



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 18, 2024 – 01:20 PM JST

PDB ID : 6JH1
Title : Crystal structure of bISG15/NS1B complex
Authors : Jiang, Y.N.; Wang, X.W.
Deposited on : 2019-02-16
Resolution : 3.00 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

<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 : 2.36
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) : 2.36

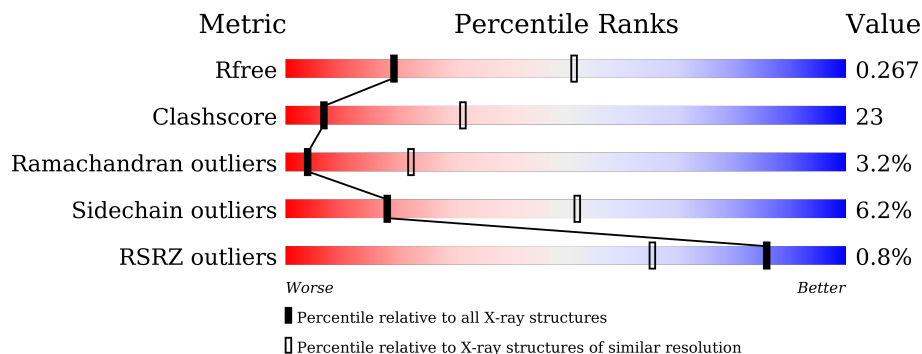
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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	A	103	 % 55% 31% 11%
1	B	103	 46% 42% 12%
2	C	154	 % 47% 45% 5%
2	D	154	 % 51% 38% 6% 5%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3795 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 Non-structural protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	92	743	467	136	135	5	0	0	0
1	B	91	732	458	135	134	5	0	0	0

- Molecule 2 is a protein called Ubiquitin-like protein ISG15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	D	147	1160	732	203	218	7	0	0	0
2	C	147	1160	732	203	218	7	0	0	0

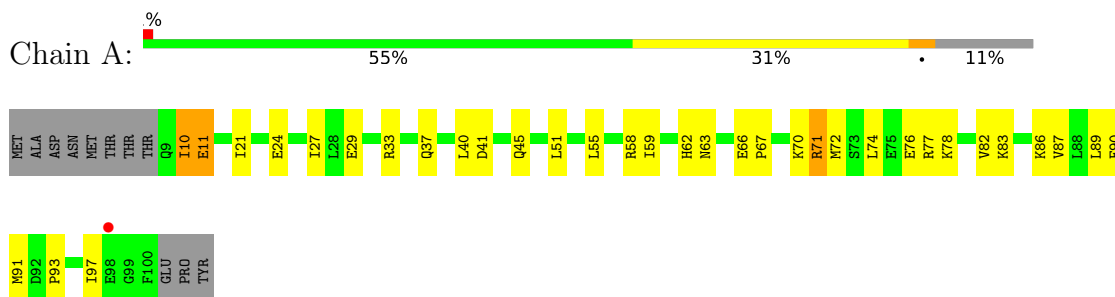
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	78	SER	CYS	engineered mutation	UNP O02741
C	78	SER	CYS	engineered mutation	UNP O02741

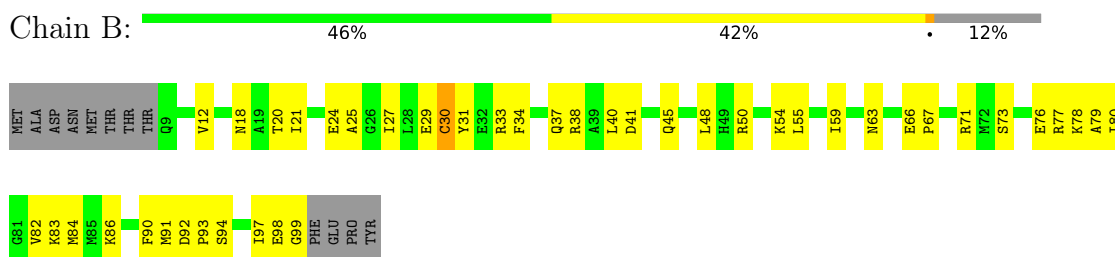
3 Residue-property plots [i](#)

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.

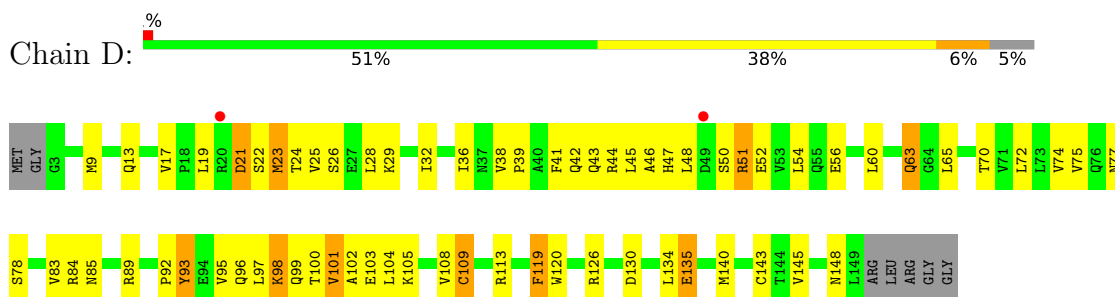
- Molecule 1: Non-structural protein 1



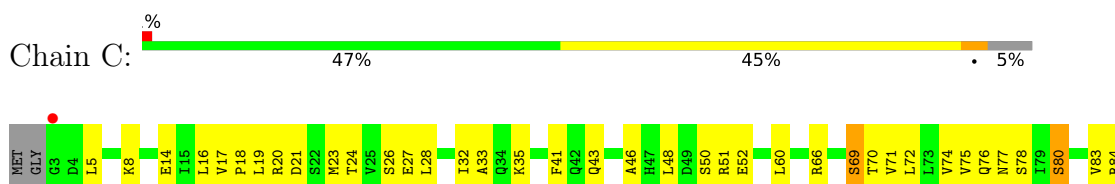
- Molecule 1: Non-structural protein 1



- Molecule 2: Ubiquitin-like protein ISG15



- Molecule 2: Ubiquitin-like protein ISG15



Y93	E94	V95	Q96	L97	K98	Q99	T100	V101	A102	E103	L104	K105	Q106	Q107	V108	C109	Q110	K111	E112	R113	D117	Q118	F119	W120	L121	S122	R126	D129	D130	E131	H132	P133	L134	E135	E136	M140	K141	G142	C143	T144	V145	F146	M147	N148	L149	ARG	LEU	ARG	ARG	GLY	GLY
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4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	59.14Å 80.05Å 109.67Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.33 – 3.00 35.93 – 3.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (33.33-3.00) 100.0 (35.93-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.13 (at 3.00Å)	Xtrriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.219 , 0.274 0.227 , 0.267	Depositor DCC
R_{free} test set	568 reflections (5.20%)	wwPDB-VP
Wilson B-factor (Å ²)	83.7	Xtrriage
Anisotropy	0.420	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 68.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3795	wwPDB-VP
Average B, all atoms (Å ²)	87.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.14% 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	0.89	0/756	0.77	0/1010
1	B	0.73	0/744	0.81	0/994
2	C	0.60	0/1176	0.76	0/1586
2	D	0.81	0/1176	0.80	0/1586
All	All	0.75	0/3852	0.78	0/5176

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 [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	743	0	752	39	0
1	B	732	0	743	43	0
2	C	1160	0	1188	63	0
2	D	1160	0	1188	61	0
All	All	3795	0	3871	178	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 23.

The worst 5 of 178 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:D:99:GLN:HE21	2:D:103:GLU:CB	1.52	1.23
2:D:99:GLN:NE2	2:D:103:GLU:HB3	1.66	1.06
2:D:99:GLN:HE21	2:D:103:GLU:HB3	0.94	1.05
2:D:92:PRO:C	2:D:93:TYR:HD1	1.61	1.02
2:D:92:PRO:C	2:D:93:TYR:CD1	2.35	0.99

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	90/103 (87%)	84 (93%)	3 (3%)	3 (3%)	4	21
1	B	89/103 (86%)	85 (96%)	3 (3%)	1 (1%)	14	50
2	C	145/154 (94%)	127 (88%)	11 (8%)	7 (5%)	2	13
2	D	145/154 (94%)	130 (90%)	11 (8%)	4 (3%)	5	25
All	All	469/514 (91%)	426 (91%)	28 (6%)	15 (3%)	4	22

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	11	GLU
1	B	98	GLU
2	C	51	ARG
2	C	77	ASN
2	C	113	ARG

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	79/89 (89%)	78 (99%)	1 (1%)	69	89
1	B	78/89 (88%)	74 (95%)	4 (5%)	24	60
2	C	131/135 (97%)	122 (93%)	9 (7%)	15	48
2	D	131/135 (97%)	119 (91%)	12 (9%)	9	34
All	All	419/448 (94%)	393 (94%)	26 (6%)	18	52

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	135	GLU
2	C	20	ARG
2	C	126	ARG
2	D	143	CYS
2	C	80	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	99	GLN
2	C	132	HIS
2	C	148	ASN
1	B	37	GLN
1	A	37	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 monosaccharides 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	92/103 (89%)	-0.33	1 (1%) 80 56	49, 76, 121, 131	0
1	B	91/103 (88%)	-0.22	0 100 100	47, 79, 114, 126	0
2	C	147/154 (95%)	-0.09	1 (0%) 87 69	54, 92, 126, 142	0
2	D	147/154 (95%)	-0.02	2 (1%) 75 49	49, 85, 134, 152	0
All	All	477/514 (92%)	-0.14	4 (0%) 86 65	47, 85, 126, 152	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	49	ASP	3.4
2	C	3	GLY	3.2
1	A	98	GLU	2.2
2	D	20	ARG	2.2

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 monosaccharides 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.