



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Mar 2, 2017 – 11:18 am GMT

PDB ID : 3IY1
EMDB ID: : EMD-5106
Title : Variable domains of the WAM of Fab B fitted into the cryoEM reconstruction of the virus-Fab B complex
Authors : Hafenstein, S.; Bowman, V.D.; Sun, T.; Nelson, C.D.; Palermo, L.M.; Battisti, A.J.; Parrish, C.R.; Rossmann, M.G.
Deposited on : 2009-04-09
Resolution : 18.00 Å(reported)

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : recalc29047

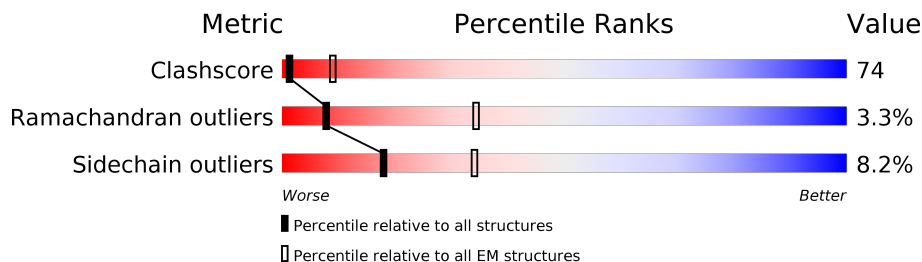
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 18.00 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)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	107	<div> <div style="width: 43%; background-color: green;"></div> <div style="width: 42%; background-color: yellow;"></div> <div style="width: 13%; background-color: orange;"></div> <div style="width: 1%; background-color: red;"></div> <div style="width: 1%; background-color: grey;"></div> </div> <div>43% 42% 13% .</div>
2	B	109	<div> <div style="width: 45%; background-color: green;"></div> <div style="width: 34%; background-color: yellow;"></div> <div style="width: 15%; background-color: orange;"></div> <div style="width: 6%; background-color: red;"></div> </div> <div>45% 34% 15% 6%</div>

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 1648 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 B, light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	107	Total	C	N	O	S	0	0
			819	517	137	162	3		

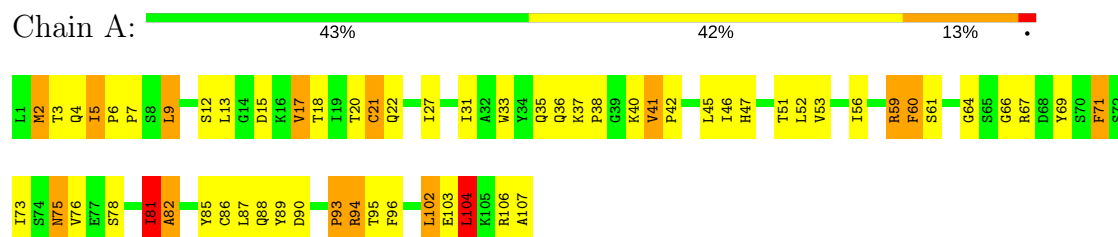
- Molecule 2 is a protein called Fab B, heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	109	Total	C	N	O	S	0	0
			829	526	130	169	4		

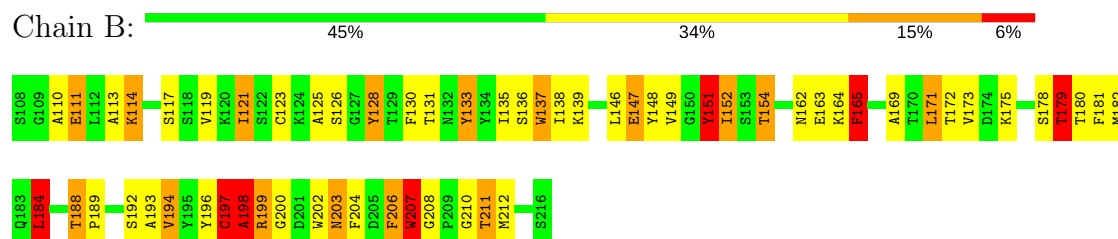
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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 B, light chain



- Molecule 2: Fab B, heavy chain



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	1126	Depositor
Resolution determination method	FSC at 0.5 cutoff	Depositor
CTF correction method	robem	Depositor
Microscope	Not provided	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	28.4	Depositor
Minimum defocus (nm)	1.7	Depositor
Maximum defocus (nm)	3.7	Depositor
Magnification	47190	Depositor
Image detector	Kodak SO-163 film	Depositor

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	$\# Z > 2$	RMSZ	$\# Z > 2$
1	A	1.04	2/837 (0.2%)	1.47	16/1132 (1.4%)
2	B	1.47	6/850 (0.7%)	2.52	48/1151 (4.2%)
All	All	1.28	8/1687 (0.5%)	2.07	64/2283 (2.8%)

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
1	A	1	0
2	B	0	4
All	All	1	4

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	207	TRP	CD2-CE2	-19.02	1.18	1.41
2	B	207	TRP	NE1-CE2	9.69	1.50	1.37
2	B	207	TRP	CZ3-CH2	-6.09	1.30	1.40
1	A	60	PHE	CG-CD2	-5.66	1.30	1.38
2	B	165	PHE	CE2-CZ	-5.47	1.26	1.37

The worst 5 of 64 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	165	PHE	CD1-CE1-CZ	-30.00	84.10	120.10
2	B	165	PHE	CZ-CE2-CD2	-24.60	90.58	120.10
2	B	207	TRP	NE1-CE2-CZ2	-19.87	108.54	130.40
2	B	154	THR	CA-CB-CG2	17.62	137.06	112.40
2	B	207	TRP	CD2-CE2-CZ2	17.41	143.19	122.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	81	ILE	CB

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	133	TYR	Sidechain
2	B	165	PHE	Sidechain
2	B	197	CYS	Mainchain
2	B	198	ALA	Mainchain

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	819	0	812	87	0
2	B	829	0	786	160	0
All	All	1648	0	1598	237	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 74.

The worst 5 of 237 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)
2:B:198:ALA:HB1	2:B:204:PHE:HB3	1.28	1.16
1:A:9:LEU:HD21	1:A:17:VAL:HG21	1.35	1.07
1:A:9:LEU:HD21	1:A:17:VAL:CG2	1.86	1.04
2:B:206:PHE:CB	2:B:207:TRP:HB3	1.91	1.01
1:A:60:PHE:HD1	1:A:71:PHE:CZ	1.77	1.01

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 PDB entries followed by that with respect to all EM entries.

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	105/107 (98%)	98 (93%)	4 (4%)	3 (3%)	5	38
2	B	107/109 (98%)	92 (86%)	11 (10%)	4 (4%)	4	33
All	All	212/216 (98%)	190 (90%)	15 (7%)	7 (3%)	8	35

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	82	ALA
2	B	111	GLU
2	B	207	TRP
2	B	211	THR
2	B	198	ALA

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 PDB entries followed by that with respect to all EM entries.

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	92/92 (100%)	84 (91%)	8 (9%)	12	40
2	B	90/90 (100%)	83 (92%)	7 (8%)	15	46
All	All	182/182 (100%)	167 (92%)	15 (8%)	18	43

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	102	LEU

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Mol	Chain	Res	Type
1	A	104	LEU
2	B	194	VAL
1	A	81	ILE
2	B	184	LEU

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

Mol	Chain	Res	Type
1	A	75	ASN
2	B	144	GLN

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.