

wwPDB X-ray Structure Validation Summary Report (i)

Nov 6, 2023 – 09:54 AM EST

PDB ID : 4GOB

Title : Low pH Crystal Structure of a reconstructed Kaede-type Red Fluorescent Pro-

tein, Least Evolved Ancestor (LEA)

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Deposited on : 2012-08-19

Resolution : 1.53 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

Mogul : 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.36

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

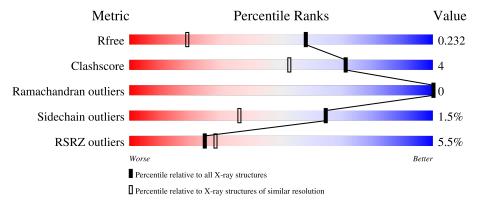
Validation Pipeline (wwPDB-VP) : 2.36

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 1.53 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	Similar resolution $(\# \text{Entries, resolution range}(\text{\AA}))$
R_{free}	130704	2556 (1.56-1.52)
Clashscore	141614	2634 (1.56-1.52)
Ramachandran outliers	138981	2580 (1.56-1.52)
Sidechain outliers	138945	2577 (1.56-1.52)
RSRZ outliers	127900	2524 (1.56-1.52)

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	228	87%	7% • 5%
1	В	228	89%	5% • •
1	С	228	87%	7% 5%
1	D	228	85%	8% • 5%



2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 7504 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 Kaede-type Fluorescent Protein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	Λ	A 217	Total	С	N	О	S	0	7	0
1	A	217	1818	1162	305	340	11	U	1	0
1	В	218	Total	С	N	О	S	2	4	0
1	Б		1802	1152	303	336	11	2		
1	C	217	Total	С	N	О	S	0	7	0
1		211	1816	1161	304	337	14	U	1	
1	1 D	217	Total	С	N	О	S	0	1	0
1		217	1774	1137	301	325	11	U	0 1	

• Molecule 2 is water.

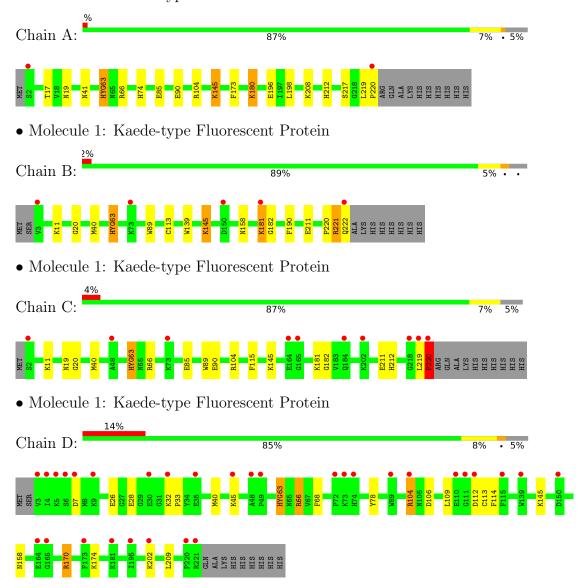
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	114	Total O 114 114	0	0
2	В	81	Total O 81 81	0	0
2	С	71	Total O 71 71	0	0
2	D	28	Total O 28 28	0	0



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: Kaede-type Fluorescent Protein





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	82.44Å 100.79Å 120.11Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.98 - 1.53	Depositor
rtesolution (A)	33.98 - 1.53	EDS
% Data completeness	94.1 (33.98-1.53)	Depositor
(in resolution range)	94.1 (33.98-1.53)	EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.26 (at 1.53Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
P. P.	0.175 , 0.231	Depositor
R, R_{free}	0.175 , 0.232	DCC
R_{free} test set	7050 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	12.0	Xtriage
Anisotropy	1.503	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.44, 53.0	EDS
L-test for twinning ²	$ < L > = 0.48, < L^2> = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7504	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.03% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities estimated from amplitudes.

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	Bo	nd lengths	Bond angles		
MIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.78	0/1839	0.80	3/2478 (0.1%)	
1	В	0.75	$4/1823 \ (0.2\%)$	0.74	0/2458	
1	С	0.65	1/1837 (0.1%)	0.76	$1/2475 \ (0.0\%)$	
1	D	0.92	4/1795~(0.2%)	0.80	0/2419	
All	All	0.78	9/7294 (0.1%)	0.77	4/9830 (0.0%)	

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

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\operatorname{\mathring{A}})$	Ideal(Å)
1	В	222	GLN	C-O	-6.24	1.11	1.23
1	В	89	TRP	CD2-CE2	5.95	1.48	1.41
1	В	139	TRP	CD2-CE2	5.66	1.48	1.41
1	С	89	TRP	CD2-CE2	5.51	1.48	1.41
1	В	221	ARG	CZ-NH2	-5.45	1.25	1.33

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	173	PHE	CB-CG-CD2	-5.89	116.67	120.80
1	С	220	PRO	CA-C-O	-5.42	107.20	120.20
1	A	173	PHE	CB-CG-CD1	5.18	124.42	120.80
1	A	180	LYS	CD-CE-NZ	5.13	123.50	111.70

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	1818	0	1737	20	0
1	В	1802	0	1722	12	0
1	С	1816	0	1736	11	0
1	D	1774	0	1708	17	0
2	A	114	0	0	2	0
2	В	81	0	0	0	0
2	С	71	0	0	1	0
2	D	28	0	0	1	0
All	All	7504	0	6903	50	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 4.

The worst 5 of 50 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} \text{Interatomic} \\ \text{distance (Å)} \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:D:158:ASN:HB3	1:D:170:ARG:HH12	1.41	0.85
1:D:158:ASN:HB3	1:D:170:ARG:NH1	1.92	0.84
1:C:219:LEU:HA	1:C:220:PRO:C	2.10	0.70
1:A:219:LEU:HA	1:A:220:PRO:C	2.11	0.69
1:B:11:LYS:HG2	1:B:113:CYS:SG	2.32	0.69

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	Percer	ntiles
1	A	$219/228 \ (96\%)$	219 (100%)	0	0	100	100
1	В	217/228~(95%)	217 (100%)	0	0	100	100
1	\mathbf{C}	$219/228 \ (96\%)$	216 (99%)	3 (1%)	0	100	100
1	D	213/228 (93%)	211 (99%)	2 (1%)	0	100	100
All	All	868/912 (95%)	863 (99%)	5 (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	Percent	iles
1	A	195/198 (98%)	192 (98%)	3 (2%)	65 3	36
1	В	193/198~(98%)	191 (99%)	2 (1%)	76 5	55
1	\mathbf{C}	195/198 (98%)	192 (98%)	3 (2%)	65 3	36
1	D	189/198 (96%)	184 (97%)	5 (3%)	46 1	16
All	All	772/792 (98%)	759 (98%)	13 (2%)	65 3	31

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	С	220	PRO
1	D	66	ARG
1	D	170	ARG
1	D	104[B]	ARG
1	D	145	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	С	81	GLN
1	D	74	HIS
1	D	81	GLN

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Mol	Chain	Res	Type
1	A	212	HIS
1	В	41	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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	Mol Type Cha	Chain	Res	Link	Bond lengths			Bond angles		
MIOI	туре	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	CR8	С	63	1	20,27,28	1.69	6 (30%)	17,37,39	2.00	5 (29%)
1	CR8	D	63	1	20,27,28	2.66	7 (35%)	17,37,39	2.56	5 (29%)
1	CR8	A	63	1	20,27,28	1.97	7 (35%)	17,37,39	2.44	4 (23%)
1	CR8	В	63	1	20,27,28	1.84	8 (40%)	17,37,39	1.58	3 (17%)

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	С	63	1	-	3/8/25/26	0/3/3/3
1	CR8	D	63	1	-	2/8/25/26	0/3/3/3
1	CR8	A	63	1	-	2/8/25/26	0/3/3/3
1	CR8	В	63	1	-	2/8/25/26	0/3/3/3

The worst 5 of 28 bond length outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	$Ideal(\AA)$
1	D	63	CR8	C2-N3	5.76	1.45	1.36
1	D	63	CR8	CA3-N3	-5.12	1.40	1.49
1	D	63	CR8	C1-N2	-4.75	1.27	1.34
1	D	63	CR8	O2-C2	-4.61	1.18	1.32
1	С	63	CR8	C2-N3	4.34	1.43	1.36

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	D	63	CR8	C3-CA3-N3	8.57	124.91	111.92
1	A	63	CR8	C3-CA3-N3	7.62	123.48	111.92
1	С	63	CR8	C3-CA3-N3	4.17	118.24	111.92
1	В	63	CR8	C3-CA3-N3	4.03	118.03	111.92
1	A	63	CR8	C12-C6-C7	-4.02	118.54	121.95

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	63	CR8	CA1-C20-C21-N22
1	A	63	CR8	CA1-C20-C21-C23
1	В	63	CR8	CA1-C20-C21-N22
1	В	63	CR8	CA1-C20-C21-C23
1	С	63	CR8	CA1-C20-C21-N22

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	С	63	CR8	1	0
1	D	63	CR8	2	0
1	A	63	CR8	1	0
1	В	63	CR8	2	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, 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	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$		$\# \mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q < 0.9
1	A	$216/228 \ (94\%)$	-0.13	2 (0%) 84 86	11, 15, 25, 54	0
1	В	$217/228 \ (95\%)$	-0.22	5 (2%) 60 66	12, 19, 34, 43	2 (0%)
1	С	216/228 (94%)	0.01	10 (4%) 32 36	12, 19, 34, 59	0
1	D	216/228 (94%)	0.86	31 (14%) 2 2	16, 35, 54, 60	0
All	All	865/912 (94%)	0.13	48 (5%) 25 28	11, 20, 46, 60	2 (0%)

The worst 5 of 48 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	220	PRO	7.5
1	D	221	ARG	6.0
1	С	220	PRO	5.3
1	A	2	SER	5.2
1	A	220	PRO	4.5

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, 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
1	CR8	D	63	25/26	0.94	0.16	26,29,39,44	0
1	CR8	С	63	25/26	0.97	0.10	13,16,18,20	0
1	CR8	В	63	25/26	0.97	0.10	13,14,19,20	0
1	CR8	A	63	25/26	0.98	0.10	10,13,15,17	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.

