Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 03:39 PM GMT

PDB ID	:	4D0B
Title	:	COMPLEX OF A B21 CHICKEN MHC CLASS I MOLECULE AND A 10MER CHICKEN PEPTIDE
Authors	:	Chappell, P.E.; Roversi, P.; Harrison, M.C.; Mears, L.E.; Kaufman, J.F.; Lea, S.M.
Deposited on	:	2014-04-25
Resolution	:	2.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

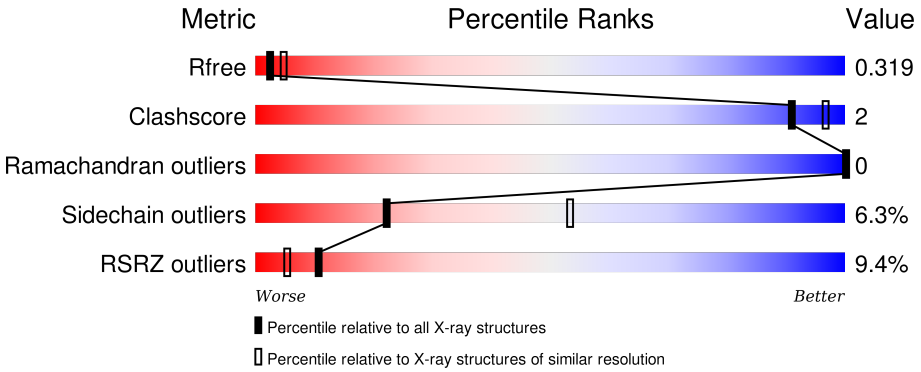
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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}	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	329	8% 76% 8% • 16%
2	B	98	8% 91% 8% •
3	C	10	30% 60% 30% 10%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 3066 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 MHC CLASS I ANTIGEN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	277	Total	C	N	O	S	0	0	1
			2208	1383	401	416	8			

There are 59 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	EXPRESSION TAG	UNP E9LUH6
A	-19	GLY	-	EXPRESSION TAG	UNP E9LUH6
A	-18	SER	-	EXPRESSION TAG	UNP E9LUH6
A	-17	CYS	-	EXPRESSION TAG	UNP E9LUH6
A	-16	GLY	-	EXPRESSION TAG	UNP E9LUH6
A	-15	ALA	-	EXPRESSION TAG	UNP E9LUH6
A	-14	LEU	-	EXPRESSION TAG	UNP E9LUH6
A	-13	GLY	-	EXPRESSION TAG	UNP E9LUH6
A	-12	LEU	-	EXPRESSION TAG	UNP E9LUH6
A	-11	GLY	-	EXPRESSION TAG	UNP E9LUH6
A	-10	LEU	-	EXPRESSION TAG	UNP E9LUH6
A	-9	LEU	-	EXPRESSION TAG	UNP E9LUH6
A	-8	LEU	-	EXPRESSION TAG	UNP E9LUH6
A	-7	ALA	-	EXPRESSION TAG	UNP E9LUH6
A	-6	ALA	-	EXPRESSION TAG	UNP E9LUH6
A	-5	VAL	-	EXPRESSION TAG	UNP E9LUH6
A	-4	CYS	-	EXPRESSION TAG	UNP E9LUH6
A	-3	GLY	-	EXPRESSION TAG	UNP E9LUH6
A	-2	ALA	-	EXPRESSION TAG	UNP E9LUH6
A	-1	ALA	-	EXPRESSION TAG	UNP E9LUH6
A	0	ALA	-	EXPRESSION TAG	UNP E9LUH6
A	271	ARG	-	EXPRESSION TAG	UNP E9LUH6
A	272	SER	-	EXPRESSION TAG	UNP E9LUH6
A	273	GLY	-	EXPRESSION TAG	UNP E9LUH6
A	274	GLY	-	EXPRESSION TAG	UNP E9LUH6
A	275	GLY	-	EXPRESSION TAG	UNP E9LUH6
A	276	LEU	-	EXPRESSION TAG	UNP E9LUH6

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Chain	Residue	Modelled	Actual	Comment	Reference
A	277	ASN	-	EXPRESSION TAG	UNP E9LUH6
A	278	ASP	-	EXPRESSION TAG	UNP E9LUH6
A	279	ILE	-	EXPRESSION TAG	UNP E9LUH6
A	280	PHE	-	EXPRESSION TAG	UNP E9LUH6
A	281	GLU	-	EXPRESSION TAG	UNP E9LUH6
A	282	ALA	-	EXPRESSION TAG	UNP E9LUH6
A	283	GLN	-	EXPRESSION TAG	UNP E9LUH6
A	284	LYS	-	EXPRESSION TAG	UNP E9LUH6
A	285	ILE	-	EXPRESSION TAG	UNP E9LUH6
A	286	GLU	-	EXPRESSION TAG	UNP E9LUH6
A	287	TRP	-	EXPRESSION TAG	UNP E9LUH6
A	288	HIS	-	EXPRESSION TAG	UNP E9LUH6
A	289	GLU	-	EXPRESSION TAG	UNP E9LUH6
A	290	ASN	-	EXPRESSION TAG	UNP E9LUH6
A	291	SER	-	EXPRESSION TAG	UNP E9LUH6
A	292	SER	-	EXPRESSION TAG	UNP E9LUH6
A	293	SER	-	EXPRESSION TAG	UNP E9LUH6
A	294	VAL	-	EXPRESSION TAG	UNP E9LUH6
A	295	ASP	-	EXPRESSION TAG	UNP E9LUH6
A	296	LYS	-	EXPRESSION TAG	UNP E9LUH6
A	297	LEU	-	EXPRESSION TAG	UNP E9LUH6
A	298	ALA	-	EXPRESSION TAG	UNP E9LUH6
A	299	ALA	-	EXPRESSION TAG	UNP E9LUH6
A	300	ALA	-	EXPRESSION TAG	UNP E9LUH6
A	301	LEU	-	EXPRESSION TAG	UNP E9LUH6
A	302	GLU	-	EXPRESSION TAG	UNP E9LUH6
A	303	HIS	-	EXPRESSION TAG	UNP E9LUH6
A	304	HIS	-	EXPRESSION TAG	UNP E9LUH6
A	305	HIS	-	EXPRESSION TAG	UNP E9LUH6
A	306	HIS	-	EXPRESSION TAG	UNP E9LUH6
A	307	HIS	-	EXPRESSION TAG	UNP E9LUH6
A	308	HIS	-	EXPRESSION TAG	UNP E9LUH6

- Molecule 2 is a protein called BETA-2-MICROGLOBULIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	97	771	495	125	146	5	0	0	0

- Molecule 3 is a protein called PEPTIDE.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	10	Total	C	N	O	0	0	0
			82	48	14	20			

- Molecule 4 is water.

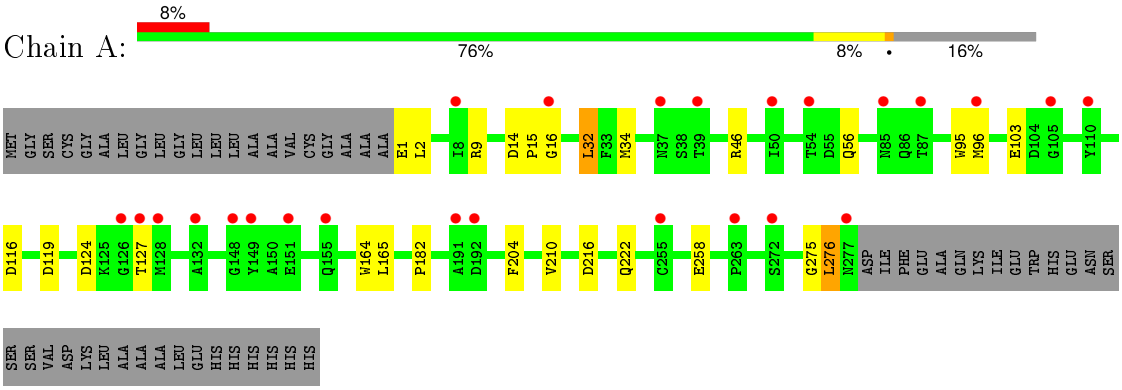
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	4	Total	O	0	0
			4	4		
4	B	1	Total	O	0	0
			1	1		

3 Residue-property plots (i)

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.

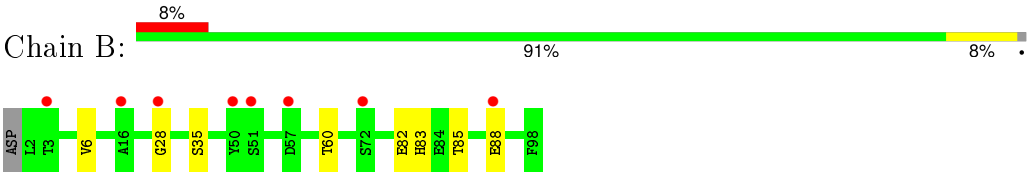
- Molecule 1: MHC CLASS I ANTIGEN

Chain A:



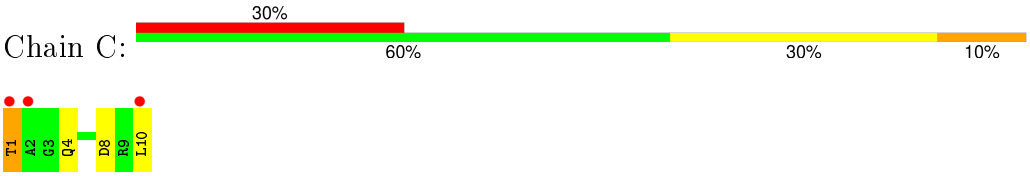
- Molecule 2: BETA-2-MICROGLOBULIN

Chain B:



- Molecule 3: PEPTIDE

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	60.92Å 69.21Å 95.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	56.03 – 2.80 56.03 – 2.80	Depositor EDS
% Data completeness (in resolution range)	89.9 (56.03-2.80) 89.9 (56.03-2.80)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.27 (at 2.81Å)	Xtriage
Refinement program	BUSTER 2.11.4	Depositor
R, R_{free}	0.275 , 0.296 0.289 , 0.319	Depositor DCC
R_{free} test set	1641 reflections (10.01%)	DCC
Wilson B-factor (Å^2)	29.2	Xtriage
Anisotropy	1.166	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 24.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Outliers	0 of 9361 reflections	Xtriage
F_o,F_c correlation	0.80	EDS
Total number of atoms	3066	wwPDB-VP
Average B, all atoms (Å^2)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.65% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

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	0.38	0/2267	0.55	0/3080
2	B	0.38	0/796	0.51	0/1081
3	C	0.43	0/82	0.69	0/108
All	All	0.38	0/3145	0.54	0/4269

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-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 hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2208	0	2094	10	0
2	B	771	0	730	3	0
3	C	82	0	72	3	0
4	A	4	0	0	0	0
4	B	1	0	0	0	0
All	All	3066	0	2896	13	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (13) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:164:TRP:CG	3:C:1:THR:HG21	1.98	0.98
1:A:164:TRP:CD2	3:C:1:THR:HG21	2.12	0.84
2:B:28:GLY:HA2	2:B:60:THR:HB	1.74	0.69
1:A:9:ARG:HB2	1:A:95:TRP:HB2	1.85	0.59
1:A:164:TRP:CD1	3:C:1:THR:HG21	2.45	0.51
2:B:35:SER:HB3	2:B:82:GLU:HB2	1.92	0.50
1:A:32:LEU:HD22	1:A:46:ARG:HD2	1.95	0.47
1:A:275:GLY:HA2	1:A:276:LEU:HA	1.76	0.47
1:A:210:VAL:HB	1:A:258:GLU:HB2	1.99	0.45
1:A:15:PRO:N	1:A:16:GLY:HA2	2.33	0.43
2:B:83:HIS:HD2	2:B:85:THR:H	1.66	0.43
1:A:182:PRO:HB3	1:A:204:PHE:HB3	2.03	0.41
1:A:1:GLU:HB3	1:A:103:GLU:HG2	2.02	0.41

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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	275/329 (84%)	256 (93%)	19 (7%)	0	100	100
2	B	95/98 (97%)	94 (99%)	1 (1%)	0	100	100
3	C	8/10 (80%)	7 (88%)	1 (12%)	0	100	100
All	All	378/437 (86%)	357 (94%)	21 (6%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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	225/263 (86%)	211 (94%)	14 (6%)	23 54
2	B	85/86 (99%)	83 (98%)	2 (2%)	57 87
3	C	8/8 (100%)	4 (50%)	4 (50%)	0 0
All	All	318/357 (89%)	298 (94%)	20 (6%)	22 53

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	LEU
1	A	14	ASP
1	A	32	LEU
1	A	34	MET
1	A	56	GLN
1	A	96	MET
1	A	116	ASP
1	A	119	ASP
1	A	124	ASP
1	A	127	THR
1	A	165	LEU
1	A	216	ASP
1	A	222	GLN
1	A	276	LEU
2	B	6	VAL
2	B	88	GLU
3	C	1	THR
3	C	4	GLN
3	C	8	ASP
3	C	10	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	232	ASN
1	A	254	GLN
2	B	83	HIS

5.3.3 RNA

There are no RNA molecules 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, 95^{th} 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	277/329 (84%)	0.87	25 (9%) 12 6	12, 28, 46, 56	0
2	B	97/98 (98%)	0.93	8 (8%) 14 7	16, 29, 43, 50	0
3	C	10/10 (100%)	1.97	3 (30%) 1 0	39, 43, 49, 53	0
All	All	384/437 (87%)	0.92	36 (9%) 11 5	12, 28, 47, 56	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	1	THR	6.5
3	C	2	ALA	5.3
2	B	50	TYR	3.9
1	A	37	ASN	3.8
1	A	277	ASN	3.5
1	A	39	THR	3.1
2	B	88	GLU	3.1
3	C	10	LEU	2.9
1	A	126	GLY	2.9
1	A	127	THR	2.7
2	B	51	SER	2.7
1	A	191	ALA	2.6
1	A	149	TYR	2.6
1	A	272	SER	2.6
1	A	263	PRO	2.6
1	A	87	THR	2.6
1	A	85	ASN	2.5
1	A	255	CYS	2.5
2	B	28	GLY	2.4
1	A	54	THR	2.4
1	A	155	GLN	2.3
2	B	72	SER	2.3
1	A	50	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	192	ASP	2.3
2	B	3	THR	2.3
2	B	16	ALA	2.2
2	B	57	ASP	2.2
1	A	8	ILE	2.2
1	A	16	GLY	2.2
1	A	128	MET	2.1
1	A	132	ALA	2.1
1	A	96	MET	2.1
1	A	151	GLU	2.1
1	A	148	GLY	2.0
1	A	110	TYR	2.0
1	A	105	GLY	2.0

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

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

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.