



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 13, 2026 – 06:54 PM UTC

PDB ID : 6FOE / pdb_00006foe
Title : BaxB01 Fab fragment
Authors : Hollerweger, J.; Schinagl, A.; Kerschbaumer, R.J.; Scheiflinger, F.; Thiele, M.;
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Deposited on : 2018-02-07
Resolution : 2.60 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	FAILED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

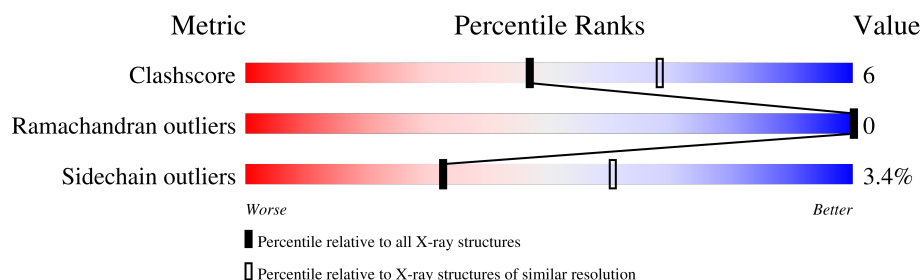
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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))
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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 $\leq 5\%$.

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	225	81% 17% .
1	H	225	85% 15%
2	B	214	81% 17% .
2	L	214	86% 14%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6727 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 BaxB01 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	225	Total	C	N	O	S	0	0	0
			1669	1046	281	334	8			
1	H	225	Total	C	N	O	S	0	0	0
			1669	1046	281	334	8			

- Molecule 2 is a protein called Fab BaxB01 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	214	Total	C	N	O	S	0	0	0
			1654	1033	281	333	7			
2	L	214	Total	C	N	O	S	0	0	0
			1654	1033	281	333	7			

- Molecule 3 is water.

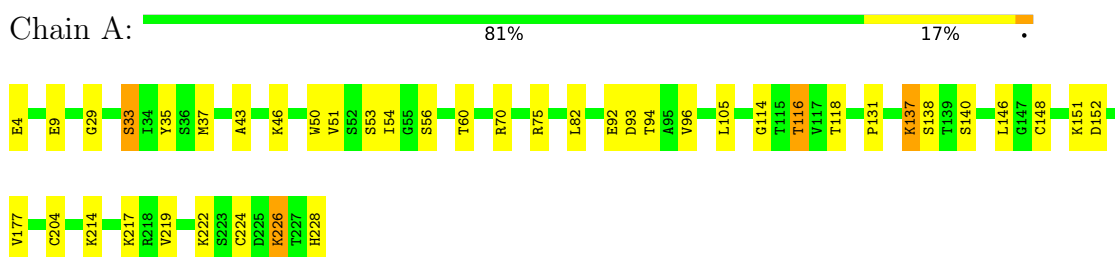
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	15	Total	O	0	0
			15	15		
3	B	23	Total	O	0	0
			23	23		
3	H	18	Total	O	0	0
			18	18		
3	L	25	Total	O	0	0
			25	25		

3 Residue-property plots

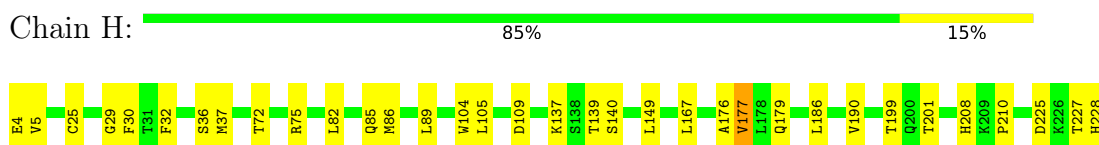
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

Note EDS failed to run properly.

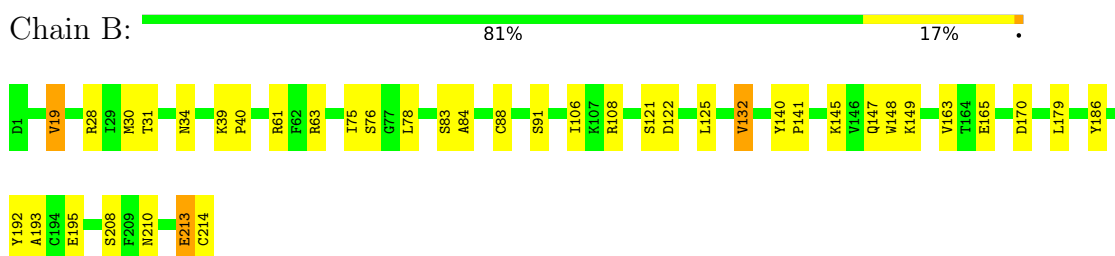
- Molecule 1: Fab BaxB01 heavy chain



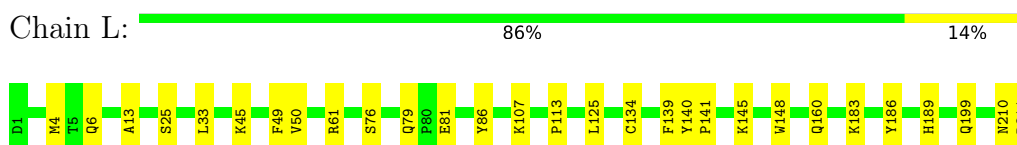
- Molecule 1: Fab BaxB01 heavy chain



- Molecule 2: Fab BaxB01 light chain



- Molecule 2: Fab BaxB01 light chain



4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	102.70Å 102.70Å 188.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	69.48 – 2.60	Depositor
% Data completeness (in resolution range)	99.5 (69.48-2.60)	Depositor
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.72 (at 2.62Å)	Xtriage
Refinement program	PHENIX 1.11.1-2575	Depositor
R, R_{free}	0.214 , 0.263	Depositor
Wilson B-factor (Å ²)	52.8	Xtriage
Anisotropy	0.119	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6727	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.87% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 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	0.19	0/1708	0.38	0/2324
1	H	0.15	0/1708	0.38	0/2324
2	B	0.19	0/1690	0.39	0/2291
2	L	0.30	1/1690 (0.1%)	0.40	0/2291
All	All	0.21	1/6796 (0.0%)	0.39	0/9230

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	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	79	GLN	C-O	-5.05	1.19	1.24

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	140	SER	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	1669	0	1623	24	0
1	H	1669	0	1623	16	0
2	B	1654	0	1610	22	0
2	L	1654	0	1610	17	0
3	A	15	0	0	0	0
3	B	23	0	0	1	0
3	H	18	0	0	1	0
3	L	25	0	0	2	0
All	All	6727	0	6466	75	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 6.

All (75) 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:214:CYS:O	3:B:301:HOH:O	1.84	0.94
2:L:189:HIS:O	2:L:211:ARG:NH2	2.23	0.72
2:L:186:TYR:O	2:L:211:ARG:NH2	2.25	0.70
2:L:45:LYS:NZ	3:L:301:HOH:O	2.24	0.69
2:B:210:ASN:HB2	2:B:213:GLU:HB2	1.77	0.66
1:A:70:ARG:NH1	1:A:93:ASP:OD2	2.30	0.65
1:H:5:VAL:HG12	1:H:30:PHE:HB3	1.80	0.63
1:H:86:MET:HB3	1:H:89:LEU:HD21	1.79	0.63
2:B:148:TRP:O	2:B:149:LYS:NZ	2.32	0.62
1:A:94:THR:HG23	1:A:118:THR:HA	1.85	0.59
1:A:37:MET:HB3	1:A:82:LEU:HD22	1.84	0.59
2:L:199:GLN:N	3:L:302:HOH:O	2.35	0.58
2:L:210:ASN:HB2	2:L:213:GLU:HB3	1.84	0.58
1:H:177:VAL:HG21	2:L:160:GLN:HB3	1.86	0.58
2:L:13:ALA:O	2:L:107:LYS:N	2.32	0.57
1:A:56:SER:O	1:A:75:ARG:NH1	2.39	0.56
1:A:37:MET:HG2	1:A:75:ARG:HH21	1.71	0.55
1:A:50:TRP:HE1	1:A:53:SER:HB3	1.73	0.54
1:H:176:ALA:HA	1:H:186:LEU:HB3	1.90	0.54
1:A:131:PRO:HD3	1:A:217:LYS:HE2	1.90	0.53
1:H:37:MET:HB3	1:H:82:LEU:HD22	1.89	0.53
2:B:147:GLN:HB3	2:B:195:GLU:HB3	1.90	0.52
1:A:222:LYS:NZ	2:B:122:ASP:OD2	2.43	0.51
2:B:83:SER:HB2	2:B:106:ILE:HG12	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:25:CYS:HB3	1:H:82:LEU:HB3	1.92	0.51
2:B:61:ARG:HB2	2:B:76:SER:O	2.11	0.51
2:B:186:TYR:O	2:B:192:TYR:OH	2.26	0.50
1:H:208:HIS:CE1	1:H:210:PRO:HG2	2.46	0.50
1:H:72:THR:HB	1:H:85:GLN:HB3	1.94	0.50
2:B:132:VAL:HG13	2:B:179:LEU:HB3	1.92	0.50
2:L:4:MET:HE1	2:L:25:SER:HB3	1.94	0.50
1:A:43:ALA:HB3	1:A:46:LYS:HB2	1.94	0.50
1:A:54:ILE:HD13	1:A:75:ARG:HG2	1.93	0.50
2:L:6:GLN:NE2	2:L:86:TYR:O	2.40	0.49
1:A:35:TYR:O	1:A:75:ARG:NH2	2.45	0.49
2:B:121:SER:O	2:B:125:LEU:HG	2.13	0.48
2:L:113:PRO:HB3	2:L:139:PHE:HB3	1.95	0.48
1:H:32:PHE:O	1:H:75:ARG:NH2	2.47	0.48
1:H:36:SER:HB3	3:H:306:HOH:O	2.13	0.48
1:H:109:ASP:OD1	1:H:109:ASP:N	2.40	0.48
2:B:145:LYS:HD3	2:B:145:LYS:HA	1.69	0.47
2:B:39:LYS:HD3	2:B:84:ALA:HB2	1.95	0.47
2:B:40:PRO:HB2	2:B:165:GLU:HG3	1.97	0.47
1:A:4:GLU:O	1:A:29:GLY:HA3	2.16	0.46
1:A:214:LYS:HB3	1:A:214:LYS:HE2	1.82	0.46
1:H:227:THR:O	1:H:228:HIS:ND1	2.49	0.46
1:A:146:LEU:HD13	1:A:219:VAL:HG21	1.98	0.46
2:B:147:GLN:HG3	2:B:149:LYS:NZ	2.30	0.46
2:B:19:VAL:HG22	2:B:75:ILE:HB	1.98	0.45
2:L:61:ARG:HB2	2:L:76:SER:O	2.17	0.45
2:L:125:LEU:O	2:L:183:LYS:HD3	2.18	0.44
1:A:37:MET:HG2	1:A:75:ARG:NH2	2.34	0.43
1:A:226:LYS:HB2	1:A:228:HIS:CD2	2.53	0.43
2:L:49:PHE:HD2	2:L:50:VAL:HG23	1.84	0.43
1:A:9:GLU:CD	1:A:114:GLY:H	2.27	0.43
1:H:104:TRP:CG	1:H:105:LEU:H	2.35	0.43
2:L:140:TYR:CG	2:L:141:PRO:HA	2.54	0.43
1:A:137:LYS:HG2	1:A:138:SER:H	1.84	0.43
2:B:108:ARG:NH1	2:B:170:ASP:O	2.50	0.42
1:H:167:LEU:HD21	1:H:190:VAL:HG21	2.01	0.42
1:A:33:SER:O	1:A:56:SER:HB2	2.21	0.41
2:B:28:ARG:NH1	2:B:28:ARG:HB2	2.36	0.41
1:H:179:GLN:HA	2:L:160:GLN:HE22	1.86	0.41
2:L:134:CYS:HB2	2:L:148:TRP:CH2	2.56	0.41
1:A:105:LEU:HD22	2:B:91:SER:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:34:ASN:O	2:B:88:CYS:HA	2.20	0.41
1:A:96:VAL:HA	1:A:116:THR:HA	2.03	0.41
1:H:4:GLU:O	1:H:29:GLY:HA3	2.21	0.41
2:L:145:LYS:HA	2:L:145:LYS:HD3	1.94	0.40
1:A:151:LYS:HG2	1:A:152:ASP:CG	2.46	0.40
2:B:193:ALA:HB2	2:B:208:SER:HB3	2.03	0.40
1:A:92:GLU:CD	1:A:92:GLU:H	2.29	0.40
1:A:226:LYS:H	1:A:226:LYS:HG2	1.63	0.40
2:B:140:TYR:CG	2:B:141:PRO:HA	2.56	0.40
2:B:30:MET:HB3	2:B:31:THR:H	1.80	0.40

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	223/225 (99%)	213 (96%)	10 (4%)	0	100	100
1	H	223/225 (99%)	214 (96%)	9 (4%)	0	100	100
2	B	212/214 (99%)	202 (95%)	10 (5%)	0	100	100
2	L	212/214 (99%)	204 (96%)	8 (4%)	0	100	100
All	All	870/878 (99%)	833 (96%)	37 (4%)	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	188/188 (100%)	178 (95%)	10 (5%)	20	43
1	H	188/188 (100%)	180 (96%)	8 (4%)	26	51
2	B	190/190 (100%)	184 (97%)	6 (3%)	34	62
2	L	190/190 (100%)	188 (99%)	2 (1%)	65	84
All	All	756/756 (100%)	730 (97%)	26 (3%)	32	60

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	SER
1	A	51	VAL
1	A	60	THR
1	A	116	THR
1	A	137	LYS
1	A	148	CYS
1	A	177	VAL
1	A	204	CYS
1	A	224	CYS
1	A	226	LYS
2	B	19	VAL
2	B	63	ARG
2	B	78	LEU
2	B	132	VAL
2	B	163	VAL
2	B	213	GLU
1	H	137	LYS
1	H	139	THR
1	H	140	SER
1	H	149	LEU
1	H	177	VAL
1	H	199	THR
1	H	201	THR
1	H	225	ASP
2	L	33	LEU
2	L	81	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	42	GLN
1	A	207	ASN
2	B	38	GLN
2	B	138	ASN
1	H	85	GLN
1	H	103	GLN
1	H	172	HIS
2	L	137	ASN
2	L	138	ASN
2	L	160	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 oligosaccharides 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

6.1 Protein, DNA and RNA chains

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

6.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

6.4 Ligands

EDS failed to run properly - this section is therefore empty.

6.5 Other polymers

EDS failed to run properly - this section is therefore empty.