



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 12:24 PM UTC

PDB ID : 2WWA / pdb_00002wwa
EMDB ID : EMD-1669
Title : Cryo-EM structure of idle yeast Ssh1 complex bound to the yeast 80S ribosome
Authors : Becker, T.; Mandon, E.; Bhushan, S.; Jarasch, A.; Armache, J.P.; Funes, S.; Jossinet, F.; Gumbart, J.; Mielke, T.; Berninghausen, O.; Schulten, K.; Westhof, E.; Gilmore, R.; Beckmann, R.
Deposited on : 2009-10-22
Resolution : 8.90 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:

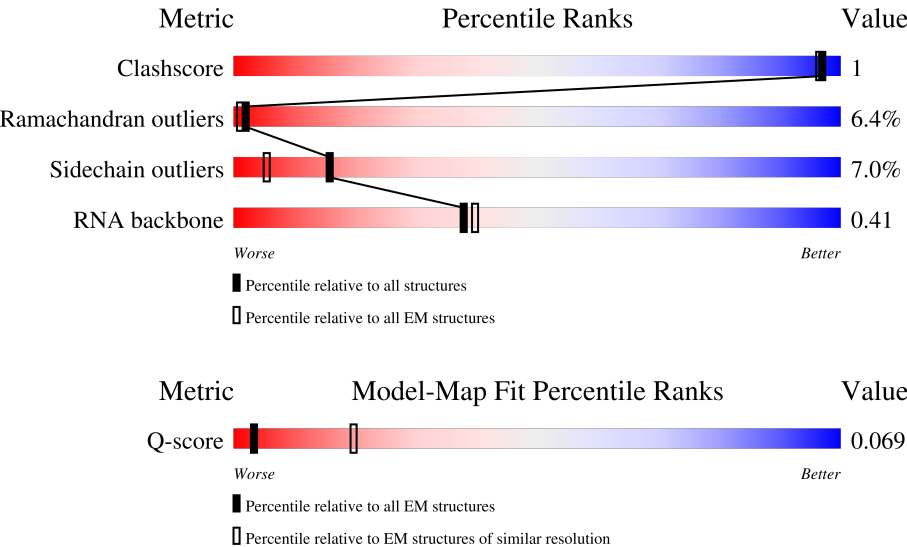
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 8.90 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	265 (8.30 - 9.30)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	490	63% 88% 10% ..
2	B	80	55% 66% 8% 25%
3	C	87	23% 22% 76%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	D	63	
5	E	34	
6	F	25	
7	G	18	
8	H	362	
9	I	184	
10	J	189	
11	K	142	
12	L	127	
13	M	113	
14	N	120	
15	O	51	

2 Entry composition

There are 15 unique types of molecules in this entry. The entry contains 14301 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 SEC SIXTY-ONE PROTEIN HOMOLOG.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	490	Total	C	N	O	S	0	0
			3770	2487	603	671	9		

- Molecule 2 is a protein called PROTEIN TRANSPORT PROTEIN SSS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	60	Total	C	N	O	S	0	0
			472	318	76	77	1		

- Molecule 3 is a protein called PROTEIN TRANSPORT PROTEIN SEB2.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	21	Total	C	N	O	0	0
			162	112	24	26		

- Molecule 4 is a RNA chain called 25S RRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	63	Total	C	N	O	P	0	0
			1347	603	245	436	63		

- Molecule 5 is a RNA chain called 25S RRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	34	Total	C	N	O	P	0	0
			740	332	148	226	34		

- Molecule 6 is a RNA chain called 25S RRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	25	Total	C	N	O	P	0	0
			536	239	99	173	25		

- Molecule 7 is a RNA chain called 25S RRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	18	Total	C	N	O	P	0	0
			379	169	64	128	18		

- Molecule 8 is a protein called 60S RIBOSOMAL PROTEIN L4-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	269	Total	C	N	O	S	0	0
			2039	1281	391	363	4		

- Molecule 9 is a protein called 60S RIBOSOMAL PROTEIN L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	153	Total	C	N	O	S	0	0
			1212	756	236	219	1		

- Molecule 10 is a protein called 60S RIBOSOMAL PROTEIN L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	53	Total	C	N	O	S	0	0
			410	254	83	72	1		

- Molecule 11 is a protein called 60S RIBOSOMAL PROTEIN L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	83	Total	C	N	O	S	0	0
			663	424	111	126	2		

- Molecule 12 is a protein called 60S RIBOSOMAL PROTEIN L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	127	Total	C	N	O	S	0	0
			1002	630	193	178	1		

- Molecule 13 is a protein called 60S RIBOSOMAL PROTEIN L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	84	Total	C	N	O	S	0	0
			706	447	140	118	1		

- Molecule 14 is a protein called 60S RIBOSOMAL PROTEIN L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	69	Total	C	N	O	S	0	0
			547	345	101	99	2		

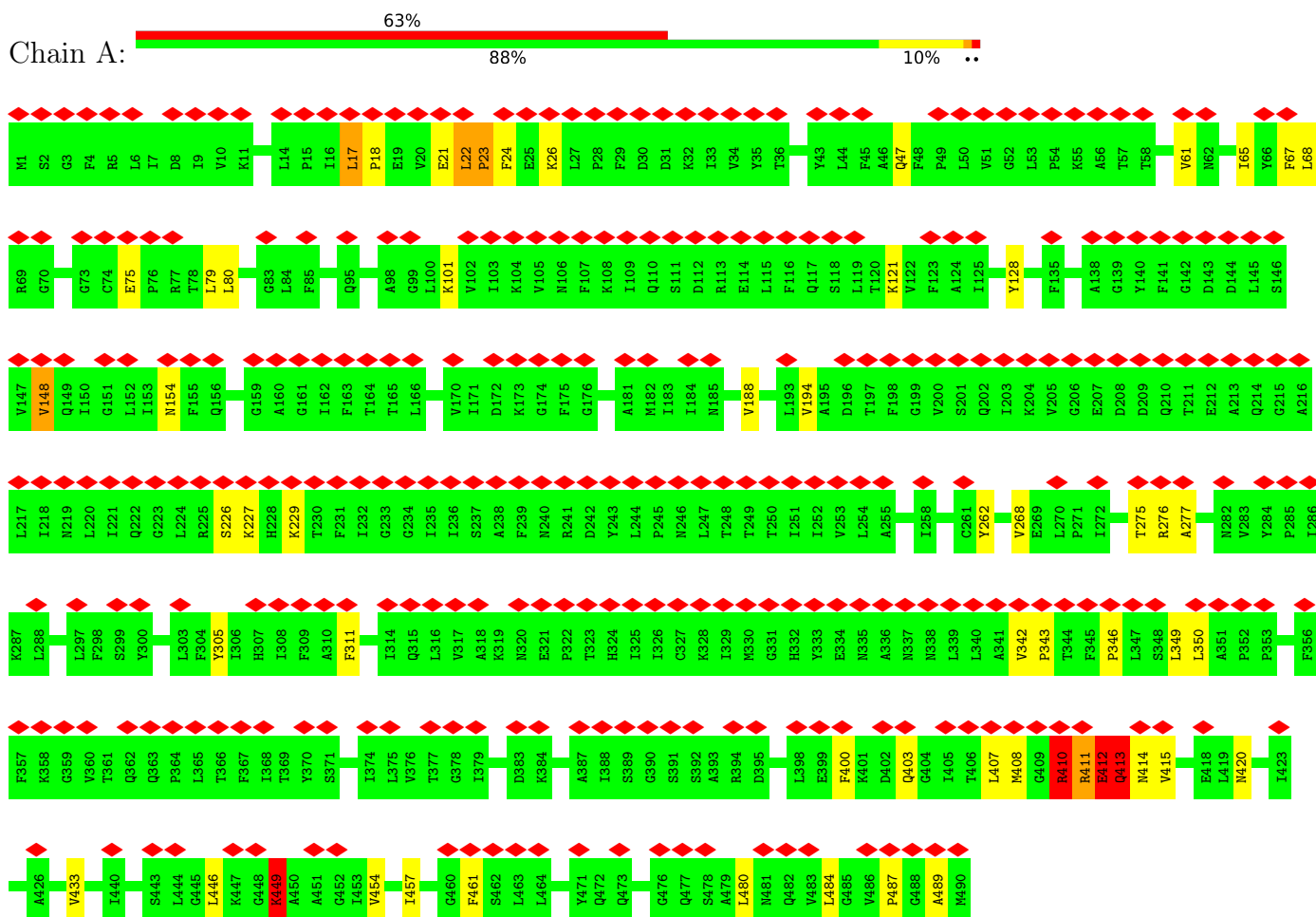
- Molecule 15 is a protein called 60S RIBOSOMAL PROTEIN L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	37	Total	C	N	O	S	0	0
			316	200	66	48	2		

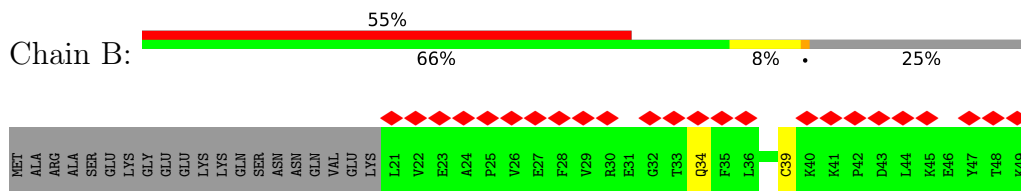
3 Residue-property plots

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 atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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: SEC SIXTY-ONE PROTEIN HOMOLOG

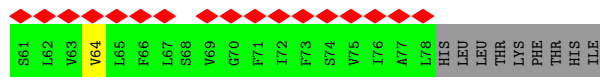
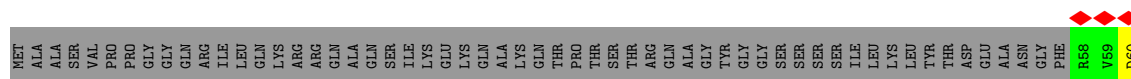


• Molecule 2: PROTEIN TRANSPORT PROTEIN SSS1

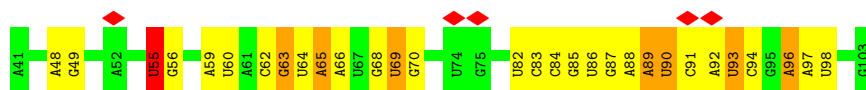




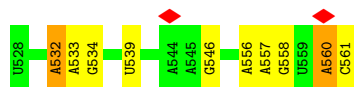
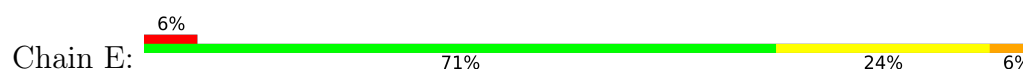
• Molecule 3: PROTEIN TRANSPORT PROTEIN SEB2



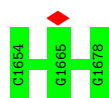
• Molecule 4: 25S RRNA



• Molecule 5: 25S RRNA



• Molecule 6: 25S RRNA



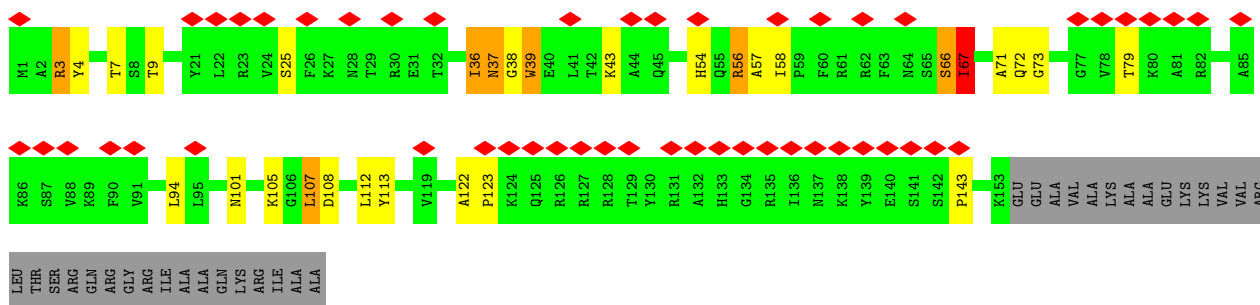
• Molecule 7: 25S RRNA



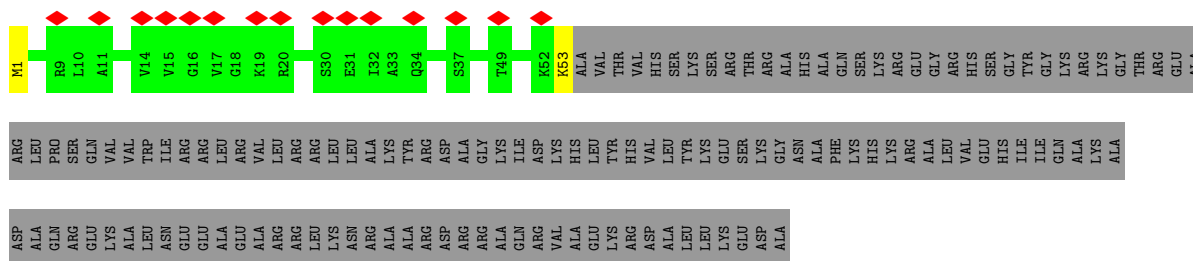
• Molecule 8: 60S RIBOSOMAL PROTEIN L4-B



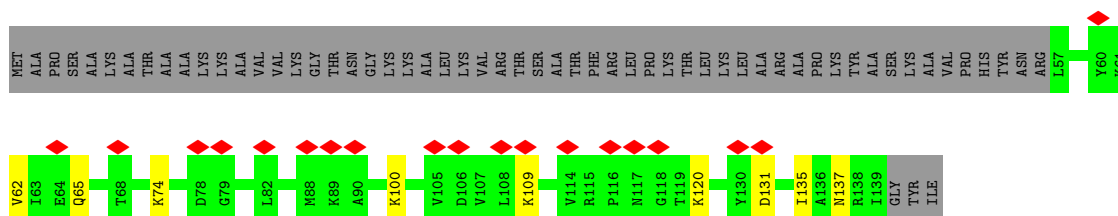
- Molecule 9: 60S RIBOSOMAL PROTEIN L17-A



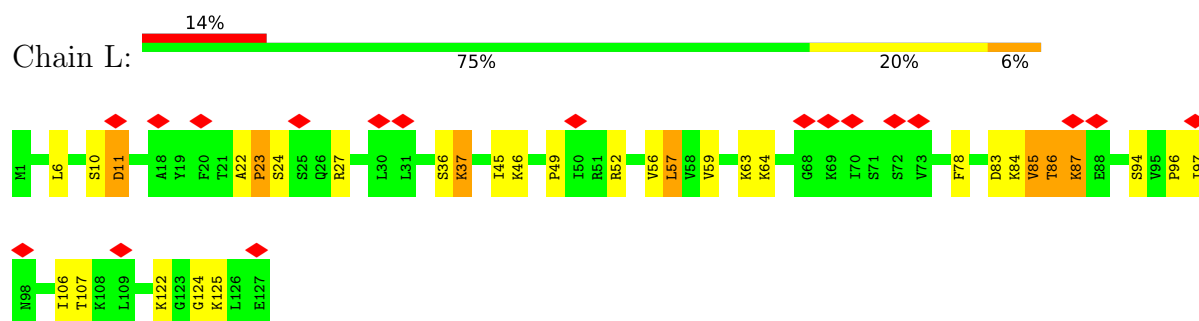
- Molecule 10: 60S RIBOSOMAL PROTEIN L19



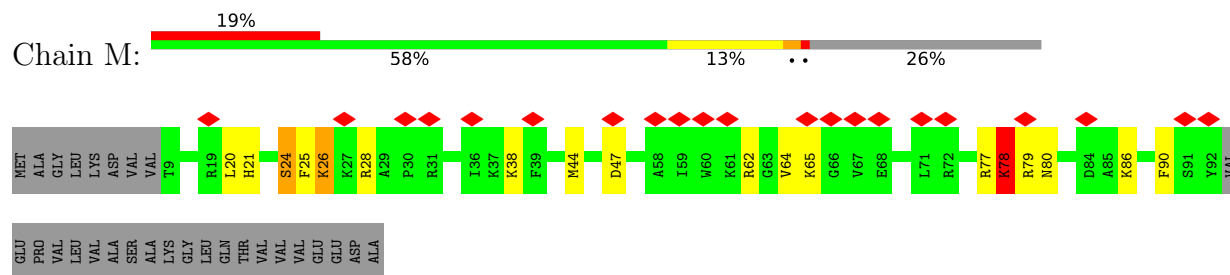
- Molecule 11: 60S RIBOSOMAL PROTEIN L25



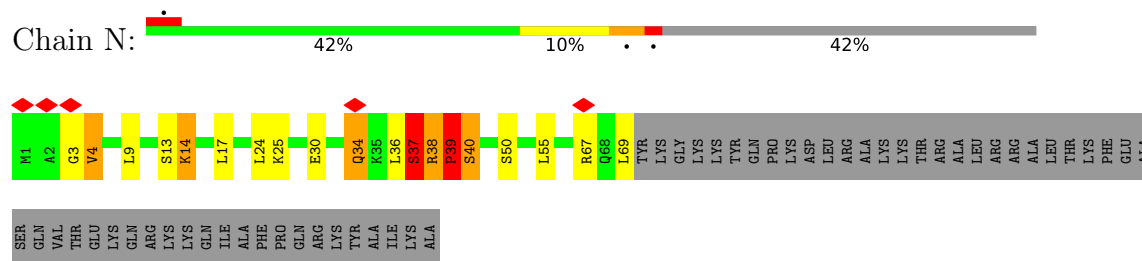
- Molecule 12: 60S RIBOSOMAL PROTEIN L26-A



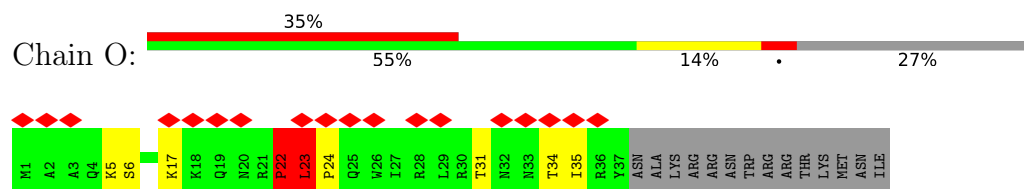
• Molecule 13: 60S RIBOSOMAL PROTEIN L31-A



• Molecule 14: 60S RIBOSOMAL PROTEIN L35



• Molecule 15: 60S RIBOSOMAL PROTEIN L39



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	20400	Depositor
Resolution determination method	Not provided	
CTF correction method	DEFOCUS GROUP VOLUMES	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	4500	Depositor
Magnification	38000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	7.747	Depositor
Minimum map value	-3.672	Depositor
Average map value	0.049	Depositor
Map value standard deviation	0.609	Depositor
Recommended contour level	1.75	Depositor
Map size ($\text{\AA}$)	455.4, 455.4, 455.4	wwPDB
Map dimensions	368, 368, 368	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.2375, 1.2375, 1.2375	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	1.14	0/3848	1.53	22/5234 (0.4%)
2	B	1.10	0/481	1.64	9/648 (1.4%)
3	C	1.14	0/164	1.46	0/222
4	D	0.89	0/1508	1.22	8/2348 (0.3%)
5	E	0.87	0/833	1.08	3/1298 (0.2%)
6	F	0.88	0/599	0.99	0/932
7	G	0.87	0/421	0.98	0/653
8	H	1.25	0/2079	1.86	46/2817 (1.6%)
9	I	1.28	0/1235	1.74	27/1662 (1.6%)
10	J	1.27	0/412	1.42	0/551
11	K	1.13	0/670	1.40	2/903 (0.2%)
12	L	1.28	0/1013	1.69	23/1351 (1.7%)
13	M	1.37	0/719	1.67	16/959 (1.7%)
14	N	1.29	1/549 (0.2%)	1.93	24/733 (3.3%)
15	O	1.30	0/321	1.81	6/426 (1.4%)
All	All	1.15	1/14852 (0.0%)	1.54	186/20737 (0.9%)

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
1	A	0	3
4	D	0	2
8	H	0	2
9	I	0	1
12	L	0	1
14	N	0	2
15	O	0	2
All	All	0	13

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	N	69	LEU	C-O	-11.56	1.00	1.23

All (186) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	532	A	P-O3'-C3'	14.40	141.80	120.20
8	H	54	GLU	CA-C-N	11.70	142.76	121.70
8	H	54	GLU	C-N-CA	11.70	142.76	121.70
4	D	69	U	P-O3'-C3'	11.41	137.31	120.20
8	H	75	PRO	CA-C-N	11.10	141.68	121.70
8	H	75	PRO	C-N-CA	11.10	141.68	121.70
8	H	59	GLN	CA-C-N	11.01	141.52	121.70
8	H	59	GLN	C-N-CA	11.01	141.52	121.70
4	D	65	A	P-O3'-C3'	10.70	136.25	120.20
4	D	90	U	P-O3'-C3'	10.53	136.00	120.20
4	D	96	A	P-O3'-C3'	10.30	135.65	120.20
4	D	55	U	P-O3'-C3'	10.06	135.29	120.20
9	I	56	ARG	CA-C-N	9.84	139.42	121.70
9	I	56	ARG	C-N-CA	9.84	139.42	121.70
9	I	36	ILE	CA-C-N	9.39	138.60	121.70
9	I	36	ILE	C-N-CA	9.39	138.60	121.70
12	L	84	LYS	CA-C-N	9.37	138.57	121.70
12	L	84	LYS	C-N-CA	9.37	138.57	121.70
8	H	184	SER	CA-C-N	9.29	138.43	121.70
8	H	184	SER	C-N-CA	9.29	138.43	121.70
2	B	54	VAL	N-CA-C	-9.28	103.89	112.43
8	H	214	GLY	CA-C-N	9.20	138.26	121.70
8	H	214	GLY	C-N-CA	9.20	138.26	121.70
14	N	39	PRO	CA-C-N	9.02	137.93	121.70
14	N	39	PRO	C-N-CA	9.02	137.93	121.70
5	E	560	A	P-O3'-C3'	8.80	133.41	120.20
12	L	10	SER	CA-C-N	8.66	137.29	121.70
12	L	10	SER	C-N-CA	8.66	137.29	121.70
4	D	93	U	P-O3'-C3'	8.55	133.03	120.20
4	D	89	A	P-O3'-C3'	8.43	132.84	120.20
8	H	60	THR	N-CA-CB	8.18	125.41	111.50
13	M	77	ARG	CA-C-N	7.97	136.05	121.70
13	M	77	ARG	C-N-CA	7.97	136.05	121.70
8	H	212	ASP	CA-C-N	7.86	135.85	121.70
8	H	212	ASP	C-N-CA	7.86	135.85	121.70
8	H	57	GLY	CA-C-N	7.84	135.81	121.70
8	H	57	GLY	C-N-CA	7.84	135.81	121.70
14	N	36	LEU	CA-C-N	7.82	135.78	121.70

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	N	36	LEU	C-N-CA	7.82	135.78	121.70
5	E	532	A	C2'-C3'-O3'	7.74	121.11	109.50
9	I	105	LYS	N-CA-C	7.64	119.69	111.36
14	N	37	SER	N-CA-CB	7.40	123.08	110.50
9	I	37	ASN	N-CA-CB	7.39	123.07	110.50
9	I	36	ILE	N-CA-CB	7.39	119.19	110.55
13	M	21	HIS	N-CA-C	-7.25	105.36	114.56
2	B	72	HIS	CA-C-N	7.25	124.80	120.24
2	B	72	HIS	C-N-CA	7.25	124.80	120.24
12	L	63	LYS	N-CA-C	-7.21	101.79	110.44
12	L	85	VAL	CA-C-N	7.09	134.46	121.70
12	L	85	VAL	C-N-CA	7.09	134.46	121.70
8	H	105	THR	CA-C-N	6.99	134.28	121.70
8	H	105	THR	C-N-CA	6.99	134.28	121.70
9	I	66	SER	CA-C-N	6.97	134.24	121.70
9	I	66	SER	C-N-CA	6.97	134.24	121.70
15	O	31	THR	CA-C-N	6.96	134.22	121.70
15	O	31	THR	C-N-CA	6.96	134.22	121.70
14	N	69	LEU	CA-C-O	-6.94	109.00	120.80
1	A	412	GLU	CA-C-N	6.91	134.73	121.54
1	A	412	GLU	C-N-CA	6.91	134.73	121.54
1	A	408	MET	CA-C-N	6.89	134.09	121.70
1	A	408	MET	C-N-CA	6.89	134.09	121.70
14	N	67	ARG	N-CA-CB	-6.89	100.27	110.53
14	N	37	SER	CA-C-N	6.83	134.00	121.70
14	N	37	SER	C-N-CA	6.83	134.00	121.70
8	H	88	GLY	CA-C-N	6.71	133.79	121.70
8	H	88	GLY	C-N-CA	6.71	133.79	121.70
8	H	89	ALA	N-CA-CB	6.65	120.38	110.40
14	N	13	SER	CA-C-N	6.61	133.60	121.70
14	N	13	SER	C-N-CA	6.61	133.60	121.70
8	H	159	ILE	CA-C-N	6.58	133.55	121.70
8	H	159	ILE	C-N-CA	6.58	133.55	121.70
8	H	86	GLY	CA-C-N	6.55	133.49	121.70
8	H	86	GLY	C-N-CA	6.55	133.49	121.70
8	H	101	ALA	CA-C-N	6.51	127.98	119.84
8	H	101	ALA	C-N-CA	6.51	127.98	119.84
13	M	64	VAL	CA-C-N	6.49	129.30	120.54
13	M	64	VAL	C-N-CA	6.49	129.30	120.54
9	I	101	ASN	N-CA-C	-6.42	105.38	113.72
14	N	3	GLY	CA-C-N	6.38	133.19	121.70
14	N	3	GLY	C-N-CA	6.38	133.19	121.70

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	H	102	PRO	N-CA-C	6.38	125.61	112.47
9	I	9	THR	CA-C-N	6.32	133.07	121.70
9	I	9	THR	C-N-CA	6.32	133.07	121.70
14	N	50	SER	N-CA-C	-6.30	105.53	113.72
12	L	37	LYS	N-CA-C	-6.28	106.58	114.56
1	A	449	LYS	N-CA-CB	6.28	121.10	110.49
9	I	3	ARG	CA-C-N	6.26	132.98	121.70
9	I	3	ARG	C-N-CA	6.26	132.98	121.70
2	B	39	CYS	CA-C-N	6.19	132.84	121.70
2	B	39	CYS	C-N-CA	6.19	132.84	121.70
9	I	38	GLY	CA-C-N	6.19	132.84	121.70
9	I	38	GLY	C-N-CA	6.19	132.84	121.70
12	L	22	ALA	CA-C-N	6.18	127.56	119.84
12	L	22	ALA	C-N-CA	6.18	127.56	119.84
8	H	25	VAL	N-CA-C	-6.18	106.71	112.83
14	N	39	PRO	CB-CA-C	6.17	121.73	111.56
9	I	39	TRP	N-CA-CB	6.16	120.97	110.50
12	L	27	ARG	N-CA-C	-6.14	105.37	112.92
1	A	349	LEU	N-CA-C	-6.14	105.37	112.92
2	B	34	GLN	CA-C-N	6.12	128.48	120.28
2	B	34	GLN	C-N-CA	6.12	128.48	120.28
8	H	213	ASN	CA-C-N	6.10	132.68	121.70
8	H	213	ASN	C-N-CA	6.10	132.68	121.70
13	M	80	ASN	CA-C-N	6.08	132.64	121.70
13	M	80	ASN	C-N-CA	6.08	132.64	121.70
12	L	23	PRO	CA-C-N	6.06	133.11	121.54
12	L	23	PRO	C-N-CA	6.06	133.11	121.54
12	L	83	ASP	CA-C-N	6.05	132.58	121.70
12	L	83	ASP	C-N-CA	6.05	132.58	121.70
15	O	5	LYS	CA-C-N	6.03	132.56	121.70
15	O	5	LYS	C-N-CA	6.03	132.56	121.70
13	M	24	SER	CA-C-N	6.01	132.52	121.70
13	M	24	SER	C-N-CA	6.01	132.52	121.70
9	I	105	LYS	CA-C-N	5.96	132.43	121.70
9	I	105	LYS	C-N-CA	5.96	132.43	121.70
8	H	243	HIS	CA-C-N	5.92	132.85	121.54
8	H	243	HIS	C-N-CA	5.92	132.85	121.54
11	K	137	ASN	N-CA-C	-5.91	106.23	113.50
1	A	23	PRO	CA-C-N	5.86	132.25	121.70
1	A	23	PRO	C-N-CA	5.86	132.25	121.70
8	H	59	GLN	N-CA-C	5.73	117.20	111.07
9	I	36	ILE	N-CA-C	5.67	115.86	110.42

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	H	83	GLY	CA-C-N	5.64	131.86	121.70
8	H	83	GLY	C-N-CA	5.64	131.86	121.70
14	N	14	LYS	N-CA-CB	5.64	120.09	110.50
14	N	30	GLU	N-CA-C	-5.64	106.24	113.23
8	H	173	GLY	CA-C-N	5.64	131.85	121.70
8	H	173	GLY	C-N-CA	5.64	131.85	121.70
1	A	420	ASN	N-CA-C	-5.63	106.08	113.17
13	M	78	LYS	N-CA-CB	5.62	120.06	110.50
9	I	4	TYR	CA-C-N	5.61	131.80	121.70
9	I	4	TYR	C-N-CA	5.61	131.80	121.70
12	L	59	VAL	N-CA-C	-5.60	107.42	112.12
8	H	212	ASP	CB-CA-C	5.58	121.53	110.42
1	A	275	THR	N-CA-C	-5.56	107.50	114.56
1	A	400	PHE	CA-C-N	5.55	127.71	120.28
1	A	400	PHE	C-N-CA	5.55	127.71	120.28
14	N	67	ARG	CA-CB-CG	5.54	125.17	114.10
1	A	413	GLN	N-CA-C	5.52	122.55	110.80
2	B	60	ALA	CA-C-N	5.50	127.99	120.46
2	B	60	ALA	C-N-CA	5.50	127.99	120.46
8	H	74	ILE	O-C-N	-5.47	114.86	121.10
8	H	59	GLN	O-C-N	-5.43	116.47	122.07
14	N	4	VAL	N-CA-CB	5.42	120.71	111.50
1	A	457	ILE	N-CA-C	-5.38	107.57	113.43
11	K	135	ILE	N-CA-C	-5.37	107.75	112.90
15	O	5	LYS	CB-CA-C	5.36	121.09	110.42
13	M	62	ARG	N-CA-C	-5.36	106.91	113.50
13	M	80	ASN	N-CA-C	5.30	117.06	111.28
4	D	63	G	P-O3'-C3'	5.30	128.15	120.20
13	M	24	SER	N-CA-CB	5.29	119.44	110.49
1	A	17	LEU	CA-C-N	5.29	126.45	119.84
1	A	17	LEU	C-N-CA	5.29	126.45	119.84
1	A	350	LEU	N-CA-C	-5.27	106.53	113.17
1	A	311	PHE	N-CA-C	5.26	116.83	111.14
8	H	63	GLU	N-CA-C	-5.21	106.45	114.16
9	I	7	THR	N-CA-C	5.21	116.96	111.28
8	H	199	TRP	N-CA-CB	5.19	119.26	110.49
8	H	13	GLY	CA-C-N	5.18	131.03	121.70
8	H	13	GLY	C-N-CA	5.18	131.03	121.70
1	A	21	GLU	N-CA-C	-5.16	100.88	108.99
12	L	124	GLY	CA-C-N	5.16	130.98	121.70
12	L	124	GLY	C-N-CA	5.16	130.98	121.70
1	A	461	PHE	N-CA-C	-5.14	107.18	113.50

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	N	24	LEU	N-CA-C	-5.11	106.73	113.17
8	H	222	VAL	N-CA-CB	5.10	118.36	111.21
9	I	58	ILE	CA-C-N	5.09	125.09	119.90
9	I	58	ILE	C-N-CA	5.09	125.09	119.90
12	L	49	PRO	CA-C-N	5.09	127.32	120.50
12	L	49	PRO	C-N-CA	5.09	127.32	120.50
13	M	26	LYS	N-CA-CB	5.08	119.08	110.49
15	O	22	PRO	N-CA-C	5.08	125.32	112.10
9	I	73	GLY	CA-C-N	5.08	130.84	121.70
9	I	73	GLY	C-N-CA	5.08	130.84	121.70
1	A	433	VAL	N-CA-C	-5.06	107.00	113.22
1	A	411	ARG	N-CA-CB	5.05	119.03	110.49
14	N	34	GLN	CA-C-N	5.05	130.79	121.70
14	N	34	GLN	C-N-CA	5.05	130.79	121.70
8	H	58	HIS	N-CA-CB	5.05	119.08	110.50
13	M	65	LYS	CA-C-N	5.04	130.77	121.70
13	M	65	LYS	C-N-CA	5.04	130.77	121.70
14	N	55	LEU	N-CA-C	-5.03	106.99	113.23
12	L	11	ASP	N-CA-CB	5.02	119.04	110.50
12	L	84	LYS	N-CA-CB	5.02	119.04	110.50
14	N	25	LYS	N-CA-C	-5.02	107.21	113.38
12	L	11	ASP	CA-CB-CG	5.00	117.60	112.60

There are no chirality outliers.

All (13) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	17	LEU	Peptide
1	A	262	TYR	Sidechain
1	A	407	LEU	Peptide
4	D	55	U	Sidechain
4	D	60	U	Sidechain
8	H	209	TYR	Sidechain
8	H	92	ASN	Peptide
9	I	122	ALA	Peptide
12	L	94	SER	Peptide
14	N	38	ARG	Peptide
14	N	40	SER	Peptide
15	O	23	LEU	Peptide
15	O	24	PRO	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	3770	0	3941	4	0
2	B	472	0	519	1	0
3	C	162	0	177	0	0
4	D	1347	0	678	0	0
5	E	740	0	369	1	0
6	F	536	0	272	0	0
7	G	379	0	195	0	0
8	H	2039	0	2106	7	0
9	I	1212	0	1231	2	0
10	J	410	0	452	0	0
11	K	663	0	699	0	0
12	L	1002	0	1093	2	0
13	M	706	0	741	1	0
14	N	547	0	613	2	0
15	O	316	0	349	0	0
All	All	14301	0	13435	20	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 1.

All (20) 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)
5:E:539:U:H3	5:E:546:G:H1	1.46	0.61
8:H:88:GLY:HA3	8:H:89:ALA:HB3	1.86	0.57
8:H:74:ILE:H	8:H:75:PRO:HA	1.76	0.50
14:N:39:PRO:HB2	14:N:40:SER:C	2.38	0.48
1:A:410:ARG:HH22	1:A:412:GLU:HG3	1.79	0.48
2:B:76:ARG:HE	2:B:76:ARG:HA	1.81	0.46
8:H:55:LYS:HD3	8:H:55:LYS:H	1.80	0.45
13:M:44:MET:HE1	13:M:78:LYS:HB2	1.98	0.44
8:H:57:GLY:HA3	8:H:58:HIS:HB2	1.99	0.44
9:I:66:SER:HA	9:I:67:ILE:HG22	1.99	0.44
8:H:87:GLN:HE21	8:H:87:GLN:HA	1.83	0.43
9:I:56:ARG:HB3	9:I:57:ALA:HB3	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:65:ILE:HD12	1:A:68:LEU:HD12	2.01	0.42
1:A:22:LEU:HB2	1:A:23:PRO:HD2	2.01	0.42
8:H:83:GLY:HA3	8:H:84:ARG:HB2	2.01	0.41
12:L:56:VAL:HG22	12:L:106:ILE:HG22	2.01	0.41
8:H:58:HIS:O	8:H:58:HIS:CG	2.73	0.41
12:L:57:LEU:HD12	12:L:107:THR:HG23	2.02	0.41
1:A:342:VAL:HB	1:A:343:PRO:HD2	2.03	0.40
14:N:37:SER:N	14:N:38:ARG:HA	2.36	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	488/490 (100%)	434 (89%)	37 (8%)	17 (4%)	3	20
2	B	58/80 (72%)	55 (95%)	3 (5%)	0	100	100
3	C	19/87 (22%)	17 (90%)	1 (5%)	1 (5%)	1	15
8	H	267/362 (74%)	187 (70%)	47 (18%)	33 (12%)	0	4
9	I	151/184 (82%)	114 (76%)	27 (18%)	10 (7%)	1	12
10	J	51/189 (27%)	49 (96%)	2 (4%)	0	100	100
11	K	81/142 (57%)	72 (89%)	6 (7%)	3 (4%)	2	20
12	L	125/127 (98%)	101 (81%)	12 (10%)	12 (10%)	0	7
13	M	82/113 (73%)	65 (79%)	11 (13%)	6 (7%)	1	10
14	N	67/120 (56%)	61 (91%)	2 (3%)	4 (6%)	1	13
15	O	35/51 (69%)	25 (71%)	5 (14%)	5 (14%)	0	3
All	All	1424/1945 (73%)	1180 (83%)	153 (11%)	91 (6%)	2	12

All (91) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	18	PRO
1	A	148	VAL
1	A	277	ALA
1	A	411	ARG
1	A	413	GLN
1	A	449	LYS
8	H	3	ARG
8	H	28	ALA
8	H	55	LYS
8	H	58	HIS
8	H	60	THR
8	H	64	SER
8	H	74	ILE
8	H	102	PRO
8	H	146	PRO
8	H	199	TRP
8	H	215	ILE
8	H	222	VAL
8	H	244	LEU
9	I	67	ILE
9	I	123	PRO
12	L	23	PRO
12	L	24	SER
12	L	85	VAL
13	M	24	SER
13	M	26	LYS
13	M	79	ARG
14	N	14	LYS
14	N	39	PRO
15	O	22	PRO
15	O	23	LEU
1	A	24	PHE
1	A	61	VAL
1	A	67	PHE
1	A	276	ARG
1	A	446	LEU
8	H	89	ALA
8	H	98	ARG
8	H	103	THR
8	H	107	ARG
8	H	110	ASN
8	H	132	ALA
8	H	173	GLY

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
8	H	264	SER
9	I	25	SER
9	I	37	ASN
9	I	54	HIS
9	I	113	TYR
11	K	62	VAL
12	L	6	LEU
12	L	11	ASP
12	L	45	ILE
12	L	87	LYS
12	L	96	PRO
13	M	78	LYS
14	N	4	VAL
14	N	37	SER
15	O	35	ILE
1	A	101	LYS
1	A	226	SER
1	A	487	PRO
1	A	489	ALA
3	C	60	ASP
8	H	54	GLU
8	H	70	ALA
8	H	96	GLY
8	H	187	LEU
8	H	253	ALA
9	I	71	ALA
9	I	107	LEU
12	L	36	SER
12	L	46	LYS
12	L	86	THR
13	M	25	PHE
13	M	90	PHE
15	O	6	SER
15	O	34	THR
1	A	410	ARG
8	H	101	ALA
8	H	131	VAL
8	H	200	THR
8	H	262	TRP
9	I	143	PRO
11	K	109	LYS
1	A	346	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
11	K	131	ASP
12	L	97	ILE
8	H	196	ASN
8	H	212	ASP
9	I	39	TRP
8	H	86	GLY

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	412/412 (100%)	386 (94%)	26 (6%)	16	37
2	B	50/67 (75%)	48 (96%)	2 (4%)	28	49
3	C	19/73 (26%)	18 (95%)	1 (5%)	20	41
8	H	209/288 (73%)	189 (90%)	20 (10%)	8	25
9	I	124/146 (85%)	114 (92%)	10 (8%)	11	31
10	J	44/154 (29%)	42 (96%)	2 (4%)	24	46
11	K	74/118 (63%)	70 (95%)	4 (5%)	20	41
12	L	110/110 (100%)	101 (92%)	9 (8%)	10	31
13	M	74/97 (76%)	69 (93%)	5 (7%)	14	36
14	N	62/105 (59%)	59 (95%)	3 (5%)	23	44
15	O	33/46 (72%)	30 (91%)	3 (9%)	9	27
All	All	1211/1616 (75%)	1126 (93%)	85 (7%)	16	35

All (85) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	LEU
1	A	26	LYS
1	A	47	GLN
1	A	75	GLU
1	A	79	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	80	LEU
1	A	121	LYS
1	A	128	TYR
1	A	148	VAL
1	A	154	ASN
1	A	188	VAL
1	A	194	VAL
1	A	227	LYS
1	A	229	LYS
1	A	268	VAL
1	A	305	TYR
1	A	403	GLN
1	A	410	ARG
1	A	412	GLU
1	A	413	GLN
1	A	414	ASN
1	A	415	VAL
1	A	449	LYS
1	A	454	VAL
1	A	480	LEU
1	A	484	LEU
2	B	52	LYS
2	B	76	ARG
3	C	64	VAL
8	H	35	VAL
8	H	43	ASN
8	H	46	LYS
8	H	48	GLN
8	H	74	ILE
8	H	90	PHE
8	H	98	ARG
8	H	102	PRO
8	H	103	THR
8	H	119	ARG
8	H	131	VAL
8	H	140	HIS
8	H	145	ILE
8	H	159	ILE
8	H	161	LYS
8	H	164	GLU
8	H	201	GLN
8	H	233	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
8	H	243	HIS
8	H	244	LEU
9	I	3	ARG
9	I	36	ILE
9	I	43	LYS
9	I	67	ILE
9	I	72	GLN
9	I	79	THR
9	I	94	LEU
9	I	107	LEU
9	I	108	ASP
9	I	112	LEU
10	J	1	MET
10	J	53	LYS
11	K	65	GLN
11	K	74	LYS
11	K	100	LYS
11	K	120	LYS
12	L	37	LYS
12	L	52	ARG
12	L	57	LEU
12	L	64	LYS
12	L	78	PHE
12	L	86	THR
12	L	87	LYS
12	L	122	LYS
12	L	125	LYS
13	M	20	LEU
13	M	28	ARG
13	M	38	LYS
13	M	47	ASP
13	M	86	LYS
14	N	9	LEU
14	N	17	LEU
14	N	34	GLN
15	O	17	LYS
15	O	22	PRO
15	O	23	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	62	ASN
1	A	87	ASN
1	A	95	GLN
1	A	110	GLN
1	A	320	ASN
1	A	324	HIS
1	A	403	GLN
1	A	481	ASN
8	H	43	ASN
8	H	87	GLN
8	H	196	ASN
8	H	201	GLN
8	H	237	GLN
9	I	64	ASN
9	I	96	GLN
9	I	120	ASN
9	I	121	GLN
9	I	125	GLN
11	K	137	ASN
12	L	91	ASN
12	L	98	ASN
13	M	21	HIS
13	M	57	GLN
13	M	80	ASN
14	N	61	GLN
15	O	33	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	D	62/63 (98%)	23 (37%)	9 (14%)
5	E	33/34 (97%)	7 (21%)	2 (6%)
6	F	24/25 (96%)	0	0
7	G	17/18 (94%)	1 (5%)	0
All	All	136/140 (97%)	31 (22%)	11 (8%)

All (31) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	D	48	A
4	D	49	G
4	D	56	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	D	59	A
4	D	62	C
4	D	63	G
4	D	64	U
4	D	66	A
4	D	68	G
4	D	70	G
4	D	82	U
4	D	83	C
4	D	84	C
4	D	85	G
4	D	86	U
4	D	87	G
4	D	88	A
4	D	90	U
4	D	91	C
4	D	92	A
4	D	94	C
4	D	97	A
4	D	98	U
5	E	533	A
5	E	534	G
5	E	556	A
5	E	557	A
5	E	558	G
5	E	560	A
5	E	561	C
7	G	1922	U

All (11) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	D	48	A
4	D	55	U
4	D	63	G
4	D	65	A
4	D	69	U
4	D	89	A
4	D	90	U
4	D	93	U
4	D	96	A
5	E	532	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	E	560	A

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.

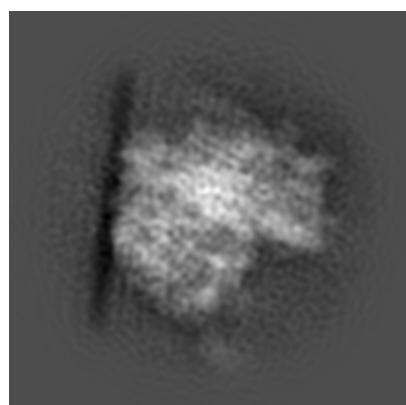
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1669. These allow visual inspection of the internal detail of the map and identification of artifacts.

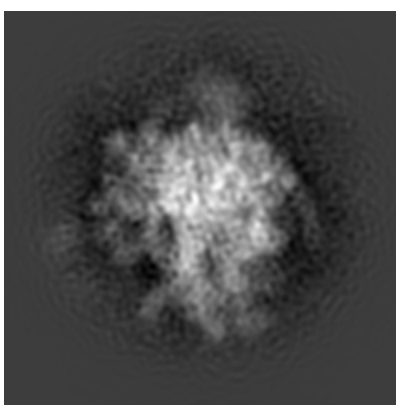
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

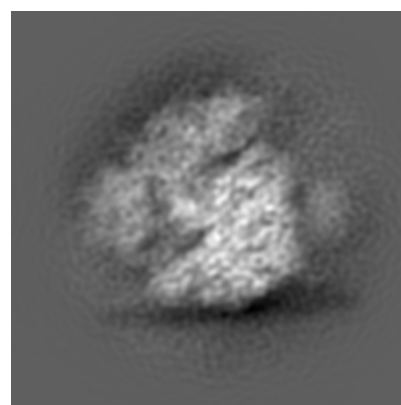
6.1.1 Primary map



X



Y

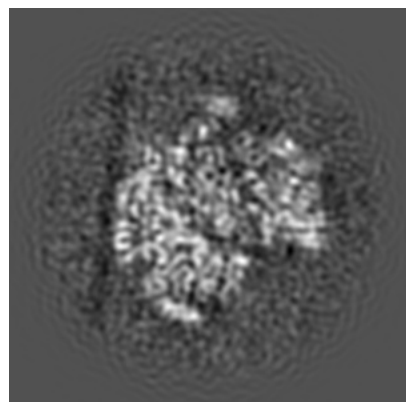


Z

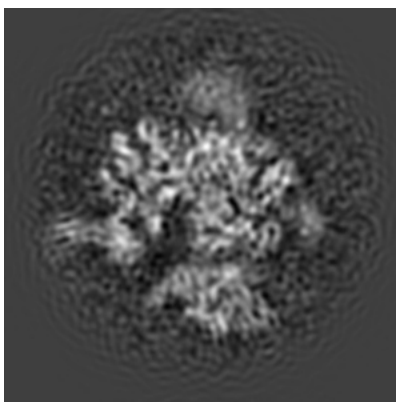
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

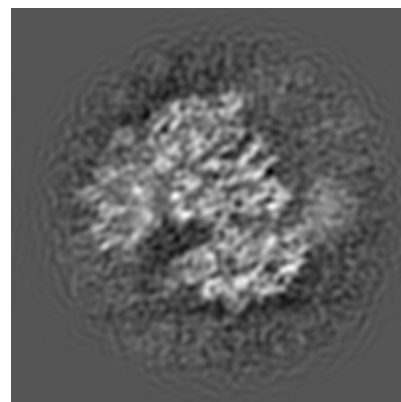
6.2.1 Primary map



X Index: 184



Y Index: 184

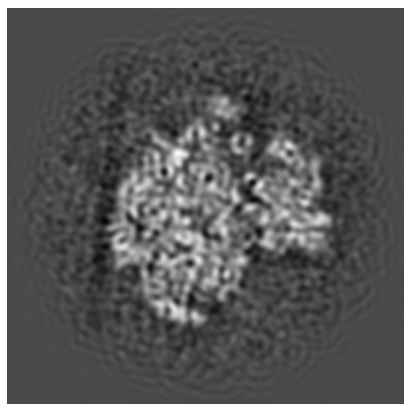


Z Index: 184

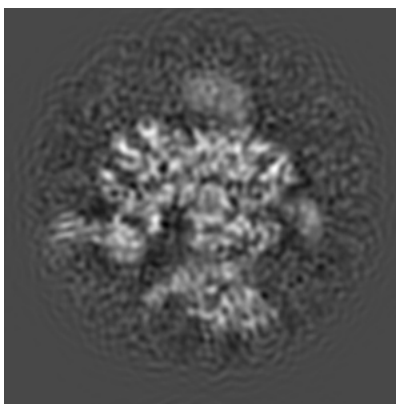
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

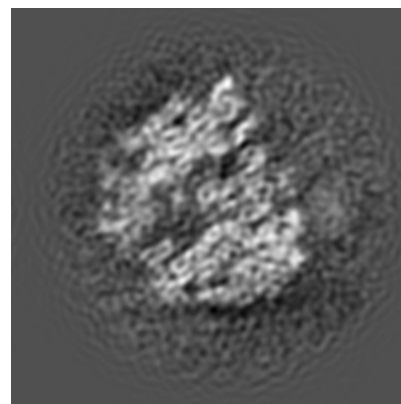
6.3.1 Primary map



X Index: 188



Y Index: 187

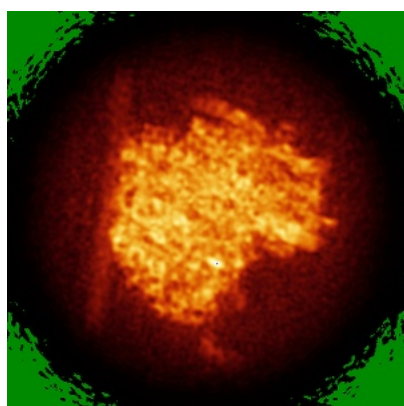


Z Index: 172

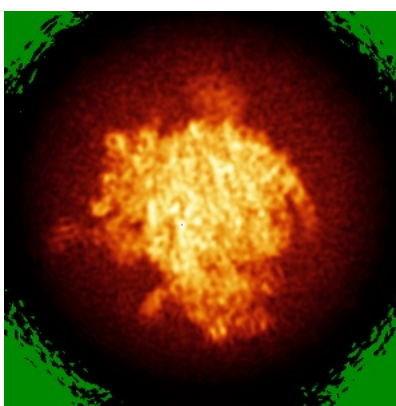
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

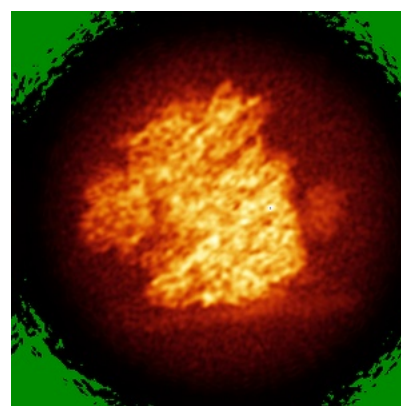
6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.75. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

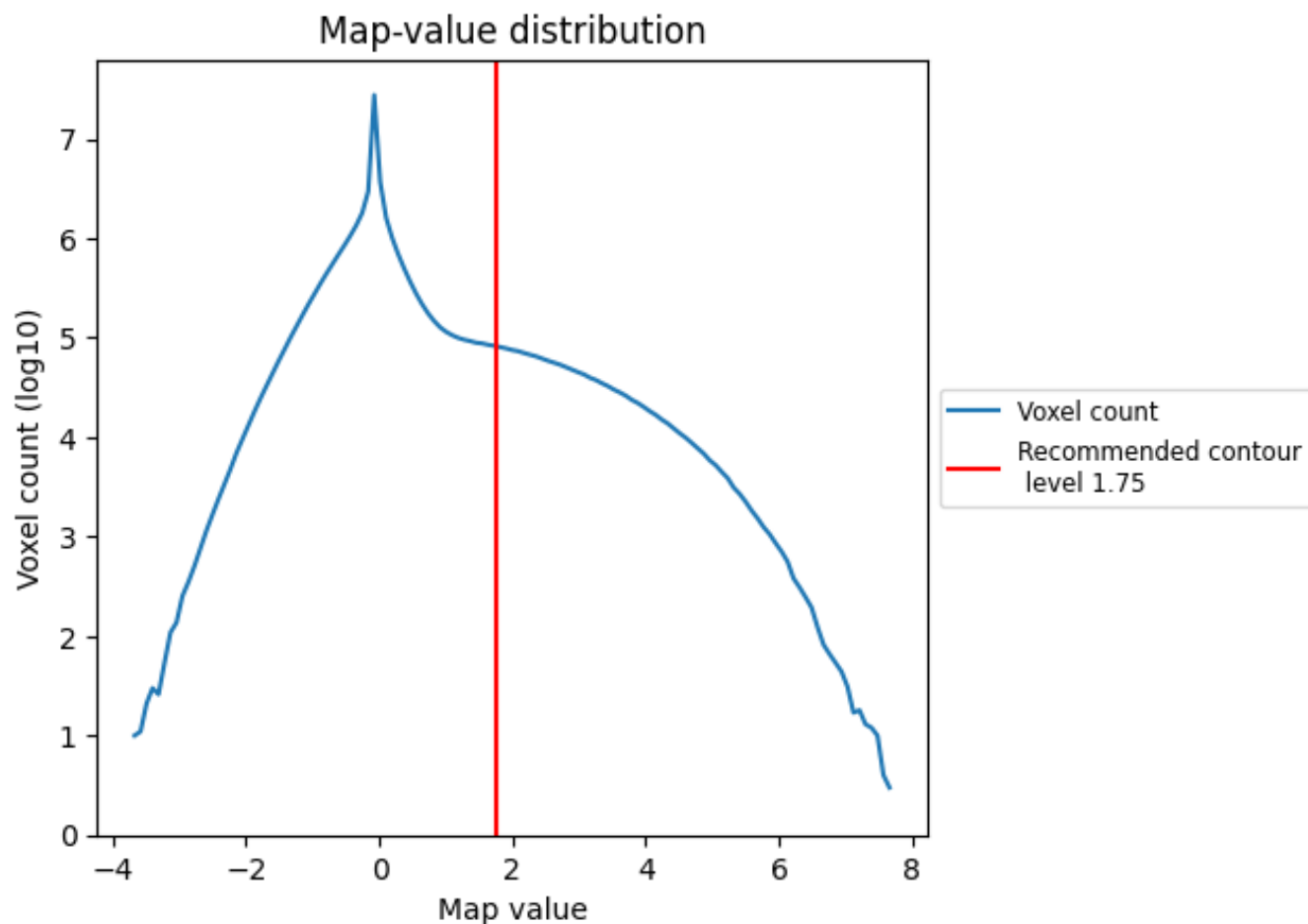
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

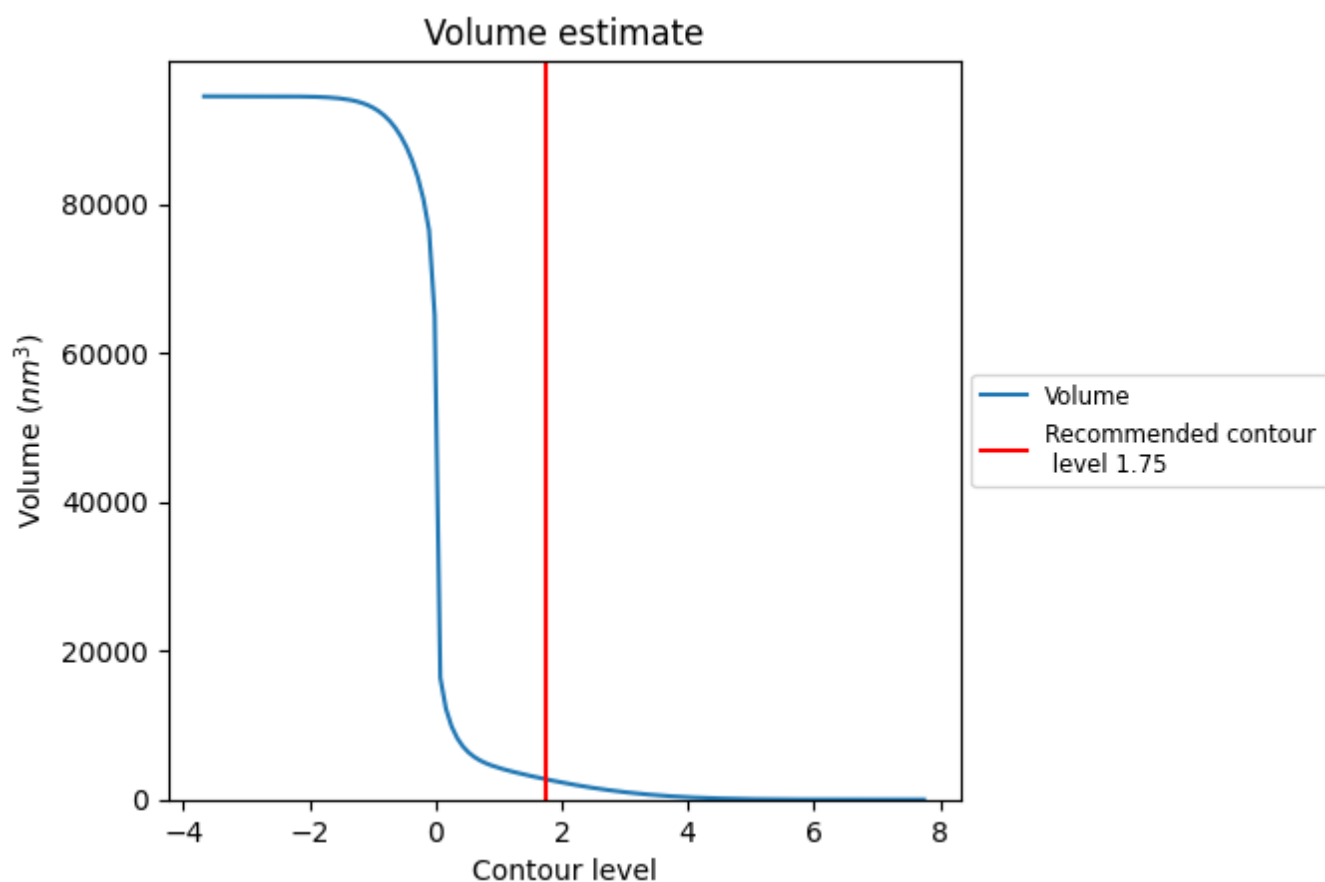
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

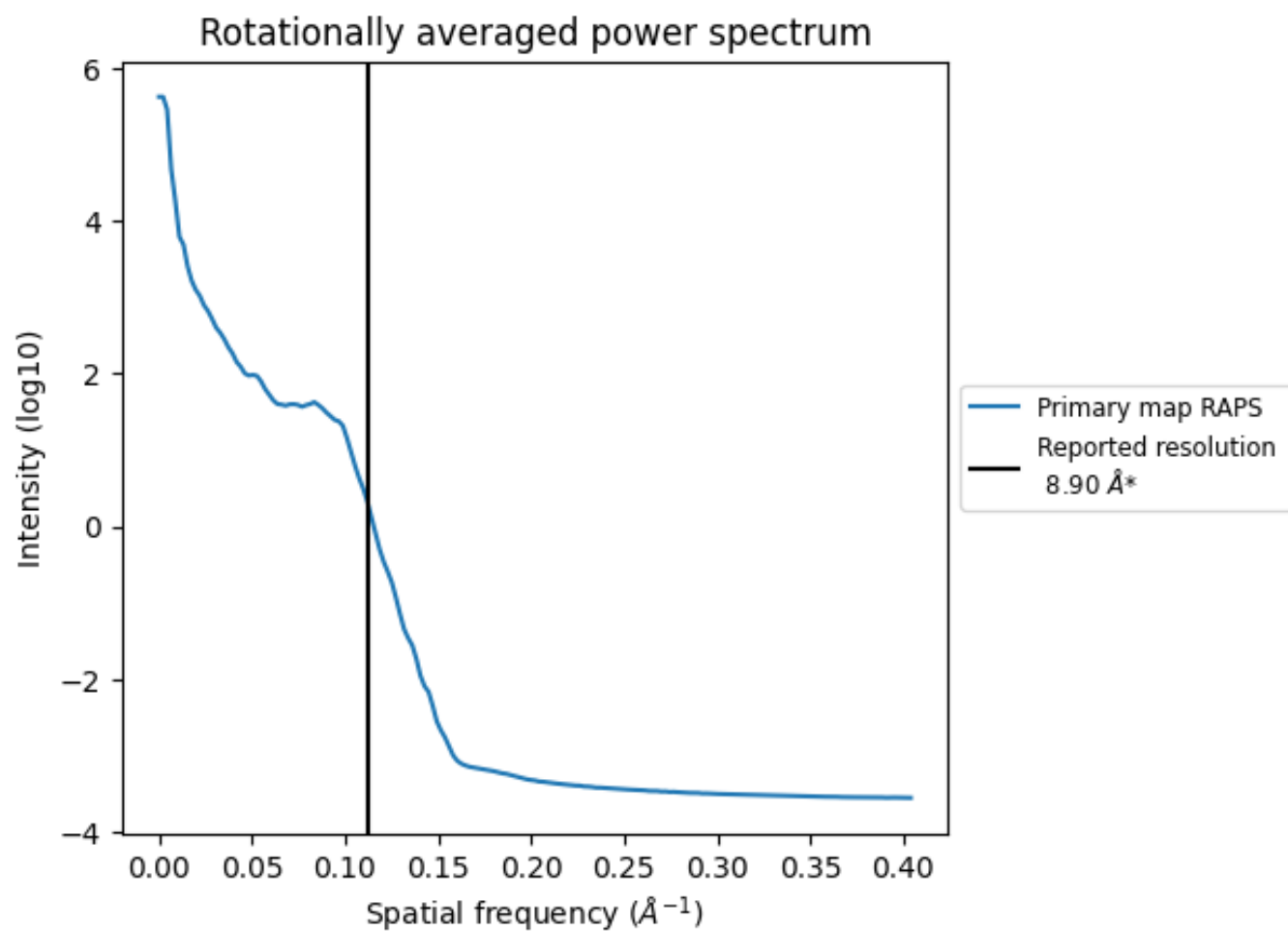
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2728 nm³; this corresponds to an approximate mass of 2464 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.112 Å⁻¹

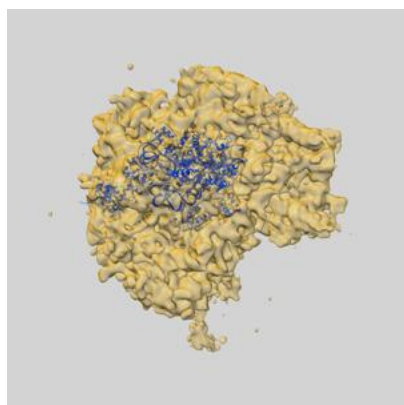
8 Fourier-Shell correlation

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

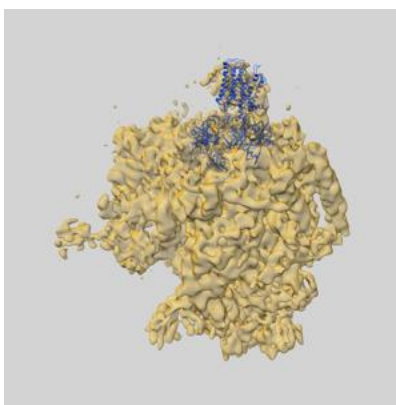
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-1669 and PDB model 2WWA. Per-residue inclusion information can be found in section 3 on page 7.

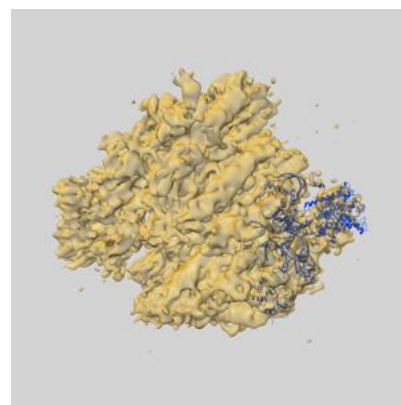
9.1 Map-model overlay [i](#)



X



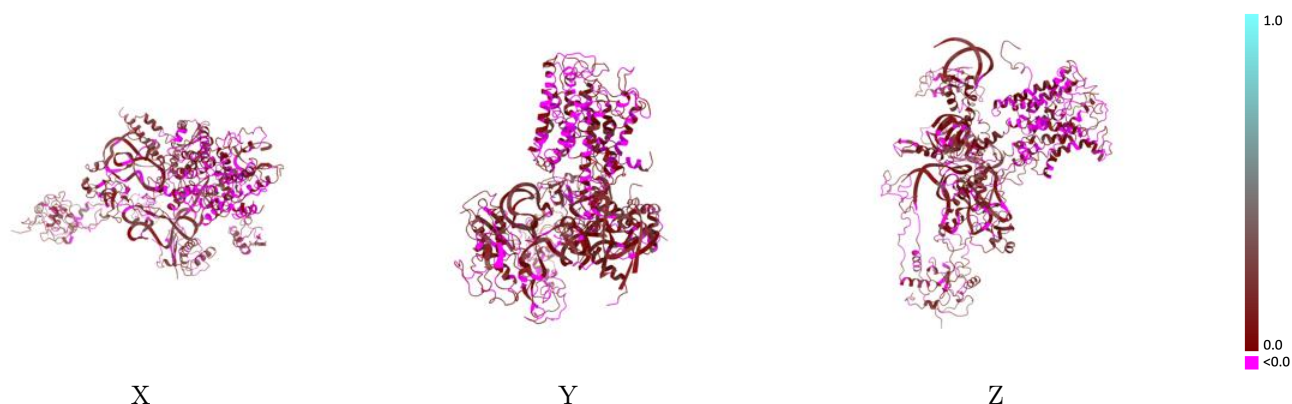
Y



Z

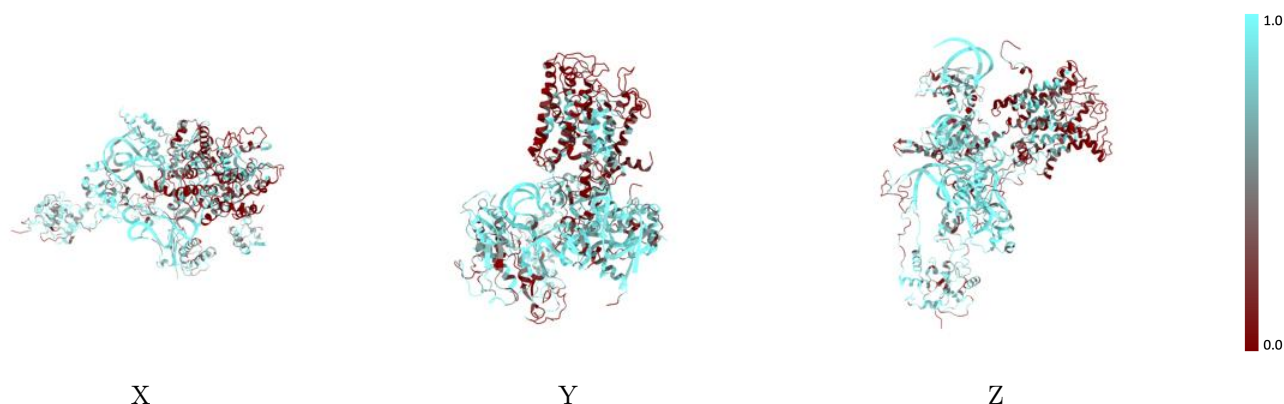
The images above show the 3D surface view of the map at the recommended contour level 1.75 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



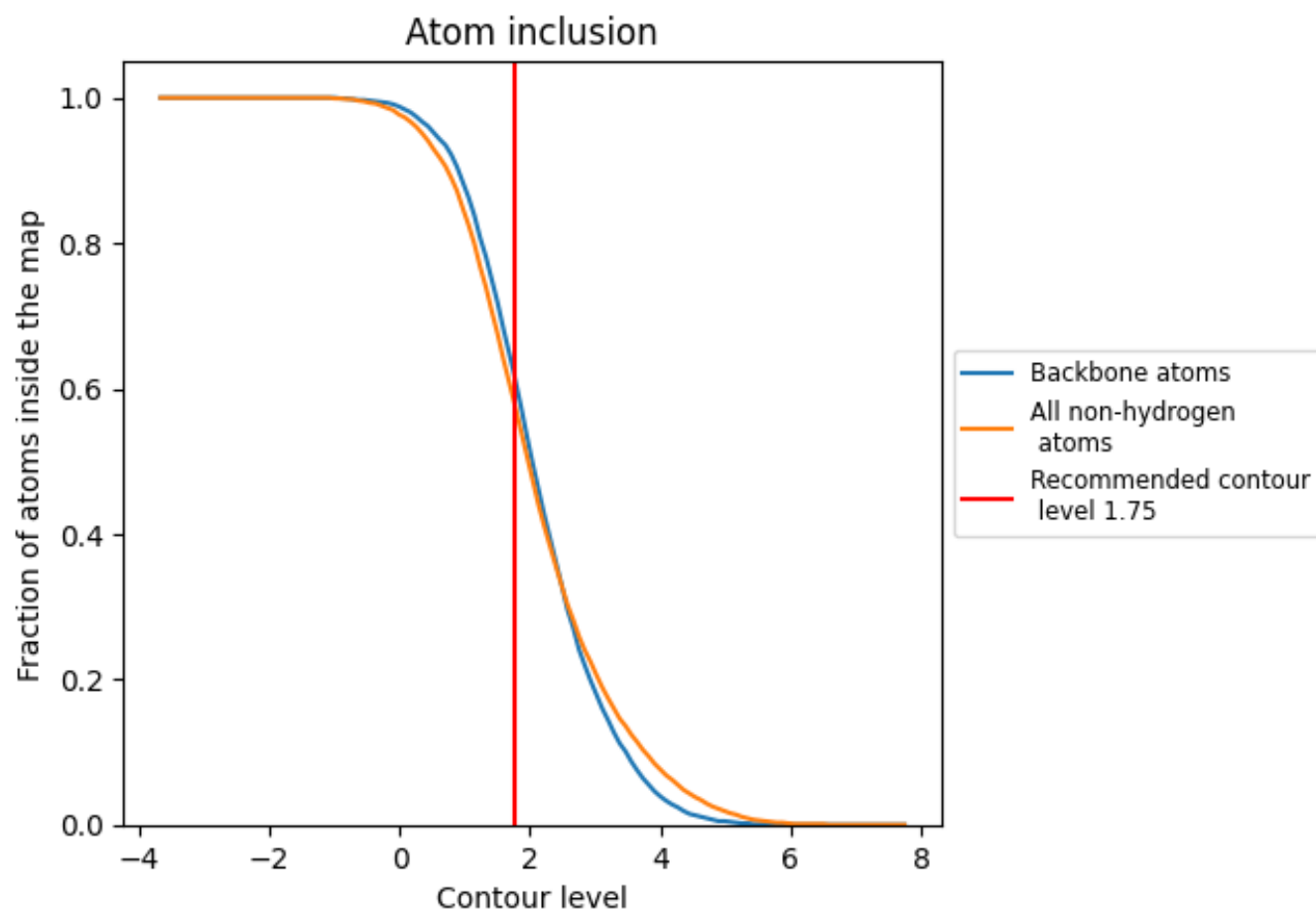
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (1.75).

9.4 Atom inclusion [i](#)



At the recommended contour level, 62% of all backbone atoms, 58% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (1.75) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5840	 0.0690
A	 0.3310	 0.0200
B	 0.2370	 -0.0190
C	 0.0810	 -0.0380
D	 0.8430	 0.0880
E	 0.9000	 0.1320
F	 0.8730	 0.1230
G	 0.8630	 0.1460
H	 0.6350	 0.0780
I	 0.5590	 0.0630
J	 0.6270	 0.1170
K	 0.6260	 0.0860
L	 0.7490	 0.0990
M	 0.6260	 0.0860
N	 0.7540	 0.1180
O	 0.4310	 0.0690

