wwPDB X-ray Structure Validation Summary Report (i)

Feb 1, 2016 – 10:12 PM GMT

PDB ID	:	4X0K
Title	:	Engineered Fab fragment specific for EYMPME (EE) peptide
Authors	:	Johnson, J.L.; Lieberman, R.L.
Deposited on	:	2014-11-21
Resolution	:	2.04 Å(reported)

This is a wwPDB X-ray Structure 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/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:

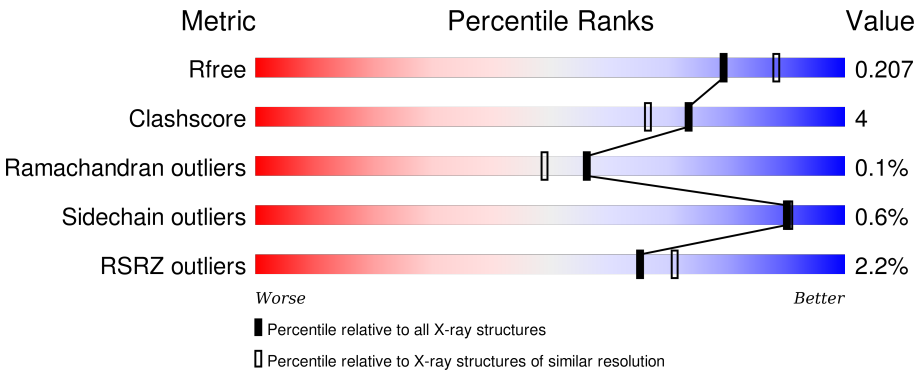
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	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 2.04 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	1192 (2.04-2.04)
Clashscore	102246	1269 (2.04-2.04)
Ramachandran outliers	100387	1258 (2.04-2.04)
Sidechain outliers	100360	1258 (2.04-2.04)
RSRZ outliers	91569	1194 (2.04-2.04)

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	242	93% 5% •
1	H	242	5% 87% 7% • 5%
2	B	234	% 93% • • •
2	L	234	3% 88% 9% •

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 7537 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 Fab fragment heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	H	229	1730	1083	292	345	10	0	2	0
1	A	235	1786	1114	303	360	9	0	5	0

- Molecule 2 is a protein called Fab fragment light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	L	226	1756	1099	306	345	6	0	1	0
2	B	226	1740	1089	301	344	6	0	0	0

- Molecule 3 is water.

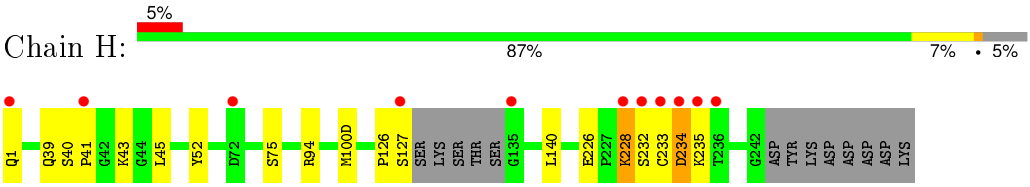
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	H	115	115	115	0	0
3	L	159	159	159	0	0
3	A	101	101	101	0	0
3	B	150	150	150	0	0

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.

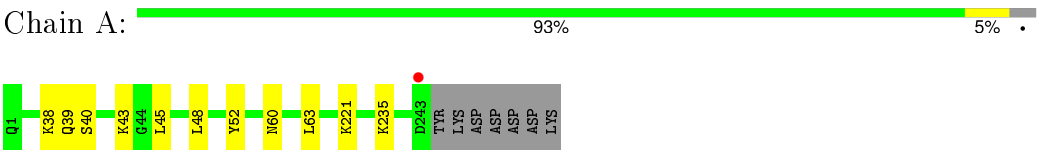
- Molecule 1: Fab fragment heavy chain

Chain H:



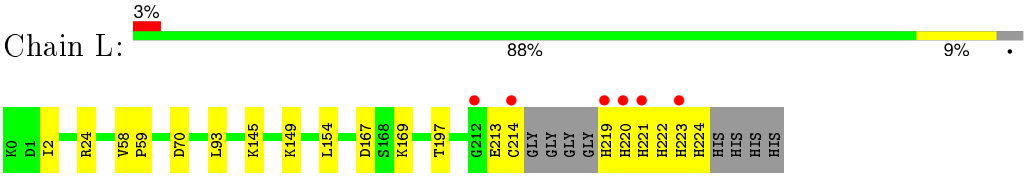
- Molecule 1: Fab fragment heavy chain

Chain A:



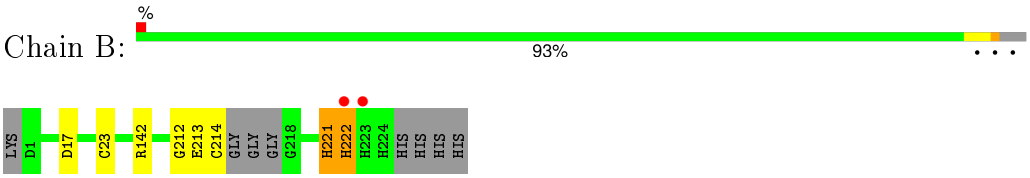
- Molecule 2: Fab fragment light chain

Chain L:



- Molecule 2: Fab fragment light chain

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	53.56Å 67.13Å 71.88Å 71.30° 78.10° 85.31°	Depositor
Resolution (Å)	32.97 – 2.04 45.68 – 2.04	Depositor EDS
% Data completeness (in resolution range)	97.7 (32.97-2.04) 85.0 (45.68-2.04)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.82 (at 2.05Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.165 , 0.207 0.164 , 0.207	Depositor DCC
R_{free} test set	2821 reflections (5.09%)	DCC
Wilson B-factor (Å^2)	29.2	Xtriage
Anisotropy	0.081	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 48.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Outliers	0 of 57696 reflections	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	7537	wwPDB-VP
Average B, all atoms (Å^2)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.23% 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 (i)

5.1 Standard geometry (i)

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	0.23	0/1832	0.43	0/2490
1	H	0.33	0/1772	0.51	2/2409 (0.1%)
2	B	0.24	0/1781	0.45	0/2413
2	L	0.26	0/1797	0.47	0/2433
All	All	0.27	0/7182	0.47	2/9745 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	H	226	GLU	C-N-CD	5.83	140.63	128.40
1	H	234	ASP	CB-CG-OD1	5.36	123.13	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	221	HIS	Peptide

5.2 Too-close contacts (i)

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	1786	0	1733	7	0
1	H	1730	0	1680	30	0
2	B	1740	0	1681	5	0
2	L	1756	0	1704	30	0
3	A	101	0	0	1	0
3	B	150	0	0	2	0
3	H	115	0	0	2	0
3	L	159	0	0	0	0
All	All	7537	0	6798	56	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 4.

The worst 5 of 56 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:H:233:CYS:HB3	2:L:214:CYS:SG	1.57	1.41
1:H:233:CYS:CB	2:L:214:CYS:SG	2.51	0.97
1:H:228:LYS:O	1:H:232:SER:OG	1.91	0.88
1:H:228:LYS:HD2	1:H:232:SER:N	1.90	0.86
1:H:233:CYS:HB3	2:L:214:CYS:HG	1.40	0.86

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	238/242 (98%)	235 (99%)	3 (1%)	0	100	100
1	H	228/242 (94%)	224 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	222/234 (95%)	215 (97%)	6 (3%)	1 (0%)	34	22
2	L	223/234 (95%)	218 (98%)	5 (2%)	0	100	100
All	All	911/952 (96%)	892 (98%)	18 (2%)	1 (0%)	56	49

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	222	HIS

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	205/207 (99%)	204 (100%)	1 (0%)	92	92
1	H	197/207 (95%)	194 (98%)	3 (2%)	72	70
2	B	198/203 (98%)	197 (100%)	1 (0%)	92	92
2	L	200/203 (98%)	200 (100%)	0	100	100
All	All	800/820 (98%)	795 (99%)	5 (1%)	90	90

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	52	TYR
1	H	75	SER
1	H	228	LYS
1	A	52	TYR
2	B	17	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	L	219	HIS

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Mol	Chain	Res	Type
2	L	223	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

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	235/242 (97%)	-0.31	1 (0%)	93	94	22, 42, 62, 120	0
1	H	229/242 (94%)	-0.07	11 (4%)	34	40	21, 40, 80, 114	0
2	B	226/234 (96%)	-0.31	2 (0%)	85	89	20, 30, 58, 96	0
2	L	226/234 (96%)	-0.25	6 (2%)	58	64	20, 31, 63, 126	0
All	All	916/952 (96%)	-0.24	20 (2%)	65	71	20, 35, 64, 126	0

The worst 5 of 20 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	L	214	CYS	6.1
1	H	235	LYS	6.0
2	L	219	HIS	5.0
1	A	243	ASP	4.1
1	H	127	SER	4.1

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.