



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2022 – 02:12 PM JST

PDB ID : 7DMX
Title : Photocleavable Fluorescent Protein in green form
Authors : Wen, Y.; Lemieux, M.J.
Deposited on : 2020-12-08
Resolution : 2.10 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.26
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)	:	2.26

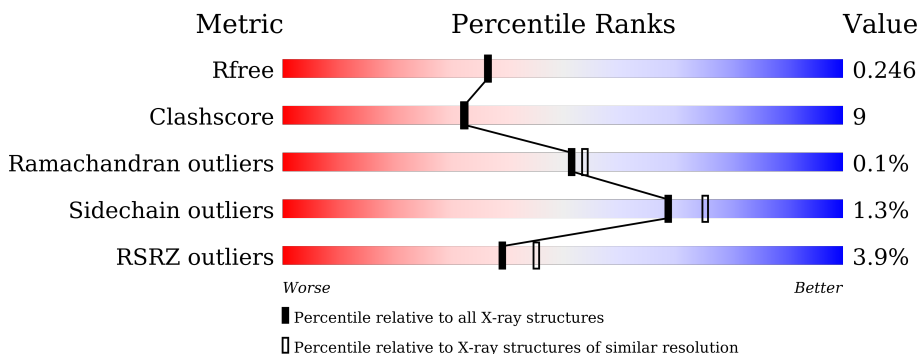
1 Overall quality at a glance

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}	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (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	A	240	<div> <div>2%</div> <div> <div></div> <div>72%</div> <div>15%</div> <div>•</div> <div>12%</div> </div> </div>
1	B	240	<div> <div>6%</div> <div> <div></div> <div>71%</div> <div>15%</div> <div>•</div> <div>12%</div> </div> </div>
1	C	240	<div> <div>3%</div> <div> <div></div> <div>71%</div> <div>14%</div> <div>•</div> <div>13%</div> </div> </div>
1	D	240	<div> <div>2%</div> <div> <div></div> <div>79%</div> <div>10%</div> <div></div> <div>10%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7204 atoms, of which 0 are hydrogens and 0 are deuteriums.

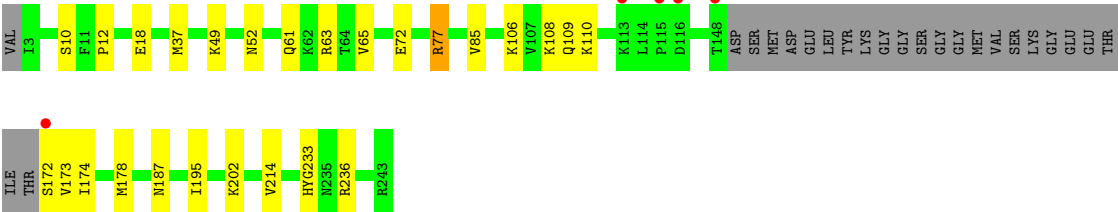
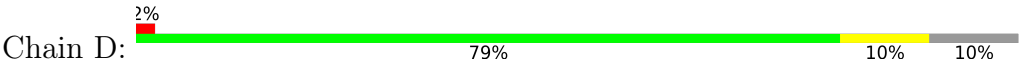
In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called PhoCl green.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	211	Total	C	N	O	S	4	3	0
			1705	1089	288	319	9			
1	B	210	Total	C	N	O	S	4	1	0
			1665	1066	276	314	9			
1	C	208	Total	C	N	O	S	4	2	0
			1680	1079	285	307	9			
1	D	216	Total	C	N	O	S	6	3	0
			1735	1111	295	320	9			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	127	Total	O	0	0
			127	127		
2	B	103	Total	O	0	0
			103	103		
2	C	92	Total	O	0	0
			92	92		
2	D	97	Total	O	0	0
			97	97		



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	60.36Å 112.76Å 144.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.39 – 2.10 44.39 – 2.10	Depositor EDS
% Data completeness (in resolution range)	73.7 (44.39-2.10) 73.7 (44.39-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.44 (at 2.10Å)	Xtriage
Refinement program	PHENIX 1.17.1 _3660	Depositor
R, R_{free}	0.205 , 0.249 0.206 , 0.246	Depositor DCC
R_{free} test set	2000 reflections (4.66%)	wwPDB-VP
Wilson B-factor (Å ²)	25.7	Xtriage
Anisotropy	0.049	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 47.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7204	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.43% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CR8

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	0.49	0/1724	0.73	3/2325 (0.1%)
1	B	0.53	0/1681	0.76	2/2274 (0.1%)
1	C	0.48	0/1696	0.72	3/2285 (0.1%)
1	D	0.51	0/1756	0.69	1/2369 (0.0%)
All	All	0.50	0/6857	0.73	9/9253 (0.1%)

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	65	VAL	CG1-CB-CG2	7.23	122.46	110.90
1	C	181	LYS	CD-CE-NZ	6.44	126.52	111.70
1	B	102	ARG	NE-CZ-NH2	-6.38	117.11	120.30
1	A	77	ARG	CB-CG-CD	-6.04	95.88	111.60
1	C	9	GLN	CA-CB-CG	5.68	125.90	113.40

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	1705	0	1616	33	0
1	B	1665	0	1541	38	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	1680	0	1601	31	0
1	D	1735	0	1652	17	0
2	A	127	0	0	13	0
2	B	103	0	0	5	1
2	C	92	0	0	6	1
2	D	97	0	0	9	0
All	All	7204	0	6410	116	1

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 9.

The worst 5 of 116 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:B:175:LYS:H	1:B:178:MET:HE1	1.13	1.09
1:C:109:GLN:NE2	2:C:301:HOH:O	1.83	1.08
1:C:40:ASP:O	1:C:178:MET:HE3	1.53	1.07
1:B:175:LYS:N	1:B:178:MET:HE1	1.80	0.96
1:B:175:LYS:H	1:B:178:MET:CE	1.79	0.95

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:387:HOH:O	2:C:383:HOH:O[3_554]	1.81	0.39

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	205/240 (85%)	199 (97%)	6 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	203/240 (85%)	197 (97%)	6 (3%)	0	100	100
1	C	201/240 (84%)	195 (97%)	5 (2%)	1 (0%)	29	26
1	D	212/240 (88%)	208 (98%)	4 (2%)	0	100	100
All	All	821/960 (86%)	799 (97%)	21 (3%)	1 (0%)	51	54

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	13	GLU

5.3.2 Protein sidechains ⓘ

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	179/207 (86%)	177 (99%)	2 (1%)	73	79
1	B	169/207 (82%)	166 (98%)	3 (2%)	59	65
1	C	173/207 (84%)	173 (100%)	0	100	100
1	D	180/207 (87%)	175 (97%)	5 (3%)	43	47
All	All	701/828 (85%)	691 (99%)	10 (1%)	69	73

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	77	ARG
1	D	172	SER
1	D	173	VAL
1	B	178	MET
1	B	202	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	47	HIS
1	B	141	HIS
1	C	9	GLN
1	D	52	ASN
1	D	187	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

4 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	CR8	A	233	1	20,27,28	2.05	7 (35%)	17,37,39	1.36	2 (11%)
1	CR8	C	233	1	20,27,28	2.00	9 (45%)	17,37,39	1.70	4 (23%)
1	CR8	D	233	1	20,27,28	2.16	9 (45%)	17,37,39	1.68	3 (17%)
1	CR8	B	233	1	20,27,28	2.09	9 (45%)	17,37,39	1.13	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	CR8	A	233	1	-	6/8/25/26	0/3/3/3
1	CR8	C	233	1	-	4/8/25/26	0/3/3/3
1	CR8	D	233	1	-	4/8/25/26	0/3/3/3
1	CR8	B	233	1	-	5/8/25/26	0/3/3/3

The worst 5 of 34 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	233	CR8	C12-N13	-4.22	1.29	1.36
1	D	233	CR8	C12-N13	-4.17	1.29	1.36
1	B	233	CR8	C12-N13	-3.79	1.30	1.36
1	B	233	CR8	C9-C8	3.68	1.55	1.41
1	C	233	CR8	C9-C8	3.54	1.54	1.41

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	233	CR8	C-C17-N13	4.21	118.31	111.92
1	C	233	CR8	C-C17-N13	3.81	117.70	111.92
1	C	233	CR8	O19-C-C17	-3.32	116.88	126.32
1	D	233	CR8	C4-C5-C7	-2.91	119.47	121.95
1	B	233	CR8	O19-C-C17	-2.63	118.85	126.32

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	233	CR8	C6-C7-C8-C9
1	A	233	CR8	C7-C8-C9-N15
1	A	233	CR8	C16-C20-C21-N22
1	A	233	CR8	C16-C20-C21-C23
1	B	233	CR8	C7-C8-C9-N15

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	233	CR8	1	0
1	C	233	CR8	1	0
1	B	233	CR8	1	0

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	210/240 (87%)	-0.14	6 (2%) 51 57	14, 25, 54, 82	3 (1%)
1	B	209/240 (87%)	0.19	14 (6%) 17 22	16, 32, 65, 105	3 (1%)
1	C	207/240 (86%)	0.08	8 (3%) 39 45	17, 32, 61, 83	3 (1%)
1	D	215/240 (89%)	-0.12	5 (2%) 60 65	15, 28, 59, 84	4 (1%)
All	All	841/960 (87%)	0.00	33 (3%) 39 45	14, 29, 62, 105	13 (1%)

The worst 5 of 33 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	174	ILE	4.7
1	A	112	VAL	4.0
1	A	111	PRO	4.0
1	B	9	GLN	3.5
1	B	176	PRO	3.4

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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, 95th 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
1	CR8	B	233	25/26	0.94	0.10	20,24,31,35	0
1	CR8	C	233	25/26	0.96	0.09	21,25,30,31	0
1	CR8	D	233	25/26	0.96	0.10	13,17,23,23	0
1	CR8	A	233	25/26	0.97	0.10	11,16,19,21	0

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.