



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 08:13 AM UTC

PDB ID : 6RBE / pdb_00006rbe
EMDB ID : EMD-4793
Title : State 2 of yeast Tsr1-TAP Rps20-Deltaloop pre-40S particles
Authors : Shayan, R.; Mitterer, V.; Ferreira-Cerca, S.; Murat, G.; Enne, T.; Rinaldi, D.; Weigl, S.; Omanic, H.; Gleizes, P.E.; Kressler, D.; Pertschy, B.; Plisson-Chastang, C.
Deposited on : 2019-04-10
Resolution : 3.80 Å (reported)
Based on initial models : ?, 4V88

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:

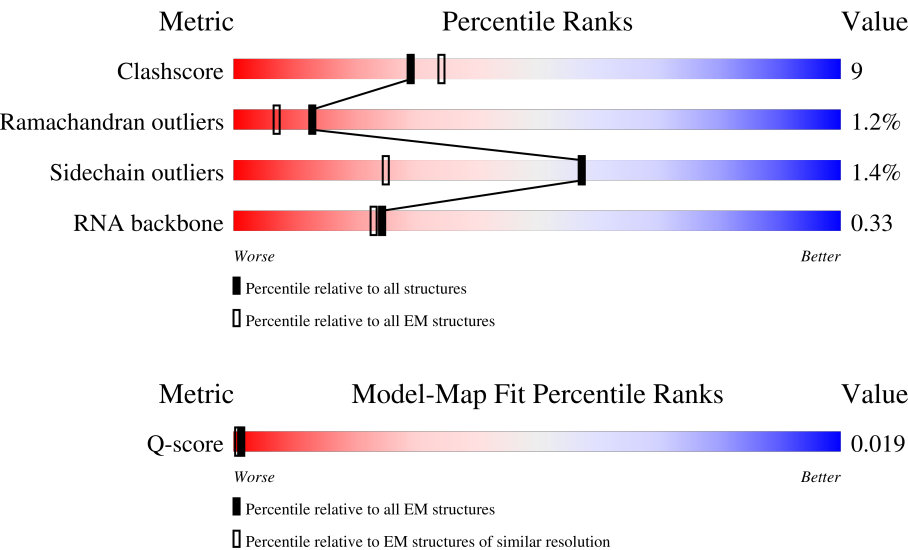
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.80 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.



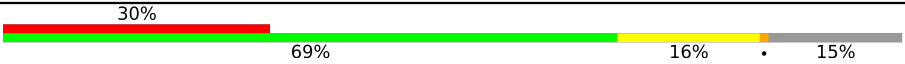
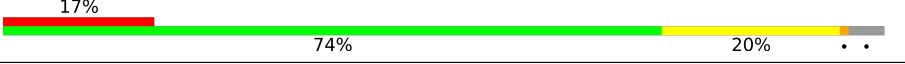
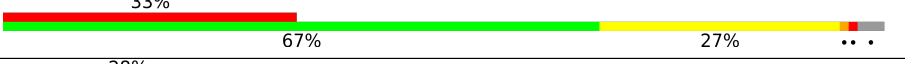
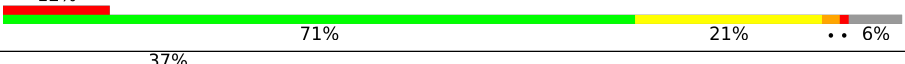
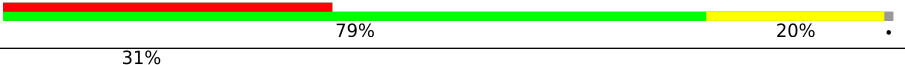
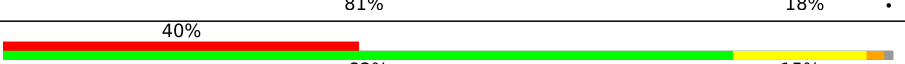
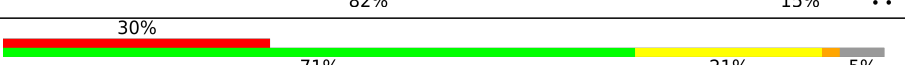
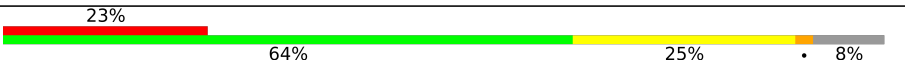
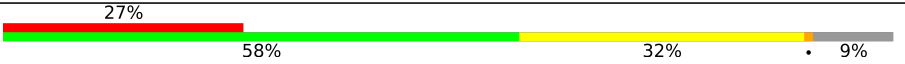
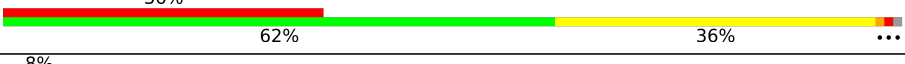
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13733 (2.97 - 3.97)

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	1800	
2	A	252	
3	B	255	

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Mol	Chain	Length	Quality of chain
4	C	254	
5	E	261	
6	G	236	
7	H	190	
8	I	200	
9	J	197	
10	L	156	
11	N	151	
12	O	137	
13	R	136	
14	V	87	
15	W	130	
16	X	145	
17	Y	135	
18	b	82	
19	d	56	
20	e	63	
21	D	240	
22	F	225	
23	K	105	
24	M	143	
25	P	142	
26	Q	143	
27	S	146	
28	T	144	

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Mol	Chain	Length	Quality of chain
29	U	121	
30	Z	108	
31	c	67	
32	f	152	
33	g	319	

2 Entry composition

There are 33 unique types of molecules in this entry. The entry contains 72721 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	1750	Total	C	N	O	P	0	0
			37285	16669	6597	12269	1750		

- Molecule 2 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	206	Total	C	N	O	S	0	0
			1577	1014	278	283	2		

- Molecule 3 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	113	Total	C	N	O	S	0	0
			918	584	169	164	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	217	Total	C	N	O	S	0	0
			1635	1047	289	297	2		

- Molecule 5 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	260	Total	C	N	O	S	0	0
			2068	1316	389	360	3		

- Molecule 6 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	226	Total	C	N	O	S	0	0
			1799	1129	346	321	3		

- Molecule 7 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	H	184	Total	C	N	O	0	0
			1481	951	265	265		

- Molecule 8 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	188	Total	C	N	O	S	0	0
			1489	925	298	264	2		

- Molecule 9 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 10 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	155	Total	C	N	O	S	0	0
			1213	774	230	206	3		

- Molecule 11 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	N	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 12 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	O	18	Total	C	N	O	0	0
			141	83	35	23		

- Molecule 13 is a protein called 40S ribosomal protein S17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	R	120	Total	C	N	O	S	0	0
			926	577	177	170	2		

- Molecule 14 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	V	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 15 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	W	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 16 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	X	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 17 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Y	134	Total	C	N	O	S	0	0
			1073	676	208	189			

- Molecule 18 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	b	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 19 is a protein called 40S ribosomal protein S29-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	d	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 20 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	e	60	Total	C	N	O	S	0	0
			475	299	98	77	1		

- Molecule 21 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	D	223	Total	C	N	O	S	0	0
			1734	1101	313	314	6		

- Molecule 22 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	F	206	Total	C	N	O	S	0	0
			1609	1007	300	299	3		

- Molecule 23 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	K	96	Total	C	N	O	S	0	0
			772	499	126	145	2		

- Molecule 24 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	M	124	Total	C	N	O	S	0	0
			890	560	156	172	2		

- Molecule 25 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	P	124	Total	C	N	O	S	0	0
			977	622	182	166	7		

- Molecule 26 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Q	141	Total	C	N	O		0	0
			1105	708	203	194			

- Molecule 27 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	S	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		

- Molecule 28 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	T	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 29 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	U	98	Total	C	N	O	S	0	0
			792	502	144	145	1		

- Molecule 30 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Z	70	Total	C	N	O		0	0
			563	360	104	99			

- Molecule 31 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	c	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 32 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	51	Total	C	N	O	S	0	0
			397	249	73	71	4		

- Molecule 33 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	318	Total	C	N	O	S	0	0
			2437	1541	418	470	8		

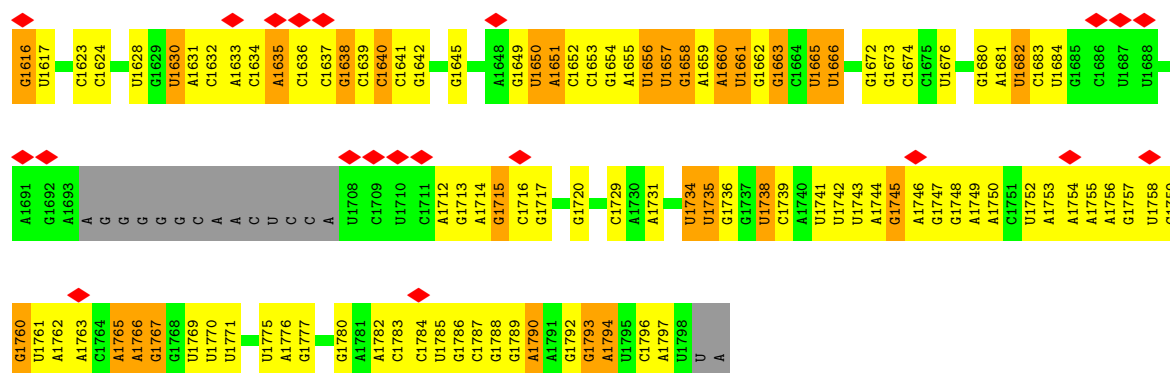
3 Residue-property plots

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.

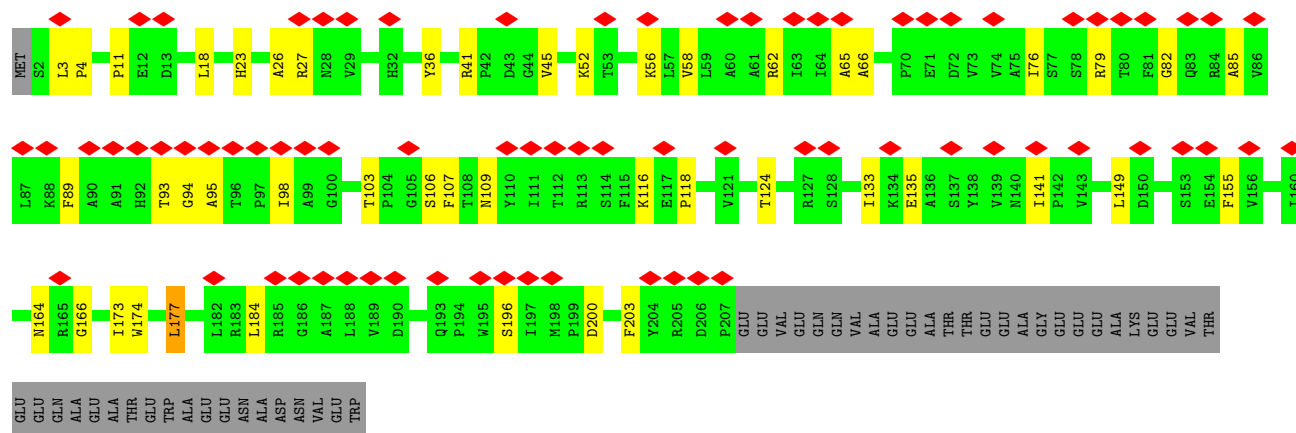
• Molecule 1: 18S ribosomal RNA



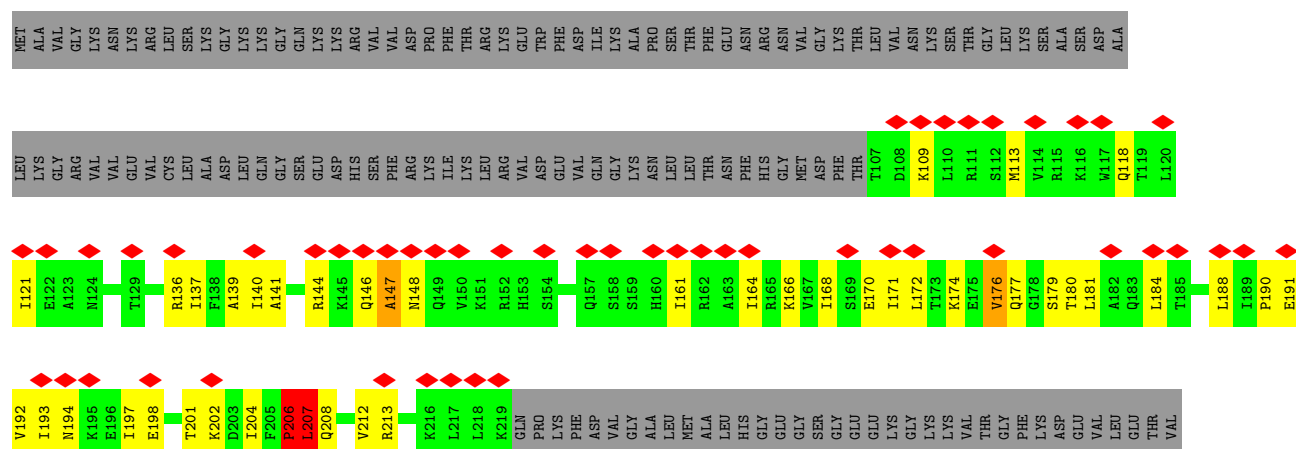




• Molecule 2: 40S ribosomal protein S0-A

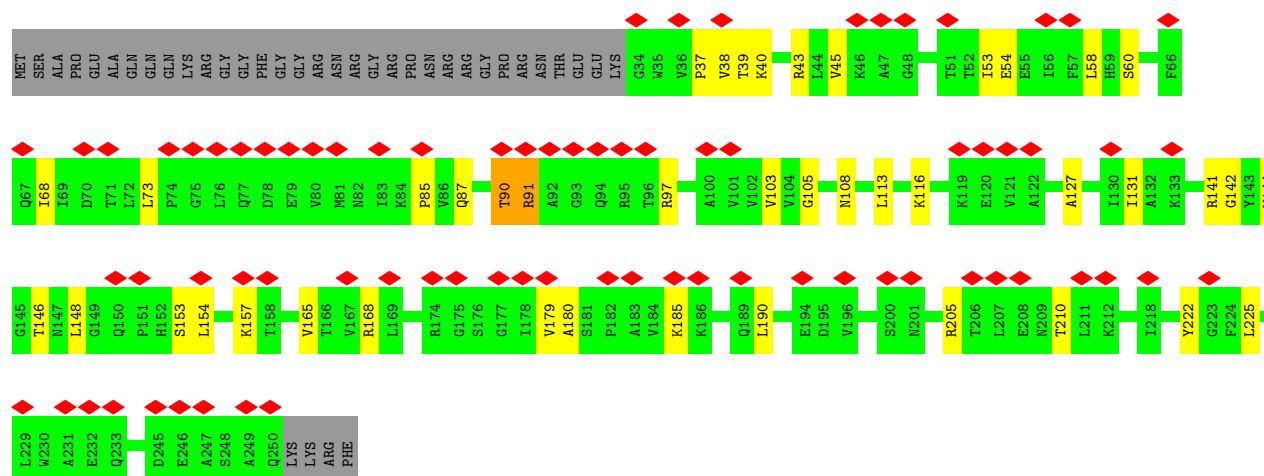


• Molecule 3: 40S ribosomal protein S1-A

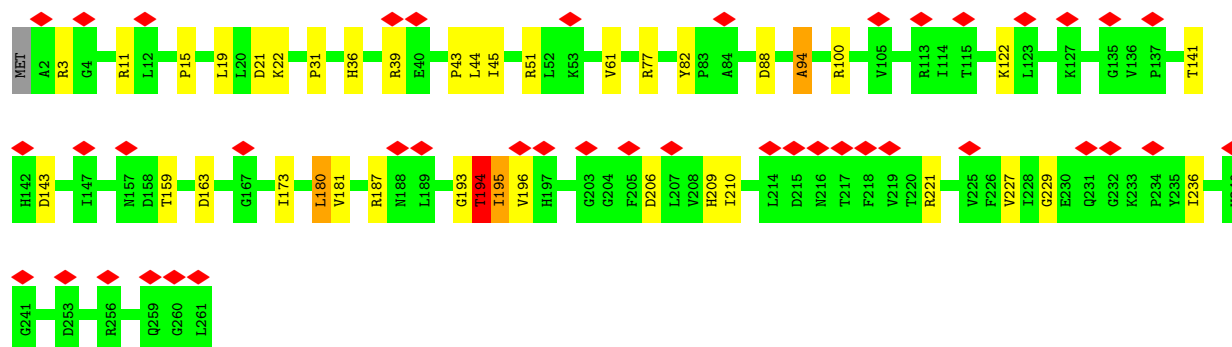
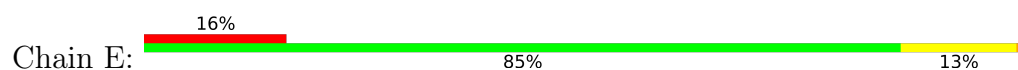


• Molecule 4: 40S ribosomal protein S2

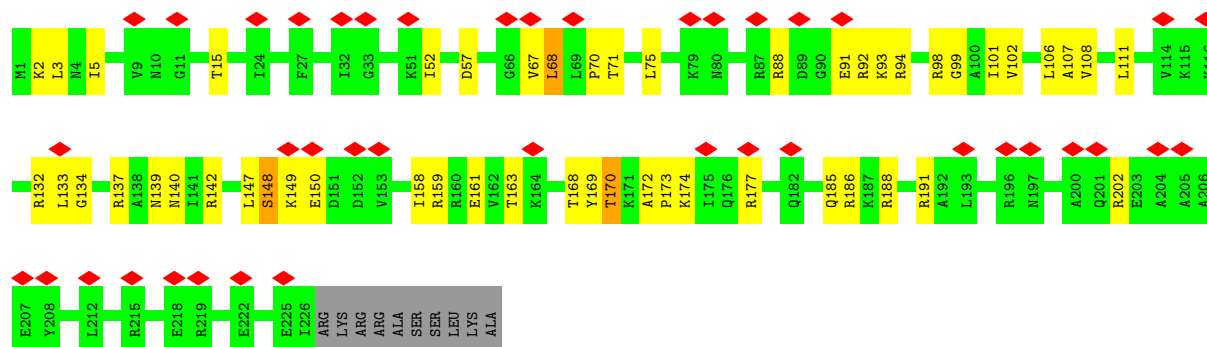
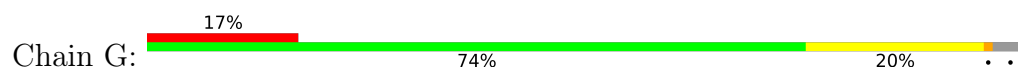




• Molecule 5: 40S ribosomal protein S4-A

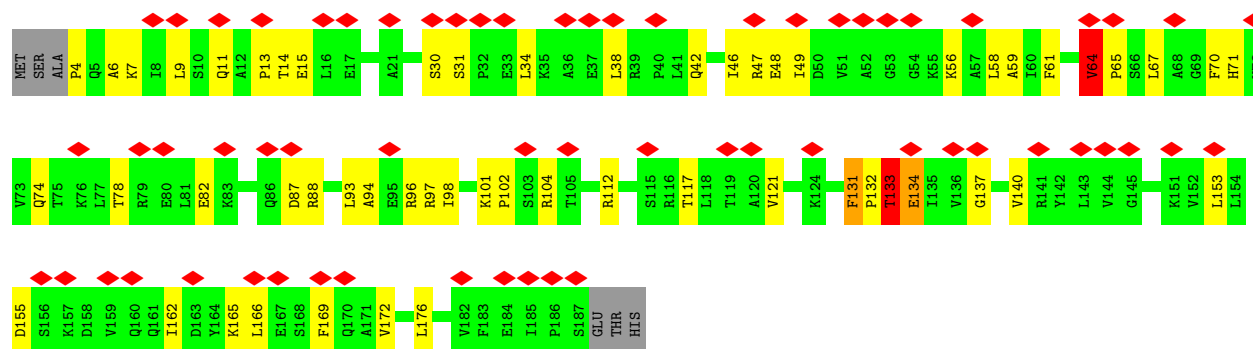


• Molecule 6: 40S ribosomal protein S6-A

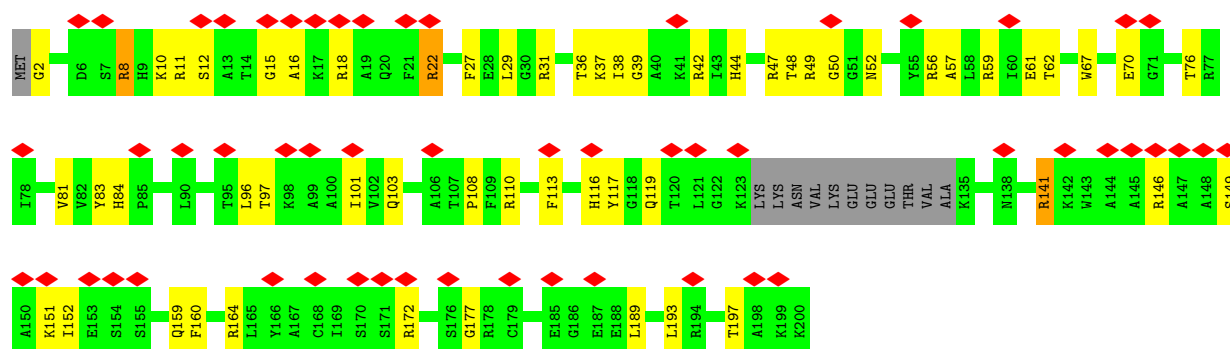


• Molecule 7: 40S ribosomal protein S7-A

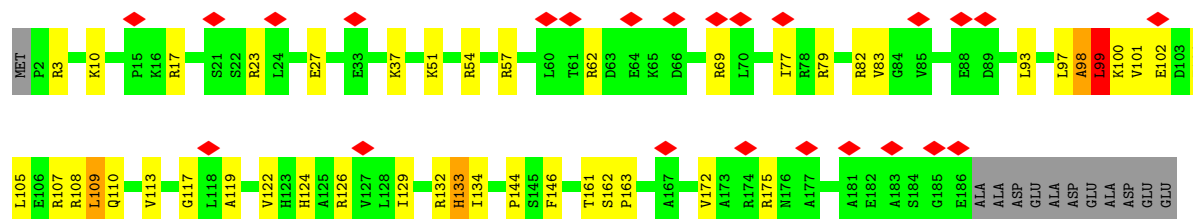




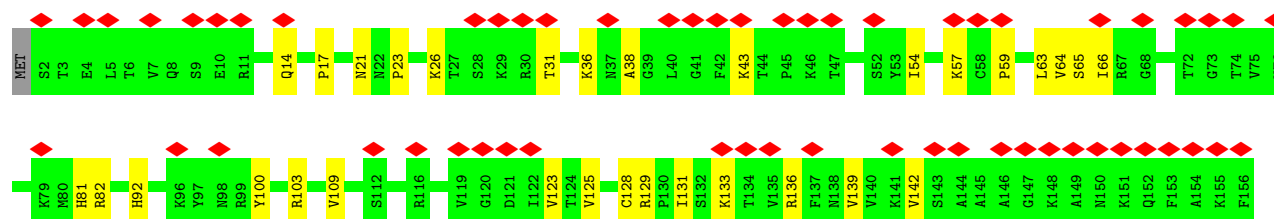
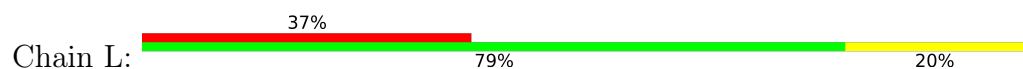
• Molecule 8: 40S ribosomal protein S8-A



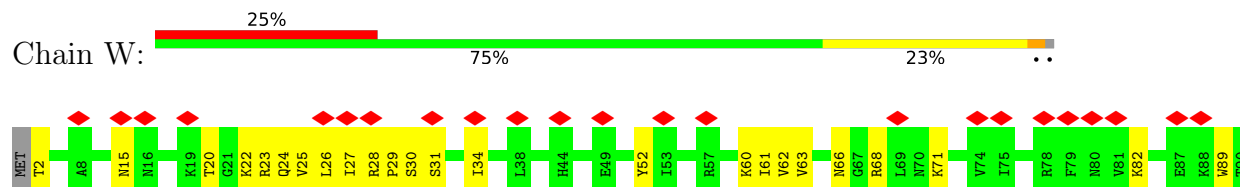
• Molecule 9: 40S ribosomal protein S9-A

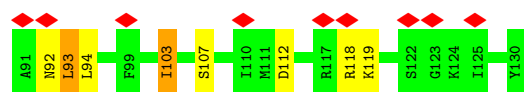


• Molecule 10: 40S ribosomal protein S11-A

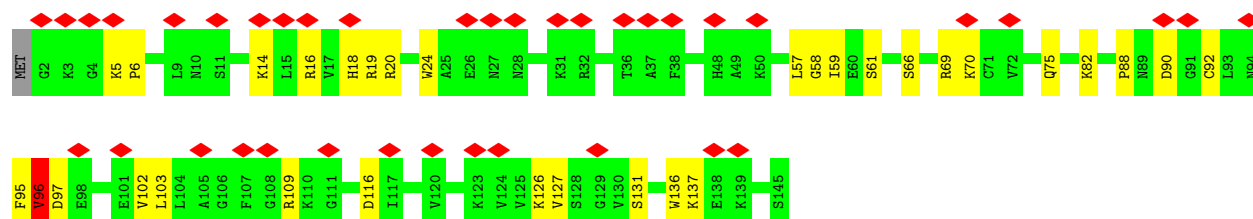
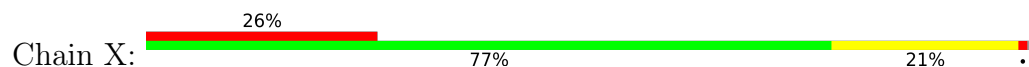


• Molecule 11: 40S ribosomal protein S13

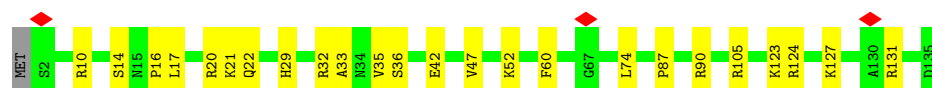
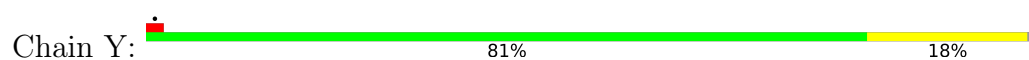




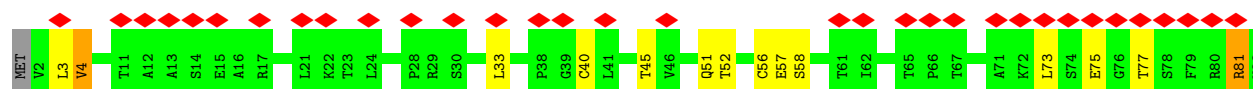
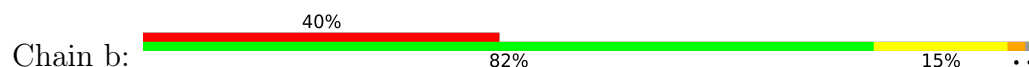
- Molecule 16: 40S ribosomal protein S23-A



- Molecule 17: 40S ribosomal protein S24-A



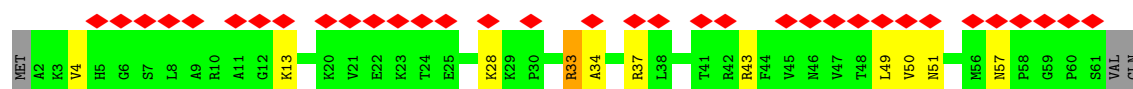
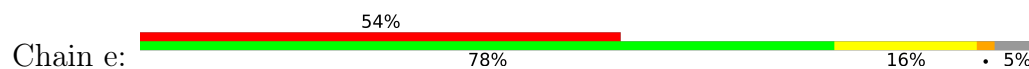
- Molecule 18: 40S ribosomal protein S27-A



- Molecule 19: 40S ribosomal protein S29-A



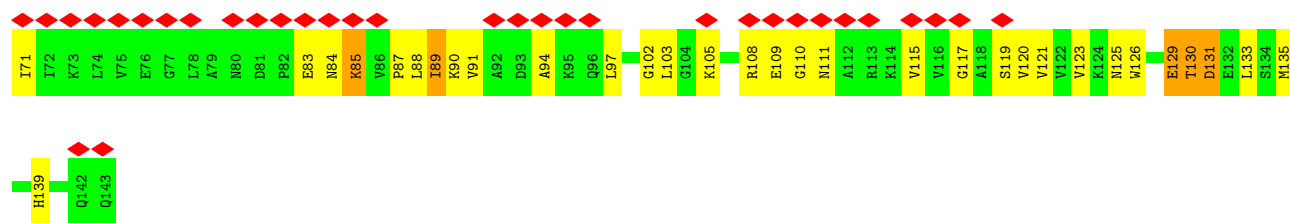
- Molecule 20: 40S ribosomal protein S30-A



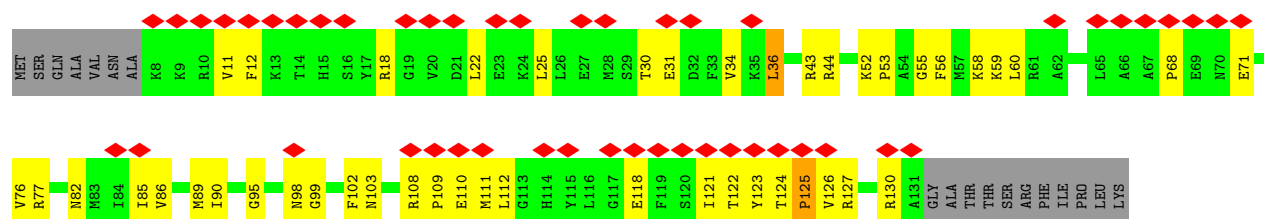
- Molecule 21: 40S ribosomal protein S3



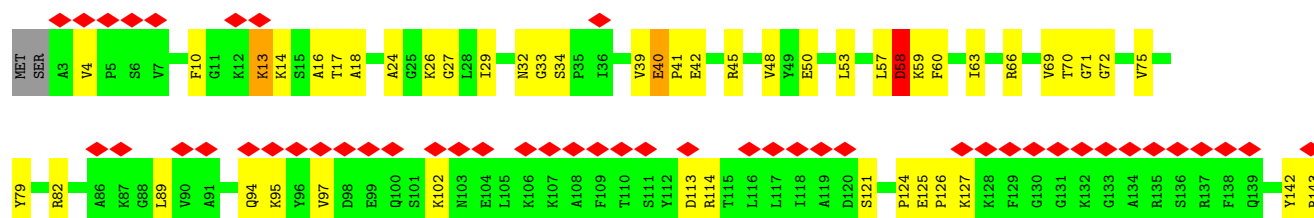




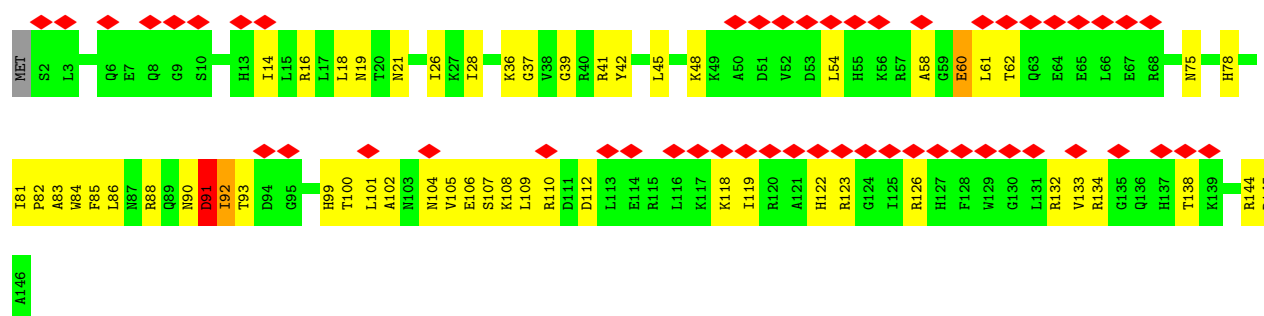
• Molecule 25: 40S ribosomal protein S15



• Molecule 26: 40S ribosomal protein S16-A



• Molecule 27: 40S ribosomal protein S18-A



• Molecule 28: 40S ribosomal protein S19-A





L301	F241	W181	M121	F61	MET
F302	S242	N182	I122	K62	A2
A303	L243	L183	I123	G63	S3
G304	A244	N184	S124	H64	N4
Y305	F245	Q185	G125	S65	E5
T306	S246	F186	S126	H66	V6
D307	P247	Q187	R127	I67	L7
N308	N248	I188	D128	V68	V8
V309	R249	E189	K129	Q69	L9
I310	Y250	A190	T130	D70	R10
R311	W251	D191	I131	C71	G11
V312	L252	F192	K132	T72	T12
W313	A253	L193	V133	L73	L13
Q314	A254	G194	W134	T74	E14
V315	A255	H195	T135	A75	G15
M316	T256	N196	I136	D76	H16
T317	A257	S197	K137	G77	M17
A318	T258	N198	G138	A78	G18
N319	G259	I199	Q139	Y79	W19
	L260	N200	C140	A80	V20
	K261	T201	L141	L81	T21
	V262	L202	A142	S82	S22
	F263	T203	T143	A83	L23
	S264	A204	L144	S84	A24
	L265	S205	L145	W85	T25
	D266	P206	G146	D86	S26
	P267	D207	H147	K87	A27
	Q268	G208	N148	T88	G28
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	V271	T211	V151	L91	N31
	D272	A212	S152	W92	L32
	D273	S213	Q153	D93	L33
	L274	A214	V154	V94	L34
	R275	G215	R155	A95	S35
	P276	T216	V156	T96	A36
	E277	D217	V157	G97	S37
	F278	G218	P158	E98	R38
	A279	E219	N159	T99	D39
	G280	T220	E160	Y100	K40
	Y281	M221	K161	Q101	T41
	S282	L222	A162	R102	L42
	A284	W223	D163	F103	I43
	A285	N224	D164	S44	S44
		L225	D165	G105	W45
	E286	A226	S166	H106	K46
	P287	A227	V167	K107	L47
	H288	K228	T168	S108	T48
	A289	K229	I169	D109	G49
	V290	A230	I170	V110	D50
	S291	M231	S171	M111	D51
	L292	T232	A172	S112	Q52
	A293	T233	G173	V113	A53
	W294	L234	N174	D114	F54
	S295	S235	D175	I115	G55
	A296	A236	K176	D116	V56
	D297	Q237	M177	K117	P57
	G298	D238	V178	K118	V58
	Q299	E239	L179	A119	A59
	T300	W240	A180	S120	S60

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	42901	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 ($e^-/\text{\AA}^2$)	32.4	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.528	Depositor
Minimum map value	-0.170	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.020	Depositor
Recommended contour level	0.075	Depositor
Map size (Å)	409.72803, 409.72803, 409.72803	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.067, 1.067, 1.067	Depositor

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	2	0.32	0/41697	0.53	9/64961 (0.0%)
2	A	0.38	0/1617	0.95	7/2215 (0.3%)
3	B	0.31	0/929	0.99	8/1250 (0.6%)
4	C	0.45	1/1665 (0.1%)	0.81	2/2263 (0.1%)
5	E	0.43	0/2109	0.91	6/2839 (0.2%)
6	G	0.36	0/1823	0.80	0/2439
7	H	0.36	0/1506	1.00	3/2028 (0.1%)
8	I	0.40	0/1514	0.87	1/2021 (0.0%)
9	J	0.40	0/1519	0.88	3/2035 (0.1%)
10	L	0.42	0/1239	0.77	0/1673
11	N	0.31	0/1215	0.96	7/1638 (0.4%)
12	O	0.36	0/142	1.08	1/185 (0.5%)
13	R	0.35	0/935	0.99	4/1254 (0.3%)
14	V	0.41	0/693	0.93	4/935 (0.4%)
15	W	0.51	0/1038	0.83	1/1395 (0.1%)
16	X	0.42	0/1139	0.94	2/1518 (0.1%)
17	Y	0.40	0/1087	0.86	2/1449 (0.1%)
18	b	0.33	0/620	0.99	2/838 (0.2%)
19	d	0.27	0/452	0.82	0/600
20	e	0.34	0/483	0.83	1/643 (0.2%)
21	D	0.30	0/1759	0.81	0/2368
22	F	0.33	0/1629	0.88	2/2202 (0.1%)
23	K	0.35	0/789	0.97	1/1067 (0.1%)
24	M	0.38	0/898	1.25	10/1220 (0.8%)
25	P	0.32	0/998	0.87	0/1341
26	Q	0.33	0/1125	1.22	7/1510 (0.5%)
27	S	0.32	0/1211	0.86	0/1628
28	T	0.38	0/1130	0.92	5/1517 (0.3%)
29	U	0.29	0/798	0.78	0/1075
30	Z	0.32	0/571	1.03	3/768 (0.4%)
31	c	0.28	0/499	0.82	0/670
32	f	0.34	0/404	0.96	0/542
33	g	0.33	0/2490	0.77	2/3389 (0.1%)
All	All	0.34	1/77723 (0.0%)	0.72	93/113476 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	A	0	3
3	B	0	2
4	C	0	4
5	E	0	2
6	G	0	1
7	H	0	4
8	I	0	2
9	J	0	6
11	N	0	4
12	O	0	1
13	R	0	2
14	V	0	4
15	W	0	2
16	X	0	3
17	Y	0	2
21	D	0	2
22	F	0	8
23	K	0	3
24	M	0	8
25	P	0	2
26	Q	0	3
27	S	0	3
28	T	0	2
29	U	0	2
30	Z	0	3
32	f	0	4
33	g	0	1
All	All	0	83

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	225	LEU	C-N	-6.55	1.20	1.33

The worst 5 of 93 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	Q	124	PRO	CA-C-N	15.63	150.63	120.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	Q	124	PRO	C-N-CA	15.63	150.63	120.94
26	Q	40	GLU	CA-C-N	13.23	136.38	119.84
26	Q	40	GLU	C-N-CA	13.23	136.38	119.84
11	N	22	ALA	CA-C-N	10.80	133.34	119.84

There are no chirality outliers.

5 of 83 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	166	GLY	Peptide
2	A	3	LEU	Peptide
2	A	94	GLY	Peptide
3	B	147	ALA	Peptide
3	B	206	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	2	37285	0	18766	523	0
2	A	1577	0	1567	25	0
3	B	918	0	987	29	0
4	C	1635	0	1722	27	0
5	E	2068	0	2154	22	0
6	G	1799	0	1879	38	0
7	H	1481	0	1572	29	0
8	I	1489	0	1525	38	0
9	J	1494	0	1573	28	0
10	L	1213	0	1257	22	0
11	N	1192	0	1255	16	0
12	O	141	0	155	4	0
13	R	926	0	930	26	0
14	V	684	0	672	19	0
15	W	1021	0	1060	22	0
16	X	1121	0	1196	22	0
17	Y	1073	0	1132	13	0
18	b	610	0	633	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	d	442	0	432	9	0
20	e	475	0	525	10	0
21	D	1734	0	1817	43	0
22	F	1609	0	1675	49	0
23	K	772	0	727	21	0
24	M	890	0	887	24	0
25	P	977	0	1002	29	0
26	Q	1105	0	1166	39	0
27	S	1192	0	1222	39	0
28	T	1112	0	1124	35	0
29	U	792	0	851	22	0
30	Z	563	0	603	12	0
31	c	497	0	535	14	0
32	f	397	0	399	17	0
33	g	2437	0	2386	73	0
All	All	72721	0	55386	1125	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 9.

The worst 5 of 1125 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)
1:2:1047:G:H1	1:2:1071:U:H3	1.04	1.04
1:2:567:A:H62	1:2:576:G:N2	1.61	0.99
1:2:996:U:H3	1:2:1008:G:H1	1.00	0.98
1:2:1170:G:H1	1:2:1469:A:N6	1.62	0.98
1:2:875:G:H1	1:2:952:A:H61	1.05	0.94

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	
2	A	204/252 (81%)	160 (78%)	42 (21%)	2 (1%)	12	43
3	B	111/255 (44%)	93 (84%)	15 (14%)	3 (3%)	4	27
4	C	215/254 (85%)	194 (90%)	20 (9%)	1 (0%)	24	57
5	E	258/261 (99%)	235 (91%)	22 (8%)	1 (0%)	30	62
6	G	224/236 (95%)	204 (91%)	15 (7%)	5 (2%)	5	30
7	H	182/190 (96%)	146 (80%)	29 (16%)	7 (4%)	2	21
8	I	184/200 (92%)	157 (85%)	25 (14%)	2 (1%)	11	41
9	J	183/197 (93%)	164 (90%)	17 (9%)	2 (1%)	11	41
10	L	153/156 (98%)	139 (91%)	14 (9%)	0	100	100
11	N	148/151 (98%)	136 (92%)	9 (6%)	3 (2%)	6	32
12	O	16/137 (12%)	13 (81%)	3 (19%)	0	100	100
13	R	116/136 (85%)	103 (89%)	11 (10%)	2 (2%)	7	34
14	V	85/87 (98%)	64 (75%)	19 (22%)	2 (2%)	4	29
15	W	127/130 (98%)	111 (87%)	16 (13%)	0	100	100
16	X	142/145 (98%)	115 (81%)	25 (18%)	2 (1%)	9	37
17	Y	132/135 (98%)	121 (92%)	11 (8%)	0	100	100
18	b	79/82 (96%)	66 (84%)	12 (15%)	1 (1%)	9	38
19	d	51/56 (91%)	48 (94%)	3 (6%)	0	100	100
20	e	58/63 (92%)	53 (91%)	5 (9%)	0	100	100
21	D	221/240 (92%)	203 (92%)	16 (7%)	2 (1%)	14	45
22	F	204/225 (91%)	177 (87%)	25 (12%)	2 (1%)	12	43
23	K	94/105 (90%)	76 (81%)	17 (18%)	1 (1%)	11	41
24	M	122/143 (85%)	88 (72%)	28 (23%)	6 (5%)	1	17
25	P	122/142 (86%)	101 (83%)	19 (16%)	2 (2%)	7	35
26	Q	139/143 (97%)	125 (90%)	11 (8%)	3 (2%)	5	30
27	S	143/146 (98%)	119 (83%)	21 (15%)	3 (2%)	5	31
28	T	141/144 (98%)	125 (89%)	16 (11%)	0	100	100
29	U	90/121 (74%)	83 (92%)	6 (7%)	1 (1%)	11	41
30	Z	68/108 (63%)	58 (85%)	9 (13%)	1 (2%)	8	36
31	c	61/67 (91%)	55 (90%)	6 (10%)	0	100	100
32	f	49/152 (32%)	37 (76%)	11 (22%)	1 (2%)	6	32
33	g	316/319 (99%)	285 (90%)	31 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	4438/5178 (86%)	3854 (87%)	529 (12%)	55 (1%)	13	40

5 of 55 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	E	195	ILE
6	G	173	PRO
9	J	99	LEU
11	N	22	ALA
14	V	81	ASN

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	164/210 (78%)	162 (99%)	2 (1%)	63	72
3	B	104/224 (46%)	103 (99%)	1 (1%)	68	74
4	C	176/205 (86%)	176 (100%)	0	100	100
5	E	221/222 (100%)	217 (98%)	4 (2%)	51	67
6	G	188/201 (94%)	186 (99%)	2 (1%)	65	73
7	H	165/170 (97%)	163 (99%)	2 (1%)	63	72
8	I	150/161 (93%)	150 (100%)	0	100	100
9	J	158/166 (95%)	155 (98%)	3 (2%)	50	66
10	L	129/137 (94%)	129 (100%)	0	100	100
11	N	127/128 (99%)	124 (98%)	3 (2%)	43	62
12	O	15/105 (14%)	15 (100%)	0	100	100
13	R	94/124 (76%)	91 (97%)	3 (3%)	34	56
14	V	74/74 (100%)	70 (95%)	4 (5%)	20	45
15	W	110/111 (99%)	108 (98%)	2 (2%)	51	67
16	X	119/120 (99%)	119 (100%)	0	100	100
17	Y	112/113 (99%)	110 (98%)	2 (2%)	51	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	b	70/71 (99%)	69 (99%)	1 (1%)	59	70
19	d	47/49 (96%)	46 (98%)	1 (2%)	47	64
20	e	51/54 (94%)	50 (98%)	1 (2%)	48	65
21	D	182/195 (93%)	178 (98%)	4 (2%)	45	63
22	F	173/191 (91%)	170 (98%)	3 (2%)	53	67
23	K	77/98 (79%)	76 (99%)	1 (1%)	61	71
24	M	88/119 (74%)	88 (100%)	0	100	100
25	P	101/118 (86%)	100 (99%)	1 (1%)	68	74
26	Q	117/119 (98%)	117 (100%)	0	100	100
27	S	128/129 (99%)	127 (99%)	1 (1%)	73	76
28	T	115/116 (99%)	112 (97%)	3 (3%)	40	60
29	U	93/114 (82%)	92 (99%)	1 (1%)	65	73
30	Z	61/89 (68%)	57 (93%)	4 (7%)	15	41
31	c	56/60 (93%)	56 (100%)	0	100	100
32	f	43/135 (32%)	41 (95%)	2 (5%)	23	48
33	g	259/262 (99%)	259 (100%)	0	100	100
All	All	3767/4390 (86%)	3716 (99%)	51 (1%)	57	70

5 of 51 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	b	4	VAL
22	F	84	LYS
32	f	108	VAL
19	d	28	THR
21	D	158	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 63 such sidechains are listed below:

Mol	Chain	Res	Type
11	N	62	GLN
30	Z	37	GLN
17	Y	34	ASN
28	T	129	GLN
33	g	69	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1743/1800 (96%)	627 (35%)	49 (2%)

5 of 627 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	4	C
1	2	14	C
1	2	20	G
1	2	23	G

5 of 49 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	782	U
1	2	1226	A
1	2	783	G
1	2	1051	G
1	2	1250	U

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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	2	2
29	U	2
4	C	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	839:U	O3'	840:U	P	4.31
1	2	1654:G	O3'	1655:A	P	4.14
1	U	84:MET	C	85:ARG	N	3.97
1	U	61:LYS	C	62:VAL	N	3.80
1	C	225:LEU	C	226:THR	N	1.20

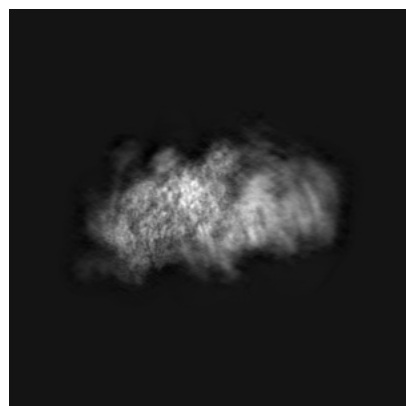
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4793. These allow visual inspection of the internal detail of the map and identification of artifacts.

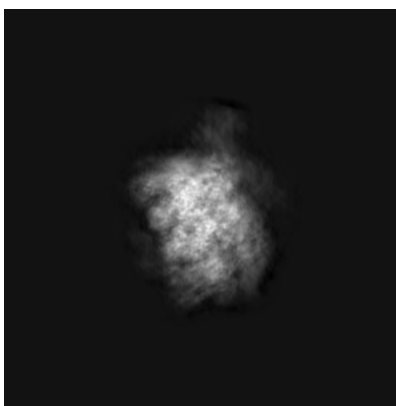
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

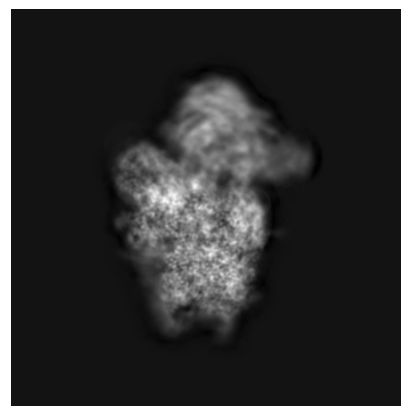
6.1.1 Primary map



X

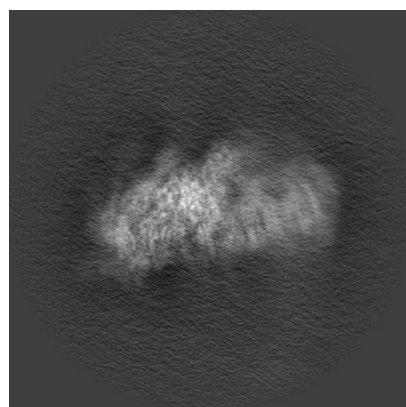


Y

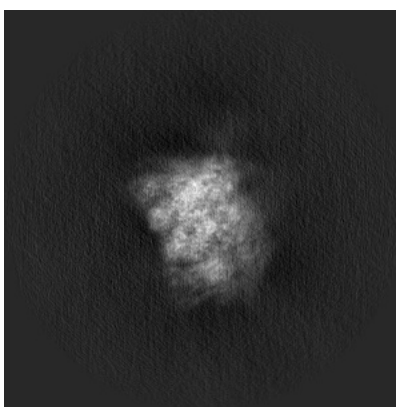


Z

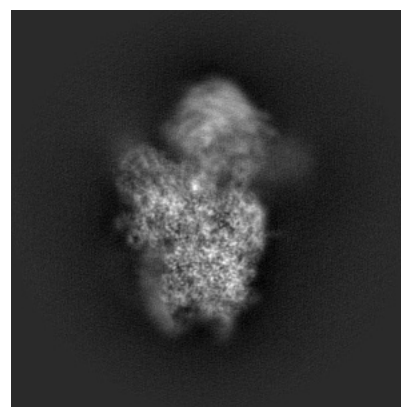
6.1.2 Raw map



X



Y

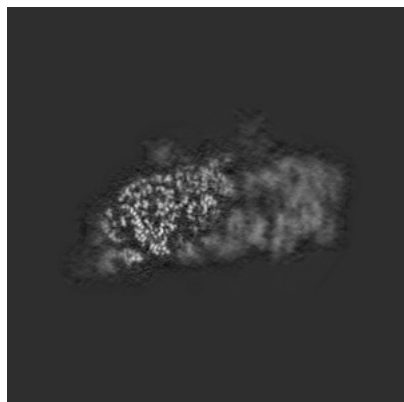


Z

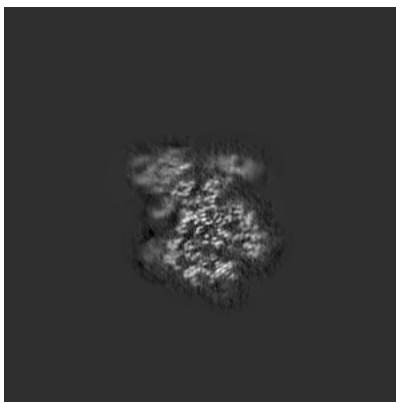
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

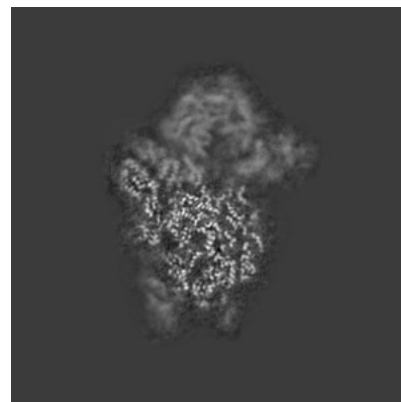
6.2.1 Primary map



X Index: 192

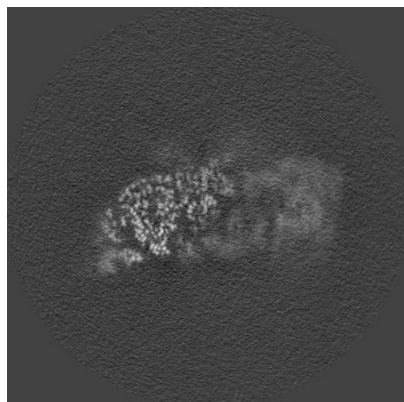


Y Index: 192

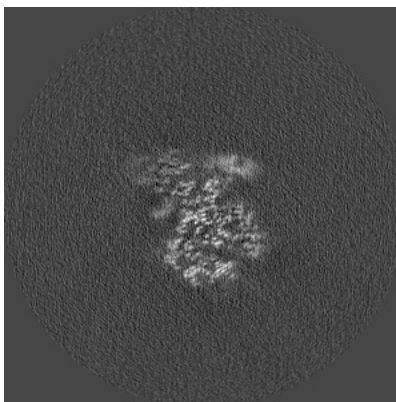


Z Index: 192

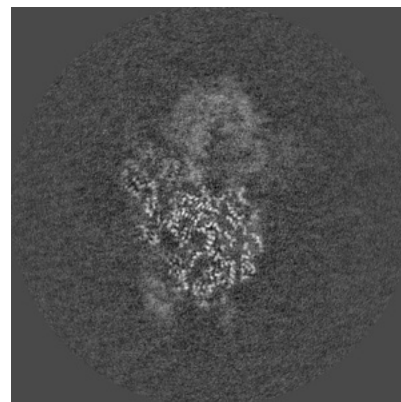
6.2.2 Raw map



X Index: 192



Y Index: 192

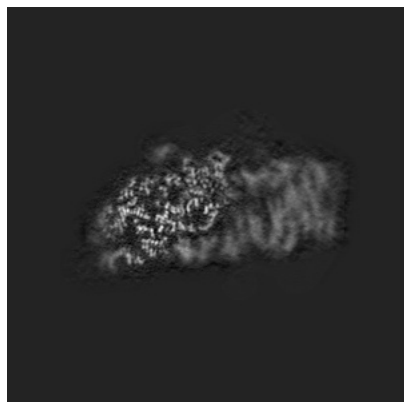


Z Index: 192

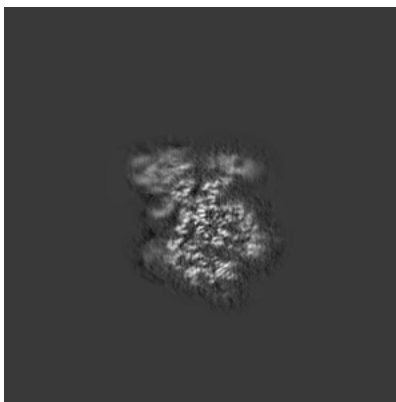
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

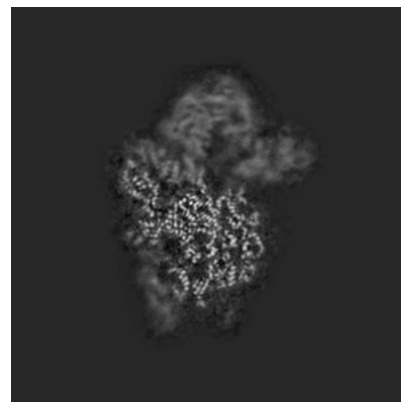
6.3.1 Primary map



X Index: 188

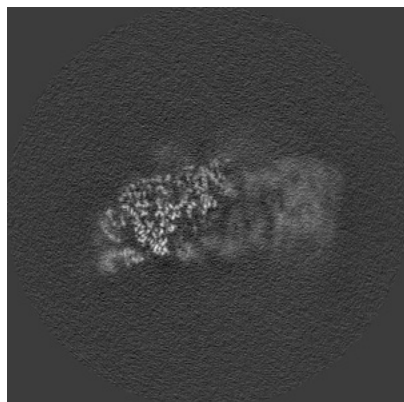


Y Index: 191

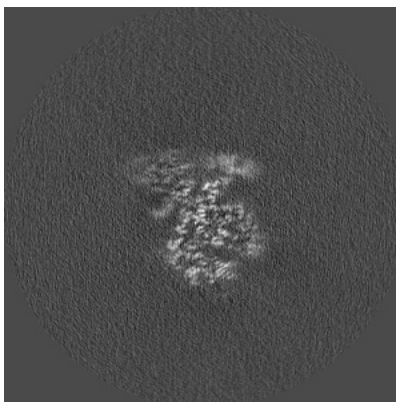


Z Index: 194

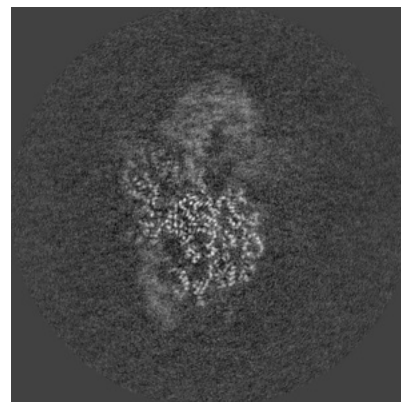
6.3.2 Raw map



X Index: 191



Y Index: 191

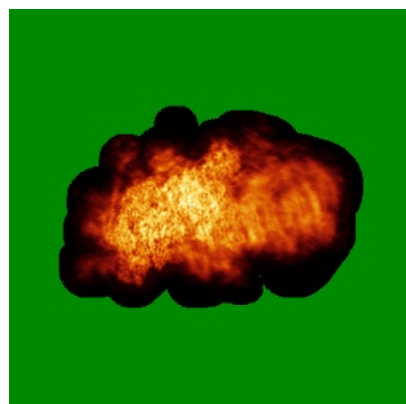


Z Index: 194

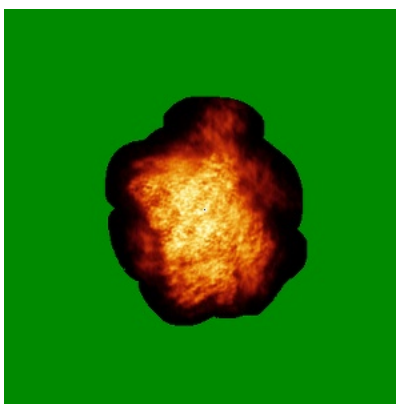
The images above show the largest variance slices of the map in three orthogonal directions.

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

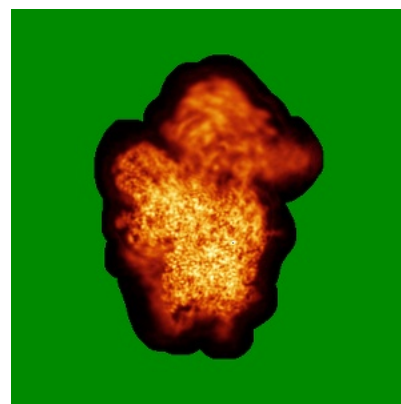
6.4.1 Primary map



X

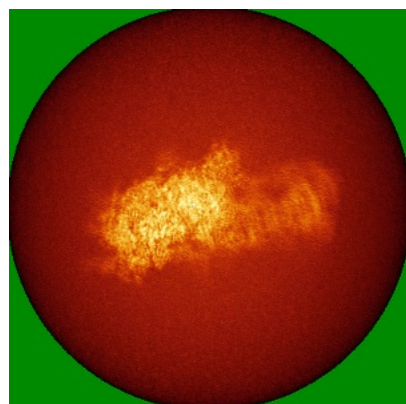


Y

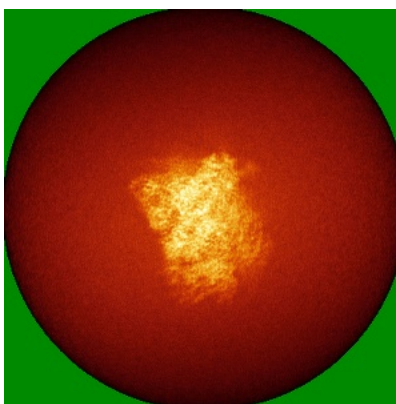


Z

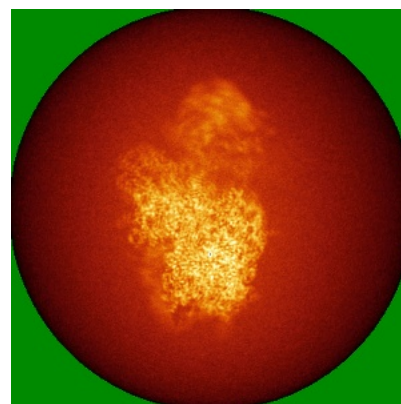
6.4.2 Raw map



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.

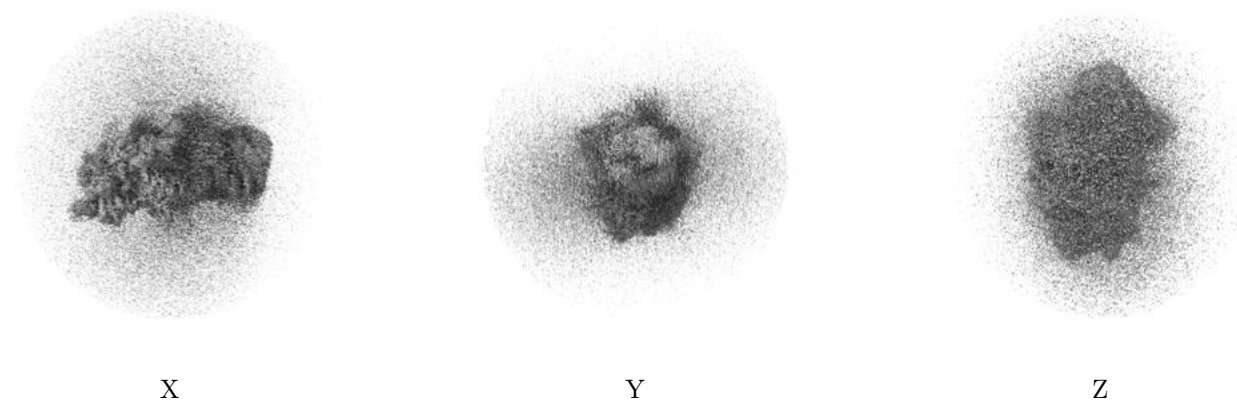
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.075. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

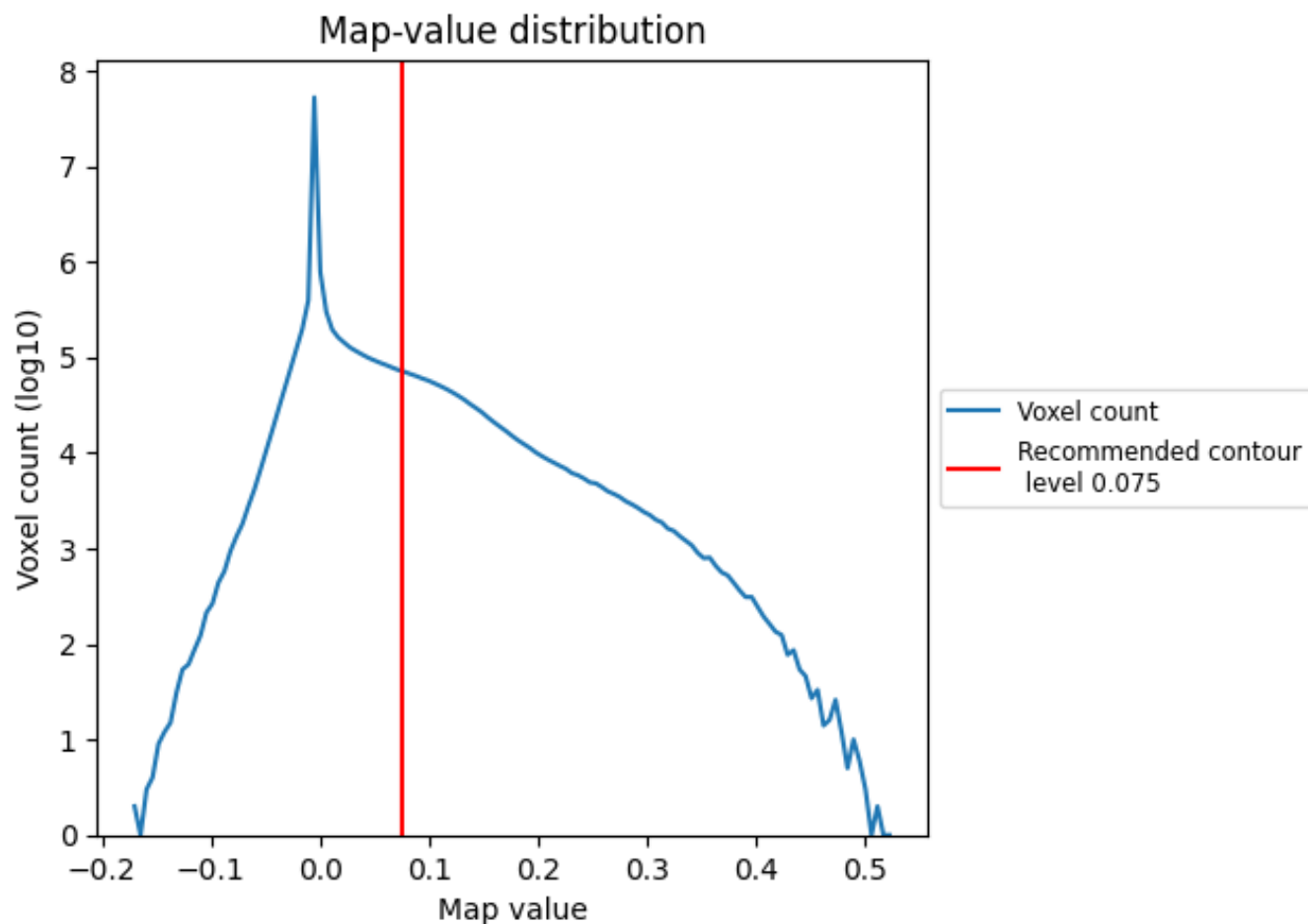
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

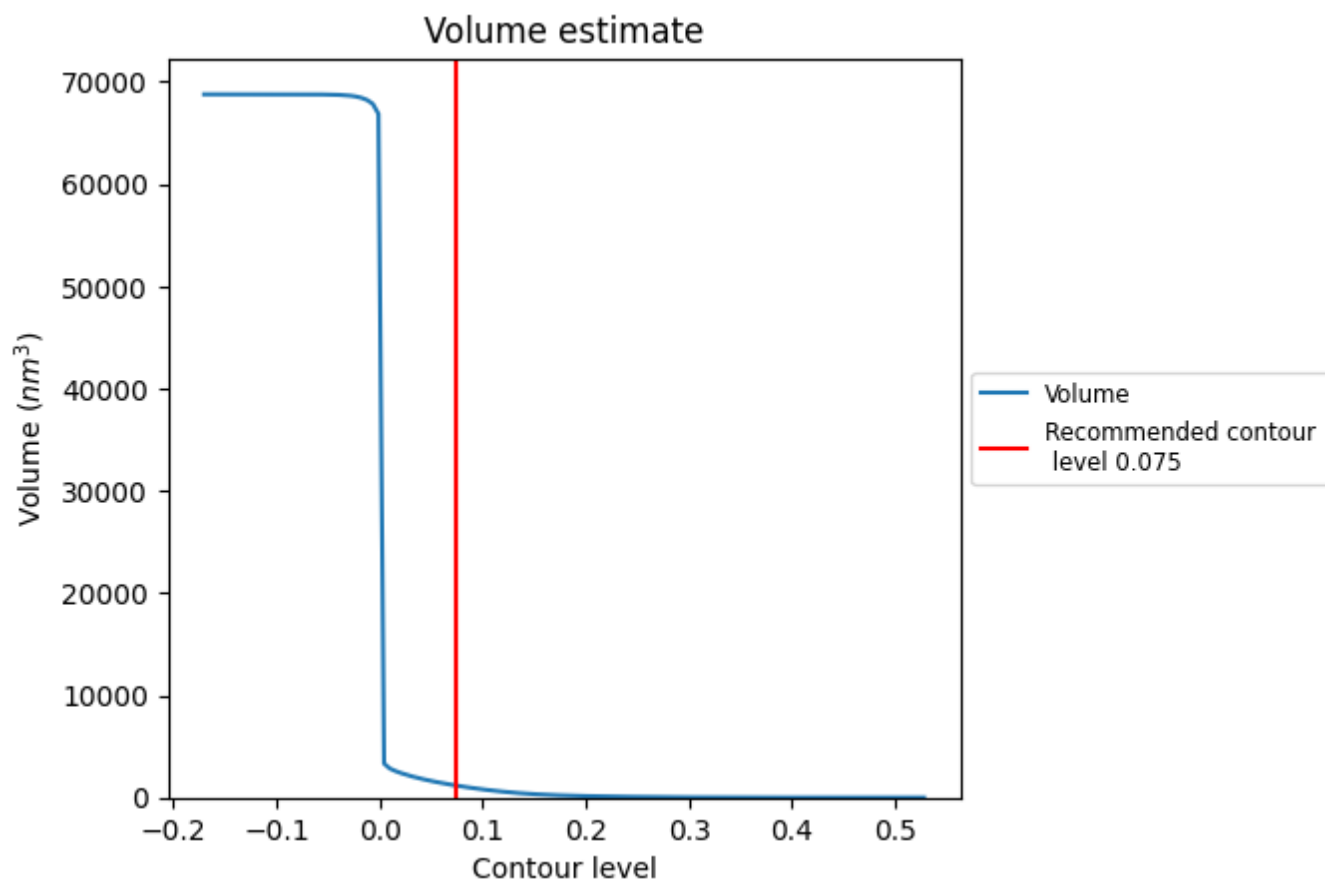
This section contains the results of statistical analysis of the map.

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.

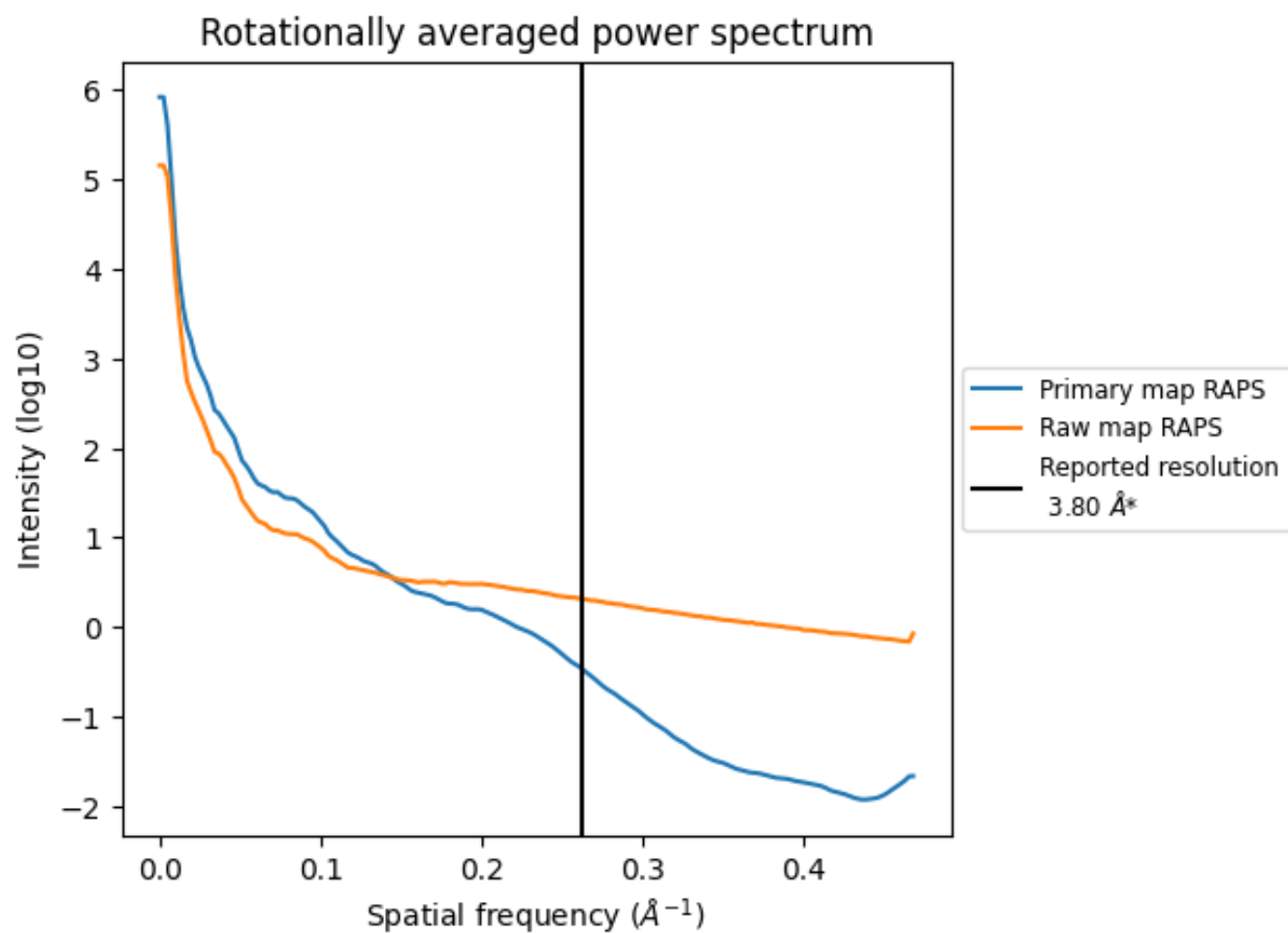
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1165 nm³; this corresponds to an approximate mass of 1053 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 ⓘ

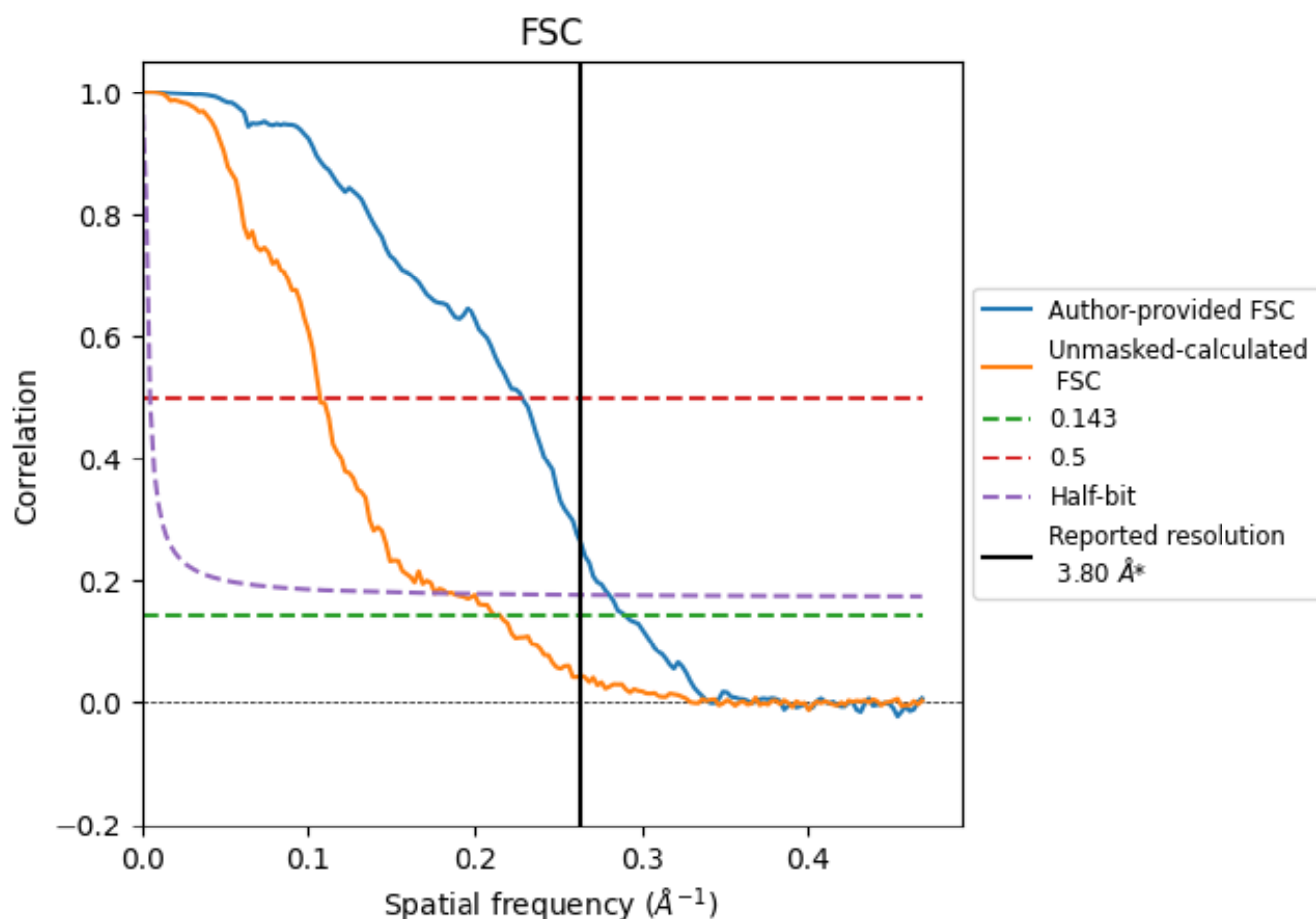


*Reported resolution corresponds to spatial frequency of $0.263 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

8.2 Resolution estimates [i](#)

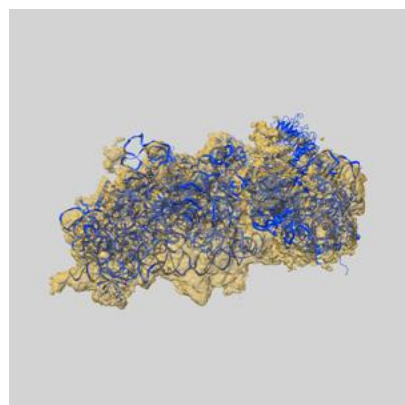
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.45	4.38	3.57
Unmasked-calculated*	4.71	9.35	5.69

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.71 differs from the reported value 3.8 by more than 10 %

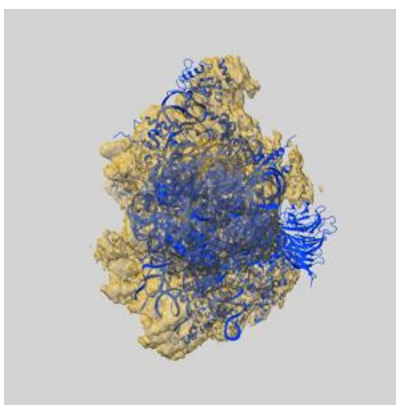
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4793 and PDB model 6RBE. Per-residue inclusion information can be found in section 3 on page 10.

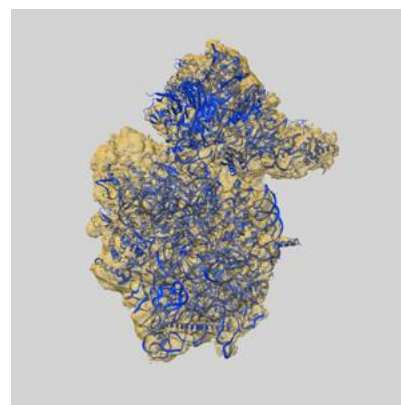
9.1 Map-model overlay [i](#)



X



Y



Z

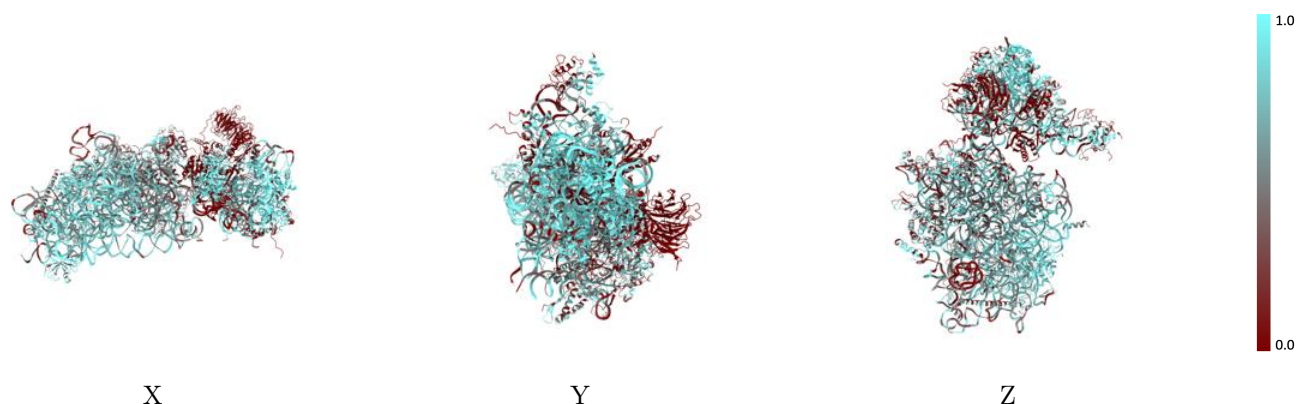
The images above show the 3D surface view of the map at the recommended contour level 0.075 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



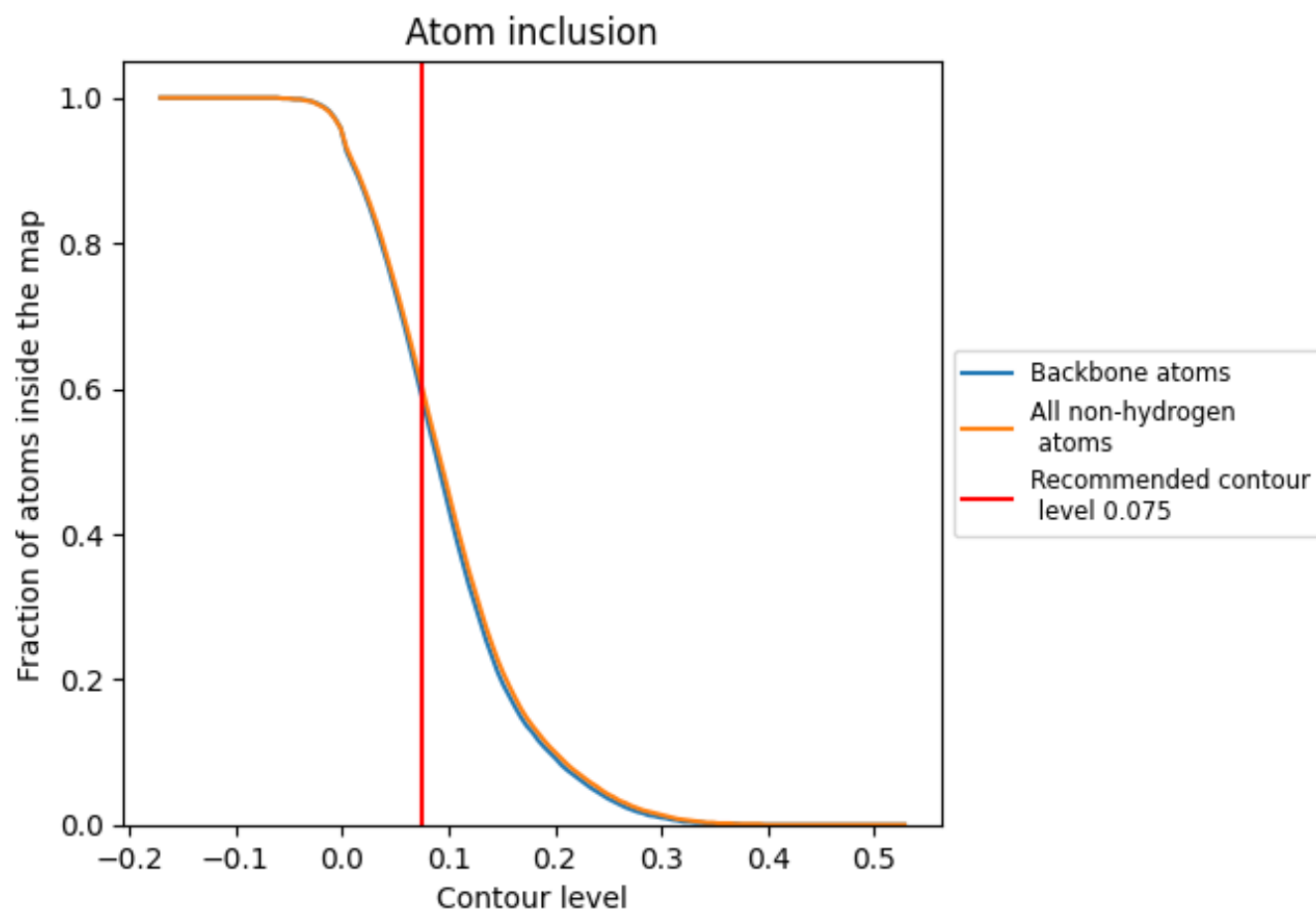
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.075).

9.4 Atom inclusion [i](#)



At the recommended contour level, 59% of all backbone atoms, 60% 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 (0.075) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6040	 0.0190
2	 0.6670	 0.0320
A	 0.5710	 -0.0250
B	 0.4790	 -0.0530
C	 0.5450	 -0.0190
D	 0.3010	 0.0160
E	 0.6850	 -0.0010
F	 0.7180	 0.0120
G	 0.6840	 0.0400
H	 0.5500	 0.0020
I	 0.5800	 -0.0250
J	 0.7120	 0.0250
K	 0.6610	 0.0130
L	 0.5190	 -0.0230
M	 0.5170	 -0.0000
N	 0.5940	 0.0000
O	 0.4660	 -0.0060
P	 0.5220	 -0.0130
Q	 0.6020	 0.0280
R	 0.3980	 0.0140
S	 0.5970	 0.0280
T	 0.8820	 0.0340
U	 0.1330	 0.0070
V	 0.6600	 0.0020
W	 0.6370	 -0.0260
X	 0.6200	 -0.0390
Y	 0.8250	 0.1970
Z	 0.5230	 -0.0290
b	 0.4810	 0.0290
c	 0.4760	 0.0590
d	 0.6050	 0.0310
e	 0.3660	 -0.0290
f	 0.0750	 -0.0000
g	 0.0030	 -0.0210

