Full wwPDB EM Validation Report

May 13, 2024 – 10:08 pm BST

PDB ID	:	6Z1G
EMDB ID	:	EMD-11029
Title	:	CryoEM structure of the interaction between Rubisco Activase small-subunit-like (SSUL) domain with Rubisco from Nostoc sp. (strain PCC7120)
Authors	:	Wang, H.; Bracher, A.; Flecken, M.; Popilka, L.; Hartl, F.U.; Hayer-Hartl, M.
Deposited on	:	2020-05-13
Resolution	:	8.20 Å(reported)

This is a Full wwPDB EM 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/EMValidationReportHelp
with specific help available everywhere you see the ⓘ 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 ⓘ) were used in the production of this report:

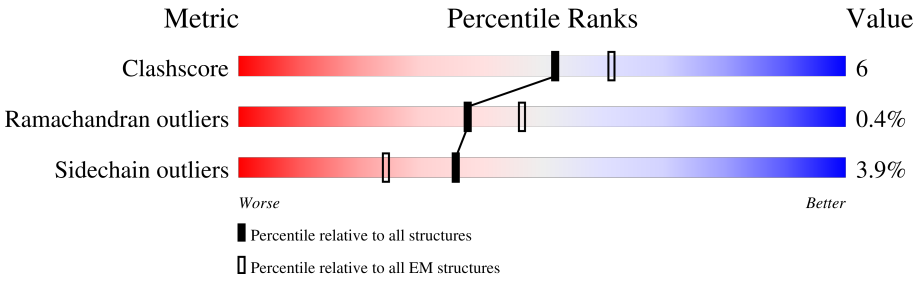
EMDB validation analysis	:	0.0.1.dev92
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	FAILED
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 8.20 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)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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%

Mol	Chain	Length	Quality of chain
1	A	90	67% 28%
2	B	476	78% 12% 9%
2	C	476	77% 13% 9%
3	D	109	89% 8%
3	E	109	86% 11%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 9262 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 Ribulose bisphosphate carboxylase/oxygenase activase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	86	Total	C	N	O	S	0	0
			688	425	127	133	3		

- Molecule 2 is a protein called Ribulose bisphosphate carboxylase large chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	435	Total	C	N	O	S	0	0
			3414	2172	603	626	13		
2	C	435	Total	C	N	O	S	0	0
			3414	2172	603	626	13		

- Molecule 3 is a protein called Ribulose bisphosphate carboxylase small chain.

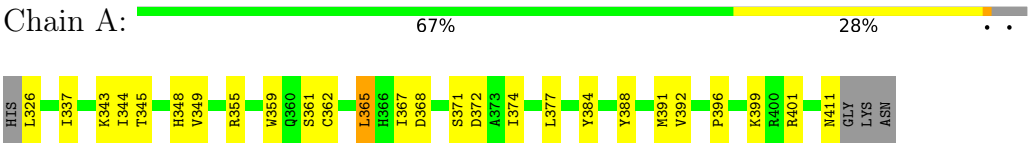
Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	106	Total	C	N	O	S	0	0
			873	568	143	159	3		
3	E	106	Total	C	N	O	S	0	0
			873	568	143	159	3		

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.

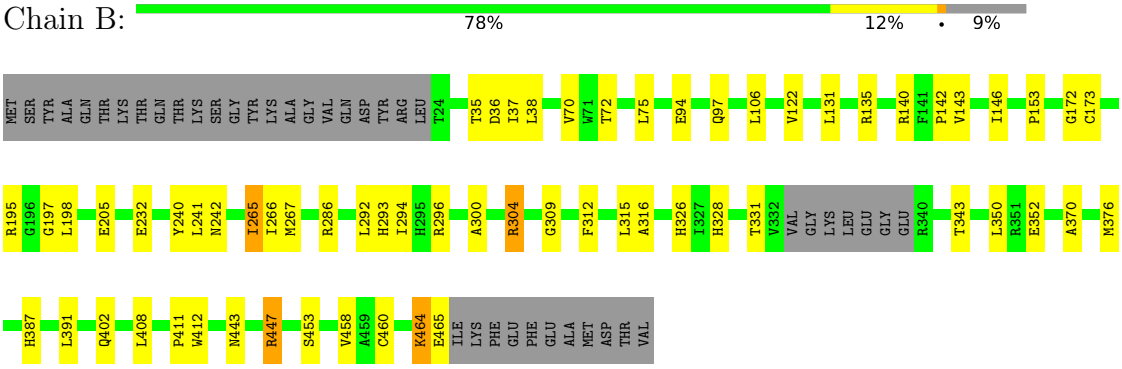
• Molecule 1: Ribulose bisphosphate carboxylase/oxygenase activase

Chain A:



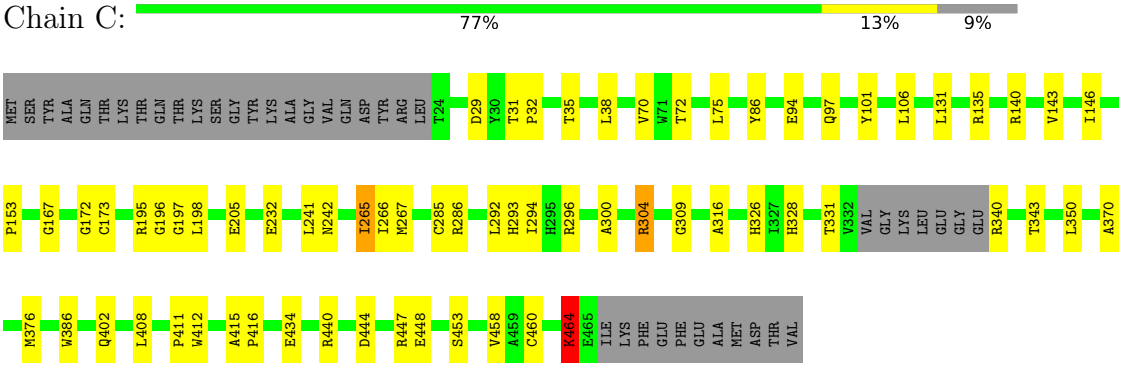
• Molecule 2: Ribulose bisphosphate carboxylase large chain

Chain B:



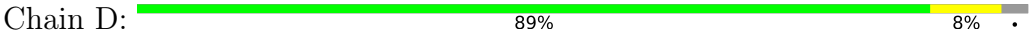
• Molecule 2: Ribulose bisphosphate carboxylase large chain

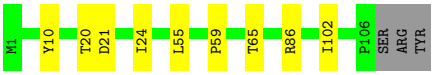
Chain C:



• Molecule 3: Ribulose bisphosphate carboxylase small chain

Chain D:





• Molecule 3: Ribulose bisphosphate carboxylase small chain

Chain E:

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	32128	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	47	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

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	0.66	0/698	0.76	0/941
2	B	0.64	0/3498	0.74	0/4752
2	C	0.65	0/3498	0.74	0/4752
3	D	0.64	0/897	0.70	0/1222
3	E	0.64	0/897	0.70	0/1222
All	All	0.65	0/9488	0.73	0/12889

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	C	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	464	LYS	Peptide

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	688	0	680	26	0
2	B	3414	0	3350	36	0
2	C	3414	0	3350	40	0
3	D	873	0	871	4	0
3	E	873	0	871	8	0
All	All	9262	0	9122	104	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 6.

All (104) 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:399:LYS:O	2:C:32:PRO:HD2	1.59	1.02
1:A:348:HIS:CD2	1:A:362:CYS:SG	2.67	0.88
1:A:326:LEU:HD13	1:A:377:LEU:HD23	1.58	0.86
2:B:326:HIS:HD2	2:B:376:MET:HB3	1.52	0.74
2:C:412:TRP:CZ2	2:C:458:VAL:HG21	2.21	0.74
2:C:326:HIS:HD2	2:C:376:MET:HB3	1.55	0.70
1:A:365:LEU:HD22	2:C:29:ASP:HB3	1.76	0.67
1:A:359:TRP:CH2	1:A:388:TYR:HB3	2.32	0.64
2:C:143:VAL:HA	2:C:146:ILE:HD12	1.80	0.64
2:B:412:TRP:CZ2	2:B:458:VAL:HG21	2.35	0.61
1:A:337:ILE:HG21	1:A:344:ILE:HG12	1.85	0.59
3:E:21:ASP:HA	3:E:24:ILE:HD12	1.85	0.59
1:A:349:VAL:HG12	1:A:388:TYR:HB2	1.83	0.59
2:B:300:ALA:O	2:B:304:ARG:HB2	2.03	0.58
2:B:241:LEU:HB2	2:B:266:ILE:HG22	1.87	0.57
1:A:362:CYS:SG	1:A:384:TYR:CE2	2.96	0.56
1:A:343:LYS:HE2	1:A:396:PRO:HG3	1.87	0.56
2:B:411:PRO:HG2	2:B:458:VAL:HG12	1.86	0.56
2:B:94:GLU:HB3	2:B:97:GLN:HB3	1.87	0.56
2:C:172:GLY:HA3	2:C:402:GLN:HE21	1.71	0.56
2:B:143:VAL:HA	2:B:146:ILE:HD12	1.88	0.56
3:D:21:ASP:HA	3:D:24:ILE:HD12	1.87	0.55
1:A:326:LEU:HD13	1:A:377:LEU:CD2	2.35	0.55
2:C:326:HIS:CD2	2:C:376:MET:HB3	2.40	0.55
2:C:411:PRO:HG2	2:C:458:VAL:HG12	1.89	0.54
2:C:300:ALA:O	2:C:304:ARG:HB2	2.08	0.54
1:A:326:LEU:HD22	1:A:374:ILE:HG23	1.90	0.53
2:B:38:LEU:HD12	2:B:140:ARG:HD3	1.90	0.53
2:B:267:MET:HB3	2:B:293:HIS:HB3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:326:LEU:CD1	1:A:377:LEU:HD23	2.34	0.53
1:A:326:LEU:HD11	1:A:374:ILE:HG12	1.91	0.53
2:B:326:HIS:CD2	2:B:376:MET:HB3	2.37	0.53
2:C:94:GLU:HB3	2:C:97:GLN:HB3	1.91	0.53
2:B:172:GLY:HA3	2:B:402:GLN:HE21	1.73	0.53
1:A:343:LYS:HD2	1:A:368:ASP:HB3	1.90	0.53
2:B:153:PRO:HA	2:B:286:ARG:HE	1.73	0.53
1:A:344:ILE:HG23	1:A:391:MET:HG3	1.92	0.52
2:B:37:ILE:HG13	2:B:142:PRO:HD2	1.92	0.52
1:A:401:ARG:HG3	2:C:31:THR:CG2	2.40	0.52
2:B:37:ILE:HG13	2:B:142:PRO:CD	2.39	0.52
2:C:153:PRO:HA	2:C:286:ARG:HE	1.74	0.52
2:B:447:ARG:HG3	2:B:447:ARG:HH11	1.74	0.51
2:B:292:LEU:HD21	2:B:294:ILE:HD11	1.93	0.51
2:C:386:TRP:HH2	2:C:447:ARG:HH11	1.59	0.51
2:C:35:THR:HB	2:C:106:LEU:HD22	1.93	0.51
1:A:326:LEU:CD1	1:A:377:LEU:CD2	2.89	0.50
2:C:143:VAL:HG13	2:C:370:ALA:HB2	1.92	0.50
2:C:38:LEU:HD12	2:C:140:ARG:HD3	1.93	0.50
2:B:195:ARG:HG3	2:B:232:GLU:OE2	2.12	0.50
2:C:267:MET:HB3	2:C:293:HIS:HB3	1.93	0.50
2:B:265:ILE:HG13	2:B:266:ILE:N	2.27	0.50
2:C:241:LEU:HB2	2:C:266:ILE:HG22	1.94	0.49
2:C:153:PRO:O	2:C:286:ARG:NE	2.46	0.49
2:C:464:LYS:HD3	2:C:464:LYS:HA	1.79	0.49
1:A:399:LYS:C	2:C:31:THR:HG23	2.33	0.48
2:C:242:ASN:HA	2:C:267:MET:HG3	1.94	0.48
1:A:344:ILE:HA	1:A:392:VAL:O	2.13	0.48
2:C:167:GLY:HA2	3:E:98:ILE:O	2.12	0.48
3:D:55:LEU:HD21	3:D:59:PRO:HD3	1.95	0.48
2:B:35:THR:HB	2:B:106:LEU:HD22	1.95	0.47
2:C:292:LEU:HD21	2:C:294:ILE:HD11	1.96	0.47
2:B:153:PRO:O	2:B:286:ARG:NE	2.47	0.47
1:A:359:TRP:HH2	1:A:388:TYR:HB3	1.80	0.47
2:C:386:TRP:CH2	2:C:447:ARG:NH1	2.83	0.47
2:B:135:ARG:HA	2:B:309:GLY:O	2.16	0.46
2:C:447:ARG:HH11	2:C:447:ARG:HG3	1.81	0.46
2:C:195:ARG:HG3	2:C:232:GLU:OE2	2.16	0.45
3:E:55:LEU:HD21	3:E:59:PRO:HD3	1.98	0.45
2:C:434:GLU:HB3	3:E:26:LYS:HE3	1.98	0.45
2:C:265:ILE:HG13	2:C:266:ILE:N	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:75:LEU:HD22	3:E:90:PHE:HB3	1.99	0.45
2:C:316:ALA:HB1	2:C:350:LEU:HD11	1.97	0.45
2:C:135:ARG:HA	2:C:309:GLY:O	2.16	0.45
2:B:173:CYS:HB2	2:B:198:LEU:HD13	1.99	0.44
2:B:242:ASN:HA	2:B:267:MET:HG3	2.00	0.44
1:A:355:ARG:HD2	2:B:352:GLU:CD	2.38	0.44
2:C:86:TYR:CZ	2:C:101:TYR:HB3	2.52	0.44
3:E:86:ARG:HB3	3:E:102:ILE:HG13	1.99	0.44
2:B:443:ASN:HB3	2:B:447:ARG:HH12	1.82	0.44
1:A:343:LYS:HA	1:A:367:ILE:O	2.18	0.43
2:B:316:ALA:HB1	2:B:350:LEU:HD11	2.00	0.43
2:B:447:ARG:HG3	2:B:447:ARG:NH1	2.34	0.43
2:C:75:LEU:HD23	2:C:75:LEU:HA	1.92	0.43
2:C:296:ARG:HG2	2:C:328:HIS:HB2	2.00	0.43
2:B:143:VAL:HG13	2:B:370:ALA:HB2	2.01	0.43
2:C:173:CYS:HB2	2:C:198:LEU:HD13	2.01	0.43
2:B:36:ASP:O	2:B:140:ARG:NH1	2.43	0.42
1:A:345:THR:O	1:A:392:VAL:N	2.47	0.42
3:D:86:ARG:HB3	3:D:102:ILE:HG13	2.01	0.42
1:A:348:HIS:HD2	1:A:362:CYS:SG	2.31	0.42
2:C:415:ALA:HB3	2:C:416:PRO:HD3	2.03	0.41
3:D:10:TYR:HB3	3:D:102:ILE:HD13	2.03	0.41
2:B:267:MET:HA	2:B:293:HIS:O	2.20	0.41
2:B:387:HIS:O	2:B:391:LEU:HG	2.21	0.41
2:C:196:GLY:HA2	3:E:4:LEU:CD2	2.50	0.41
2:C:304:ARG:HA	2:C:304:ARG:HD2	1.86	0.41
2:C:196:GLY:HA2	3:E:4:LEU:HD21	2.02	0.41
1:A:344:ILE:CG2	1:A:391:MET:HG3	2.51	0.41
2:B:304:ARG:HD2	2:B:304:ARG:HA	1.87	0.41
2:B:312:PHE:HA	2:B:315:LEU:HD12	2.01	0.41
2:B:447:ARG:HH11	2:B:447:ARG:CG	2.34	0.40
1:A:361:SER:HB2	1:A:365:LEU:HD11	2.03	0.40
2:B:296:ARG:HG2	2:B:328:HIS:HB2	2.03	0.40
2:C:444:ASP:O	2:C:448:GLU:HG3	2.21	0.40

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 PDB entries followed by that with respect to all EM entries.

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	Percentiles	
1	A	84/90 (93%)	78 (93%)	6 (7%)	0	100	100
2	B	431/476 (90%)	409 (95%)	19 (4%)	3 (1%)	22	63
2	C	431/476 (90%)	411 (95%)	18 (4%)	2 (0%)	29	69
3	D	104/109 (95%)	99 (95%)	5 (5%)	0	100	100
3	E	104/109 (95%)	98 (94%)	6 (6%)	0	100	100
All	All	1154/1260 (92%)	1095 (95%)	54 (5%)	5 (0%)	38	72

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	464	LYS
2	B	464	LYS
2	B	197	GLY
2	C	197	GLY
2	B	122	VAL

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 PDB entries followed by that with respect to all EM entries.

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	76/79 (96%)	72 (95%)	4 (5%)	22	47
2	B	351/386 (91%)	336 (96%)	15 (4%)	29	53
2	C	351/386 (91%)	336 (96%)	15 (4%)	29	53
3	D	98/102 (96%)	96 (98%)	2 (2%)	55	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	E	98/102 (96%)	96 (98%)	2 (2%)	55 74
All	All	974/1055 (92%)	936 (96%)	38 (4%)	36 56

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	365	LEU
1	A	371	SER
1	A	372	ASP
1	A	411	ASN
2	B	70	VAL
2	B	72	THR
2	B	131	LEU
2	B	205	GLU
2	B	240	TYR
2	B	265	ILE
2	B	304	ARG
2	B	331	THR
2	B	343	THR
2	B	408	LEU
2	B	447	ARG
2	B	453	SER
2	B	460	CYS
2	B	464	LYS
2	B	465	GLU
2	C	70	VAL
2	C	72	THR
2	C	131	LEU
2	C	205	GLU
2	C	265	ILE
2	C	285	CYS
2	C	304	ARG
2	C	331	THR
2	C	340	ARG
2	C	343	THR
2	C	408	LEU
2	C	440	ARG
2	C	453	SER
2	C	460	CYS
2	C	464	LYS
3	D	20	THR
3	D	65	THR

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Mol	Chain	Res	Type
3	E	20	THR
3	E	65	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	348	HIS
2	B	154	HIS
2	B	213	GLN
2	B	278	ASN
2	C	213	GLN
2	C	278	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-11029. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Map analysis

This section contains the results of statistical analysis of the map.

7.1 Map-value distribution

This section was not generated.

7.2 Volume estimate versus contour level

This section was not generated.

7.3 Rotationally averaged power spectrum

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

This section was not generated.