



Full wwPDB EM Validation Report ⓘ

Mar 19, 2026 – 11:56 PM UTC

PDB ID : 7KAL / pdb_00007kal
EMDB ID : EMD-22774
Title : Cryo-EM structure of the Sec complex from *T. lanuginosus*, wild-type, class with Sec62, plug-open conformation
Authors : Itskanov, S.; Park, E.
Deposited on : 2020-10-01
Resolution : 4.00 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.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

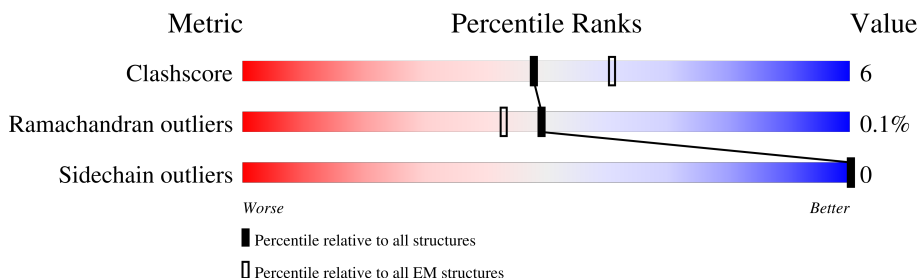
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.00 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	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	480	
2	C	70	
3	B	125	
4	D	719	
5	E	243	
6	F	214	
7	G	402	

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 10789 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 Protein transport channel Sec61 complex, alpha subunit (Sec61).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	437	Total	C	N	O	S	0	0
			3264	2142	537	565	20		

- Molecule 2 is a protein called Protein transport channel Sec61 complex, gamma subunit (Sss1).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	57	Total	C	N	O	S	0	0
			440	291	76	69	4		

- Molecule 3 is a protein called Protein transport channel Sec61 complex, beta subunit (Sbh1).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	32	Total	C	N	O	S	0	0
			245	168	41	35	1		

- Molecule 4 is a protein called Protein transport protein Sec63.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	475	Total	C	N	O	S	0	0
			3673	2399	617	646	11		

- Molecule 5 is a protein called Protein transport protein Sec66/Sec71.

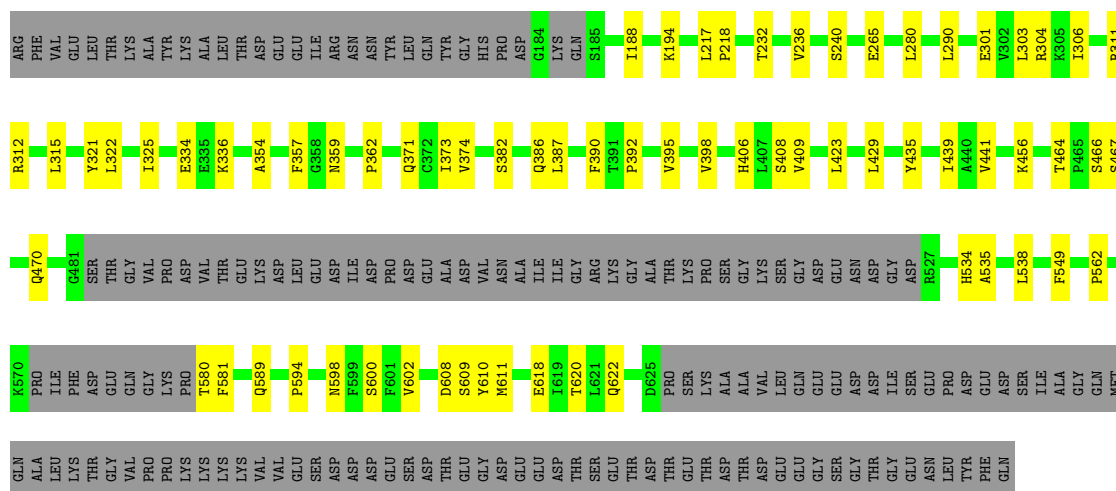
Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	172	Total	C	N	O	S	0	0
			1359	873	255	226	5		

- Molecule 6 is a protein called Protein transport protein Sec72.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	194	Total	C	N	O	S	0	0
			1454	919	264	265	6		

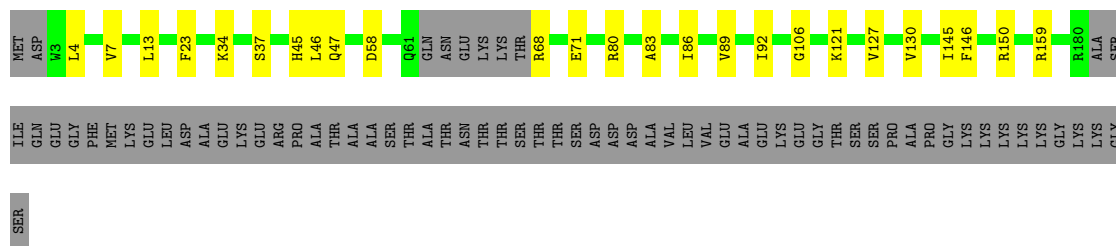
- Molecule 7 is a protein called Protein transport protein Sec62.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	G	62	Total	C	N	O	0	0
			354	229	63	62		



• Molecule 5: Protein transport protein Sec66/Sec71

Chain E: 60% 10% 29%



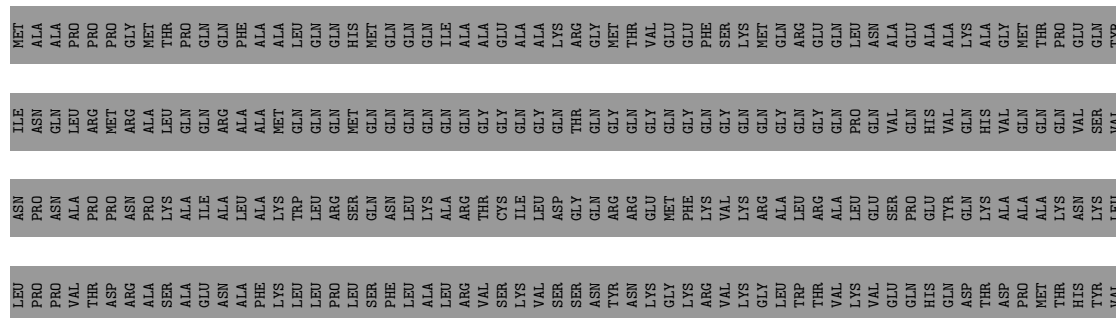
• Molecule 6: Protein transport protein Sec72

Chain F: 77% 14% 9%



• Molecule 7: Protein transport protein Sec62

Chain G: 14% 85%



TRP	ALA
LEU	ALA
TYR	VAL
E244	SER
G245	LYS
P246	SER
	GLN
A254	GLU
	LYS
V258	GLY
	ALA
I261	ALA
	PRO
I264	THR
	THR
I272	ALA
	ALA
V305	PRO
THR	GLU
VAL	ALA
PHE	PRO
VAL	THR
VAL	ALA
PRO	THR
PRO	THR
GLY	THR
ILE	SER
TRP	SER
LEU	GLU
PHE	ALA
PRO	GLN
ASN	PRO
LEU	SER
PHE	SER
GLU	SER
ASP	SER
VAL	GLY
GLY	THR
PHE	ALA
ILE	SER
ASP	LYS
SER	ARG
PHE	ASN
LYS	LEU
PRO	ALA
LEU	ALA
TRP	SER
ALA	VAL
TRP	GLU
ASN	ASP
GLU	ALA
LYS	GLU
LYS	GLY
LYS	SER
LYS	
PRO	
LYS	
LYS	
ALA	
LYS	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	114704	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50.0	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	43860	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor

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	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.11	0/3331	0.29	0/4533
2	C	0.12	0/449	0.25	0/602
3	B	0.12	0/249	0.26	0/339
4	D	0.11	0/3756	0.30	0/5101
5	E	0.11	0/1389	0.28	0/1883
6	F	0.10	0/1490	0.27	0/2032
7	G	0.19	0/360	0.46	1/498 (0.2%)
All	All	0.11	0/11024	0.29	1/14988 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	G	246	PRO	N-CA-CB	6.19	110.14	103.33

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	3264	0	3345	35	0
2	C	440	0	467	4	0
3	B	245	0	273	3	0
4	D	3673	0	3728	55	0
5	E	1359	0	1354	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	F	1454	0	1411	19	0
7	G	354	0	247	3	0
All	All	10789	0	10825	127	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 (127) 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:151:VAL:HA	1:A:154:ILE:HD12	1.68	0.73
4:D:535:ALA:HB1	4:D:538:LEU:HD21	1.72	0.69
1:A:155:VAL:HG21	5:E:13:LEU:HD21	1.74	0.69
4:D:63:GLN:NE2	4:D:334:GLU:OE2	2.26	0.68
4:D:374:VAL:HG11	4:D:609:SER:HA	1.76	0.68
1:A:39:THR:HG23	1:A:167:LEU:HD23	1.78	0.65
4:D:392:PRO:HA	4:D:395:VAL:HG12	1.78	0.65
1:A:243:ASN:OD1	1:A:246:ASN:ND2	2.30	0.64
4:D:466:SER:HB3	4:D:594:PRO:HB3	1.80	0.64
4:D:10:GLU:O	4:D:13:GLN:NE2	2.32	0.63
5:E:4:LEU:HA	5:E:7:VAL:HG12	1.81	0.62
5:E:159:ARG:NH1	6:F:106:ALA:O	2.33	0.62
4:D:359:ASN:HB3	4:D:362:PRO:HD2	1.81	0.61
4:D:371:GLN:NE2	4:D:610:TYR:O	2.28	0.61
4:D:306:ILE:HD12	4:D:311:ARG:HG2	1.84	0.59
4:D:395:VAL:HA	4:D:398:VAL:HG12	1.86	0.58
1:A:134:VAL:HG11	1:A:154:ILE:HG12	1.86	0.57
6:F:130:GLN:OE1	6:F:162:ARG:NH2	2.38	0.57
5:E:86:ILE:HA	5:E:89:VAL:HG12	1.86	0.57
6:F:93:GLU:HA	6:F:96:ARG:HD2	1.87	0.56
7:G:261:ILE:HA	7:G:264:ILE:HG22	1.87	0.56
1:A:52:TYR:HD1	3:B:114:HIS:HD2	1.54	0.55
4:D:13:GLN:HG3	4:D:97:THR:HG21	1.89	0.55
4:D:56:HIS:HB3	4:D:59:ILE:HD13	1.88	0.55
6:F:108:ARG:HH22	6:F:116:LEU:HD22	1.71	0.55
3:B:98:VAL:HA	5:E:23:PHE:HE2	1.72	0.55
4:D:435:TYR:CZ	4:D:439:ILE:HD11	2.41	0.55
4:D:290:LEU:HD23	4:D:325:ILE:HD11	1.89	0.55
4:D:301:GLU:OE1	4:D:304:ARG:NH1	2.40	0.54
6:F:108:ARG:HD3	6:F:109:PRO:HD2	1.89	0.54
4:D:15:PHE:CD2	4:D:16:PRO:HD3	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:16:PRO:HB2	4:D:94:ILE:HD11	1.90	0.54
1:A:224:THR:HG23	1:A:225:TRP:HD1	1.72	0.54
4:D:386:GLN:NE2	4:D:611:MET:H	2.06	0.54
4:D:321:TYR:HB2	4:D:336:LYS:HG2	1.89	0.53
1:A:17:LEU:HD13	1:A:119:LYS:HE3	1.89	0.53
1:A:92:PHE:HE2	1:A:118:GLN:HA	1.72	0.53
6:F:71:ARG:HD2	6:F:108:ARG:HE	1.73	0.53
6:F:72:SER:O	6:F:76:THR:HG23	2.10	0.52
1:A:323:LEU:O	1:A:341:ILE:N	2.43	0.52
5:E:89:VAL:HA	5:E:92:ILE:HG22	1.91	0.52
1:A:318:LEU:HD23	1:A:321:ARG:HH12	1.75	0.52
5:E:45:HIS:HE1	5:E:47:GLN:HB2	1.74	0.52
6:F:180:ILE:HG21	6:F:201:LEU:HB2	1.91	0.52
4:D:232:THR:OG1	5:E:106:GLY:O	2.28	0.51
1:A:275:ARG:HD2	4:D:464:THR:HG21	1.92	0.51
4:D:240:SER:HB2	4:D:265:GLU:HB2	1.91	0.51
4:D:602:VAL:HG12	4:D:618:GLU:HB3	1.92	0.51
4:D:600:SER:HA	4:D:620:THR:HA	1.93	0.50
4:D:303:LEU:HD13	4:D:315:LEU:HD22	1.94	0.49
1:A:88:SER:OG	1:A:118:GLN:NE2	2.45	0.49
4:D:382:SER:OG	4:D:406:HIS:ND1	2.36	0.49
6:F:77:LYS:O	6:F:81:THR:HG23	2.12	0.49
4:D:23:THR:HA	4:D:26:VAL:HG12	1.94	0.49
6:F:71:ARG:O	6:F:75:ILE:HG12	2.12	0.49
1:A:203:ILE:HG12	4:D:188:ILE:HG22	1.96	0.48
1:A:132:VAL:O	1:A:136:THR:HG22	2.14	0.48
1:A:246:ASN:HB2	1:A:439:GLY:O	2.14	0.47
4:D:90:MET:O	4:D:94:ILE:HG12	2.14	0.47
4:D:382:SER:HG	4:D:406:HIS:HD1	1.42	0.47
5:E:80:ARG:HH22	6:F:44:GLN:HB3	1.80	0.47
1:A:17:LEU:HD11	1:A:116:THR:HG22	1.96	0.47
1:A:390:VAL:HB	1:A:413:LEU:HD21	1.97	0.47
1:A:139:TYR:O	1:A:141:GLN:NE2	2.48	0.46
4:D:10:GLU:HG2	4:D:194:LYS:HB2	1.97	0.46
4:D:15:PHE:CG	4:D:16:PRO:HD3	2.51	0.46
4:D:78:ILE:HG13	4:D:79:ALA:N	2.29	0.46
1:A:300:CYS:HA	1:A:303:VAL:HG12	1.97	0.46
5:E:47:GLN:HG2	5:E:80:ARG:HG3	1.96	0.46
2:C:56:LYS:O	2:C:60:ILE:HG12	2.16	0.46
6:F:164:GLY:HA3	6:F:180:ILE:HD11	1.98	0.45
1:A:149:ILE:HD12	1:A:152:LEU:HD12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:296:GLN:NE2	1:A:368:MET:SD	2.90	0.45
1:A:243:ASN:H	1:A:246:ASN:HD21	1.65	0.45
1:A:17:LEU:O	1:A:17:LEU:HD12	2.17	0.44
1:A:243:ASN:O	1:A:246:ASN:ND2	2.51	0.44
4:D:13:GLN:C	4:D:16:PRO:HD2	2.42	0.44
6:F:177:ARG:O	6:F:181:GLU:HG2	2.18	0.44
1:A:431:LEU:HD23	1:A:431:LEU:HA	1.89	0.43
4:D:387:LEU:HD12	4:D:390:PHE:CE2	2.53	0.43
7:G:258:VAL:HA	7:G:261:ILE:HG12	2.00	0.43
7:G:254:ALA:O	7:G:258:VAL:HG13	2.18	0.43
4:D:19:VAL:HG13	4:D:90:MET:HG3	2.01	0.43
5:E:71:GLU:H	5:E:71:GLU:CD	2.27	0.43
5:E:127:VAL:HA	5:E:130:VAL:HG12	2.00	0.43
1:A:134:VAL:HG11	1:A:154:ILE:CG1	2.49	0.43
1:A:211:PHE:HZ	4:D:14:PHE:HB3	1.83	0.42
5:E:34:LYS:O	5:E:37:SER:OG	2.33	0.42
5:E:86:ILE:HD13	5:E:150:ARG:HB3	2.00	0.42
3:B:112:GLY:HA2	3:B:115:VAL:HG12	2.01	0.42
4:D:217:LEU:HB3	4:D:218:PRO:HD3	2.01	0.42
1:A:162:LEU:HA	1:A:165:ILE:HG22	2.01	0.42
1:A:352:LYS:HA	1:A:355:LEU:HG	2.02	0.42
2:C:30:ASP:OD2	2:C:33:GLU:HG2	2.20	0.42
4:D:322:LEU:HD21	4:D:373:ILE:HG12	2.02	0.42
5:E:58:ASP:OD1	5:E:68:ARG:NH1	2.52	0.42
6:F:57:PRO:HB2	6:F:58:PRO:HD3	2.01	0.42
1:A:44:LEU:HD13	2:C:52:GLY:HA2	2.01	0.42
4:D:580:THR:OG1	4:D:581:PHE:N	2.52	0.42
5:E:46:LEU:HD22	6:F:41:GLU:HG2	2.01	0.42
6:F:170:MET:SD	6:F:172:ARG:NH2	2.93	0.42
4:D:441:VAL:HG21	4:D:534:HIS:HE1	1.85	0.42
5:E:121:LYS:HE2	5:E:121:LYS:HB3	1.91	0.42
4:D:423:LEU:HA	4:D:429:LEU:HD13	2.01	0.42
4:D:598:ASN:HD22	4:D:622:GLN:HE22	1.66	0.42
4:D:549:PHE:HB3	4:D:562:PRO:HB3	2.03	0.41
6:F:174:ASP:N	6:F:174:ASP:OD1	2.53	0.41
1:A:316:ASP:OD1	1:A:316:ASP:N	2.49	0.41
5:E:83:ALA:O	5:E:86:ILE:HG22	2.20	0.41
5:E:145:ILE:HG13	5:E:146:PHE:N	2.35	0.41
4:D:354:ALA:HA	4:D:357:PHE:HD2	1.84	0.41
4:D:464:THR:O	4:D:467:SER:OG	2.27	0.41
4:D:608:ASP:OD1	4:D:608:ASP:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:88:ARG:HH11	6:F:90:ASN:N	2.18	0.41
1:A:52:TYR:HB3	1:A:156:GLN:HE22	1.86	0.41
2:C:60:ILE:HB	2:C:61:PRO:HD3	2.03	0.41
4:D:232:THR:HG22	4:D:236:VAL:O	2.20	0.41
4:D:280:LEU:HD11	4:D:312:ARG:HG2	2.03	0.41
4:D:456:LYS:HE2	4:D:456:LYS:HB3	1.91	0.41
1:A:208:GLY:HA2	1:A:209:PRO:HD3	1.96	0.41
4:D:470:GLN:HA	4:D:589:GLN:HA	2.03	0.41
4:D:75:LYS:HE3	4:D:75:LYS:HB3	1.86	0.40
1:A:85:ILE:H	1:A:85:ILE:HD12	1.86	0.40
4:D:408:SER:OG	4:D:409:VAL:N	2.55	0.40
6:F:48:LEU:HD23	6:F:48:LEU:HA	1.89	0.40
4:D:17:PHE:O	4:D:21:THR:HG22	2.22	0.40
4:D:371:GLN:HG2	4:D:608:ASP:HA	2.02	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	429/480 (89%)	417 (97%)	12 (3%)	0	100	100
2	C	55/70 (79%)	54 (98%)	1 (2%)	0	100	100
3	B	30/125 (24%)	30 (100%)	0	0	100	100
4	D	464/719 (64%)	448 (97%)	16 (3%)	0	100	100
5	E	168/243 (69%)	168 (100%)	0	0	100	100
6	F	188/214 (88%)	183 (97%)	5 (3%)	0	100	100
7	G	60/402 (15%)	57 (95%)	2 (3%)	1 (2%)	7	36
All	All	1394/2253 (62%)	1357 (97%)	36 (3%)	1 (0%)	49	81

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	G	272	ILE

5.3.2 Protein sidechains ⓘ

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	338/398 (85%)	338 (100%)	0	100	100
2	C	46/60 (77%)	46 (100%)	0	100	100
3	B	28/94 (30%)	28 (100%)	0	100	100
4	D	382/613 (62%)	382 (100%)	0	100	100
5	E	129/200 (64%)	129 (100%)	0	100	100
6	F	142/169 (84%)	142 (100%)	0	100	100
7	G	13/325 (4%)	13 (100%)	0	100	100
All	All	1078/1859 (58%)	1078 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	118	GLN
1	A	141	GLN
1	A	156	GLN
1	A	246	ASN
4	D	61	GLN
4	D	375	GLN
4	D	386	GLN
4	D	529	GLN
4	D	534	HIS
4	D	595	GLN
5	E	95	GLN
5	E	97	GLN

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Mol	Chain	Res	Type
6	F	10	HIS
6	F	49	HIS
6	F	127	ASN

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 Map visualisation

This section contains visualisations of the EMDB entry EMD-22774. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

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

9 Map-model fit

This section was not generated.