



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:38 PM UTC

PDB ID : 8VBQ / pdb_00008vbq
Title : Structure of bovine anti-HIV Fab Bess7
Authors : Stanfield, R.L.; Wilson, I.A.
Deposited on : 2023-12-12
Resolution : 2.10 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	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

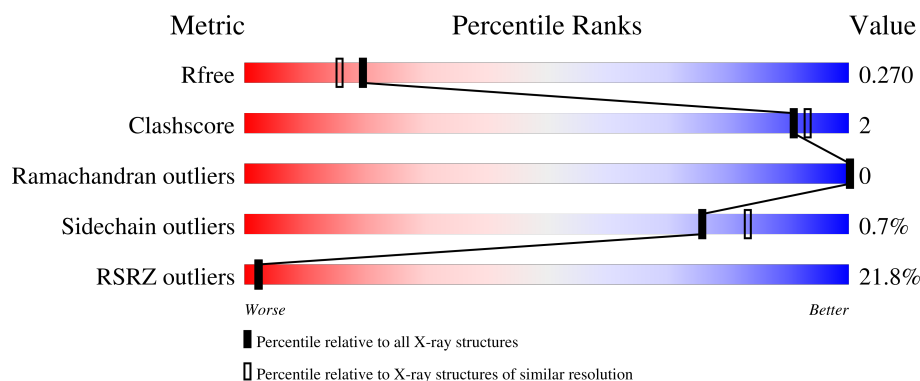
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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 $\leq 5\%$. 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	H	272	29% 93% 6%
2	L	216	12% 98% .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7134 atoms, of which 3423 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 Bovine Fab Bess7 heavy chain.

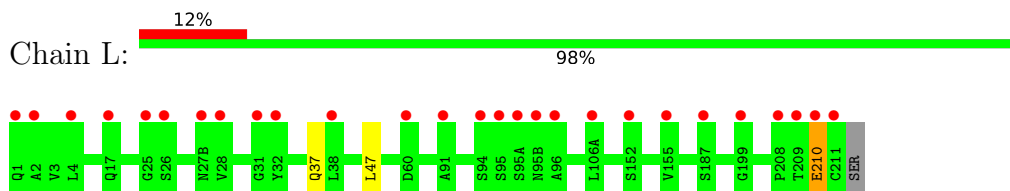
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	H	271	Total	C	H	N	O	S	0	0	0
			3910	1243	1916	329	409	13			

- Molecule 2 is a protein called Bovine Fab Bess7 light chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	L	215	Total	C	H	N	O	S	0	0	0
			3082	971	1507	266	333	5			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	H	78	Total	O	0	0
			78	78		
3	L	64	Total	O	0	0
			64	64		



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	83.00Å 69.78Å 87.52Å 90.00° 103.52° 90.00°	Depositor
Resolution (Å)	48.29 – 2.10 48.29 – 2.10	Depositor EDS
% Data completeness (in resolution range)	98.8 (48.29-2.10) 98.7 (48.29-2.10)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.34 (at 2.10Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.232 , 0.268 0.233 , 0.270	Depositor DCC
R_{free} test set	1348 reflections (4.74%)	wwPDB-VP
Wilson B-factor (Å ²)	31.8	Xtriage
Anisotropy	0.463	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 29.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7134	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.76% 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

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	H	0.09	0/2041	0.26	0/2790
2	L	0.09	0/1608	0.25	0/2196
All	All	0.09	0/3649	0.25	0/4986

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	H	1994	1916	1918	10	0
2	L	1575	1507	1513	2	0
3	H	78	0	0	0	0
3	L	64	0	0	0	0
All	All	3711	3423	3431	12	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 (12) 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:31:ASP:HA	1:H:53:THR:HG22	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:67:LEU:CD2	1:H:82:VAL:HG22	2.33	0.58
1:H:51:VAL:HG12	1:H:78:ILE:HD12	1.86	0.58
2:L:210:GLU:N	2:L:210:GLU:OE1	2.42	0.53
1:H:231:LEU:HD12	1:H:231:LEU:C	2.34	0.53
1:H:17:THR:HG23	1:H:81:THR:HG23	1.94	0.49
1:H:103:LYS:NZ	1:H:125:ASP:OD2	2.47	0.48
2:L:37:GLN:HB2	2:L:47:LEU:HD11	1.96	0.48
1:H:104:GLU:O	1:H:144:SER:N	2.50	0.45
1:H:17:THR:CG2	1:H:81:THR:HG23	2.49	0.42
1:H:64:LYS:N	1:H:65:PRO:CD	2.83	0.41
1:H:5:ARG:NH2	1:H:25:SER:OG	2.50	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	H	269/272 (99%)	255 (95%)	14 (5%)	0	100	100
2	L	213/216 (99%)	204 (96%)	9 (4%)	0	100	100
All	All	482/488 (99%)	459 (95%)	23 (5%)	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	H	230/231 (100%)	228 (99%)	2 (1%)	70	78
2	L	179/180 (99%)	178 (99%)	1 (1%)	78	86
All	All	409/411 (100%)	406 (99%)	3 (1%)	76	83

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	75	LYS
1	H	78	ILE
2	L	210	GLU

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

Mol	Chain	Res	Type
1	H	96	HIS
1	H	97	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

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	H	271/272 (99%)	1.20	79 (29%)	1 1	25, 43, 109, 121	0
2	L	215/216 (99%)	0.83	27 (12%)	8 8	23, 43, 78, 106	0
All	All	486/488 (99%)	1.03	106 (21%)	2 2	23, 43, 103, 121	0

All (106) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	27	PHE	6.3
1	H	145	VAL	5.6
1	H	29	LEU	5.6
1	H	2	VAL	5.4
1	H	149	TYR	5.2
1	H	111	TRP	5.1
1	H	96	HIS	5.1
1	H	146	ALA	5.0
2	L	25	GLY	4.9
1	H	33	ALA	4.6
2	L	211	CYS	4.4
1	H	101	THR	4.4
1	H	269	CYS	4.3
1	H	51	VAL	4.0
1	H	108	GLY	3.9
1	H	249	CYS	3.9
1	H	53	THR	3.9
1	H	152	TYR	3.9
1	H	140	TYR	3.8
1	H	99	THR	3.8
1	H	130	GLY	3.8
2	L	27(B)	ASN	3.7
2	L	2	ALA	3.7
1	H	30	ASN	3.7

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Mol	Chain	Res	Type	RSRZ
1	H	97	GLN	3.7
1	H	131	GLY	3.7
1	H	28	SER	3.6
1	H	32	LYS	3.6
1	H	102	THR	3.6
1	H	129	TRP	3.5
1	H	151	TRP	3.5
1	H	132	VAL	3.5
1	H	124	ALA	3.5
1	H	119	LEU	3.5
1	H	143	CYS	3.4
1	H	117	SER	3.4
1	H	147	HIS	3.3
1	H	144	SER	3.3
2	L	95(A)	SER	3.3
1	H	109	TYR	3.3
1	H	78	ILE	3.3
1	H	59	TYR	3.2
1	H	123	GLY	3.2
1	H	56	SER	3.2
1	H	98	THR	3.2
2	L	91	ALA	3.2
2	L	1	GLN	3.2
1	H	57	THR	3.2
1	H	148	THR	3.2
2	L	187	SER	3.1
1	H	60	ASN	3.1
1	H	95	VAL	3.1
1	H	31	ASP	3.1
2	L	31	GLY	3.0
2	L	95(B)	ASN	3.0
1	H	127	CYS	3.0
1	H	106	PRO	3.0
2	L	209	THR	3.0
1	H	58	THR	2.9
1	H	94	THR	2.9
1	H	54	GLY	2.9
1	H	52	SER	2.8
2	L	26	SER	2.8
1	H	182	LYS	2.8
2	L	152	SER	2.8
2	L	96	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
2	L	4	LEU	2.8
1	H	268	SER	2.7
2	L	94	SER	2.7
2	L	32	TYR	2.7
1	H	105	CYS	2.7
1	H	61	PRO	2.7
1	H	5	ARG	2.6
1	H	139	LEU	2.5
1	H	122	GLY	2.5
1	H	125	ASP	2.5
1	H	74	SER	2.5
2	L	60	ASP	2.5
2	L	155	VAL	2.4
2	L	17	GLN	2.4
2	L	106(A)	LEU	2.3
1	H	26	GLY	2.3
1	H	34	VAL	2.3
1	H	128	CYS	2.3
1	H	142	CYS	2.3
1	H	110	ASN	2.3
1	H	154	ASP	2.3
1	H	180	SER	2.3
1	H	24	VAL	2.3
1	H	72	ASP	2.3
1	H	120	GLY	2.3
1	H	141	SER	2.2
1	H	43	ARG	2.2
2	L	208	PRO	2.2
1	H	116	GLY	2.2
2	L	95	SER	2.2
1	H	112	ASP	2.2
1	H	3	GLN	2.1
1	H	135	TYR	2.1
2	L	210	GLU	2.1
2	L	28	VAL	2.1
1	H	100	LYS	2.1
1	H	50	SER	2.1
2	L	38	LEU	2.0
1	H	73	ASN	2.0
2	L	199	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 oligosaccharides 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.