

HMNPIVVVHGGGAGPISKDRKERVHQGMVRAATVGYGILREGGSAV
DAVEGAVVALEDDPEFNAGCGSVLNTNGEVEMDASIMDGKDL SAGA
VSAVQCIANPIKLARLVMEKTPHCFLTDQGAAQFAAAMGVPEIPGEKL
VTERNKKRLEKEKHEKGAQKTD CQKNLGTVGAVALDCKGNVAYATSTG
GIVNKMVGRVGDSPCLGAGGYADNDIGAVSTTGHGESILKVNLARLTL
FHIEQGKTVEEAADLSLGYMKSRVKGLGGLIVVSKTGDWVAKWTSTS
MPWAAAK DGKLHFGIDPDDTTITDLP

Figure S1. Amino acid sequence of Homo sapiens Asparaginase 4O0H extracted from the Protein Data Bank website.

LPNITILATGGTIAGGGDSATKSNYTVGKVGVENLVNAV PQLKDIANVK
GEQV V NIGSQDMNDNVWLT LAKKINTDCDKTDG FVITHGTDTMEET
AYFLDLTVKCDKPVVMVGAMRPSTSMSADGPFNLNAVVT AADKASA
NRGVLVVMNDTVLDGRDVTKTNTTDVATFKSVNYG PLGYIHNGKIDY
QRTPARKHTSDTPFDVSKLNELPKVGIVYNYANASDLP AKALVDAGYD
GIVSAGVGNGNLYKSVFDTLATAAKTGTAVVRSSRVPTGATTQDAEVD
DAKYGFV ASGTLNPQKARVLLQLALTQTKDPQQIQQIFNQY

Figure S2. Amino acid sequence of Escherichia coli Asparaginase 3ECA extracted from the Protein Data Bank website.

LPNITILATGGTIAGGGDSATKSNYTVGKVG **VDAVEGAVVALEDDPNV**
KGEQV V NIGSQDMNDNVWLT LAKKINTDCDKTDG FVITHGTDTMEE
TAYFLDLTVKCDKPVVMVGAMRPSTSMSA **ANPIKLARLVMEKTPKAS**
ANRGVLVVMNDTVLDGRDVTKTNTTDVATFKSVNYG PLGYIHNGKID
YQRTPARKHTSDTPFDVSKLNELPKVGIVYNYANASDLP AKALVDAGYD
GIVSAGVGNGNLYKSVFDTLATAAKTGTAVVRSSRVPTGATTQDAEVD
DAKYGFV ASGTLNPQKARVLLQLALTQTKDPQQIQQIFNQY

Figure S3. Amino acid sequence of Humanized Chimeric Asparaginase engineered with human asparaginase fragments. The residues corresponding to human asparaginase that were inserted as substituents in the E.coli enzyme are highlighted in blue.

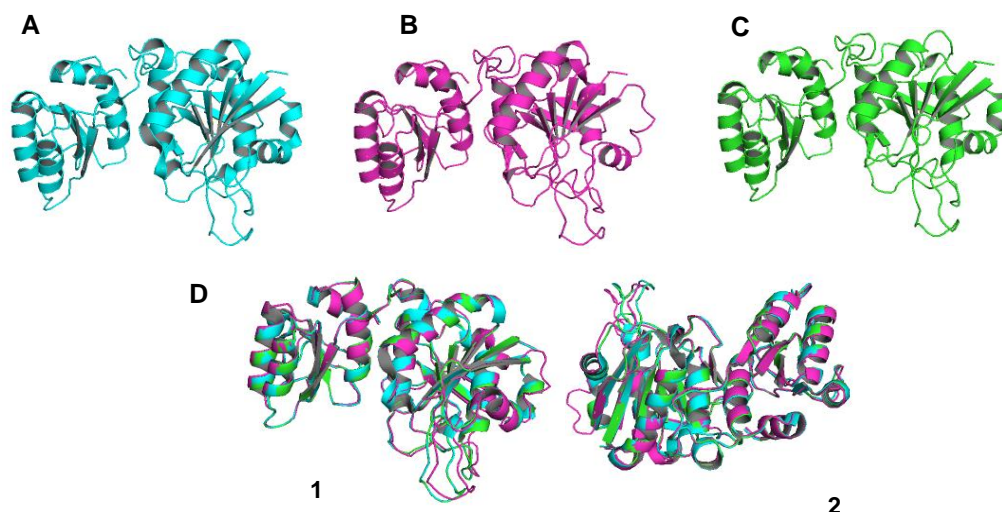


Figure S4. Validation of the three-dimensional structure of the humanized 3ECA chimeric enzyme predicted by the SWISS Model server by similarity analysis of its AC dimers with the BD dimers of the native 3ECA protein and the chimeric protein model predicted by AlphaFold 2. **A.** Structure of the BD dimer of the native 3ECA protein. **B.** BD dimer structure of the humanized 3ECA chimeric protein obtained from the AlphaFold2 server. **C.** Structure of the BD dimer of the humanized 3ECA chimeric protein obtained from the SWISS Model server. **D.** Alienation of the 3 structures with a view from two different psotions. The root mean square deviation (RMSD) was used to calculate the quality of aliasing and reported an RMSD value of 0.47 . All visualized structures were performed with PyMOL 2.4.0 Molecular Graphics System software as well as the alignment.

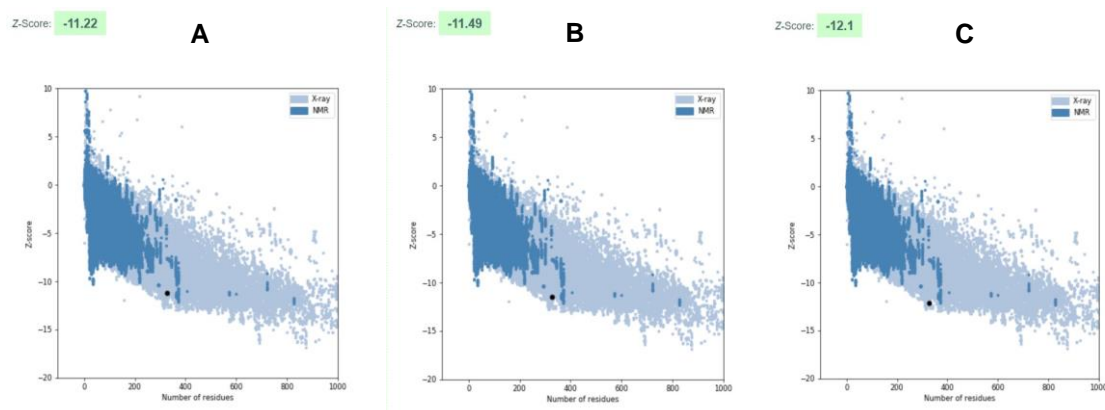


Figure S5. Graph of Protein Data Bank (PDB) protein structures (blue), (A) 3ECA chimeric enzyme predicted by the SWISS Model server (black), (B) the chimeric protein model predicted by AlphaFold 2 and (C) native 3ECA protein (black) , all with z-scores computed by ProSA-web server. PDB structures determined by X-ray crystallography and nuclear magnetic resonance (NMR) were shown in light blue and dark blue, respectively. Models generated by SWISS-MODEL , Alpha Fold and 3ECA Native from PDB server were shown in circle.

Table S1. Output of the NetMHCIIpan version 4.0 program. for the 3ECA protein. Of a total of 2025 fragmented peptides, only those that bind to MHCII either weakly or strongly and are therefore considered antigenic are presented. In green The antigenic peptides that additionally present allergenicity, determined by the AllerTOP server, are represented for the DRB1_0401 and DRB1_0701 allele. Additionally in blue the peptides that were selected as surrogates for designing the humanized chimeric asparaginase are indicated.

```
# NetMHCIIpan version 4.0
# Input is in FASTA format
# Peptide length 9,10,11,12,13,14,15
# Prediction Mode: EL
# Threshold for Strong binding peptides (%Rank) 1%
# Threshold for Weak binding peptides (%Rank) 5%
# Allele: DRB1_0101
```

Pos	MHC	Peptide	Of	Core	Core_Rel	Identity	Score_EL	%Rank_EL	Exp_Bind	BindLevel
215	DRB1_0101	GIVYNYANASDLPA	3	YNYANASDL	0.987	3ECA_A_PDBID_CH	0.856610	0.60	NA	<=SB
216	DRB1_0101	IVYNYANASDLPAK	2	YNYANASDL	0.987	3ECA_A_PDBID_CH	0.805187	0.85	NA	<=SB
233	DRB1_0101	DAGYDGIVSAGVGN	3	YDGIVSAGV	1.000	3ECA_A_PDBID_CH	0.776991	0.98	NA	<=SB
214	DRB1_0101	VGIVYNYANASDLPA	4	YNYANASDL	0.967	3ECA_A_PDBID_CH	0.842813	0.67	NA	<=SB
215	DRB1_0101	GIVYNYANASDLPAK	3	YNYANASDL	1.000	3ECA_A_PDBID_CH	0.939400	0.26	NA	<=SB
232	DRB1_0101	VDAGYDGIVSAGVGN	4	YDGIVSAGV	1.000	3ECA_A_PDBID_CH	0.787291	0.94	NA	<=SB
233	DRB1_0101	DAGYDGIVSAGVNG	3	YDGIVSAGV	1.000	3ECA_A_PDBID_CH	0.889292	0.47	NA	<=SB
286	DRB1_0101	DARYGFVASGTLNFPQ	3	YGFVASGTL	1.000	3ECA_A_PDBID_CH	0.789841	0.92	NA	<=SB
42	DRB1_0101	LKDIANVKGEQVV	3	IANVKGEQV	1.000	3ECA_A_PDBID_CH	0.453290	2.93	NA	<=WB
43	DRB1_0101	KDIANVKGEQVVN	2	IANVKGEQV	1.000	3ECA_A_PDBID_CH	0.587101	1.95	NA	<=WB
80	DRB1_0101	TDGPFVITHGTDTM	3	FVITHGTD	1.000	3ECA_A_PDBID_CH	0.395657	3.45	NA	<=WB
81	DRB1_0101	DGPFVITHGTDTME	2	FVITHGTD	1.000	3ECA_A_PDBID_CH	0.365173	3.76	NA	<=WB
213	DRB1_0101	KVGIVYNYANASD	3	IVYNYANAS	1.000	3ECA_A_PDBID_CH	0.431889	3.12	NA	<=WB
215	DRB1_0101	GIVYNYANASDLP	3	YNYANASDL	0.967	3ECA_A_PDBID_CH	0.692847	1.39	NA	<=WB

216	DRB1_0101	IVYNYANASDLPA	2	YNYANASDL	1.000	3ECA_A_PDBID_CH	0.626087	1.73	NA	<=WB
217	DRB1_0101	VYNYANASDLPAK	1	YNYANASDL	0.833	3ECA_A_PDBID_CH	0.423387	3.19	NA	<=WB
233	DRB1_0101	DAGYDGIVSAGVG	3	YDGIVSAGV	1.000	3ECA_A_PDBID_CH	0.566505	2.08	NA	<=WB
234	DRB1_0101	AGYDGIVSAGVGN	2	YDGIVSAGV	1.000	3ECA_A_PDBID_CH	0.519855	2.39	NA	<=WB
286	DRB1_0101	DAKYGFVASGTLN	3	YGFVASGTL	0.993	3ECA_A_PDBID_CH	0.412389	3.29	NA	<=WB
287	DRB1_0101	AKYGFVASGTLNP	2	YGFVASGTL	0.987	3ECA_A_PDBID_CH	0.385619	3.54	NA	<=WB
294	DRB1_0101	SGTLNPQKARVLL	3	LNPKQKARVL	1.000	3ECA_A_PDBID_CH	0.293319	4.59	NA	<=WB
295	DRB1_0101	GTLNPQKARVLLQ	2	LNPKQKARVL	1.000	3ECA_A_PDBID_CH	0.269743	4.94	NA	<=WB
3	DRB1_0101	NITILATGGTIAGG	3	ILATGGTIA	0.993	3ECA_A_PDBID_CH	0.318591	4.28	NA	<=WB
41	DRB1_0101	QLKDIANVKGEQVV	4	IANVKGEQV	1.000	3ECA_A_PDBID_CH	0.413779	3.28	NA	<=WB
42	DRB1_0101	LKDIANVKGEQVVN	3	IANVKGEQV	1.000	3ECA_A_PDBID_CH	0.683266	1.44	NA	<=WB
43	DRB1_0101	KDIANVKGEQVVNI	2	IANVKGEQV	1.000	3ECA_A_PDBID_CH	0.582497	1.98	NA	<=WB
79	DRB1_0101	KTDGFVITHGTDTM	4	FVITHGTD	1.000	3ECA_A_PDBID_CH	0.353500	3.88	NA	<=WB
80	DRB1_0101	TDGFVITHGTDME	3	FVITHGTD	1.000	3ECA_A_PDBID_CH	0.570299	2.06	NA	<=WB
81	DRB1_0101	DGFVITHGTDME	2	FVITHGTD	1.000	3ECA_A_PDBID_CH	0.444882	3.00	NA	<=WB
94	DRB1_0101	ETAYFLDLTVKCDK	3	YFLDLTVKC	0.980	3ECA_A_PDBID_CH	0.288631	4.66	NA	<=WB
144	DRB1_0101	RGVLVVMNDTVLDG	3	LVVMNDTVL	0.993	3ECA_A_PDBID_CH	0.382118	3.58	NA	<=WB
145	DRB1_0101	GVLVVMNDTVLDGR	2	LVVMNDTVL	0.980	3ECA_A_PDBID_CH	0.276061	4.85	NA	<=WB
212	DRB1_0101	PKVGIVYNYANASD	4	IVYNYANAS	1.000	3ECA_A_PDBID_CH	0.392505	3.48	NA	<=WB
213	DRB1_0101	KVGIVYNYANASDL	3	IVYNYANAS	0.907	3ECA_A_PDBID_CH	0.445260	3.00	NA	<=WB
214	DRB1_0101	VGIVYNYANASDLP	4	YNYANASDL	0.833	3ECA_A_PDBID_CH	0.675097	1.48	NA	<=WB
217	DRB1_0101	VYNYANASDLPAKA	1	YNYANASDL	0.533	3ECA_A_PDBID_CH	0.389067	3.51	NA	<=WB
232	DRB1_0101	VDAGYDGIVSAGVG	4	YDGIVSAGV	1.000	3ECA_A_PDBID_CH	0.518277	2.40	NA	<=WB
234	DRB1_0101	AGYDGIVSAGVGNG	2	YDGIVSAGV	1.000	3ECA_A_PDBID_CH	0.648984	1.61	NA	<=WB
285	DRB1_0101	DDAKYGFVASGTLN	4	YGFVASGTL	0.987	3ECA_A_PDBID_CH	0.348675	3.93	NA	<=WB
286	DRB1_0101	DAKYGFVASGTLNP	3	YGFVASGTL	0.993	3ECA_A_PDBID_CH	0.663099	1.54	NA	<=WB

287	DRB1_0101	AKYGFVASGTLNPQ	2	YGFVASGTL	0.980	3ECA_A_PDBID_CH	0.486700	2.64	NA	<=WB
294	DRB1_0101	SGTLNPQKARVLLQ	3	LNPKQKARVL	1.000	3ECA_A_PDBID_CH	0.455215	2.91	NA	<=WB
2	DRB1_0101	PNITILATGGTIAGG	4	ILATGGTIA	0.853	3ECA_A_PDBID_CH	0.331687	4.12	NA	<=WB
3	DRB1_0101	NITILATGGTIAGGG	3	ILATGGTIA	1.000	3ECA_A_PDBID_CH	0.493740	2.58	NA	<=WB
40	DRB1_0101	PQLKDIANVKGEQVV	5	IANVKGEQV	0.967	3ECA_A_PDBID_CH	0.342488	3.99	NA	<=WB
41	DRB1_0101	QLKDIANVKGEQVVN	4	IANVKGEQV	1.000	3ECA_A_PDBID_CH	0.680513	1.45	NA	<=WB
42	DRB1_0101	LKDIANVKGEQVVNI	3	IANVKGEQV	1.000	3ECA_A_PDBID_CH	0.692057	1.39	NA	<=WB
43	DRB1_0101	KDIANVKGEQVVNIG	2	IANVKGEQV	0.987	3ECA_A_PDBID_CH	0.475962	2.73	NA	<=WB
62	DRB1_0101	NDNVWLTLLAKKINTD	3	VWLTLLAKKI	0.953	3ECA_A_PDBID_CH	0.266068	5.00	NA	<=WB
78	DRB1_0101	DKTDFGVITHGTDTM	5	FVITHGTD	1.000	3ECA_A_PDBID_CH	0.300074	4.49	NA	<=WB
79	DRB1_0101	KTDGFEVITHGTDME	4	FVITHGTD	1.000	3ECA_A_PDBID_CH	0.570440	2.06	NA	<=WB
80	DRB1_0101	TDGFEVITHGTDME	3	FVITHGTD	1.000	3ECA_A_PDBID_CH	0.690766	1.40	NA	<=WB
81	DRB1_0101	DGFEVITHGTDMEET	2	FVITHGTD	1.000	3ECA_A_PDBID_CH	0.362081	3.79	NA	<=WB
93	DRB1_0101	EETAYFLDLTVKCDK	4	YFLDLTVKC	0.993	3ECA_A_PDBID_CH	0.272270	4.90	NA	<=WB
94	DRB1_0101	ETAYFLDLTVKCDKP	3	YFLDLTVKC	0.993	3ECA_A_PDBID_CH	0.415586	3.27	NA	<=WB
124	DRB1_0101	DGPFNLNAVVTAAAD	3	FNLYNAVVT	0.987	3ECA_A_PDBID_CH	0.393252	3.47	NA	<=WB
143	DRB1_0101	NRGVLVVMNDTVLDG	4	LVVMNDTVL	0.947	3ECA_A_PDBID_CH	0.388702	3.51	NA	<=WB
144	DRB1_0101	RGVLVVMNDTVLDGR	3	LVVMNDTVL	1.000	3ECA_A_PDBID_CH	0.571900	2.05	NA	<=WB
211	DRB1_0101	LPKVGIVYNYANASD	5	IVYNYANAS	1.000	3ECA_A_PDBID_CH	0.325031	4.20	NA	<=WB
212	DRB1_0101	PKVGIVYNYANASDL	4	IVYNYANAS	0.933	3ECA_A_PDBID_CH	0.404097	3.37	NA	<=WB
213	DRB1_0101	KVGIVYNYANASDLP	5	YNYANASDL	0.467	3ECA_A_PDBID_CH	0.710908	1.30	NA	<=WB
216	DRB1_0101	IVYNYANASDLPAKA	2	YNYANASDL	0.907	3ECA_A_PDBID_CH	0.715427	1.27	NA	<=WB
217	DRB1_0101	VYNYANASDLPAKAL	3	YANASDLPA	0.513	3ECA_A_PDBID_CH	0.307190	4.41	NA	<=WB
231	DRB1_0101	LVDAGYDGIVSAGVG	5	YDGIVSAGV	1.000	3ECA_A_PDBID_CH	0.477626	2.72	NA	<=WB
234	DRB1_0101	AGYDGIVSAGVGNGN	2	YDGIVSAGV	0.987	3ECA_A_PDBID_CH	0.562906	2.11	NA	<=WB
247	DRB1_0101	GNLYKSVFDTLATAA	3	YKSVFDTLA	1.000	3ECA_A_PDBID_CH	0.268710	4.96	NA	<=WB

284	DRB1_0101	VDDAKYGFVASGTLN	5	YGFVASGTL	0.993	3ECA_A_PDBID_CH	0.299478	4.50	NA	<=WB
285	DRB1_0101	DDAKYGFVASGTLNP	4	YGFVASGTL	0.993	3ECA_A_PDBID_CH	0.653044	1.59	NA	<=WB
287	DRB1_0101	AKYGFVASGTLNPQK	2	YGFVASGTL	0.920	3ECA_A_PDBID_CH	0.389288	3.50	NA	<=WB
293	DRB1_0101	ASGTLNPQKARVLLQ	4	LNPQKARVL	1.000	3ECA_A_PDBID_CH	0.419235	3.23	NA	<=WB
294	DRB1_0101	SGTLNPQKARVLLQL	3	LNPQKARVL	1.000	3ECA_A_PDBID_CH	0.376540	3.64	NA	<=WB

Allele: DRB1_0301

100	DRB1_0301	DLTVKCDKPVVMV	3	VKCDKPVVM	1.000	3ECA_A_PDBID_CH	0.377936	2.99	NA	<=WB
101	DRB1_0301	LTVKCDKPVVMVG	2	VKCDKPVVM	1.000	3ECA_A_PDBID_CH	0.295409	3.85	NA	<=WB
184	DRB1_0301	NGKIDYQRTPAR	3	IDYQRTPAR	1.000	3ECA_A_PDBID_CH	0.270114	4.21	NA	<=WB
185	DRB1_0301	GKIDYQRTPARKH	2	IDYQRTPAR	1.000	3ECA_A_PDBID_CH	0.226714	4.92	NA	<=WB
213	DRB1_0301	KVGIVYNYANASD	3	IVYNYANAS	1.000	3ECA_A_PDBID_CH	0.305954	3.72	NA	<=WB
99	DRB1_0301	LDLTVKCDKPVVMV	4	VKCDKPVVM	1.000	3ECA_A_PDBID_CH	0.340310	3.34	NA	<=WB
100	DRB1_0301	DLTVKCDKPVVMVG	3	VKCDKPVVM	1.000	3ECA_A_PDBID_CH	0.481993	2.17	NA	<=WB
101	DRB1_0301	LTVKCDKPVVMVGA	2	VKCDKPVVM	1.000	3ECA_A_PDBID_CH	0.322670	3.50	NA	<=WB
145	DRB1_0301	GVLVVMNDTVLDGR	3	VVMNDTVLD	0.533	3ECA_A_PDBID_CH	0.240197	4.69	NA	<=WB
146	DRB1_0301	VLVVMNDTVLDGRD	3	VMNDTVLDG	0.700	3ECA_A_PDBID_CH	0.299411	3.80	NA	<=WB
178	DRB1_0301	PLGYIHNGKIDYQR	3	YIHNGKIDY	0.947	3ECA_A_PDBID_CH	0.230814	4.85	NA	<=WB
183	DRB1_0301	HNGKIDYQRTPAR	4	IDYQRTPAR	1.000	3ECA_A_PDBID_CH	0.255598	4.43	NA	<=WB
184	DRB1_0301	NGKIDYQRTPARKH	3	IDYQRTPAR	1.000	3ECA_A_PDBID_CH	0.327924	3.45	NA	<=WB
185	DRB1_0301	GKIDYQRTPARKHT	2	IDYQRTPAR	0.987	3ECA_A_PDBID_CH	0.231616	4.84	NA	<=WB
212	DRB1_0301	PKVGIVYNYANASD	4	IVYNYANAS	0.993	3ECA_A_PDBID_CH	0.277959	4.09	NA	<=WB
213	DRB1_0301	KVGIVYNYANASDL	3	IVYNYANAS	0.993	3ECA_A_PDBID_CH	0.286539	3.97	NA	<=WB

94	DRB1_0301	ETAYFLDLTVKCDKP	3	YFLDLTVKC	0.993	3ECA_A_PDBID_CH	0.262903	4.32	NA	<=WB
98	DRB1_0301	FLDLTVKCDKPVVMV	5	VKCDKPVVM	1.000	3ECA_A_PDBID_CH	0.304364	3.74	NA	<=WB
99	DRB1_0301	LDLTVKCDKPVVMVG	4	VKCDKPVVM	1.000	3ECA_A_PDBID_CH	0.475115	2.22	NA	<=WB
100	DRB1_0301	DLTVKCDKPVVMVGA	3	VKCDKPVVM	1.000	3ECA_A_PDBID_CH	0.537227	1.80	NA	<=WB
101	DRB1_0301	LTVKCDKPVVMVGAM	2	VKCDKPVVM	1.000	3ECA_A_PDBID_CH	0.256839	4.41	NA	<=WB
118	DRB1_0301	STSMSADGPFNLYNA	3	MSADGPFNL	1.000	3ECA_A_PDBID_CH	0.267122	4.26	NA	<=WB
144	DRB1_0301	RGVLVVMNDTVLDGR	4	VVMNDTVLD	0.507	3ECA_A_PDBID_CH	0.271332	4.19	NA	<=WB
145	DRB1_0301	GVLVVMNDTVLDGRD	4	VMNDTVLDG	0.533	3ECA_A_PDBID_CH	0.409175	2.73	NA	<=WB
146	DRB1_0301	VLVVMNDTVLDGRDV	3	VMNDTVLDG	0.773	3ECA_A_PDBID_CH	0.331094	3.42	NA	<=WB
150	DRB1_0301	MNDTVLDGRDVTCTN	3	TVLDGRDVT	0.993	3ECA_A_PDBID_CH	0.275046	4.13	NA	<=WB
178	DRB1_0301	PLGYIHNGKIDYQRT	3	YIHNGKIDY	0.953	3ECA_A_PDBID_CH	0.237083	4.74	NA	<=WB
182	DRB1_0301	IHNGKIDYQRTPAR	5	IDYQRTPAR	0.993	3ECA_A_PDBID_CH	0.266253	4.27	NA	<=WB
183	DRB1_0301	HNGKIDYQRTPARKH	4	IDYQRTPAR	1.000	3ECA_A_PDBID_CH	0.359918	3.16	NA	<=WB
184	DRB1_0301	NGKIDYQRTPARKHT	3	IDYQRTPAR	1.000	3ECA_A_PDBID_CH	0.379228	2.98	NA	<=WB
211	DRB1_0301	LPKVGIVYNYANASD	5	IVYNYANAS	0.980	3ECA_A_PDBID_CH	0.256249	4.42	NA	<=WB
212	DRB1_0301	PKVGIVYNYANASDL	4	IVYNYANAS	1.000	3ECA_A_PDBID_CH	0.288226	3.94	NA	<=WB
213	DRB1_0301	KVGIVYNYANASDLP	3	IVYNYANAS	0.987	3ECA_A_PDBID_CH	0.374633	3.02	NA	<=WB

Allele: DRB1_0401

218	DRB1_0401	YNYANASDLPAK	2	YANASDLPA	1.000	3ECA_A_PDBID_CH	0.699347	0.84	NA	<=SB
213	DRB1_0401	KVGIVYNYANASD	3	IVYNYANAS	1.000	3ECA_A_PDBID_CH	0.736986	0.67	NA	<=SB
217	DRB1_0401	VYNYANASDLPAK	3	YANASDLPA	1.000	3ECA_A_PDBID_CH	0.909565	0.13	NA	<=SB
218	DRB1_0401	YNYANASDLPAKA	2	YANASDLPA	1.000	3ECA_A_PDBID_CH	0.894517	0.16	NA	<=SB
39	DRB1_0401	VPQLKDIANVKGEQ	3	LKDIANVKG	1.000	3ECA_A_PDBID_CH	0.671939	0.96	NA	<=SB
94	DRB1_0401	ETAYFLDLTVKCDK	3	YFLDLTVKC	0.993	3ECA_A_PDBID_CH	0.688832	0.88	NA	<=SB

212	DRB1_0401	PKVGIVYNYANASD	4	IVYNYANAS	1.000	3ECA_A_PDBID_CH	0.715918	0.76	NA	<=SB
213	DRB1_0401	KVGIVYNYANASDL	3	IVYNYANAS	0.993	3ECA_A_PDBID_CH	0.727693	0.70	NA	<=SB
216	DRB1_0401	IVYNYANASDLPAK	4	YANASDLPA	1.000	3ECA_A_PDBID_CH	0.895092	0.16	NA	<=SB
217	DRB1_0401	VYNYANASDLPAKA	3	YANASDLPA	1.000	3ECA_A_PDBID_CH	0.945743	0.06	NA	<=SB
218	DRB1_0401	YNYANASDLPAKAL	2	YANASDLPA	1.000	3ECA_A_PDBID_CH	0.845737	0.30	NA	<=SB
247	DRB1_0401	GNLYKSVFDTLATA	3	YKSVFDTLA	1.000	3ECA_A_PDBID_CH	0.670025	0.97	NA	<=SB
288	DRB1_0401	KYGFVASGTLNPQK	3	FVASGTLNP	1.000	3ECA_A_PDBID_CH	0.709457	0.79	NA	<=SB
38	DRB1_0401	AVPQLKDIANVKGEQ	4	LKDIANVKG	1.000	3ECA_A_PDBID_CH	0.663240	1.00	NA	<=SB
39	DRB1_0401	VPQLKDIANVKGEQV	3	LKDIANVKG	1.000	3ECA_A_PDBID_CH	0.676495	0.94	NA	<=SB
94	DRB1_0401	ETAYFLDLTVKCDKP	3	YFLDLTVKC	1.000	3ECA_A_PDBID_CH	0.769601	0.55	NA	<=SB
126	DRB1_0401	PFNLNAVVTAAADKA	4	YNAVVTAAAD	0.693	3ECA_A_PDBID_CH	0.681508	0.92	NA	<=SB
127	DRB1_0401	FNLYNAVVTAAADKAS	3	YNAVVTAAAD	0.987	3ECA_A_PDBID_CH	0.689372	0.88	NA	<=SB
213	DRB1_0401	KVGIVYNYANASDLP	3	IVYNYANAS	0.993	3ECA_A_PDBID_CH	0.758515	0.59	NA	<=SB
215	DRB1_0401	GIVYNYANASDLPAK	5	YANASDLPA	0.967	3ECA_A_PDBID_CH	0.859535	0.26	NA	<=SB
216	DRB1_0401	IVYNYANASDLPAKA	4	YANASDLPA	1.000	3ECA_A_PDBID_CH	0.936469	0.07	NA	<=SB
217	DRB1_0401	VYNYANASDLPAKAL	3	YANASDLPA	1.000	3ECA_A_PDBID_CH	0.916075	0.11	NA	<=SB
218	DRB1_0401	YNYANASDLPAKALV	2	YANASDLPA	1.000	3ECA_A_PDBID_CH	0.761364	0.58	NA	<=SB
247	DRB1_0401	GNLYKSVFDTLATAA	3	YKSVFDTLA	1.000	3ECA_A_PDBID_CH	0.723465	0.72	NA	<=SB
287	DRB1_0401	AKYGFVASGTLNPQK	4	FVASGTLNP	0.993	3ECA_A_PDBID_CH	0.664480	1.00	NA	<=SB
288	DRB1_0401	KYGFVASGTLNPQKA	3	FVASGTLNP	1.000	3ECA_A_PDBID_CH	0.725718	0.71	NA	<=SB
128	DRB1_0401	NLYNAVVTAAADK	2	YNAVVTAAAD	0.960	3ECA_A_PDBID_CH	0.345675	3.77	NA	<=WB
214	DRB1_0401	VGIVYNYANASD	2	IVYNYANAS	1.000	3ECA_A_PDBID_CH	0.382356	3.26	NA	<=WB
217	DRB1_0401	VYNYANASDLPA	3	YANASDLPA	0.973	3ECA_A_PDBID_CH	0.323084	4.13	NA	<=WB
219	DRB1_0401	NYANASDLPAKA	1	YANASDLPA	1.000	3ECA_A_PDBID_CH	0.479246	2.28	NA	<=WB
39	DRB1_0401	VPQLKDIANVKGE	3	LKDIANVKG	1.000	3ECA_A_PDBID_CH	0.550328	1.72	NA	<=WB
40	DRB1_0401	PQLKDIANVKGEQ	2	LKDIANVKG	1.000	3ECA_A_PDBID_CH	0.531248	1.86	NA	<=WB

94	DRB1_0401	ETAYFLDLTVKCD	3	YFLDLTVKC	1.000	3ECA_A_PDBID_CH	0.537989	1.81	NA	<=WB
95	DRB1_0401	TAYFLDLTVKCDK	2	YFLDLTVKC	0.980	3ECA_A_PDBID_CH	0.528021	1.89	NA	<=WB
96	DRB1_0401	AYFLDLTVKCDKP	1	YFLDLTVKC	0.947	3ECA_A_PDBID_CH	0.286146	4.80	NA	<=WB
127	DRB1_0401	FNLYNAVVTAAADK	3	YNAVVTAAAD	0.887	3ECA_A_PDBID_CH	0.528900	1.88	NA	<=WB
128	DRB1_0401	NLYNAVVTAAADKA	2	YNAVVTAAAD	0.967	3ECA_A_PDBID_CH	0.589305	1.44	NA	<=WB
212	DRB1_0401	PKVGIVYNYANAS	4	IVYNYANAS	0.987	3ECA_A_PDBID_CH	0.326994	4.06	NA	<=WB
214	DRB1_0401	VGIVYNYANASDL	2	IVYNYANAS	0.987	3ECA_A_PDBID_CH	0.516516	1.97	NA	<=WB
215	DRB1_0401	GIVYNYANASDLP	1	IVYNYANAS	0.767	3ECA_A_PDBID_CH	0.305171	4.43	NA	<=WB
216	DRB1_0401	IVYNYANASDLPA	4	YANASDLPA	0.920	3ECA_A_PDBID_CH	0.455856	2.47	NA	<=WB
219	DRB1_0401	NYANASDLPAKAL	1	YANASDLPA	1.000	3ECA_A_PDBID_CH	0.551685	1.71	NA	<=WB
247	DRB1_0401	GNLYKSVFDTLAT	3	YKSVFDTLA	1.000	3ECA_A_PDBID_CH	0.558782	1.66	NA	<=WB
248	DRB1_0401	NLYKSVFDTLATA	2	YKSVFDTLA	1.000	3ECA_A_PDBID_CH	0.407716	2.95	NA	<=WB
288	DRB1_0401	KYGFVASGTLNPQ	3	FVASGTLNP	0.987	3ECA_A_PDBID_CH	0.534775	1.84	NA	<=WB
289	DRB1_0401	YGFVASGTLNPQK	2	FVASGTLNP	1.000	3ECA_A_PDBID_CH	0.475145	2.31	NA	<=WB
38	DRB1_0401	AVPQLKDIANVKGE	4	LKDIANVKG	1.000	3ECA_A_PDBID_CH	0.530749	1.87	NA	<=WB
40	DRB1_0401	PQLKDIANVKGEQV	2	LKDIANVKG	1.000	3ECA_A_PDBID_CH	0.532987	1.85	NA	<=WB
93	DRB1_0401	EETAYFLDLTVKCD	4	YFLDLTVKC	1.000	3ECA_A_PDBID_CH	0.477869	2.29	NA	<=WB
95	DRB1_0401	TAYFLDLTVKCDKP	2	YFLDLTVKC	0.973	3ECA_A_PDBID_CH	0.615284	1.27	NA	<=WB
126	DRB1_0401	PFNLYNAVVTAAADK	4	YNAVVTAAAD	0.627	3ECA_A_PDBID_CH	0.566013	1.61	NA	<=WB
127	DRB1_0401	FNLYNAVVTAAADKA	3	YNAVVTAAAD	0.913	3ECA_A_PDBID_CH	0.630319	1.18	NA	<=WB
128	DRB1_0401	NLYNAVVTAAADKAS	2	YNAVVTAAAD	0.993	3ECA_A_PDBID_CH	0.624347	1.22	NA	<=WB
130	DRB1_0401	YNAVVTAAADKASAN	3	VVTAADKAS	0.813	3ECA_A_PDBID_CH	0.313628	4.29	NA	<=WB
131	DRB1_0401	NAVVTAAADKASANR	2	VVTAADKAS	0.813	3ECA_A_PDBID_CH	0.321282	4.16	NA	<=WB
144	DRB1_0401	RGVLVVMNDTVLDG	3	LVVMNDTVL	0.680	3ECA_A_PDBID_CH	0.392752	3.12	NA	<=WB
145	DRB1_0401	GVLVVMNDTVLDGR	3	VVMNDTVLD	0.600	3ECA_A_PDBID_CH	0.454569	2.48	NA	<=WB
146	DRB1_0401	VLVVMNDTVLDGRD	2	VVMNDTVLD	0.540	3ECA_A_PDBID_CH	0.369872	3.41	NA	<=WB

184	DRB1_0401	NGKIDYQRTPARKH	3	IDYQRTPAR	0.953	3ECA_A_PDBID_CH	0.283986	4.84	NA	<=WB
214	DRB1_0401	VGIVYNYANASDLP	2	IVYNYANAS	0.947	3ECA_A_PDBID_CH	0.603462	1.34	NA	<=WB
215	DRB1_0401	GIVYNYANASDLPA	5	YANASDLPA	0.613	3ECA_A_PDBID_CH	0.434539	2.68	NA	<=WB
219	DRB1_0401	NYANASDLPAKALV	1	YANASDLPA	0.993	3ECA_A_PDBID_CH	0.406808	2.96	NA	<=WB
233	DRB1_0401	DAGYDGIVSAGVGN	3	YDGIVSAGV	1.000	3ECA_A_PDBID_CH	0.360469	3.54	NA	<=WB
246	DRB1_0401	NGNLYKSVFDTLAT	4	YKSVFDTLA	1.000	3ECA_A_PDBID_CH	0.474676	2.32	NA	<=WB
248	DRB1_0401	NLYKSVFDTLATAA	2	YKSVFDTLA	1.000	3ECA_A_PDBID_CH	0.428596	2.74	NA	<=WB
287	DRB1_0401	AKYGFVASGTLNPQ	4	FVASGTLNP	0.967	3ECA_A_PDBID_CH	0.478671	2.28	NA	<=WB
289	DRB1_0401	YGFVASGTLNPQKA	2	FVASGTLNP	1.000	3ECA_A_PDBID_CH	0.505138	2.06	NA	<=WB
37	DRB1_0401	NAVPLKDIANVKGE	5	LKDIANVKG	1.000	3ECA_A_PDBID_CH	0.472183	2.34	NA	<=WB
40	DRB1_0401	PQLKDIANVKGEQVV	2	LKDIANVKG	0.993	3ECA_A_PDBID_CH	0.434920	2.68	NA	<=WB
92	DRB1_0401	MEETAYFLDLTVKCD	5	YFLDLTVKC	0.993	3ECA_A_PDBID_CH	0.404740	2.98	NA	<=WB
93	DRB1_0401	EETAYFLDLTVKCDK	4	YFLDLTVKC	0.993	3ECA_A_PDBID_CH	0.660361	1.02	NA	<=WB
95	DRB1_0401	TAYFLDLTVKCDKPV	2	YFLDLTVKC	0.947	3ECA_A_PDBID_CH	0.510534	2.02	NA	<=WB
112	DRB1_0401	VGAMRPSTSMSADGP	3	MRPSTSMSA	1.000	3ECA_A_PDBID_CH	0.333296	3.96	NA	<=WB
125	DRB1_0401	GPFNLNAVVTAAADK	5	YNAVVTAAAD	0.600	3ECA_A_PDBID_CH	0.526624	1.90	NA	<=WB
128	DRB1_0401	NLYNAVVTAAADKASA	2	YNAVVTAAAD	0.907	3ECA_A_PDBID_CH	0.562629	1.63	NA	<=WB
129	DRB1_0401	LYNAVVTAAADKASAN	4	VVTAADKAS	0.667	3ECA_A_PDBID_CH	0.352420	3.66	NA	<=WB
130	DRB1_0401	YNAVVTAAADKASANR	3	VVTAADKAS	0.900	3ECA_A_PDBID_CH	0.448748	2.54	NA	<=WB
143	DRB1_0401	NRGVLVVMNDTVLDG	4	LVVMNDTVL	0.627	3ECA_A_PDBID_CH	0.361094	3.53	NA	<=WB
144	DRB1_0401	RGVLVVMNDTVLDGR	3	LVVMNDTVL	0.633	3ECA_A_PDBID_CH	0.565814	1.61	NA	<=WB
145	DRB1_0401	GVLVVMNDTVLDGRD	3	VVMNDTVLD	0.707	3ECA_A_PDBID_CH	0.525129	1.91	NA	<=WB
146	DRB1_0401	VLVVMNDTVLDGRDV	3	VMNDTVLDG	0.567	3ECA_A_PDBID_CH	0.297957	4.57	NA	<=WB
184	DRB1_0401	NGKIDYQRTPARKHT	3	IDYQRTPAR	0.853	3ECA_A_PDBID_CH	0.299151	4.54	NA	<=WB
211	DRB1_0401	LPKVGIVYNYANASD	5	IVYNYANAS	0.993	3ECA_A_PDBID_CH	0.619601	1.24	NA	<=WB
212	DRB1_0401	PKVGIVYNYANASDL	4	IVYNYANAS	1.000	3ECA_A_PDBID_CH	0.661767	1.01	NA	<=WB

214	DRB1_0401	VGIVYNYANASDLPA	2	IVYNYANAS	0.707	3ECA_A_PDBID_CH	0.514557	1.99	NA	<=WB
219	DRB1_0401	NYANASDLPAKALVD	1	YANASDLPA	0.967	3ECA_A_PDBID_CH	0.287351	4.77	NA	<=WB
232	DRB1_0401	VDAGYDGIVSAGVGN	4	YDGIVSAGV	1.000	3ECA_A_PDBID_CH	0.370250	3.41	NA	<=WB
233	DRB1_0401	DAGYDGIVSAGVGNG	3	YDGIVSAGV	0.993	3ECA_A_PDBID_CH	0.465963	2.39	NA	<=WB
245	DRB1_0401	GNGNLYKSVFDTLAT	5	YKSVFDTLA	1.000	3ECA_A_PDBID_CH	0.391449	3.14	NA	<=WB
246	DRB1_0401	NGNLYKSVFDTLATA	4	YKSVFDTLA	1.000	3ECA_A_PDBID_CH	0.633199	1.16	NA	<=WB
248	DRB1_0401	NLYKSVFDTLATAAK	2	YKSVFDTLA	0.947	3ECA_A_PDBID_CH	0.311644	4.32	NA	<=WB
265	DRB1_0401	TAVVRSSRVPTGATT	3	VRSSRVPTG	1.000	3ECA_A_PDBID_CH	0.278164	4.95	NA	<=WB
286	DRB1_0401	DAKYGFVASGTLNPQ	5	FVASGTLNP	0.807	3ECA_A_PDBID_CH	0.417653	2.85	NA	<=WB
289	DRB1_0401	YGFVASGTLNPQKAR	2	FVASGTLNP	0.987	3ECA_A_PDBID_CH	0.365708	3.47	NA	<=WB

Allele: DRB1_0701

42	DRB1_0701	LKDIANVKGEQVV	3	IANVKGEQV	1.000	3ECA_A_PDBID_CH	0.712443	0.67	NA	<=SB
43	DRB1_0701	KDIANVKGEQVVN	2	IANVKGEQV	1.000	3ECA_A_PDBID_CH	0.706160	0.69	NA	<=SB
61	DRB1_0701	MNDNVWLTAKKI	4	VWLTAKKI	1.000	3ECA_A_PDBID_CH	0.665523	0.85	NA	<=SB
62	DRB1_0701	NDNVWLTAKKIN	3	VWLTAKKI	1.000	3ECA_A_PDBID_CH	0.853420	0.26	NA	<=SB
63	DRB1_0701	DNVWLTAKKINT	2	VWLTAKKI	1.000	3ECA_A_PDBID_CH	0.745309	0.56	NA	<=SB
80	DRB1_0701	TDGFVITHGTDTM	3	FVITHGTD	1.000	3ECA_A_PDBID_CH	0.700966	0.71	NA	<=SB
215	DRB1_0701	GIVYNYANASDLP	3	YNYANASDL	1.000	3ECA_A_PDBID_CH	0.727702	0.62	NA	<=SB
233	DRB1_0701	DAGYDGIVSAGVG	3	YDGIVSAGV	1.000	3ECA_A_PDBID_CH	0.672671	0.82	NA	<=SB
286	DRB1_0701	DAKYGFVASGTLN	3	YGFVASGTL	1.000	3ECA_A_PDBID_CH	0.798901	0.41	NA	<=SB
287	DRB1_0701	AKYGFVASGTLNP	2	YGFVASGTL	1.000	3ECA_A_PDBID_CH	0.732577	0.60	NA	<=SB
41	DRB1_0701	QLKDIANVKGEQVV	4	IANVKGEQV	1.000	3ECA_A_PDBID_CH	0.707213	0.69	NA	<=SB
42	DRB1_0701	LKDIANVKGEQVVN	3	IANVKGEQV	1.000	3ECA_A_PDBID_CH	0.779984	0.46	NA	<=SB

43	DRB1_0701	KDIANVKGEQVUNI	2	IANVKGEQV	1.000	3ECA_A_PDBID_CH	0.688739	0.76	NA	<=SB
61	DRB1_0701	MNDNVWLTAKKIN	4	VWLTAKKI	1.000	3ECA_A_PDBID_CH	0.841039	0.29	NA	<=SB
62	DRB1_0701	NDNVWLTAKKINT	3	VWLTAKKI	1.000	3ECA_A_PDBID_CH	0.867377	0.23	NA	<=SB
63	DRB1_0701	DNVWLTAKKINTD	2	VWLTAKKI	1.000	3ECA_A_PDBID_CH	0.804759	0.39	NA	<=SB
79	DRB1_0701	KTDGFVITHGDTM	4	FVITHGDT	1.000	3ECA_A_PDBID_CH	0.699313	0.72	NA	<=SB
80	DRB1_0701	TDGFVITHGDTME	3	FVITHGDT	1.000	3ECA_A_PDBID_CH	0.774179	0.47	NA	<=SB
81	DRB1_0701	DGFVITHGDTMEE	2	FVITHGDT	1.000	3ECA_A_PDBID_CH	0.675938	0.81	NA	<=SB
214	DRB1_0701	VGIVYNYANASDLP	4	YNYANASDL	0.947	3ECA_A_PDBID_CH	0.728071	0.62	NA	<=SB
215	DRB1_0701	GIVYNYANASDLPA	3	YNYANASDL	1.000	3ECA_A_PDBID_CH	0.786162	0.44	NA	<=SB
216	DRB1_0701	IVYNYANASDLPAK	2	YNYANASDL	0.993	3ECA_A_PDBID_CH	0.716844	0.65	NA	<=SB
232	DRB1_0701	VDAGYDGIVSAGVG	4	YDGIVSAGV	1.000	3ECA_A_PDBID_CH	0.666211	0.85	NA	<=SB
233	DRB1_0701	DAGYDGIVSAGVGN	3	YDGIVSAGV	1.000	3ECA_A_PDBID_CH	0.751984	0.54	NA	<=SB
285	DRB1_0701	DDAKYGFVASGTLN	4	YGFVASGTL	1.000	3ECA_A_PDBID_CH	0.786890	0.44	NA	<=SB
286	DRB1_0701	DAKYGFVASGTLNP	3	YGFVASGTL	1.000	3ECA_A_PDBID_CH	0.876850	0.21	NA	<=SB
287	DRB1_0701	AKYGFVASGTLNPQ	2	YGFVASGTL	0.973	3ECA_A_PDBID_CH	0.774316	0.47	NA	<=SB
40	DRB1_0701	PQLKDIANVKGEQVV	5	IANVKGEQV	1.000	3ECA_A_PDBID_CH	0.674838	0.82	NA	<=SB
41	DRB1_0701	QLKDIANVKGEQVVN	4	IANVKGEQV	1.000	3ECA_A_PDBID_CH	0.790399	0.43	NA	<=SB
42	DRB1_0701	LKDIANVKGEQVUNI	3	IANVKGEQV	1.000	3ECA_A_PDBID_CH	0.766696	0.49	NA	<=SB
60	DRB1_0701	DMNDNVWLTAKKIN	5	VWLTAKKI	1.000	3ECA_A_PDBID_CH	0.808590	0.38	NA	<=SB
61	DRB1_0701	MNDNVWLTAKKINT	4	VWLTAKKI	1.000	3ECA_A_PDBID_CH	0.863347	0.24	NA	<=SB
62	DRB1_0701	NDNVWLTAKKINTD	3	VWLTAKKI	1.000	3ECA_A_PDBID_CH	0.909089	0.14	NA	<=SB
63	DRB1_0701	DNVWLTAKKINTDC	2	VWLTAKKI	1.000	3ECA_A_PDBID_CH	0.738558	0.58	NA	<=SB
78	DRB1_0701	DKTDGFVITHGDTM	5	FVITHGDT	1.000	3ECA_A_PDBID_CH	0.664701	0.85	NA	<=SB
79	DRB1_0701	KTDGFVITHGDTME	4	FVITHGDT	1.000	3ECA_A_PDBID_CH	0.778442	0.46	NA	<=SB
80	DRB1_0701	TDGFVITHGDTMEE	3	FVITHGDT	1.000	3ECA_A_PDBID_CH	0.819944	0.35	NA	<=SB
213	DRB1_0701	KVGIVYNYANASDLP	5	YNYANASDL	0.867	3ECA_A_PDBID_CH	0.724649	0.63	NA	<=SB

214	DRB1_0701	VGIVYNYANASDLPA	4	YNYANASDL	0.987	3ECA_A_PDBID_CH	0.802615	0.40	NA	<=SB
215	DRB1_0701	GIVYNYANASDLPAK	3	YNYANASDL	1.000	3ECA_A_PDBID_CH	0.865203	0.23	NA	<=SB
231	DRB1_0701	LVDAGYDGIVSAGVG	5	YDGIVSAGV	1.000	3ECA_A_PDBID_CH	0.685672	0.78	NA	<=SB
232	DRB1_0701	VDAGYDGIVSAGVGN	4	YDGIVSAGV	1.000	3ECA_A_PDBID_CH	0.797549	0.41	NA	<=SB
233	DRB1_0701	DAGYDGIVSAGVGNG	3	YDGIVSAGV	1.000	3ECA_A_PDBID_CH	0.827671	0.33	NA	<=SB
284	DRB1_0701	VDDAKYGFVASGTLN	5	YGFVASGTL	1.000	3ECA_A_PDBID_CH	0.761717	0.51	NA	<=SB
285	DRB1_0701	DDAKYGFVASGTLNP	4	YGFVASGTL	1.000	3ECA_A_PDBID_CH	0.884281	0.20	NA	<=SB
286	DRB1_0701	DAKYGFVASGTLNPQ	3	YGFVASGTL	1.000	3ECA_A_PDBID_CH	0.909081	0.14	NA	<=SB
287	DRB1_0701	AKYGFVASGTLNPQK	2	YGFVASGTL	0.887	3ECA_A_PDBID_CH	0.719580	0.65	NA	<=SB
63	DRB1_0701	DNVWLTAKKI	2	VWLTAKKI	1.000	3ECA_A_PDBID_CH	0.248919	4.79	NA	<=WB
42	DRB1_0701	LKDIANVKGEQV	3	IANVKGEQV	1.000	3ECA_A_PDBID_CH	0.389642	2.71	NA	<=WB
43	DRB1_0701	KDIANVKGEQVV	2	IANVKGEQV	1.000	3ECA_A_PDBID_CH	0.512511	1.69	NA	<=WB
62	DRB1_0701	NDNVWLTAKKI	3	VWLTAKKI	1.000	3ECA_A_PDBID_CH	0.565667	1.37	NA	<=WB
63	DRB1_0701	DNVWLTAKKIN	2	VWLTAKKI	1.000	3ECA_A_PDBID_CH	0.605028	1.14	NA	<=WB
64	DRB1_0701	NVWLTAKKINT	1	VWLTAKKI	1.000	3ECA_A_PDBID_CH	0.242034	4.93	NA	<=WB
80	DRB1_0701	TDGFVITHGTD	3	FVITHGTD	1.000	3ECA_A_PDBID_CH	0.469179	2.00	NA	<=WB
81	DRB1_0701	DGFVITHGTD	2	FVITHGTD	1.000	3ECA_A_PDBID_CH	0.411896	2.48	NA	<=WB
215	DRB1_0701	GIVYNYANASDL	3	YNYANASDL	0.953	3ECA_A_PDBID_CH	0.290386	4.03	NA	<=WB
216	DRB1_0701	IVYNYANASDLP	2	YNYANASDL	1.000	3ECA_A_PDBID_CH	0.371573	2.90	NA	<=WB
233	DRB1_0701	DAGYDGIVSAGV	3	YDGIVSAGV	1.000	3ECA_A_PDBID_CH	0.278445	4.24	NA	<=WB
234	DRB1_0701	AGYDGIVSAGVG	2	YDGIVSAGV	1.000	3ECA_A_PDBID_CH	0.305089	3.80	NA	<=WB
286	DRB1_0701	DAKYGFVASGTL	3	YGFVASGTL	1.000	3ECA_A_PDBID_CH	0.390455	2.70	NA	<=WB
287	DRB1_0701	AKYGFVASGTLN	2	YGFVASGTL	1.000	3ECA_A_PDBID_CH	0.445933	2.20	NA	<=WB
3	DRB1_0701	NITILATGGTIAG	3	ILATGGTIA	0.993	3ECA_A_PDBID_CH	0.299446	3.89	NA	<=WB
41	DRB1_0701	QLKDIANVKGEQV	4	IANVKGEQV	1.000	3ECA_A_PDBID_CH	0.512210	1.69	NA	<=WB
44	DRB1_0701	DIANVKGEQVNI	1	IANVKGEQV	0.960	3ECA_A_PDBID_CH	0.243349	4.90	NA	<=WB

64	DRB1_0701	NVWLTAKKINTD	1	VWLTAKKI	1.000	3ECA_A_PDBID_CH	0.453146	2.14	NA	<=WB
79	DRB1_0701	KTDGFVITHGTD	4	FVITHGTD	1.000	3ECA_A_PDBID_CH	0.584234	1.26	NA	<=WB
81	DRB1_0701	DGFVITHGTDME	2	FVITHGTD	1.000	3ECA_A_PDBID_CH	0.617517	1.07	NA	<=WB
82	DRB1_0701	GFVITHGTDME	1	FVITHGTD	1.000	3ECA_A_PDBID_CH	0.281681	4.18	NA	<=WB
112	DRB1_0701	VGAMRPSTMSAD	3	MRPSTMSA	1.000	3ECA_A_PDBID_CH	0.301500	3.86	NA	<=WB
127	DRB1_0701	FNLYNAVVTAAK	3	YNAVVTAA	0.933	3ECA_A_PDBID_CH	0.328074	3.46	NA	<=WB
128	DRB1_0701	NLYNAVVTAAKA	2	YNAVVTAA	0.953	3ECA_A_PDBID_CH	0.341037	3.28	NA	<=WB
157	DRB1_0701	GRDVTKTNTDVA	3	VTKTNTDV	1.000	3ECA_A_PDBID_CH	0.343739	3.25	NA	<=WB
176	DRB1_0701	YGPLGYIHNGKID	3	LGYIHNGKI	1.000	3ECA_A_PDBID_CH	0.397489	2.62	NA	<=WB
177	DRB1_0701	GPLGYIHNGKIDY	2	LGYIHNGKI	0.987	3ECA_A_PDBID_CH	0.308939	3.75	NA	<=WB
185	DRB1_0701	GKIDYQRTPAKH	4	YQRTPAKH	0.960	3ECA_A_PDBID_CH	0.272242	4.34	NA	<=WB
186	DRB1_0701	KIDYQRTPAKHT	3	YQRTPAKH	1.000	3ECA_A_PDBID_CH	0.390310	2.70	NA	<=WB
187	DRB1_0701	IDYQRTPAKH	2	YQRTPAKH	1.000	3ECA_A_PDBID_CH	0.252354	4.72	NA	<=WB
200	DRB1_0701	DTPFDVSKLNEP	3	FDVSKLNE	1.000	3ECA_A_PDBID_CH	0.349988	3.16	NA	<=WB
201	DRB1_0701	TPFDVSKLNEPK	2	FDVSKLNE	1.000	3ECA_A_PDBID_CH	0.282173	4.17	NA	<=WB
213	DRB1_0701	KVGIVYNYANASD	3	IVYNYANAS	0.987	3ECA_A_PDBID_CH	0.240914	4.95	NA	<=WB
214	DRB1_0701	VGIVYNYANASDL	4	YNYANASDL	0.880	3ECA_A_PDBID_CH	0.442759	2.22	NA	<=WB
216	DRB1_0701	IVYNYANASDLPA	2	YNYANASDL	1.000	3ECA_A_PDBID_CH	0.612015	1.10	NA	<=WB
217	DRB1_0701	VYNYANASDLPAK	1	YNYANASDL	0.833	3ECA_A_PDBID_CH	0.373666	2.88	NA	<=WB
232	DRB1_0701	VDAGYDGIVSAGV	4	YDGIVSAGV	1.000	3ECA_A_PDBID_CH	0.401027	2.59	NA	<=WB
234	DRB1_0701	AGYDGIVSAGVGN	2	YDGIVSAGV	1.000	3ECA_A_PDBID_CH	0.546725	1.47	NA	<=WB
285	DRB1_0701	DDAKYGFVASGTL	4	YGFVASGTL	1.000	3ECA_A_PDBID_CH	0.520377	1.64	NA	<=WB
288	DRB1_0701	KYGFVASGTLNPQ	1	YGFVASGTL	0.753	3ECA_A_PDBID_CH	0.442341	2.23	NA	<=WB
2	DRB1_0701	PNITILATGGTIAG	4	ILATGGTIA	0.967	3ECA_A_PDBID_CH	0.280080	4.21	NA	<=WB
3	DRB1_0701	NITILATGGTIAGG	3	ILATGGTIA	0.987	3ECA_A_PDBID_CH	0.370175	2.91	NA	<=WB
40	DRB1_0701	PQLKDIANVKGEQV	5	IANVKGEQV	0.993	3ECA_A_PDBID_CH	0.447518	2.18	NA	<=WB

60	DRB1_0701	DMNDNVWLTAKKI	5	VWLTAKKI	1.000	3ECA_A_PDBID_CH	0.592580	1.20	NA	<=WB
64	DRB1_0701	NVWLTAKKINTDC	1	VWLTAKKI	1.000	3ECA_A_PDBID_CH	0.333043	3.39	NA	<=WB
78	DRB1_0701	DKTGDFVITHGTDI	5	FVITHGTDI	1.000	3ECA_A_PDBID_CH	0.524814	1.62	NA	<=WB
111	DRB1_0701	MVGAMPSTSMSAD	4	MRPSTMSA	1.000	3ECA_A_PDBID_CH	0.288332	4.07	NA	<=WB
112	DRB1_0701	VGAMPSTSMSADG	3	MRPSTMSA	1.000	3ECA_A_PDBID_CH	0.378213	2.83	NA	<=WB
113	DRB1_0701	GAMPSTSMSADGP	2	MRPSTMSA	0.993	3ECA_A_PDBID_CH	0.303119	3.83	NA	<=WB
126	DRB1_0701	PFNLNAVVTAAADK	4	YNAVVTAAAD	0.807	3ECA_A_PDBID_CH	0.315092	3.65	NA	<=WB
127	DRB1_0701	FNLYNAVVTAAADKA	3	YNAVVTAAAD	0.953	3ECA_A_PDBID_CH	0.395714	2.64	NA	<=WB
128	DRB1_0701	NLYNAVVTAAADKAS	2	YNAVVTAAAD	0.953	3ECA_A_PDBID_CH	0.368699	2.93	NA	<=WB
156	DRB1_0701	DGRDVTKTNTTDVA	4	VTKTNTTDV	1.000	3ECA_A_PDBID_CH	0.333816	3.38	NA	<=WB
157	DRB1_0701	GRDVTKTNTTDVAT	3	VTKTNTTDV	1.000	3ECA_A_PDBID_CH	0.400437	2.59	NA	<=WB
165	DRB1_0701	TTDVATFKSVNYGP	3	VATFKSVNY	0.993	3ECA_A_PDBID_CH	0.266777	4.44	NA	<=WB
175	DRB1_0701	NYGPLGYIHNGKID	4	LGYIHNGKI	1.000	3ECA_A_PDBID_CH	0.385308	2.75	NA	<=WB
176	DRB1_0701	YGPLGYIHNGKIDY	3	LGYIHNGKI	1.000	3ECA_A_PDBID_CH	0.416118	2.44	NA	<=WB
177	DRB1_0701	GPLGYIHNGKIDYQ	2	LGYIHNGKI	0.987	3ECA_A_PDBID_CH	0.339867	3.30	NA	<=WB
185	DRB1_0701	GKIDYQRTTPARKHT	4	YQRTTPARKH	0.967	3ECA_A_PDBID_CH	0.374103	2.87	NA	<=WB
186	DRB1_0701	KIDYQRTTPARKHTS	3	YQRTTPARKH	1.000	3ECA_A_PDBID_CH	0.411950	2.48	NA	<=WB
187	DRB1_0701	IDYQRTTPARKHTSD	2	YQRTTPARKH	1.000	3ECA_A_PDBID_CH	0.302471	3.84	NA	<=WB
199	DRB1_0701	SDTPFDVSKLNELP	4	FDVSKLNEL	1.000	3ECA_A_PDBID_CH	0.344300	3.24	NA	<=WB
200	DRB1_0701	DTPFDVSKLNELPK	3	FDVSKLNEL	1.000	3ECA_A_PDBID_CH	0.471167	1.99	NA	<=WB
201	DRB1_0701	TPFDVSKLNELPKV	2	FDVSKLNEL	1.000	3ECA_A_PDBID_CH	0.272067	4.35	NA	<=WB
213	DRB1_0701	KVGIVYNYANASDL	5	YNYANASDL	0.660	3ECA_A_PDBID_CH	0.422519	2.39	NA	<=WB
217	DRB1_0701	VYNYANASDLPAKA	1	YNYANASDL	0.653	3ECA_A_PDBID_CH	0.311991	3.70	NA	<=WB
231	DRB1_0701	LVDAGYDGIVSAGV	5	YDGIVSAGV	1.000	3ECA_A_PDBID_CH	0.330752	3.42	NA	<=WB
234	DRB1_0701	AGYDGIVSAGVGNG	2	YDGIVSAGV	1.000	3ECA_A_PDBID_CH	0.588434	1.23	NA	<=WB
284	DRB1_0701	VDDAKYGFVASGTL	5	YGFVASGTL	1.000	3ECA_A_PDBID_CH	0.430511	2.32	NA	<=WB

288	DRB1_0701	KYGFVASGTLNPQK	1	YGFVASGTL	0.533	3ECA_A_PDBID_CH	0.392252	2.68	NA	<=WB
1	DRB1_0701	LPNITILATGGTIAG	5	ILATGGTIA	0.953	3ECA_A_PDBID_CH	0.261920	4.52	NA	<=WB
2	DRB1_0701	PNITILATGGTIAGG	4	ILATGGTIA	0.973	3ECA_A_PDBID_CH	0.401303	2.58	NA	<=WB
3	DRB1_0701	NITILATGGTIAGGG	3	ILATGGTIA	1.000	3ECA_A_PDBID_CH	0.461918	2.06	NA	<=WB
39	DRB1_0701	VPQLKDIANVKGEQV	6	IANVKGEQV	0.973	3ECA_A_PDBID_CH	0.394537	2.66	NA	<=WB
43	DRB1_0701	KDIANVKGEQVVNIG	2	IANVKGEQV	0.993	3ECA_A_PDBID_CH	0.610748	1.11	NA	<=WB
50	DRB1_0701	GEQVVNIGSQDMNDN	3	VVNIGSQDM	0.987	3ECA_A_PDBID_CH	0.258517	4.59	NA	<=WB
59	DRB1_0701	QDMNDNVWLTIAKKI	6	VWLTIAKKI	1.000	3ECA_A_PDBID_CH	0.512699	1.69	NA	<=WB
64	DRB1_0701	NVWLTIAKKINTDCD	1	VWLTIAKKI	1.000	3ECA_A_PDBID_CH	0.261120	4.54	NA	<=WB
77	DRB1_0701	CDKTDGFEVITHGTD	6	FVITHGTD	1.000	3ECA_A_PDBID_CH	0.454399	2.13	NA	<=WB
81	DRB1_0701	DGFVITHGTDMEET	2	FVITHGTD	1.000	3ECA_A_PDBID_CH	0.602218	1.15	NA	<=WB
110	DRB1_0701	VMVGAMRPSTSMSAD	5	MRPSTMSA	0.987	3ECA_A_PDBID_CH	0.253941	4.69	NA	<=WB
111	DRB1_0701	MVGAMRPSTSMSADG	4	MRPSTMSA	1.000	3ECA_A_PDBID_CH	0.388613	2.72	NA	<=WB
112	DRB1_0701	VGAMRPSTSMSADGP	3	MRPSTMSA	1.000	3ECA_A_PDBID_CH	0.498589	1.80	NA	<=WB
113	DRB1_0701	GAMRPSTSMSADGPF	2	MRPSTMSA	0.993	3ECA_A_PDBID_CH	0.245624	4.86	NA	<=WB
123	DRB1_0701	ADGPFNLYNAVVTAA	4	FNLYNAVVT	0.993	3ECA_A_PDBID_CH	0.245882	4.85	NA	<=WB
124	DRB1_0701	DGPFNLYNAVVTAAD	3	FNLYNAVVT	0.887	3ECA_A_PDBID_CH	0.367421	2.94	NA	<=WB
125	DRB1_0701	GPFNLYNAVVTAADK	5	YNAVVTAAD	0.627	3ECA_A_PDBID_CH	0.334752	3.37	NA	<=WB
126	DRB1_0701	PFNLYNAVVTAADKA	4	YNAVVTAAD	0.887	3ECA_A_PDBID_CH	0.423410	2.38	NA	<=WB
127	DRB1_0701	FNLYNAVVTAADKAS	3	YNAVVTAAD	0.953	3ECA_A_PDBID_CH	0.462859	2.06	NA	<=WB
128	DRB1_0701	NLYNAVVTAADKASA	2	YNAVVTAAD	0.933	3ECA_A_PDBID_CH	0.320465	3.57	NA	<=WB
155	DRB1_0701	LDGRDVTKTNTTDVA	5	VTKTNTTDV	0.993	3ECA_A_PDBID_CH	0.325953	3.49	NA	<=WB
156	DRB1_0701	DGRDVTKTNTTDVAT	4	VTKTNTTDV	1.000	3ECA_A_PDBID_CH	0.435618	2.28	NA	<=WB
157	DRB1_0701	GRDVTKTNTTDVATF	3	VTKTNTTDV	1.000	3ECA_A_PDBID_CH	0.427199	2.35	NA	<=WB
164	DRB1_0701	NTTDVATFKSVNYGP	4	VATFKSVNY	0.993	3ECA_A_PDBID_CH	0.281528	4.18	NA	<=WB
165	DRB1_0701	TTDVATFKSVNYGPL	3	VATFKSVNY	0.793	3ECA_A_PDBID_CH	0.258512	4.59	NA	<=WB

174	DRB1_0701	VNYGPLGYIHNGKID	5	LGYIHNGKI	0.993	3ECA_A_PDBID_CH	0.357957	3.06	NA	<=WB
175	DRB1_0701	NYGPLGYIHNGKIDY	4	LGYIHNGKI	1.000	3ECA_A_PDBID_CH	0.424361	2.37	NA	<=WB
176	DRB1_0701	YGPLGYIHNGKIDYQ	3	LGYIHNGKI	1.000	3ECA_A_PDBID_CH	0.469305	2.00	NA	<=WB
177	DRB1_0701	GPLGYIHNGKIDYQR	2	LGYIHNGKI	0.960	3ECA_A_PDBID_CH	0.276477	4.27	NA	<=WB
184	DRB1_0701	NGKIDYQRTPARKHT	5	YQRTPARKH	0.947	3ECA_A_PDBID_CH	0.340392	3.29	NA	<=WB
185	DRB1_0701	GKIDYQRTPARKHTS	4	YQRTPARKH	0.993	3ECA_A_PDBID_CH	0.407740	2.51	NA	<=WB
186	DRB1_0701	KIDYQRTPARKHTSD	3	YQRTPARKH	1.000	3ECA_A_PDBID_CH	0.497606	1.81	NA	<=WB
187	DRB1_0701	IDYQRTPARKHTSDT	2	YQRTPARKH	1.000	3ECA_A_PDBID_CH	0.243646	4.90	NA	<=WB
198	DRB1_0701	TSDTPFDVSKLNELP	5	FDVSKLNEL	0.993	3ECA_A_PDBID_CH	0.312669	3.69	NA	<=WB
199	DRB1_0701	SDTPFDVSKLNELPK	4	FDVSKLNEL	1.000	3ECA_A_PDBID_CH	0.479037	1.93	NA	<=WB
200	DRB1_0701	DTPFDVSKLNELPKV	3	FDVSKLNEL	1.000	3ECA_A_PDBID_CH	0.482865	1.90	NA	<=WB
212	DRB1_0701	PKVGIVYNYANASDL	6	YNYANASDL	0.647	3ECA_A_PDBID_CH	0.362950	2.99	NA	<=WB
216	DRB1_0701	IVYNYANASDLPAKA	2	YNYANASDL	0.933	3ECA_A_PDBID_CH	0.629302	1.01	NA	<=WB
217	DRB1_0701	VYNYANASDLPAKAL	1	YNYANASDL	0.633	3ECA_A_PDBID_CH	0.245904	4.85	NA	<=WB
230	DRB1_0701	ALVDAGYDGIVSAGV	6	YDGIVSAGV	1.000	3ECA_A_PDBID_CH	0.310335	3.72	NA	<=WB
234	DRB1_0701	AGYDGIVSAGVGNGN	2	YDGIVSAGV	0.993	3ECA_A_PDBID_CH	0.551129	1.45	NA	<=WB
261	DRB1_0701	AKTGTAVVRSSRVPT	4	TAVVRSSRV	0.993	3ECA_A_PDBID_CH	0.254231	4.68	NA	<=WB
262	DRB1_0701	KTGTAVVRSSRVPTG	3	TAVVRSSRV	0.987	3ECA_A_PDBID_CH	0.310394	3.72	NA	<=WB
283	DRB1_0701	EVDDAKYGFVASGTL	6	YGFVASGTL	1.000	3ECA_A_PDBID_CH	0.386416	2.74	NA	<=WB
288	DRB1_0701	KYGFVASGTLNPQKA	3	FVASGTLNP	0.640	3ECA_A_PDBID_CH	0.393850	2.66	NA	<=WB

Allele: DRB1_0801

127	DRB1_0801	FNLYNAVVTAAADK	3	YNAVVTAAAD	1.000	3ECA_A_PDBID_CH	0.816422	0.53	NA	<=SB
128	DRB1_0801	NLYNAVVTAAADKA	2	YNAVVTAAAD	1.000	3ECA_A_PDBID_CH	0.855517	0.35	NA	<=SB

126	DRB1_0801	PFNLYNAVVTAAADK	4	YNAVVTAAAD	0.987	3ECA_A_PDBID_CH	0.794670	0.65	NA	<=SB
127	DRB1_0801	FNLYNAVVTAAADKA	3	YNAVVTAAAD	1.000	3ECA_A_PDBID_CH	0.865691	0.31	NA	<=SB
128	DRB1_0801	NLYNAVVTAAADKAS	2	YNAVVTAAAD	0.993	3ECA_A_PDBID_CH	0.875745	0.27	NA	<=SB
125	DRB1_0801	GPFNLYNAVVTAAADK	5	YNAVVTAAAD	0.987	3ECA_A_PDBID_CH	0.757895	0.86	NA	<=SB
126	DRB1_0801	PFNLYNAVVTAAADKA	4	YNAVVTAAAD	0.987	3ECA_A_PDBID_CH	0.858004	0.34	NA	<=SB
127	DRB1_0801	FNLYNAVVTAAADKAS	3	YNAVVTAAAD	1.000	3ECA_A_PDBID_CH	0.889852	0.22	NA	<=SB
128	DRB1_0801	NLYNAVVTAAADKASA	2	YNAVVTAAAD	0.993	3ECA_A_PDBID_CH	0.832305	0.45	NA	<=SB
128	DRB1_0801	NLYNAVVTAAADK	2	YNAVVTAAAD	1.000	3ECA_A_PDBID_CH	0.696661	1.33	NA	<=WB
129	DRB1_0801	LYNAVVTAAADKA	1	YNAVVTAAAD	1.000	3ECA_A_PDBID_CH	0.477379	3.93	NA	<=WB
22	DRB1_0801	KSNYTVGKVGVEN	3	YTVGKVGVE	0.947	3ECA_A_PDBID_CH	0.423505	5.00	NA	<=WB
63	DRB1_0801	DNVWLTAKKINT	3	WLTAKKIN	0.967	3ECA_A_PDBID_CH	0.611940	2.11	NA	<=WB
64	DRB1_0801	NVWLTAKKINTD	2	WLTAKKIN	0.740	3ECA_A_PDBID_CH	0.575930	2.51	NA	<=WB
129	DRB1_0801	LYNAVVTAAADKAS	1	YNAVVTAAAD	0.993	3ECA_A_PDBID_CH	0.633457	1.88	NA	<=WB
213	DRB1_0801	KVGIVYNYANASD	3	IVYNYANAS	0.920	3ECA_A_PDBID_CH	0.456524	4.32	NA	<=WB
33	DRB1_0801	ENLVNAVPLKDIA	3	VNAVPLKLD	0.967	3ECA_A_PDBID_CH	0.525880	3.17	NA	<=WB
62	DRB1_0801	NDNVWLTAKKINT	4	WLTAKKIN	0.920	3ECA_A_PDBID_CH	0.576310	2.50	NA	<=WB
63	DRB1_0801	DNVWLTAKKINTD	3	WLTAKKIN	0.873	3ECA_A_PDBID_CH	0.715579	1.17	NA	<=WB
129	DRB1_0801	LYNAVVTAAADKASA	1	YNAVVTAAAD	0.847	3ECA_A_PDBID_CH	0.561338	2.69	NA	<=WB
131	DRB1_0801	NAVVTAAADKASANR	3	VTAADKASA	0.973	3ECA_A_PDBID_CH	0.539697	2.97	NA	<=WB
212	DRB1_0801	PKVGIVYNYANASD	4	IVYNYANAS	0.900	3ECA_A_PDBID_CH	0.442398	4.60	NA	<=WB
213	DRB1_0801	KVGIVYNYANASDL	3	IVYNYANAS	0.873	3ECA_A_PDBID_CH	0.438295	4.69	NA	<=WB
32	DRB1_0801	VENLVNAVPLKDIA	4	VNAVPLKLD	0.960	3ECA_A_PDBID_CH	0.506812	3.46	NA	<=WB
33	DRB1_0801	ENLVNAVPLKDIAN	3	VNAVPLKLD	1.000	3ECA_A_PDBID_CH	0.577867	2.48	NA	<=WB
61	DRB1_0801	MNDNVWLTAKKINT	5	WLTAKKIN	0.907	3ECA_A_PDBID_CH	0.486842	3.78	NA	<=WB
62	DRB1_0801	NDNVWLTAKKINTD	4	WLTAKKIN	0.873	3ECA_A_PDBID_CH	0.687441	1.40	NA	<=WB
63	DRB1_0801	DNVWLTAKKINTDC	3	WLTAKKIN	0.833	3ECA_A_PDBID_CH	0.509373	3.42	NA	<=WB

129	DRB1_0801	LYNAVVTAAADKASAN	1	YNAVVTAAAD	0.587	3ECA_A_PDBID_CH	0.550730	2.83	NA	<=WB
130	DRB1_0801	YNAVVTAAADKASANR	4	VTAADKASA	0.953	3ECA_A_PDBID_CH	0.514749	3.34	NA	<=WB
131	DRB1_0801	NAVVTAAADKASANRG	3	VTAADKASA	0.993	3ECA_A_PDBID_CH	0.571167	2.57	NA	<=WB
145	DRB1_0801	GVLVVMNDTVLDGRD	3	VVMNDTVLD	0.967	3ECA_A_PDBID_CH	0.462530	4.21	NA	<=WB
213	DRB1_0801	KVGIVYNYANASDLP	3	IVYNYANAS	0.820	3ECA_A_PDBID_CH	0.503477	3.51	NA	<=WB

Allele: DRB1_1101

63	DRB1_1101	DNVWLTLLAKKINTD	3	WLTLLAKKIN	0.907	3ECA_A_PDBID_CH	0.821043	0.84	NA	<=SB
131	DRB1_1101	NAVVTAAADKASANRG	3	VTAADKASA	1.000	3ECA_A_PDBID_CH	0.832963	0.77	NA	<=SB
63	DRB1_1101	DNVWLTLLAKKINT	3	WLTLLAKKIN	0.993	3ECA_A_PDBID_CH	0.686725	1.61	NA	<=WB
64	DRB1_1101	NVWLTLLAKKINTD	2	WLTLLAKKIN	0.720	3ECA_A_PDBID_CH	0.689332	1.59	NA	<=WB
131	DRB1_1101	NAVVTAAADKASAN	3	VTAADKASA	1.000	3ECA_A_PDBID_CH	0.511718	2.95	NA	<=WB
132	DRB1_1101	AVVTAADKASANR	2	VTAADKASA	1.000	3ECA_A_PDBID_CH	0.516289	2.91	NA	<=WB
178	DRB1_1101	PLGYIHNGKIDYQ	3	YIHNGKIDY	0.987	3ECA_A_PDBID_CH	0.377640	4.50	NA	<=WB
213	DRB1_1101	KVGIVYNYANASD	3	IVYNYANAS	0.993	3ECA_A_PDBID_CH	0.470140	3.40	NA	<=WB
264	DRB1_1101	GTAVVRSSRVPTG	3	VVRSSRVPT	1.000	3ECA_A_PDBID_CH	0.407132	4.14	NA	<=WB
62	DRB1_1101	NDNVWLTLLAKKINT	4	WLTLLAKKIN	0.987	3ECA_A_PDBID_CH	0.643721	1.88	NA	<=WB
64	DRB1_1101	NVWLTLLAKKINTDC	2	WLTLLAKKIN	0.620	3ECA_A_PDBID_CH	0.459464	3.52	NA	<=WB
130	DRB1_1101	YNAVVTAAADKASAN	4	VTAADKASA	0.987	3ECA_A_PDBID_CH	0.517292	2.90	NA	<=WB
131	DRB1_1101	NAVVTAAADKASANR	3	VTAADKASA	1.000	3ECA_A_PDBID_CH	0.762907	1.16	NA	<=WB
132	DRB1_1101	AVVTAADKASANRG	2	VTAADKASA	1.000	3ECA_A_PDBID_CH	0.633116	1.95	NA	<=WB
177	DRB1_1101	GPLGYIHNGKIDYQ	4	YIHNGKIDY	0.907	3ECA_A_PDBID_CH	0.363575	4.72	NA	<=WB
178	DRB1_1101	PLGYIHNGKIDYQR	3	YIHNGKIDY	0.993	3ECA_A_PDBID_CH	0.551048	2.60	NA	<=WB
212	DRB1_1101	PKVGIVYNYANASD	4	IVYNYANAS	0.993	3ECA_A_PDBID_CH	0.455360	3.57	NA	<=WB

213	DRB1_1101	KVGIVYNYANASDL	3	IVYNYANAS	0.987	3ECA_A_PDBID_CH	0.479862	3.29	NA	<=WB
263	DRB1_1101	TGTAVVRSSRVPTG	4	VVRSSRVPT	1.000	3ECA_A_PDBID_CH	0.386141	4.39	NA	<=WB
264	DRB1_1101	GTAVVRSSRVPTGA	3	VVRSSRVPT	0.993	3ECA_A_PDBID_CH	0.572548	2.42	NA	<=WB
61	DRB1_1101	MNDNVWLTAKKINT	5	WLTAKKIN	0.993	3ECA_A_PDBID_CH	0.552126	2.59	NA	<=WB
62	DRB1_1101	NDNVWLTAKKINTD	4	WLTAKKIN	0.973	3ECA_A_PDBID_CH	0.789760	1.02	NA	<=WB
63	DRB1_1101	DNVWLTAKKINTDC	3	WLTAKKIN	0.873	3ECA_A_PDBID_CH	0.638302	1.91	NA	<=WB
64	DRB1_1101	NVWLTAKKINTDCD	3	LTLAKKINT	0.653	3ECA_A_PDBID_CH	0.427659	3.89	NA	<=WB
127	DRB1_1101	FNLYNAVVTAAKAS	3	YNAVVTAA	0.993	3ECA_A_PDBID_CH	0.370538	4.61	NA	<=WB
129	DRB1_1101	LYNAVVTAAKASAN	5	VTAADKASA	0.953	3ECA_A_PDBID_CH	0.469117	3.41	NA	<=WB
130	DRB1_1101	YNAVVTAAKASANR	4	VTAADKASA	1.000	3ECA_A_PDBID_CH	0.766093	1.14	NA	<=WB
132	DRB1_1101	AVVTAADKASARGV	2	VTAADKASA	1.000	3ECA_A_PDBID_CH	0.537141	2.72	NA	<=WB
177	DRB1_1101	GPLGYIHNGKIDYQR	4	YIHNGKIDY	0.960	3ECA_A_PDBID_CH	0.500025	3.07	NA	<=WB
178	DRB1_1101	PLGYIHNGKIDYQRT	3	YIHNGKIDY	0.993	3ECA_A_PDBID_CH	0.525776	2.82	NA	<=WB
186	DRB1_1101	KIDYQRTPARKHTSD	3	YQRTPARKH	1.000	3ECA_A_PDBID_CH	0.385684	4.40	NA	<=WB
211	DRB1_1101	LPKVGIVYNYANASD	5	IVYNYANAS	0.987	3ECA_A_PDBID_CH	0.379786	4.47	NA	<=WB
212	DRB1_1101	PKVGIVYNYANASDL	4	IVYNYANAS	1.000	3ECA_A_PDBID_CH	0.440919	3.74	NA	<=WB
213	DRB1_1101	KVGIVYNYANASDLP	3	IVYNYANAS	0.993	3ECA_A_PDBID_CH	0.566517	2.47	NA	<=WB
263	DRB1_1101	TGTAVVRSSRVPTGA	4	VVRSSRVPT	1.000	3ECA_A_PDBID_CH	0.519380	2.88	NA	<=WB
264	DRB1_1101	GTAVVRSSRVPTGAT	3	VVRSSRVPT	0.980	3ECA_A_PDBID_CH	0.564436	2.48	NA	<=WB

Allele: DRB1_1301

184	DRB1_1301	NGKIDYQRTPARKH	3	IDYQRTPAR	0.987	3ECA_A_PDBID_CH	0.756006	0.90	NA	<=SB
183	DRB1_1301	HNGKIDYQRTPARKH	4	IDYQRTPAR	0.973	3ECA_A_PDBID_CH	0.749549	0.94	NA	<=SB
184	DRB1_1301	NGKIDYQRTPARKHT	3	IDYQRTPAR	0.973	3ECA_A_PDBID_CH	0.770490	0.81	NA	<=SB
165	DRB1_1301	TTDVATFKSVNYG	3	VATFKSVNY	1.000	3ECA_A_PDBID_CH	0.495974	3.74	NA	<=WB

166	DRB1_1301	TDVATFKSVNYGP	2	VATFKSVNY	0.993	3ECA_A_PDBID_CH	0.480626	3.99	NA	<=WB
184	DRB1_1301	NGKIDYQRTPARK	3	IDYQRTPAR	0.993	3ECA_A_PDBID_CH	0.656866	1.71	NA	<=WB
185	DRB1_1301	GKIDYQRTPARKH	2	IDYQRTPAR	0.987	3ECA_A_PDBID_CH	0.623093	2.09	NA	<=WB
213	DRB1_1301	KVGIVYNYANASD	3	IVYNYANAS	0.987	3ECA_A_PDBID_CH	0.565993	2.73	NA	<=WB
264	DRB1_1301	GTAVVRSSRVPTG	3	VVRSSRVPT	0.987	3ECA_A_PDBID_CH	0.448059	4.59	NA	<=WB
131	DRB1_1301	NAVVTAAADKASANR	3	VTAAADKASA	0.980	3ECA_A_PDBID_CH	0.578727	2.58	NA	<=WB
132	DRB1_1301	AVVTAADKASANRG	2	VTAAADKASA	0.980	3ECA_A_PDBID_CH	0.457973	4.40	NA	<=WB
164	DRB1_1301	NTTDVATFKSVNYG	4	VATFKSVNY	1.000	3ECA_A_PDBID_CH	0.470290	4.18	NA	<=WB
165	DRB1_1301	TTDVATFKSVNYGP	3	VATFKSVNY	0.993	3ECA_A_PDBID_CH	0.621143	2.11	NA	<=WB
183	DRB1_1301	HNGKIDYQRTPARK	4	IDYQRTPAR	0.980	3ECA_A_PDBID_CH	0.662992	1.65	NA	<=WB
185	DRB1_1301	GKIDYQRTPARKHT	2	IDYQRTPAR	0.980	3ECA_A_PDBID_CH	0.661536	1.66	NA	<=WB
212	DRB1_1301	PKVGIVYNYANASD	4	IVYNYANAS	0.967	3ECA_A_PDBID_CH	0.554197	2.88	NA	<=WB
213	DRB1_1301	KVGIVYNYANASDL	3	IVYNYANAS	0.973	3ECA_A_PDBID_CH	0.576071	2.61	NA	<=WB
214	DRB1_1301	VGIVYNYANASDLP	2	IVYNYANAS	0.947	3ECA_A_PDBID_CH	0.452728	4.50	NA	<=WB
264	DRB1_1301	GTAVVRSSRVPTGA	3	VVRSSRVPT	0.987	3ECA_A_PDBID_CH	0.563172	2.77	NA	<=WB
130	DRB1_1301	YNAVVTAAADKASANR	4	VTAAADKASA	0.960	3ECA_A_PDBID_CH	0.608891	2.24	NA	<=WB
131	DRB1_1301	NAVVTAAADKASANRG	3	VTAAADKASA	0.987	3ECA_A_PDBID_CH	0.684887	1.44	NA	<=WB
163	DRB1_1301	TNTTDVATFKSVNYG	5	VATFKSVNY	0.993	3ECA_A_PDBID_CH	0.453859	4.48	NA	<=WB
164	DRB1_1301	NTTDVATFKSVNYGP	4	VATFKSVNY	1.000	3ECA_A_PDBID_CH	0.648380	1.81	NA	<=WB
165	DRB1_1301	TTDVATFKSVNYGPL	3	VATFKSVNY	0.993	3ECA_A_PDBID_CH	0.600451	2.33	NA	<=WB
182	DRB1_1301	IHNGKIDYQRTPARK	5	IDYQRTPAR	0.980	3ECA_A_PDBID_CH	0.636649	1.94	NA	<=WB
185	DRB1_1301	GKIDYQRTPARKHTS	2	IDYQRTPAR	0.960	3ECA_A_PDBID_CH	0.607344	2.26	NA	<=WB
211	DRB1_1301	LPKVGIVYNYANASD	5	IVYNYANAS	0.947	3ECA_A_PDBID_CH	0.502494	3.63	NA	<=WB
212	DRB1_1301	PKVGIVYNYANASDL	4	IVYNYANAS	0.973	3ECA_A_PDBID_CH	0.550376	2.92	NA	<=WB
213	DRB1_1301	KVGIVYNYANASDLP	3	IVYNYANAS	0.980	3ECA_A_PDBID_CH	0.646161	1.84	NA	<=WB
263	DRB1_1301	TGTAVVRSSRVPTGA	4	VVRSSRVPT	0.980	3ECA_A_PDBID_CH	0.529964	3.21	NA	<=WB

264	DRB1_1301	GTAVVRSSRVPTGAT	3	VVRSSRVPT	0.973	3ECA_A_PDBID_CH	0.571609	2.66	NA	<=WB
-----	-----------	-----------------	---	-----------	-------	-----------------	----------	------	----	------

Allele: DRB1_1501

42	DRB1_1501	LKDIANVKGEQVVN	3	IANVKGEQV	1.000	3ECA_A_PDBID_CH	0.731120	0.72	NA	<=SB
165	DRB1_1501	TTDVATFKSVNYGP	3	VATFKSVNY	1.000	3ECA_A_PDBID_CH	0.673522	0.90	NA	<=SB
41	DRB1_1501	QLKDIANVKGEQVVN	4	IANVKGEQV	1.000	3ECA_A_PDBID_CH	0.715774	0.76	NA	<=SB
42	DRB1_1501	LKDIANVKGEQVVNI	3	IANVKGEQV	1.000	3ECA_A_PDBID_CH	0.709645	0.78	NA	<=SB
124	DRB1_1501	DGPFNLYNAVVTAA	3	FNLYNAVVT	1.000	3ECA_A_PDBID_CH	0.690907	0.84	NA	<=SB
144	DRB1_1501	RGVLVVMNDTVLDGR	3	LVVMNDTVL	0.960	3ECA_A_PDBID_CH	0.694990	0.82	NA	<=SB
164	DRB1_1501	NTTDVATFKSVNYGP	4	VATFKSVNY	1.000	3ECA_A_PDBID_CH	0.658345	0.96	NA	<=SB
176	DRB1_1501	YGPLGYIHNGKIDYQ	3	LGYIHNGKI	1.000	3ECA_A_PDBID_CH	0.650172	0.99	NA	<=SB
43	DRB1_1501	KDIANVKGEQVV	2	IANVKGEQV	0.993	3ECA_A_PDBID_CH	0.313248	3.15	NA	<=WB
125	DRB1_1501	GPFNLYNAVVTAA	2	FNLYNAVVT	1.000	3ECA_A_PDBID_CH	0.249286	3.98	NA	<=WB
166	DRB1_1501	TDVATFKSVNYG	2	VATFKSVNY	1.000	3ECA_A_PDBID_CH	0.247827	4.00	NA	<=WB
177	DRB1_1501	GPLGYIHNGKID	2	LGYIHNGKI	0.973	3ECA_A_PDBID_CH	0.205518	4.87	NA	<=WB
42	DRB1_1501	LKDIANVKGEQVV	3	IANVKGEQV	1.000	3ECA_A_PDBID_CH	0.570010	1.34	NA	<=WB
43	DRB1_1501	KDIANVKGEQVVN	2	IANVKGEQV	1.000	3ECA_A_PDBID_CH	0.638603	1.04	NA	<=WB
123	DRB1_1501	ADGPFNLYNAVVT	4	FNLYNAVVT	0.973	3ECA_A_PDBID_CH	0.219501	4.58	NA	<=WB
124	DRB1_1501	DGPFNLYNAVVTAA	3	FNLYNAVVT	1.000	3ECA_A_PDBID_CH	0.555055	1.41	NA	<=WB
125	DRB1_1501	GPFNLYNAVVTAA	2	FNLYNAVVT	1.000	3ECA_A_PDBID_CH	0.465939	1.88	NA	<=WB
126	DRB1_1501	PFNLYNAVVTAA	1	FNLYNAVVT	0.993	3ECA_A_PDBID_CH	0.208326	4.81	NA	<=WB
144	DRB1_1501	RGVLVVMNDTVLD	3	LVVMNDTVL	0.907	3ECA_A_PDBID_CH	0.443797	2.02	NA	<=WB
145	DRB1_1501	GVLVVMNDTVLDG	2	LVVMNDTVL	0.940	3ECA_A_PDBID_CH	0.323788	3.03	NA	<=WB
165	DRB1_1501	TTDVATFKSVNYG	3	VATFKSVNY	1.000	3ECA_A_PDBID_CH	0.532377	1.51	NA	<=WB

166	DRB1_1501	TDVATFKSVNYGP	2	VATFKSVNY	1.000	3ECA_A_PDBID_CH	0.514772	1.61	NA	<=WB
176	DRB1_1501	YGPLGYIHNGKID	3	LGYIHNGKI	0.993	3ECA_A_PDBID_CH	0.447847	1.99	NA	<=WB
177	DRB1_1501	GPLGYIHNGKIDY	2	LGYIHNGKI	1.000	3ECA_A_PDBID_CH	0.454826	1.95	NA	<=WB
213	DRB1_1501	KVGIVYNYANASD	3	IVYNYANAS	0.620	3ECA_A_PDBID_CH	0.239978	4.16	NA	<=WB
214	DRB1_1501	VGIVYNYANASDL	3	VYNYANASD	0.733	3ECA_A_PDBID_CH	0.265123	3.76	NA	<=WB
215	DRB1_1501	GIVYNYANASDLP	2	VYNYANASD	0.887	3ECA_A_PDBID_CH	0.257497	3.87	NA	<=WB
39	DRB1_1501	VPQLKDIANVKGEQ	3	LKDIANVKG	1.000	3ECA_A_PDBID_CH	0.317961	3.10	NA	<=WB
40	DRB1_1501	PQLKDIANVKGEQV	2	LKDIANVKG	0.693	3ECA_A_PDBID_CH	0.234792	4.27	NA	<=WB
41	DRB1_1501	QLKDIANVKGEQVV	4	IANVKGEQV	0.993	3ECA_A_PDBID_CH	0.544961	1.46	NA	<=WB
43	DRB1_1501	KDIANVKGEQVVNI	2	IANVKGEQV	1.000	3ECA_A_PDBID_CH	0.627026	1.09	NA	<=WB
50	DRB1_1501	GEQVVNIGSQDMND	3	VVNIGSQDM	1.000	3ECA_A_PDBID_CH	0.287652	3.45	NA	<=WB
123	DRB1_1501	ADGPFNLYNAVVT	4	FNLYNAVVT	0.987	3ECA_A_PDBID_CH	0.520855	1.57	NA	<=WB
124	DRB1_1501	DGPFNLYNAVVTAA	3	FNLYNAVVT	1.000	3ECA_A_PDBID_CH	0.627178	1.09	NA	<=WB
125	DRB1_1501	GPFNLYNAVVTAAD	2	FNLYNAVVT	1.000	3ECA_A_PDBID_CH	0.546174	1.45	NA	<=WB
143	DRB1_1501	NRGVLVVMNDTVLD	4	LVVMNDTVL	0.747	3ECA_A_PDBID_CH	0.463977	1.89	NA	<=WB
144	DRB1_1501	RGVLVVMNDTVLDG	3	LVVMNDTVL	0.907	3ECA_A_PDBID_CH	0.581248	1.29	NA	<=WB
145	DRB1_1501	GVLVVMNDTVLDGR	2	LVVMNDTVL	0.953	3ECA_A_PDBID_CH	0.462374	1.90	NA	<=WB
164	DRB1_1501	NTTDVATFKSVNYG	4	VATFKSVNY	1.000	3ECA_A_PDBID_CH	0.491604	1.73	NA	<=WB
166	DRB1_1501	TDVATFKSVNYGPL	2	VATFKSVNY	1.000	3ECA_A_PDBID_CH	0.425956	2.16	NA	<=WB
175	DRB1_1501	NYGPLGYIHNGKID	4	LGYIHNGKI	0.980	3ECA_A_PDBID_CH	0.419418	2.21	NA	<=WB
176	DRB1_1501	YGPLGYIHNGKIDY	3	LGYIHNGKI	1.000	3ECA_A_PDBID_CH	0.571267	1.33	NA	<=WB
177	DRB1_1501	GPLGYIHNGKIDYQ	2	LGYIHNGKI	1.000	3ECA_A_PDBID_CH	0.533160	1.51	NA	<=WB
184	DRB1_1501	NGKIDYQRTPARKH	3	IDYQRTPAR	0.993	3ECA_A_PDBID_CH	0.206038	4.86	NA	<=WB
212	DRB1_1501	PKVGIVYNYANASD	4	IVYNYANAS	0.520	3ECA_A_PDBID_CH	0.257007	3.87	NA	<=WB
213	DRB1_1501	KVGIVYNYANASDL	4	VYNYANASD	0.533	3ECA_A_PDBID_CH	0.329602	2.97	NA	<=WB
214	DRB1_1501	VGIVYNYANASDLP	3	VYNYANASD	0.773	3ECA_A_PDBID_CH	0.404756	2.32	NA	<=WB

215	DRB1_1501	GIVYNYANASDLPA	2	VYNYANASD	0.940	3ECA_A_PDBID_CH	0.326109	3.00	NA	<=WB
38	DRB1_1501	AVPQLKDIANVKGEQ	4	LKDIANVKG	1.000	3ECA_A_PDBID_CH	0.327560	2.99	NA	<=WB
39	DRB1_1501	VPQLKDIANVKGEQV	3	LKDIANVKG	0.913	3ECA_A_PDBID_CH	0.369752	2.60	NA	<=WB
40	DRB1_1501	PQLKDIANVKGEQVV	5	IANVKGEQV	0.867	3ECA_A_PDBID_CH	0.486444	1.76	NA	<=WB
43	DRB1_1501	KDIANVKGEQVVNIG	2	IANVKGEQV	1.000	3ECA_A_PDBID_CH	0.524740	1.55	NA	<=WB
49	DRB1_1501	KGEQVVNIGSQDMND	4	VVNIGSQDM	1.000	3ECA_A_PDBID_CH	0.292557	3.40	NA	<=WB
50	DRB1_1501	GEQVVNIGSQDMNDN	3	VVNIGSQDM	1.000	3ECA_A_PDBID_CH	0.405126	2.32	NA	<=WB
122	DRB1_1501	SADGPFNLYNAVVT	5	FNLYNAVVT	0.987	3ECA_A_PDBID_CH	0.442219	2.03	NA	<=WB
123	DRB1_1501	ADGPFNLYNAVVTAA	4	FNLYNAVVT	1.000	3ECA_A_PDBID_CH	0.587291	1.26	NA	<=WB
125	DRB1_1501	GPFNLYNAVVTAAADK	2	FNLYNAVVT	0.993	3ECA_A_PDBID_CH	0.430430	2.12	NA	<=WB
142	DRB1_1501	ANRGVLVVMNDTVLD	5	LVVMNDTVL	0.753	3ECA_A_PDBID_CH	0.414541	2.25	NA	<=WB
143	DRB1_1501	NRGVLVVMNDTVLDG	4	LVVMNDTVL	0.780	3ECA_A_PDBID_CH	0.609664	1.16	NA	<=WB
145	DRB1_1501	GVLVVMNDTVLDGRD	2	LVVMNDTVL	0.953	3ECA_A_PDBID_CH	0.378788	2.52	NA	<=WB
163	DRB1_1501	TNTTDVATFKSVNYG	5	VATFKSVNY	1.000	3ECA_A_PDBID_CH	0.424914	2.17	NA	<=WB
165	DRB1_1501	TTDVATFKSVNYGPL	3	VATFKSVNY	1.000	3ECA_A_PDBID_CH	0.609214	1.16	NA	<=WB
166	DRB1_1501	TDVATFKSVNYGPLG	2	VATFKSVNY	1.000	3ECA_A_PDBID_CH	0.317866	3.10	NA	<=WB
174	DRB1_1501	VNYGPLGYIHNGKID	5	LGYIHNGKI	0.987	3ECA_A_PDBID_CH	0.341831	2.86	NA	<=WB
175	DRB1_1501	NYGPLGYIHNGKIDY	4	LGYIHNGKI	0.993	3ECA_A_PDBID_CH	0.540256	1.48	NA	<=WB
177	DRB1_1501	GPLGYIHNGKIDYQR	2	LGYIHNGKI	1.000	3ECA_A_PDBID_CH	0.420828	2.20	NA	<=WB
184	DRB1_1501	NGKIDYQRTPARKHT	3	IDYQRTPAR	0.987	3ECA_A_PDBID_CH	0.217859	4.61	NA	<=WB
211	DRB1_1501	LPKVGIVYNYANASD	3	VGIVYNYAN	0.413	3ECA_A_PDBID_CH	0.244185	4.08	NA	<=WB
212	DRB1_1501	PKVGIVYNYANASDL	5	VYNYANASD	0.440	3ECA_A_PDBID_CH	0.298246	3.33	NA	<=WB
213	DRB1_1501	KVGIVYNYANASDLP	4	VYNYANASD	0.633	3ECA_A_PDBID_CH	0.469879	1.86	NA	<=WB
214	DRB1_1501	VGIVYNYANASDLPA	3	VYNYANASD	0.933	3ECA_A_PDBID_CH	0.497247	1.70	NA	<=WB
215	DRB1_1501	GIVYNYANASDLPAK	2	VYNYANASD	0.873	3ECA_A_PDBID_CH	0.280540	3.54	NA	<=WB

Table S2. Output of the NetMHCIIpan version 4.0 program. for the 400H protein. Of a total of 2086 fragmented peptides, only those that bind to MHCII either weakly or strongly and are therefore considered antigenic are presented.

NetMHCIIpan version 4.0

Input is in FASTA format

Peptide length 9,10,11,12,13,14,15

Prediction Mode: EL

Threshold for Strong binding peptides (%Rank) 1%

Threshold for Weak binding peptides (%Rank) 5%

Allele: DRB1_0101

Pos	MHC	Peptide	Of	Core	Core_Rel	Identity	Score_EL	%Rank_EL	Exp_Bind	BindLevel
235	DRB1_0101	TLFHIEQGKTVE	2	FHIEQGKTV	1.000	400H_PDBID	0.794961	0.90	NA	<=SB
234	DRB1_0101	LTLFHIEQGKTVE	3	FHIEQGKTV	1.000	400H_PDBID	0.921956	0.33	NA	<=SB
235	DRB1_0101	TLFHIEQGKTVEE	2	FHIEQGKTV	1.000	400H_PDBID	0.947656	0.21	NA	<=SB
236	DRB1_0101	LFHIEQGKTVEEA	1	FHIEQGKTV	1.000	400H_PDBID	0.779704	0.97	NA	<=SB
233	DRB1_0101	RLTLFHIEQGKTVE	4	FHIEQGKTV	1.000	400H_PDBID	0.907577	0.39	NA	<=SB
234	DRB1_0101	LTLFHIEQGKTVEE	3	FHIEQGKTV	1.000	400H_PDBID	0.963580	0.13	NA	<=SB
235	DRB1_0101	TLFHIEQGKTVEEA	2	FHIEQGKTV	1.000	400H_PDBID	0.965539	0.12	NA	<=SB
232	DRB1_0101	ARLTLFHIEQGKTVE	5	FHIEQGKTV	1.000	400H_PDBID	0.844460	0.67	NA	<=SB
233	DRB1_0101	RLTLFHIEQGKTVEE	4	FHIEQGKTV	1.000	400H_PDBID	0.950899	0.20	NA	<=SB
234	DRB1_0101	LTLFHIEQGKTVEEA	3	FHIEQGKTV	1.000	400H_PDBID	0.968406	0.11	NA	<=SB
235	DRB1_0101	TLFHIEQGKTVEEAA	2	FHIEQGKTV	1.000	400H_PDBID	0.932854	0.28	NA	<=SB
257	DRB1_0101	KSRVKGLGGLIVVSK	3	VKGLGGLIV	1.000	400H_PDBID	0.843803	0.67	NA	<=SB
3	DRB1_0101	NPIVVHGGGAG	2	IVVHGGGA	1.000	400H_PDBID	0.266913	4.98	NA	<=WB
234	DRB1_0101	LTLFHIEQGKTV	3	FHIEQGKTV	1.000	400H_PDBID	0.321740	4.24	NA	<=WB
236	DRB1_0101	LFHIEQGKTVEE	1	FHIEQGKTV	1.000	400H_PDBID	0.540090	2.26	NA	<=WB

2	DRB1_0101	MNPIVVVHGGGAG	3	IVVVHGGGA	1.000	4O0H_PDBID	0.523037	2.37	NA	<=WB
3	DRB1_0101	NPIVVVHGGGAGP	2	IVVVHGGGA	1.000	4O0H_PDBID	0.626272	1.73	NA	<=WB
35	DRB1_0101	YGILREGGSAVD	3	ILREGGSAV	0.973	4O0H_PDBID	0.375503	3.65	NA	<=WB
36	DRB1_0101	YGILREGGSAVDA	2	ILREGGSAV	1.000	4O0H_PDBID	0.345526	3.96	NA	<=WB
105	DRB1_0101	LARLVMEKTPHCF	3	LVMEKTPHC	1.000	4O0H_PDBID	0.335812	4.07	NA	<=WB
106	DRB1_0101	ARLVMEKTPHCFL	2	LVMEKTPHC	1.000	4O0H_PDBID	0.298515	4.52	NA	<=WB
233	DRB1_0101	RLTLFHIEQGKTV	4	FHIEQGKTV	1.000	4O0H_PDBID	0.467340	2.81	NA	<=WB
257	DRB1_0101	KSRVKGLGGLIVV	3	VKGLGGLIV	1.000	4O0H_PDBID	0.605052	1.84	NA	<=WB
258	DRB1_0101	SRVKGLGGLIVVS	2	VKGLGGLIV	1.000	4O0H_PDBID	0.451764	2.94	NA	<=WB
1	DRB1_0101	HMNPIVVVHGGGAG	4	IVVVHGGGA	1.000	4O0H_PDBID	0.484795	2.66	NA	<=WB
2	DRB1_0101	MNPIVVVHGGGAGP	3	IVVVHGGGA	1.000	4O0H_PDBID	0.720307	1.24	NA	<=WB
3	DRB1_0101	NPIVVVHGGGAGPI	2	IVVVHGGGA	1.000	4O0H_PDBID	0.610306	1.82	NA	<=WB
34	DRB1_0101	VGYGILREGGSAVD	4	ILREGGSAV	0.847	4O0H_PDBID	0.364254	3.77	NA	<=WB
35	DRB1_0101	YGILREGGSAVDA	3	ILREGGSAV	0.993	4O0H_PDBID	0.611734	1.81	NA	<=WB
36	DRB1_0101	YGILREGGSAVDAV	2	ILREGGSAV	1.000	4O0H_PDBID	0.359834	3.81	NA	<=WB
104	DRB1_0101	KLARLVMEKTPHCF	4	LVMEKTPHC	1.000	4O0H_PDBID	0.289687	4.65	NA	<=WB
105	DRB1_0101	LARLVMEKTPHCFL	3	LVMEKTPHC	1.000	4O0H_PDBID	0.337699	4.05	NA	<=WB
106	DRB1_0101	ARLVMEKTPHCFLT	2	LVMEKTPHC	1.000	4O0H_PDBID	0.320367	4.25	NA	<=WB
123	DRB1_0101	AAQFAAAMGVPEIP	3	FAAAMGVPE	1.000	4O0H_PDBID	0.377623	3.63	NA	<=WB
124	DRB1_0101	AQFAAAMGVPEIPG	2	FAAAMGVPE	1.000	4O0H_PDBID	0.285966	4.70	NA	<=WB
180	DRB1_0101	NVAYATSTGGIVNK	3	YATSTGGIV	1.000	4O0H_PDBID	0.484222	2.66	NA	<=WB
188	DRB1_0101	GGIVNKMVGRVGDS	3	VNKMVGRVG	0.980	4O0H_PDBID	0.343882	3.98	NA	<=WB
232	DRB1_0101	ARLTLFHIEQGKTV	5	FHIEQGKTV	1.000	4O0H_PDBID	0.337233	4.06	NA	<=WB
236	DRB1_0101	LFHIEQGKTVEEAA	1	FHIEQGKTV	1.000	4O0H_PDBID	0.660758	1.55	NA	<=WB
256	DRB1_0101	MKSRVKGLGGLIVV	4	VKGLGGLIV	1.000	4O0H_PDBID	0.537931	2.27	NA	<=WB
257	DRB1_0101	KSRVKGLGGLIVVS	3	VKGLGGLIV	1.000	4O0H_PDBID	0.756743	1.09	NA	<=WB

258	DRB1_0101	SRVKGLGGLIVVSK	2	VKGLGGLIV	1.000	400H_PDBID	0.621928	1.75	NA	<=WB
1	DRB1_0101	HMNPIVVVHGGGAGP	4	IVVVHGGGA	1.000	400H_PDBID	0.734173	1.18	NA	<=WB
2	DRB1_0101	MNPIVVVHGGGAGPI	3	IVVVHGGGA	1.000	400H_PDBID	0.733037	1.18	NA	<=WB
3	DRB1_0101	NPIVVVHGGGAGPIS	2	IVVVHGGGA	0.987	400H_PDBID	0.540890	2.25	NA	<=WB
33	DRB1_0101	TVGYGILREGGSAVD	5	ILREGGSAV	0.627	400H_PDBID	0.360550	3.81	NA	<=WB
34	DRB1_0101	VGYGILREGGSAVDA	4	ILREGGSAV	0.987	400H_PDBID	0.600244	1.87	NA	<=WB
35	DRB1_0101	GYGILREGGSAVDAV	3	ILREGGSAV	1.000	400H_PDBID	0.655353	1.58	NA	<=WB
43	DRB1_0101	GSAVDAVEGAVVALE	3	VDAVEGAVV	0.993	400H_PDBID	0.301235	4.48	NA	<=WB
59	DRB1_0101	DPEFNAGCGSVLNTN	3	FNAGCGSVL	1.000	400H_PDBID	0.276263	4.85	NA	<=WB
104	DRB1_0101	KLARLVMEKTPHCFL	4	LVMEKTPHC	1.000	400H_PDBID	0.308310	4.40	NA	<=WB
105	DRB1_0101	LARLVMEKTPHCFLT	3	LVMEKTPHC	1.000	400H_PDBID	0.367026	3.74	NA	<=WB
122	DRB1_0101	GAAQFAAAMGVPEIP	4	FAAAMGVPE	1.000	400H_PDBID	0.369261	3.71	NA	<=WB
123	DRB1_0101	AAQFAAAMGVPEIPG	3	FAAAMGVPE	1.000	400H_PDBID	0.528276	2.33	NA	<=WB
178	DRB1_0101	KGNVAYATSTGGIVN	3	VAYATSTGG	0.547	400H_PDBID	0.274336	4.87	NA	<=WB
179	DRB1_0101	GNVAYATSTGGIVNK	4	YATSTGGIV	0.993	400H_PDBID	0.463845	2.84	NA	<=WB
180	DRB1_0101	NVAYATSTGGIVNKM	3	YATSTGGIV	1.000	400H_PDBID	0.457679	2.89	NA	<=WB
187	DRB1_0101	TGGIVNKMVGRVGDS	4	VNKMVGRVG	0.953	400H_PDBID	0.354398	3.87	NA	<=WB
188	DRB1_0101	GGIVNKMVGRVGDSP	3	VNKMVGRVG	0.993	400H_PDBID	0.503391	2.50	NA	<=WB
236	DRB1_0101	LFHIEQGKTVEEAAD	1	FHIEQGKTV	1.000	400H_PDBID	0.484952	2.65	NA	<=WB
255	DRB1_0101	YMKSRVKGLGGLIVV	5	VKGLGGLIV	1.000	400H_PDBID	0.447356	2.98	NA	<=WB
256	DRB1_0101	MKSRVKGLGGLIVVS	4	VKGLGGLIV	1.000	400H_PDBID	0.709083	1.31	NA	<=WB
258	DRB1_0101	SRVKGLGGLIVVSKT	2	VKGLGGLIV	1.000	400H_PDBID	0.487787	2.63	NA	<=WB
283	DRB1_0101	SMPWAAAKDGKLFHG	3	WAAAKDGKL	1.000	400H_PDBID	0.395875	3.44	NA	<=WB

Allele: DRB1_0301

13	DRB1_0301	AGPISKDRKERV	3	ISKDRKERV	1.000	400H_PDBID	0.795437	0.60	NA	<=SB
14	DRB1_0301	GPISKDRKERVH	2	ISKDRKERV	1.000	400H_PDBID	0.888930	0.29	NA	<=SB
15	DRB1_0301	PISKDRKERVHQ	1	ISKDRKERV	1.000	400H_PDBID	0.729421	0.87	NA	<=SB
12	DRB1_0301	GAGPISKDRKERV	4	ISKDRKERV	1.000	400H_PDBID	0.853889	0.40	NA	<=SB
13	DRB1_0301	AGPISKDRKERVH	3	ISKDRKERV	1.000	400H_PDBID	0.951725	0.09	NA	<=SB
14	DRB1_0301	GPISKDRKERVHQ	2	ISKDRKERV	1.000	400H_PDBID	0.941981	0.11	NA	<=SB
15	DRB1_0301	PISKDRKERVHQG	1	ISKDRKERV	1.000	400H_PDBID	0.835588	0.46	NA	<=SB
11	DRB1_0301	GGAGPISKDRKERV	5	ISKDRKERV	1.000	400H_PDBID	0.807664	0.55	NA	<=SB
12	DRB1_0301	GAGPISKDRKERVH	4	ISKDRKERV	1.000	400H_PDBID	0.948722	0.10	NA	<=SB
13	DRB1_0301	AGPISKDRKERVHQ	3	ISKDRKERV	1.000	400H_PDBID	0.961202	0.05	NA	<=SB
14	DRB1_0301	GPISKDRKERVHQG	2	ISKDRKERV	1.000	400H_PDBID	0.944649	0.10	NA	<=SB
15	DRB1_0301	PISKDRKERVHQGM	1	ISKDRKERV	1.000	400H_PDBID	0.767790	0.70	NA	<=SB
170	DRB1_0301	VGAVALDCKGNVAY	3	VALDCKGNV	1.000	400H_PDBID	0.732741	0.85	NA	<=SB
10	DRB1_0301	GGGAGPISKDRKERV	6	ISKDRKERV	1.000	400H_PDBID	0.730762	0.86	NA	<=SB
11	DRB1_0301	GGAGPISKDRKERVH	5	ISKDRKERV	1.000	400H_PDBID	0.932647	0.14	NA	<=SB
12	DRB1_0301	GAGPISKDRKERVHQ	4	ISKDRKERV	1.000	400H_PDBID	0.954829	0.07	NA	<=SB
13	DRB1_0301	AGPISKDRKERVHQG	3	ISKDRKERV	1.000	400H_PDBID	0.960116	0.05	NA	<=SB
14	DRB1_0301	GPISKDRKERVHQGM	2	ISKDRKERV	1.000	400H_PDBID	0.921955	0.18	NA	<=SB
73	DRB1_0301	NGEVEMDASIMDGKD	3	VEMDASIMD	1.000	400H_PDBID	0.763901	0.72	NA	<=SB
169	DRB1_0301	TVGAVALDCKGNVAY	4	VALDCKGNV	1.000	400H_PDBID	0.706531	0.96	NA	<=SB
170	DRB1_0301	VGAVALDCKGNVAYA	3	VALDCKGNV	1.000	400H_PDBID	0.745860	0.79	NA	<=SB
14	DRB1_0301	GPISKDRKERV	2	ISKDRKERV	1.000	400H_PDBID	0.563047	1.67	NA	<=WB
15	DRB1_0301	PISKDRKERVH	1	ISKDRKERV	1.000	400H_PDBID	0.536466	1.80	NA	<=WB
171	DRB1_0301	GAVALDCKGNVA	2	VALDCKGNV	1.000	400H_PDBID	0.406877	2.75	NA	<=WB
73	DRB1_0301	NGEVEMDASIMDG	3	VEMDASIMD	1.000	400H_PDBID	0.416057	2.67	NA	<=WB
74	DRB1_0301	GEVEMDASIMDGK	2	VEMDASIMD	1.000	400H_PDBID	0.450544	2.39	NA	<=WB

136	DRB1_0301	PGEKLVTERNKKR	4	LVTERNKKR	0.987	400H_PDBID	0.251198	4.50	NA	<=WB
137	DRB1_0301	GEKLVTERNKKRL	3	LVTERNKKR	1.000	400H_PDBID	0.420967	2.62	NA	<=WB
138	DRB1_0301	EKLVTERNKKRLE	2	LVTERNKKR	1.000	400H_PDBID	0.355246	3.20	NA	<=WB
169	DRB1_0301	TVGAVALDCKGNV	4	VALDCKGNV	1.000	400H_PDBID	0.307280	3.70	NA	<=WB
170	DRB1_0301	VGAVALDCKGNVA	3	VALDCKGNV	1.000	400H_PDBID	0.693143	1.02	NA	<=WB
171	DRB1_0301	GAVALDCKGNVAY	2	VALDCKGNV	1.000	400H_PDBID	0.621616	1.35	NA	<=WB
172	DRB1_0301	AVALDCKGNVAYA	1	VALDCKGNV	1.000	400H_PDBID	0.241995	4.66	NA	<=WB
295	DRB1_0301	HFGIDPDDTTITD	3	IDPDDTTIT	0.967	400H_PDBID	0.279165	4.07	NA	<=WB
72	DRB1_0301	TNGEVEMDASIMDG	4	VEMDASIMD	1.000	400H_PDBID	0.395541	2.84	NA	<=WB
73	DRB1_0301	NGEVEMDASIMDGK	3	VEMDASIMD	1.000	400H_PDBID	0.626170	1.33	NA	<=WB
74	DRB1_0301	GEVEMDASIMDGKD	2	VEMDASIMD	0.993	400H_PDBID	0.528498	1.85	NA	<=WB
136	DRB1_0301	PGEKLVTERNKKRL	4	LVTERNKKR	1.000	400H_PDBID	0.395662	2.84	NA	<=WB
137	DRB1_0301	GEKLVTERNKKRLE	3	LVTERNKKR	1.000	400H_PDBID	0.483708	2.16	NA	<=WB
138	DRB1_0301	EKLVTERNKKRLEK	2	LVTERNKKR	0.993	400H_PDBID	0.412246	2.70	NA	<=WB
168	DRB1_0301	GTVGAVALDCKGNV	5	VALDCKGNV	1.000	400H_PDBID	0.229031	4.88	NA	<=WB
169	DRB1_0301	TVGAVALDCKGNVA	4	VALDCKGNV	1.000	400H_PDBID	0.657289	1.19	NA	<=WB
171	DRB1_0301	GAVALDCKGNVAYA	2	VALDCKGNV	1.000	400H_PDBID	0.634596	1.29	NA	<=WB
285	DRB1_0301	PWAAAKDGKLFHFI	3	AAKDGKLFH	1.000	400H_PDBID	0.238018	4.72	NA	<=WB
294	DRB1_0301	LHFGIDPDDTTITD	4	IDPDDTTIT	0.893	400H_PDBID	0.272281	4.18	NA	<=WB
295	DRB1_0301	HFGIDPDDTTITDL	3	IDPDDTTIT	0.987	400H_PDBID	0.296260	3.84	NA	<=WB
296	DRB1_0301	FGIDPDDTTITDLP	2	IDPDDTTIT	1.000	400H_PDBID	0.228716	4.89	NA	<=WB
15	DRB1_0301	PISKDRKERVHQGMV	1	ISKDRKERV	1.000	400H_PDBID	0.678569	1.08	NA	<=WB
51	DRB1_0301	GAVVALEDDPEFNAG	5	LEDDPEFN	0.620	400H_PDBID	0.242519	4.65	NA	<=WB
71	DRB1_0301	NTNGEVEMDASIMDG	5	VEMDASIMD	1.000	400H_PDBID	0.415130	2.68	NA	<=WB
72	DRB1_0301	TNGEVEMDASIMDGK	4	VEMDASIMD	1.000	400H_PDBID	0.687719	1.04	NA	<=WB
74	DRB1_0301	GEVEMDASIMDGKDL	2	VEMDASIMD	1.000	400H_PDBID	0.533156	1.82	NA	<=WB

114	DRB1_0301	PHCFLTDQGAAQFAA	3	FLTDQGAAQ	1.000	400H_PDBID	0.244545	4.61	NA	<=WB
135	DRB1_0301	IPGEKLVTERNKKRL	5	LVTERNKKR	0.993	400H_PDBID	0.392786	2.87	NA	<=WB
136	DRB1_0301	PGEKLVTERNKKRLE	4	LVTERNKKR	1.000	400H_PDBID	0.513817	1.94	NA	<=WB
137	DRB1_0301	GEKLVTERNKKRLEK	3	LVTERNKKR	1.000	400H_PDBID	0.591510	1.51	NA	<=WB
138	DRB1_0301	EKLVTERNKKRLEKE	2	LVTERNKKR	0.993	400H_PDBID	0.384751	2.94	NA	<=WB
168	DRB1_0301	GTVGAVALDCKGNVA	5	VALDCKGNV	1.000	400H_PDBID	0.593264	1.50	NA	<=WB
171	DRB1_0301	GAVALDCKGNVAYAT	2	VALDCKGNV	1.000	400H_PDBID	0.530504	1.84	NA	<=WB
284	DRB1_0301	MPWAAAKDGKLHFGI	4	AAKDGKLHF	1.000	400H_PDBID	0.240768	4.68	NA	<=WB
285	DRB1_0301	PWAAAKDGKLHFGID	3	AAKDGKLHF	1.000	400H_PDBID	0.330045	3.43	NA	<=WB
293	DRB1_0301	KLHFGIDPDDTTITD	5	IDPDDTTIT	0.747	400H_PDBID	0.307529	3.70	NA	<=WB
294	DRB1_0301	LHFGIDPDDTTITDL	4	IDPDDTTIT	0.967	400H_PDBID	0.329248	3.44	NA	<=WB
295	DRB1_0301	HFGIDPDDTTITDLP	3	IDPDDTTIT	0.987	400H_PDBID	0.432742	2.52	NA	<=WB

Allele: DRB1_0401

106	DRB1_0401	ARLVMEKTPHCF	2	LVMEKTPHC	1.000	400H_PDBID	0.369495	3.42	NA	<=WB
73	DRB1_0401	NGEVEMDASIMDG	3	VEMDASIMD	1.000	400H_PDBID	0.295383	4.62	NA	<=WB
74	DRB1_0401	GEVEMDASIMDGK	2	VEMDASIMD	1.000	400H_PDBID	0.318607	4.20	NA	<=WB
104	DRB1_0401	KLARLVMEKTPHC	4	LVMEKTPHC	1.000	400H_PDBID	0.278960	4.94	NA	<=WB
105	DRB1_0401	LARLVMEKTPHCF	3	LVMEKTPHC	1.000	400H_PDBID	0.583614	1.47	NA	<=WB
106	DRB1_0401	ARLVMEKTPHCFL	2	LVMEKTPHC	1.000	400H_PDBID	0.469519	2.36	NA	<=WB
114	DRB1_0401	PHCFLTDQGAAQF	3	FLTDQGAAQ	1.000	400H_PDBID	0.531471	1.86	NA	<=WB
115	DRB1_0401	HCFLTDQGAAQFA	2	FLTDQGAAQ	1.000	400H_PDBID	0.372406	3.38	NA	<=WB
178	DRB1_0401	KGNVAYATSTGGI	3	VAYATSTGG	0.987	400H_PDBID	0.279827	4.92	NA	<=WB
293	DRB1_0401	KLHFGIDPDDTTI	3	FGIDPDDTT	0.973	400H_PDBID	0.293047	4.66	NA	<=WB
73	DRB1_0401	NGEVEMDASIMDGK	3	VEMDASIMD	1.000	400H_PDBID	0.527907	1.89	NA	<=WB

74	DRB1_0401	GEVEMDASIMDGKD	2	VEMDASIMD	1.000	400H_PDBID	0.404888	2.98	NA	<=WB
104	DRB1_0401	KLARLVMEKTPHCF	4	LVMEKTPHC	1.000	400H_PDBID	0.539727	1.80	NA	<=WB
105	DRB1_0401	LARLVMEKTPHCFL	3	LVMEKTPHC	1.000	400H_PDBID	0.513852	1.99	NA	<=WB
106	DRB1_0401	ARLVMEKTPHCFLT	2	LVMEKTPHC	1.000	400H_PDBID	0.456011	2.47	NA	<=WB
113	DRB1_0401	TPHCFLTDQGAAQF	4	FLTDQGAAQ	1.000	400H_PDBID	0.471377	2.34	NA	<=WB
114	DRB1_0401	PHCFLTDQGAAQFA	3	FLTDQGAAQ	1.000	400H_PDBID	0.625057	1.21	NA	<=WB
115	DRB1_0401	HCFLTDQGAAQFAA	2	FLTDQGAAQ	1.000	400H_PDBID	0.386352	3.20	NA	<=WB
178	DRB1_0401	KGNVAYATSTGGIV	3	VAYATSTGG	1.000	400H_PDBID	0.332082	3.98	NA	<=WB
293	DRB1_0401	KLHFGIDPDDTTIT	3	FGIDPDDTT	0.987	400H_PDBID	0.378625	3.30	NA	<=WB
294	DRB1_0401	LHFGIDPDDTTITD	2	FGIDPDDTT	0.533	400H_PDBID	0.302679	4.48	NA	<=WB
50	DRB1_0401	EGAVVALEDDPEFNA	3	VVALEDDPE	0.867	400H_PDBID	0.304441	4.45	NA	<=WB
72	DRB1_0401	TNGEVEMDASIMDGK	4	VEMDASIMD	1.000	400H_PDBID	0.513649	1.99	NA	<=WB
73	DRB1_0401	NGEVEMDASIMDGKD	3	VEMDASIMD	1.000	400H_PDBID	0.636779	1.14	NA	<=WB
74	DRB1_0401	GEVEMDASIMDGKDL	2	VEMDASIMD	1.000	400H_PDBID	0.330792	4.00	NA	<=WB
103	DRB1_0401	IKLARLVMEKTPHCF	5	LVMEKTPHC	1.000	400H_PDBID	0.427185	2.75	NA	<=WB
104	DRB1_0401	KLARLVMEKTPHCFL	4	LVMEKTPHC	1.000	400H_PDBID	0.446446	2.56	NA	<=WB
105	DRB1_0401	LARLVMEKTPHCFLT	3	LVMEKTPHC	1.000	400H_PDBID	0.474297	2.32	NA	<=WB
106	DRB1_0401	ARLVMEKTPHCFLTD	2	LVMEKTPHC	1.000	400H_PDBID	0.325840	4.08	NA	<=WB
112	DRB1_0401	KTPHCFLTDQGAAQF	5	FLTDQGAAQ	1.000	400H_PDBID	0.355881	3.61	NA	<=WB
113	DRB1_0401	TPHCFLTDQGAAQFA	4	FLTDQGAAQ	1.000	400H_PDBID	0.557882	1.67	NA	<=WB
114	DRB1_0401	PHCFLTDQGAAQFAA	3	FLTDQGAAQ	1.000	400H_PDBID	0.626289	1.20	NA	<=WB
123	DRB1_0401	AAQFAAAMGVPEIPG	3	FAAAMGVPE	0.993	400H_PDBID	0.285592	4.81	NA	<=WB
177	DRB1_0401	CKGNVAYATSTGGIV	4	VAYATSTGG	1.000	400H_PDBID	0.329979	4.01	NA	<=WB
178	DRB1_0401	KGNVAYATSTGGIVN	3	VAYATSTGG	1.000	400H_PDBID	0.435767	2.67	NA	<=WB
283	DRB1_0401	SMPWAAAKDGKLHFG	3	WAAAKDGKL	1.000	400H_PDBID	0.285509	4.81	NA	<=WB
292	DRB1_0401	GKLHFGIDPDDTTIT	4	FGIDPDDTT	0.967	400H_PDBID	0.353531	3.65	NA	<=WB

293	DRB1_0401	KLHFGIDPDDTTITD	3	FGIDPDDTT	0.813	400H_PDBID	0.511403	2.01	NA	<=WB
295	DRB1_0401	HFGIDPDDTTITDLP	3	IDPDDTTIT	0.953	400H_PDBID	0.299212	4.54	NA	<=WB

Allele: DRB1_0701

180	DRB1_0701	NVAYATSTGGIVN	3	YATSTGGIV	1.000	400H_PDBID	0.692139	0.75	NA	<=SB
181	DRB1_0701	VAYATSTGGIVNK	2	YATSTGGIV	1.000	400H_PDBID	0.632000	0.99	NA	<=SB
179	DRB1_0701	GNVAYATSTGGIVN	4	YATSTGGIV	0.993	400H_PDBID	0.669566	0.84	NA	<=SB
180	DRB1_0701	NVAYATSTGGIVNK	3	YATSTGGIV	1.000	400H_PDBID	0.810703	0.37	NA	<=SB
178	DRB1_0701	KGNVAYATSTGGIVN	5	YATSTGGIV	0.927	400H_PDBID	0.636043	0.97	NA	<=SB
179	DRB1_0701	GNVAYATSTGGIVNK	4	YATSTGGIV	0.973	400H_PDBID	0.804572	0.39	NA	<=SB
180	DRB1_0701	NVAYATSTGGIVNKM	3	YATSTGGIV	1.000	400H_PDBID	0.769086	0.49	NA	<=SB
180	DRB1_0701	NVAYATSTGGIV	3	YATSTGGIV	0.973	400H_PDBID	0.267935	4.42	NA	<=WB
181	DRB1_0701	VAYATSTGGIVN	2	YATSTGGIV	1.000	400H_PDBID	0.318897	3.59	NA	<=WB
123	DRB1_0701	AAQFAAAMGVPEI	3	FAAAMGVPE	0.980	400H_PDBID	0.253273	4.70	NA	<=WB
164	DRB1_0701	QKNLGTVGAVALD	3	LGTVGAVAL	1.000	400H_PDBID	0.323134	3.53	NA	<=WB
179	DRB1_0701	GNVAYATSTGGIV	4	YATSTGGIV	0.900	400H_PDBID	0.387379	2.73	NA	<=WB
234	DRB1_0701	LTLFHIEQGKTVE	3	FHIEQGKTV	1.000	400H_PDBID	0.331161	3.42	NA	<=WB
235	DRB1_0701	TLFHIEQGKTVEE	2	FHIEQGKTV	0.993	400H_PDBID	0.336301	3.35	NA	<=WB
252	DRB1_0701	SLGYMKSRVKGLG	3	YMKSRVKGL	1.000	400H_PDBID	0.474788	1.96	NA	<=WB
253	DRB1_0701	LGYSMKSRVKGLGG	2	YMKSRVKGL	1.000	400H_PDBID	0.355080	3.09	NA	<=WB
283	DRB1_0701	SMPWAAAKDGKLH	3	WAAAKDGKL	1.000	400H_PDBID	0.349419	3.17	NA	<=WB
122	DRB1_0701	GAAQFAAAMGVPEI	4	FAAAMGVPE	0.907	400H_PDBID	0.239993	4.97	NA	<=WB
123	DRB1_0701	AAQFAAAMGVPEIP	3	FAAAMGVPE	0.987	400H_PDBID	0.376377	2.85	NA	<=WB
124	DRB1_0701	AQFAAAMGVPEIPG	2	FAAAMGVPE	0.987	400H_PDBID	0.250850	4.75	NA	<=WB
163	DRB1_0701	CQKNLGTVGAVALD	4	LGTVGAVAL	1.000	400H_PDBID	0.297312	3.92	NA	<=WB

178	DRB1_0701	KGNVAYATSTGGIV	5	YATSTGGIV	0.760	400H_PDBID	0.339423	3.31	NA	<=WB
181	DRB1_0701	VAYATSTGGIVNKM	2	YATSTGGIV	1.000	400H_PDBID	0.555918	1.42	NA	<=WB
233	DRB1_0701	RLTLFHIEQGKTVE	4	FHIEQGKTV	1.000	400H_PDBID	0.314186	3.67	NA	<=WB
234	DRB1_0701	LTLFHIEQGKTVEE	3	FHIEQGKTV	0.993	400H_PDBID	0.403341	2.56	NA	<=WB
235	DRB1_0701	TLFHIEQGKTVEEA	2	FHIEQGKTV	0.987	400H_PDBID	0.370295	2.91	NA	<=WB
251	DRB1_0701	LSLGYMKSRVKGLG	4	YMKSRVKGL	1.000	400H_PDBID	0.426749	2.35	NA	<=WB
252	DRB1_0701	SLGYMKSRVKGLGG	3	YMKSRVKGL	1.000	400H_PDBID	0.522432	1.63	NA	<=WB
253	DRB1_0701	LGYSMKSRVKGLGGL	2	YMKSRVKGL	1.000	400H_PDBID	0.258149	4.60	NA	<=WB
282	DRB1_0701	TSMFWAAAKDGKLH	4	WAAAKDGKL	1.000	400H_PDBID	0.339025	3.31	NA	<=WB
283	DRB1_0701	SMPWAAAKDGKLHF	3	WAAAKDGKL	1.000	400H_PDBID	0.350708	3.15	NA	<=WB
1	DRB1_0701	HMNPVVHGGGAGP	4	IVVVHGGGA	0.993	400H_PDBID	0.263757	4.49	NA	<=WB
2	DRB1_0701	MNPVVHGGGAGPI	3	IVVVHGGGA	0.953	400H_PDBID	0.250739	4.75	NA	<=WB
121	DRB1_0701	QGAAQFAAAMGVPEI	5	FAAAMGVPE	0.693	400H_PDBID	0.248672	4.79	NA	<=WB
122	DRB1_0701	GAAQFAAAMGVPEIP	4	FAAAMGVPE	0.973	400H_PDBID	0.385080	2.76	NA	<=WB
123	DRB1_0701	AAQFAAAMGVPEIPG	3	FAAAMGVPE	0.987	400H_PDBID	0.449923	2.16	NA	<=WB
162	DRB1_0701	DCQKNLGTVGAVALD	5	LGTVGAVAL	0.993	400H_PDBID	0.283205	4.16	NA	<=WB
164	DRB1_0701	QKNLGTVGAVALDCK	3	LGTVGAVAL	0.993	400H_PDBID	0.286821	4.09	NA	<=WB
177	DRB1_0701	CKGNVAYATSTGGIV	6	YATSTGGIV	0.700	400H_PDBID	0.293971	3.98	NA	<=WB
181	DRB1_0701	VAYATSTGGIVNKMV	2	YATSTGGIV	0.993	400H_PDBID	0.449922	2.16	NA	<=WB
232	DRB1_0701	ARLTLFHIEQGKTVE	5	FHIEQGKTV	0.987	400H_PDBID	0.259722	4.57	NA	<=WB
233	DRB1_0701	RLTLFHIEQGKTVEE	4	FHIEQGKTV	0.993	400H_PDBID	0.381479	2.79	NA	<=WB
234	DRB1_0701	LTLFHIEQGKTVEEA	3	FHIEQGKTV	1.000	400H_PDBID	0.420689	2.40	NA	<=WB
235	DRB1_0701	TLFHIEQGKTVEEAA	2	FHIEQGKTV	0.967	400H_PDBID	0.281718	4.18	NA	<=WB
250	DRB1_0701	DLSLGYMKSRVKGLG	5	YMKSRVKGL	0.987	400H_PDBID	0.362089	3.00	NA	<=WB
251	DRB1_0701	LSLGYMKSRVKGLGG	4	YMKSRVKGL	1.000	400H_PDBID	0.503141	1.76	NA	<=WB
252	DRB1_0701	SLGYMKSRVKGLGGL	3	YMKSRVKGL	1.000	400H_PDBID	0.433228	2.30	NA	<=WB

281	DRB1_0701	STSMPWAAAKDGKLH	5	WAAAKDGKL	1.000	400H_PDBID	0.341089	3.28	NA	<=WB
282	DRB1_0701	TSMPWAAAKDGKLHF	4	WAAAKDGKL	1.000	400H_PDBID	0.385034	2.76	NA	<=WB
283	DRB1_0701	SMPWAAAKDGKLHFG	3	WAAAKDGKL	1.000	400H_PDBID	0.434615	2.29	NA	<=WB

Allele: DRB1_0801

263	DRB1_0801	LGGLIVVSKTGDW	3	LIVVSKTGD	1.000	400H_PDBID	0.847285	0.38	NA	<=SB
264	DRB1_0801	GGLIVVSKTGDWV	2	LIVVSKTGD	1.000	400H_PDBID	0.835851	0.43	NA	<=SB
262	DRB1_0801	GLGGLIVVSKTGDW	4	LIVVSKTGD	1.000	400H_PDBID	0.821740	0.50	NA	<=SB
263	DRB1_0801	LGGLIVVSKTGDWV	3	LIVVSKTGD	1.000	400H_PDBID	0.840129	0.41	NA	<=SB
264	DRB1_0801	GGLIVVSKTGDWVA	2	LIVVSKTGD	1.000	400H_PDBID	0.853021	0.36	NA	<=SB
261	DRB1_0801	KGLGGLIVVSKTGDW	5	LIVVSKTGD	1.000	400H_PDBID	0.767702	0.80	NA	<=SB
262	DRB1_0801	GLGGLIVVSKTGDWV	4	LIVVSKTGD	1.000	400H_PDBID	0.819479	0.51	NA	<=SB
263	DRB1_0801	LGGLIVVSKTGDWVA	3	LIVVSKTGD	1.000	400H_PDBID	0.857689	0.34	NA	<=SB
264	DRB1_0801	GGLIVVSKTGDWVAK	2	LIVVSKTGD	0.993	400H_PDBID	0.767018	0.81	NA	<=SB
263	DRB1_0801	LGGLIVVSKTGD	3	LIVVSKTGD	1.000	400H_PDBID	0.526083	3.17	NA	<=WB
264	DRB1_0801	GGLIVVSKTGDW	2	LIVVSKTGD	1.000	400H_PDBID	0.717812	1.16	NA	<=WB
262	DRB1_0801	GLGGLIVVSKTGD	4	LIVVSKTGD	0.987	400H_PDBID	0.656790	1.66	NA	<=WB
265	DRB1_0801	GLIVVSKTGDWVA	1	LIVVSKTGD	0.993	400H_PDBID	0.518842	3.28	NA	<=WB
261	DRB1_0801	KGLGGLIVVSKTGD	5	LIVVSKTGD	0.980	400H_PDBID	0.557018	2.75	NA	<=WB
272	DRB1_0801	TGDWVAKWTSTSM	3	WVAKWTSTS	0.953	400H_PDBID	0.482560	3.85	NA	<=WB
260	DRB1_0801	VKGLGGLIVVSKTGD	6	LIVVSKTGD	0.967	400H_PDBID	0.436428	4.73	NA	<=WB
271	DRB1_0801	KTGDWVAKWTSTSM	4	WVAKWTSTS	0.960	400H_PDBID	0.459674	4.26	NA	<=WB

Allele: DRB1_1101

2	DRB1_1101	MNPIVVVHGGGAGP	3	IVVVHGGGA	0.980	400H_PDBID	0.370587	4.61	NA	<=WB
146	DRB1_1101	KKRLEKEKHEKGAQ	3	LEKEKHEKG	1.000	400H_PDBID	0.412402	4.08	NA	<=WB
263	DRB1_1101	LGGLIVVSKTGDWV	3	LIVVSKTGD	1.000	400H_PDBID	0.395112	4.29	NA	<=WB
264	DRB1_1101	GGLIVVSKTGDWVA	2	LIVVSKTGD	0.993	400H_PDBID	0.416927	4.02	NA	<=WB
1	DRB1_1101	HMNPIVVVHGGGAGP	4	IVVVHGGGA	0.960	400H_PDBID	0.390631	4.34	NA	<=WB
2	DRB1_1101	MNPIVVVHGGGAGPI	3	IVVVHGGGA	0.973	400H_PDBID	0.360103	4.78	NA	<=WB
33	DRB1_1101	TVGYGILREGGSAVD	3	YGILREGGS	1.000	400H_PDBID	0.421324	3.97	NA	<=WB
145	DRB1_1101	NKKRLEKEKHEKGAQ	4	LEKEKHEKG	1.000	400H_PDBID	0.394799	4.29	NA	<=WB
146	DRB1_1101	KKRLEKEKHEKGAQK	3	LEKEKHEKG	1.000	400H_PDBID	0.512616	2.94	NA	<=WB
262	DRB1_1101	GLGGLIVVSKTGDWV	4	LIVVSKTGD	1.000	400H_PDBID	0.383862	4.42	NA	<=WB
263	DRB1_1101	LGGLIVVSKTGDWVA	3	LIVVSKTGD	1.000	400H_PDBID	0.505084	3.01	NA	<=WB

Allele: DRB1_1301

137	DRB1_1301	GEKLVTERNKKRLE	3	LVTERNKKR	0.667	400H_PDBID	0.775160	0.78	NA	<=SB
138	DRB1_1301	EKLVTERNKKRLEK	3	VTERNKKRL	0.573	400H_PDBID	0.804879	0.58	NA	<=SB
136	DRB1_1301	PGEKLVTERNKKRLE	4	LVTERNKKR	0.680	400H_PDBID	0.751393	0.92	NA	<=SB
137	DRB1_1301	GEKLVTERNKKRLEK	3	LVTERNKKR	0.593	400H_PDBID	0.839923	0.39	NA	<=SB
138	DRB1_1301	EKLVTERNKKRLEKE	3	VTERNKKRL	0.740	400H_PDBID	0.801169	0.61	NA	<=SB
13	DRB1_1301	AGPISKDRKERVH	3	ISKDRKERV	0.967	400H_PDBID	0.523783	3.30	NA	<=WB
14	DRB1_1301	GPISKDRKERVHQ	2	ISKDRKERV	0.993	400H_PDBID	0.500647	3.66	NA	<=WB
137	DRB1_1301	GEKLVTERNKKRL	3	LVTERNKKR	0.840	400H_PDBID	0.628310	2.03	NA	<=WB
138	DRB1_1301	EKLVTERNKKRLE	3	VTERNKKRL	0.520	400H_PDBID	0.700606	1.31	NA	<=WB

139	DRB1_1301	KLVTERNKKRLEK	2	VTERNKKRL	0.713	400H_PDBID	0.617134	2.15	NA	<=WB
2	DRB1_1301	MNPVVHGGGAGP	3	IVVVHGGGA	0.640	400H_PDBID	0.436216	4.81	NA	<=WB
12	DRB1_1301	GAGPISKDRKERVH	4	ISKDRKERV	0.920	400H_PDBID	0.534821	3.14	NA	<=WB
13	DRB1_1301	AGPISKDRKERVHQ	3	ISKDRKERV	0.987	400H_PDBID	0.628198	2.03	NA	<=WB
14	DRB1_1301	GPISKDRKERVHQG	2	ISKDRKERV	1.000	400H_PDBID	0.569367	2.69	NA	<=WB
136	DRB1_1301	PGEKLVTERNKKRL	4	LVTERNKKR	0.860	400H_PDBID	0.610364	2.22	NA	<=WB
139	DRB1_1301	KLVTERNKKRLEKE	2	VTERNKKRL	0.820	400H_PDBID	0.640646	1.90	NA	<=WB
187	DRB1_1301	TGGIVNKMVGRVGD	3	IVNKMVGRV	0.967	400H_PDBID	0.521849	3.33	NA	<=WB
188	DRB1_1301	GGIVNKMVGRVGDS	2	IVNKMVGRV	0.887	400H_PDBID	0.431720	4.90	NA	<=WB
1	DRB1_1301	HMNPIVVHGGGAGP	4	IVVVHGGGA	0.667	400H_PDBID	0.469446	4.20	NA	<=WB
2	DRB1_1301	MNPVVHGGGAGPI	3	IVVVHGGGA	0.567	400H_PDBID	0.501903	3.64	NA	<=WB
3	DRB1_1301	NPIVVHGGGAGPIS	3	VVVHGGGAG	0.633	400H_PDBID	0.469823	4.19	NA	<=WB
11	DRB1_1301	GGAGPISKDRKERVH	5	ISKDRKERV	0.873	400H_PDBID	0.495831	3.74	NA	<=WB
12	DRB1_1301	GAGPISKDRKERVHQ	4	ISKDRKERV	0.927	400H_PDBID	0.629941	2.01	NA	<=WB
13	DRB1_1301	AGPISKDRKERVHQG	3	ISKDRKERV	0.980	400H_PDBID	0.676421	1.52	NA	<=WB
14	DRB1_1301	GPISKDRKERVHQGM	2	ISKDRKERV	0.993	400H_PDBID	0.508031	3.54	NA	<=WB
135	DRB1_1301	IPGEKLVTERNKKRL	5	LVTERNKKR	0.867	400H_PDBID	0.545423	2.98	NA	<=WB
139	DRB1_1301	KLVTERNKKRLEKEK	2	VTERNKKRL	0.813	400H_PDBID	0.546870	2.97	NA	<=WB
186	DRB1_1301	STGGIVNKMVGRVGD	4	IVNKMVGRV	0.960	400H_PDBID	0.528945	3.22	NA	<=WB
187	DRB1_1301	TGGIVNKMVGRVGDS	3	IVNKMVGRV	0.960	400H_PDBID	0.590800	2.44	NA	<=WB

Allele: DRB1_1501

3	DRB1_1501	NPIVVHGGGAG	2	IVVVHGGGA	0.993	400H_PDBID	0.261895	3.81	NA	<=WB
2	DRB1_1501	MNPVVHGGGAG	3	IVVVHGGGA	1.000	400H_PDBID	0.479346	1.80	NA	<=WB

3	DRB1_1501	NPIVVVHGGGAGP	2	IVVVHGGGA	0.960	400H_PDBID	0.535023	1.50	NA	<=WB
257	DRB1_1501	KSRVKGLGGLIVV	3	VKGLGGLIV	1.000	400H_PDBID	0.210067	4.77	NA	<=WB
273	DRB1_1501	GDWVAKWTSTSM	3	VAKWTSTSM	0.993	400H_PDBID	0.271760	3.67	NA	<=WB
1	DRB1_1501	HMNPIVVVHGGGAG	4	IVVVHGGGA	0.993	400H_PDBID	0.454273	1.95	NA	<=WB
2	DRB1_1501	MNPIVVVHGGGAGP	3	IVVVHGGGA	0.987	400H_PDBID	0.623864	1.10	NA	<=WB
3	DRB1_1501	NPIVVVHGGGAGPI	2	IVVVHGGGA	0.907	400H_PDBID	0.520709	1.58	NA	<=WB
257	DRB1_1501	KSRVKGLGGLIVVS	3	VKGLGGLIV	1.000	400H_PDBID	0.317373	3.11	NA	<=WB
258	DRB1_1501	SRVKGLGGLIVVSK	2	VKGLGGLIV	1.000	400H_PDBID	0.200532	4.97	NA	<=WB
272	DRB1_1501	TGDWVAKWTSTSM	4	VAKWTSTSM	0.980	400H_PDBID	0.244537	4.07	NA	<=WB
273	DRB1_1501	GDWVAKWTSTSM	3	VAKWTSTSM	1.000	400H_PDBID	0.291959	3.40	NA	<=WB
1	DRB1_1501	HMNPIVVVHGGGAGP	4	IVVVHGGGA	0.987	400H_PDBID	0.624314	1.10	NA	<=WB
2	DRB1_1501	MNPIVVVHGGGAGPI	3	IVVVHGGGA	0.947	400H_PDBID	0.624292	1.10	NA	<=WB
3	DRB1_1501	NPIVVVHGGGAGPIS	2	IVVVHGGGA	0.827	400H_PDBID	0.469541	1.86	NA	<=WB
35	DRB1_1501	GYGILREGGSAVDAV	3	ILREGGSAV	0.993	400H_PDBID	0.210121	4.77	NA	<=WB
256	DRB1_1501	MKSRVKGLGGLIVVS	4	VKGLGGLIV	1.000	400H_PDBID	0.283149	3.51	NA	<=WB
257	DRB1_1501	KSRVKGLGGLIVVSK	3	VKGLGGLIV	1.000	400H_PDBID	0.427525	2.15	NA	<=WB
271	DRB1_1501	KTGDWVAKWTSTSM	5	VAKWTSTSM	0.960	400H_PDBID	0.209546	4.78	NA	<=WB
272	DRB1_1501	TGDWVAKWTSTSM	4	VAKWTSTSM	0.993	400H_PDBID	0.290189	3.42	NA	<=WB
273	DRB1_1501	GDWVAKWTSTSM	3	VAKWTSTSM	1.000	400H_PDBID	0.395839	2.39	NA	<=WB

Table S3 Epitope density of the 3ECA ,400H and 3ECA Humanized Chimeric Protein proteins. To calculate the relative frequency, the formula $f_i = n_i / N$ was used, where n_i is the number of predicted immunogenic epitopes, and N is the total number of epitopes determined by the program (immunogenic and nonimmunogenic). The epitope density of each protein was determined for the alleles HLA-DRB1*01:01, HLA-DRB1*03:01, HLA-DRB1*04:01, HLA-DRB1*07:01, HLA-DRB1*08:01, HLA-DRB1*11:01, HLA-DRB1*13:01 and HLA-DRB1*15:01, which are reference alleles in the literature with a wide global frequency.

Allele	3ECA Protien			400H Protein		
	Total Immunogenic Epitopes (ni)	Total Epitopes (N)	fi	Total Immunogenic Epitopes (ni)	Total Epitopes (N)	fi
HLA-DRB1*01:01	71	2205	0.032	64	2086	0.031
HLA-DRB1*03:01	33	2205	0.014	64	2086	0.031
HLA-DRB1*04:01	94	2205	0.042	39	2086	0.019
HLA-DRB1*07:01	162	2205	0.073	50	2086	0.024
HLA-DRB1*08:01	33	2205	0.014	17	2086	0.008
HLA-DRB1*11:01	36	2205	0.016	11	2086	0.005
HLA-DRB1*13:01	31	2205	0.014	29	2086	0.014
HLA-DRB1*15:01	72	2205	0.032	21	2086	0.010

Allele	3ECA Humanized Chimera Protein		
	Total Immunogenic Epitopes (ni)	Total Epitopes (N)	fi
HLA-DRB1*01:01	76	2205	0.034
HLA-DRB1*03:01	40	2205	0.018
HLA-DRB1*04:01	105	2205	0.048
HLA-DRB1*07:01	148	2205	0.067
HLA-DRB1*08:01	22	2205	0.010
HLA-DRB1*11:01	36	2205	0.016
HLA-DRB1*13:01	28	2205	0.013
HLA-DRB1*15:01	53	2205	0.024

Table S4. Affinity results of 7 ligands evaluated in retrospective docking with Chimeric Asparaginase.

The asparagine value appears in blue.

The ligands were chosen at random, conserving glutamine and asparagine: glutamine(5961), ATP(5957), leucine(6106) ,phenylalanine(994), tyrosine(6075), tryptophan(6305), asparagine(6267).

Ligand	Binding Affinity	rmsd/ub	rmsd/lb
recpetor6_6106	-4.7	0.0	0.0
recpetor6_6106	-4.6	14.218	13.704
recpetor6_6106	-4.6	24.905	24.07
recpetor6_6106	-4.6	12.513	11.765
recpetor6_6106	-4.5	25.568	24.34
recpetor6_6106	-4.5	26.509	25.414
recpetor6_6106	-4.5	33.083	31.617
recpetor6_6106	-4.5	20.956	19.886
recpetor6_6106	-4.4	27.881	26.661
recpetor6_5957	-7.9	0.0	0.0
recpetor6_5957	-7.6	15.225	12.788
recpetor6_5957	-7.6	14.934	12.216
recpetor6_5957	-7.4	15.815	13.528
recpetor6_5957	-7.2	5.255	3.033
recpetor6_5957	-7.2	15.617	13.358
recpetor6_5957	-7.1	14.856	12.146
recpetor6_5957	-7.1	6.886	4.195
recpetor6_5957	-7.1	5.725	4.259
recpetor6_6305	-6.7	0.0	0.0
recpetor6_6305	-6.6	11.988	10.524
recpetor6_6305	-6.6	5.838	4.309
recpetor6_6305	-6.4	2.251	1.688
recpetor6_6305	-6.4	17.587	16.113
recpetor6_6305	-6.4	24.662	23.536
recpetor6_6305	-6.3	18.273	16.779
recpetor6_6305	-6.2	2.961	2.318
recpetor6_6305	-6.1	30.02	28.437
recpetor6_6057	-6.5	0.0	0.0
recpetor6_6057	-6.3	38.012	36.756
recpetor6_6057	-6.2	23.791	22.529
recpetor6_6057	-6.2	37.511	36.288
recpetor6_6057	-6.2	38.026	37.053
recpetor6_6057	-6.2	13.536	12.375
recpetor6_6057	-6.1	16.368	14.91
recpetor6_6057	-6.1	25.283	24.11
recpetor6_6057	-6.1	37.08	36.074
recpetor6_994	-6.0	0.0	0.0
recpetor6_994	-5.9	12.264	11.3
recpetor6_994	-5.9	25.553	24.613
recpetor6_994	-5.9	19.581	18.578
recpetor6_994	-5.8	16.055	14.762
recpetor6_994	-5.8	5.978	4.597
recpetor6_994	-5.7	17.316	16.249
recpetor6_994	-5.6	19.232	17.884
recpetor6_994	-5.6	29.337	27.709

recpetor6_5961	-5.7	0.0	0.0
recpetor6_5961	-5.1	4.324	2.047
recpetor6_5961	-5.0	16.51	15.663
recpetor6_5961	-5.0	17.922	17.108
recpetor6_5961	-4.9	29.228	28.392
recpetor6_5961	-4.9	39.943	39.208
recpetor6_5961	-4.7	22.375	21.551
recpetor6_5961	-4.7	23.583	22.604
recpetor6_5961	-4.7	15.388	14.57
recpetor6_6267	-5.9	0.0	0.0
recpetor6_6267	-5.9	28.312	26.825
recpetor6_6267	-5.8	16.66	15.655
recpetor6_6267	-5.7	16.643	15.667
recpetor6_6267	-5.7	28.275	26.577
recpetor6_6267	-5.7	3.793	2.024
recpetor6_6267	-5.5	11.221	10.456
recpetor6_6267	-5.5	7.378	6.081
recpetor6_6267	-5.4	11.102	10.313

Table S5. Docking of the native enzyme 3ECA with the ligand asparagine. Affinity Results

Ligand	Binding Affinity	rmsd/ub	rmsd/lb
3eca_cleaned_6267_uff_E=44.03	-5.6	0.0	0.0
3eca_cleaned_6267_uff_E=44.03	-5.5	3.805	1.551
3eca_cleaned_6267_uff_E=44.03	-5.5	29.988	28.166
3eca_cleaned_6267_uff_E=44.03	-5.4	29.74	28.281
3eca_cleaned_6267_uff_E=44.03	-5.4	30.121	28.93
3eca_cleaned_6267_uff_E=44.03	-5.4	6.634	6.056
3eca_cleaned_6267_uff_E=44.03	-5.2	4.03	2.14
3eca_cleaned_6267_uff_E=44.03	-5.2	6.861	5.852
3eca_cleaned_6267_uff_E=44.03	-5.2	7.076	6.322