.7	50.00	Sequence
IAb	14	PYALNAVSDDERADI	PYALNAVSD	0.2173	4764.8	50.00	Sequence
IAb	97	AIAGVGLGAFGLGVLT	GAFGLGVLT	0.2166	4798.3	50.00	Sequence
IAb	116	PPTVAEQVLTAPDVR	QVLTAPDVR	0.2165	4804.9	50.00	Sequence
IAb	216	GSPQPTGTILAELPL	GSPQPTGTI	0.2158	4839.2	50.00	Sequence
IAb	96	AAIAVGLGAFGLGVL	AAIAVGLGA	0.2110	5100.5	50.00	Sequence
IAb	163	SRGTVYQMWLLGGAK	YQMWLLGGA	0.2101	5151.1	50.00	Sequence
IAb	65	PPAHLRTAILDATKP	LRTAILDAT	0.2061	5374.4	50.00	Sequence
IAb	38	PVAAAFNDEVRAVRE	VAAAFNDEV	0.2055	5409.4	50.00	Sequence
IAb	44	NDEVRAVRETMAVVS	RAVRETMAV	0.2055	5412.6	50.00	Sequence
IAb	94	SAAAIAVGLGAFGLG	SAAAIAVGL	0.2021	5615.4	50.00	Sequence
IAb	136	LGAGTATVVF SRDRN	LGAGTATVV	0.2014	5657.0	50.00	Sequence
IAb	95	AAIAVGLGAFGLGV	AAIAVGLGA	0.2000	5742.2	50.00	Sequence
IAb	63	AEPHAHLRTAILDAT	EPPAHLRTA	0.1991	5799.0	50.00	Sequence
IAb	39	VAAAFNDEVRAVRET	VAAAFNDEV	0.1987	5826.5	50.00	Sequence
IAb	64	EPPAHLRTAILDATK	AHLRTAILD	0.1985	5835.4	50.00	Sequence
IAb	157	NNVAPPSRGTVYQMW	NNVAPPSRG	0.1976	5892.2	50.00	Sequence
IAb	123	VLTA PDVRTVSRPLG	VLTA PDVRT	0.1973	5912.5	50.00	Sequence
IAb	113	PSPPPTVAEQVLTAP	PSPPPTVAE	0.1937	6149.6	50.00	Sequence
IAb	40	AAAFNDEVRAVRETM	AAFNDEVRA	0.1857	6702.9	50.00	Sequence
IAb	115	PPPTVAEQVLTAPDV	TVAEQVLT	0.1804	7102.0	50.00	Sequence
IAb	217	SPQPTGTILAELPLG	PQPTGTILA	0.1785	7249.7	50.00	Sequence
IAb	193	STTATLTDLGASTAL	TDLGASTAL	0.1775	7325.7	50.00	Sequence
IAb	23	DERADIDRRVAAAPS	DRRVAAAPS	0.1765	7409.0	50.00	Sequence
IAb	43	FNDEVRAVRETMAVV	VRAVRETM	0.1740	7606.4	50.00	Sequence
IAb	148	DRNTGLLVMNNVAPP	LVMNNVAPP	0.1605	8810.1	50.00	Sequence
IAb	62	TAEPHAHLRTAILDA	EPPAHLRTA	0.1603	8824.9	50.00	Sequence
IAb	114	SPPPTVAEQVLTAPD	TVAEQVLT	0.1540	9444.3	50.00	Sequence
IAb	42	AFNDEVRAVRETM	VRAVRETM	0.1532	9534.9	50.00	Sequence
IAb	158	NVAPPSRGTVYQMWL	NVAPPSRG	0.1504	9825.5	50.00	Sequence
IAb	192	PSTTATLTDLGASTA	LTDLGASTA	0.1501	9854.2	50.00	Sequence
IAb	162	PSRGTVYQMWLLGGA	YQMWLLGGA	0.1489	9987.3	50.00	Sequence
IAb	191	TPSTTATLTDLGAST	TPSTTATLT	0.1344	11683.9	50.00	Sequence
IAb	78	KPEVRRQSRWRTAaf	QSRWRTAaf	0.1282	12492.4	50.00	Sequence
IAb	159	VAPPSRGTVYQMWLL	VAPPSRGTV	0.1277	12562.0	50.00	Sequence
IAb	15	YALNAVSDDERADID	YALNAVSD	0.1242	13038.7	50.00	Sequence
IAb	41	AAFNDEVRAVRETM	VRAVRETM	0.1223	13318.9	50.00	Sequence
IAb	2	EHTDFELLELATPYA	FELLELATP	0.1218	13383.4	50.00	Sequence
IAb	73	ILDATKPEVRRQSRW	LDATKPEVR	0.1199	13662.8	50.00	Sequence
IAb	147	RDRNTGLLVMNNVAP	LLVMNNVAP	0.1160	14256.0	50.00	Sequence
IAb	142	TVVFSRDRNTGLLVM	VVFSRDRNT	0.1152	14369.8	50.00	Sequence
IAb	141	ATVVFSRDRNTGLLV	VVFSRDRNT	0.1120	14879.1	50.00	Sequence
IAb	140	TATVVFSRDRNTGLL	VVFSRDRNT	0.1052	16014.1	50.00	Sequence
IAb	137	GAGTATVVFSRDRNT	VVFSRDRNT	0.1050	16062.2	50.00	Sequence
IAb	138	AGTATVVFSRDRNTG	VVFSRDRNT	0.1022	16540.4	50.00	Sequence
IAb	160	APPSRGTVYQMWLLG	APPSRGTVY	0.0986	17212.7	50.00	Sequence
IAb	143	VVFSRDRNTGLLVMN	VVFSRDRNT	0.0973	17442.7	50.00	Sequence
IAb	139	GTATVVFSRDRNTGL	VVFSRDRNT	0.0962	17661.9	50.00	Sequence
IAb	146	SRRNTGLLVMNNVA	RDRNTGLLV	0.0958	17732.4	50.00	Sequence
IAb	22	DDERADIDRRVAAAP	IDRRVAAAP	0.0914	18588.9	50.00	Sequence
IAb	145	FSRDRNTGLLVMNNV	RDRNTGLLV	0.0909	18693.4	50.00	Sequence
IAb	74	LDATKPEVRRQSRWR	LDATKPEVR	0.0901	18854.9	50.00	Sequence

IAb	161	PPSRGTVYQMWLLGG	GTVYQMWLL	0.0900	18879.8	50.00	Sequence
IAb	77	TKPEVRRQSRWRATA	VRRQSRWRT	0.0886	19178.9	50.00	Sequence
IAb	144	VFSRDRNTGLLVMMN	RDRNTGLLV	0.0879	19324.7	50.00	Sequence
IAb	1	TEHTDFELLELATPY	FELLELATP	0.0778	21540.4	50.00	Sequence
IAb	0	MTEHTDFELLELATP	FELLELATP	0.0723	22869.8	50.00	Sequence
IAb	76	ATKPEVRRQSRWRATA	VRRQSRWRT	0.0664	24383.4	50.00	Sequence
IAb	75	DATKPEVRRQSRWRATA	VRRQSRWRT	0.0445	30878.0	50.00	Sequence
IAb	21	SDDERADIDRRVAAA	DIDRRVAAA	0.0223	39276.4	50.00	Sequence
IAb	16	ALNAVSDDERADIDR	AVSDDERAD	0.0221	39357.2	50.00	Sequence
IAb	17	LNAVSDDERADIDRR	LNAVSDDER	0.0199	40316.2	50.00	Sequence
IAb	18	NAVSDDERADIDRRV	NAVSDDERA	0.0178	41257.0	50.00	Sequence
IAb	19	AVSDDERADIDRRVA	AVSDDERAD	0.0155	42263.6	50.00	Sequence
IAb	20	VSDDERADIDRRVAA	ERADIDRRV	0.0133	43302.8	50.00	Sequence

Allele: IAb. Number of high binders 14. Number of weak binders 48. Number of peptides 218

Allele	pos	peptide	core	l-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
IAd	48	RAVRETMVVSAATT	RETMVVSA	0.7263	19.3	SB	0.01	Sequence
IAd	49	AVRETMVVSAATTA	RETMVVSA	0.7202	20.6	SB	0.01	Sequence
IAd	47	VRAVRETMVVSAAT	RETMVVSA	0.6851	30.2	SB	0.01	Sequence
IAd	50	VRETMVVSAATTAET	RETMVVSA	0.6758	33.4	SB	0.01	Sequence
IAd	46	EVRAVRETMVVSA	RETMVVSA	0.6696	35.7	SB	0.01	Sequence
IAd	51	RETMVVSAATTAEP	RETMVVSA	0.6135	65.5	WB	0.05	Sequence
IAd	45	DEVRAVRETMVVSA	RETMVVSA	0.5602	116.6	WB	0.15	Sequence
IAd	87	WRTAAFASAAAIAV	WRTAAFASA	0.4970	231.1	WB	0.80	Sequence
IAd	86	RWRTAAFASAAAIAV	WRTAAFASA	0.4716	303.9	WB	0.80	Sequence
IAd	82	RRQSRWRTAAFASAA	WRTAAFASA	0.4620	337.4	WB	1.00	Sequence
IAd	179	PRSAGTMGTAAVTPS	RSAGTMGTA	0.4613	340.0	WB	1.00	Sequence
IAd	89	TAAFASAAAIAVGLG	FASAAAIAV	0.4568	356.7	WB	1.00	Sequence
IAd	90	AAFASAAAIAVGLGA	FASAAAIAV	0.4551	363.5	WB	1.00	Sequence
IAd	84	QSRWRTAAFASAAAIA	WRTAAFASA	0.4547	365.0	WB	1.00	Sequence
IAd	81	VRRQSRWRTAAFASAA	WRTAAFASA	0.4492	387.5	WB	1.00	Sequence
IAd	85	SRWRTAAFASAAAIA	WRTAAFASA	0.4430	414.3	WB	2.00	Sequence
IAd	180	RSAGTMGTAAVTPST	RSAGTMGTA	0.4406	425.3	WB	2.00	Sequence
IAd	91	AFASAAAIAVGLGAF	FASAAAIAV	0.4399	428.2	WB	2.00	Sequence
IAd	83	RQSRWRTAAFASAAA	WRTAAFASA	0.4338	457.8	WB	2.00	Sequence
IAd	88	RTAAFASAAAIAVGL	FASAAAIAV	0.4275	490.1	WB	2.00	Sequence
IAd	52	ETMAVVSAATTAEP	ETMAVVSA	0.4208	526.9		2.00	Sequence
IAd	92	FASAAAIAVGLGAF	FASAAAIAV	0.4103	590.3		2.00	Sequence
IAd	178	GPRSAGTMGTAAVTP	RSAGTMGTA	0.3704	908.7		4.00	Sequence
IAd	177	KGPRSAGTMGTAAVT	PRSAGTMGT	0.3685	928.2		4.00	Sequence
IAd	174	GGAKGPRSAGTMGTA	RSAGTMGTA	0.3675	938.0		4.00	Sequence
IAd	175	GAKGPRSAGTMGTA	RSAGTMGTA	0.3670	943.3		4.00	Sequence
IAd	176	AKGPRSAGTMGTA	RSAGTMGTA	0.3656	957.0		4.00	Sequence
IAd	23	DERADIDRRVAAAPS	DRRVAAAPS	0.3106	1736.0		8.00	Sequence
IAd	44	NDEVRAVRETMVVSA	VRETMVVSA	0.3103	1740.6		8.00	Sequence
IAd	24	ERADIDRRVAAAPSP	RRVAAAPSP	0.3046	1852.3		8.00	Sequence
IAd	80	EVRRQSRWRTAAFASA	RRQSRWRTA	0.3019	1907.9		8.00	Sequence
IAd	165	GTVYQMWLLGGAKGP	YQMWLLGGA	0.3013	1919.5		8.00	Sequence
IAd	181	SAGTMGTAAVTPSTT	MGTAAVTPS	0.2992	1963.9		16.00	Sequence
IAd	164	RGTVYQMWLLGGAKG	YQMWLLGGA	0.2980	1988.3		16.00	Sequence
IAd	28	IDRRVAAAPSPVAAA	AAPSPVAAA	0.2956	2041.1		16.00	Sequence
IAd	27	DIDRRVAAAPSPVAAA	RRVAAAPSP	0.2938	2081.7		16.00	Sequence
IAd	25	RADIDRRVAAAPSPV	RADIDRRVA	0.2910	2144.7		16.00	Sequence
IAd	167	VYQMWLLGGAKGPRS	YQMWLLGGA	0.2893	2186.0		16.00	Sequence
IAd	93	ASAAAIAVGLGAFGL	AAIAVGLGA	0.2872	2236.2		16.00	Sequence
IAd	182	AGTMGTAAVTPSTTA	MGTAAVTPS	0.2857	2272.4		16.00	Sequence
IAd	166	TVYQMWLLGGAKGPR	YQMWLLGGA	0.2852	2283.7		16.00	Sequence
IAd	163	SRGTVYQMWLLGGAK	YQMWLLGGA	0.2852	2283.9		16.00	Sequence
IAd	29	DRRVAAAPSPVAAAF	RVAAAPSPV	0.2815	2377.0		16.00	Sequence
IAd	76	ATKPEVRRQSRWRATA	RRQSRWRATA	0.2806	2400.3		16.00	Sequence
IAd	168	YQMWLLGGAKGPRSA	YQMWLLGGA	0.2799	2419.8		16.00	Sequence
IAd	26	ADIDRRVAAAPSPVA	DRRVAAAPS	0.2767	2504.8		16.00	Sequence
IAd	118	TVAEQVLTAPDVRT	VLTAPDVRT	0.2755	2537.6		16.00	Sequence
IAd	183	GTMGTAAVTPSTTAT	MGTAAVTPS	0.2754	2540.4		16.00	Sequence
IAd	79	PEVRRQSRWRTAAFASA	RRQSRWRATA	0.2747	2560.3		16.00	Sequence
IAd	184	TMGTAAVTPSTTATL	MGTAAVTPS	0.2693	2713.0		16.00	Sequence
IAd	20	VSDDERADIDRRVAAA	RADIDRRVA	0.2662	2807.4		16.00	Sequence
IAd	117	PTVAEQVLTAPDVRT	VLTAPDVRT	0.2639	2877.1		16.00	Sequence
IAd	22	DDERADIDRRVAAAP	RADIDRRVA	0.2637	2883.3		16.00	Sequence
IAd	78	KPEVRRQSRWRATAAF	RRQSRWRATA	0.2634	2891.0		16.00	Sequence
IAd	162	PSRGTVYQMWLLGGA	YQMWLLGGA	0.2634	2893.5		16.00	Sequence
IAd	185	MGTAAVTPSTTATLT	MGTAAVTPS	0.2621	2934.9		16.00	Sequence

IAd	21	SDDERADIDRRVAAA	RADIDRRVA	0.2615	2951.6	16.00	Sequence
IAd	19	AVSDDERADIDRRVA	RADIDRRVA	0.2570	3098.6	16.00	Sequence
IAd	30	RRVAAAPSPVAAAAN	AAAPSPVAA	0.2567	3110.6	16.00	Sequence
IAd	65	PPAHLRTAILDATKP	LRTAILDAT	0.2548	3174.2	16.00	Sequence
IAd	53	TMAVVSAATTAEPPE	MAVSAATT	0.2524	3258.0	16.00	Sequence
IAd	195	TATLTDLDGASTALAF	ATLTDLDGAS	0.2521	3268.3	16.00	Sequence
IAd	67	AHLRTAILDATKPEV	LRTAILDAT	0.2497	3355.9	16.00	Sequence
IAd	66	PAHLRTAILDATKPE	HLRTAILDA	0.2491	3377.1	16.00	Sequence
IAd	192	PSTTATLTDLDGASTA	LTDLDGASTA	0.2480	3418.5	16.00	Sequence
IAd	77	TKPEVRRQSRWRATA	RRQSRWRATA	0.2466	3470.5	16.00	Sequence
IAd	133	SRPLGAGTATVVFSR	GTATVVFSR	0.2458	3500.9	16.00	Sequence
IAd	193	STTATLTDLDGASTAL	ATLTDLDGAS	0.2390	3765.4	32.00	Sequence
IAd	134	RPLGAGTATVVFSRD	GTATVVFSR	0.2365	3869.8	32.00	Sequence
IAd	191	TPSTTATLTDLDGAST	ATLTDLDGAS	0.2358	3899.0	32.00	Sequence
IAd	54	MAVVSAATTAEPPEAH	MAVSAATT	0.2335	3995.9	32.00	Sequence
IAd	64	EPPAHLRTAILDATK	LRTAILDAT	0.2329	4025.1	32.00	Sequence
IAd	31	RVAAAPSPVAAAANFND	AAPSPVAAA	0.2274	4271.3	32.00	Sequence
IAd	135	PLGAGTATVVFSRDR	GTATVVFSR	0.2269	4294.1	32.00	Sequence
IAd	43	FNDEVRAVRETMAVV	VRVRETMA	0.2261	4330.8	32.00	Sequence
IAd	190	VTPSTTATLTDLDGAS	ATLTDLDGAS	0.2252	4371.5	32.00	Sequence
IAd	12	ATPYALNAVSDDERA	ATPYALNAV	0.2252	4374.9	32.00	Sequence
IAd	68	HLRTAILDATKPEVR	LRTAILDAT	0.2246	4402.5	32.00	Sequence
IAd	136	LGAGTATVVFSRDRN	GTATVVFSR	0.2212	4568.2	32.00	Sequence
IAd	116	PPTVAEQVLTAPDVR	TVAEQVLT	0.2210	4573.7	32.00	Sequence
IAd	217	SPQPTGTILAEPLG	PQPTGTILA	0.2204	4607.2	32.00	Sequence
IAd	194	TTATLTDLDGASTALA	ATLTDLDGAS	0.2200	4627.1	32.00	Sequence
IAd	115	PPPTVAEQVLTAPDV	TVAEQVLT	0.2164	4809.7	32.00	Sequence
IAd	119	VAEQVLTAPDVVRTVS	VLTAPDVRT	0.2152	4872.7	32.00	Sequence
IAd	94	SAAAIAVGLGAFGLG	AAAVGLG	0.2151	4875.2	32.00	Sequence
IAd	196	ATLTDLDGASTALAF	ATLTDLDGAS	0.2147	4901.2	32.00	Sequence
IAd	63	AEPHAHLRTAILDAT	LRTAILDAT	0.2106	5121.4	32.00	Sequence
IAd	11	LATPYALNAVSDDER	ATPYALNAV	0.2058	5395.2	32.00	Sequence
IAd	201	LGASTALAFVTEPGT	ASTALAFV	0.2030	5560.0	32.00	Sequence
IAd	42	AFNDEVRAVRETMAV	VRVRETMA	0.2018	5633.0	32.00	Sequence
IAd	128	DVRTVSRPLGAGTAT	SRPLGAGTA	0.2013	5661.7	32.00	Sequence
IAd	18	NAVSDDERADIDRRV	ERADIDRRV	0.2011	5678.5	32.00	Sequence
IAd	137	GAGTATVVFSRDRNT	GTATVVFSR	0.2000	5745.3	32.00	Sequence
IAd	198	LTDLDGASTALAFVTE	ASTALAFV	0.1995	5776.5	32.00	Sequence
IAd	120	AEQVLTAPDVVRTVS	VLTAPDVRT	0.1994	5782.9	32.00	Sequence
IAd	200	DLGASTALAFVTEPG	ASTALAFV	0.1963	5976.9	32.00	Sequence
IAd	197	TLTDLGASTALAFVTE	ASTALAFV	0.1962	5987.7	32.00	Sequence
IAd	216	GSPQPTGTILAEPL	PQPTGTILA	0.1927	6212.5	32.00	Sequence
IAd	6	FELLELATPYALNAV	LELATPYAL	0.1912	6314.0	32.00	Sequence
IAd	121	EQVLTAPDVVRTVSRP	VLTAPDVRT	0.1887	6488.5	32.00	Sequence
IAd	127	PDVRTVSRPLGAGTA	RTVSRPLGA	0.1874	6579.3	32.00	Sequence
IAd	8	LLELATPYALNAVSD	LELATPYAL	0.1866	6636.5	32.00	Sequence
IAd	173	LGGAKGPRASAGTMGT	PRASAGTMGT	0.1865	6643.3	32.00	Sequence
IAd	130	RTVSRPLGAGTATVV	SRPLGAGTA	0.1859	6691.2	32.00	Sequence
IAd	75	DATKPEVRRQSRWR	VRRQSRWR	0.1858	6695.6	32.00	Sequence
IAd	7	ELLELATPYALNAV	LELATPYAL	0.1855	6716.2	32.00	Sequence
IAd	132	VSRPLGAGTATVVFS	AGTATVVFS	0.1854	6728.1	32.00	Sequence
IAd	32	VAAAPSPVAAAANFND	AAPSPVAAA	0.1840	6831.6	32.00	Sequence
IAd	129	VRTVSRPLGAGTATV	SRPLGAGTA	0.1833	6877.8	32.00	Sequence
IAd	199	TDLGASTALAFVTEP	ASTALAFV	0.1825	6938.2	32.00	Sequence
IAd	9	LELATPYALNAVSD	LELATPYAL	0.1803	7110.5	32.00	Sequence
IAd	138	AGTATVVFSRDRNTG	GTATVVFSR	0.1798	7148.5	32.00	Sequence
IAd	55	AVVSAATTAEPPEAHL	AVVSAATTA	0.1795	7173.1	32.00	Sequence
IAd	69	LRTAILDATKPEVRR	LRTAILDAT	0.1753	7506.5	50.00	Sequence
IAd	95	AAAVGLGAFGLGV	AAAVGLGA	0.1742	7592.3	50.00	Sequence
IAd	17	LNAVSDDERADIDRR	DERADIDRR	0.1742	7593.3	50.00	Sequence
IAd	10	ELATPYALNAVSDDE	ATPYALNAV	0.1725	7733.5	50.00	Sequence
IAd	114	SPPPTVAEQVLTAPD	TVAEQVLT	0.1696	7980.1	50.00	Sequence
IAd	58	SAATTAEPPEAHLRTA	AATTAEPPE	0.1657	8326.1	50.00	Sequence
IAd	41	AAFNDEVRAVRETMA	VRVRETMA	0.1641	8473.9	50.00	Sequence
IAd	57	VSAATTAEPPEAHLRT	AATTAEPPE	0.1616	8702.9	50.00	Sequence
IAd	33	AAAPSPVAAAANFND	AAPSPVAAA	0.1596	8890.1	50.00	Sequence
IAd	145	FSRDRNTGLLVMNNV	RDRNTGLLV	0.1584	9008.5	50.00	Sequence
IAd	131	TVSRPLGAGTATVV	SRPLGAGTA	0.1567	9180.7	50.00	Sequence
IAd	202	GASTALAFVTEPGTGS	ASTALAFV	0.1544	9407.3	50.00	Sequence
IAd	56	VVSAATTAEPPEAHLR	AATTAEPPE	0.1537	9479.1	50.00	Sequence
IAd	215	TGSPQPTGTILAEPL	PQPTGTILA	0.1534	9510.9	50.00	Sequence
IAd	189	AVTPSTTATLTDLDGA	TATLTDLDGA	0.1491	9957.9	50.00	Sequence
IAd	203	ASTALAFVTEPGTGS	ASTALAFV	0.1474	10143.0	50.00	Sequence
IAd	214	GTGSPQPTGTILAEPL	PQPTGTILA	0.1446	10461.0	50.00	Sequence
IAd	113	PSPPPTVAEQVLTAP	TVAEQVLT	0.1429	10656.9	50.00	Sequence
IAd	146	SRDRNTGLLVMNNVA	RDRNTGLLV	0.1423	10727.9	50.00	Sequence
IAd	213	PGTGSPQPTGTILAE	PQPTGTILA	0.1421	10741.1	50.00	Sequence

IAd	13	TPYALNAVSDDERAD	PYALNAVSD	0.1420	10757.2	50.00	Sequence
IAd	3	HTDFELLELATPYAL	LLELATPYA	0.1398	11013.8	50.00	Sequence
IAd	5	DFELLELATPYALNA	FELLELATP	0.1379	11245.0	50.00	Sequence
IAd	150	NTGLLVMMNNVAPPSR	TGLLVMMNNV	0.1360	11474.4	50.00	Sequence
IAd	147	RDRNTGLLVMMNNVAP	RDRNTGLLV	0.1316	12044.3	50.00	Sequence
IAd	151	TGLLVMMNNVAPPSRG	TGLLVMMNNV	0.1314	12058.8	50.00	Sequence
IAd	101	QLGAFGLGVLTRPSL	AFGLGVLTR	0.1302	12221.3	50.00	Sequence
IAd	122	VLTPADVVRTVSRPL	VLTPADVVRT	0.1279	12534.4	50.00	Sequence
IAd	186	GTAAVTPSTTATLTD	GTAAVTPST	0.1277	12561.8	50.00	Sequence
IAd	62	TAEPPAHLRTAILDA	HLRTAILDA	0.1274	12594.1	50.00	Sequence
IAd	126	APDVRTVSRPLGAGT	VRTVSRPLG	0.1273	12606.1	50.00	Sequence
IAd	14	PYALNAVSDDERADI	PYALNAVSD	0.1271	12641.6	50.00	Sequence
IAd	102	LGAFFGLGVLTRPSP	FGLGVLTRP	0.1257	12826.3	50.00	Sequence
IAd	96	AAIAVGLGAFGLGV	AAIAVGLGA	0.1254	12877.9	50.00	Sequence
IAd	70	RTAILDATKPEVRRQ	ATKPEVRRQ	0.1252	12906.2	50.00	Sequence
IAd	100	VGLGAFGLGVLTRPS	AFGLGVLTR	0.1244	13013.1	50.00	Sequence
IAd	34	AAPSPVAAAFAFDEV	AAPSPVAAA	0.1234	13162.1	50.00	Sequence
IAd	59	AATTAEPHAHLRTAI	AATTAEPPI	0.1232	13187.4	50.00	Sequence
IAd	15	YALNAVSDDERADID	NAVSDDERA	0.1223	13320.2	50.00	Sequence
IAd	149	RNTGLLVMMNNVAPPS	VMNNVAPPS	0.1200	13655.4	50.00	Sequence
IAd	123	VLTPADVVRTVSRPLG	VLTPADVVRT	0.1188	13830.0	50.00	Sequence
IAd	187	TAAVTPSTTATLTDL	AAVTPSTTA	0.1187	13837.5	50.00	Sequence
IAd	4	TDFELLELATPYALN	LLELATPYA	0.1175	14030.0	50.00	Sequence
IAd	2	EHTDFELLELATPYA	LLELATPYA	0.1168	14125.8	50.00	Sequence
IAd	148	DRNTGLLVMMNNVAPP	TGLLVMMNNV	0.1158	14281.2	50.00	Sequence
IAd	161	PPSRGTVYQMWLLGG	VYQMWLLGG	0.1147	14449.5	50.00	Sequence
IAd	188	AAVTPSTTATLTDLG	AAVTPSTTA	0.1146	14464.8	50.00	Sequence
IAd	112	RPSPPTVAEQVLT	TVAEQVLT	0.1143	14514.0	50.00	Sequence
IAd	40	AAAFNDEVRAVRETM	AAFNDEVRA	0.1142	14525.2	50.00	Sequence
IAd	139	GTATVVFSDRNTGL	GTATVVFSD	0.1128	14749.6	50.00	Sequence
IAd	99	AVGLGAFGLGVLTRP	AFGLGVLTR	0.1099	15217.0	50.00	Sequence
IAd	169	QMWLLGGAKGPRSAG	QMWLLGGAK	0.1096	15276.8	50.00	Sequence
IAd	16	ALNAVSDDERADIDR	NAVSDDERA	0.1074	15637.6	50.00	Sequence
IAd	125	TAPDVRTVSRPLGAG	APDVRTVSR	0.1074	15643.7	50.00	Sequence
IAd	103	GAFGLGVLTRPSPPP	FGLGVLTRP	0.1052	16015.3	50.00	Sequence
IAd	39	VAAAFNDEVRAVRET	AAFNDEVRA	0.1014	16688.2	50.00	Sequence
IAd	38	PVAAAFNDEVRAVRE	AAFNDEVRA	0.0994	17048.7	50.00	Sequence
IAd	104	AFGLGVLTRPSPPTT	FGLGVLTRP	0.0969	17529.6	50.00	Sequence
IAd	212	EPGTGSPQPTGTILA	PQPTGTILA	0.0958	17736.8	50.00	Sequence
IAd	144	VFSRDRNTGLLVMMN	RNTGLLVMMN	0.0947	17955.3	50.00	Sequence
IAd	143	VVFSRDRNTGLLVMMN	RNTGLLVMMN	0.0943	18022.9	50.00	Sequence
IAd	36	PSPVAAAFNDEVRAV	AAFNDEVRA	0.0941	18067.0	50.00	Sequence
IAd	124	LTAPDVRTVSRPLGA	LTAPDVRTV	0.0919	18498.2	50.00	Sequence
IAd	35	APSPVAAAFNDEVRA	AAFNDEVRA	0.0910	18674.6	50.00	Sequence
IAd	37	SPVAAAFNDEVRAVR	AAFNDEVRA	0.0889	19103.8	50.00	Sequence
IAd	160	APPSRGTVYQMWLLG	PSRGTVYQM	0.0842	20108.4	50.00	Sequence
IAd	159	VAPPSRGTVYQMWLL	PSRGTVYQM	0.0823	20523.4	50.00	Sequence
IAd	71	TAILDATKPEVRRQS	ATKPEVRRQ	0.0804	20960.6	50.00	Sequence
IAd	98	IAVGLGAFGLGVLTR	AFGLGVLTR	0.0801	21028.5	50.00	Sequence
IAd	0	MTEHTDFELLELATP	MTEHTDFEL	0.0798	21085.5	50.00	Sequence
IAd	74	LDATKPEVRRQSRWR	ATKPEVRRQ	0.0786	21361.0	50.00	Sequence
IAd	152	GLLVMMNNVAPPSRGT	GLLVMMNNVA	0.0778	21551.4	50.00	Sequence
IAd	61	TTAEPHAHLRTAILD	AHLRTAILD	0.0773	21670.9	50.00	Sequence
IAd	153	LLVMNNVAPPSRGTV	VMNNVAPPS	0.0762	21920.6	50.00	Sequence
IAd	97	AIAGVGLGAFGLGVLT	AIAGVGLGAF	0.0742	22395.5	50.00	Sequence
IAd	60	ATTAEPHAHLRTAIL	EPPAHLRTA	0.0740	22463.0	50.00	Sequence
IAd	156	MNNVAPPSRGTVYQM	PSRGTVYQM	0.0740	22463.7	50.00	Sequence
IAd	204	STALAFVTEPGTGSP	ALAFVTEPG	0.0712	23151.7	50.00	Sequence
IAd	158	NVAPPSRGTVYQMWL	PSRGTVYQM	0.0706	23292.1	50.00	Sequence
IAd	142	TVVFSRDRNTGLLVMM	DRNTGLLVMM	0.0697	23528.7	50.00	Sequence
IAd	1	TEHTDFELLELATPY	FELLELATP	0.0690	23711.4	50.00	Sequence
IAd	73	ILDATKPEVRRQSRW	ATKPEVRRQ	0.0658	24544.1	50.00	Sequence
IAd	157	NNVAPPSRGTVYQMW	PSRGTVYQM	0.0653	24674.6	50.00	Sequence
IAd	105	FGLGVLTRPSPPTTV	FGLGVLTRP	0.0644	24913.0	50.00	Sequence
IAd	205	TALAFVTEPGTGSPQ	ALAFVTEPG	0.0635	25147.9	50.00	Sequence
IAd	72	AILDATKPEVRRQSR	ATKPEVRRQ	0.0615	25694.9	50.00	Sequence
IAd	171	WLLGGAKGPRSAGTM	KGPRSAGTM	0.0612	25772.9	50.00	Sequence
IAd	154	LVMMNNVAPPSRGTVY	VMNNVAPPS	0.0612	25779.6	50.00	Sequence
IAd	172	LLGGAKGPRSAGTMG	KGPRSAGTM	0.0604	26003.4	50.00	Sequence
IAd	111	TRPSPPTVAEQVLT	PTVAEQVLT	0.0593	26333.5	50.00	Sequence
IAd	206	ALAFVTEPGTGSPQP	ALAFVTEPG	0.0570	26975.8	50.00	Sequence
IAd	207	LAFVTEPGTGSPQPT	PGTGSPQPT	0.0551	27543.2	50.00	Sequence
IAd	170	MWLLGGAKGPRSAGT	GAKGPRSAG	0.0544	27749.0	50.00	Sequence
IAd	110	LTRPSPPTVAEQVL	PPPTVAEQV	0.0536	27996.6	50.00	Sequence
IAd	106	GLGVLTRPSPPTTVA	GLGVLTRPS	0.0531	28162.8	50.00	Sequence
IAd	141	ATVVFSDRNTGLLV	ATVVFSDRDR	0.0514	28673.2	50.00	Sequence
IAd	109	VLTRPSPPTVAEQV	PPPTVAEQV	0.0439	31108.1	50.00	Sequence

IAd	155	VMNNVAPPSRGTVYQ	VMNNVAPPS	0.0438	31126.9	50.00	Sequence
IAd	208	AFTVEPGTGSPQPTG	PGTGSPQPT	0.0436	31185.9	50.00	Sequence
IAd	211	VEPGTGSPQPTGTIL	PGTGSPQPT	0.0401	32408.8	50.00	Sequence
IAd	209	FTVEPGTGSPQPTGT	PGTGSPQPT	0.0382	33064.8	50.00	Sequence
IAd	107	LGVLTRPSPPTVAE	LTRPSPPT	0.0360	33857.6	50.00	Sequence
IAd	140	TATVVFSRDRNTGLL	TATVVFSRD	0.0341	34590.8	50.00	Sequence
IAd	210	TVEPGTGSPQPTGTI	PGTGSPQPT	0.0319	35405.3	50.00	Sequence
IAd	108	GVLTRPSPPTVAEQ	LTRPSPPT	0.0206	40022.4	50.00	Sequence

Allele: IAd. Number of high binders 5. Number of weak binders 15. Number of peptides 218

Allele	pos	peptide	core	1-log50k(aff)	affinity(nM)	Bind Level	%Random	Identity
IAs	25	RADIDRRVAAAPSPV	RRVAAAPSP	0.4367	443.6	WB	0.40	Sequence
IAs	26	ADIDRRVAAAPSPVA	RRVAAAPSP	0.4221	519.2		0.80	Sequence
IAs	28	IDRRVAAAPSPVAAA	RRVAAAPSP	0.4085	601.5		0.80	Sequence
IAs	27	DIDRRVAAAPSPVAA	RRVAAAPSP	0.4078	606.1		0.80	Sequence
IAs	30	RRVAAAPSPVAAAFN	RRVAAAPSP	0.3982	673.0		0.80	Sequence
IAs	116	PPTVAEQVLTAPDVR	QVLTAPDVR	0.3941	703.2		0.80	Sequence
IAs	29	DRRVAAAPSPVAAAF	RRVAAAPSP	0.3866	763.0		0.80	Sequence
IAs	54	MAVVSAATTAEPPEAH	SAATTAEPP	0.3791	826.8		0.80	Sequence
IAs	117	PTVAEQVLTAPDVRT	QVLTAPDVR	0.3777	839.7		0.80	Sequence
IAs	55	AVVSAATTAEPPEAHL	SAATTAEPP	0.3718	895.2		1.00	Sequence
IAs	57	VSAATTAEPPEAHLRT	SAATTAEPP	0.3717	895.6		1.00	Sequence
IAs	56	VVSAATTAEPPEAHLR	SAATTAEPP	0.3689	924.0		1.00	Sequence
IAs	53	TMAVVSAATTAEPPEA	SAATTAEPP	0.3650	963.9		1.00	Sequence
IAs	118	TVAEQVLTAPDVRTV	QVLTAPDVR	0.3595	1022.2		2.00	Sequence
IAs	58	SAATTAEPPEAHLRRTA	SAATTAEPP	0.3572	1048.4		2.00	Sequence
IAs	119	VAEQVLTAPDVRTVS	QVLTAPDVR	0.3454	1190.9		2.00	Sequence
IAs	52	ETMAVVSAATTAEPPE	SAATTAEPP	0.3432	1220.4		2.00	Sequence
IAs	24	ERADIDRRVAAAPSP	RRVAAAPSP	0.3411	1248.0		2.00	Sequence
IAs	120	AEQVLTAPDVRTVSR	QVLTAPDVR	0.3099	1749.6		4.00	Sequence
IAs	121	EQVLTAPDVRTVSRP	QVLTAPDVR	0.2975	2000.0		4.00	Sequence
IAs	122	QVLTAPDVRTVSRPL	QVLTAPDVR	0.2776	2480.1		4.00	Sequence
IAs	68	HLRTAILDATKPEVR	LDATKPEVR	0.2749	2553.1		4.00	Sequence
IAs	31	RVAAAPSPVAAAFND	RVAAAPSPV	0.2710	2663.0		4.00	Sequence
IAs	102	LGAFGLGVLTRPSPPP	GVLTRPSPPP	0.2681	2749.1		4.00	Sequence
IAs	69	LRTAILDATKPEVRR	LDATKPEVR	0.2601	2997.9		8.00	Sequence
IAs	103	GAFGLGVLTRPSPPPP	GVLTRPSPPP	0.2573	3091.4		8.00	Sequence
IAs	104	AFGLGVLTRPSPPPP	GVLTRPSPPP	0.2461	3486.9		8.00	Sequence
IAs	105	FGLGVLTRPSPPPPTV	GVLTRPSPPP	0.2387	3779.0		8.00	Sequence
IAs	106	GLGVLTRPSPPPPTVA	GVLTRPSPPP	0.2272	4277.3		8.00	Sequence
IAs	108	GVLTRPSPPTVAEQ	GVLTRPSPPP	0.2265	4311.7		8.00	Sequence
IAs	107	LGVLTRPSPPTVAE	GVLTRPSPPP	0.2254	4363.3		8.00	Sequence
IAs	70	RTAILDATKPEVRRQ	LDATKPEVR	0.2240	4431.7		8.00	Sequence
IAs	71	TAILDATKPEVRRQS	TAILDATKP	0.2203	4612.1		8.00	Sequence
IAs	59	AATTAEPPEAHLRTAI	AATTAEPPEA	0.1980	5872.2		16.00	Sequence
IAs	72	AILDATKPEVRRQSR	LDATKPEVR	0.1961	5992.8		16.00	Sequence
IAs	217	SPQPTGTILAEPLG	TGTILAEPL	0.1949	6069.6		16.00	Sequence
IAs	73	ILDATKPEVRRQSRW	LDATKPEVR	0.1939	6134.9		16.00	Sequence
IAs	212	EPGTGSPQPTGTILA	EPGTGSPQP	0.1889	6473.5		16.00	Sequence
IAs	216	GSPQPTGTILAEPL	TGTILAEPL	0.1880	6536.4		16.00	Sequence
IAs	67	AHLRTAILDATKPEV	TAILDATKP	0.1875	6577.5		16.00	Sequence
IAs	85	SRWRTAAFASAAAIA	AFASAAAIA	0.1873	6588.2		16.00	Sequence
IAs	207	LAFTVEPGTGSPQPT	EPGTGSPQP	0.1832	6890.7		16.00	Sequence
IAs	208	AFTVEPGTGSPQPTG	EPGTGSPQP	0.1810	7050.7		16.00	Sequence
IAs	211	VEPGTGSPQPTGTIL	EPGTGSPQP	0.1804	7101.1		16.00	Sequence
IAs	86	RWRTAAFASAAAIAV	AFASAAAIA	0.1775	7329.1		16.00	Sequence
IAs	180	RSAGTMGTAAVTPST	RSAGTMGTA	0.1743	7588.3		16.00	Sequence
IAs	115	PPPTVAEQVLTAPDV	EQVLTAPDV	0.1738	7627.9		16.00	Sequence
IAs	210	TVEPGTGSPQPTGTI	EPGTGSPQP	0.1736	7642.5		16.00	Sequence
IAs	88	RTAAFASAAAIAVGL	AFASAAAIA	0.1732	7674.6		16.00	Sequence
IAs	66	PAHLRTAILDATKPE	TAILDATKP	0.1731	7684.4		16.00	Sequence
IAs	209	FTVEPGTGSPQPTGT	EPGTGSPQP	0.1724	7746.2		16.00	Sequence
IAs	184	TMGTAAVTPSTTATL	TMGTAAVTP	0.1720	7773.3		16.00	Sequence
IAs	87	WRTAAFASAAAIAV	AFASAAAIA	0.1719	7787.5		16.00	Sequence
IAs	181	SAGTMGTAAVTPSTT	TAAVTPSTT	0.1714	7823.9		16.00	Sequence
IAs	182	AGTMGTAAVTPSTTA	TAAVTPSTT	0.1700	7947.8		16.00	Sequence
IAs	183	GTMGTAAVTPSTTAT	TMGTAAVTP	0.1683	8097.6		16.00	Sequence
IAs	124	LTAPDVRTVSRPLGA	RTVSRPLGA	0.1682	8104.7		16.00	Sequence
IAs	74	LDATKPEVRRQSRWR	LDATKPEVR	0.1673	8178.3		16.00	Sequence
IAs	3	HTDFELLELATPYAL	FELLELATP	0.1663	8272.9		16.00	Sequence
IAs	4	TDFELLELATPYALN	FELLELATP	0.1643	8454.9		16.00	Sequence
IAs	206	ALAFTVEPGTGSPQP	EPGTGSPQP	0.1640	8476.1		16.00	Sequence

IAs	6	FELLELEATPYALNAV	FELLELEATP	0.1630	8569.1	16.00	Sequence
IAs	154	LVMNNVAPPSRGTVY	LVMNNVAPP	0.1601	8849.0	16.00	Sequence
IAs	5	DFELLELEATPYALNA	FELLELEATP	0.1600	8849.9	16.00	Sequence
IAs	51	RETMVAVSAATTAEP	VSAATTAEP	0.1594	8906.9	32.00	Sequence
IAs	151	TGLLVMMNNVAPPSRG	LVMNNVAPP	0.1593	8919.3	32.00	Sequence
IAs	1	TEHTDFELLELEATPY	FELLELEATP	0.1575	9100.4	32.00	Sequence
IAs	2	EHTDFELLELEATPYA	FELLELEATP	0.1564	9202.7	32.00	Sequence
IAs	152	GLLVMMNNVAPPSRGT	LVMNNVAPP	0.1554	9308.2	32.00	Sequence
IAs	153	LLVMNNVAPPSRGTV	LVMNNVAPP	0.1547	9378.4	32.00	Sequence
IAs	125	TAPDVRTVSRPLGAG	RTVSRPLGA	0.1546	9388.7	32.00	Sequence
IAs	114	SPPPTVAEQVLTAPD	PPPTVAEQV	0.1505	9814.0	32.00	Sequence
IAs	126	APDVRTVSRPLGAGT	RTVSRPLGA	0.1488	9992.3	32.00	Sequence
IAs	185	MGTAAVTPSTTATLT	TAAVTPSTT	0.1451	10401.7	32.00	Sequence
IAs	90	AAFASAAAIAVGLGA	AFASAAAIA	0.1446	10462.7	32.00	Sequence
IAs	127	PDVRTVSRPLGAGTA	RTVSRPLGA	0.1424	10707.1	32.00	Sequence
IAs	65	PPAHLRTAILDATKP	TAILDATKP	0.1417	10795.1	32.00	Sequence
IAs	84	QSRWRTAAFASAAAIA	AAFASAAAIA	0.1406	10921.7	32.00	Sequence
IAs	176	AKGPRSAGTMGTAAV	KGPRSAGTM	0.1392	11087.0	32.00	Sequence
IAs	202	GASTALAFVTEPGTG	AFTVEPGTG	0.1370	11360.2	32.00	Sequence
IAs	89	TAAFASAAAIAVGLG	AFASAAAIA	0.1360	11478.3	32.00	Sequence
IAs	101	GLGAFGLVLTTRPSP	GLGVLTRPS	0.1318	12013.6	32.00	Sequence
IAs	109	VLTRPSPPTVAEQV	VLTRPSPPP	0.1317	12021.6	32.00	Sequence
IAs	60	ATTAEPHAHLRTAIL	ATTAEPHAH	0.1316	12035.9	32.00	Sequence
IAs	171	WLLGGAKGPRSAGTM	KGPRSAGTM	0.1306	12175.6	32.00	Sequence
IAs	179	RSAGTMGTAAVTPS	RSAGTMGTA	0.1298	12281.9	32.00	Sequence
IAs	113	PSPPTVAEQVLTAP	PPPTVAEQV	0.1281	12508.2	32.00	Sequence
IAs	175	GAKGPRSAGTMGTAA	KGPRSAGTM	0.1273	12613.7	32.00	Sequence
IAs	174	GGAKGPRSAGTMGTA	KGPRSAGTM	0.1260	12794.2	32.00	Sequence
IAs	215	TGSPQPTGTILAEPL	TGTILAEPL	0.1256	12845.4	32.00	Sequence
IAs	7	ELLELEATPYALNAV	ELLELEATPY	0.1254	12869.6	32.00	Sequence
IAs	129	VRTVSRPLGAGTATV	RTVSRPLGA	0.1246	12980.2	32.00	Sequence
IAs	177	KGPRSAGTMGTAAVT	KGPRSAGTM	0.1245	12993.1	32.00	Sequence
IAs	203	ASTALAFVTEPGTGS	AFTVEPGTG	0.1245	12994.8	32.00	Sequence
IAs	205	TALAFVTEPGTGSPQ	AFTVEPGTG	0.1239	13082.3	32.00	Sequence
IAs	204	STALAFVTEPGTGSP	AFTVEPGTG	0.1228	13235.8	32.00	Sequence
IAs	112	RPSPPPTVAEQVLT	RPSPPPTVA	0.1218	13389.4	32.00	Sequence
IAs	128	DVRTVSRPLGAGTAT	RTVSRPLGA	0.1215	13431.5	32.00	Sequence
IAs	49	AVRETMVAVSAATTA	AVVSAATTA	0.1185	13867.6	32.00	Sequence
IAs	149	RNTGLLVMMNNVAPPS	LVMNNVAPP	0.1185	13876.3	32.00	Sequence
IAs	111	TRPSPPTVAEQVLT	RPSPPPTVA	0.1180	13946.4	32.00	Sequence
IAs	178	GPRSAGTMGTAAVTP	RSAGTMGTA	0.1166	14162.7	32.00	Sequence
IAs	201	LGASTALAFVTEPGT	ALAFVTEPG	0.1152	14369.0	32.00	Sequence
IAs	50	VRETMVAVSAATTA	AVVSAATTA	0.1151	14388.8	32.00	Sequence
IAs	110	LTRPSPPTVAEQVLT	RPSPPPTVA	0.1149	14417.3	32.00	Sequence
IAs	61	TTAEPHAHLRTAILD	AHLRTAILD	0.1139	14575.3	32.00	Sequence
IAs	130	RTVSRPLGAGTATVV	RTVSRPLGA	0.1130	14714.7	32.00	Sequence
IAs	172	LLGGAKGPRSAGTMG	KGPRSAGTM	0.1128	14751.0	32.00	Sequence
IAs	150	NTGLLVMMNNVAPPSR	LVMNNVAPP	0.1126	14781.9	32.00	Sequence
IAs	200	DLGASTALAFVTEPG	ALAFVTEPG	0.1122	14851.3	32.00	Sequence
IAs	100	VGLGAFGLVLTTRPS	GLGVLTRPS	0.1117	14930.1	32.00	Sequence
IAs	148	DRNTGLLVMMNNVAPP	LVMNNVAPP	0.1091	15355.2	50.00	Sequence
IAs	155	VMMNNVAPPSRGTVYQ	NNVAPPSRG	0.1066	15779.8	50.00	Sequence
IAs	91	AFASAAAIAVGLGAF	AFASAAAIA	0.1055	15962.0	50.00	Sequence
IAs	173	LGGAKGPRSAGTMGT	KGPRSAGTM	0.1046	16115.4	50.00	Sequence
IAs	23	DERADIDRRVAAAPS	DRRVAAAPS	0.1046	16127.5	50.00	Sequence
IAs	64	EPPAHLRTAILDATK	AHLRTAILD	0.1025	16501.3	50.00	Sequence
IAs	186	GTAAVTPSTTATLTD	TAAVTPSTT	0.1011	16747.0	50.00	Sequence
IAs	63	AEPHAHLRTAILDAT	AHLRTAILD	0.0986	17205.2	50.00	Sequence
IAs	93	ASAAAIAVGLGAFGL	ASAAAIAVG	0.0959	17722.0	50.00	Sequence
IAs	213	PGTGSPQPTGTILAE	PGTGSPQPT	0.0945	17990.3	50.00	Sequence
IAs	62	TAEPHAHLRTAILDA	AHLRTAILD	0.0932	18249.7	50.00	Sequence
IAs	168	YQMWLLGGAKGPRSA	GGAKGPRSA	0.0926	18349.7	50.00	Sequence
IAs	48	RAVRETMVAVSAATT	MAVVSAATT	0.0913	18626.2	50.00	Sequence
IAs	123	VTAPDVRTVSRPLG	PDVRTVSRP	0.0911	18651.6	50.00	Sequence
IAs	188	AAVTPSTTATLTDLG	TTATLTDLG	0.0904	18795.0	50.00	Sequence
IAs	170	MWLLGGAKGPRSAGT	GGAKGPRSA	0.0891	19061.6	50.00	Sequence
IAs	166	TVYQMWLLGGAKGPR	LLGGAKGPR	0.0882	19253.0	50.00	Sequence
IAs	163	SRGTVYQMWLLGGAK	SRGTVYQMW	0.0879	19309.5	50.00	Sequence
IAs	92	FASAAAIAVGLGAFG	SAAAIAVGL	0.0860	19714.0	50.00	Sequence
IAs	189	AVTPSTTATLTDLGA	TTATLTDLG	0.0851	19910.8	50.00	Sequence
IAs	160	APPSRGTVYQMWLLG	APPSRGTVY	0.0851	19920.9	50.00	Sequence
IAs	193	STTATLTDLGGASTAL	TTATLTDLG	0.0840	20150.2	50.00	Sequence
IAs	191	TPSTTATLTDLGGAST	TTATLTDLG	0.0834	20270.1	50.00	Sequence
IAs	187	TAAVTPSTTATLTDL	TAAVTPSTT	0.0828	20406.3	50.00	Sequence
IAs	190	VTPSTTATLTDLGGAS	TTATLTDLG	0.0826	20462.4	50.00	Sequence
IAs	167	VYQMWLLGGAKGPRS	LLGGAKGPR	0.0824	20505.0	50.00	Sequence
IAs	157	NNVAPPSRGTVYQMW	NNVAPPSRG	0.0813	20738.8	50.00	Sequence

IAs	156	MNNVAPPSRGTVYQM	NNVAPPSRG	0.0799	21066.3	50.00	Sequence
IAs	159	VAPPSRGTVYQMWLL	GTVYQMWLL	0.0778	21537.8	50.00	Sequence
IAs	192	PSTTATLTDLGASTA	TTATLTDLG	0.0778	21552.3	50.00	Sequence
IAs	99	AVGLGAFGLGVLTRP	FGLGVLTRP	0.0769	21757.5	50.00	Sequence
IAs	169	QMWLLGGAKGPRSAG	GGAKGPRSA	0.0759	22000.7	50.00	Sequence
IAs	47	VRAVRETMAVVSAA	RAVRETMAV	0.0757	22037.3	50.00	Sequence
IAs	32	VAAAPSPVAAAFNDE	VAAAPSPVA	0.0754	22114.3	50.00	Sequence
IAs	161	PSRGTVYQMWLLGG	SRGTVYQMW	0.0750	22209.4	50.00	Sequence
IAs	162	PSRGTVYQMWLLGGA	SRGTVYQMW	0.0748	22255.4	50.00	Sequence
IAs	83	RQSRWRTAAAFASAAA	RTAAAFASAA	0.0738	22506.7	50.00	Sequence
IAs	34	AAPSPVAAAFNDEVR	APSPVAAAF	0.0734	22585.6	50.00	Sequence
IAs	133	SRPLGAGTATVVF	RPLGAGTAT	0.0715	23073.6	50.00	Sequence
IAs	131	TVSRPLGAGTATVVF	RPLGAGTAT	0.0714	23095.8	50.00	Sequence
IAs	8	LLELATPYALNAVSD	LELATPYAL	0.0711	23165.4	50.00	Sequence
IAs	9	LELATPYALNAVSD	LELATPYAL	0.0707	23258.6	50.00	Sequence
IAs	82	RRQSRWRTAAAFASAA	RTAAAFASAA	0.0704	23350.1	50.00	Sequence
IAs	132	VSRPLGAGTATVVF	RPLGAGTAT	0.0700	23454.5	50.00	Sequence
IAs	165	GTVYQMWLLGGAKGP	GTVYQMWLL	0.0689	23730.1	50.00	Sequence
IAs	33	AAAPSPVAAAFNDEV	SPVAAAFND	0.0684	23843.9	50.00	Sequence
IAs	94	SAAAIAVGLGAFGLG	VGLGAFGLG	0.0683	23890.1	50.00	Sequence
IAs	22	DDERADIDRRVAAAP	IDRRVAAAP	0.0669	24250.3	50.00	Sequence
IAs	145	FSRDRNTGLLVMNNV	TGLLVMNNV	0.0666	24324.9	50.00	Sequence
IAs	46	EVRVRETMAVVSAA	RAVRETMAV	0.0657	24563.8	50.00	Sequence
IAs	158	NVAPPSRGTVYQMWL	SRGTVYQMW	0.0650	24757.7	50.00	Sequence
IAs	147	RDRNTGLLVMNNVAP	TGLLVMNNV	0.0648	24791.5	50.00	Sequence
IAs	42	AFNDEVRAVRETMAV	RAVRETMAV	0.0643	24923.0	50.00	Sequence
IAs	0	MTEHTDFELLELATP	TDFELLELA	0.0641	24983.8	50.00	Sequence
IAs	146	SRDRNTGLLVMNNVA	TGLLVMNNV	0.0635	25153.3	50.00	Sequence
IAs	198	LTDLGASTALAF	LGASTALAF	0.0630	25280.2	50.00	Sequence
IAs	35	APSPVAAAFNDEVRA	APSPVAAAF	0.0627	25363.7	50.00	Sequence
IAs	43	FNDEVRAVRETMAV	RAVRETMAV	0.0627	25381.0	50.00	Sequence
IAs	199	TDLGASTALAF	LGASTALAF	0.0625	25422.2	50.00	Sequence
IAs	95	AAAIAVGLGAFGLGV	VGLGAFGLG	0.0622	25522.3	50.00	Sequence
IAs	79	PEVRRQSRWRTAAFA	SRWRTAAFA	0.0620	25556.8	50.00	Sequence
IAs	134	RPLGAGTATVVF	RPLGAGTAT	0.0608	25884.4	50.00	Sequence
IAs	164	RGTVYQMWLLGGAKG	RGTVYQMWL	0.0601	26096.7	50.00	Sequence
IAs	44	NDEVRAVRETMAVVS	RAVRETMAV	0.0600	26125.2	50.00	Sequence
IAs	214	GTGSPQPTGTILAE	GTGSPQPTG	0.0591	26372.0	50.00	Sequence
IAs	81	VRQSRWRTAAAFASA	SRWRTAAFA	0.0584	26580.0	50.00	Sequence
IAs	197	TLTDLGASTALAF	LGASTALAF	0.0575	26846.2	50.00	Sequence
IAs	196	ATLTDLGASTALAF	LGASTALAF	0.0570	26989.2	50.00	Sequence
IAs	76	ATKPEVRRQSRWRTA	PEVRRQSRW	0.0564	27170.3	50.00	Sequence
IAs	45	DEVRAVRETMAVVS	RAVRETMAV	0.0554	27463.2	50.00	Sequence
IAs	75	DATKPEVRRQSRWRT	PEVRRQSRW	0.0548	27640.2	50.00	Sequence
IAs	80	EVRQSRWRTAAAFAS	SRWRTAAFA	0.0546	27680.9	50.00	Sequence
IAs	137	GAGTATVVF	GAGTATVVF	0.0527	28267.5	50.00	Sequence
IAs	136	LGAGTATVVF	LGAGTATVVF	0.0525	28332.1	50.00	Sequence
IAs	96	AAIAVGLGAFGLGVL	VGLGAFGLG	0.0515	28626.7	50.00	Sequence
IAs	135	PLGAGTATVVF	PLGAGTATV	0.0515	28630.4	50.00	Sequence
IAs	10	ELATPYALNAVSDDE	ALNAVSDDE	0.0511	28756.4	50.00	Sequence
IAs	194	TTATLTDLGASTALA	TTATLTDLG	0.0501	29071.8	50.00	Sequence
IAs	98	IAVGLGAFGLGVLTR	VGLGAFGLG	0.0494	29301.7	50.00	Sequence
IAs	97	IAVGLGAFGLGVL	IAVGLGAF	0.0492	29372.8	50.00	Sequence
IAs	37	SPVAAAFNDEVRAVR	SPVAAAFND	0.0488	29489.6	50.00	Sequence
IAs	11	LATPYALNAVSDDER	TPYALNAV	0.0479	29780.8	50.00	Sequence
IAs	144	VFSRDRNTGLLVMNN	RNTGLLVMN	0.0477	29842.4	50.00	Sequence
IAs	36	PSPVAAAFNDEVRAV	SPVAAAFND	0.0475	29909.6	50.00	Sequence
IAs	39	VAAAFNDEVRAVRET	DEVRAVRET	0.0474	29926.8	50.00	Sequence
IAs	138	AGTATVVF	AGTATVVF	0.0471	30052.4	50.00	Sequence
IAs	195	TATLTDLGASTALAF	LGASTALAF	0.0469	30086.2	50.00	Sequence
IAs	140	TATVVF	TATVVF	0.0468	30134.8	50.00	Sequence
IAs	78	KPEVRRQSRWRTAAF	PEVRRQSRW	0.0450	30732.4	50.00	Sequence
IAs	139	GTATVVF	GTATVVF	0.0446	30876.7	50.00	Sequence
IAs	41	AAFNDEVRAVRETMA	VRAVRETMA	0.0439	31082.2	50.00	Sequence
IAs	77	TKPEVRRQSRWRTAA	PEVRRQSRW	0.0439	31109.8	50.00	Sequence
IAs	40	AAAFNDEVRAVRET	DEVRAVRET	0.0431	31350.0	50.00	Sequence
IAs	15	YALNAVSDDERADID	SDDERADID	0.0425	31568.2	50.00	Sequence
IAs	16	ALNAVSDDERADIDR	SDDERADID	0.0407	32183.1	50.00	Sequence
IAs	12	ATPYALNAVSDDERA	NAVSDDERA	0.0400	32419.7	50.00	Sequence
IAs	143	VVF	VVF	0.0359	33892.1	50.00	Sequence
IAs	13	TPYALNAVSDDERAD	TPYALNAV	0.0356	34004.9	50.00	Sequence
IAs	38	PVAAAFNDEVRAVRE	AAAFNDEV	0.0348	34310.9	50.00	Sequence
IAs	14	PYALNAVSDDERADI	ALNAVSDDE	0.0347	34332.4	50.00	Sequence
IAs	20	VSDDERADIDRRVAA	SDDERADID	0.0323	35257.3	50.00	Sequence
IAs	19	AVSDDERADIDRRVA	SDDERADID	0.0318	35434.8	50.00	Sequence
IAs	18	NAVSDDERADIDRRV	SDDERADID	0.0318	35460.5	50.00	Sequence
IAs	17	LNNAVSDDERADIDRR	SDDERADID	0.0309	35786.2	50.00	Sequence

IAs	141	ATVVFSRDRNTGLLV	ATVVFSRDR	0.0305	35952.3	50.00	Sequence
IAs	21	SDDERADIDRRVAAA	SDDERADID	0.0294	36372.5	50.00	Sequence
IAs	142	TVVFSRDRNTGLLVM	TVVFSRDRN	0.0280	36950.1	50.00	Sequence

Allele: IAs. Number of high binders 0. Number of weak binders 1. Number of peptides 218

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