



wwPDB EM Validation Summary Report ⓘ

Jun 25, 2025 – 02:41 pm BST

PDB ID : 6ZOJ / pdb_00006zoj
EMDB ID : EMD-11320
Title : SARS-CoV-2-Nsp1-40S complex, composite map
Authors : Schubert, K.; Karousis, E.D.; Jomaa, A.; Scaiola, A.; Echeverria, B.; Gurzeler, L.-A.; Leibundgut, M.L.; Thiel, V.; Muehlemann, O.; Ban, N.
Deposited on : 2020-07-07
Resolution : 2.80 Å(reported)

This is a wwPDB EM Validation Summary 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.dev118
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.44

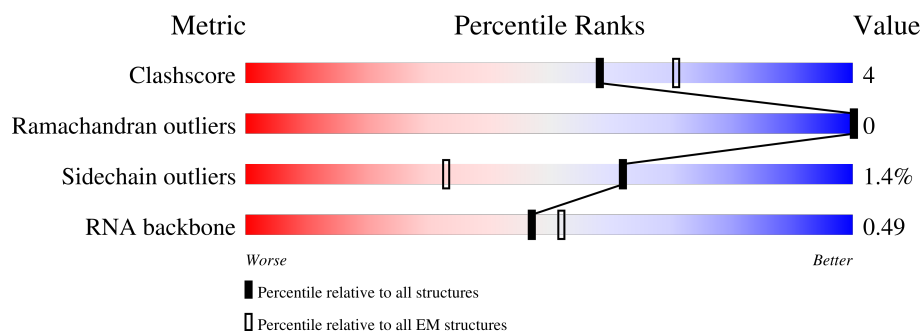
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	2	1869	
2	A	295	
3	B	264	
4	C	293	
5	D	243	
6	E	263	
7	F	204	

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Mol	Chain	Length	Quality of chain
8	G	249	
9	H	194	
10	I	208	
11	J	194	
12	K	165	
13	L	158	
14	M	132	
15	N	151	
16	O	151	
17	P	145	
18	Q	146	
19	R	135	
20	S	152	
21	T	145	
22	U	119	
23	V	83	
24	W	130	
25	X	143	
26	Y	130	
27	Z	125	
28	a	101	
29	b	82	
30	c	61	
31	d	55	
32	e	56	

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Mol	Chain	Length	Quality of chain
33	f	72	<div><div></div><div>51%</div><div></div><div>85%</div><div></div><div>14%</div><div>.</div></div>
34	g	315	<div><div></div><div>12%</div><div></div><div>82%</div><div></div><div>17%</div></div>
35	j	180	<div><div>.</div><div></div><div>17%</div><div>..</div><div></div><div>82%</div></div>
36	h	25	<div><div></div><div>44%</div><div></div><div>80%</div><div></div><div>20%</div></div>

2 Entry composition

There are 38 unique types of molecules in this entry. The entry contains 75783 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 RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	1704	Total	C	N	O	P	0	0
			36367	16233	6526	11904	1704		

- Molecule 2 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	216	Total	C	N	O	S	0	0
			1705	1083	299	315	8		

- Molecule 3 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 4 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	218	Total	C	N	O	S	0	0
			1690	1094	289	297	10		

- Molecule 5 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	225	Total	C	N	O	S	0	0
			1752	1117	315	313	7		

- Molecule 6 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 7 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	190	Total	C	N	O	S	0	0
			1501	939	285	270	7		

- Molecule 8 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	230	Total	C	N	O	S	0	0
			1862	1164	371	320	7		

- Molecule 9 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	186	Total	C	N	O	S	0	0
			1501	957	276	267	1		

- Molecule 10 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	205	Total	C	N	O	S	0	0
			1682	1056	331	290	5		

- Molecule 11 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	180	Total	C	N	O	S	0	0
			1499	955	300	242	2		

- Molecule 12 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	97	Total	C	N	O	S	0	0
			816	533	144	133	6		

- Molecule 13 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	151	Total	C	N	O	S	0	0
			1229	782	230	211	6		

- Molecule 14 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	123	Total	C	N	O	S	0	0
			953	598	169	177	9		

- Molecule 15 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 16 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	135	Total	C	N	O	S	0	0
			1010	618	198	188	6		

- Molecule 17 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	124	Total	C	N	O	S	0	0
			1016	644	192	173	7		

- Molecule 18 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 19 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 20 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	143	Total	C	N	O	S	0	0
			1184	743	240	200	1		

- Molecule 21 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	144	Total	C	N	O	S	0	0
			1122	703	217	199	3		

- Molecule 22 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	101	Total	C	N	O	S	0	0
			803	504	153	142	4		

- Molecule 23 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 24 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 25 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	X	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 26 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	124	Total	C	N	O	S	0	0
			1014	641	198	170	5		

- Molecule 27 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	72	Total	C	N	O	S	0	0
			574	368	104	101	1		

- Molecule 28 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

- Molecule 29 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	82	Total	C	N	O	S	0	0
			640	402	118	113	7		

- Molecule 30 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	61	Total	C	N	O	S	0	0
			479	292	95	90	2		

- Molecule 31 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	55	Total	C	N	O	S	0	0
			458	286	94	73	5		

- Molecule 32 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	56	Total	C	N	O	S	0	0
			441	273	96	71	1		

- Molecule 33 is a protein called Ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	72	Total	C	N	O	S	0	0
			585	366	114	97	8		

- Molecule 34 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	314	Total	C	N	O	S	0	0
			2440	1537	425	466	12		

- Molecule 35 is a protein called Non-structural protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j	33	Total	C	N	O	S	0	0
			267	162	47	57	1		

- Molecule 36 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	h	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 37 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
37	2	159	Total	Mg	0
			159	159	
37	G	1	Total	Mg	0
			1	1	
37	O	2	Total	Mg	0
			2	2	
37	S	2	Total	Mg	0
			2	2	
37	T	1	Total	Mg	0
			1	1	
37	X	1	Total	Mg	0
			1	1	

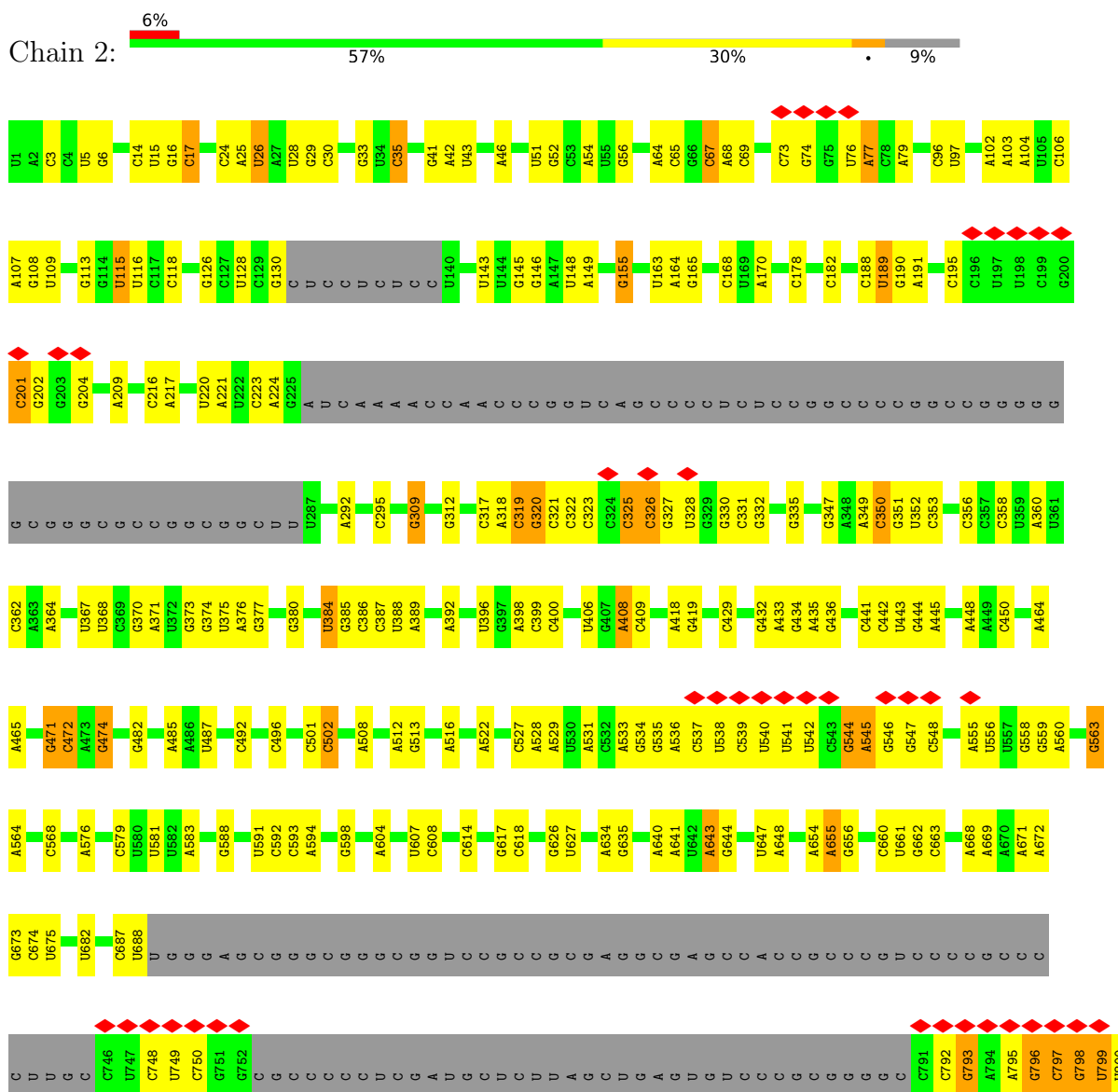
- Molecule 38 is ZINC ION (CCD ID: ZN) (formula: Zn).

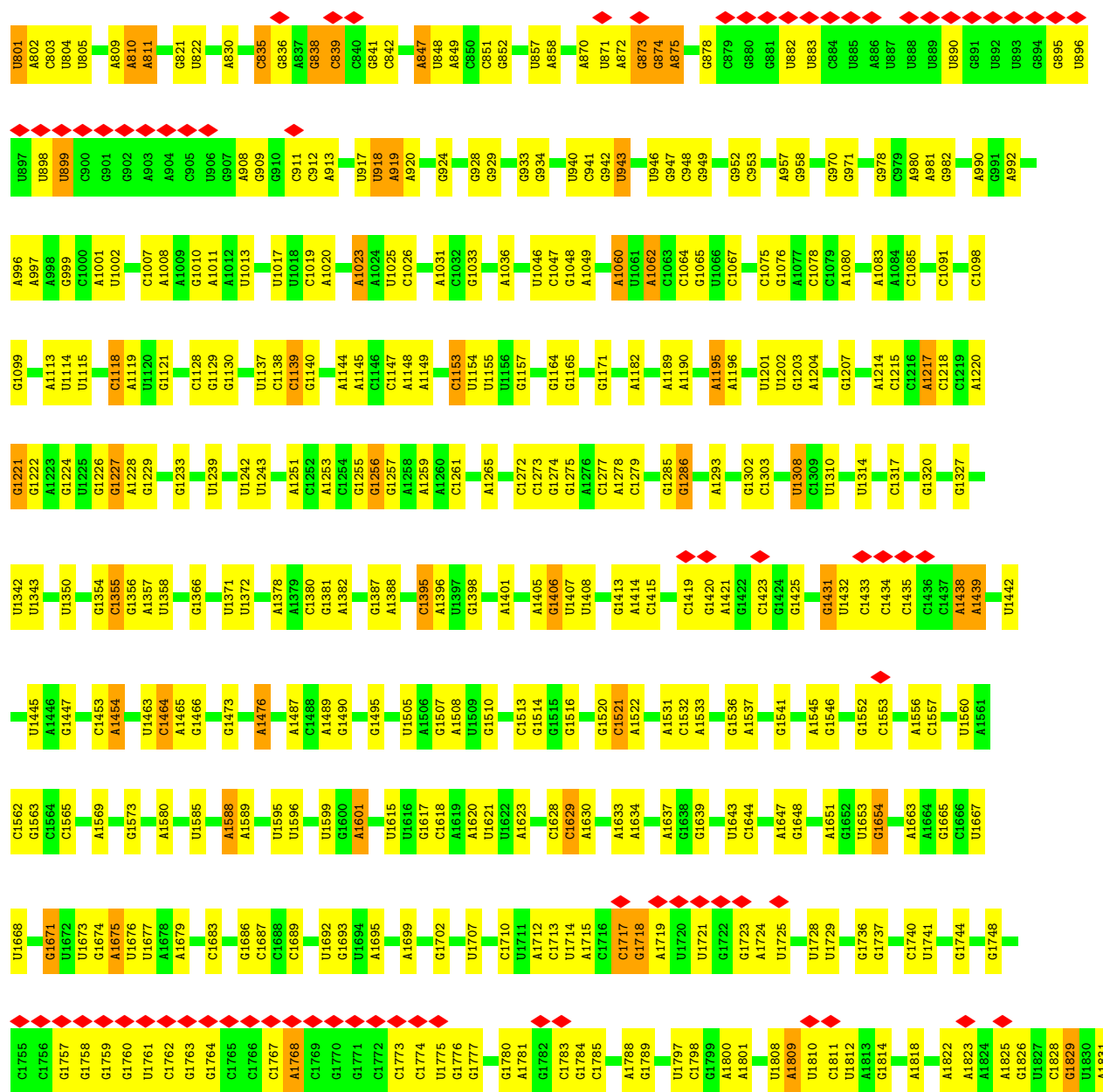
Mol	Chain	Residues	Atoms		AltConf
38	a	1	Total	Zn	0
			1	1	
38	d	1	Total	Zn	0
			1	1	
38	f	1	Total	Zn	0
			1	1	

3 Residue-property plots

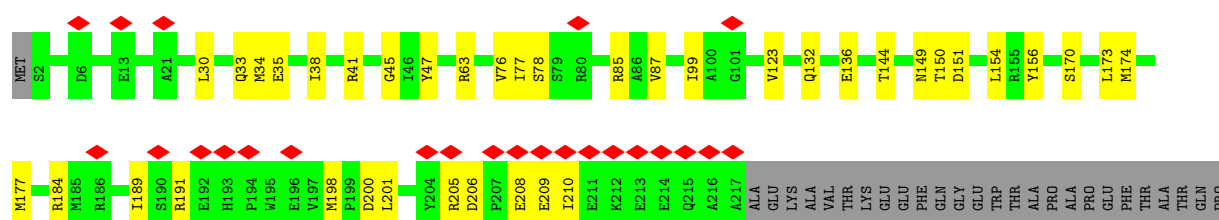
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 18S ribosomal RNA

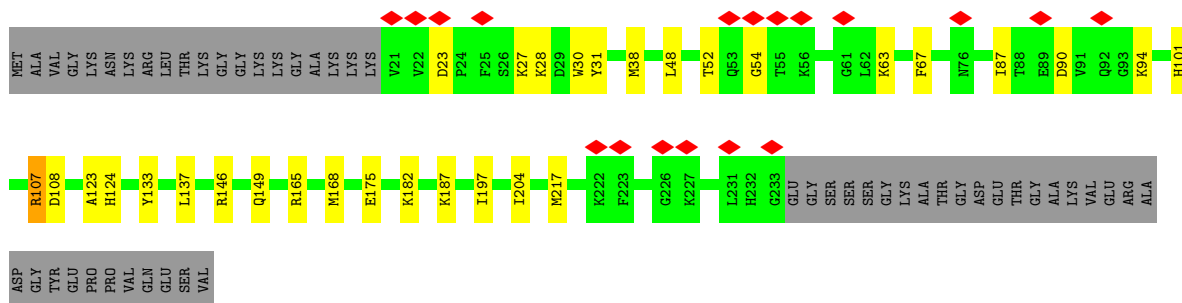




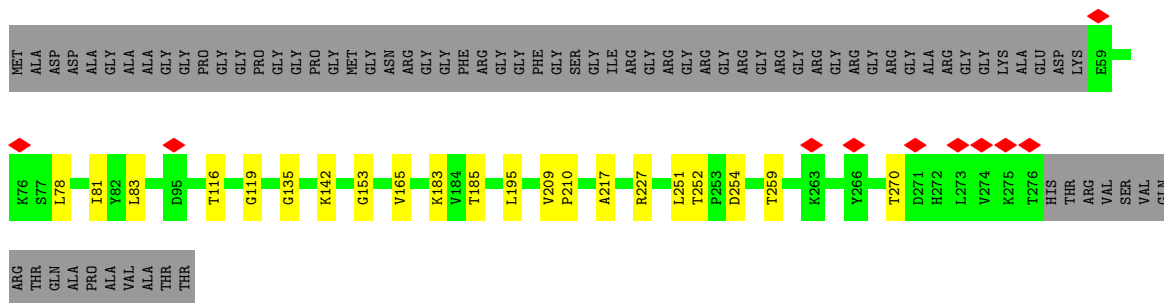
• Molecule 2: 40S ribosomal protein SA



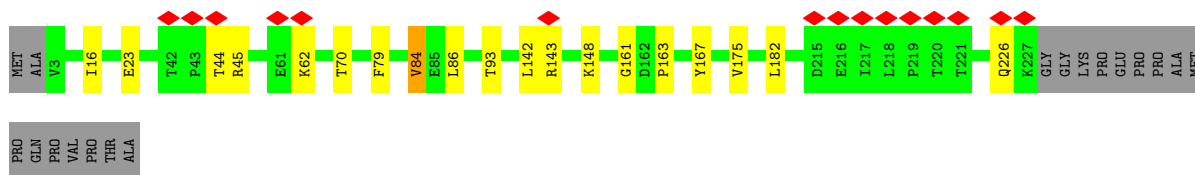
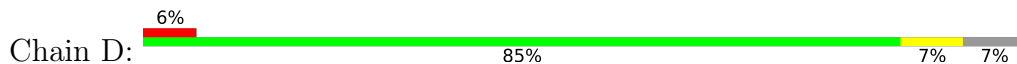
- Molecule 3: 40S ribosomal protein S3a



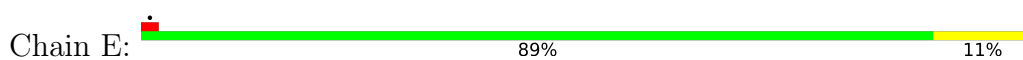
- Molecule 4: 40S ribosomal protein S2



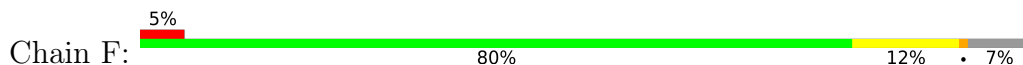
- Molecule 5: 40S ribosomal protein S3

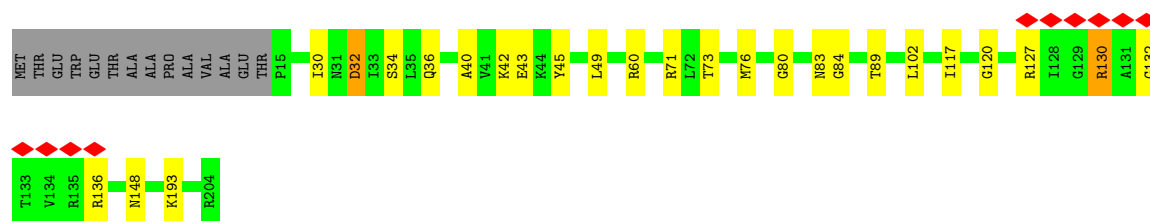


- Molecule 6: 40S ribosomal protein S4, X isoform

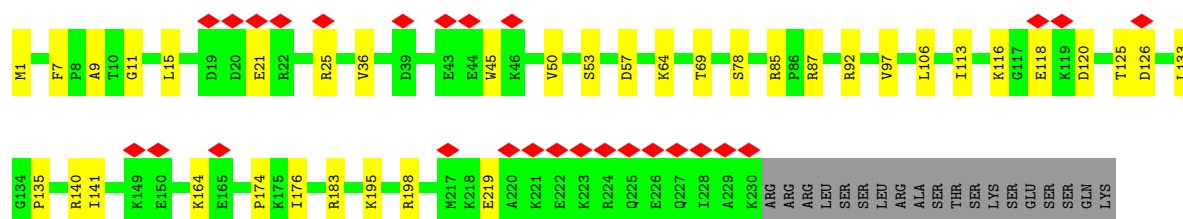
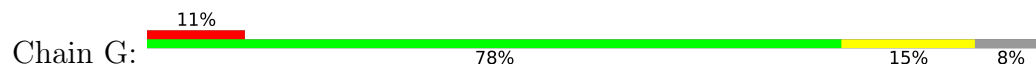


- Molecule 7: 40S ribosomal protein S5

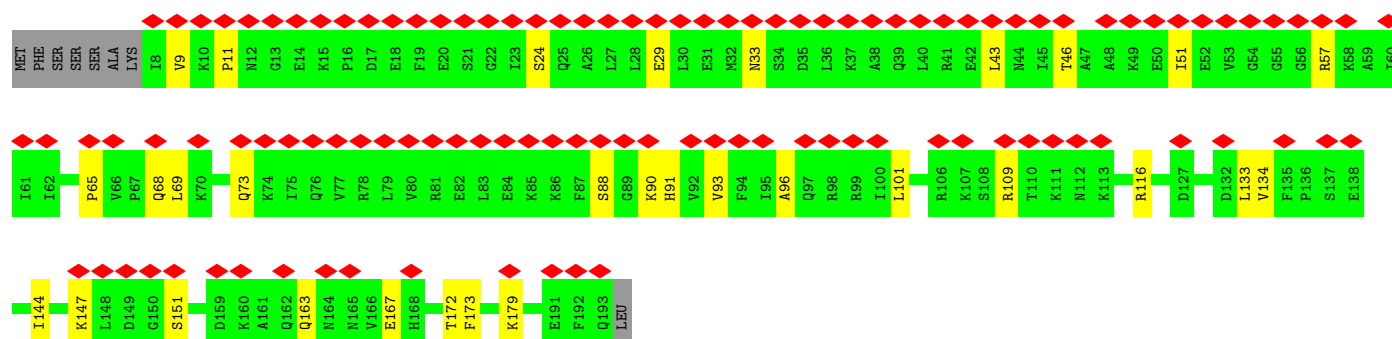
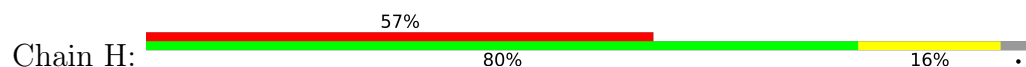




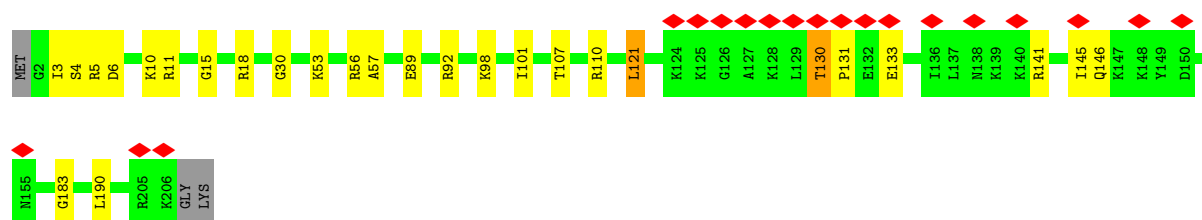
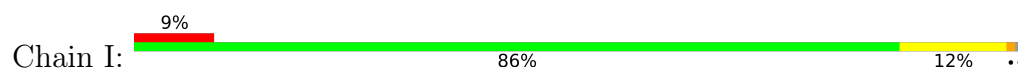
• Molecule 8: 40S ribosomal protein S6



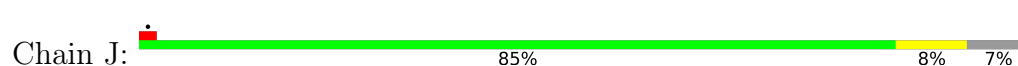
• Molecule 9: 40S ribosomal protein S7



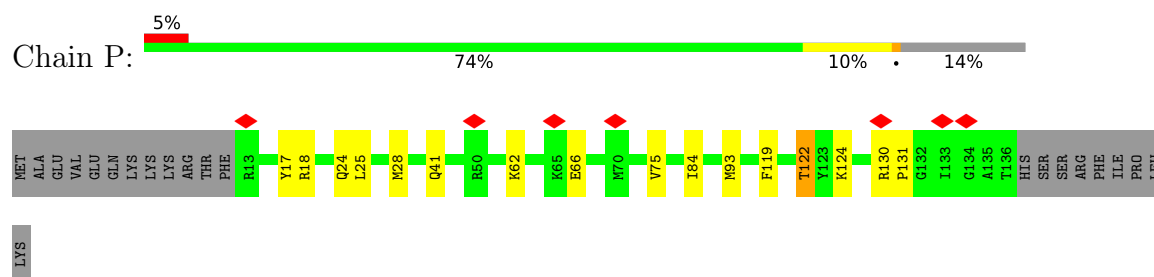
• Molecule 10: 40S ribosomal protein S8



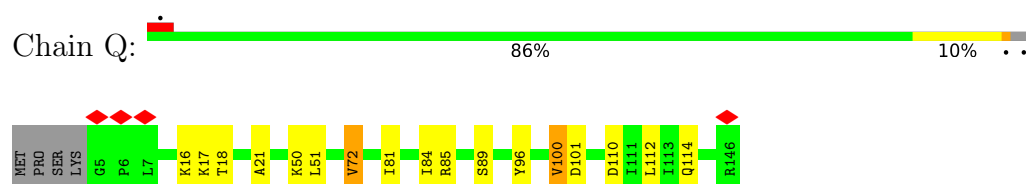
• Molecule 11: 40S ribosomal protein S9



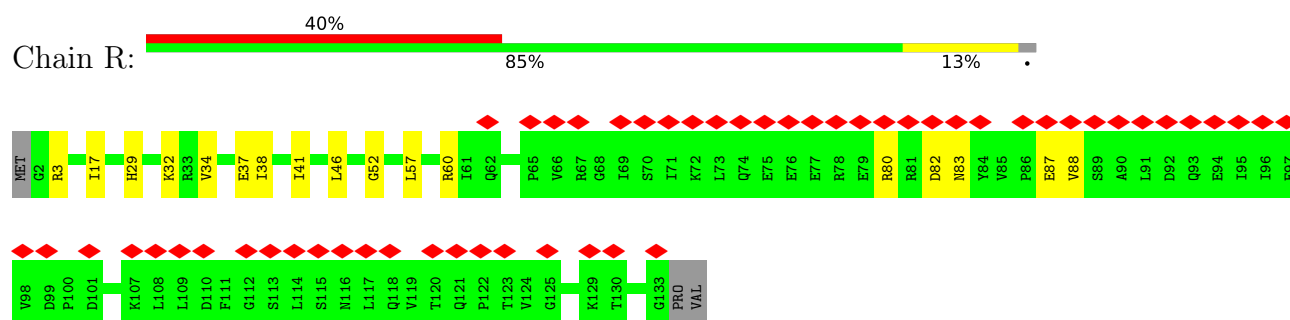
- Molecule 17: 40S ribosomal protein S15



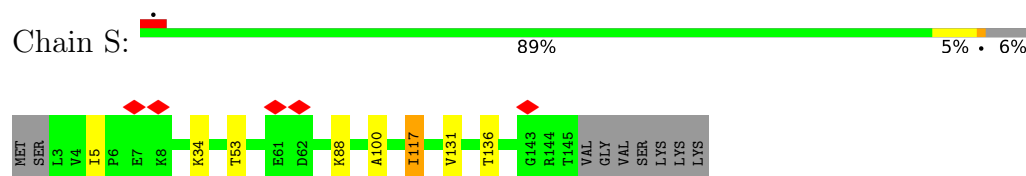
- Molecule 18: 40S ribosomal protein S16



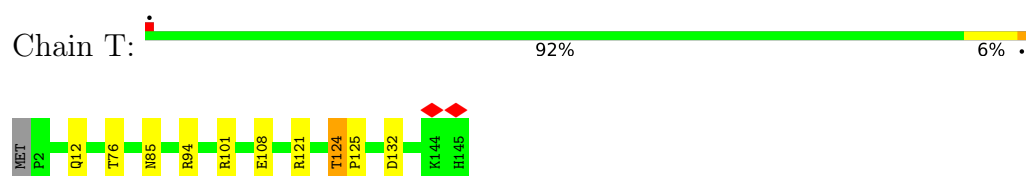
- Molecule 19: 40S ribosomal protein S17



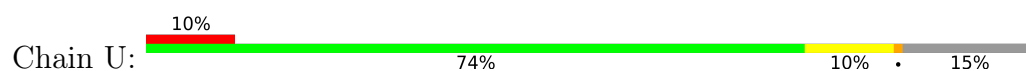
- Molecule 20: 40S ribosomal protein S18

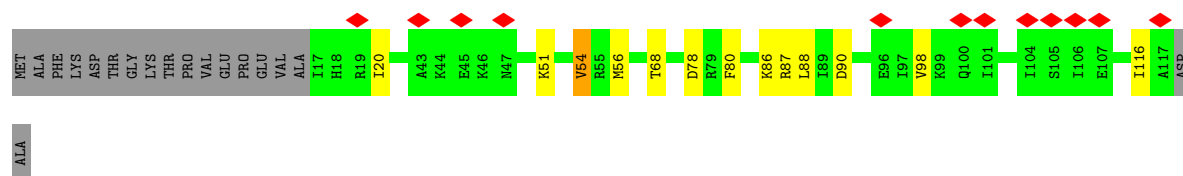


- Molecule 21: 40S ribosomal protein S19

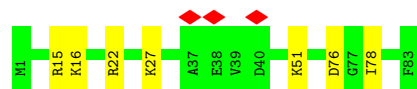


- Molecule 22: 40S ribosomal protein S20

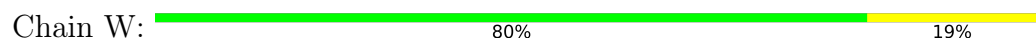




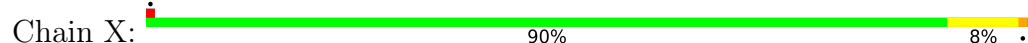
- Molecule 23: 40S ribosomal protein S21



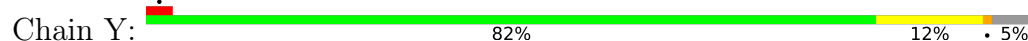
- Molecule 24: 40S ribosomal protein S15a



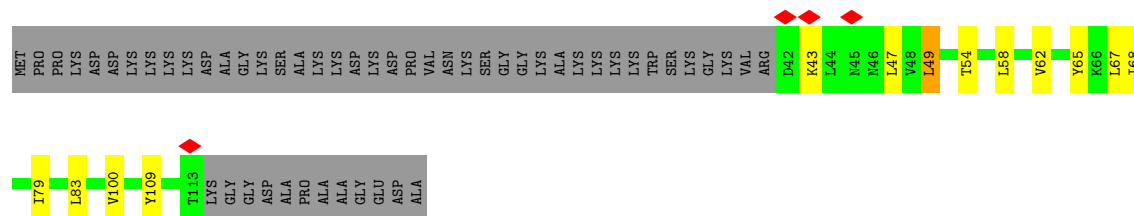
- Molecule 25: 40S ribosomal protein S23



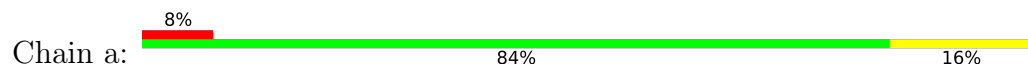
- Molecule 26: 40S ribosomal protein S24

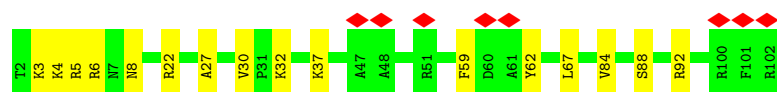


- Molecule 27: 40S ribosomal protein S25

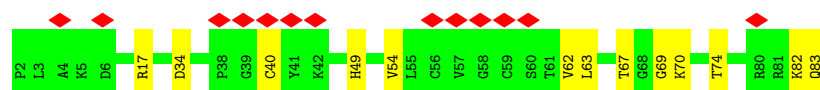
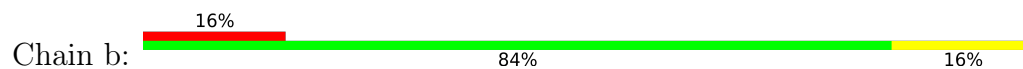


- Molecule 28: 40S ribosomal protein S26

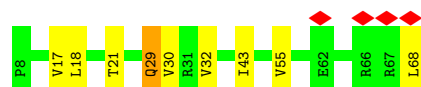
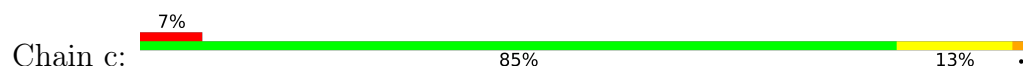




- Molecule 29: 40S ribosomal protein S27



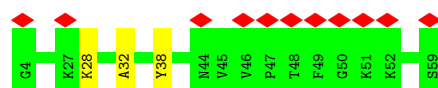
- Molecule 30: 40S ribosomal protein S28



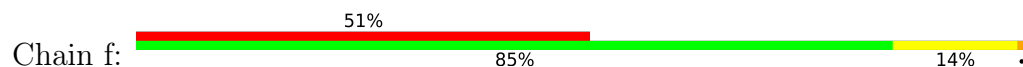
- Molecule 31: 40S ribosomal protein S29



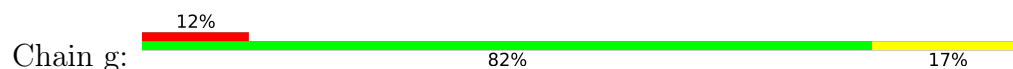
- Molecule 32: 40S ribosomal protein S30

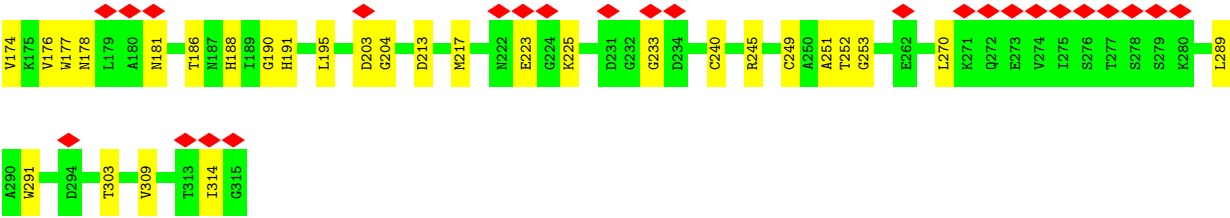


- Molecule 33: Ribosomal protein S27a

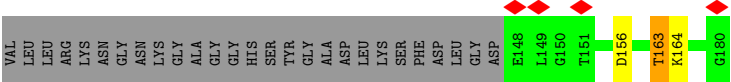
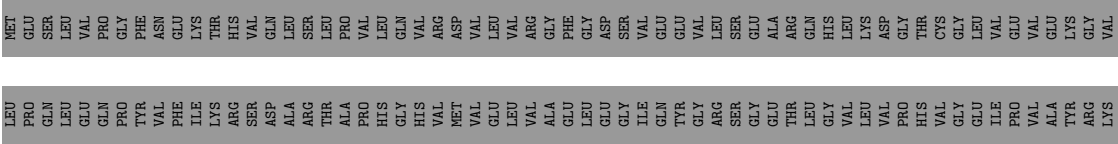


- Molecule 34: Receptor of activated protein C kinase 1

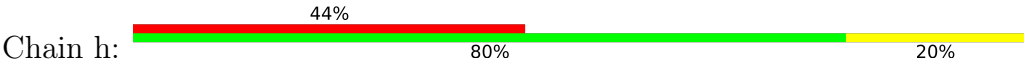




• Molecule 35: Non-structural protein 1



• Molecule 36: 60S ribosomal protein L41



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	118765	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	6.548	Depositor
Minimum map value	-2.295	Depositor
Average map value	-0.003	Depositor
Map value standard deviation	0.138	Depositor
Recommended contour level	0.9	Depositor
Map size (Å)	604.80005, 604.80005, 604.80005	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN

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	2	0.12	0/40667	0.26	0/63387
2	A	0.12	0/1742	0.29	0/2367
3	B	0.11	0/1756	0.30	0/2350
4	C	0.12	0/1726	0.29	0/2332
5	D	0.13	0/1780	0.33	0/2397
6	E	0.12	0/2118	0.32	0/2849
7	F	0.15	0/1523	0.36	0/2048
8	G	0.12	0/1885	0.32	0/2510
9	H	0.11	0/1524	0.31	0/2042
10	I	0.11	0/1711	0.31	0/2282
11	J	0.13	0/1524	0.36	0/2035
12	K	0.13	0/840	0.35	0/1133
13	L	0.11	0/1250	0.29	0/1673
14	M	0.11	0/963	0.31	0/1291
15	N	0.12	0/1226	0.29	0/1649
16	O	0.13	0/1023	0.37	0/1372
17	P	0.12	0/1035	0.29	0/1383
18	Q	0.15	0/1146	0.37	0/1534
19	R	0.12	0/1082	0.32	0/1452
20	S	0.14	0/1202	0.35	0/1610
21	T	0.12	0/1142	0.28	0/1530
22	U	0.14	0/813	0.36	0/1092
23	V	0.10	0/643	0.29	0/860
24	W	0.12	0/1051	0.31	0/1406
25	X	0.12	0/1116	0.35	0/1490
26	Y	0.11	0/1031	0.31	0/1370
27	Z	0.12	0/580	0.32	0/780
28	a	0.14	0/828	0.34	0/1109
29	b	0.11	0/653	0.32	0/876
30	c	0.14	0/481	0.36	0/643
31	d	0.13	0/469	0.33	0/623
32	e	0.12	0/446	0.33	0/587

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	f	0.11	0/595	0.33	0/785
34	g	0.12	0/2497	0.34	0/3399
35	j	0.10	0/272	0.27	0/366
36	h	0.14	0/240	0.40	0/305
All	All	0.12	0/80580	0.29	0/116917

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
7	F	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	F	130	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	2	36367	0	18368	298	0
2	A	1705	0	1706	23	0
3	B	1729	0	1803	21	0
4	C	1690	0	1777	11	0
5	D	1752	0	1848	13	0
6	E	2076	0	2177	17	0
7	F	1501	0	1557	18	0
8	G	1862	0	2018	25	0
9	H	1501	0	1593	19	0
10	I	1682	0	1769	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	J	1499	0	1618	12	0
12	K	816	0	841	6	0
13	L	1229	0	1302	8	0
14	M	953	0	990	12	0
15	N	1202	0	1289	9	0
16	O	1010	0	1034	11	0
17	P	1016	0	1066	10	0
18	Q	1128	0	1195	12	0
19	R	1068	0	1121	13	0
20	S	1184	0	1244	5	0
21	T	1122	0	1153	7	0
22	U	803	0	873	8	0
23	V	636	0	637	6	0
24	W	1034	0	1080	15	0
25	X	1098	0	1167	6	0
26	Y	1014	0	1082	11	0
27	Z	574	0	627	10	0
28	a	814	0	863	9	0
29	b	640	0	663	6	0
30	c	479	0	507	5	0
31	d	458	0	448	4	0
32	e	441	0	487	2	0
33	f	585	0	615	9	0
34	g	2440	0	2396	34	0
35	j	267	0	238	4	0
36	h	239	0	289	4	0
37	2	159	0	0	0	0
37	G	1	0	0	0	0
37	O	2	0	0	0	0
37	S	2	0	0	0	0
37	T	1	0	0	0	0
37	X	1	0	0	0	0
38	a	1	0	0	0	0
38	d	1	0	0	0	0
38	f	1	0	0	0	0
All	All	75783	0	59441	593	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 4.

The worst 5 of 593 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)
1:2:190:G:O2'	1:2:209:A:N6	2.15	0.80
1:2:164:A:H3'	1:2:165:G:H21	1.49	0.78
1:2:1147:C:OP1	28:a:6:ARG:NH1	2.21	0.74
1:2:1091:C:HO2'	24:W:2:VAL:N	1.86	0.73
21:T:76:THR:HG22	21:T:94:ARG:HB3	1.71	0.73

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	
2	A	214/295 (72%)	208 (97%)	6 (3%)	0	100	100
3	B	211/264 (80%)	209 (99%)	2 (1%)	0	100	100
4	C	216/293 (74%)	213 (99%)	3 (1%)	0	100	100
5	D	223/243 (92%)	221 (99%)	2 (1%)	0	100	100
6	E	260/263 (99%)	258 (99%)	2 (1%)	0	100	100
7	F	188/204 (92%)	179 (95%)	9 (5%)	0	100	100
8	G	228/249 (92%)	224 (98%)	4 (2%)	0	100	100
9	H	184/194 (95%)	176 (96%)	8 (4%)	0	100	100
10	I	203/208 (98%)	201 (99%)	2 (1%)	0	100	100
11	J	178/194 (92%)	173 (97%)	5 (3%)	0	100	100
12	K	95/165 (58%)	91 (96%)	4 (4%)	0	100	100
13	L	149/158 (94%)	146 (98%)	3 (2%)	0	100	100
14	M	121/132 (92%)	117 (97%)	4 (3%)	0	100	100
15	N	147/151 (97%)	143 (97%)	4 (3%)	0	100	100
16	O	133/151 (88%)	129 (97%)	4 (3%)	0	100	100
17	P	122/145 (84%)	121 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	Q	140/146 (96%)	138 (99%)	2 (1%)	0	100	100
19	R	130/135 (96%)	129 (99%)	1 (1%)	0	100	100
20	S	141/152 (93%)	138 (98%)	3 (2%)	0	100	100
21	T	142/145 (98%)	139 (98%)	3 (2%)	0	100	100
22	U	99/119 (83%)	98 (99%)	1 (1%)	0	100	100
23	V	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
24	W	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
25	X	139/143 (97%)	137 (99%)	2 (1%)	0	100	100
26	Y	122/130 (94%)	121 (99%)	1 (1%)	0	100	100
27	Z	70/125 (56%)	68 (97%)	2 (3%)	0	100	100
28	a	99/101 (98%)	98 (99%)	1 (1%)	0	100	100
29	b	80/82 (98%)	76 (95%)	4 (5%)	0	100	100
30	c	59/61 (97%)	59 (100%)	0	0	100	100
31	d	53/55 (96%)	53 (100%)	0	0	100	100
32	e	54/56 (96%)	54 (100%)	0	0	100	100
33	f	70/72 (97%)	63 (90%)	7 (10%)	0	100	100
34	g	312/315 (99%)	294 (94%)	18 (6%)	0	100	100
35	j	31/180 (17%)	30 (97%)	1 (3%)	0	100	100
36	h	23/25 (92%)	23 (100%)	0	0	100	100
All	All	4844/5564 (87%)	4732 (98%)	112 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	
2	A	180/243 (74%)	180 (100%)	0	100	100
3	B	194/231 (84%)	193 (100%)	1 (0%)	86	95

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	C	184/225 (82%)	181 (98%)	3 (2%)	58	85
5	D	189/202 (94%)	185 (98%)	4 (2%)	48	80
6	E	224/225 (100%)	222 (99%)	2 (1%)	75	92
7	F	160/170 (94%)	159 (99%)	1 (1%)	84	95
8	G	200/218 (92%)	195 (98%)	5 (2%)	42	75
9	H	167/174 (96%)	166 (99%)	1 (1%)	84	95
10	I	178/180 (99%)	175 (98%)	3 (2%)	56	84
11	J	160/168 (95%)	159 (99%)	1 (1%)	84	95
12	K	88/136 (65%)	86 (98%)	2 (2%)	45	78
13	L	135/142 (95%)	133 (98%)	2 (2%)	60	86
14	M	104/108 (96%)	103 (99%)	1 (1%)	73	91
15	N	130/131 (99%)	130 (100%)	0	100	100
16	O	105/119 (88%)	103 (98%)	2 (2%)	52	82
17	P	110/130 (85%)	109 (99%)	1 (1%)	75	92
18	Q	117/121 (97%)	115 (98%)	2 (2%)	56	84
19	R	119/122 (98%)	119 (100%)	0	100	100
20	S	124/132 (94%)	121 (98%)	3 (2%)	44	77
21	T	114/115 (99%)	112 (98%)	2 (2%)	54	83
22	U	93/107 (87%)	91 (98%)	2 (2%)	47	79
23	V	67/67 (100%)	67 (100%)	0	100	100
24	W	112/113 (99%)	111 (99%)	1 (1%)	75	92
25	X	113/115 (98%)	109 (96%)	4 (4%)	31	65
26	Y	108/112 (96%)	106 (98%)	2 (2%)	52	82
27	Z	64/103 (62%)	63 (98%)	1 (2%)	58	85
28	a	88/88 (100%)	85 (97%)	3 (3%)	32	66
29	b	74/74 (100%)	72 (97%)	2 (3%)	40	74
30	c	54/54 (100%)	52 (96%)	2 (4%)	29	63
31	d	48/48 (100%)	48 (100%)	0	100	100
32	e	45/45 (100%)	45 (100%)	0	100	100
33	f	65/65 (100%)	64 (98%)	1 (2%)	60	86
34	g	272/273 (100%)	268 (98%)	4 (2%)	60	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	j	29/151 (19%)	28 (97%)	1 (3%)	32	66
36	h	24/24 (100%)	24 (100%)	0	100	100
All	All	4238/4731 (90%)	4179 (99%)	59 (1%)	62	87

5 of 59 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	P	122	THR
34	g	132	TRP
21	T	124	THR
34	g	113	PHE
29	b	17	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
25	X	16	HIS
33	f	111	ASN
25	X	20	GLN
27	Z	64	ASN
34	g	56	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1699/1869 (90%)	341 (20%)	0

5 of 341 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	3	C
1	2	17	C
1	2	26	U
1	2	33	G
1	2	35	C

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 169 ligands modelled in this entry, 169 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

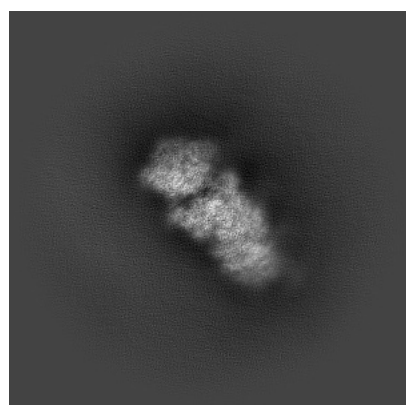
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11320. These allow visual inspection of the internal detail of the map and identification of artifacts.

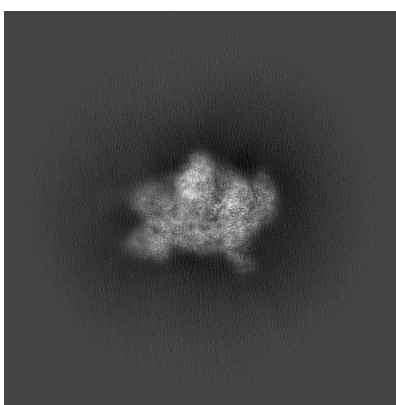
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

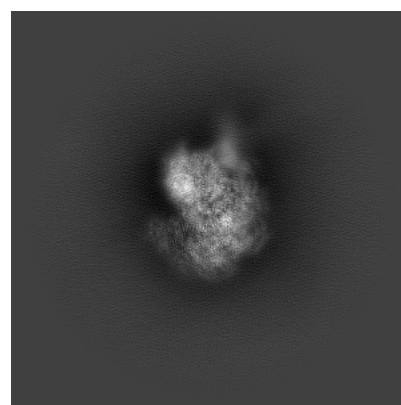
6.1.1 Primary map



X



Y

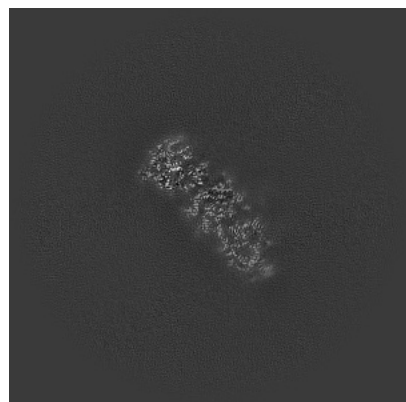


Z

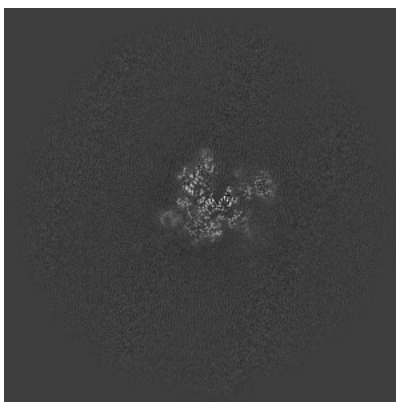
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

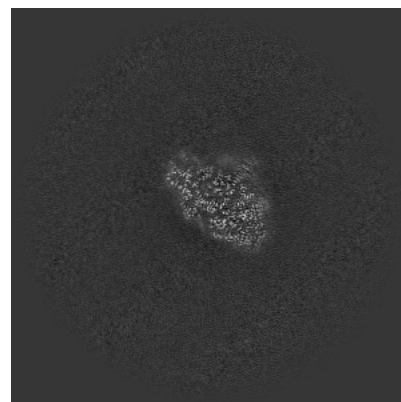
6.2.1 Primary map



X Index: 280



Y Index: 280

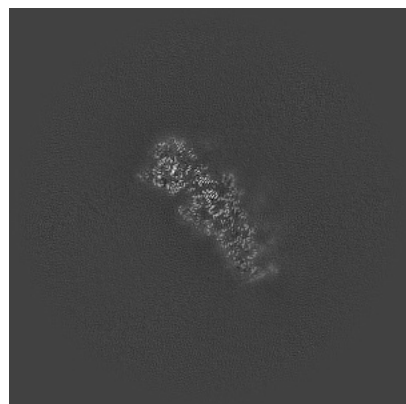


Z Index: 280

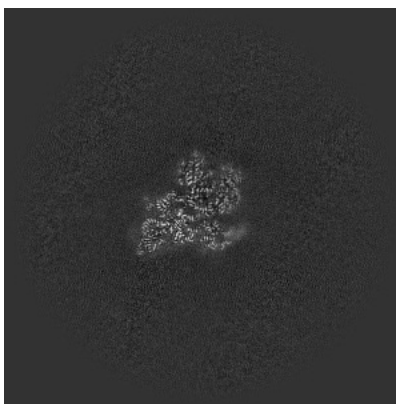
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

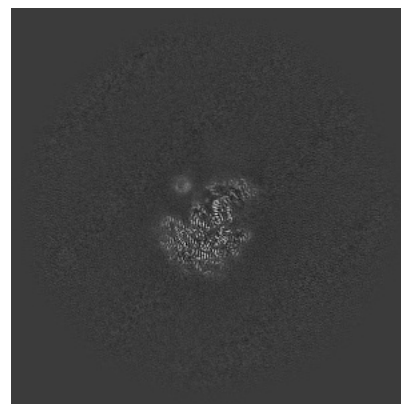
6.3.1 Primary map



X Index: 287



Y Index: 310

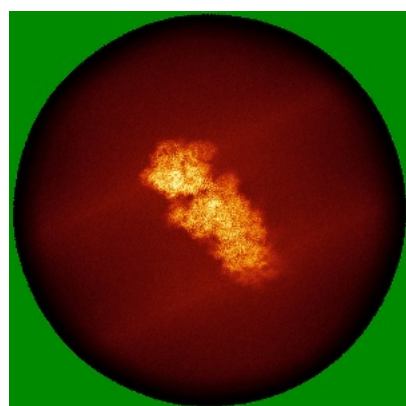


Z Index: 316

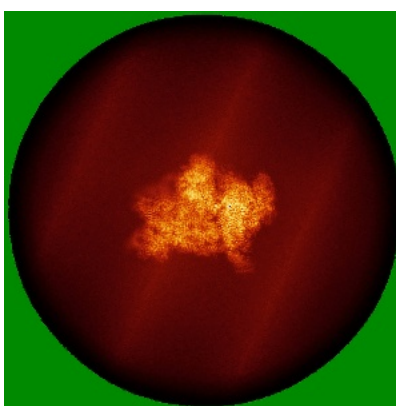
The images above show the largest variance slices of the map in three orthogonal directions.

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

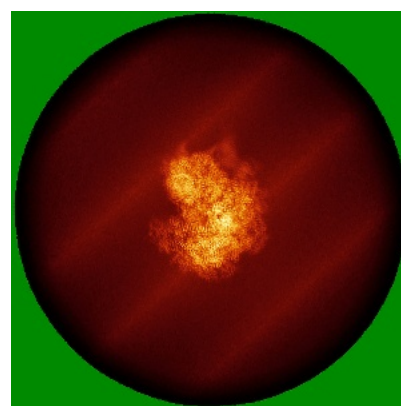
6.4.1 Primary map



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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.9. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

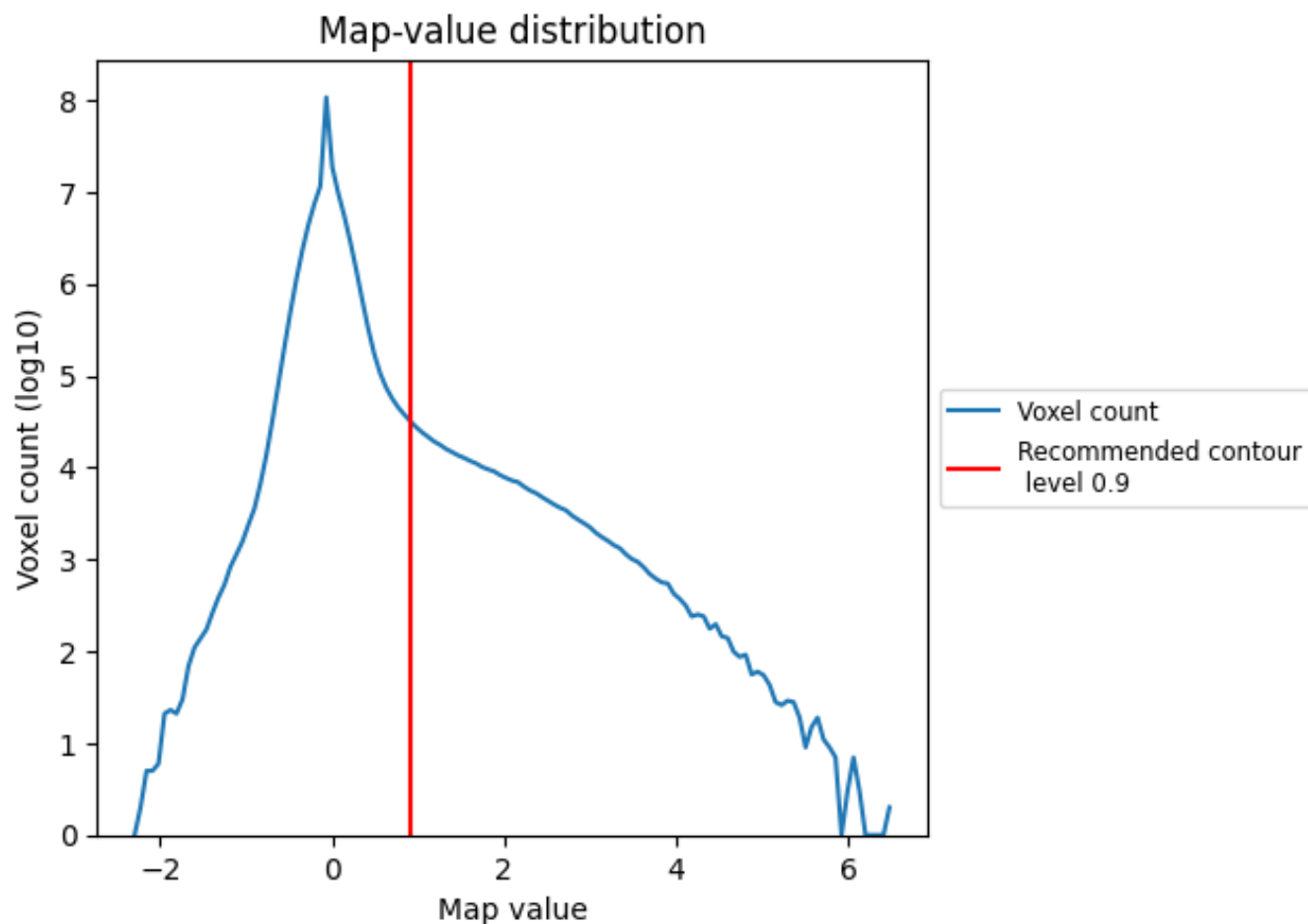
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

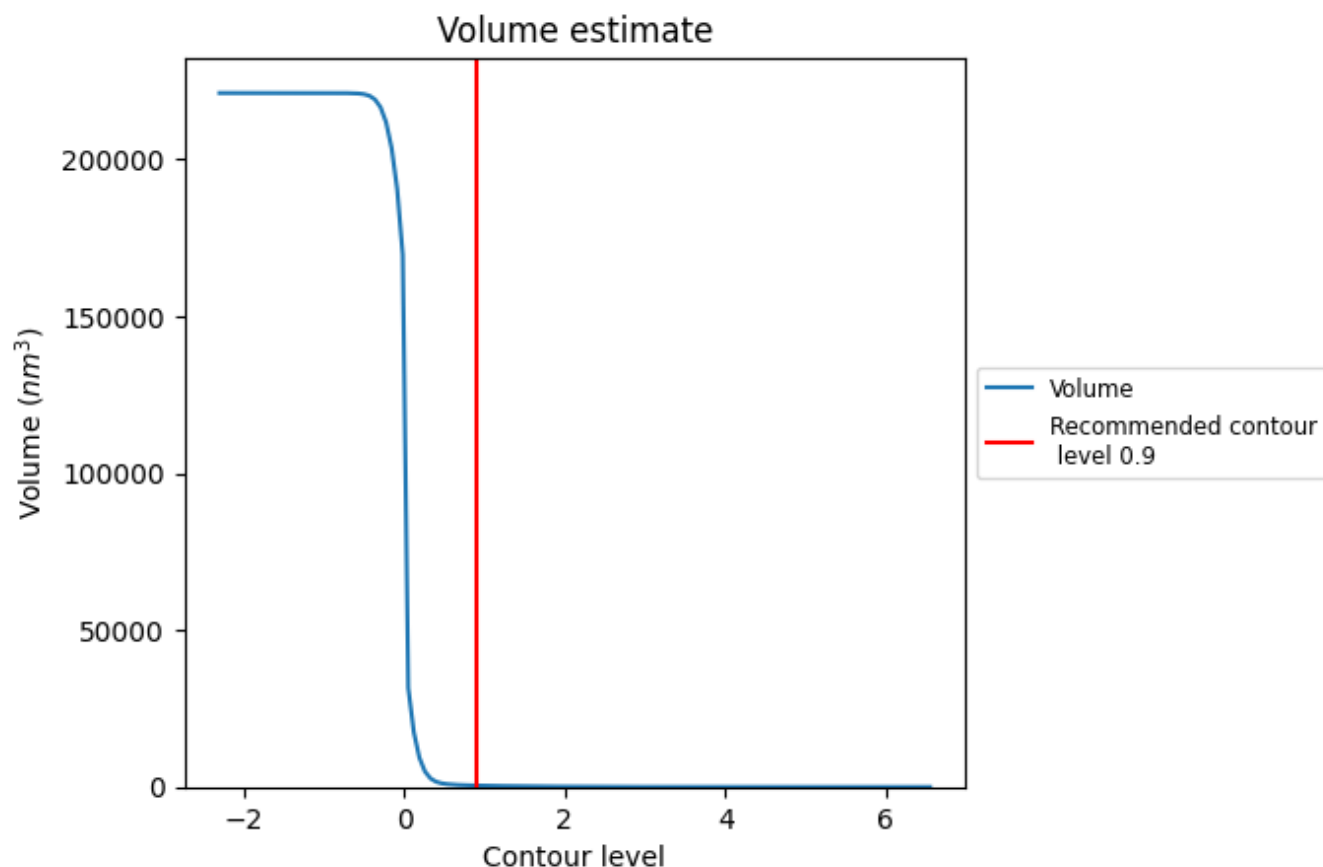
This section contains the results of statistical analysis of the map.

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.

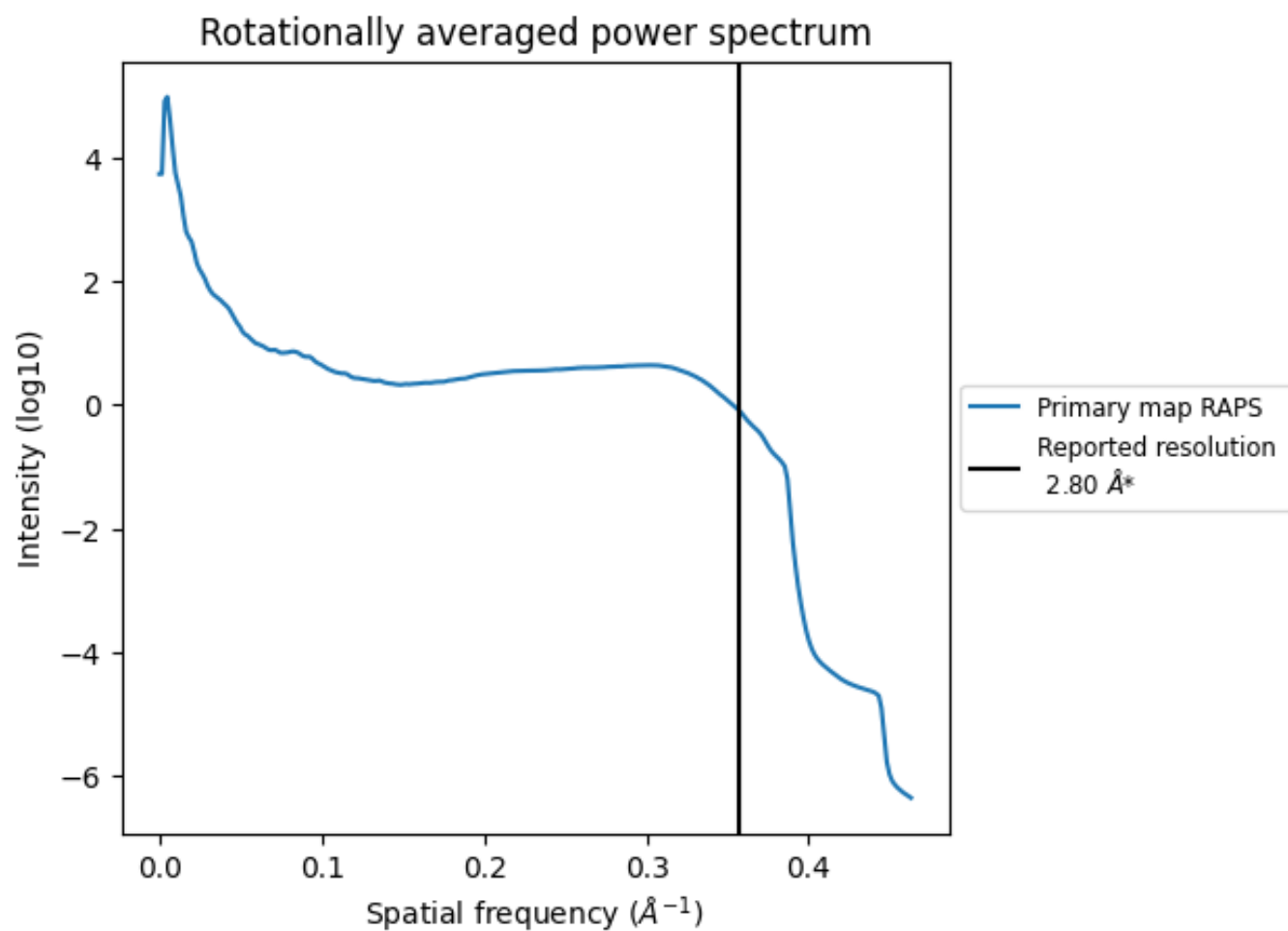
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 443 nm^3 ; this corresponds to an approximate mass of 400 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 0.357 Å⁻¹

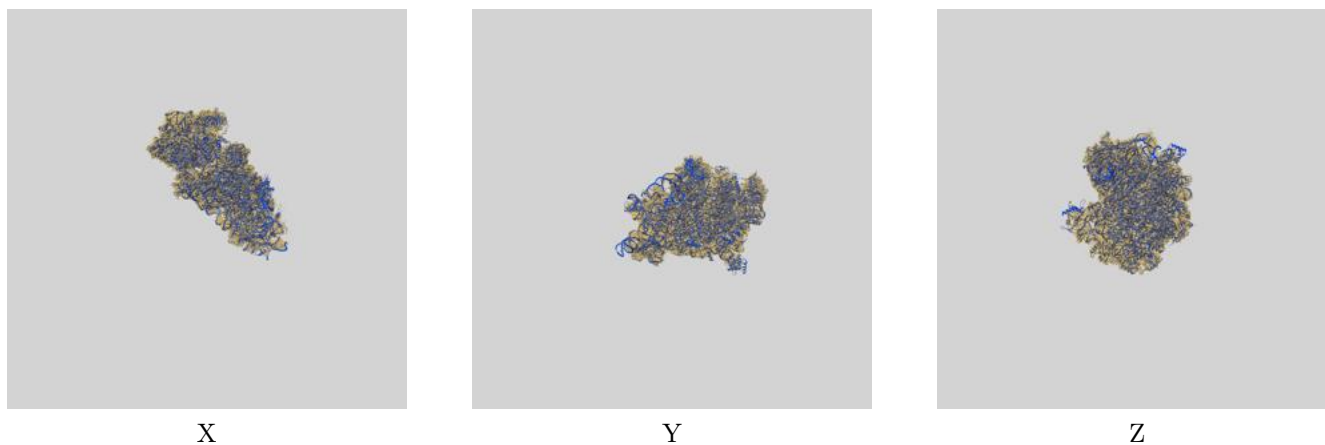
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

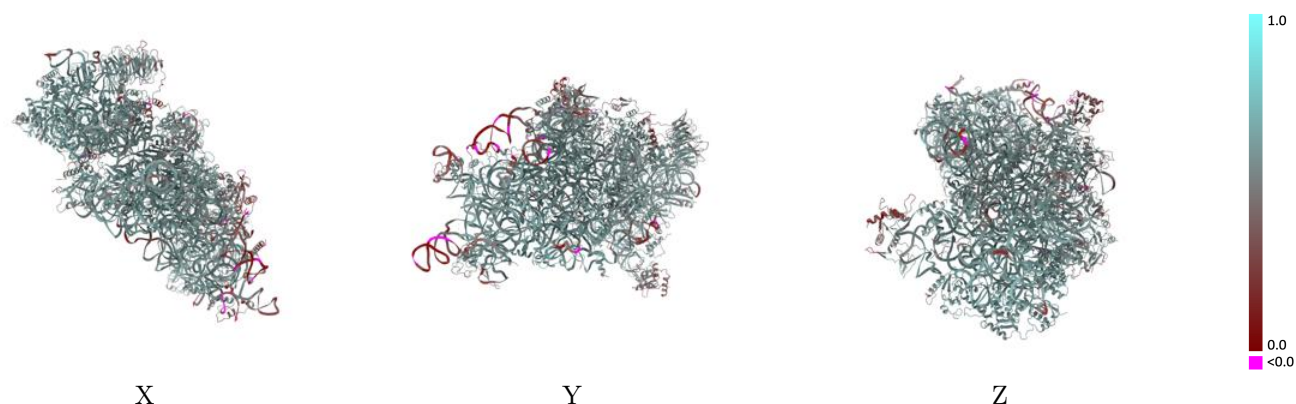
This section contains information regarding the fit between EMDB map EMD-11320 and PDB model 6ZMJ. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



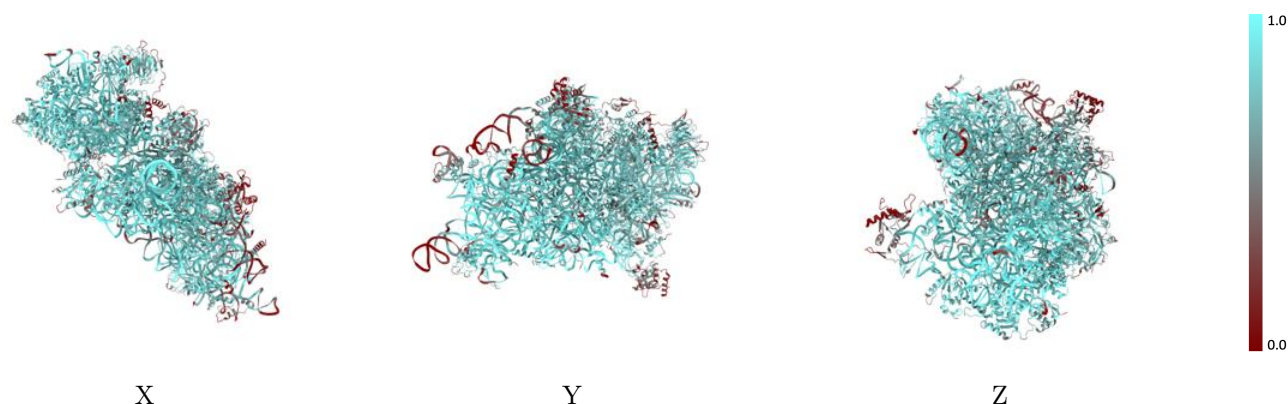
The images above show the 3D surface view of the map at the recommended contour level 0.9 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



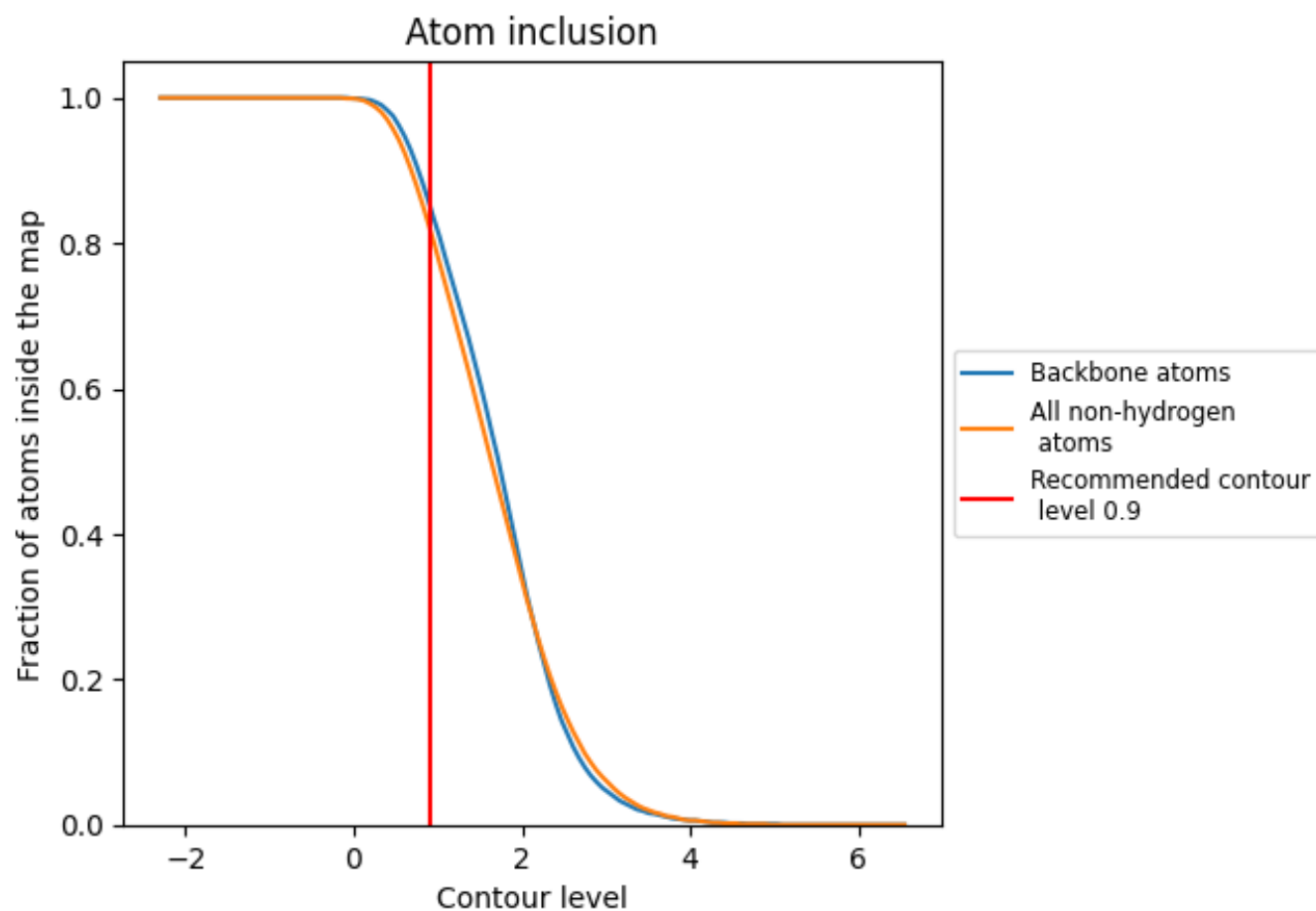
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.9).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 85% of all backbone atoms, 82% 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 (0.9) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8220	 0.5580
2	 0.8950	 0.5610
A	 0.7130	 0.5440
B	 0.7630	 0.5580
C	 0.7910	 0.5700
D	 0.7530	 0.5480
E	 0.8760	 0.6080
F	 0.8560	 0.5860
G	 0.7550	 0.5460
H	 0.3500	 0.4070
I	 0.7710	 0.5610
J	 0.8460	 0.5870
K	 0.8000	 0.5760
L	 0.7650	 0.5740
M	 0.2680	 0.3870
N	 0.7860	 0.5610
O	 0.7790	 0.5470
P	 0.8490	 0.5880
Q	 0.9110	 0.6170
R	 0.5560	 0.4730
S	 0.8560	 0.5970
T	 0.9030	 0.6050
U	 0.7560	 0.5610
V	 0.6910	 0.5500
W	 0.8390	 0.5990
X	 0.8470	 0.6010
Y	 0.8780	 0.5970
Z	 0.7450	 0.5660
a	 0.7920	 0.5550
b	 0.6700	 0.5360
c	 0.7700	 0.5590
d	 0.9140	 0.6180
e	 0.7040	 0.5420
f	 0.4140	 0.4340
g	 0.7270	 0.5320



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Chain	Atom inclusion	Q-score
h	 0.4860	 0.4870
j	 0.6470	 0.5350