Full wwPDB X-ray Structure Validation Report ⓘ

Jun 24, 2024 – 12:24 PM EDT

PDB ID	:	6GFB
Title	:	Structure of the BTB/POZ domain of human 90K
Authors	:	Ssebyatika, G.; Krey, T.
Deposited on	:	2018-04-29
Resolution	:	2.08 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:

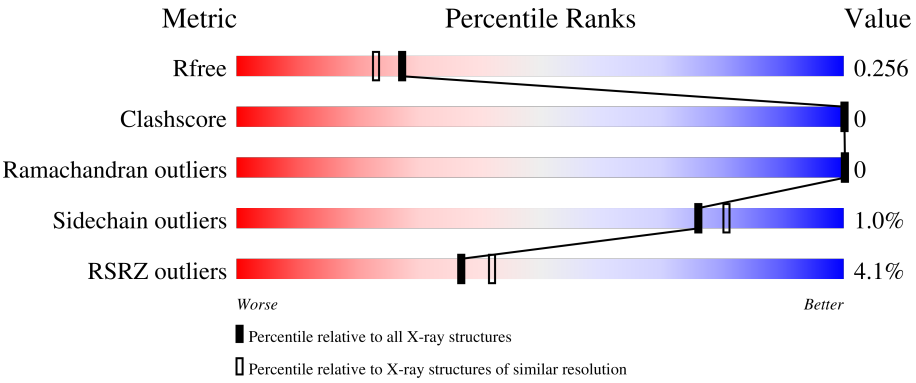
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 2.08 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}	130704	6189 (2.10-2.06)
Clashscore	141614	6738 (2.10-2.06)
Ramachandran outliers	138981	6663 (2.10-2.06)
Sidechain outliers	138945	6664 (2.10-2.06)
RSRZ outliers	127900	6057 (2.10-2.06)

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 <=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	166	5% 71% · 28%
1	B	166	% 73% · 26%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	ZN	B	302	-	-	-	X

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 1905 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 Galectin-3-binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	119	Total	C	N	O	S	0	0	0
			917	574	159	177	7			
1	B	123	Total	C	N	O	S	0	0	0
			944	592	163	182	7			

There are 78 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	122	ARG	-	expression tag	UNP Q08380
A	123	SER	-	expression tag	UNP Q08380
A	251	SER	-	expression tag	UNP Q08380
A	252	ARG	-	expression tag	UNP Q08380
A	253	ASP	-	expression tag	UNP Q08380
A	254	ASP	-	expression tag	UNP Q08380
A	255	ASP	-	expression tag	UNP Q08380
A	256	ASP	-	expression tag	UNP Q08380
A	257	LYS	-	expression tag	UNP Q08380
A	258	ALA	-	expression tag	UNP Q08380
A	259	GLY	-	expression tag	UNP Q08380
A	260	TRP	-	expression tag	UNP Q08380
A	261	SER	-	expression tag	UNP Q08380
A	262	HIS	-	expression tag	UNP Q08380
A	263	PRO	-	expression tag	UNP Q08380
A	264	GLN	-	expression tag	UNP Q08380
A	265	PHE	-	expression tag	UNP Q08380
A	266	GLU	-	expression tag	UNP Q08380
A	267	LYS	-	expression tag	UNP Q08380
A	268	GLY	-	expression tag	UNP Q08380
A	269	GLY	-	expression tag	UNP Q08380
A	270	GLY	-	expression tag	UNP Q08380
A	271	SER	-	expression tag	UNP Q08380
A	272	GLY	-	expression tag	UNP Q08380
A	273	GLY	-	expression tag	UNP Q08380

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	274	GLY	-	expression tag	UNP Q08380
A	275	SER	-	expression tag	UNP Q08380
A	276	GLY	-	expression tag	UNP Q08380
A	277	GLY	-	expression tag	UNP Q08380
A	278	GLY	-	expression tag	UNP Q08380
A	279	SER	-	expression tag	UNP Q08380
A	280	TRP	-	expression tag	UNP Q08380
A	281	SER	-	expression tag	UNP Q08380
A	282	HIS	-	expression tag	UNP Q08380
A	283	PRO	-	expression tag	UNP Q08380
A	284	GLN	-	expression tag	UNP Q08380
A	285	PHE	-	expression tag	UNP Q08380
A	286	GLU	-	expression tag	UNP Q08380
A	287	LYS	-	expression tag	UNP Q08380
B	122	ARG	-	expression tag	UNP Q08380
B	123	SER	-	expression tag	UNP Q08380
B	251	SER	-	expression tag	UNP Q08380
B	252	ARG	-	expression tag	UNP Q08380
B	253	ASP	-	expression tag	UNP Q08380
B	254	ASP	-	expression tag	UNP Q08380
B	255	ASP	-	expression tag	UNP Q08380
B	256	ASP	-	expression tag	UNP Q08380
B	257	LYS	-	expression tag	UNP Q08380
B	258	ALA	-	expression tag	UNP Q08380
B	259	GLY	-	expression tag	UNP Q08380
B	260	TRP	-	expression tag	UNP Q08380
B	261	SER	-	expression tag	UNP Q08380
B	262	HIS	-	expression tag	UNP Q08380
B	263	PRO	-	expression tag	UNP Q08380
B	264	GLN	-	expression tag	UNP Q08380
B	265	PHE	-	expression tag	UNP Q08380
B	266	GLU	-	expression tag	UNP Q08380
B	267	LYS	-	expression tag	UNP Q08380
B	268	GLY	-	expression tag	UNP Q08380
B	269	GLY	-	expression tag	UNP Q08380
B	270	GLY	-	expression tag	UNP Q08380
B	271	SER	-	expression tag	UNP Q08380
B	272	GLY	-	expression tag	UNP Q08380
B	273	GLY	-	expression tag	UNP Q08380
B	274	GLY	-	expression tag	UNP Q08380
B	275	SER	-	expression tag	UNP Q08380
B	276	GLY	-	expression tag	UNP Q08380

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	277	GLY	-	expression tag	UNP Q08380
B	278	GLY	-	expression tag	UNP Q08380
B	279	SER	-	expression tag	UNP Q08380
B	280	TRP	-	expression tag	UNP Q08380
B	281	SER	-	expression tag	UNP Q08380
B	282	HIS	-	expression tag	UNP Q08380
B	283	PRO	-	expression tag	UNP Q08380
B	284	GLN	-	expression tag	UNP Q08380
B	285	PHE	-	expression tag	UNP Q08380
B	286	GLU	-	expression tag	UNP Q08380
B	287	LYS	-	expression tag	UNP Q08380

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Zn 1 1	0	0
2	B	2	Total Zn 2 2	0	1

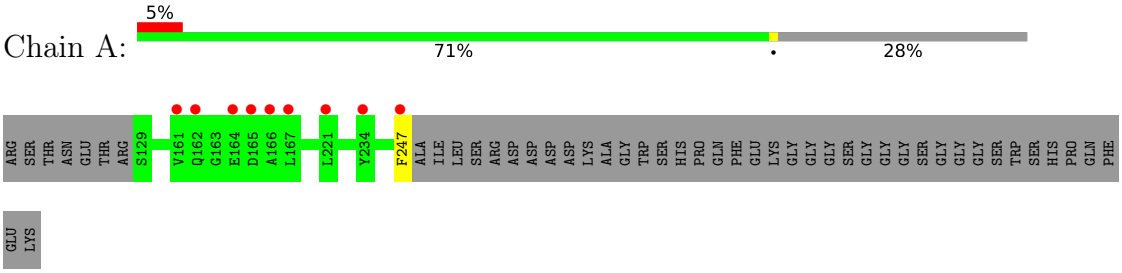
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	19	Total O 19 19	0	0
3	B	22	Total O 22 22	0	0

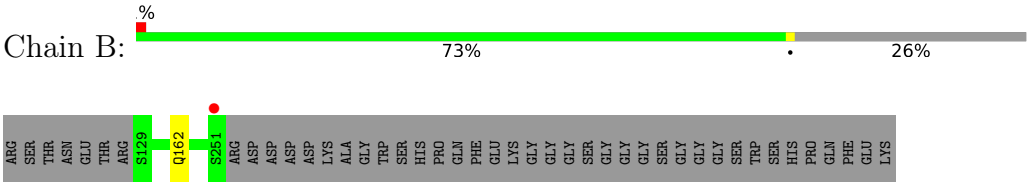
3 Residue-property plots (i)

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 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: Galectin-3-binding protein



• Molecule 1: Galectin-3-binding protein



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	70.34Å 70.34Å 105.51Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.77 – 2.08 39.88 – 2.08	Depositor EDS
% Data completeness (in resolution range)	99.2 (20.77-2.08) 99.2 (39.88-2.08)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.28 (at 2.08Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.208 , 0.243 0.221 , 0.256	Depositor DCC
R_{free} test set	936 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å^2)	47.9	Xtriage
Anisotropy	0.433	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 50.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.024 for -h,-k,l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	1905	wwPDB-VP
Average B, all atoms (Å^2)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.96% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	0.47	0/932	0.63	0/1260
1	B	0.52	0/959	0.64	0/1297
All	All	0.50	0/1891	0.63	0/2557

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	917	0	897	0	0
1	B	944	0	929	0	0
2	A	1	0	0	0	0
2	B	2	0	0	0	0
3	A	19	0	0	0	0
3	B	22	0	0	0	0
All	All	1905	0	1826	0	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 0.

There are no clashes within the asymmetric unit.

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	117/166 (70%)	116 (99%)	1 (1%)	0	100	100
1	B	121/166 (73%)	120 (99%)	1 (1%)	0	100	100
All	All	238/332 (72%)	236 (99%)	2 (1%)	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	101/136 (74%)	100 (99%)	1 (1%)	76	81
1	B	104/136 (76%)	103 (99%)	1 (1%)	76	81
All	All	205/272 (75%)	203 (99%)	2 (1%)	76	81

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	247	PHE
1	B	162	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	172	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 monosaccharides in this entry.

5.6 Ligand geometry

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	119/166 (71%)	0.18	9 (7%) 13 17	41, 55, 84, 109	0
1	B	123/166 (74%)	-0.03	1 (0%) 86 87	38, 50, 73, 110	0
All	All	242/332 (72%)	0.07	10 (4%) 37 42	38, 53, 80, 110	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	165	ASP	6.1
1	A	234	TYR	5.1
1	A	162	GLN	4.9
1	A	167	LEU	4.6
1	B	251	SER	3.9
1	A	166	ALA	3.8
1	A	164	GLU	3.8
1	A	247	PHE	3.4
1	A	161	VAL	3.2
1	A	221	LEU	2.5

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

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

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	ZN	B	302	1/1	0.77	1.77	300,300,300,300	0
2	ZN	B	301[L]	1/1	0.95	0.22	48,48,48,48	0
2	ZN	A	301	1/1	0.96	0.08	93,93,93,93	0

6.5 Other polymers

There are no such residues in this entry.