



# Full wwPDB X-ray Structure Validation Report ⓘ

Dec 12, 2023 – 02:44 pm GMT

PDB ID : 8BXP  
Title : SfGFP C148 F206 mutant  
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Deposited on : 2022-12-09  
Resolution : 1.79 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

<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>.

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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 : 1.8.4, CSD as541be (2020)  
Xtrriage (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

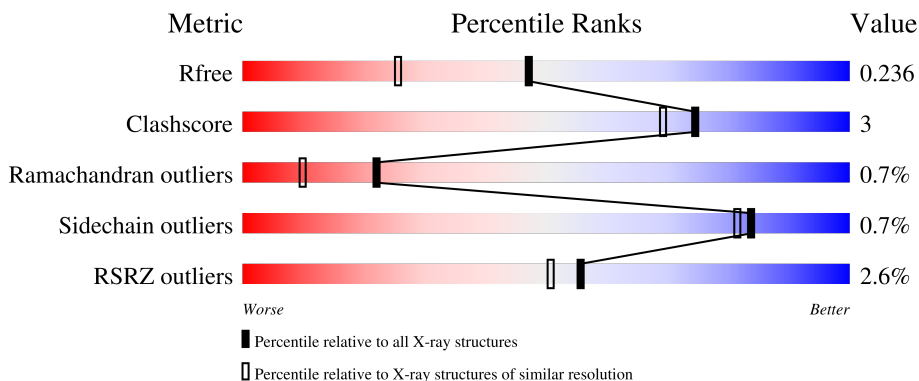
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.79 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	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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  $\geq 3$ , 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	232	 2% 89% 10%
1	B	232	 3% 88% 10%

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4078 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 fluorescent protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	232	1913	1207	329	368	9	0	8	0
1	B	230	1890	1191	325	366	8	0	7	0

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	VAL	-	insertion	UNP P42212
A	30	ARG	SER	conflict	UNP P42212
A	39	ASN	TYR	conflict	UNP P42212
A	64	LEU	PHE	conflict	UNP P42212
A	66	CRO	SER	chromophore	UNP P42212
A	66	CRO	TYR	chromophore	UNP P42212
A	66	CRO	GLY	chromophore	UNP P42212
A	80	ARG	GLN	conflict	UNP P42212
A	99	SER	PHE	conflict	UNP P42212
A	105	THR	ASN	conflict	UNP P42212
A	145	PHE	TYR	conflict	UNP P42212
A	148	CYS	HIS	conflict	UNP P42212
A	153	THR	MET	conflict	UNP P42212
A	163	ALA	VAL	conflict	UNP P42212
A	171	VAL	ILE	conflict	UNP P42212
A	206	PHE	ALA	conflict	UNP P42212
B	1	VAL	-	insertion	UNP P42212
B	30	ARG	SER	conflict	UNP P42212
B	39	ASN	TYR	conflict	UNP P42212
B	64	LEU	PHE	conflict	UNP P42212
B	66	CRO	SER	chromophore	UNP P42212
B	66	CRO	TYR	chromophore	UNP P42212
B	66	CRO	GLY	chromophore	UNP P42212
B	80	ARG	GLN	conflict	UNP P42212
B	99	SER	PHE	conflict	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
B	105	THR	ASN	conflict	UNP P42212
B	145	PHE	TYR	conflict	UNP P42212
B	148	CYS	HIS	conflict	UNP P42212
B	153	THR	MET	conflict	UNP P42212
B	163	ALA	VAL	conflict	UNP P42212
B	171	VAL	ILE	conflict	UNP P42212
B	206	PHE	ALA	conflict	UNP P42212

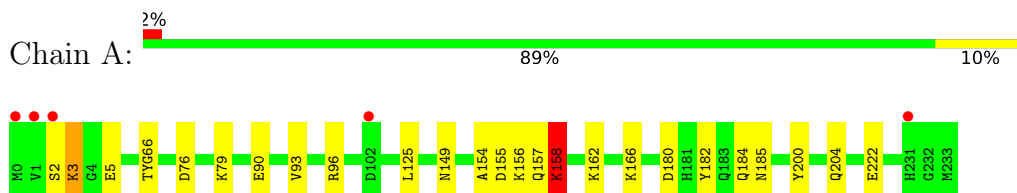
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	145	Total O 145 145	0	0
2	B	130	Total O 130 130	0	0

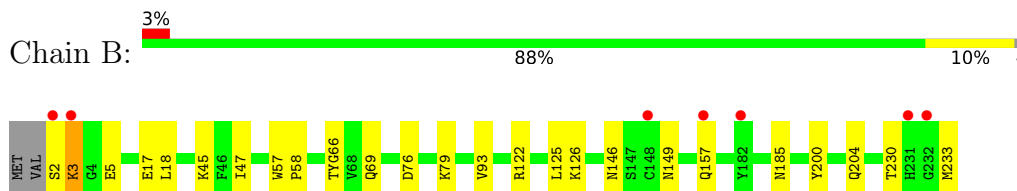
### 3 Residue-property plots [i](#)

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: Green fluorescent protein



- Molecule 1: Green fluorescent protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	67.80Å 75.02Å 125.77Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.30 – 1.79 50.30 – 1.79	Depositor EDS
% Data completeness (in resolution range)	99.8 (50.30-1.79) 97.0 (50.30-1.79)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.02 (at 1.78Å)	Xtrriage
Refinement program	REFMAC 5.8.0267	Depositor
R, $R_{free}$	0.200 , 0.234 0.204 , 0.236	Depositor DCC
$R_{free}$ test set	2964 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	34.9	Xtrriage
Anisotropy	0.381	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 34.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	4078	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	44.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.89% 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 [i](#)

### 5.1 Standard geometry [i](#)

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

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	0.88	5/1930 (0.3%)	0.99	0/2606
1	B	0.80	0/1907	0.95	0/2575
All	All	0.84	5/3837 (0.1%)	0.97	0/5181

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	5	GLU	CD-OE2	11.03	1.37	1.25
1	A	222	GLU	CD-OE2	-7.78	1.17	1.25
1	A	158	LYS	C-O	5.64	1.34	1.23
1	A	90	GLU	CD-OE2	5.22	1.31	1.25
1	A	5	GLU	CD-OE1	5.14	1.31	1.25

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	1913	0	1857	10	1
1	B	1890	0	1825	14	1
2	A	145	0	0	1	0
2	B	130	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	4078	0	3682	24	2

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 3.

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:162:LYS:HE2	1:A:184[B]:GLN:HG3	1.81	0.62
1:B:126:LYS:HD2	2:B:430:HOH:O	2.03	0.59
1:B:17:GLU:OE2	1:B:122:ARG:NH1	2.36	0.57
1:A:154:ALA:O	1:A:156:LYS:HE2	2.05	0.56
1:A:166:LYS:HG2	1:A:180[B]:ASP:OD1	2.10	0.51
1:B:2:SER:O	1:B:5:GLU:HG2	2.12	0.50
1:A:157:GLN:O	1:A:158:LYS:HB3	2.11	0.50
1:A:76:ASP:O	1:A:79:LYS:HG2	2.13	0.49
1:B:76:ASP:O	1:B:79:LYS:HG2	2.14	0.48
1:B:157:GLN:OE1	1:B:157:GLN:N	2.41	0.47
1:B:69:GLN:HA	2:B:405:HOH:O	2.14	0.47
1:B:93:VAL:O	1:B:185:ASN:HA	2.16	0.46
1:B:45:LYS:HE2	1:B:47:ILE:HD11	1.98	0.45
1:A:3:LYS:HG3	2:A:346:HOH:O	2.17	0.44
1:A:93:VAL:O	1:A:185:ASN:HA	2.16	0.44
1:A:155:ASP:OD2	1:A:184[A]:GLN:OE1	2.36	0.43
1:A:125:LEU:C	1:A:125:LEU:HD23	2.40	0.42
1:B:125:LEU:C	1:B:125:LEU:HD23	2.40	0.41
1:B:146:ASN:OD1	2:B:301:HOH:O	2.21	0.41
1:B:230:THR:O	1:B:233:MET:HG2	2.20	0.41
1:B:18:LEU:HD23	1:B:18:LEU:C	2.41	0.41
1:A:96:ARG:HA	1:A:182:TYR:O	2.21	0.41
1:B:57:TRP:N	1:B:58:PRO:CD	2.84	0.41
1:B:3:LYS:HE3	1:B:3:LYS:HB2	1.91	0.40

All (2) 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)
1:B:200:TYR:OH	1:B:204[A]:GLN:OE1[4_545]	2.16	0.04
1:A:200:TYR:OH	1:A:204[A]:GLN:OE1[3_555]	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	235/232 (101%)	227 (97%)	6 (3%)	2 (1%)	17	6
1	B	232/232 (100%)	225 (97%)	6 (3%)	1 (0%)	34	21
All	All	467/464 (101%)	452 (97%)	12 (3%)	3 (1%)	22	12

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	149	ASN
1	A	158	LYS
1	B	149	ASN

### 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	210/202 (104%)	208 (99%)	2 (1%)	76	71
1	B	207/202 (102%)	206 (100%)	1 (0%)	88	87
All	All	417/404 (103%)	414 (99%)	3 (1%)	84	81

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	SER
1	A	3	LYS
1	B	3	LYS

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](#)

2 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	CRO	A	66	1	23,23,24	0.69	0	30,32,34	1.33	4 (13%)
1	CRO	B	66	1	23,23,24	0.87	0	30,32,34	1.20	2 (6%)

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	CRO	A	66	1	-	0/12/31/32	0/2/2/2
1	CRO	B	66	1	-	0/12/31/32	0/2/2/2

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	66	CRO	CA2-C2-N3	4.05	105.28	103.37
1	A	66	CRO	O3-C3-CA3	-3.95	114.46	126.39
1	B	66	CRO	O3-C3-CA3	-3.72	115.14	126.39
1	A	66	CRO	CG2-CB2-CA2	2.68	133.23	129.94
1	A	66	CRO	C2-CA2-N2	-2.34	107.30	108.93
1	A	66	CRO	CA2-N2-C1	2.16	107.36	105.77

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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<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	231/232 (99%)	0.18	5 (2%) 62 57	28, 41, 65, 87	0
1	B	229/232 (98%)	0.28	7 (3%) 49 43	33, 43, 64, 97	0
All	All	460/464 (99%)	0.23	12 (2%) 56 51	28, 42, 65, 97	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	2	SER	6.6
1	A	1	VAL	5.6
1	B	232	GLY	5.4
1	B	231	HIS	4.3
1	B	182	TYR	3.9
1	B	148[A]	CYS	3.3
1	B	157	GLN	2.7
1	B	3	LYS	2.5
1	A	0	MET	2.3
1	A	231	HIS	2.2
1	A	102	ASP	2.2
1	A	2	SER	2.2

### 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<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	B-factors(Å <sup>2</sup> )	Q<0.9
1	CRO	A	66	22/23	0.97	0.09	28,31,33,34	0
1	CRO	B	66	22/23	0.97	0.09	30,33,41,43	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.