wwPDB X-ray Structure Validation Summary Report (i)

Nov 15, 2023 – 01:46 PM JST

PDB ID	:	6J7H
Title	:	Crystal structure of blue fluorescent protein from metagenomic library
Authors	:	Seo, P.W.; Kim, J.S.
Deposited on	:	2019-01-18
Resolution	:	2.31 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 (i) 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 (1)) were used in the production of this report:

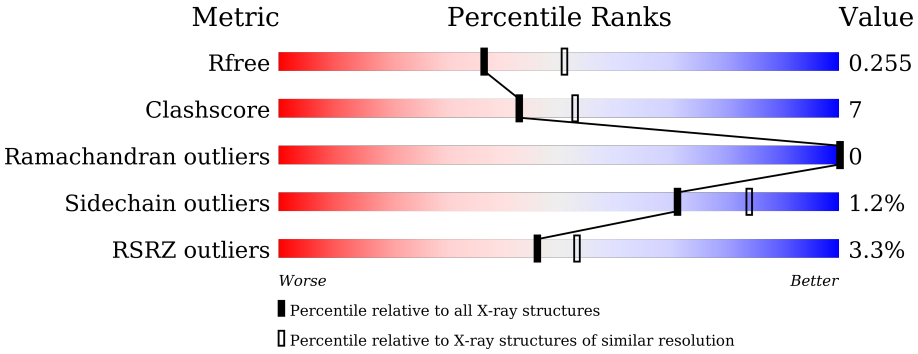
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.31 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	261	3% 81% 13% 6%
1	B	261	2% 84% 10% • 5%
1	C	261	3% 84% 11% 5%
1	D	261	5% 81% 13% 5%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 7364 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 Blue fluorescent protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	246	1766	1095	326	339	6	0	0	0
1	B	247	1775	1100	328	341	6	0	0	0
1	C	247	1775	1100	328	341	6	0	0	0
1	D	247	1775	1100	328	341	6	0	0	0

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP D6NKF4
A	2	ARG	-	expression tag	UNP D6NKF4
A	3	GLY	-	expression tag	UNP D6NKF4
A	4	SER	-	expression tag	UNP D6NKF4
A	5	HIS	-	expression tag	UNP D6NKF4
A	6	HIS	-	expression tag	UNP D6NKF4
A	7	HIS	-	expression tag	UNP D6NKF4
A	8	HIS	-	expression tag	UNP D6NKF4
A	9	HIS	-	expression tag	UNP D6NKF4
A	10	HIS	-	expression tag	UNP D6NKF4
A	11	GLY	-	expression tag	UNP D6NKF4
A	12	SER	-	expression tag	UNP D6NKF4
A	13	ALA	-	expression tag	UNP D6NKF4
A	14	CYS	-	expression tag	UNP D6NKF4
B	1	MET	-	expression tag	UNP D6NKF4
B	2	ARG	-	expression tag	UNP D6NKF4
B	3	GLY	-	expression tag	UNP D6NKF4
B	4	SER	-	expression tag	UNP D6NKF4
B	5	HIS	-	expression tag	UNP D6NKF4
B	6	HIS	-	expression tag	UNP D6NKF4
B	7	HIS	-	expression tag	UNP D6NKF4

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Chain	Residue	Modelled	Actual	Comment	Reference
B	8	HIS	-	expression tag	UNP D6NKF4
B	9	HIS	-	expression tag	UNP D6NKF4
B	10	HIS	-	expression tag	UNP D6NKF4
B	11	GLY	-	expression tag	UNP D6NKF4
B	12	SER	-	expression tag	UNP D6NKF4
B	13	ALA	-	expression tag	UNP D6NKF4
B	14	CYS	-	expression tag	UNP D6NKF4
C	1	MET	-	expression tag	UNP D6NKF4
C	2	ARG	-	expression tag	UNP D6NKF4
C	3	GLY	-	expression tag	UNP D6NKF4
C	4	SER	-	expression tag	UNP D6NKF4
C	5	HIS	-	expression tag	UNP D6NKF4
C	6	HIS	-	expression tag	UNP D6NKF4
C	7	HIS	-	expression tag	UNP D6NKF4
C	8	HIS	-	expression tag	UNP D6NKF4
C	9	HIS	-	expression tag	UNP D6NKF4
C	10	HIS	-	expression tag	UNP D6NKF4
C	11	GLY	-	expression tag	UNP D6NKF4
C	12	SER	-	expression tag	UNP D6NKF4
C	13	ALA	-	expression tag	UNP D6NKF4
C	14	CYS	-	expression tag	UNP D6NKF4
D	1	MET	-	expression tag	UNP D6NKF4
D	2	ARG	-	expression tag	UNP D6NKF4
D	3	GLY	-	expression tag	UNP D6NKF4
D	4	SER	-	expression tag	UNP D6NKF4
D	5	HIS	-	expression tag	UNP D6NKF4
D	6	HIS	-	expression tag	UNP D6NKF4
D	7	HIS	-	expression tag	UNP D6NKF4
D	8	HIS	-	expression tag	UNP D6NKF4
D	9	HIS	-	expression tag	UNP D6NKF4
D	10	HIS	-	expression tag	UNP D6NKF4
D	11	GLY	-	expression tag	UNP D6NKF4
D	12	SER	-	expression tag	UNP D6NKF4
D	13	ALA	-	expression tag	UNP D6NKF4
D	14	CYS	-	expression tag	UNP D6NKF4

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	74	74	74	0	0
			Total	O		
2	B	79	79	79	0	0

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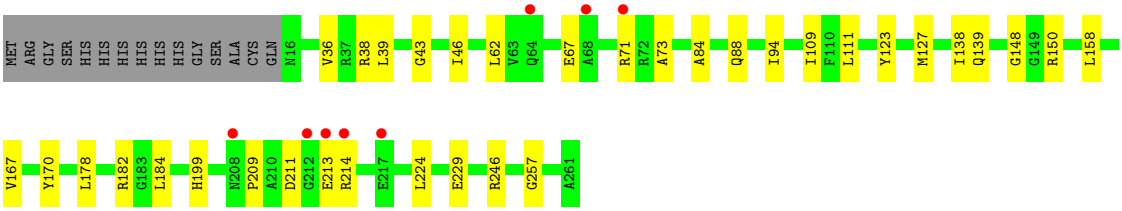
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	C	67	67	67	0	0
			Total	O		
2	D	53	53	53	0	0

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.

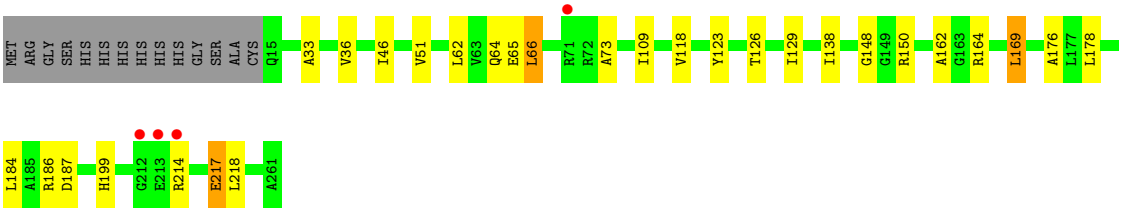
• Molecule 1: Blue fluorescent protein

Chain A:



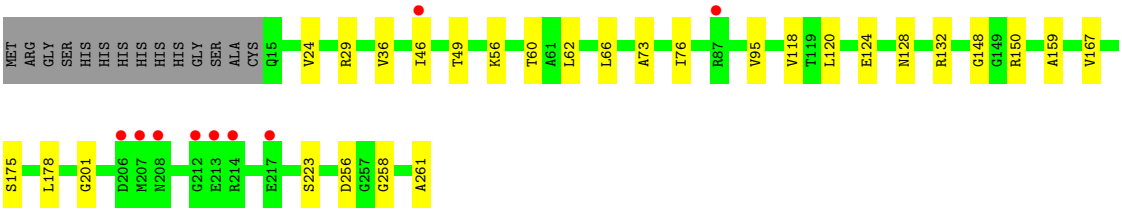
• Molecule 1: Blue fluorescent protein

Chain B:



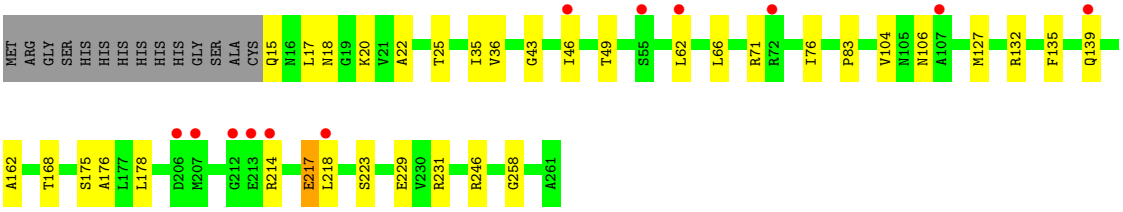
• Molecule 1: Blue fluorescent protein

Chain C:



• Molecule 1: Blue fluorescent protein

Chain D:


MET
ARG
GLY
SER
HIS
HIS
HIS
HIS
HIS
GLY
SER
ALA
CYS
Q15
N16
L17
N18
G19
K20
V21
A22
T25
I35
V36
G43
I46
T49
S55
L62
L66
R71
R72
I76
P83
V104
N105
N106
A107
M127
R132
F135
Q139
A162
T168
S175
A176
L177
L178
D206
M207
G212
E213
R214
E217
L218
S223
E229
V230
R231
R246
G258
A261

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	56.28Å 90.56Å 171.53Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.35 – 2.31 48.35 – 2.31	Depositor EDS
% Data completeness (in resolution range)	99.1 (48.35-2.31) 99.1 (48.35-2.31)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.50 (at 2.32Å)	Xtriage
Refinement program	PHENIX (1.12_2829: ???)	Depositor
R, R_{free}	0.205 , 0.256 0.205 , 0.255	Depositor DCC
R_{free} test set	1562 reflections (4.00%)	wwPDB-VP
Wilson B-factor (Å^2)	31.1	Xtriage
Anisotropy	0.642	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 37.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	7364	wwPDB-VP
Average B, all atoms (Å^2)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 22.48 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.6555e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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 (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	0.53	0/1788	0.62	0/2427
1	B	0.66	2/1797 (0.1%)	0.66	0/2439
1	C	0.59	0/1797	0.63	0/2439
1	D	0.42	0/1797	0.57	0/2439
All	All	0.56	2/7179 (0.0%)	0.62	0/9744

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	65	GLU	CD-OE2	-6.44	1.18	1.25
1	B	169	LEU	C-O	-5.24	1.13	1.23

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	1766	0	1781	32	0
1	B	1775	0	1789	24	0
1	C	1775	0	1789	26	0
1	D	1775	0	1789	24	0
2	A	74	0	0	4	0
2	B	79	0	0	5	0
2	C	67	0	0	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	53	0	0	1	0
All	All	7364	0	7148	97	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 7.

The worst 5 of 97 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:A:43:GLY:HA2	1:A:71:ARG:NH2	1.39	1.38
1:A:43:GLY:HA2	1:A:71:ARG:CZ	1.70	1.21
1:A:43:GLY:CA	1:A:71:ARG:NH2	2.21	1.02
1:B:186:ARG:HH21	1:C:261:ALA:HB2	1.27	1.00
1:A:43:GLY:CA	1:A:71:ARG:HH21	1.84	0.90

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	244/261 (94%)	239 (98%)	5 (2%)	0	100	100
1	B	245/261 (94%)	242 (99%)	3 (1%)	0	100	100
1	C	245/261 (94%)	241 (98%)	4 (2%)	0	100	100
1	D	245/261 (94%)	243 (99%)	2 (1%)	0	100	100
All	All	979/1044 (94%)	965 (99%)	14 (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	173/185 (94%)	172 (99%)	1 (1%)	86	94
1	B	174/185 (94%)	171 (98%)	3 (2%)	60	76
1	C	174/185 (94%)	173 (99%)	1 (1%)	86	94
1	D	174/185 (94%)	171 (98%)	3 (2%)	60	76
All	All	695/740 (94%)	687 (99%)	8 (1%)	71	84

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	246	ARG
1	D	218	LEU
1	C	95	VAL
1	B	217	GLU
1	D	217	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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	246/261 (94%)	0.08	8 (3%)	46	53	22, 31, 55, 91	0
1	B	247/261 (94%)	0.00	4 (1%)	72	77	21, 30, 50, 80	0
1	C	247/261 (94%)	0.21	9 (3%)	42	49	20, 32, 57, 95	0
1	D	247/261 (94%)	0.33	12 (4%)	29	36	22, 35, 63, 100	0
All	All	987/1044 (94%)	0.16	33 (3%)	46	53	20, 32, 58, 100	0

The worst 5 of 33 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	213	GLU	7.9
1	C	214	ARG	7.0
1	A	212	GLY	5.3
1	C	206	ASP	4.9
1	C	213	GLU	4.8

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.