



# wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 9JVR / pdb\_00009jvr  
Title : De novo designed GFP 1GFL-15  
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Deposited on : 2024-10-09  
Resolution : 2.61 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](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 : 4-5-2 with Phenix2.0  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.46

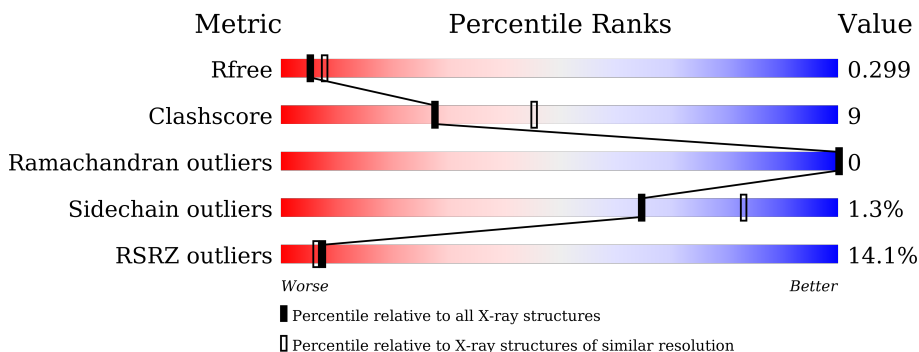
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.61 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))
$R_{free}$	164625	4623 (2.64-2.60)
Clashscore	180529	5071 (2.64-2.60)
Ramachandran outliers	177936	5006 (2.64-2.60)
Sidechain outliers	177891	5006 (2.64-2.60)
RSRZ outliers	164620	4622 (2.64-2.60)

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	237	<div> <div>9%</div> <div>76%</div> <div>19%</div> <div>.</div> </div>
1	B	237	<div> <div>13%</div> <div>78%</div> <div>17%</div> <div>..</div> </div>
1	C	237	<div> <div>10%</div> <div>76%</div> <div>19%</div> <div>..</div> </div>
1	D	237	<div> <div>22%</div> <div>74%</div> <div>22%</div> <div>.</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7402 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 De novo designed 1GFL-15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	228	Total	C	N	O	S	0	0	0
			1823	1167	309	340	7			
1	B	228	Total	C	N	O	S	0	0	0
			1823	1167	309	340	7			
1	C	228	Total	C	N	O	S	0	0	0
			1823	1167	309	340	7			
1	D	228	Total	C	N	O	S	0	0	0
			1823	1167	309	340	7			

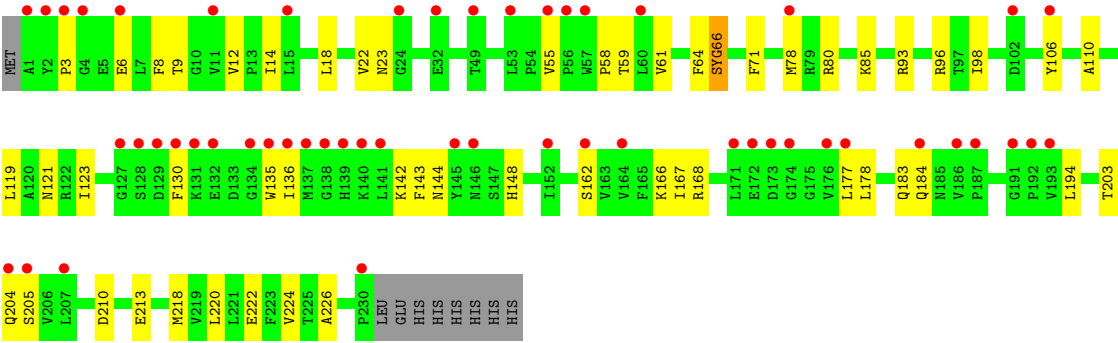
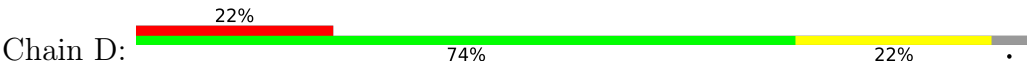
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	38	Total	O	0	0
			38	38		
2	B	32	Total	O	0	0
			32	32		
2	C	17	Total	O	0	0
			17	17		
2	D	23	Total	O	0	0
			23	23		



- Molecule 1: De novo designed 1GFL-15





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	51.70Å 65.80Å 88.49Å 70.31° 89.84° 74.36°	Depositor
Resolution (Å)	27.64 – 2.61 27.64 – 2.61	Depositor EDS
% Data completeness (in resolution range)	98.5 (27.64-2.61) 98.7 (27.64-2.61)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	7.07 (at 2.61Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, $R_{free}$	0.247 , 0.300 0.247 , 0.299	Depositor DCC
$R_{free}$ test set	1549 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	34.3	Xtriage
Anisotropy	0.212	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 55.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.53$ , $\langle L^2 \rangle = 0.37$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.88	EDS
Total number of atoms	7402	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.17% 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: GYS

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	0.11	0/1847	0.28	0/2499
1	B	0.11	0/1847	0.28	0/2499
1	C	0.10	0/1847	0.27	0/2499
1	D	0.10	0/1847	0.26	0/2499
All	All	0.10	0/7388	0.27	0/9996

There are no bond length outliers.

There are no bond angle outliers.

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	1823	0	1780	32	0
1	B	1823	0	1780	25	0
1	C	1823	0	1781	35	0
1	D	1823	0	1780	37	0
2	A	38	0	0	4	0
2	B	32	0	0	0	0
2	C	17	0	0	2	0
2	D	23	0	0	4	0
All	All	7402	0	7121	128	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 9.

The worst 5 of 128 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:57:TRP:HB3	1:B:218:MET:HE3	1.61	0.83
1:D:144:ASN:HD22	1:D:168:ARG:HD3	1.49	0.76
1:D:18:LEU:HD23	1:D:123:ILE:HB	1.69	0.74
1:B:108:THR:HG22	1:B:125:LEU:HD23	1.66	0.74
1:D:58:PRO:HB3	1:D:143:PHE:HB2	1.69	0.73

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	223/237 (94%)	219 (98%)	4 (2%)	0	100	100
1	B	223/237 (94%)	219 (98%)	4 (2%)	0	100	100
1	C	223/237 (94%)	217 (97%)	6 (3%)	0	100	100
1	D	223/237 (94%)	219 (98%)	4 (2%)	0	100	100
All	All	892/948 (94%)	874 (98%)	18 (2%)	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	198/207 (96%)	196 (99%)	2 (1%)	73	87
1	B	198/207 (96%)	195 (98%)	3 (2%)	60	80
1	C	198/207 (96%)	194 (98%)	4 (2%)	50	73
1	D	198/207 (96%)	197 (100%)	1 (0%)	86	95
All	All	792/828 (96%)	782 (99%)	10 (1%)	65	83

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

Mol	Chain	Res	Type
1	C	167	ILE
1	C	177	LEU
1	D	142	LYS
1	B	123	ILE
1	B	220	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	184	GLN
1	D	23	ASN
1	D	73	HIS
1	B	73	HIS
1	A	121	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	GYS	A	66	1	22,22,23	3.93	5 (22%)	27,30,32	3.57	7 (25%)
1	GYS	C	66	1	22,22,23	4.05	4 (18%)	27,30,32	3.74	8 (29%)
1	GYS	B	66	1	22,22,23	4.02	4 (18%)	27,30,32	3.88	9 (33%)
1	GYS	D	66	1	22,22,23	4.01	4 (18%)	27,30,32	3.61	7 (25%)

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	GYS	A	66	1	-	3/9/29/30	0/2/2/2
1	GYS	C	66	1	-	1/9/29/30	0/2/2/2
1	GYS	B	66	1	-	2/9/29/30	0/2/2/2
1	GYS	D	66	1	-	4/9/29/30	0/2/2/2

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	66	GYS	CB2-CA2	17.10	1.49	1.35
1	B	66	GYS	CB2-CA2	16.95	1.49	1.35
1	D	66	GYS	CB2-CA2	16.70	1.49	1.35
1	A	66	GYS	CB2-CA2	16.28	1.48	1.35
1	D	66	GYS	O2-C2	5.97	1.35	1.23

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	66	GYS	CA2-C2-N3	12.71	109.38	103.37
1	C	66	GYS	CA2-C2-N3	12.39	109.23	103.37
1	D	66	GYS	CA2-C2-N3	12.34	109.21	103.37
1	B	66	GYS	CA2-C2-N3	12.30	109.19	103.37
1	B	66	GYS	O2-C2-CA2	-11.45	124.53	130.96

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	66	GYS	N1-CA1-CB1-OG1
1	A	66	GYS	C1-CA1-CB1-OG1

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Mol	Chain	Res	Type	Atoms
1	A	66	GYS	C3-CA3-N3-C2
1	B	66	GYS	C3-CA3-N3-C1
1	B	66	GYS	C3-CA3-N3-C2

There are no ring outliers.

4 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	66	GYS	5	0
1	C	66	GYS	2	0
1	B	66	GYS	1	0
1	D	66	GYS	1	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides 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	227/237 (95%)	0.76	21 (9%) 16 14	17, 30, 52, 73	0
1	B	227/237 (95%)	1.11	31 (13%) 8 7	19, 34, 70, 88	0
1	C	227/237 (95%)	0.90	23 (10%) 14 12	18, 36, 57, 70	0
1	D	227/237 (95%)	1.35	53 (23%) 2 2	24, 41, 77, 104	0
All	All	908/948 (95%)	1.03	128 (14%) 7 6	17, 36, 65, 104	0

The worst 5 of 128 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	1	ALA	7.1
1	D	135	TRP	6.8
1	C	77	HIS	5.6
1	B	135	TRP	5.4
1	D	3	PRO	5.4

### 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, 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	GYS	A	66	21/22	0.76	0.18	18,28,32,37	0
1	GYS	D	66	21/22	0.79	0.17	27,35,46,52	0
1	GYS	B	66	21/22	0.83	0.14	19,28,35,37	0
1	GYS	C	66	21/22	0.86	0.13	17,23,30,39	0

### 6.3 Carbohydrates [i](#)

There are no oligosaccharides 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.