



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 04:17 PM UTC

PDB ID : 2WW9 / pdb_00002ww9
EMDB ID : EMD-1667
Title : Cryo-EM structure of the active 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 : 8.60 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:

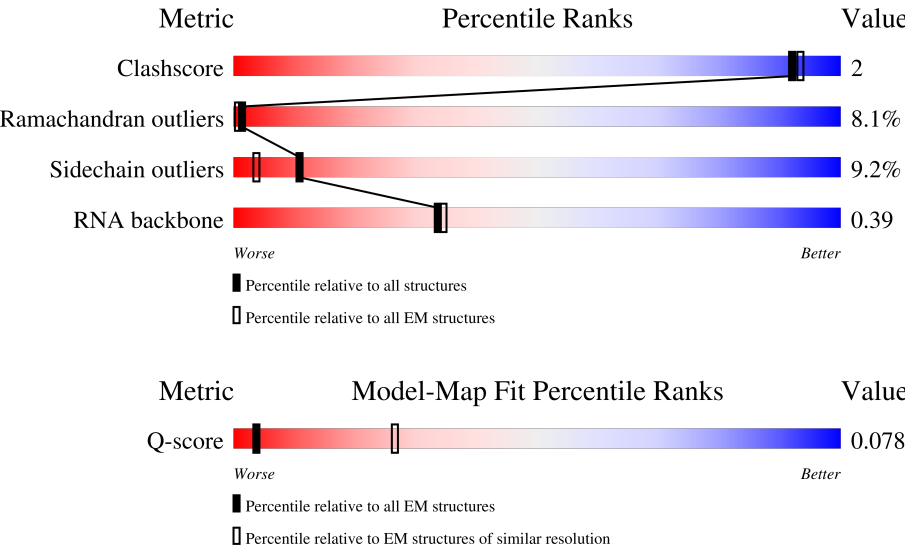
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 8.60 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	292 (8.10 - 9.10)

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	37% 82% 14% • •
2	B	80	14% 66% 8% • 25%
3	C	87	15% 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		

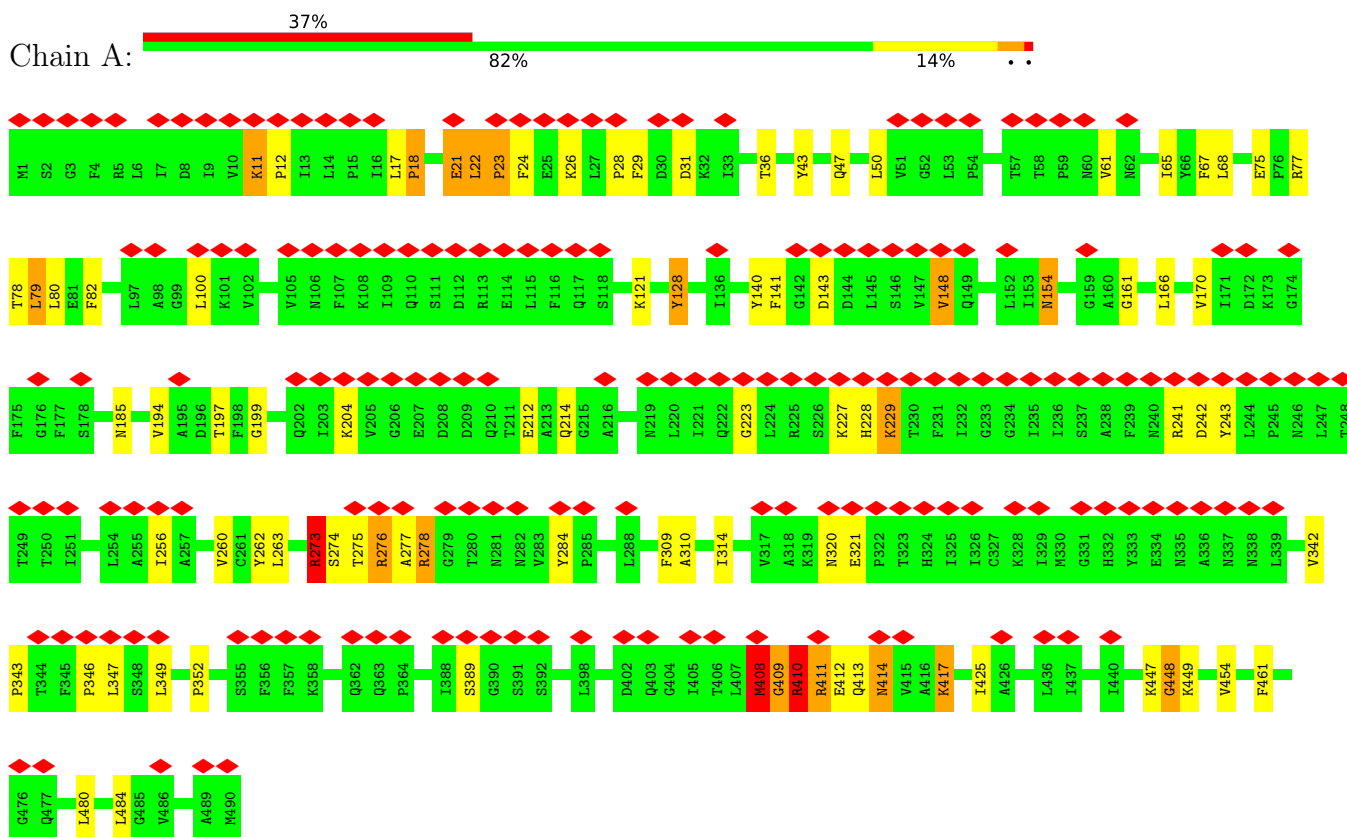
- Molecule 15 is a protein called 60S RIBOSOMAL PROTEIN L39.

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

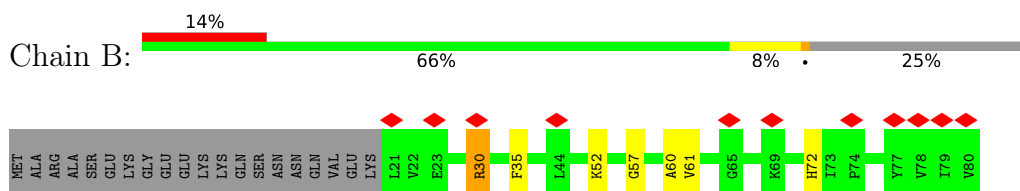
3 Residue-property plots

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

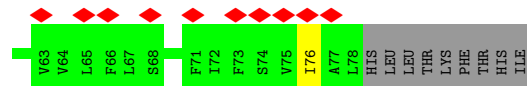
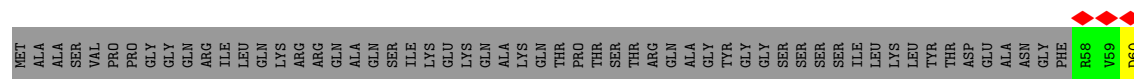


• Molecule 2: PROTEIN TRANSPORT PROTEIN SSS1

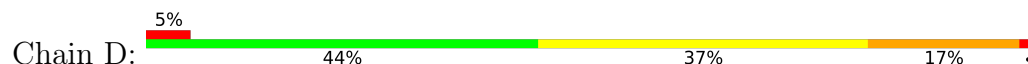


• Molecule 3: PROTEIN TRANSPORT PROTEIN SEB2





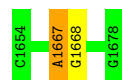
• Molecule 4: 25S rRNA



• Molecule 5: 25S rRNA



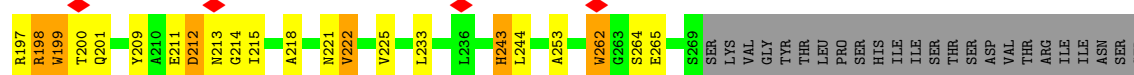
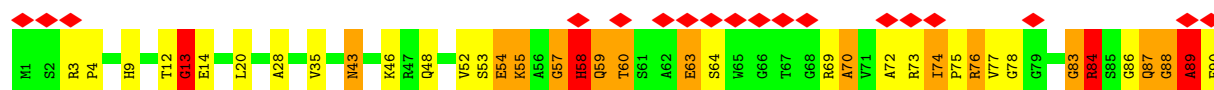
• Molecule 6: 25S rRNA

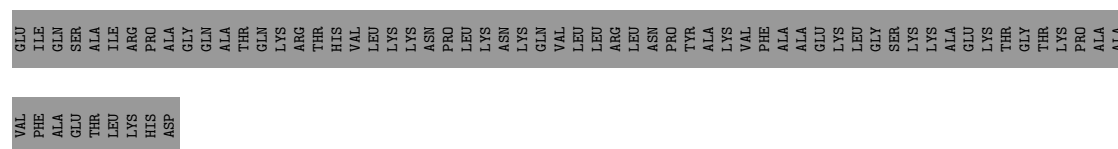


• Molecule 7: 25S rRNA

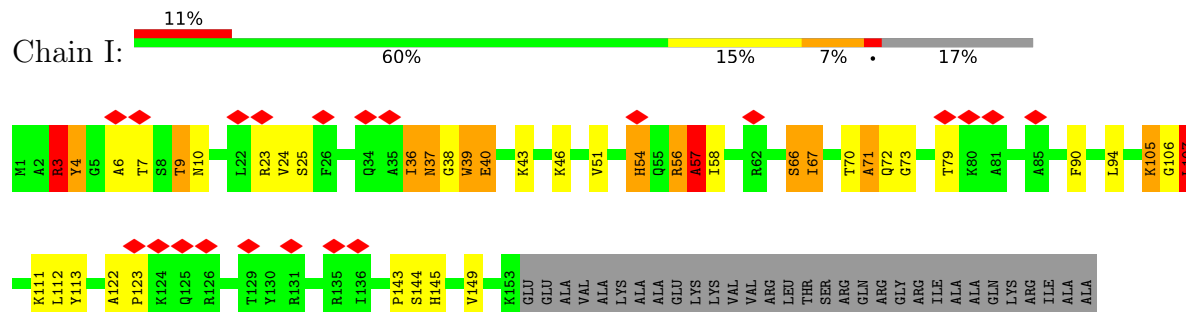


• Molecule 8: 60S RIBOSOMAL PROTEIN L4-B

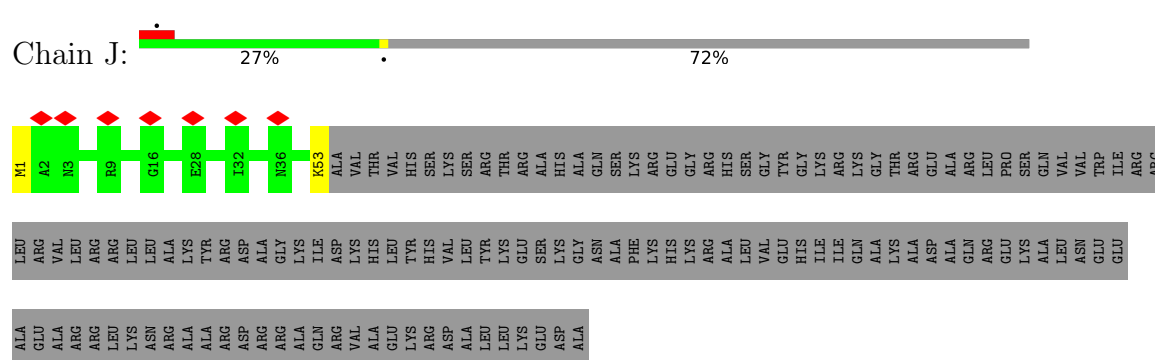




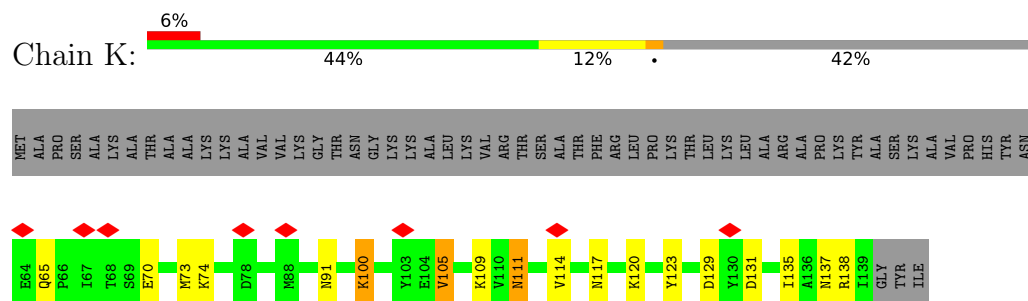
• Molecule 9: 60S RIBOSOMAL PROTEIN L17-A



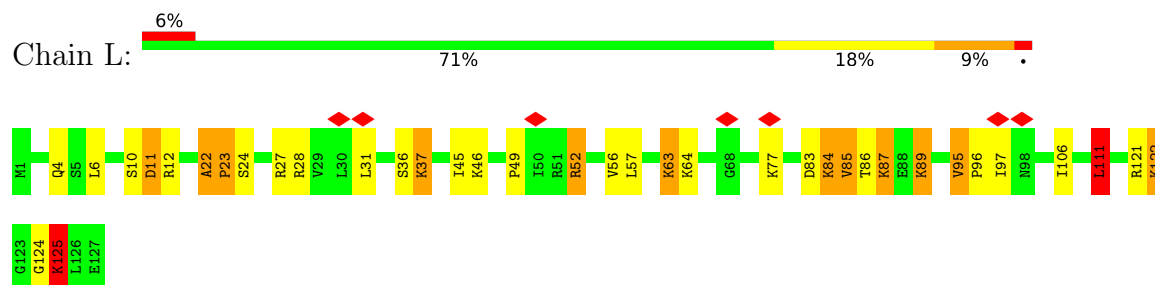
• Molecule 10: 60S RIBOSOMAL PROTEIN L19



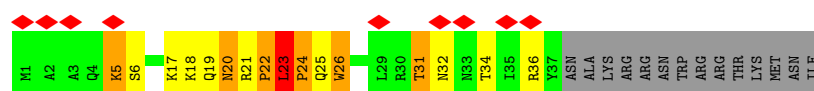
• Molecule 11: 60S RIBOSOMAL PROTEIN L25



• Molecule 12: 60S RIBOSOMAL PROTEIN L26-A



• Molecule 13: 60S RIBOSOMAL PROTEIN L31-A



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	35800	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	9.043	Depositor
Minimum map value	-4.082	Depositor
Average map value	0.051	Depositor
Map value standard deviation	0.671	Depositor
Recommended contour level	1.5	Depositor
Map size ($\text{\AA}$)	455.4, 455.4, 455.4	wwPDB
Map dimensions	368, 368, 368	wwPDB
Map angles ($^\circ$)	90, 90, 90	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	1.17	0/3848	1.56	44/5234 (0.8%)
2	B	1.14	0/481	1.59	4/648 (0.6%)
3	C	1.16	0/164	1.53	0/222
4	D	0.92	0/1508	1.27	9/2348 (0.4%)
5	E	0.87	0/833	1.11	3/1298 (0.2%)
6	F	0.89	0/599	1.04	1/932 (0.1%)
7	G	0.88	0/421	0.97	0/653
8	H	1.26	0/2079	1.93	73/2817 (2.6%)
9	I	1.30	0/1235	1.91	42/1662 (2.5%)
10	J	1.28	0/412	1.45	0/551
11	K	1.16	0/670	1.53	8/903 (0.9%)
12	L	1.27	0/1013	1.76	32/1351 (2.4%)
13	M	1.37	0/719	1.73	17/959 (1.8%)
14	N	1.33	1/549 (0.2%)	2.02	23/733 (3.1%)
15	O	1.33	0/321	1.82	9/426 (2.1%)
All	All	1.17	1/14852 (0.0%)	1.60	265/20737 (1.3%)

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	9
2	B	0	1
4	D	0	7
5	E	0	2
6	F	0	1
8	H	0	7
9	I	0	2
11	K	0	2
12	L	0	6
14	N	0	3

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
15	O	0	5
All	All	0	45

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	N	69	LEU	C-O	-11.53	1.00	1.23

All (265) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	532	A	P-O3'-C3'	14.15	141.42	120.20
9	I	56	ARG	CA-C-N	12.43	144.07	121.70
9	I	56	ARG	C-N-CA	12.43	144.07	121.70
8	H	184	SER	CA-C-N	11.97	143.25	121.70
8	H	184	SER	C-N-CA	11.97	143.25	121.70
4	D	69	U	P-O3'-C3'	11.49	137.43	120.20
8	H	75	PRO	CA-C-N	10.81	141.17	121.70
8	H	75	PRO	C-N-CA	10.81	141.17	121.70
4	D	93	U	P-O3'-C3'	10.70	136.26	120.20
14	N	36	LEU	N-CA-C	-10.35	98.02	110.44
4	D	90	U	P-O3'-C3'	10.26	135.58	120.20
4	D	55	U	P-O3'-C3'	10.06	135.29	120.20
9	I	36	ILE	CA-C-N	9.83	139.40	121.70
9	I	36	ILE	C-N-CA	9.83	139.40	121.70
8	H	54	GLU	CA-C-N	9.80	139.33	121.70
8	H	54	GLU	C-N-CA	9.80	139.33	121.70
14	N	39	PRO	CA-C-N	9.76	139.26	121.70
14	N	39	PRO	C-N-CA	9.76	139.26	121.70
8	H	101	ALA	CA-C-N	9.47	131.68	119.84
8	H	101	ALA	C-N-CA	9.47	131.68	119.84
4	D	65	A	P-O3'-C3'	9.47	134.40	120.20
4	D	96	A	P-O3'-C3'	9.38	134.27	120.20
12	L	84	LYS	CA-C-N	9.35	138.54	121.70
12	L	84	LYS	C-N-CA	9.35	138.54	121.70
9	I	105	LYS	N-CA-C	9.22	121.09	111.14
12	L	10	SER	CA-C-N	9.14	138.15	121.70
12	L	10	SER	C-N-CA	9.14	138.15	121.70
9	I	36	ILE	N-CA-C	8.85	119.65	110.62
8	H	214	GLY	CA-C-N	8.83	137.59	121.70
8	H	214	GLY	C-N-CA	8.83	137.59	121.70
13	M	77	ARG	CA-C-N	8.46	136.93	121.70

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	M	77	ARG	C-N-CA	8.46	136.93	121.70
8	H	57	GLY	CA-C-N	8.36	136.75	121.70
8	H	57	GLY	C-N-CA	8.36	136.75	121.70
8	H	159	ILE	CA-C-N	8.32	136.68	121.70
8	H	159	ILE	C-N-CA	8.32	136.68	121.70
8	H	86	GLY	CA-C-N	8.18	136.43	121.70
8	H	86	GLY	C-N-CA	8.18	136.43	121.70
5	E	560	A	P-O3'-C3'	8.11	132.36	120.20
4	D	63	G	P-O3'-C3'	8.06	132.29	120.20
14	N	3	GLY	CA-C-N	7.97	136.05	121.70
14	N	3	GLY	C-N-CA	7.97	136.05	121.70
8	H	89	ALA	N-CA-CB	7.97	122.36	110.40
6	F	1667	A	P-O3'-C3'	7.97	132.15	120.20
4	D	89	A	P-O3'-C3'	7.95	132.12	120.20
8	H	88	GLY	CA-C-N	7.63	135.44	121.70
8	H	88	GLY	C-N-CA	7.63	135.44	121.70
8	H	43	ASN	CA-CB-CG	7.58	120.18	112.60
5	E	532	A	C2'-C3'-O3'	7.56	120.83	109.50
8	H	212	ASP	CA-C-N	7.51	135.22	121.70
8	H	212	ASP	C-N-CA	7.51	135.22	121.70
14	N	50	SER	N-CA-C	-7.47	104.30	113.41
14	N	13	SER	CA-C-N	7.43	135.08	121.70
14	N	13	SER	C-N-CA	7.43	135.08	121.70
9	I	66	SER	CA-C-N	7.33	134.90	121.70
9	I	66	SER	C-N-CA	7.33	134.90	121.70
8	H	60	THR	N-CA-CB	7.27	122.77	110.49
8	H	102	PRO	N-CA-C	7.21	127.31	112.47
12	L	11	ASP	CA-CB-CG	7.19	119.79	112.60
8	H	73	ARG	N-CA-C	-7.13	104.73	113.50
8	H	105	THR	CA-C-N	7.11	134.50	121.70
8	H	105	THR	C-N-CA	7.11	134.50	121.70
9	I	37	ASN	N-CA-CB	7.08	122.53	110.50
9	I	9	THR	CA-C-N	7.07	134.43	121.70
9	I	9	THR	C-N-CA	7.07	134.43	121.70
15	O	31	THR	CA-C-N	7.00	134.31	121.70
15	O	31	THR	C-N-CA	7.00	134.31	121.70
9	I	56	ARG	CB-CA-C	6.99	124.32	110.42
9	I	36	ILE	N-CA-CB	6.96	120.01	110.54
14	N	67	ARG	N-CA-CB	-6.95	99.95	110.73
14	N	69	LEU	CA-C-O	-6.94	109.00	120.80
1	A	411	ARG	N-CA-CB	6.87	122.10	110.49
14	N	36	LEU	CA-C-N	6.86	134.05	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	6.86	134.05	121.70
9	I	3	ARG	CA-C-N	6.85	134.03	121.70
9	I	3	ARG	C-N-CA	6.85	134.03	121.70
12	L	83	ASP	CA-C-N	6.85	134.04	121.70
12	L	83	ASP	C-N-CA	6.85	134.04	121.70
12	L	85	VAL	CA-C-N	6.83	134.00	121.70
12	L	85	VAL	C-N-CA	6.83	134.00	121.70
1	A	154	ASN	CA-CB-CG	6.82	119.42	112.60
8	H	58	HIS	N-CA-CB	6.79	122.05	110.50
2	B	72	HIS	CA-C-N	6.74	124.48	120.24
2	B	72	HIS	C-N-CA	6.74	124.48	120.24
9	I	105	LYS	CA-C-N	6.72	133.79	121.70
9	I	105	LYS	C-N-CA	6.72	133.79	121.70
9	I	39	TRP	N-CA-CB	6.70	121.89	110.50
8	H	88	GLY	N-CA-C	-6.68	103.23	111.45
13	M	64	VAL	CA-C-N	6.67	129.52	120.38
13	M	64	VAL	C-N-CA	6.67	129.52	120.38
8	H	60	THR	N-CA-C	-6.62	96.69	110.80
8	H	12	THR	CA-C-N	6.60	133.59	121.70
8	H	12	THR	C-N-CA	6.60	133.59	121.70
1	A	414	ASN	CA-CB-CG	6.56	119.16	112.60
12	L	27	ARG	N-CA-C	-6.55	105.03	113.16
11	K	137	ASN	N-CA-C	-6.55	104.60	112.59
1	A	278	ARG	N-CA-C	-6.54	96.87	110.80
1	A	349	LEU	N-CA-C	-6.53	104.94	113.17
12	L	95	VAL	N-CA-CB	6.45	120.23	111.21
1	A	408	MET	N-CA-CB	6.44	121.38	110.49
1	A	409	GLY	CA-C-N	6.43	133.27	121.70
1	A	409	GLY	C-N-CA	6.43	133.27	121.70
1	A	273	ARG	CA-C-N	6.42	133.81	121.54
1	A	273	ARG	C-N-CA	6.42	133.81	121.54
9	I	7	THR	N-CA-C	6.42	120.69	112.34
9	I	36	ILE	CA-C-O	-6.42	114.27	120.95
11	K	111	ASN	CA-CB-CG	6.42	119.02	112.60
13	M	24	SER	CA-C-N	6.41	133.23	121.70
13	M	24	SER	C-N-CA	6.41	133.23	121.70
8	H	84	ARG	N-CA-CB	6.35	121.30	110.50
8	H	211	GLU	CA-C-N	6.35	133.68	121.54
8	H	211	GLU	C-N-CA	6.35	133.68	121.54
13	M	80	ASN	CA-C-N	6.27	132.98	121.70
13	M	80	ASN	C-N-CA	6.27	132.98	121.70
8	H	63	GLU	N-CA-C	-6.26	97.47	110.80

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	23	PRO	CA-C-N	6.24	132.93	121.70
1	A	23	PRO	C-N-CA	6.24	132.93	121.70
9	I	38	GLY	CA-C-N	6.20	132.85	121.70
9	I	38	GLY	C-N-CA	6.20	132.85	121.70
8	H	59	GLN	CA-C-N	6.19	133.36	121.54
8	H	59	GLN	C-N-CA	6.19	133.36	121.54
14	N	34	GLN	CA-C-N	6.16	132.78	121.70
14	N	34	GLN	C-N-CA	6.16	132.78	121.70
14	N	14	LYS	N-CA-CB	6.14	120.93	110.50
8	H	262	TRP	CA-C-N	6.13	132.74	121.70
8	H	262	TRP	C-N-CA	6.13	132.74	121.70
8	H	185	LYS	N-CA-C	6.11	128.12	111.00
11	K	129	ASP	CA-C-N	6.11	128.38	120.44
11	K	129	ASP	C-N-CA	6.11	128.38	120.44
1	A	276	ARG	N-CA-CB	6.09	120.79	110.49
1	A	410	ARG	N-CA-CB	6.07	120.82	110.50
15	O	5	LYS	CA-C-N	6.07	132.62	121.70
15	O	5	LYS	C-N-CA	6.07	132.62	121.70
8	H	55	LYS	N-CA-C	6.05	127.93	111.00
14	N	56	THR	N-CA-CB	6.04	119.10	110.16
8	H	158	SER	CA-C-N	6.03	128.58	120.50
8	H	158	SER	C-N-CA	6.03	128.58	120.50
8	H	13	GLY	CA-C-N	6.00	132.50	121.70
8	H	13	GLY	C-N-CA	6.00	132.50	121.70
14	N	4	VAL	N-CA-CB	5.99	121.69	111.50
12	L	63	LYS	N-CA-C	-5.99	103.25	110.44
13	M	21	HIS	N-CA-C	-5.99	106.30	113.97
1	A	417	LYS	N-CA-C	-5.98	106.15	113.50
9	I	70	THR	CA-C-N	5.94	132.40	121.70
9	I	70	THR	C-N-CA	5.94	132.40	121.70
12	L	89	LYS	N-CA-C	-5.92	100.54	109.95
8	H	155	ASP	CA-C-N	5.91	128.80	120.28
8	H	155	ASP	C-N-CA	5.91	128.80	120.28
8	H	173	GLY	CA-C-N	5.88	132.28	121.70
8	H	173	GLY	C-N-CA	5.88	132.28	121.70
8	H	20	LEU	CA-C-N	5.85	125.86	119.89
8	H	20	LEU	C-N-CA	5.85	125.86	119.89
1	A	141	PHE	CA-CB-CG	-5.85	107.95	113.80
12	L	124	GLY	CA-C-N	5.82	132.18	121.70
12	L	124	GLY	C-N-CA	5.82	132.18	121.70
1	A	320	ASN	CA-C-N	5.82	127.36	120.09
1	A	320	ASN	C-N-CA	5.82	127.36	120.09

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	L	37	LYS	N-CA-C	-5.82	107.17	114.56
8	H	175	HIS	CA-C-N	5.81	128.65	120.28
8	H	175	HIS	C-N-CA	5.81	128.65	120.28
9	I	4	TYR	CA-C-N	5.81	132.16	121.70
9	I	4	TYR	C-N-CA	5.81	132.16	121.70
11	K	138	ARG	N-CA-C	-5.80	105.10	114.09
12	L	84	LYS	N-CA-CB	5.79	120.34	110.50
13	M	26	LYS	N-CA-CB	5.76	120.23	110.49
8	H	64	SER	N-CA-C	-5.75	98.55	110.80
8	H	88	GLY	O-C-N	-5.75	119.34	123.08
9	I	56	ARG	N-CA-CB	5.74	120.18	110.49
2	B	60	ALA	CA-C-N	5.70	128.27	120.46
2	B	60	ALA	C-N-CA	5.70	128.27	120.46
8	H	83	GLY	CA-C-N	5.64	131.85	121.70
8	H	83	GLY	C-N-CA	5.64	131.85	121.70
15	O	5	LYS	CB-CA-C	5.62	121.60	110.42
9	I	6	ALA	CA-C-N	5.61	129.66	120.63
9	I	6	ALA	C-N-CA	5.61	129.66	120.63
1	A	413	GLN	CB-CA-C	5.60	121.56	110.42
9	I	73	GLY	CA-C-N	5.59	131.77	121.70
9	I	73	GLY	C-N-CA	5.59	131.77	121.70
13	M	25	PHE	N-CA-CB	5.56	119.95	110.50
8	H	213	ASN	CA-C-N	5.55	131.68	121.70
8	H	213	ASN	C-N-CA	5.55	131.68	121.70
8	H	199	TRP	N-CA-CB	5.53	119.83	110.49
8	H	243	HIS	CA-C-N	5.53	132.10	121.54
8	H	243	HIS	C-N-CA	5.53	132.10	121.54
8	H	198	ARG	CA-C-N	5.52	132.09	121.54
8	H	198	ARG	C-N-CA	5.52	132.09	121.54
12	L	23	PRO	CA-C-N	5.51	132.06	121.54
12	L	23	PRO	C-N-CA	5.51	132.06	121.54
1	A	100	LEU	N-CA-C	-5.49	106.42	113.23
9	I	106	GLY	CA-C-N	5.49	132.02	121.54
9	I	106	GLY	C-N-CA	5.49	132.02	121.54
13	M	78	LYS	N-CA-CB	5.39	119.67	110.50
1	A	276	ARG	N-CA-C	-5.37	99.36	110.80
12	L	31	LEU	N-CA-C	-5.37	105.95	112.88
8	H	140	HIS	CA-CB-CG	5.35	119.15	113.80
12	L	111	LEU	N-CA-CB	5.33	117.88	110.04
9	I	57	ALA	N-CA-C	5.33	125.92	111.00
9	I	71	ALA	N-CA-CB	5.32	118.39	110.40
12	L	22	ALA	CA-C-N	5.31	126.48	119.84

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	L	22	ALA	C-N-CA	5.31	126.48	119.84
14	N	40	SER	CA-C-N	5.31	131.26	121.70
14	N	40	SER	C-N-CA	5.31	131.26	121.70
15	O	20	ASN	CA-CB-CG	5.31	117.91	112.60
1	A	448	GLY	N-CA-C	-5.30	107.79	115.27
14	N	37	SER	CA-C-N	5.30	131.24	121.70
14	N	37	SER	C-N-CA	5.30	131.24	121.70
9	I	56	ARG	O-C-N	-5.30	115.55	122.59
1	A	214	GLN	N-CA-C	-5.28	100.69	108.99
9	I	90	PHE	CA-CB-CG	5.28	119.08	113.80
1	A	75	GLU	N-CA-C	-5.27	98.16	109.81
8	H	103	THR	N-CA-CB	5.26	119.38	110.49
13	M	81	GLU	CA-C-N	5.26	127.33	120.28
13	M	81	GLU	C-N-CA	5.26	127.33	120.28
12	L	95	VAL	CA-C-N	5.25	126.40	119.84
12	L	95	VAL	C-N-CA	5.25	126.40	119.84
15	O	21	ARG	CA-C-O	-5.25	114.77	119.59
1	A	78	THR	CA-C-N	5.24	127.30	120.28
1	A	78	THR	C-N-CA	5.24	127.30	120.28
9	I	9	THR	CB-CA-C	5.23	120.82	110.42
15	O	19	GLN	CA-C-N	5.20	131.48	121.54
15	O	19	GLN	C-N-CA	5.20	131.48	121.54
1	A	275	THR	CA-C-N	5.20	131.47	121.54
1	A	275	THR	C-N-CA	5.20	131.47	121.54
1	A	223	GLY	CA-C-N	5.20	127.25	120.28
1	A	223	GLY	C-N-CA	5.20	127.25	120.28
8	H	70	ALA	N-CA-C	-5.18	99.77	110.80
8	H	212	ASP	CB-CA-C	5.18	120.73	110.42
1	A	410	ARG	CA-C-N	5.17	131.43	121.54
1	A	410	ARG	C-N-CA	5.17	131.43	121.54
12	L	125	LYS	N-CA-CB	5.17	119.29	110.50
8	H	9	HIS	CA-CB-CG	-5.16	108.64	113.80
13	M	49	VAL	N-CA-C	-5.16	100.88	108.11
9	I	145	HIS	N-CA-C	-5.16	102.15	110.14
14	N	67	ARG	NE-CZ-NH2	5.15	123.84	119.20
1	A	347	LEU	N-CA-C	-5.14	107.00	113.28
1	A	352	PRO	CA-C-O	-5.14	116.67	120.73
12	L	49	PRO	CA-C-N	5.12	127.47	120.35
12	L	49	PRO	C-N-CA	5.12	127.47	120.35
11	K	135	ILE	N-CA-C	-5.12	107.76	112.83
8	H	57	GLY	N-CA-C	-5.11	101.08	113.18
1	A	143	ASP	CA-CB-CG	5.09	117.69	112.60

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	L	12	ARG	CA-C-N	5.09	127.51	120.29
12	L	12	ARG	C-N-CA	5.09	127.51	120.29
1	A	263	LEU	CA-C-N	5.08	129.21	120.72
1	A	263	LEU	C-N-CA	5.08	129.21	120.72
4	D	65	A	C2'-C3'-O3'	5.08	121.31	113.70
8	H	222	VAL	N-CA-CB	5.08	118.31	111.21
1	A	29	PHE	CA-C-N	5.07	127.07	120.28
1	A	29	PHE	C-N-CA	5.07	127.07	120.28
1	A	461	PHE	CA-CB-CG	5.07	118.87	113.80
12	L	4	GLN	CA-C-N	5.06	130.81	121.70
12	L	4	GLN	C-N-CA	5.06	130.81	121.70
9	I	24	VAL	CA-C-N	5.05	131.20	121.54
9	I	24	VAL	C-N-CA	5.05	131.20	121.54
1	A	243	TYR	N-CA-CB	5.05	117.37	109.85
1	A	241	ARG	CA-C-N	5.04	127.03	120.28
1	A	241	ARG	C-N-CA	5.04	127.03	120.28
11	K	91	ASN	CA-C-N	5.03	127.02	120.28
11	K	91	ASN	C-N-CA	5.03	127.02	120.28
8	H	221	ASN	N-CA-CB	5.02	118.98	110.49
13	M	65	LYS	CA-C-N	5.02	130.74	121.70
13	M	65	LYS	C-N-CA	5.02	130.74	121.70
9	I	3	ARG	CB-CA-C	5.02	120.40	110.42
14	N	24	LEU	N-CA-C	-5.01	107.02	113.23
1	A	82	PHE	CA-CB-CG	-5.00	108.80	113.80

There are no chirality outliers.

All (45) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	140	TYR	Sidechain
1	A	17	LEU	Peptide
1	A	21	GLU	Peptide
1	A	262	TYR	Sidechain
1	A	273	ARG	Sidechain
1	A	408	MET	Peptide
1	A	409	GLY	Peptide
1	A	412	GLU	Peptide
1	A	43	TYR	Sidechain
2	B	30	ARG	Sidechain
4	D	49	G	Sidechain
4	D	55	U	Sidechain
4	D	56	G	Sidechain

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
4	D	62	C	Sidechain
4	D	76	C	Sidechain
4	D	77	A	Sidechain
4	D	87	G	Sidechain
5	E	536	A	Sidechain
5	E	543	A	Sidechain
6	F	1667	A	Sidechain
8	H	110	ASN	Peptide
8	H	197	ARG	Peptide
8	H	209	TYR	Sidechain
8	H	59	GLN	Peptide
8	H	74	ILE	Peptide
8	H	76	ARG	Peptide
8	H	92	ASN	Peptide
9	I	122	ALA	Peptide
9	I	23	ARG	Sidechain
11	K	105	VAL	Peptide
11	K	57	LEU	Peptide
12	L	111	LEU	Peptide
12	L	121	ARG	Peptide
12	L	125	LYS	Peptide
12	L	52	ARG	Sidechain
12	L	63	LYS	Peptide
12	L	89	LYS	Peptide
14	N	32	LYS	Peptide
14	N	36	LEU	Peptide
14	N	38	ARG	Peptide
15	O	23	LEU	Peptide
15	O	24	PRO	Peptide
15	O	31	THR	Peptide
15	O	32	ASN	Peptide
15	O	36	ARG	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	11	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	13	0
9	I	1212	0	1231	6	0
10	J	410	0	452	0	0
11	K	663	0	699	2	0
12	L	1002	0	1093	1	0
13	M	706	0	741	2	0
14	N	547	0	613	4	0
15	O	316	0	349	1	0
All	All	14301	0	13435	42	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 2.

All (42) 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)
11:K:100:LYS:HA	11:K:105:VAL:HG22	1.81	0.63
5:E:539:U:H3	5:E:546:G:H1	1.51	0.57
1:A:228:HIS:CG	1:A:229:LYS:H	2.23	0.57
1:A:65:ILE:HD12	1:A:68:LEU:HD12	1.88	0.54
12:L:56:VAL:HG22	12:L:106:ILE:HG22	1.89	0.53
8:H:184:SER:HA	8:H:186:LYS:H	1.73	0.52
9:I:3:ARG:HB2	9:I:4:TYR:HA	1.93	0.51
9:I:9:THR:HG23	9:I:10:ASN:HA	1.93	0.50
1:A:310:ALA:H	1:A:314:ILE:HD12	1.77	0.50
1:A:447:LYS:HG2	1:A:448:GLY:H	1.77	0.50
13:M:44:MET:HE1	13:M:78:LYS:HB2	1.94	0.50
8:H:88:GLY:HA3	8:H:89:ALA:HB3	1.93	0.49
14:N:41:LEU:H	14:N:44:ILE:HD12	1.77	0.49
8:H:77:VAL:HG12	8:H:87:GLN:HA	1.93	0.48
1:A:11:LYS:H	1:A:12:PRO:HD2	1.78	0.47
15:O:26:TRP:CD1	15:O:26:TRP:H	2.34	0.46
8:H:83:GLY:HA3	8:H:84:ARG:HB2	1.98	0.45
8:H:184:SER:HA	8:H:186:LYS:N	2.31	0.45
8:H:57:GLY:HA3	8:H:58:HIS:HB2	1.98	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:342:VAL:HB	1:A:343:PRO:HD2	1.98	0.45
1:A:79:LEU:HD22	1:A:79:LEU:H	1.81	0.44
8:H:77:VAL:HG13	8:H:78:GLY:H	1.83	0.44
8:H:77:VAL:HG21	8:H:90:PHE:CD1	2.53	0.44
8:H:52:VAL:HG22	8:H:53:SER:H	1.83	0.44
8:H:77:VAL:HG13	8:H:78:GLY:N	2.33	0.43
13:M:44:MET:HE3	13:M:46:THR:HB	1.99	0.43
1:A:260:VAL:HG11	1:A:454:VAL:HG12	2.01	0.43
14:N:37:SER:N	14:N:38:ARG:HA	2.34	0.43
8:H:152:VAL:HG12	8:H:153:SER:H	1.84	0.42
1:A:22:LEU:HB2	1:A:23:PRO:CD	2.50	0.42
9:I:57:ALA:HB1	9:I:58:ILE:H	1.58	0.42
1:A:128:TYR:CZ	1:A:161:GLY:HA3	2.55	0.42
2:B:57:GLY:O	2:B:61:VAL:HG23	2.19	0.42
8:H:13:GLY:H	8:H:14:GLU:HB2	1.85	0.41
1:A:256:ILE:O	1:A:260:VAL:HG12	2.20	0.41
9:I:105:LYS:HD3	9:I:105:LYS:H	1.86	0.41
8:H:160:GLN:H	8:H:218:ALA:HB3	1.86	0.41
11:K:73:MET:HA	11:K:73:MET:HE2	2.03	0.41
14:N:34:GLN:CA	14:N:36:LEU:H	2.33	0.41
9:I:40:GLU:CD	9:I:40:GLU:H	2.29	0.40
9:I:107:LEU:HD12	9:I:107:LEU:H	1.86	0.40
14:N:34:GLN:HA	14:N:36:LEU:H	1.87	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%)	428 (88%)	41 (8%)	19 (4%)	2	19
2	B	58/80 (72%)	57 (98%)	1 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	19/87 (22%)	17 (90%)	1 (5%)	1 (5%)	1	15
8	H	267/362 (74%)	186 (70%)	38 (14%)	43 (16%)	0	2
9	I	151/184 (82%)	113 (75%)	24 (16%)	14 (9%)	0	8
10	J	51/189 (27%)	46 (90%)	5 (10%)	0	100	100
11	K	81/142 (57%)	71 (88%)	7 (9%)	3 (4%)	2	20
12	L	125/127 (98%)	101 (81%)	8 (6%)	16 (13%)	0	4
13	M	82/113 (73%)	64 (78%)	11 (13%)	7 (8%)	0	9
14	N	67/120 (56%)	60 (90%)	2 (3%)	5 (8%)	1	10
15	O	35/51 (69%)	25 (71%)	2 (6%)	8 (23%)	0	1
All	All	1424/1945 (73%)	1168 (82%)	140 (10%)	116 (8%)	1	9

All (116) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	18	PRO
1	A	148	VAL
1	A	274	SER
1	A	276	ARG
1	A	410	ARG
1	A	449	LYS
8	H	3	ARG
8	H	28	ALA
8	H	55	LYS
8	H	58	HIS
8	H	70	ALA
8	H	87	GLN
8	H	89	ALA
8	H	98	ARG
8	H	102	PRO
8	H	103	THR
8	H	146	PRO
8	H	185	LYS
8	H	199	TRP
8	H	212	ASP
8	H	215	ILE
8	H	222	VAL
8	H	244	LEU
9	I	37	ASN
9	I	56	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	I	57	ALA
9	I	67	ILE
9	I	107	LEU
9	I	113	TYR
9	I	123	PRO
9	I	143	PRO
12	L	23	PRO
12	L	24	SER
12	L	85	VAL
13	M	26	LYS
13	M	78	LYS
13	M	79	ARG
14	N	4	VAL
14	N	14	LYS
14	N	39	PRO
15	O	22	PRO
15	O	23	LEU
15	O	24	PRO
1	A	61	VAL
1	A	277	ALA
1	A	389	SER
1	A	484	LEU
3	C	60	ASP
8	H	13	GLY
8	H	72	ALA
8	H	93	MET
8	H	107	ARG
8	H	160	GLN
8	H	173	GLY
8	H	187	LEU
8	H	200	THR
8	H	262	TRP
8	H	264	SER
9	I	71	ALA
9	I	111	LYS
11	K	62	VAL
12	L	11	ASP
12	L	45	ILE
12	L	46	LYS
12	L	96	PRO
12	L	122	LYS
13	M	25	PHE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
13	M	90	PHE
14	N	5	LYS
14	N	37	SER
15	O	6	SER
15	O	20	ASN
1	A	67	PHE
1	A	278	ARG
1	A	408	MET
1	A	411	ARG
8	H	54	GLU
8	H	60	THR
8	H	63	GLU
8	H	69	ARG
8	H	76	ARG
9	I	3	ARG
9	I	25	SER
9	I	54	HIS
12	L	36	SER
12	L	87	LYS
12	L	125	LYS
13	M	24	SER
1	A	11	LYS
8	H	74	ILE
8	H	84	ARG
8	H	106	TRP
8	H	110	ASN
8	H	132	ALA
8	H	253	ALA
8	H	265	GLU
9	I	39	TRP
11	K	109	LYS
12	L	6	LEU
12	L	86	THR
15	O	34	THR
1	A	28	PRO
1	A	346	PRO
8	H	131	VAL
8	H	196	ASN
8	H	198	ARG
11	K	131	ASP
12	L	84	LYS
12	L	97	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
13	M	51	LEU
15	O	25	GLN
1	A	284	TYR
12	L	22	ALA
15	O	5	LYS
1	A	199	GLY
8	H	96	GLY

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	412/412 (100%)	378 (92%)	34 (8%)	10	30
2	B	50/67 (75%)	47 (94%)	3 (6%)	17	39
3	C	19/73 (26%)	18 (95%)	1 (5%)	20	41
8	H	209/288 (73%)	188 (90%)	21 (10%)	7	24
9	I	124/146 (85%)	109 (88%)	15 (12%)	5	17
10	J	44/154 (29%)	42 (96%)	2 (4%)	24	46
11	K	74/118 (63%)	65 (88%)	9 (12%)	5	17
12	L	110/110 (100%)	99 (90%)	11 (10%)	7	24
13	M	74/97 (76%)	68 (92%)	6 (8%)	11	31
14	N	62/105 (59%)	58 (94%)	4 (6%)	15	37
15	O	33/46 (72%)	28 (85%)	5 (15%)	3	12
All	All	1211/1616 (75%)	1100 (91%)	111 (9%)	11	27

All (111) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	PRO
1	A	21	GLU
1	A	22	LEU
1	A	24	PHE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	26	LYS
1	A	31	ASP
1	A	36	THR
1	A	47	GLN
1	A	50	LEU
1	A	77	ARG
1	A	79	LEU
1	A	80	LEU
1	A	121	LYS
1	A	128	TYR
1	A	148	VAL
1	A	154	ASN
1	A	166	LEU
1	A	170	VAL
1	A	185	ASN
1	A	194	VAL
1	A	197	THR
1	A	204	LYS
1	A	212	GLU
1	A	227	LYS
1	A	229	LYS
1	A	242	ASP
1	A	273	ARG
1	A	309	PHE
1	A	321	GLU
1	A	410	ARG
1	A	414	ASN
1	A	417	LYS
1	A	425	ILE
1	A	480	LEU
2	B	30	ARG
2	B	35	PHE
2	B	52	LYS
3	C	76	ILE
8	H	4	PRO
8	H	35	VAL
8	H	43	ASN
8	H	46	LYS
8	H	48	GLN
8	H	98	ARG
8	H	103	THR
8	H	104	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
8	H	119	ARG
8	H	131	VAL
8	H	136	LEU
8	H	140	HIS
8	H	145	ILE
8	H	159	ILE
8	H	161	LYS
8	H	164	GLU
8	H	180	LYS
8	H	201	GLN
8	H	225	VAL
8	H	233	LEU
8	H	243	HIS
9	I	36	ILE
9	I	40	GLU
9	I	43	LYS
9	I	46	LYS
9	I	51	VAL
9	I	54	HIS
9	I	66	SER
9	I	67	ILE
9	I	72	GLN
9	I	79	THR
9	I	94	LEU
9	I	107	LEU
9	I	112	LEU
9	I	144	SER
9	I	149	VAL
10	J	1	MET
10	J	53	LYS
11	K	65	GLN
11	K	70	GLU
11	K	74	LYS
11	K	100	LYS
11	K	111	ASN
11	K	114	VAL
11	K	117	ASN
11	K	120	LYS
11	K	123	TYR
12	L	28	ARG
12	L	37	LYS
12	L	52	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
12	L	57	LEU
12	L	64	LYS
12	L	77	LYS
12	L	87	LYS
12	L	95	VAL
12	L	111	LEU
12	L	122	LYS
12	L	125	LYS
13	M	20	LEU
13	M	24	SER
13	M	38	LYS
13	M	47	ASP
13	M	67	VAL
13	M	86	LYS
14	N	5	LYS
14	N	9	LEU
14	N	34	GLN
14	N	37	SER
15	O	17	LYS
15	O	18	LYS
15	O	22	PRO
15	O	23	LEU
15	O	26	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	62	ASN
1	A	87	ASN
1	A	95	GLN
1	A	149	GLN
1	A	154	ASN
1	A	214	GLN
1	A	320	ASN
1	A	324	HIS
1	A	386	GLN
1	A	403	GLN
1	A	414	ASN
1	A	472	GLN
8	H	5	GLN
8	H	36	HIS
8	H	43	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
8	H	160	GLN
8	H	196	ASN
8	H	234	ASN
9	I	34	GLN
9	I	137	ASN
10	J	39	ASN
11	K	117	ASN
12	L	91	ASN
14	N	20	GLN
15	O	4	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	D	62/63 (98%)	27 (43%)	10 (16%)
5	E	33/34 (97%)	7 (21%)	2 (6%)
6	F	24/25 (96%)	1 (4%)	0
7	G	17/18 (94%)	1 (5%)	0
All	All	136/140 (97%)	36 (26%)	12 (8%)

All (36) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	D	48	A
4	D	49	G
4	D	51	G
4	D	56	G
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	71	A
4	D	79	A
4	D	82	U
4	D	83	C
4	D	84	C
4	D	85	G
4	D	86	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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	95	G
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
6	F	1668	G
7	G	922	U

All (12) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	D	48	A
4	D	51	G
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
5	E	560	A

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 [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.

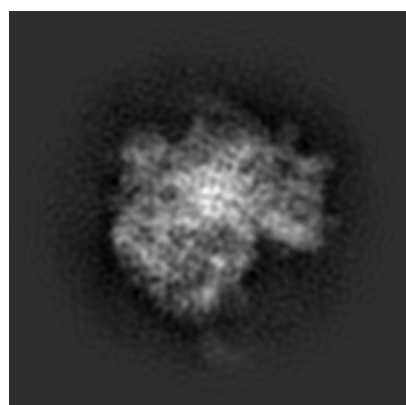
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1667. These allow visual inspection of the internal detail of the map and identification of artifacts.

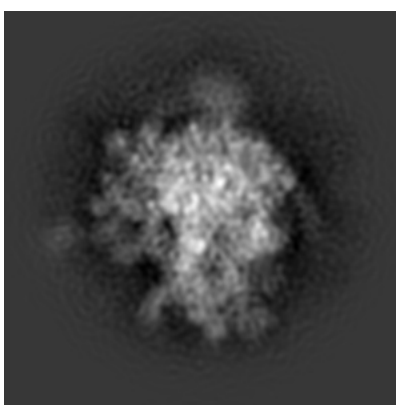
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

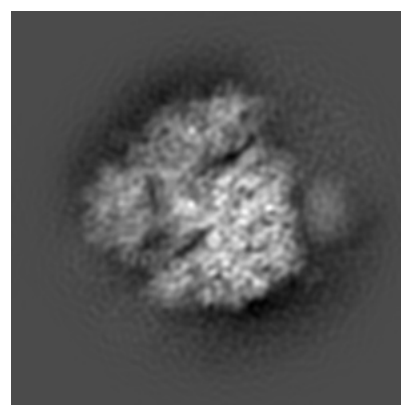
6.1.1 Primary map



X



Y

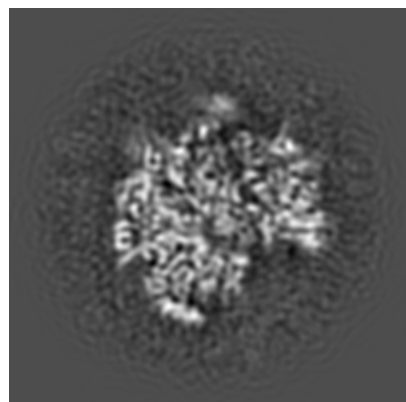


Z

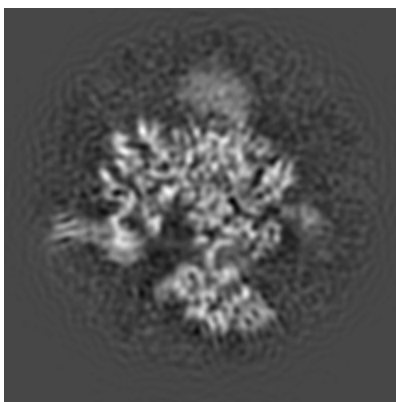
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

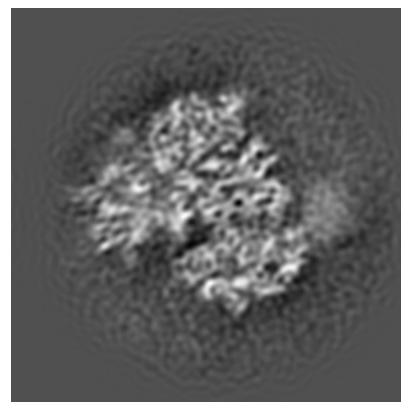
6.2.1 Primary map



X Index: 184



Y Index: 184

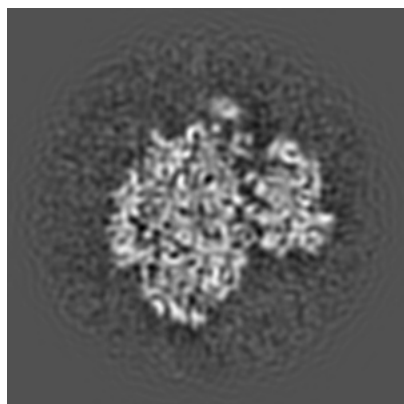


Z Index: 184

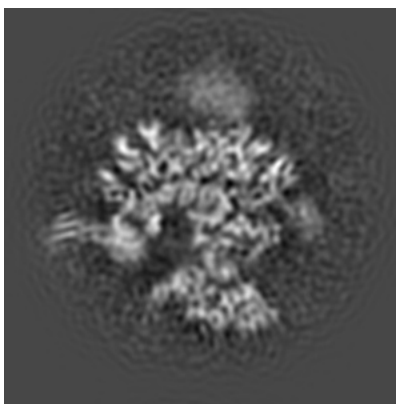
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

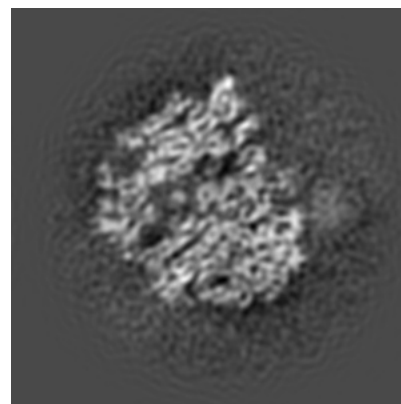
6.3.1 Primary map



X Index: 190



Y Index: 187

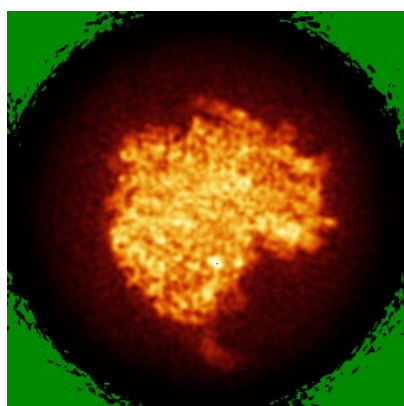


Z Index: 172

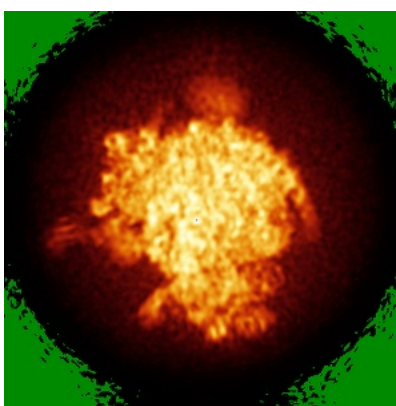
The images above show the largest variance slices of the map in three orthogonal directions.

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

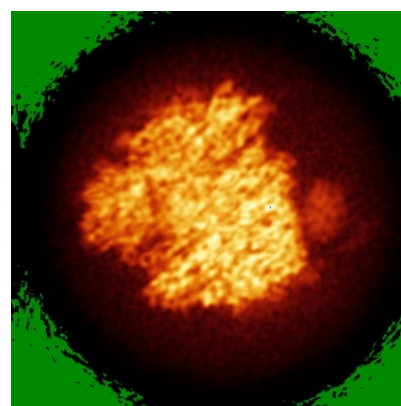
6.4.1 Primary map



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 1.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

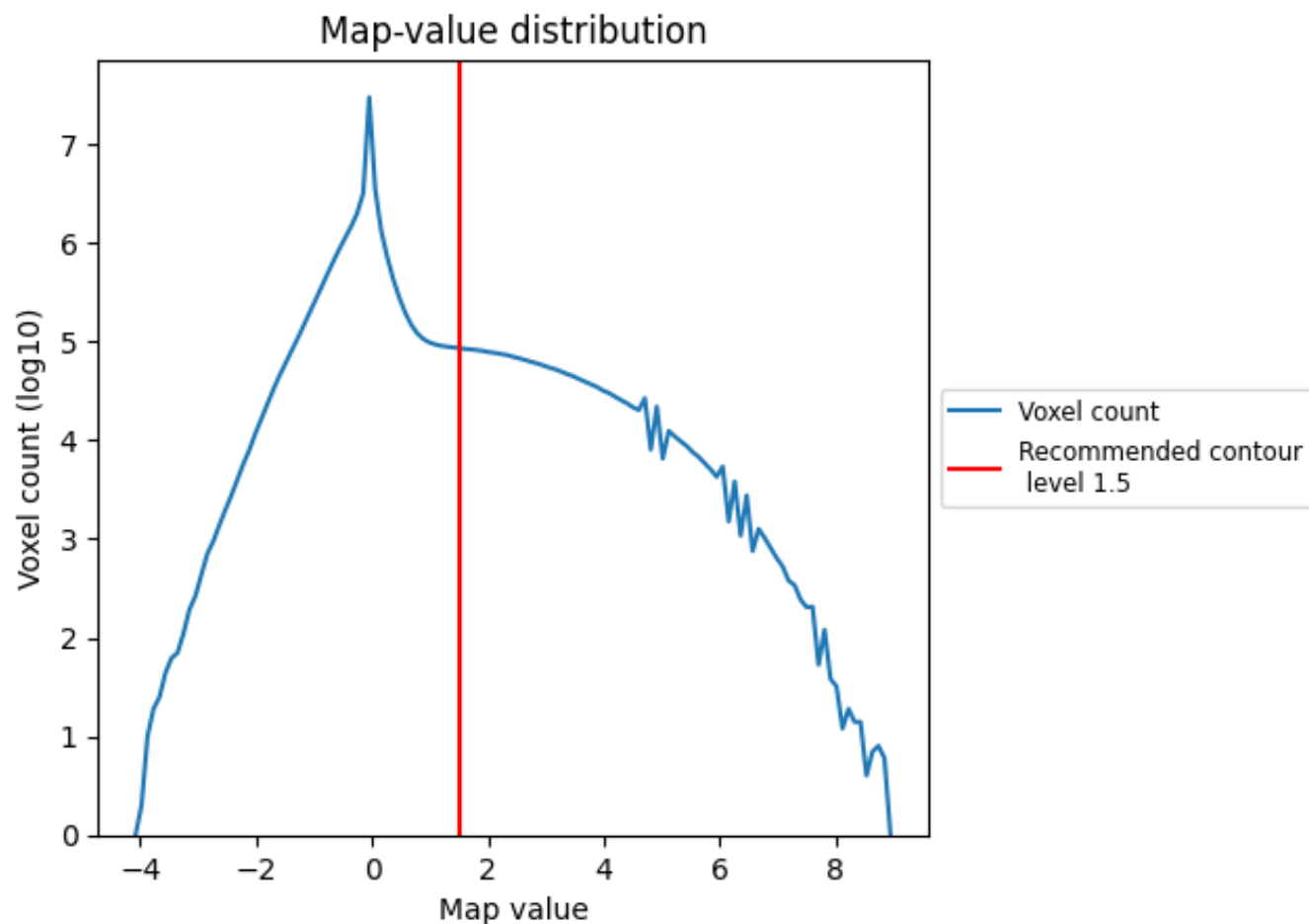
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

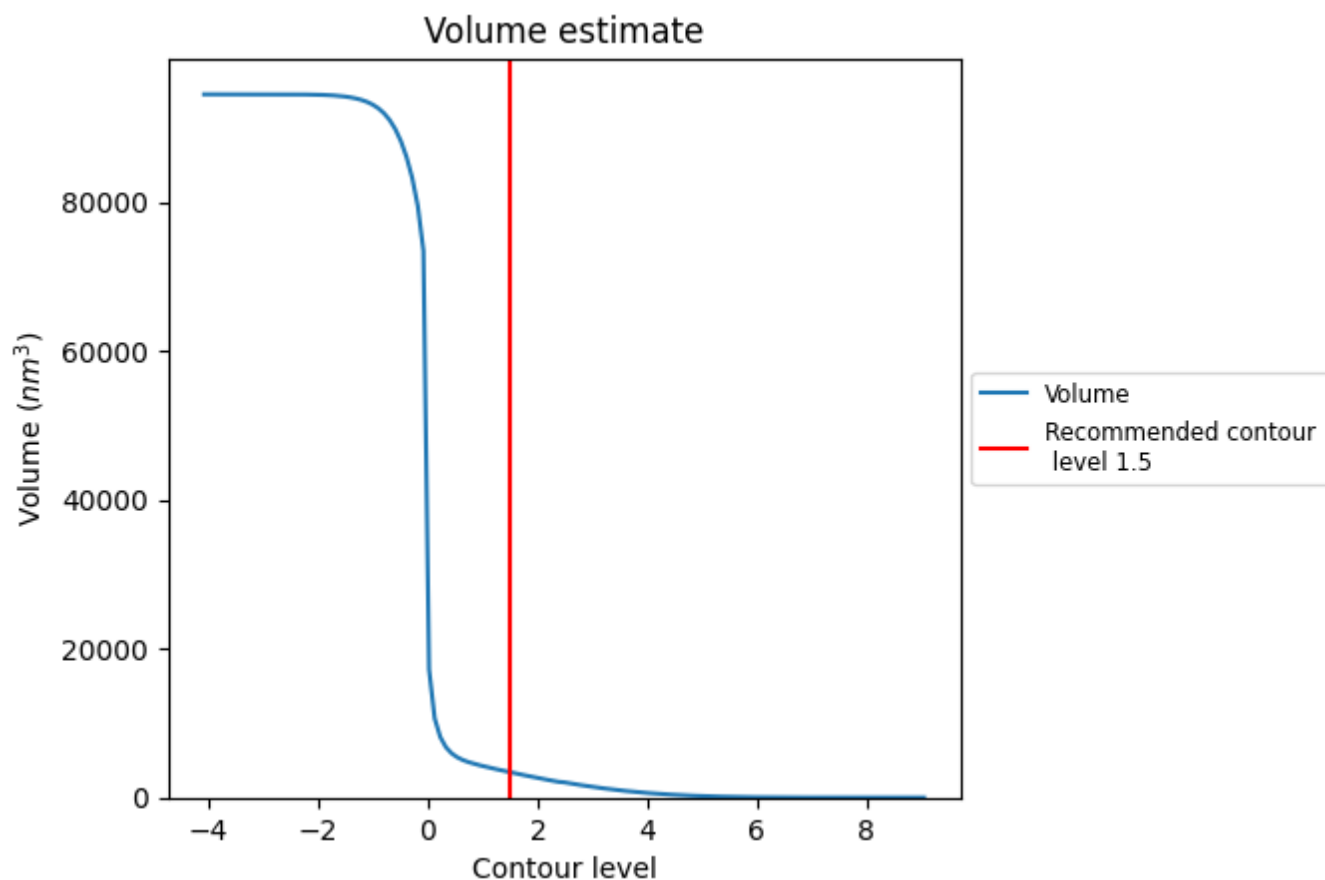
This section contains the results of statistical analysis of the map.

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.

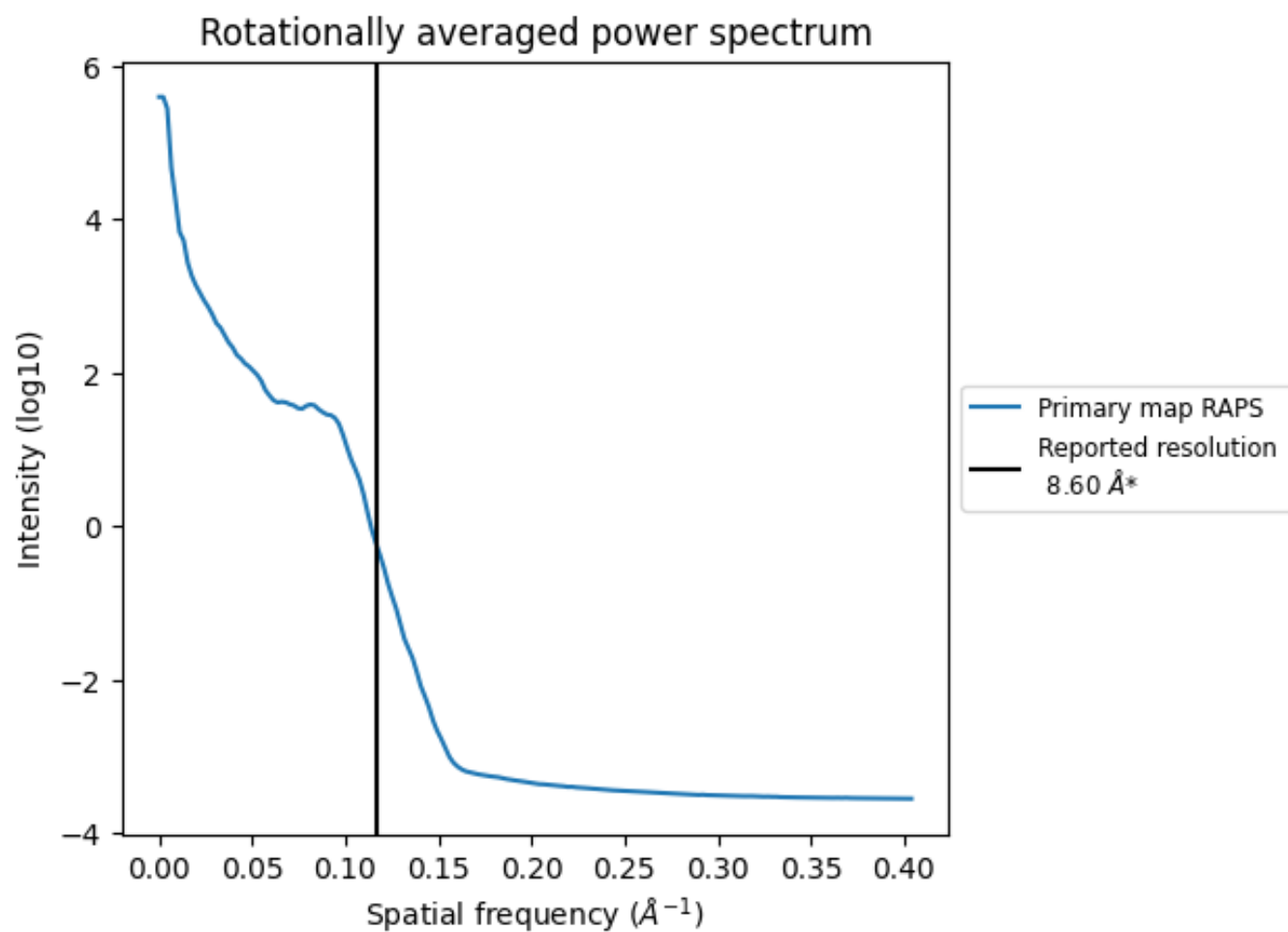
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3399 nm³; this corresponds to an approximate mass of 3071 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 0.116 Å⁻¹

8 Fourier-Shell correlation ⓘ

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

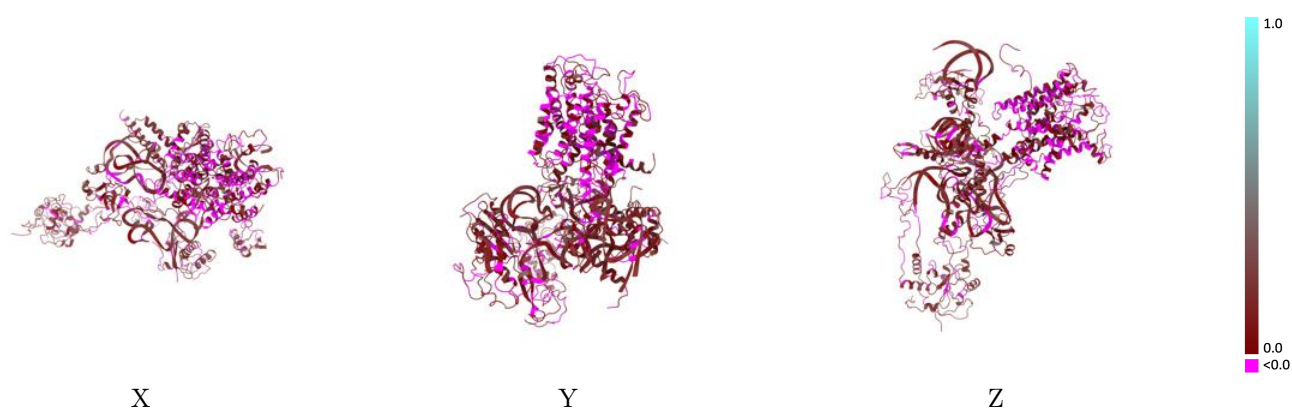
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-1667 and PDB model 2WW9. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)

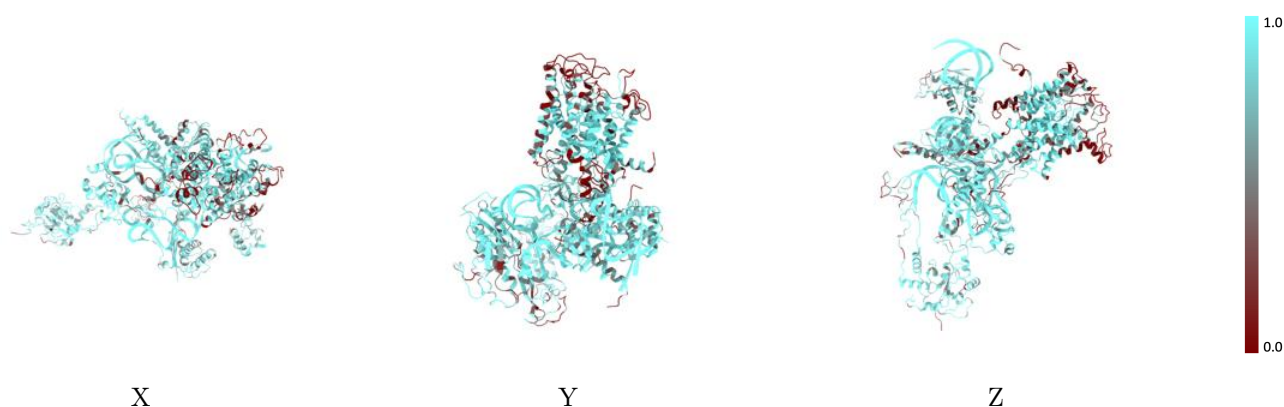
This section was not generated.

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



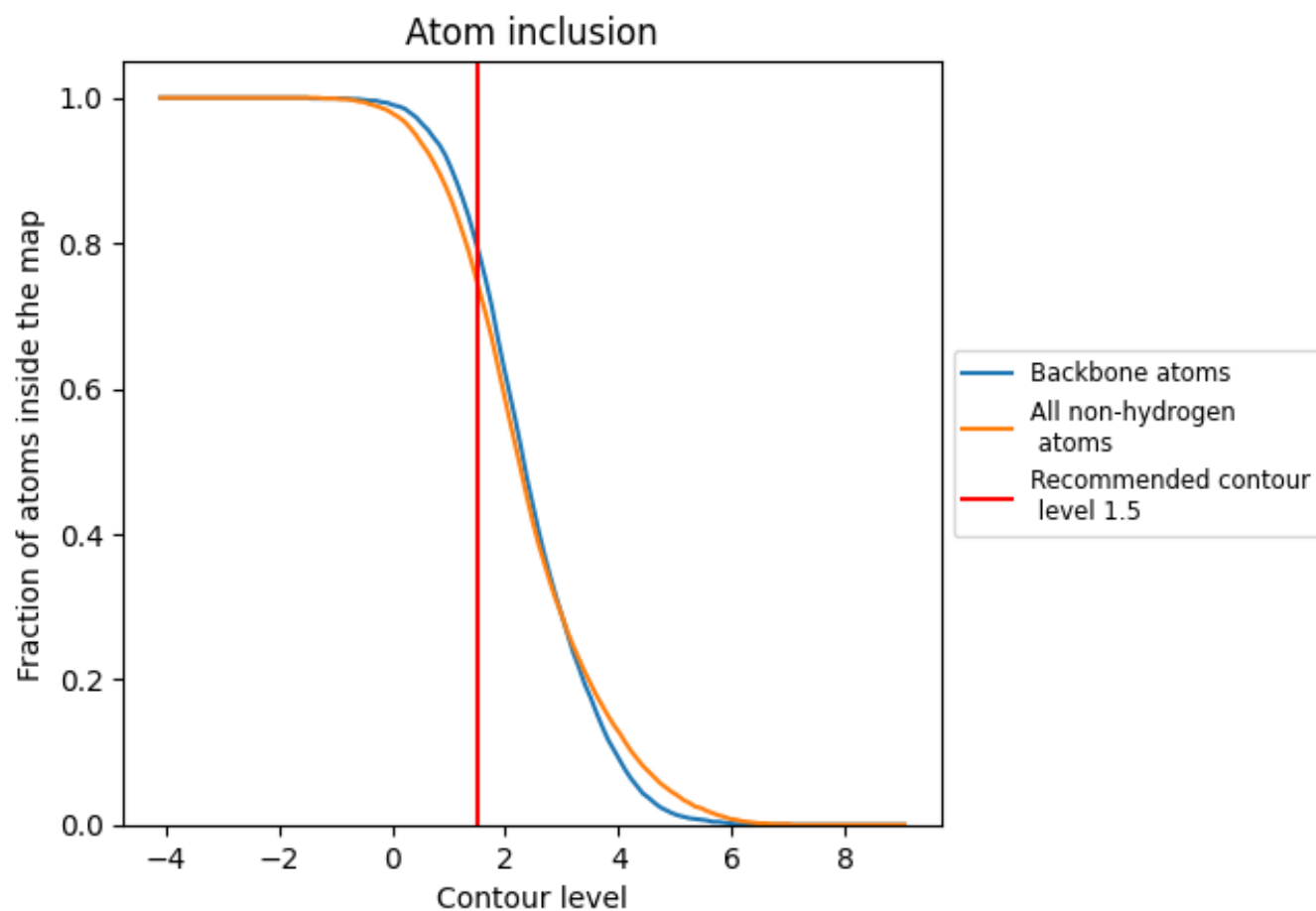
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 75% 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 (1.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7480	 0.0780
A	 0.5940	 0.0130
B	 0.7360	 0.0330
C	 0.4000	 0.0320
D	 0.8930	 0.0950
E	 0.9540	 0.1480
F	 0.9440	 0.1510
G	 0.9550	 0.1670
H	 0.7720	 0.0950
I	 0.7270	 0.0800
J	 0.7020	 0.1060
K	 0.7710	 0.1060
L	 0.8450	 0.1000
M	 0.7440	 0.0870
N	 0.8170	 0.1340
O	 0.5920	 0.0940

