

wwPDB X-ray Structure Validation Summary Report (i)

Nov 26, 2024 – 10:16 AM JST

PDB ID	:	8Y1U
Title	:	Crystal structure of ASB7-Elongin B/C bound to the LZTS1-degron
Authors	:	Dong, C.; Yan, X.; Zhou, M.
Deposited on		
Resolution	:	2.41 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* 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:

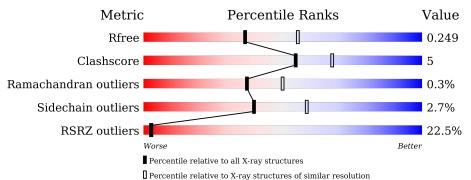
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.21
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

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 2.41 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}	164625	5670 (2.44-2.40)
Clashscore	180529	6299 (2.44-2.40)
Ramachandran outliers	177936	6232 (2.44-2.40)
Sidechain outliers	177891	6233 (2.44-2.40)
RSRZ outliers	164620	5670 (2.44-2.40)

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 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	309	12%		85%			13%	
2	В	23	4%		83%			13%	•
3	С	104	26% 28%	6%		66%			_
4	D	96	30%	60%		••	38%		



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 3191 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 Ankyrin repeat and SOCS box protein 7.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	А	305	Total 2324	C 1447	N 431	0 435	S 11	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	10	GLY	-	expression tag	UNP Q9H672

• Molecule 2 is a protein called Peptide from Leucine zipper putative tumor suppressor 1.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	В	23	Total 201	C 123	N 36	0 41	S 1	0	0	0

• Molecule 3 is a protein called Elongin-B.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
3	С	35	Total 201	C 121	N 36	0 43	S 1	0	0	0

• Molecule 4 is a protein called Elongin-C.

Mol	Chain	Residues		Ato	\mathbf{ms}			ZeroOcc	AltConf	Trace
4	D	60	Total 380	C 235	N 70	0 74	S 1	0	0	0

• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	64	Total O 64 64	0	0

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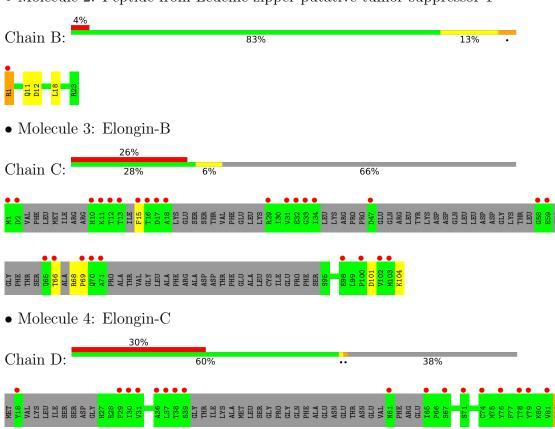
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	В	14	Total O 14 14	0	0
5	С	6	Total O 6 6	0	0
5	D	1	Total O 1 1	0	0



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.

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- Molecule 1: Ankyrin repeat and SOCS box protein 7



• Molecule 2: Peptide from Leucine zipper putative tumor suppressor 1







4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	48.15Å 43.72Å 159.23Å	Depositor
a, b, c, α , β , γ	90.00° 92.00° 90.00°	Depositor
Resolution (Å)	48.12 - 2.41	Depositor
Resolution (A)	48.12 - 2.41	EDS
% Data completeness	99.4 (48.12-2.41)	Depositor
(in resolution range)	99.5(48.12-2.41)	EDS
R _{merge}	0.09	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.11 (at 2.39 \text{\AA})$	Xtriage
Refinement program	PHENIX (1.17.1_3660: ???)	Depositor
R, R_{free}	0.215 , 0.243	Depositor
n, nfree	0.227 , 0.249	DCC
R_{free} test set	24069 reflections $(7.68%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	46.0	Xtriage
Anisotropy	0.361	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.29,81.1	EDS
L-test for twinning ²	$< L > = 0.50, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.012 for h,-k,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	3191	wwPDB-VP
Average B, all atoms $(Å^2)$	86.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 10.96% 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	
			# Z > 5	RMSZ	# Z > 5
1	А	0.46	0/2366	0.62	0/3206
2	В	0.44	0/201	0.64	0/265
3	С	0.43	0/196	0.65	0/258
4	D	0.51	0/386	0.68	0/529
All	All	0.46	0/3149	0.63	0/4258

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	2324	0	2217	21	1
2	В	201	0	207	4	0
3	С	201	0	126	5	0
4	D	380	0	267	2	0
5	А	64	0	0	0	0
5	В	14	0	0	0	0
5	С	6	0	0	1	0
5	D	1	0	0	0	0
All	All	3191	0	2817	28	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 5.



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:283:ARG:O	1:A:287:ARG:HG3	1.93	0.69
3:C:101:ASP:HA	3:C:104:LYS:HG2	1.74	0.68
1:A:260:SER:HA	1:A:265:LEU:HD21	1.80	0.63
1:A:14:GLU:HA	1:A:17:GLN:HG2	1.79	0.63
1:A:251:LEU:HD11	1:A:269:GLN:HA	1.87	0.57

The worst 5 of 28 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

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)
1:A:15:GLU:OE2	1:A:224:ARG:NH1[2_456]	1.78	0.42

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	entiles
1	А	303/309~(98%)	291~(96%)	11 (4%)	1 (0%)	37	50
2	В	21/23~(91%)	21 (100%)	0	0	100	100
3	С	18/104~(17%)	15 (83%)	3~(17%)	0	100	100
4	D	54/96~(56%)	47 (87%)	7~(13%)	0	100	100
All	All	396/532~(74%)	374 (94%)	21~(5%)	1 (0%)	37	50

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	260	SER



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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Perce	ntiles
1	А	232/262~(88%)	226~(97%)	6 (3%)	41	60
2	В	23/23~(100%)	22~(96%)	1 (4%)	25	40
3	С	11/92~(12%)	11 (100%)	0	100	100
4	D	25/85~(29%)	24 (96%)	1 (4%)	27	43
All	All	291/462~(63%)	283~(97%)	8 (3%)	40	58

5 of 8 residues with a non-rotameric side chain are listed below:

Mol	Chain	\mathbf{Res}	Type
4	D	82	ARG
2	В	1	ARG
1	А	299	ASP
1	А	276	ARG
1	А	314	LYS

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. There are no such side chains 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)

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

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^{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	$\langle RSRZ \rangle$	#RSRZ>2	$\mathbf{OWAB}(\mathbf{\AA}^2)$	Q<0.9
1	А	305/309~(98%)	0.67	38 (12%) 9 8	31, 65, 144, 170	0
2	В	23/23~(100%)	0.24	1 (4%) 40 38	35, 47, 79, 116	0
3	С	35/104 (33%)	2.79	27 (77%) 0 0	109, 161, 225, 259	0
4	D	60/96~(62%)	2.22	29 (48%) 0 1	110, 151, 185, 195	0
All	All	423/532 (79%)	1.04	95 (22%) 3 3	31, 77, 178, 259	0

The worst 5 of 95 RSRZ outliers are listed below:

Mol	Chain	\mathbf{Res}	Type	RSRZ
4	D	109	PHE	6.5
4	D	18	TYR	6.1
4	D	61	ASN	5.3
1	А	222	ALA	5.3
3	С	18	ALA	5.3

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.

