

wwPDB X-ray Structure Validation Summary Report (i)

Dec 5, 2023 - 01:57 am GMT

PDB ID	:	2C0G
Title	:	Structure of PDI-related Chaperone, Wind mutant-Y53S
Authors	:	Sevvana, M.; Ma, Q.; Barnewitz, K.; Guo, C.; Soling, HD.; Ferrari, D.M.;
		Sheldrick, G.M.
Deposited on		
Resolution	:	1.75 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:

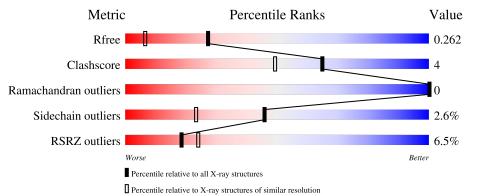
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)		
Ideal geometry (DNA, RNA)		
Validation Pipeline (wwPDB-VP)	:	2.36

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 1.75 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	2340(1.76-1.76)
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)
RSRZ outliers	127900	2298 (1.76-1.76)

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	- •			
1	А	248	% 82%	8%	• 8%	
1	В	248	83%	6%	11%	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:



Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	CL	В	2245	-	-	Х	-



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 3473 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 WINDBEUTEL PROTEIN.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Δ	228	Total	С	Ν	0	\mathbf{S}	0	1	0
		220	1773	1144	294	331	4	0		
1	Р	221	Total	С	Ν	0	S	0	0 0	0
	D	221	1531	980	257	290	4	0		0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1053	SER	TYR	engineered mutation	UNP 044342
В	1053	SER	TYR	engineered mutation	UNP 044342

• Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	Total Na 1 1	0	0

• Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

[Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
	3	В	1	Total 1	Cl 1	0	0

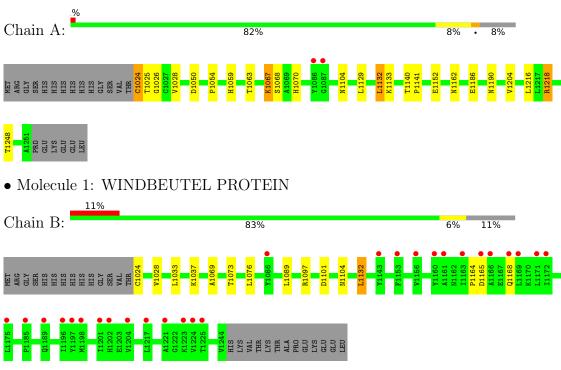
• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	125	Total O 125 125	0	0
4	В	42	$\begin{array}{cc} \text{Total} & \text{O} \\ 42 & 42 \end{array}$	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: WINDBEUTEL PROTEIN



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	108.48Å 50.56Å 98.90Å	Depositor
a, b, c, α , β , γ	90.00° 112.06° 90.00°	Depositor
Resolution (Å)	25.00 - 1.75	Depositor
Resolution (A)	50.27 - 1.72	EDS
% Data completeness	$100.0\ (25.00-1.75)$	Depositor
(in resolution range)	94.6 (50.27-1.72)	EDS
R _{merge}	0.04	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$3.08 (at 1.72 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
D D.	0.219 , 0.268	Depositor
R, R_{free}	0.218 , 0.262	DCC
R_{free} test set	9779 reflections (4.97%)	wwPDB-VP
Wilson B-factor $(Å^2)$	24.6	Xtriage
Anisotropy	0.177	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.35 , 48.5	EDS
L-test for twinning ²	$ \langle L \rangle = 0.49, \langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3473	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 7.49% 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)

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

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	Bo	nd lengths	Bond angles		
Mol Chain		RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	1.00	2/1808~(0.1%)	0.97	3/2444~(0.1%)	
1	В	0.96	6/1559~(0.4%)	0.84	2/2104~(0.1%)	
All	All	0.98	8/3367~(0.2%)	0.91	5/4548~(0.1%)	

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	В	1165	ASP	N-CA	7.72	1.61	1.46
1	В	1164	PRO	CA-C	7.16	1.67	1.52
1	В	1168	GLN	CD-OE1	6.91	1.39	1.24
1	В	1168	GLN	CD-NE2	6.68	1.49	1.32
1	А	1152	GLU	CD-OE1	6.24	1.32	1.25

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
1	А	1218	ARG	NE-CZ-NH1	-10.35	115.12	120.30
1	А	1050	ASP	CB-CG-OD1	8.22	125.69	118.30
1	В	1132	LEU	CB-CG-CD1	7.42	123.61	111.00
1	В	1097	ARG	NE-CZ-NH2	-5.96	117.32	120.30
1	А	1132	LEU	CB-CG-CD1	5.64	120.59	111.00

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



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	А	1773	0	1734	20	0
1	В	1531	0	1321	10	0
2	А	1	0	0	0	0
3	В	1	0	0	2	0
4	А	125	0	0	4	0
4	В	42	0	0	0	0
All	All	3473	0	3055	26	0

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.

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.

The worst 5 of 26 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:1248:THR:HG23	4:A:2072:HOH:O	1.62	0.99
1:B:1101:ASP:H	1:B:1104:ASN:HD22	1.20	0.88
1:A:1025:THR:HB	1:A:1067:LYS:HE2	1.59	0.84
1:B:1069:ALA:O	1:B:1073:THR:HG22	1.85	0.75
1:A:1248:THR:HG21	4:A:2069:HOH:O	1.92	0.69

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	227/248~(92%)	224~(99%)	3~(1%)	0	100	100
1	В	219/248~(88%)	210 (96%)	9~(4%)	0	100	100
All	All	446/496~(90%)	434 (97%)	12 (3%)	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	178/218~(82%)	173~(97%)	5(3%)	43 20		
1	В	125/218~(57%)	122~(98%)	3~(2%)	49 26		
All	All	303/436~(70%)	295~(97%)	8(3%)	46 23		

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

Mol	Chain	Res	Type
1	В	1132	LEU
1	В	1089	LEU
1	А	1204	VAL
1	А	1132	LEU
1	В	1024	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	1070	HIS
1	В	1104	ASN
1	В	1120	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.



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5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	$OWAB(Å^2)$	Q<0.9
1	А	228/248~(91%)	-0.04	2 (0%) 84 89	14, 26, 41, 59	0
1	В	221/248~(89%)	0.59	27 (12%) 4 6	17, 39, 76, 86	0
All	All	449/496~(90%)	0.27	29 (6%) 18 24	14, 30, 69, 86	0

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	1161	ALA	9.4
1	В	1166	ALA	7.3
1	В	1221	ALA	7.1
1	В	1217	LEU	4.2
1	В	1171	LEU	3.9

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)

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^{th} 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 ²)	Q < 0.9
2	NA	А	2252	1/1	0.95	0.10	33,33,33,33	0
3	CL	В	2245	1/1	0.99	0.11	36,36,36,36	0

6.5 Other polymers (i)

There are no such residues in this entry.

