

Full wwPDB X-ray Structure Validation Report (i)

May 21, 2020 – 08:14 pm BST

PDB ID : 4U2J

Title : N-terminal domain of C. Reinhardtii SAS-6 homolog bld12p variant Q93E

F145W (NN27)

Authors : Hilbert, M.; Kraatz, S.H.W.

Deposited on : 2014-07-17

Resolution : 2.00 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 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 : 2.11

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Refmac: 5.8.0158

 $\begin{array}{cccc} & CCP4 & : & 7.0.044 \; (Gargrove) \\ Ideal \; geometry \; (proteins) & : & Engh \; \& \; Huber \; (2001) \end{array}$

Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

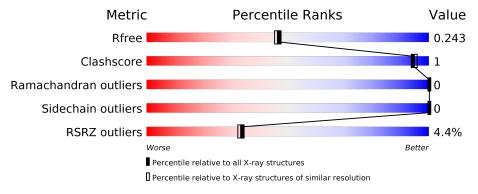
Validation Pipeline (wwPDB-VP) : 2.11

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.00 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries,\ resolution\ range(\AA)}) \end{array}$
R_{free}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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 >=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	A	161	86%	•	12%
1	В	161	6% 86%	•	12%
1	С	161	81%		14%
1	D	161	6% 85%	•	12%



2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 9549 atoms, of which 4578 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 Centriole protein.

Mol	Chain	Residues		Atoms				ZeroOcc	AltConf	Trace	
1	Λ	142	Total	С	Η	N	О	S	0	0	0
1	A	142	2291	735	1147	197	211	1	U	U	
1	С	138	Total	С	Н	N	О	S	0	1	0
1		130	2254	724	1131	194	204	1	0	1	
1	D	142	Total	С	Н	N	О	S	0	0	0
1	ע	142	2291	735	1147	197	211	1	0	0	0
1	1 B	142	Total	С	Н	N	О	S	0	1	0
	D	142	2306	740	1153	198	214	1	U	1	U

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP A9CQL4
A	0	SER	_	expression tag	UNP A9CQL4
A	93	GLU	GLN	engineered mutation	UNP A9CQL4
A	145	TRP	PHE	engineered mutation	UNP A9CQL4
С	-1	GLY	_	expression tag	UNP A9CQL4
С	0	SER	_	expression tag	UNP A9CQL4
С	93	GLU	GLN	engineered mutation	UNP A9CQL4
С	145	TRP	PHE	engineered mutation	UNP A9CQL4
D	-1	GLY	_	expression tag	UNP A9CQL4
D	0	SER	-	expression tag	UNP A9CQL4
D	93	GLU	GLN	engineered mutation	UNP A9CQL4
D	145	TRP	PHE	engineered mutation	UNP A9CQL4
В	-1	GLY	_	expression tag	UNP A9CQL4
В	0	SER	=	expression tag	UNP A9CQL4
В	93	GLU	GLN	engineered mutation	UNP A9CQL4
В	145	TRP	PHE	engineered mutation	UNP A9CQL4

• Molecule 2 is water.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	135	Total O 135 135	0	0
2	С	62	Total O 62 62	0	0
2	D	120	Total O 120 120	0	0
2	В	90	Total O 90 90	0	0



3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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: Centriole protein Chain A: 12% • Molecule 1: Centriole protein Chain C: GLY
MET
MET
PRO
PRO
LIEU
LIEU
LIEU
LIYS
GLY
RASP
PRO
GLY
COLN
THR
ASP
PRO
THR
ASP • Molecule 1: Centriole protein Chain D: 85% 12% GGLY
SER MET
MET
PRO
LLEU
LLEU
LLEU
LLEV
LLEV
LLEV
LLYS
LLYS
LLYS
GGLY
ASP
PRO
GGLY
ASP • Molecule 1: Centriole protein Chain B: 86% 12%



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	40.15Å 97.00Å 142.81Å	Danagitar
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	80.24 - 2.00	Depositor
Resolution (A)	80.24 - 2.00	EDS
% Data completeness	100.0 (80.24-2.00)	Depositor
(in resolution range)	100.0 (80.24-2.00)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.42 (at 2.00Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
D D.	0.191 , 0.240	Depositor
R, R_{free}	0.197 , 0.243	DCC
R_{free} test set	1933 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	25.2	Xtriage
Anisotropy	0.119	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.40 , 48.3	EDS
L-test for twinning ²	$< L >=0.48, < L^2>=0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9549	wwPDB-VP
Average B, all atoms $(Å^2)$	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.85% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of <|L|>, $< L^2>$ 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
WIOI		RMSZ	# Z >5	RMSZ	# Z > 5
1	A	0.25	0/1169	0.43	0/1584
1	В	0.23	0/1178	0.39	0/1596
1	С	0.22	0/1148	0.38	0/1555
1	D	0.26	0/1169	0.42	0/1584
All	All	0.24	0/4664	0.41	0/6319

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	A	1144	1147	1152	3	0
1	В	1153	1153	1157	2	0
1	С	1123	1131	1135	4	0
1	D	1144	1147	1152	4	0
2	A	135	0	0	0	2
2	В	90	0	0	1	1
2	С	62	0	0	1	0
2	D	120	0	0	1	4
All	All	4971	4578	4596	12	5

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 1.



All (12) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{aligned} ext{Interatomic} \ ext{distance} \ (ext{Å}) \end{aligned}$	Clash overlap (Å)
1:D:117:GLN:O	1:D:123:ARG:NH1	2.12	0.82
1:B:147:GLN:NE2	2:B:201:HOH:O	2.15	0.77
1:A:64:ARG:NH1	1:A:159:ASN:O	2.21	0.73
1:A:64:ARG:NH2	1:A:80:GLU:OE2	2.22	0.72
1:C:64:ARG:NH1	1:C:80:GLU:OE1	2.39	0.56
1:D:120:ASP:O	1:D:123:ARG:NH1	2.42	0.53
1:C:87:GLN:NE2	2:C:248:HOH:O	2.42	0.51
1:C:35:GLN:OE1	1:C:36:GLN:NE2	2.45	0.50
1:A:159:ASN:ND2	1:D:85:ASP:OD1	2.46	0.48
1:D:149:PRO:O	2:D:266:HOH:O	2.21	0.46
1:C:27:ARG:NH1	1:C:28:PRO:HD2	2.32	0.45
1:B:134:GLU:OE2	1:B:156:ARG:CZ	2.69	0.41

All (5) 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	$egin{array}{l} ext{Interatomic} \ ext{distance} \ (ext{Å}) \end{array}$	$egin{aligned} ext{Clash} \ ext{overlap } (ext{Å}) \end{aligned}$
2:D:226:HOH:O	2:D:234:HOH:O[4_445]	1.91	0.29
2:A:252:HOH:O	2:D:231:HOH:O[1_655]	2.05	0.15
2:D:239:HOH:O	2:D:246:HOH:O[4_545]	2.09	0.11
2:A:235:HOH:O	2:B:240:HOH:O[3_645]	2.13	0.07
2:D:209:HOH:O	2:D:234:HOH:O[4_445]	2.18	0.02

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	${f Analysed}$	Favoured	Allowed	Outliers	Perce	\mathbf{ntiles}
1	A	140/161 (87%)	134 (96%)	6 (4%)	0	100	100
1	В	141/161 (88%)	131 (93%)	10 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	ntiles
1	С	137/161 (85%)	130 (95%)	7 (5%)	0	100	100
1	D	140/161 (87%)	134 (96%)	6 (4%)	0	100	100
All	All	558/644 (87%)	529 (95%)	29 (5%)	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	129/144~(90%)	129 (100%)	0	100 100
1	В	130/144 (90%)	130 (100%)	0	100 100
1	С	126/144 (88%)	126 (100%)	0	100 100
1	D	129/144 (90%)	129 (100%)	0	100 100
All	All	514/576 (89%)	514 (100%)	0	100 100

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

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

Mol	Chain	Res	Type
1	С	36	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 carbohydrates 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 $>$	$\#\mathrm{RSRZ}{>}2$	$OWAB(\AA^2)$	Q < 0.9
1	A	142/161 (88%)	-0.07	1 (0%) 87 87	15, 24, 56, 65	0
1	В	142/161 (88%)	0.27	9 (6%) 20 19	18, 30, 67, 78	0
1	С	138/161 (85%)	0.23	6 (4%) 35 34	21, 34, 61, 91	0
1	D	142/161 (88%)	0.03	9 (6%) 20 19	12, 21, 69, 89	0
All	All	564/644 (87%)	0.12	25 (4%) 34 33	12, 28, 64, 91	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	36	GLN	4.9
1	В	132	GLY	4.4
1	D	159	ASN	4.3
1	D	121	SER	4.1
1	D	119	GLY	3.9
1	В	119	GLY	3.8
1	В	118	PRO	3.7
1	D	120	ASP	3.3
1	D	38	ARG	3.1
1	В	134	GLU	3.0
1	D	37	ASP	3.0
1	В	18	LEU	2.8
1	В	36	GLN	2.7
1	С	74	PHE	2.6
1	С	36	GLN	2.6
1	D	56	GLN	2.5
1	С	134	GLU	2.5
1	D	118	PRO	2.3
1	В	133	GLY	2.3
1	С	40	ASP	2.2
1	A	121	SER	2.1

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Mol	Chain	Res	Type	RSRZ
1	В	116	ALA	2.1
1	С	37	ASP	2.1
1	С	27	ARG	2.1
1	В	37	ASP	2.0

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 carbohydrates 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.

