



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 14, 2020 – 05:10 AM BST

PDB ID : 6O35  
Title : Crystal structure of a de novo designed octameric helical-bundle protein  
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Deposited on : 2019-02-25  
Resolution : 2.40 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.

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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  
Xtrriage (Phenix) : 1.13  
EDS : **FAILED**  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.14.4.dev1

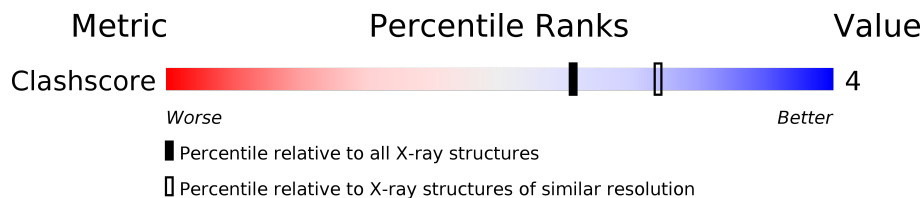
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 Å.


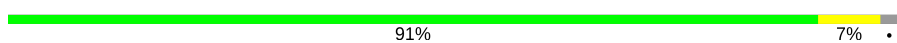


Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	4398 (2.40-2.40)

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 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  $\leq 5\%$

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	102	 89%                      10% .
1	B	102	 91%                      7% .
1	C	102	 87%                      12% .
1	D	102	 88%                      9% .

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5641 atoms, of which 2710 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 WSHC8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	A	101	1345	448	639	123	133	2	0	0	0
1	B	100	1443	473	704	123	141	2	0	0	0
1	C	101	1426	469	684	127	144	2	0	0	1
1	D	99	1410	464	683	125	136	2	0	0	0

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	4	Total 4 4	0	0
2	B	7	Total 7 7	0	0
2	C	4	Total 4 4	0	0
2	D	2	Total 2 2	0	0

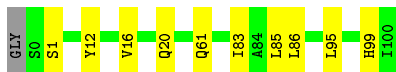
### 3 Residue-property plots [i](#)

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. 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. 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.

Note EDS failed to run properly.

- Molecule 1: de novo designed WSHC8

Chain A:  89% 10%



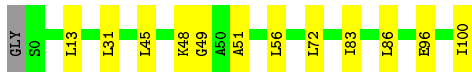
- Molecule 1: de novo designed WSHC8

Chain B:  91% 7%




- Molecule 1: de novo designed WSHC8

Chain C:  87% 12%



- Molecule 1: de novo designed WSHC8

Chain D:  88% 9%



## 4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	59.44Å 103.68Å 72.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.44 – 2.40	Depositor
% Data completeness (in resolution range)	99.5 (34.44-2.40)	Depositor
$R_{merge}$	0.19	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.04 (at 2.00Å)	Xtrriage
Refinement program	PHENIX (dev_3112: ???)	Depositor
R, $R_{free}$	0.261 , 0.298	Depositor
Wilson B-factor (Å <sup>2</sup> )	27.9	Xtrriage
Anisotropy	0.384	Xtrriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	5641	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	64.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 24.56 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.7444e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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

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	0.24	0/710	0.34	0/958
1	B	0.24	0/745	0.34	0/1003
1	C	0.24	0/748	0.33	0/1008
1	D	0.24	0/733	0.33	0/987
All	All	0.24	0/2936	0.34	0/3956

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	706	639	633	10	0
1	B	739	704	698	10	0
1	C	742	684	682	12	0
1	D	727	683	677	8	0
2	A	4	0	0	1	0
2	B	7	0	0	0	0
2	C	4	0	0	0	0
2	D	2	0	0	0	0
All	All	2931	2710	2690	25	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.

All (25) 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:86:LEU:HD23	1:B:88:LEU:HD13	1.39	1.04
1:D:16:VAL:HG12	1:D:85:LEU:HD11	1.74	0.69
1:B:86:LEU:HD21	1:C:13:LEU:HD12	1.76	0.67
1:B:68:LEU:HD21	1:C:31:LEU:HD13	1.75	0.67
1:A:86:LEU:HD21	1:B:13:LEU:CD2	2.26	0.65
1:D:20:GLN:NE2	1:D:85:LEU:HD12	2.12	0.64
1:A:86:LEU:HD21	1:B:13:LEU:HD23	1.80	0.62
1:A:1:SER:OG	2:A:201:HOH:O	2.16	0.62
1:B:53:GLU:OE1	1:C:48:LYS:NZ	2.34	0.61
1:A:12:TYR:O	1:A:16:VAL:HG23	2.04	0.57
1:C:86:LEU:HD21	1:D:13:LEU:HD12	1.86	0.57
1:C:45:LEU:O	1:C:49:GLY:N	2.40	0.55
1:C:96:GLU:O	1:C:100:ILE:N	2.40	0.55
1:C:86:LEU:HD23	1:D:88:LEU:HD13	1.90	0.54
1:C:83:ILE:HD11	1:D:20:GLN:OE1	2.09	0.53
1:A:61:GLN:OE1	1:B:38:SER:OG	2.30	0.49
1:B:68:LEU:HD21	1:C:31:LEU:CD1	2.43	0.47
1:A:20:GLN:CD	1:A:85:LEU:HD11	2.35	0.47
1:C:51:ALA:HB3	1:C:56:LEU:HG	1.97	0.46
1:A:83:ILE:HD13	1:B:84:ALA:HB3	2.00	0.43
1:A:83:ILE:HG23	1:B:88:LEU:HD11	2.00	0.43
1:D:43:ARG:O	1:D:47:GLU:HG3	2.19	0.42
1:C:72:LEU:HD21	1:D:27:PHE:CE1	2.55	0.42
1:C:83:ILE:HG21	1:D:84:ALA:HB1	2.01	0.41
1:A:95:LEU:O	1:A:99:HIS:N	2.53	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [\(i\)](#)

### 5.3.1 Protein backbone [\(i\)](#)

There are no protein backbone outliers to report in this entry.

### 5.3.2 Protein sidechains [\(i\)](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

### 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

### 6.1 Protein, DNA and RNA chains

EDS failed to run properly - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains

EDS failed to run properly - this section is therefore empty.

### 6.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

### 6.4 Ligands

EDS failed to run properly - this section is therefore empty.

### 6.5 Other polymers

EDS failed to run properly - this section is therefore empty.