



wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 12:18 PM GMT

PDB ID : 1T5X
Title : HLA-DR1 in complex with a synthetic peptide (AAYSDQATPLLLSPR) and the superantigen SEC3-3B2
Authors : Zavala-Ruiz, Z.; Strug, I.; Anderson, M.W.; Gorski, J.; Stern, L.J.
Deposited on : 2004-05-05
Resolution : 2.50 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

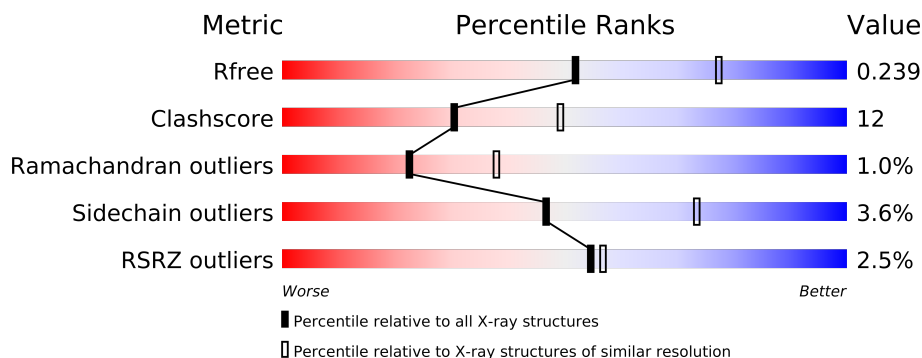
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	2784 (2.50-2.50)
Clashscore	79885	3562 (2.50-2.50)
Ramachandran outliers	78287	3480 (2.50-2.50)
Sidechain outliers	78261	3482 (2.50-2.50)
RSRZ outliers	66119	2785 (2.50-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	181	
2	B	190	
3	C	15	
4	D	239	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5226 atoms, of which 0 are hydrogen and 0 are deuterium.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called HLA class II histocompatibility antigen, DR alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	179	Total	C	N	O	S	0	0	0
			1470	952	239	274	5			

- Molecule 2 is a protein called HLA class II histocompatibility antigen, DRB1-1 beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	190	Total	C	N	O	S	0	0	0
			1557	979	279	293	6			

- Molecule 3 is a protein called 15-mer peptide fragment of Regulatory protein MIG1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	13	Total	C	N	O	0	0	0
			94	60	14	20			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	0	ALA	-	INSERTION	UNP P27705
C	1	ALA	-	INSERTION	UNP P27705
C	2	TYR	-	INSERTION	UNP P27705
C	3	SER	-	INSERTION	UNP P27705
C	4	ASP	-	INSERTION	UNP P27705
C	5	GLN	-	INSERTION	UNP P27705
C	6	ALA	-	INSERTION	UNP P27705

- Molecule 4 is a protein called Enterotoxin type C-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	230	Total	C	N	O	S	0	0	0
			1884	1196	306	372	10			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	43	SER	LYS	ENGINEERED	UNP P0A0L5
D	45	PHE	LEU	ENGINEERED	UNP P0A0L5
D	46	LYS	ALA	ENGINEERED	UNP P0A0L5
D	47	TRP	HIS	ENGINEERED	UNP P0A0L5

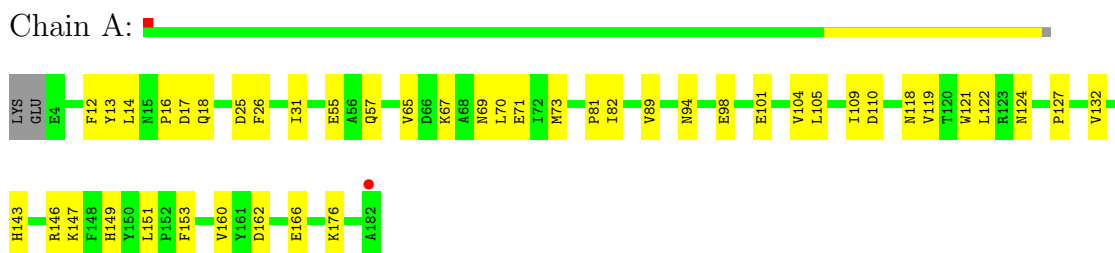
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	76	Total	O	0	0
			76	76		
5	B	54	Total	O	0	0
			54	54		
5	C	2	Total	O	0	0
			2	2		
5	D	89	Total	O	0	0
			89	89		

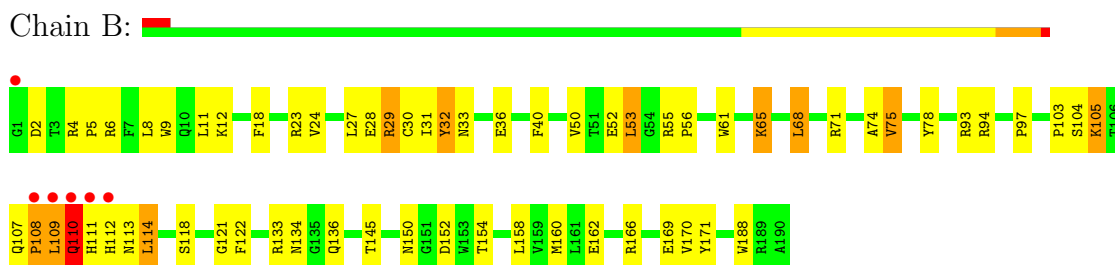
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

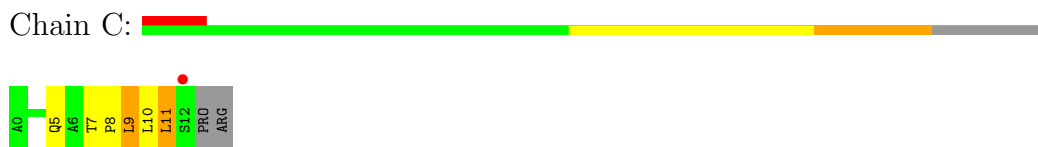
- Molecule 1: HLA class II histocompatibility antigen, DR alpha chain



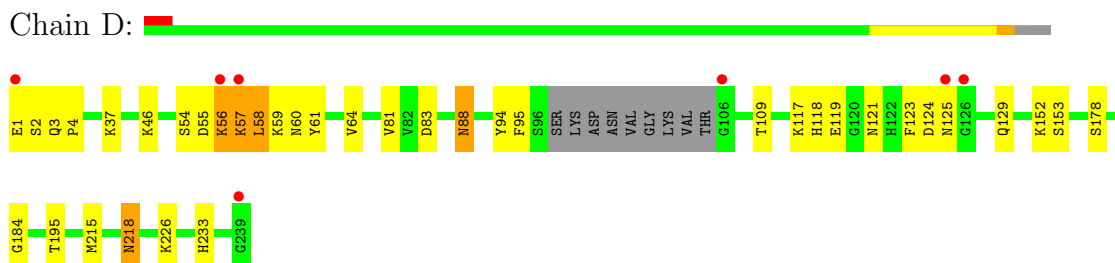
- Molecule 2: HLA class II histocompatibility antigen, DRB1-1 beta chain



- Molecule 3: 15-mer peptide fragment of Regulatory protein MIG1



- Molecule 4: Enterotoxin type C-3



4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	173.21Å 173.21Å 121.54Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.80 – 2.50 29.78 – 2.39	Depositor EDS
% Data completeness (in resolution range)	98.8 (29.80-2.50) 98.7 (29.78-2.39)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.96 (at 2.39Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.208 , 0.241 0.210 , 0.239	Depositor DCC
R_{free} test set	4691 reflections (10.09%)	DCC
Wilson B-factor (Å ²)	41.2	Xtriage
Anisotropy	0.145	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 27.5	EDS
Estimated twinning fraction	0.026 for h,-h-k,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 53191 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5226	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.40% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.39	0/1515	0.64	0/2065
2	B	0.35	0/1597	0.61	0/2168
3	C	0.42	0/95	0.66	0/130
4	D	0.38	0/1926	0.59	0/2592
All	All	0.37	0/5133	0.61	0/6955

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1470	0	1406	35	0
2	B	1557	0	1488	60	0
3	C	94	0	95	15	0
4	D	1884	0	1811	27	0
5	A	76	0	0	1	0
5	B	54	0	0	2	0
5	C	2	0	0	0	0
5	D	89	0	0	0	0
All	All	5226	0	4800	117	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 12.

The worst 5 of 117 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:150:ASN:HD22	2:B:154:THR:HG22	1.17	1.05
2:B:65:LYS:HE3	2:B:65:LYS:H	1.30	0.93
2:B:109:LEU:HD23	2:B:109:LEU:H	1.32	0.90
2:B:108:PRO:HG2	2:B:109:LEU:HD23	1.53	0.90
2:B:150:ASN:ND2	2:B:154:THR:HG22	1.89	0.88

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	177/181 (98%)	172 (97%)	5 (3%)	0	100	100
2	B	188/190 (99%)	175 (93%)	9 (5%)	4 (2%)	11	16
3	C	11/15 (73%)	10 (91%)	1 (9%)	0	100	100
4	D	226/239 (95%)	217 (96%)	7 (3%)	2 (1%)	25	42
All	All	602/625 (96%)	574 (95%)	22 (4%)	6 (1%)	22	38

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	110	GLN
2	B	108	PRO
2	B	111	HIS
4	D	57	LYS
2	B	32	TYR

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	163/165 (99%)	160 (98%)	3 (2%)	71	91
2	B	171/171 (100%)	160 (94%)	11 (6%)	25	43
3	C	10/12 (83%)	8 (80%)	2 (20%)	2	3
4	D	212/220 (96%)	208 (98%)	4 (2%)	69	90
All	All	556/568 (98%)	536 (96%)	20 (4%)	47	73

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	105	LYS
2	B	109	LEU
4	D	56	LYS
2	B	71	ARG
2	B	75	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
4	D	60	ASN
4	D	88	ASN
4	D	148	GLN
2	B	156	GLN
4	D	52	ASN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	179/181 (98%)	-0.46	1 (0%) 86 88	19, 34, 77, 162	0
2	B	190/190 (100%)	-0.36	6 (3%) 45 47	21, 40, 95, 162	0
3	C	13/15 (86%)	0.01	1 (7%) 13 13	33, 49, 73, 114	0
4	D	230/239 (96%)	-0.43	7 (3%) 48 50	23, 36, 77, 110	0
All	All	612/625 (97%)	-0.41	15 (2%) 54 57	19, 38, 84, 162	0

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	109	LEU	6.1
2	B	1	GLY	3.8
2	B	111	HIS	3.7
2	B	110	GLN	3.2
1	A	182	ALA	3.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.