



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 28, 2017 – 05:49 PM EST

PDB ID : 5OQ9  
Title : XFEL structure of the off state of a reversibly photoswitching fluorescent protein determined using the droplet on demand injection method  
Authors : Hutchison, C.D.M.; Cordon-Preciado, V.; Morgan, R.M.L.; van Thor, J.J.  
Deposited on : unknown  
Resolution : 1.51 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20030345  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20030345

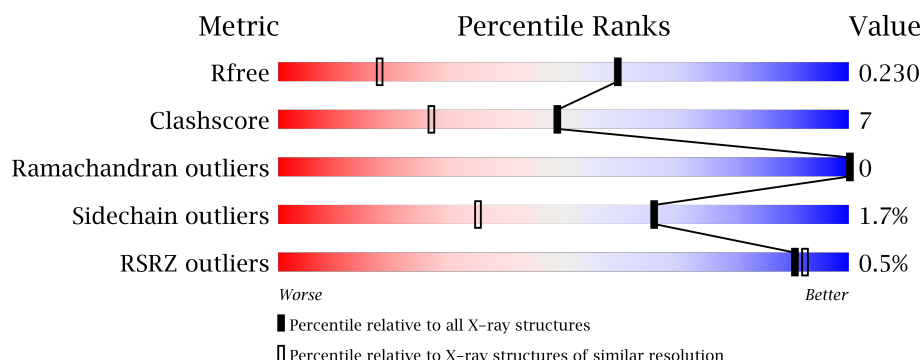
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.51 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))
$R_{free}$	100719	2964 (1.54-1.50)
Clashscore	112137	3216 (1.54-1.50)
Ramachandran outliers	110173	3145 (1.54-1.50)
Sidechain outliers	110143	3143 (1.54-1.50)
RSRZ outliers	101464	2990 (1.54-1.50)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	224	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1991 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 Green to red photoconvertible GFP-like protein EosFP.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	216	Total	C	N	O	S	0	9	0
			1781	1150	295	325	11			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	11	LYS	ASN	engineered mutation	UNP Q5S6Z9
A	62	VYA	HIS	chromophore	UNP Q5S6Z9
A	62	VYA	GLY	chromophore	UNP Q5S6Z9
A	70	LYS	GLU	engineered mutation	UNP Q5S6Z9
A	74	ASN	HIS	engineered mutation	UNP Q5S6Z9
A	121	TYR	HIS	engineered mutation	UNP Q5S6Z9
A	123	THR	VAL	engineered mutation	UNP Q5S6Z9
A	157	VAL	ILE	engineered mutation	UNP Q5S6Z9
A	158	GLU	THR	engineered mutation	UNP Q5S6Z9
A	189	ALA	TYR	engineered mutation	UNP Q5S6Z9

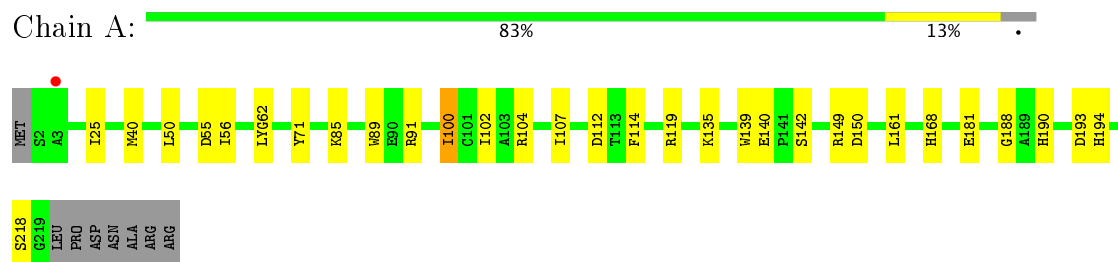
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	207	Total	O	0	3
			210	210		

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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: Green to red photoconvertible GFP-like protein EosFP



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	39.80Å 74.60Å 79.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	54.30 – 1.51 37.30 – 1.51	Depositor EDS
% Data completeness (in resolution range)	78.3 (54.30-1.51) 78.9 (37.30-1.51)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	16.69 (at 1.52Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, $R_{free}$	0.175 , 0.234 0.172 , 0.230	Depositor DCC
$R_{free}$ test set	1471 reflections (5.23%)	DCC
Wilson B-factor (Å <sup>2</sup> )	28.0	Xtriage
Anisotropy	0.026	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 54.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.98	EDS
Total number of atoms	1991	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.47% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 ⓘ

### 5.1 Standard geometry ⓘ

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

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	1.08	2/1831 (0.1%)	1.04	7/2465 (0.3%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	139	TRP	CD2-CE2	6.12	1.48	1.41
1	A	89	TRP	CD2-CE2	5.51	1.48	1.41

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	193	ASP	CB-CG-OD1	6.34	124.01	118.30
1	A	119	ARG	NE-CZ-NH1	5.69	123.15	120.30
1	A	112	ASP	CB-CG-OD1	5.54	123.28	118.30
1	A	91	ARG	NE-CZ-NH2	-5.25	117.67	120.30
1	A	150	ASP	CB-CG-OD2	-5.14	113.67	118.30
1	A	193	ASP	CB-CG-OD2	-5.14	113.68	118.30
1	A	135	LYS	CD-CE-NZ	-5.04	100.11	111.70

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	1781	0	1729	24	0
2	A	210	0	0	17	1
All	All	1991	0	1729	24	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 7.

All (24) 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:56:ILE:HG22	2:A:584:HOH:O	1.29	1.29
1:A:142:SER:HB3	2:A:450:HOH:O	0.85	1.02
1:A:25:ILE:HD11	2:A:601:HOH:O	0.83	1.01
1:A:102:ILE:HG22	2:A:558:HOH:O	1.72	0.89
1:A:50:LEU:HD11	2:A:601:HOH:O	1.80	0.80
1:A:40:MET:HE3	2:A:480:HOH:O	1.82	0.78
1:A:149:ARG:HD3	2:A:511:HOH:O	1.93	0.67
1:A:194:HIS:HD2	2:A:482:HOH:O	1.78	0.67
1:A:142:SER:CB	2:A:450:HOH:O	1.69	0.63
1:A:194:HIS:CD2	2:A:482:HOH:O	2.53	0.62
1:A:102:ILE:HD11	2:A:593:HOH:O	2.02	0.58
1:A:71:TYR:OH	1:A:190:HIS:HE1	1.88	0.56
1:A:102:ILE:CG2	2:A:558:HOH:O	2.42	0.55
1:A:140:GLU:OE2	1:A:168:HIS:HE1	1.90	0.55
1:A:100:ILE:HB	2:A:542:HOH:O	2.07	0.55
1:A:107[B]:ILE:CD1	1:A:114:PHE:HB3	2.40	0.51
1:A:107[B]:ILE:HD11	1:A:114:PHE:CD1	2.47	0.49
1:A:56:ILE:CG2	2:A:584:HOH:O	2.14	0.46
1:A:55:ASP:HB3	1:A:161:LEU:HD21	1.99	0.44
1:A:188:GLY:O	1:A:190:HIS:HD2	2.01	0.43
1:A:104:ARG:HG2	2:A:519:HOH:O	2.17	0.43
1:A:62:VYA:C3	2:A:480:HOH:O	2.67	0.42
1:A:71:TYR:OH	1:A:190:HIS:CE1	2.71	0.41
1:A:181:GLU:HG3	2:A:541:HOH:O	2.21	0.41

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:A:504:HOH:O	2:A:552:HOH:O[1_655]	2.19	0.01

## 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	222/224 (99%)	220 (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	190/190 (100%)	186 (98%)	4 (2%)	59	25

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	85	LYS
1	A	100	ILE
1	A	218[A]	SER
1	A	218[B]	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	168	HIS
1	A	190	HIS
1	A	194	HIS
1	A	206	ASN



### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	VYA	A	62	1	24,24,25	3.60	7 (29%)	31,33,35	4.21	9 (29%)

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	VYA	A	62	1	-	0/11/31/32	0/2/2/2

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	62	VYA	O3-C1	-4.12	1.27	1.37
1	A	62	VYA	C9-C12	-3.75	1.44	1.48
1	A	62	VYA	C12-N13	-2.85	1.32	1.39
1	A	62	VYA	O19-C	2.53	1.35	1.19
1	A	62	VYA	C14-N15	3.06	1.36	1.32
1	A	62	VYA	O25-C12	9.18	1.43	1.23
1	A	62	VYA	C8-C9	12.40	1.46	1.35

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	62	VYA	O25-C12-C9	-6.97	127.22	130.97
1	A	62	VYA	C8-C9-N15	-5.83	119.95	128.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	62	VYA	C12-C9-N15	-4.62	105.55	108.93
1	A	62	VYA	O19-C-C17	-3.88	113.54	126.38
1	A	62	VYA	C14-C16-N	-3.01	97.70	108.88
1	A	62	VYA	C5-C7-C6	2.03	120.67	117.63
1	A	62	VYA	C17-N13-C14	2.08	129.64	127.20
1	A	62	VYA	C8-C9-C12	7.45	131.70	122.32
1	A	62	VYA	C9-C12-N13	18.24	111.44	103.30

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	62	VYA	1	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	215/224 (95%)	-0.47	1 (0%) 90 92	19, 26, 44, 74	2 (0%)

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	3	ALA	2.5

### 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
1	VYA	A	62	23/24	0.96	0.06	-0.17	19,21,30,37	0

### 6.3 Carbohydrates [i](#)

There are no carbohydrates 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.