

Full wwPDB X-ray Structure Validation Report (i)

Nov 21, 2023 – 03:59 AM JST

PDB ID	:	7EP1
Title	:	Crystal structure of ZYG11B bound to GFLH degron
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Deposited on	:	2021-04-26
Resolution	:	1.85 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* 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:

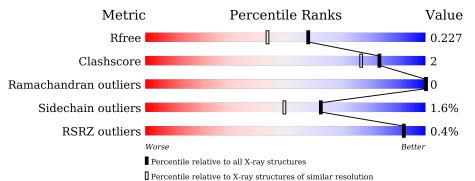
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)		
Ideal geometry (DNA, RNA)		
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 1.85 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	2469(1.86-1.86)
Clashscore	141614	2625(1.86-1.86)
Ramachandran outliers	138981	2592 (1.86-1.86)
Sidechain outliers	138945	2592(1.86-1.86)
RSRZ outliers	127900	2436 (1.86-1.86)

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	А	250	% 91%	7% •
1	В	250	91%	9%



2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 4179 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.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	Δ	245	Total	С	Ν	0	\mathbf{S}	0	0	0
	A	240	1964	1257	333	364	10	0	0	0
1	р	249	Total	С	Ν	0	S	0	0	0
	D	249	1998	1280	340	368	10	0	0	0

• Molecule 1 is a protein called Protein zyg-11 homolog B.

Chain	Residue	Modelled	Actual	Comment	Reference
A	479	GLY	-	expression tag	UNP Q9C0D3
А	480	PHE	-	expression tag	UNP Q9C0D3
А	481	LEU	-	expression tag	UNP Q9C0D3
А	482	HIS	-	expression tag	UNP Q9C0D3
A	483	VAL	-	expression tag	UNP Q9C0D3
А	484	GLY	-	expression tag	UNP Q9C0D3
В	479	GLY	-	expression tag	UNP Q9C0D3
В	480	PHE	-	expression tag	UNP Q9C0D3
В	481	LEU	-	expression tag	UNP Q9C0D3
В	482	HIS	-	expression tag	UNP Q9C0D3
В	483	VAL	-	expression tag	UNP Q9C0D3
В	484	GLY	_	expression tag	UNP Q9C0D3

There are 12 discrepancies between the modelled and reference sequences:

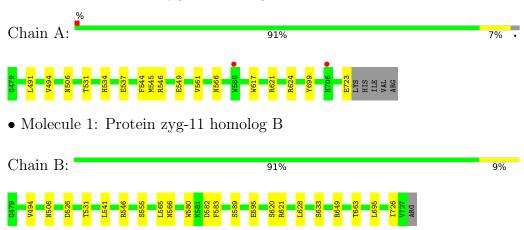
• Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	121	Total O 121 121	0	0
2	В	96	Total O 96 96	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: Protein zyg-11 homolog B



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	53.09Å 97.58Å 121.87Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.84 - 1.85	Depositor
	76.17 - 1.85	EDS
% Data completeness	98.2(25.84-1.85)	Depositor
(in resolution range)	96.0(76.17-1.85)	EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.53 (at 1.86 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.184 , 0.227	Depositor
It, Itfree	0.183 , 0.227	DCC
R_{free} test set	1995 reflections (3.72%)	wwPDB-VP
Wilson B-factor (Å ²)	29.1	Xtriage
Anisotropy	0.172	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.37, 39.4	EDS
L-test for twinning ²	$ \langle L \rangle = 0.49, \langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4179	wwPDB-VP
Average B, all atoms $(Å^2)$	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.68% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities estimated from amplitudes.

5 Model quality (i)

5.1 Standard geometry (i)

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	
	Ullaill	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.39	0/2012	0.50	0/2736
1	В	0.37	0/2047	0.48	0/2783
All	All	0.38	0/4059	0.49	0/5519

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 (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	А	1964	0	1933	8	0
1	В	1998	0	1973	11	0
2	А	121	0	0	1	0
2	В	96	0	0	0	0
All	All	4179	0	3906	19	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 2.

All (19) 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:506:ASN:OD1	1:B:546:ARG:NH2	2.01	0.92



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Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:506:ASN:OD1	1:A:546:ARG:NH2	2.23	0.69
1:B:555:SER:OG	1:B:595:GLU:OE2	2.09	0.68
1:B:628:LEU:HD11	1:B:663:THR:HG22	1.78	0.64
1:B:526:ASP:OD2	1:B:649:ARG:HD3	1.98	0.63
1:B:695:LEU:HD11	1:B:726:ILE:HD11	1.80	0.62
1:B:628:LEU:HD21	1:B:663:THR:HB	1.89	0.55
1:A:617:TRP:CG	1:A:624:ARG:HD2	2.42	0.54
1:B:565:LEU:HD13	1:B:583:PHE:HE1	1.74	0.53
1:A:699:TYR:OH	1:A:723:GLU:OE2	2.18	0.51
1:B:541:LEU:HD11	1:B:583:PHE:CD1	2.46	0.51
1:A:537:GLU:OE2	2:A:801:HOH:O	2.20	0.46
1:B:580:TRP:CE2	1:B:582:ASP:HB2	2.50	0.46
1:B:494:VAL:HG21	1:B:531:THR:HG23	1.98	0.46
1:A:491:LEU:HD22	1:A:534:HIS:CG	2.53	0.44
1:A:544:PHE:CD2	1:A:561:VAL:HG13	2.54	0.42
1:A:545:MET:O	1:A:549:GLU:HG3	2.21	0.41
1:B:628:LEU:HD23	1:B:628:LEU:HA	1.85	0.41
1:A:494:VAL:HG21	1:A:531:THR:HG23	2.03	0.41

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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	Perce	ntiles
1	А	243/250~(97%)	240 (99%)	3~(1%)	0	100	100
1	В	247/250~(99%)	244 (99%)	3~(1%)	0	100	100
All	All	490/500 (98%)	484 (99%)	6 (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	А	221/226~(98%)	219~(99%)	2(1%)	78 72
1	В	225/226~(100%)	220~(98%)	5 (2%)	52 36
All	All	446/452~(99%)	439~(98%)	7 (2%)	62 49

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	566	ASN
1	А	621	ARG
1	В	566	ASN
1	В	589	SER
1	В	620	SER
1	В	621	ARG
1	В	633	SER

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such side chains are listed below:

Mol	Chain	Res	Type
1	В	615	GLN

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 (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	Analysed	<RSRZ $>$	#RSRZ>2	$OWAB(Å^2)$	Q<0.9
1	А	245/250~(98%)	-0.12	2 (0%) 86 86	19, 29, 44, 68	0
1	В	249/250~(99%)	-0.10	0 100 100	19, 32, 47, 60	0
All	All	494/500~(98%)	-0.11	2 (0%) 92 92	19, 31, 46, 68	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	706	HIS	4.2
1	А	580	TRP	3.0

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

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

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.

