

Additional File 1

pDOCK: A new technique for rapid and accurate docking of peptide ligands to Major Histocompatibility Complexes

Javed M. Khan and Shoba Ranganathan

Table S1 – Application of pDOCK to the 186 (149 MHC-I and 37 MHC-II) non-redundant structures from MPID-T2 database.

C α RMSD values are calculated only for the nonameric core (shown in bold) forming the MHC binding register for peptides with more than 9 residues in the X-ray crystal structures. X: Chemical mimics.

Allele	PDB code	Peptide Sequence	Peptide Length	Res. (Å)	C α RMSD (Å)
MHC-I					
HLA-A*0101	1w72	EADPTGHSY	9	2.15	0.42
HLA-A*1101	1qvo	QVPLRPMTYK	10	2.22	0.24
HLA-A*1101	1x7q	KTFPPTEPK	9	1.45	0.36
HLA-A*1101	2hn7	AIMPARFYPK	10	1.60	1.40
HLA-A*1101	1q94	AIFQSSMTK	9	2.40	1.52
HLA-A*0201	1oga	GILGFVFTL	9	1.40	0.16
HLA-A*0201	1t1y	SLYNVVATL	9	2.00	0.78
HLA-A*0201	1s8d	SLANTVATL	9	2.20	0.65
HLA-A*0201	2gtz	ALGIGILTV	9	1.70	0.95
HLA-A*0201	1duy	LFGYPVYV	8	2.15	1.12
HLA-A*0201	2p5w	SLLMWITQC	9	2.20	0.35
HLA-A*0201	2v2w	SLYNTVATL	9	1.60	0.55
HLA-A*0201	2v2x	SLFNTVATL	9	1.60	0.78
HLA-A*0201	1qr1	IISAVVGIL	9	2.40	0.29
HLA-A*0201	1qrn	LLFGYAVYV	9	2.80	0.91
HLA-A*0201	1qse	LLFGYPRYV	9	2.80	0.31
HLA-A*0201	1qsf	LLFGYPVAV	9	2.80	0.34
HLA-A*0201	1hhg	TLTSCNTSV	9	2.60	1.18
HLA-A*0201	1lp9	ALWGFFPVL	9	2.00	0.26
HLA-A*0201	1s9x	SLLMWITQA	9	2.50	0.44
HLA-A*0201	1s9y	SLLMWITQS	9	2.30	0.39
HLA-A*0201	1tvb	ITDQVPFSV	9	1.80	0.38
HLA-A*0201	1tvh	IMDQVPFSV	9	1.80	0.43
HLA-A*0201	1akj	ILKEPVHGV	9	2.65	0.39
HLA-A*0201	1eey	ILSALVGIV	9	2.25	0.92
HLA-A*0201	2guo	AAGIGILTV	9	1.90	2.14
HLA-A*0201	1t20	SLYNNTIATL	9	2.20	0.82
HLA-A*0201	1ao7	LLFGYPVYV	9	2.60	0.58
HLA-A*0201	1eez	ILSALVGIL	9	2.30	0.71

Allele	PDB code	Peptide Sequence	Peptide Length	Res. (Å)	Cα RMSD (Å)
HLA-A*0201	2gj6	LLFGKPVYV	9	2.56	0.97
HLA-A*0201	1hhh	FLPSDFFPSV	10	3.00	0.49
HLA-A*0201	1i1f	FLKEPVHGV	9	2.80	0.64
HLA-A*0201	2clr	MLLSVPLLIG	10	2.00	1.01
HLA-A*0201	2gt9	EAAGIGILTV	10	1.75	0.26
HLA-A*0201	1i7r	FAPGFFPYL	9	2.20	0.47
HLA-A*0201	1i7t	ALWGVFPVL	9	2.80	0.42
HLA-A*0201	1i7u	ALWGFVPVL	9	1.80	0.29
HLA-A*0201	1jf1	ELAGIGILTV	10	1.85	0.30
HLA-A*0201	1t1x	SLYLTVATL	9	2.20	1.72
HLA-A*0201	1i1y	YLKEPVHGV	9	2.20	0.66
HLA-A*0201	1t1z	ALYNNTAAAL	9	1.90	1.15
HLA-A*0201	2bnq	SLLMWITQV	9	1.70	0.55
HLA-A*0201	2c7u	SLFNTIAVL	9	2.38	0.86
HLA-A*0201	1i4f	GVYDGREHTV	10	1.40	1.25
HLA-A*0201	1bd2	LLFGYPVYV	9	2.50	0.33
HLA-A*0201	2gtw	LAGIGILTV	9	1.55	3.08
HLA-A*2402	2bck	VYGFVRACL	9	2.80	0.79
HLA-A*6801	1tmc	EVAPPEYHRK	10	2.30	0.54
HLA-B*0801	1agc	GGKKKYQL	8	2.10	0.23
HLA-B*0801	1agd	GGKKKYKL	8	2.05	0.45
HLA-B*0801	1agb	GGRKKYKL	8	2.20	0.28
HLA-B*0801	1mi5	FLRGRAYGL	9	2.50	0.37
HLA-B*1501	1xr8	LEKARGSTY	9	2.30	1.15
HLA-B*1501	3c9n	VQQESSFVM	9	1.87	0.80
HLA-B*2101	3bev	GHAEETYGAETL	11	2.10	0.90
HLA-B*2101	3bew	REVDEQLLSV	10	2.60	0.33
HLA-B*2705	1uxs	RRRWRRRLTV	9	1.55	0.75
HLA-B*2705	1ogt	RRKWRRWHL	9	1.47	0.18
HLA-B*2705	2bsr	RRIYDLIEL	9	2.30	1.72
HLA-B*2705	2bst	SRYWAIRTR	9	2.10	1.36
HLA-B*2705	2a83	RRRWHRWRL	9	1.40	0.18
HLA-B*2705	1w0v	RRLPIFSRL	9	2.27	1.41
HLA-B*2709	1w0w	RRLPIFSRL	9	2.10	0.64
HLA-B*2709	1k5n	GRFAAAIAK	9	1.09	0.75
HLA-B*2709	1uxw	RRRWRRRLTV	9	1.71	0.47
HLA-B*2709	1jgd	RRLLRGHNQY	10	1.90	1.42
HLA-B*3501	2cik	KPIVVLHGY	9	1.75	0.26
HLA-B*3501	2axg	APQPAPENAY	10	2.00	1.14
HLA-B*3501	1a9b	LPPLDITPY	9	3.20	0.39
HLA-B*3501	1qew	FLWGPRALV	9	2.20	0.53
HLA-B*3501	1a1n	VPLRPMTY	8	2.00	0.39
HLA-B*3508	3bw9	CPSQEPMISIYVV	12	1.75	0.27
HLA-B*3508	3bwA	FPTKDVAL	8	1.30	0.26
HLA-B*3508	2ak4	LPEPLPQQQLTAY	13	2.50	1.09

Allele	PDB code	Peptide Sequence	Peptide Length	Res. (Å)	Cα RMSD (Å)
HLA-B*3508	2axf	APQPAPENAY	10	1.80	0.51
HLA-B*4402	1m6o	EEFGRAFSF	9	1.60	1.33
HLA-B*4403	1sys	EEPTVIKKY	9	2.40	0.65
HLA-B*4403	1n2r	EEFGRAFSF	9	1.70	0.99
HLA-B*4405	1syv	EEFGRAFSF	9	1.70	0.77
HLA-B*5101	1e27	LPPVVAKEI	9	2.20	0.18
HLA-B*5101	1e28	TAFTIPSI	8	3.00	0.26
HLA-B*5301	1a1m	TPYDINQML	9	2.30	0.28
HLA-B*5301	1a1o	KPIVQYDNF	9	2.30	0.84
HLA-B*5703	2bvq	KAFSPEVIP	9	2.00	0.50
HLA-B*5703	2bvo	KAFSPEVIPMF	11	1.65	2.17
HLA-B*5703	2bpv	ISPRTLDAW	9	1.35	0.65
HLA-Cw*0304	1efx	GAVDPLLAL	9	3.00	0.35
HLA-Cw*0401	1im9	QYDDAVYKL	9	2.80	0.34
HLA-E*0101	2esv	VMAPRTLIL	9	2.60	0.66
HLA-E*0103	1kpr	VMAPRTVLL	9	2.80	1.02
HLA-E*0103	1ktl	VTAPRTLLL	9	3.10	0.45
HLA-E*0103	3cdg	VMAPRTLFL	9	3.40	1.97
HLA-G*0101	2dyp	RIIPRHLQL	9	2.50	0.16
H2-Db	1jpf	SGVENPGGYCL	11	2.18	0.36
H2-Db	1jpg	FQPQNGQFI	9	2.20	0.38
H2-Db	1juf	SSVIGVWYL	9	2.00	0.29
H2-Db	1bz9	FAPGVFPYM	9	2.80	1.19
H2-Db	1ce6	FAPGNYPAL	9	2.90	0.24
H2-Db	1hoc	ASNENMETM	9	2.40	0.46
H2-Db	1ffo	AAVYNFATM	9	2.65	0.25
H2-Db	1ffp	SAVYNFATM	9	2.60	0.33
H2-Db	1fg2	KAVYNFATC	9	2.75	0.19
H2-Db	1inq	SSVVGWYL	9	2.20	0.42
H2-Db	1n3n	SNLQNAASIA	10	3.00	1.34
H2-Db	1qlf	FAPSNYPAL	9	2.65	0.26
H2-Db	1s7v	KAVYNLATM	9	2.20	0.27
H2-Db	1s7w	KALYNFATM	9	2.40	0.62
H2-Db	1s7x	KAVFNFATM	9	2.41	0.47
H2-Db	1wbx	SQLKNNAKEI	10	1.90	0.38
H2-Db	1wby	SSLENFRAYV	10	2.30	0.31
H2-Db	1yn7	SSLENFAAYV	10	2.20	0.14
H2-Db	2f74	KAVYNFATM	9	2.70	0.27
H2-Db	3buy	LSLRNPILV	9	2.60	0.23
H2-Dd	1qo3	RGPGRAFVTI	10	2.30	0.17
H2-Kb	1g6r	SIYRYYGL	8	2.80	0.34
H2-Kb	1s7q	KAVYNFATM	9	1.99	0.09
H2-Kb	1s7r	KAVYNLATM	9	2.95	1.26
H2-Kb	1s7s	KALYNFATM	9	1.99	0.28
H2-Kb	1s7t	KAVFNFATM	9	2.30	0.19

Allele	PDB code	Peptide Sequence	Peptide Length	Res. (Å)	Cα RMSD (Å)
H2-Kb	1g7p	SRDHHSRTPM	9	1.50	0.17
H2-Kb	1g7q	SAPDTRPA	8	1.60	0.36
H2-Kb	1kg	RGYVYXGL	8	2.20	0.47
H2-Kb	1t0m	SSIEFARL	8	2.00	0.21
H2-Kb	1vac	SIINFEKL	8	2.50	0.22
H2-Kb	1wbz	SSYRRPVGI	9	2.00	0.19
H2-Kb	1rjz	SEIEFARL	8	2.60	0.48
H2-Kb	1kj2	KVITFIDL	8	2.71	0.38
H2-Kb	1lk2	GNYSFYAL	8	1.35	0.53
H2-Kb	1zhb	KALYNYAPI	9	2.70	0.24
H2-Kb	1mwa	EQYKFYSV	8	2.40	0.27
H2-Kb	2fo4	SAPDFRPL	8	2.70	0.60
H2-Kb	1n59	AVYNFATM	8	2.95	0.44
H2-Kb	2ol3	SQYYYNSL	8	2.90	0.30
H2-Kb	1nam	RGYVYQGL	8	2.70	0.38
H2-Kb	1fo0	INFDFNTI	8	2.50	0.34
H2-Kb	1osz	RGYLYQGL	8	2.10	0.28
H2-Kd	1vgk	SYVNTNMGL	9	2.06	0.25
H2-Kd	2fwo	TYQRTRALV	9	2.60	0.26
H2-Kk	1zt1	FEANGNLI	8	2.50	0.45
H2-Kk	1zt7	SEFLLEKRI	9	3.00	0.45
H2-Ld	1ldp	APAAAAAAM	9	3.10	0.59
H2-Ld	1ld9	YPNVNIHNF	9	2.40	0.56
H2-Ld	2e7l	QLSPFPFDL	9	2.50	0.35
H2-Ld	2oi9	QLSPFPFDL	9	2.35	0.55
H2-M3	1mhc	MYFINILTL	9	2.10	1.16
H2-Qa-2	1k8d	ILMEHIHKL	9	2.30	0.55
Mamu-A*01	1zvs	TTPESANL	8	2.80	0.65
RT1.Aa	1kjm	AQFSASASR	9	2.35	0.49
RT1-A1C	1kjv	NPRAMQALL	9	1.48	0.33

MHC-II

HLA-DQB1*0201	1s9v	LQPFPQPELPY	11	2.22	0.33
HLA-DQB1*0302	1jk8	LVEALYLVCGERGG	14	2.40	0.31
HLA-DQB1*0302	2nna	SGEGSFQPSQENP	13	2.10	0.22
HLA-DQB1*0602	1uvq	MNL PSTKVSWAAVGGGGSLV	20	1.80	0.23
HLA-DRA*0101	1zgl	VHHFKNIVTPRTPG	14	2.80	1.27
HLA-DRB1*0101	1aqd	GSDWRFLRGYHQYA	14	2.45	0.28
HLA-DRB1*0101	1fty	PKYVKQNTLKLAT	13	2.60	0.23
HLA-DRB1*0101	1klu	GELIGTLNAAKVPAD	15	1.93	0.20
HLA-DRB1*0101	1pyw	FVKQNAXAL	9	2.10	0.81
HLA-DRB1*0101	1sje	PEVIPMFSALSEGAT	15	2.45	0.46
HLA-DRB1*0101	1sjh	PEVIPMFSALSEG	13	2.25	0.22
HLA-DRB1*0101	1t5w	AAYSDQATPLLLS	13	2.40	0.25
HLA-DRB1*0101	2fse	AGFKGEQGPKGEPG	14	3.10	0.64

Allele	PDB code	Peptide Sequence	Peptide Length	Res. (Å)	C α RMSD (Å)
HLA-DRB1*0101	2iam	GELIGILNAAKVPAD	15	2.80	0.24
HLA-DRB1*0301	1a6a	PVSK M RMATPLLMQA	15	2.75	0.30
HLA-DRB1*0401	1d5m	XXRAMXSX	8	2.00	0.13
HLA-DRB1*0401	1d5x	XXRXXX	6	2.45	0.11
HLA-DRB1*0401	1d5z	XXRAXSX	7	2.00	0.22
HLA-DRB1*0401	1d6e	XXRXMASX	8	2.45	0.14
HLA-DRB1*0401	1j8h	PKYVKQNTLKLAT	13	2.40	0.20
HLA-DRB1*0401	2seb	AY M RADAAGGA	12	2.50	0.31
HLA-DRB1*1501	1ymm	ENPV V HFFKNIVTP	14	3.50	0.28
HLA-DRB3*0101	2q6w	AWRSDEALPLG	11	2.25	0.30
HLA-DRB5*0101	1fv1	NPVVHFF K NIVTPRTPPPSQ	20	1.90	0.59
HLA-DRB5*0101	1h15	GGVYHFVKKHVHES	14	3.10	0.22
HLA-DRB5*0101	1hqr	VHFFKNIVTP	10	3.20	0.56
I-Ab	1muj	PVSK M RMATPLLMQA	15	2.15	0.15
I-Ad	1iao	RG S QAVHAAHAEI	14	2.60	0.27
I-Ad	2iad	GHAT Q GVTAAASSHE	14	2.40	0.56
I-A(G7)	1es0	YE I APVFVLLEYVT	14	2.60	0.38
I-Ak	1f3j	AMKRH G LDNYRGYS	14	3.10	0.28
I-Ak	1iak	STD Y GILQINSRW	13	1.90	0.23
I-Ak	1jl4	GNSHRGAIEWEGIESG	16	4.30	0.35
I-Au	1u3h	SRGGAS Q YRPSQ	12	2.42	0.95
I-Au	2pxy	RGGAS Q YRPSQ	11	2.23	0.28
I-Ek	1r5v	ADLIAY P KAATKF	13	2.50	0.28
I-Ek	1r5w	ADLIAY F KAATKF	13	2.90	1.26