



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 07:53 AM UTC

PDB ID : 7SSW / pdb_00007ssw
EMDB ID : EMD-25415
Title : Late translocation intermediate with EF-G dissociated (Structure VI)
Authors : Carbone, C.E.; Korostelev, A.A.
Deposited on : 2021-11-11
Resolution : 3.80 Å(reported)
Based on initial model : 5U9F

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:

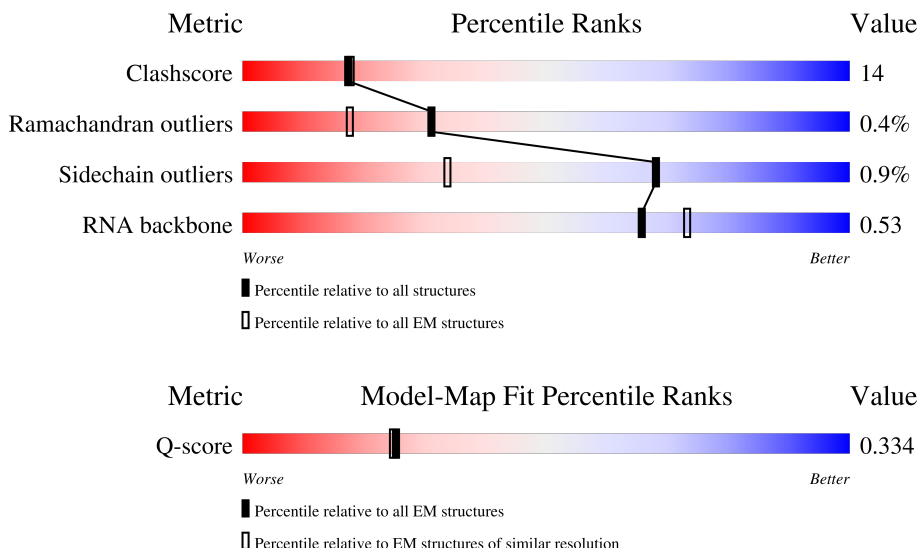
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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.



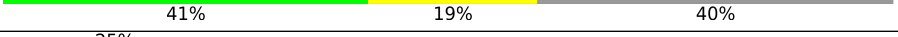
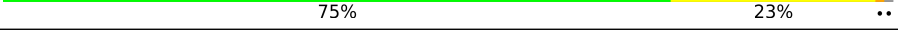
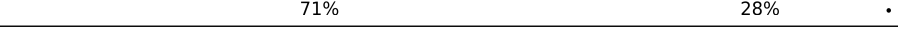
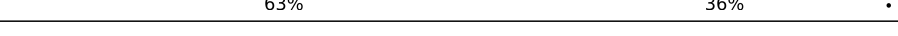
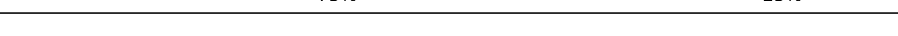
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10198 (3.30 - 4.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	3	1539	
2	1	2903	
3	2	120	

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Mol	Chain	Length	Quality of chain
4	6	77	
5	b	271	
6	c	209	
7	d	201	
8	e	177	
9	f	176	
10	g	149	
11	a	223	
12	i	142	
13	j	142	
14	k	122	
15	l	143	
16	m	136	
17	n	120	
18	o	116	
19	p	114	
20	q	117	
21	r	103	
22	s	110	
23	t	93	
24	u	102	
25	v	94	
26	w	75	
27	x	77	
28	y	63	

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Mol	Chain	Length	Quality of chain
29	z	58	
30	B	56	
31	C	50	
32	D	46	
33	E	64	
34	F	38	
35	4	39	
36	5	77	
37	G	225	
38	H	206	
39	I	205	
40	J	157	
41	K	100	
42	L	151	
43	M	129	
44	N	127	
45	O	98	
46	P	116	
47	Q	123	
48	R	114	
49	S	100	
50	T	88	
51	U	82	
52	V	80	
53	W	65	

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Mol	Chain	Length	Quality of chain
54	X	79	 61% 38% .
55	Y	85	 67% 33%
56	Z	65	 66% 31% . .

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 147596 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 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	3	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 2 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	2903	Total	C	N	O	P	0	0
			62317	27801	11468	20146	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 802133627

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	120	A	-	insertion	GB 1266961702

- Molecule 4 is a RNA chain called tRNA fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	6	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 5 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	b	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

- Molecule 6 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	c	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 7 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	d	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 8 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	e	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

- Molecule 9 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	f	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 10 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	g	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 11 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	a	134	Total	C	N	O	S	0	0
			1027	645	186	194	2		

- Molecule 12 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	i	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 13 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	j	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 14 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	k	122	Total	C	N	O	S	0	0
			939	587	180	166	6		

- Molecule 15 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	l	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 16 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	m	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 17 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	n	120	Total	C	N	O	S	0	0
			961	593	196	167	5		

- Molecule 18 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	o	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 19 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	p	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 20 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	q	117	Total	C	N	O	S	0	0
			947	604	192	151			

- Molecule 21 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	r	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 22 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	s	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 23 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	t	93	Total	C	N	O	S	0	0
			739	466	139	132	2		

- Molecule 24 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	u	102	Total	C	N	O	S	0	0
			780	492	146	142			

- Molecule 25 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	v	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 26 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	w	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 27 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	x	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 28 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 29 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	z	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 30 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	B	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 31 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	C	50	Total	C	N	O	0	0
			410	263	75	72		

- Molecule 32 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	D	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 33 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	E	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 34 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	F	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 35 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	4	20	Total	C	N	O	P	0	0
			436	195	87	134	20		

- Molecule 36 is a RNA chain called tRNA Pro.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	5	77	Total	C	N	O	P	0	0
			1647	733	295	542	77		

- Molecule 37 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	G	218	Total	C	N	O	S	0	0
			1705	1081	305	312	7		

- Molecule 38 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	H	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 39 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	I	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 40 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	J	157	Total	C	N	O	S	0	0
			1157	719	218	214	6		

- Molecule 41 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	K	100	Total	C	N	O	S	0	0
			818	515	148	149	6		

- Molecule 42 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	L	151	Total	C	N	O	S	0	0
			1182	735	227	216	4		

- Molecule 43 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	M	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 44 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	N	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 45 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	O	98	Total	C	N	O	S	0	0
			787	493	150	143	1		

- Molecule 46 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	P	116	Total	C	N	O	S	0	0
			870	535	173	159	3		

- Molecule 47 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Q	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 48 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	R	114	Total	C	N	O	S	0	0
			884	546	178	157	3		

- Molecule 49 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 50 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	T	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 51 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	U	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 52 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	V	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 53 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	W	65	Total	C	N	O	S	0	0
			536	339	100	96	1		

- Molecule 54 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	X	79	Total	C	N	O	S	0	0
			638	408	120	108	2		

- Molecule 55 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Y	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

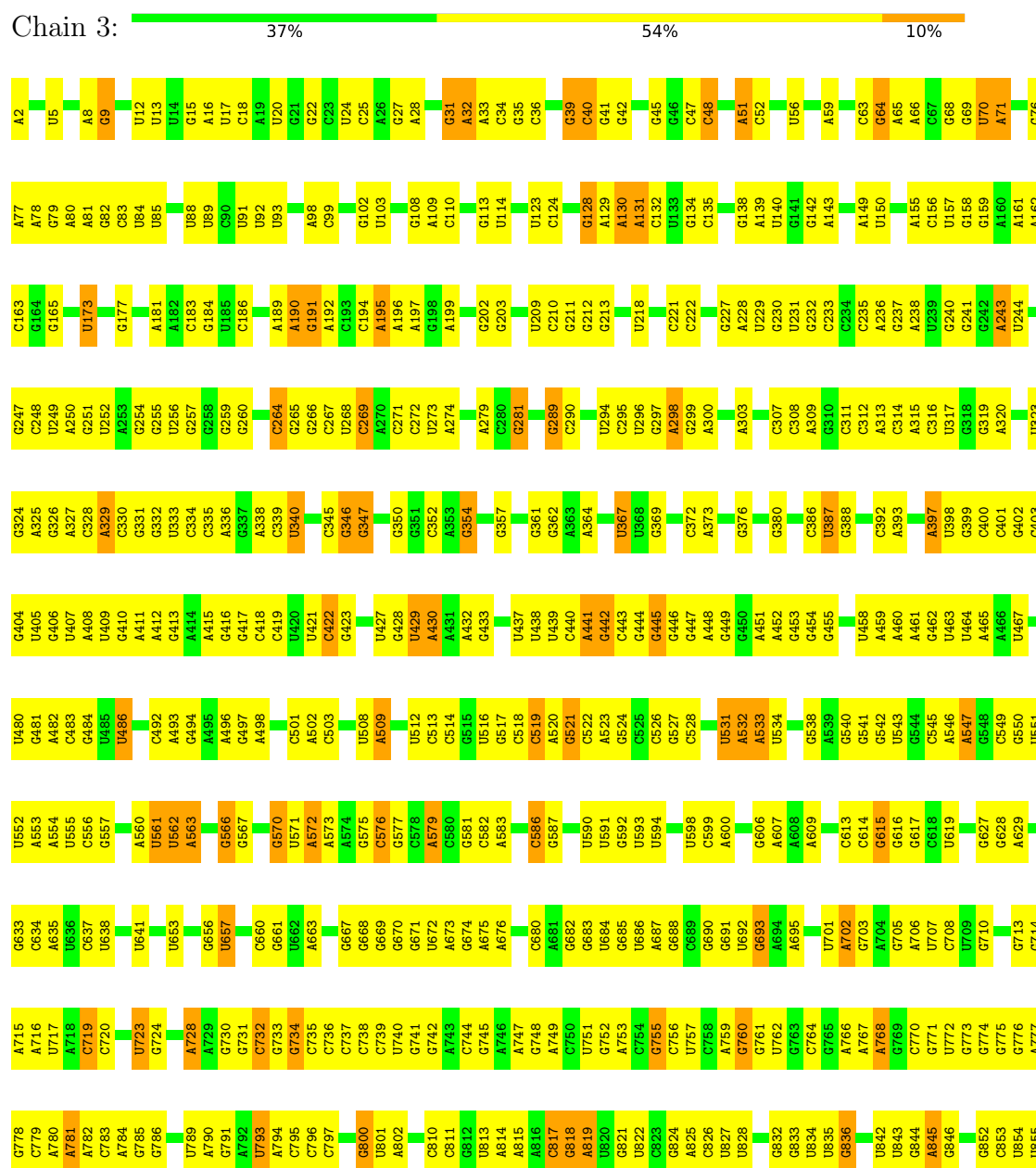
- Molecule 56 is a protein called 30S ribosomal protein S21.

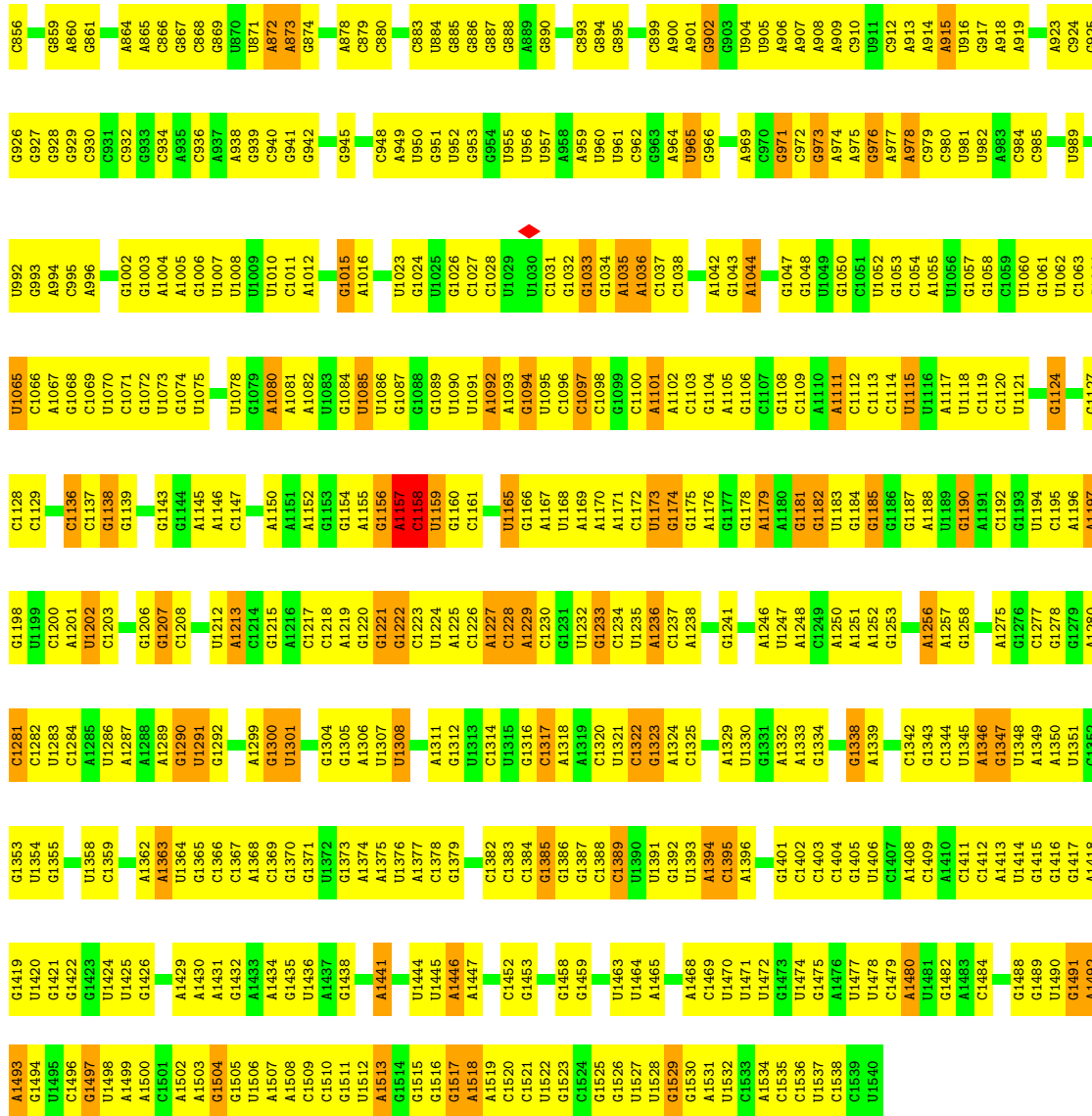
Mol	Chain	Residues	Atoms					AltConf	Trace
56	Z	65	Total	C	N	O	S	0	0
			545	335	117	92	1		

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.

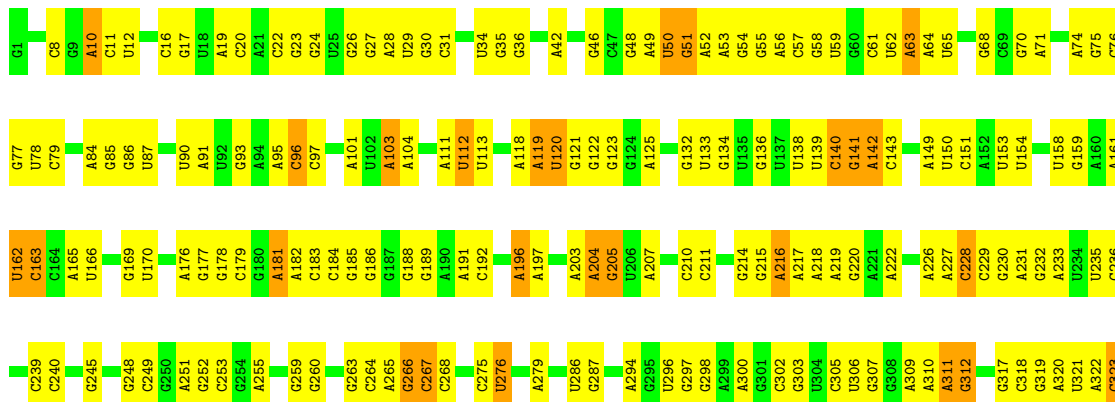
• Molecule 1: 16S rRNA





• Molecule 2: 23S rRNA

Chain 1: 42% 48% 10%

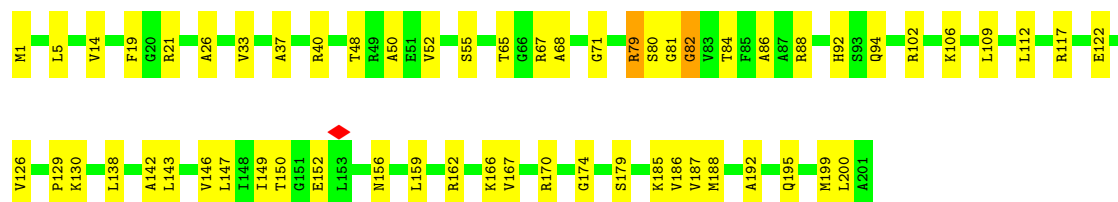


G1436	A1347	G1346	U1097	C1013	A943	C873	U807	A739	C660	A574	A507	G425	A324
C1437	A1348	U1173	A1098	U1018	C946	C876	C808	G740	A661	A575	A508	C426	G325
A1438	C1270	U1174	U1019	U1019	A947	A877	U809	U741	G662	U576	C509	G326	G327
A1363	U1175	U1101	U1101	G1022	C948	A878	U810	A742	G663	U580	C510	A432	U328
U1440	U1176	C1102	C879	G1022	G949	A879	U811	G743	G664	C581	G511	C433	G329
U1442	G1177	A1103	C880	G1022	G949	C880	U813	G744	U665	A582	G512	C434	U330
U1443	C1104	C1104	C815	C1030	G952	C881	C815	G745	A666	C436	A513	C435	A330
G1361	U1179	U1108	C818	U1033	G953	G882	C818	U746	A670	C437	A514	C436	U339
C1362	U1180	U1109	C819	U1033	G954	G883	C819	U747	C671	U588	A515	C438	A340
G1448	U1181	C1109	C885	U1033	G955	G884	C819	G748	C672	U589	C516	A439	C341
G1449	U1182	C1110	C886	U1033	U956	U884	C819	A752	C673	A590	C517	C440	A346
A1365	U1183	A1111	C887	G1038	C957	C885	A819	A753	G674	U591	G520	U441	A346
A1366	G1186	A1112	C888	A1040	U958	A886	G822	U754	A675	U591	U521	C442	A346
A1367	U1187	U1113	C889	G1041	A959	C888	C823	U755	A676	U594	A522	A443	U349
A1368	U1188	C1117	C890	U1042	A960	C889	U824	A756	A677	C595	C523	A444	U349
A1369	U1189	C1118	C891	C1043	C961	C890	U825	G760	C678	U599	G524	C445	U349
A1370	U1190	G1124	C892	G1044	G962	C891	U826	G761	C679	A603	A526	A449	U358
A1371	U1191	G1125	C893	U1045	U963	C892	U827	U762	C680	A604	A527	A450	U359
A1372	G1197	G1128	C894	U1046	C964	A892	U828	U763	C681	U606	C528	A451	U360
A1373	U1198	U1129	C895	A1048	G966	U894	C831	A764	G684	U607	A529	C455	U361
A1374	U1199	U1130	U895	G1051	G966	U895	U832	A765	A685	A608	A530	C456	G363
A1375	U1200	U1131	A896	G1051	G966	A896	A833	U766	U686	A609	C531	A457	G370
A1376	U1201	U1132	C898	G1051	G966	C898	G834	U767	C687	A609	A532	A458	A371
A1377	U1202	U1133	C899	G1051	G966	C899	C835	U768	U688	A610	A533	G458	G372
A1378	U1203	U1134	C901	G1051	G966	C901	U839	U769	A689	G612	G536	U464	G380
A1379	U1204	A1134	C902	U1056	G974	C902	U840	U770	A690	A613	G537	G465	G381
A1380	A1205	U1135	C903	U1057	A975	C903	C841	G771	C691	A614	G538	A466	G382
A1381	G1206	G1136	C904	U1058	G976	C904	U842	C772	C692	U615	A539	G467	A382
A1382	U1207	U1137	C905	U1059	G977	C905	U843	C773	A693	A616	G540	G468	C383
A1383	U1208	U1138	C906	U1060	G977	C906	U844	C774	U694	G617	C541	G469	A384
A1384	U1209	U1139	C907	U1061	A980	C907	A845	G775	C695	G618	C542	A470	C385
A1385	U1210	U1140	C908	U1062	A981	C908	U846	G776	C696	A621	C543	A471	G386
A1386	U1211	U1141	C909	U1063	A982	C909	U847	G777	G697	A622	C544	A472	U387
A1387	U1212	U1142	C910	U1064	A983	C910	C848	U778	U703	A623	A547	A478	C393
A1388	U1213	U1143	C911	U1065	A984	C911	U849	U779	A704	A624	G548	A479	C394
A1389	U1214	U1144	C912	U1066	A985	C912	U850	G780	A705	A625	G549	A480	U395
A1390	U1215	U1145	C913	U1067	A986	C913	C851	A781	A706	A626	C550	A481	G396
A1391	U1216	U1146	C914	U1068	A987	C914	U852	A782	G711	A627	U554	A482	A404
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A1393	U1218	U1148	C916	U1070	A989	C916	C854	A784	G713	A629	C556	G487	G406
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A1395	U1220	U1150	C918	U1072	A991	C918	C856	G786	G715	A631	U558	G489	G408
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A1405	U1230	U1160	C928	U1082	A1001	C928	A866	G796	U725	A641	U568	A502	C418
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A1407	U1232	U1162	C930	U1084	A1003	C930	A868	G798	A727	A643	U570	A504	C420
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A1409	U1234	U1164	C932	U1086	U1005	C932	U870	G800	A729	A645	U572	A506	G507
A1410	U1235	U1165	C933	U1087	U1006	C933	U871	A801	G730	A646	U573	A507	G508
A1411	U1236	U1166	C934	U1088	U1007	C934	U872	A802	A731	A647	U574	A508	G509
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A1415	U1240	U1170	C938	U1092	U1011	C938	U876	A806	A735	A651	U578	A512	G513
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A1417	U1242	U1172	C940	U1094	U1013	C940	U878	A808	A737	A653	U580	A514	G515
A1418	U1243	U1173	C941	U1095	U1014	C941	U879	A809	A738	A654	U581	A515	G516
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A1421	U1246	U1176	C944	U1098	U1017	C944	U882	A812	A741	A657	U584	A518	G519
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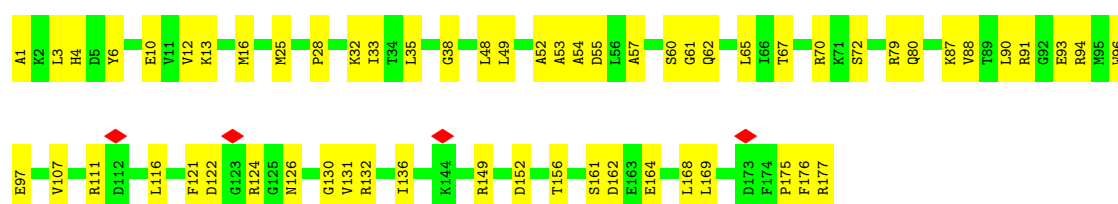
- Molecule 7: 50S ribosomal protein L4

Chain d:  71% 28%



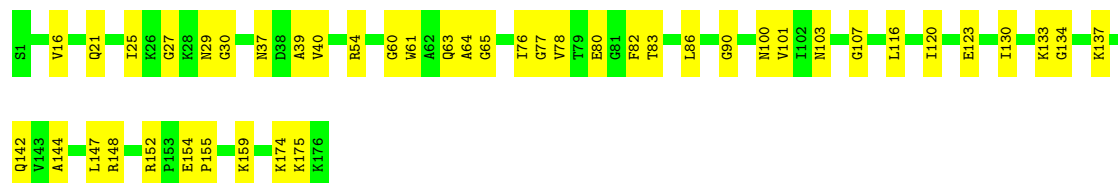
- Molecule 8: 50S ribosomal protein L5

Chain e:  66% 34%



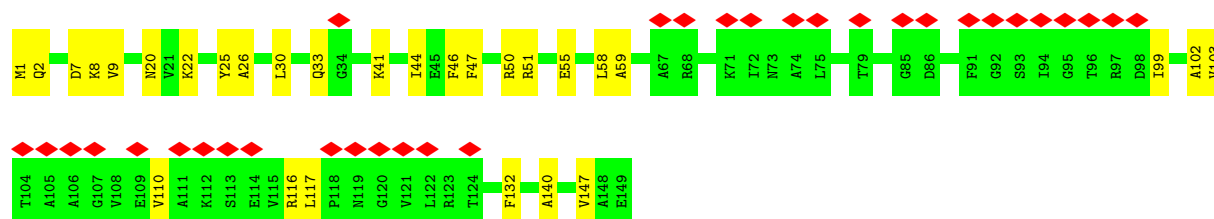
- Molecule 9: 50S ribosomal protein L6

Chain f:  75% 25%

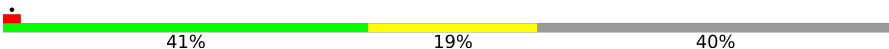


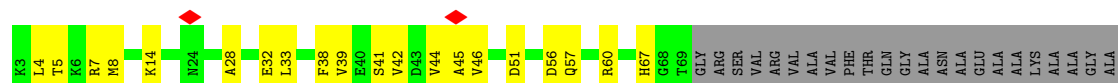
- Molecule 10: 50S ribosomal protein L9

Chain g:  22% 81% 19%



- Molecule 11: 50S ribosomal protein L1

Chain a:  41% 19% 40%



LEU VAL ASN GLY MET LYS GLU ASP LEU ALA ASP ALA GLN ILE LYS LYS GLY GLU MET MET ASP PHE ASP VAL ILE ALA SER PRO ASP ALA MET MET ARG VAL VAL GLY GLN LEU GLY VAL LEU GLY PRO ARG GLY LEU MET PRO ASN PRO PRO LYS VAL GLY THR VAL THR PRO PRO ASN VAL ALA GLU ALA VAL

LYS ASN ALA LYS ALA G159 R162 Y163 R164 N165 D166 G169 I170 I171 H172 T173 T174 T175 G176 K177 V178 D179 K184 L185 N188 T202 Q203 G206 I209 V212 T216 T217 M218 D225

• Molecule 12: 50S ribosomal protein L11

Chain i: 25% 75% 23% ..

MET A1 V4 Q5 K9 Y12 A13 A14 G15 M16 M18 N18 P19 S20 P21 P22 A26 V32 F37 C38 K39 A40 F41 T45 D46 S47 I48 E49 K50 G51 L52 P53 I54 V55 V56 V57 I58 T59 V60 Y61 A62 D63 F68 K71 T72 P73 P74 A75 A76 V77 L78

• Molecule 13: 50S ribosomal protein L13

Chain j: 69% 31%

M1 T5 A6 K7 Y16 D19 K23 R27 R34 R35 L36 R37 G38 K41 Y44 T45 V48 D49 T50 Y53 I54 I55 V56 L57 V64 T65 K68 R69 V73 T78 G79 R80 I81 T88 F89 E90 E98 E102 G112 P113 L114 G115

• Molecule 14: 50S ribosomal protein L14

Chain k: 71% 28%

M1 D12 N13 V19 V24 L25 G26 H29 R30 R31 Y32 A33 G34 V35 G36 D37 I38 I39 K40 I43 K44 P48 R49 K53 L58 K59 R64 T65 G68 V69 D73 N82 N89 I99 R105 R108 M113 K114 E121 V122

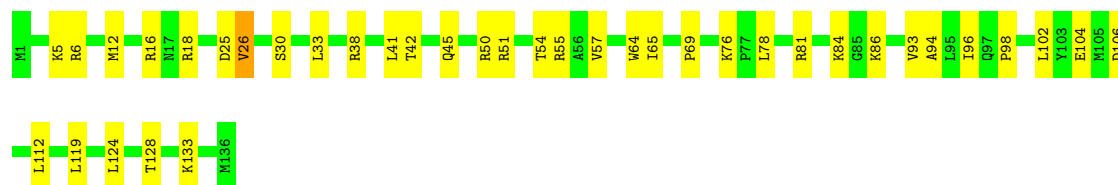
• Molecule 15: 50S ribosomal protein L15

Chain l: 74% 25%

R2 K13 L19 G22 I23 G28 K29 T30 H35 K36 G37 Q38 K39 R47 R48 Y58 F66 T67 S68 A71 A72 I73 L79 S80 D81 K84 V85 E86 G87 K86 I101 G102 I103 E106 V110 I111 L112 A113 G114 E115 V127 T128 E136

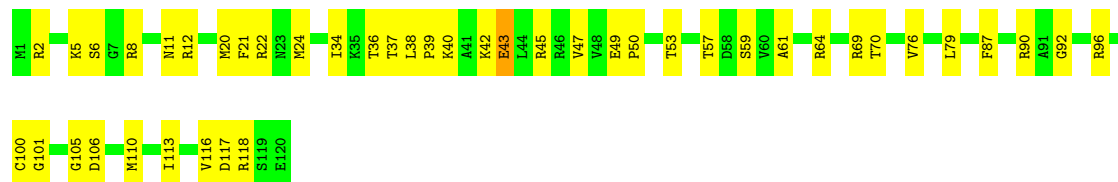
• Molecule 16: 50S ribosomal protein L16

Chain m: 72% 27%



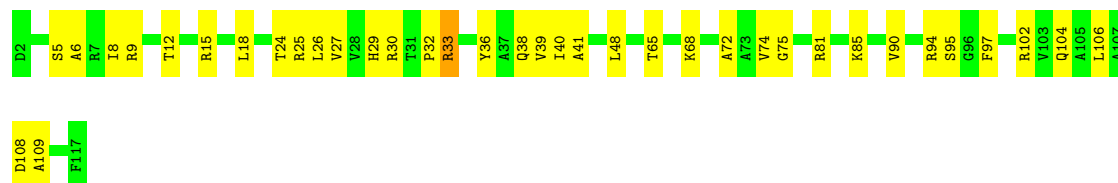
- Molecule 17: 50S ribosomal protein L17

Chain n: 63% 36%



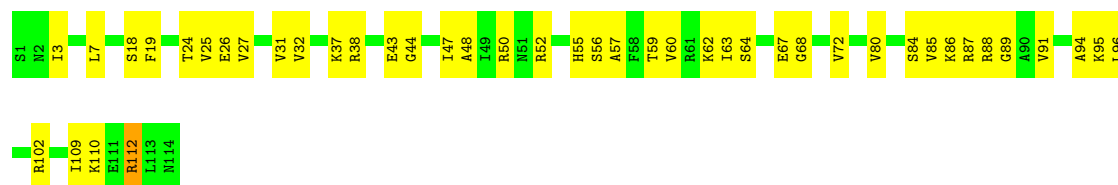
- Molecule 18: 50S ribosomal protein L18

Chain o: 68% 31%



- Molecule 19: 50S ribosomal protein L19

Chain p: 61% 38%



- Molecule 20: 50S ribosomal protein L20

Chain q: 68% 32%



- Molecule 21: 50S ribosomal protein L21

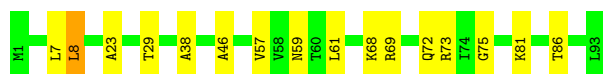
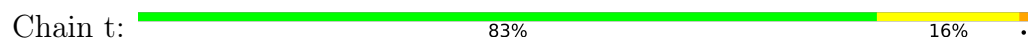
Chain r: 79% 21%



- Molecule 22: 50S ribosomal protein L22



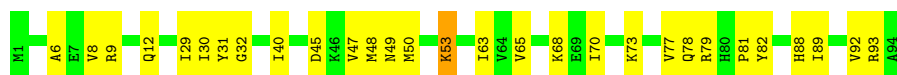
- Molecule 23: 50S ribosomal protein L23



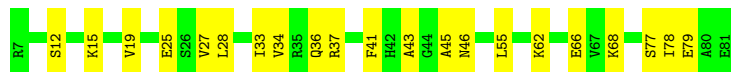
- Molecule 24: 50S ribosomal protein L24



- Molecule 25: 50S ribosomal protein L25



- Molecule 26: 50S ribosomal protein L27



- Molecule 27: 50S ribosomal protein L28



- Molecule 28: 50S ribosomal protein L29

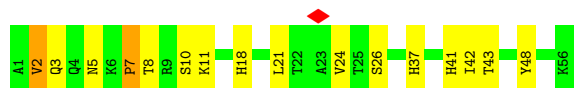




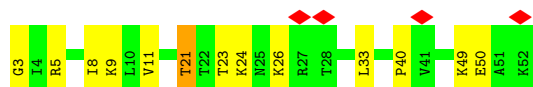
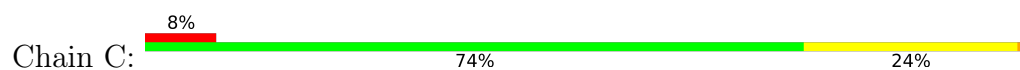
- Molecule 29: 50S ribosomal protein L30



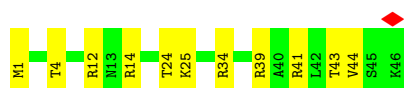
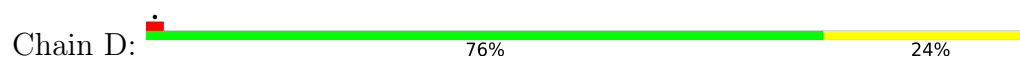
- Molecule 30: 50S ribosomal protein L32



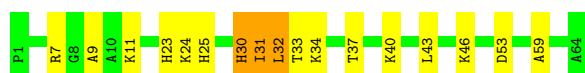
- Molecule 31: 50S ribosomal protein L33



- Molecule 32: 50S ribosomal protein L34



- Molecule 33: 50S ribosomal protein L35



- Molecule 34: 50S ribosomal protein L36



- Molecule 35: mRNA





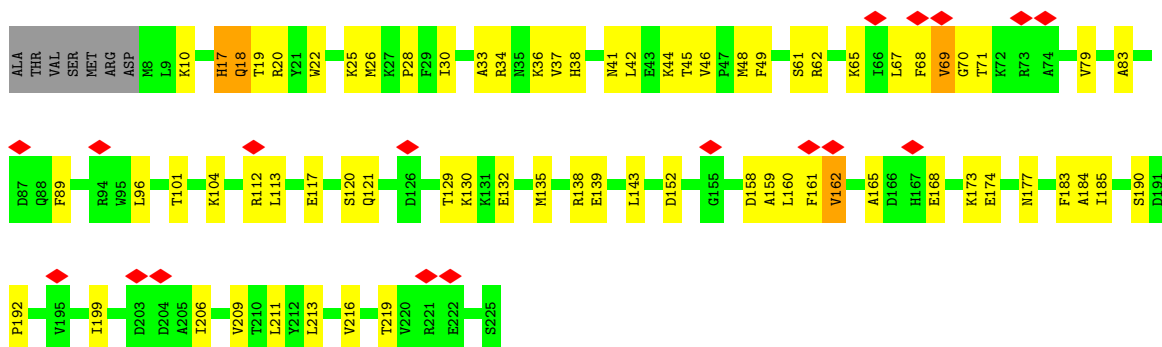
• Molecule 36: tRNA Pro

Chain 5: 43% 48% 9%



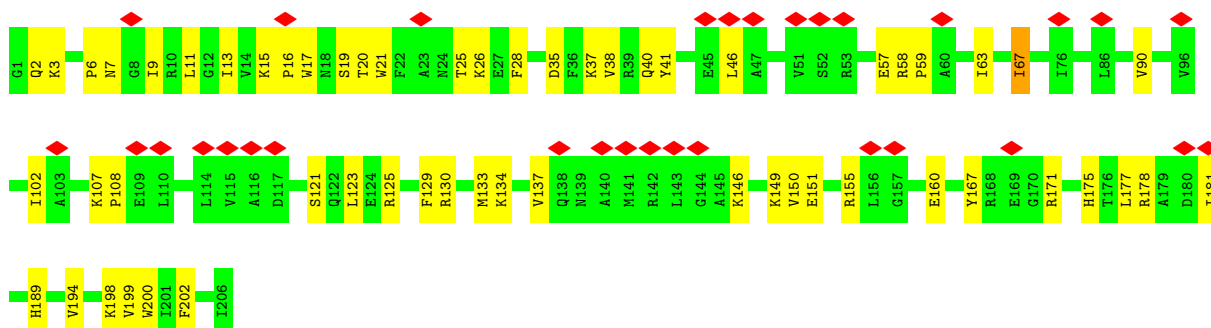
• Molecule 37: 30S ribosomal protein S2

Chain G: 8% 65% 30%



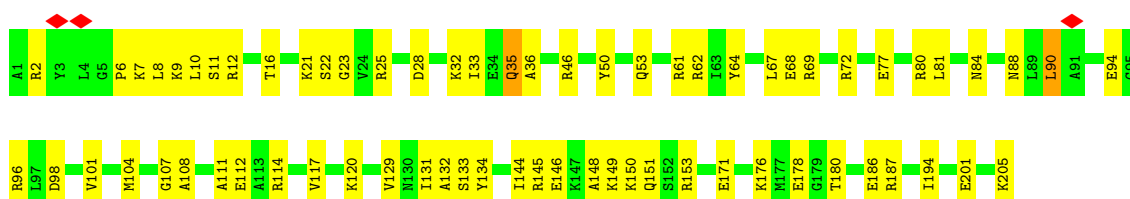
• Molecule 38: 30S ribosomal protein S3

Chain H: 15% 72% 27%

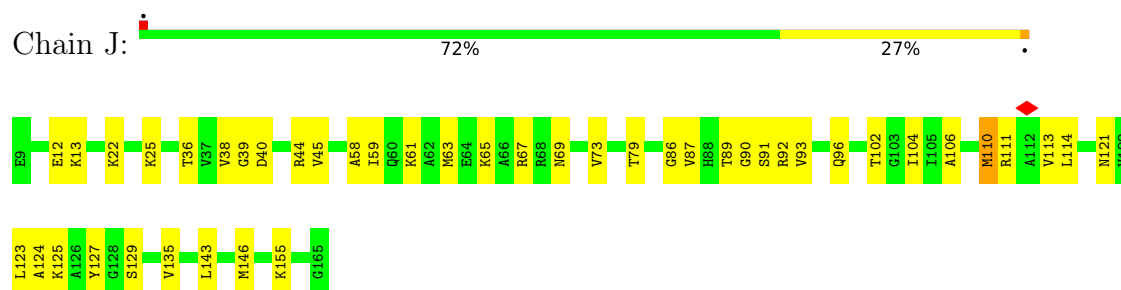


• Molecule 39: 30S ribosomal protein S4

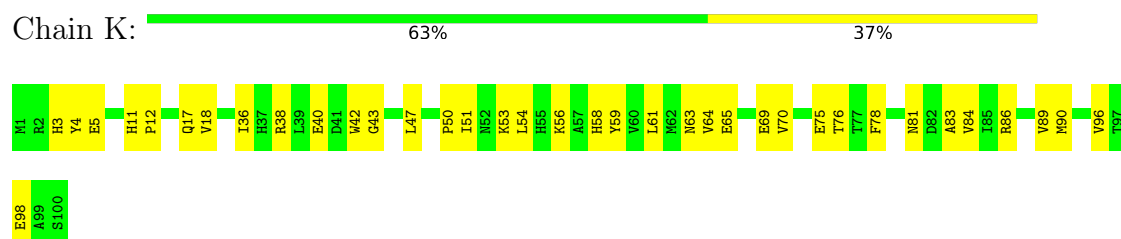
Chain I: 67% 32%



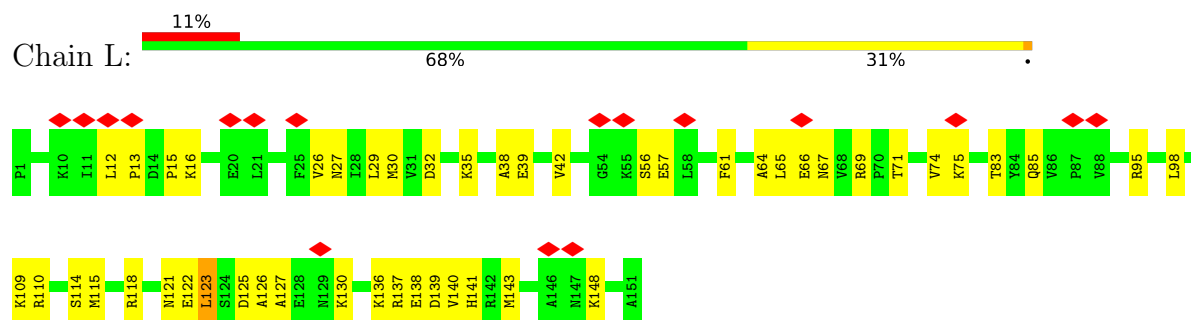
- Molecule 40: 30S ribosomal protein S5



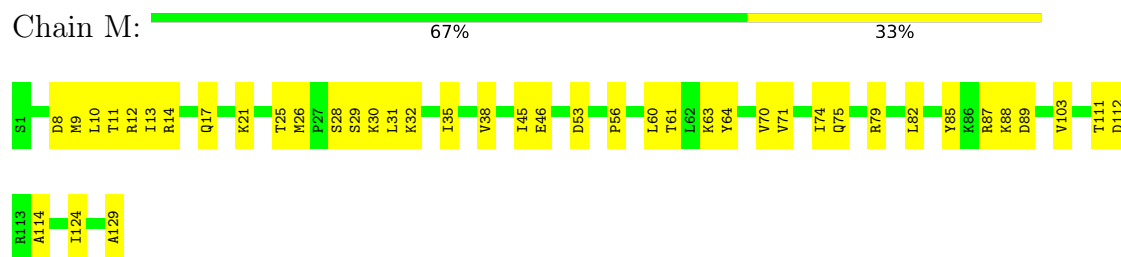
- Molecule 41: 30S ribosomal protein S6



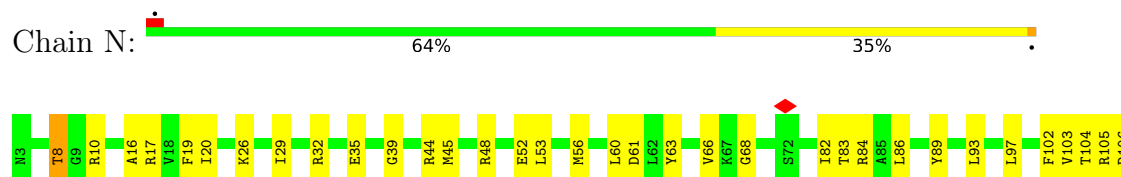
- Molecule 42: 30S ribosomal protein S7

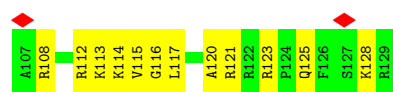


- Molecule 43: 30S ribosomal protein S8

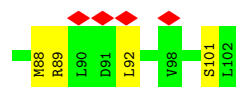
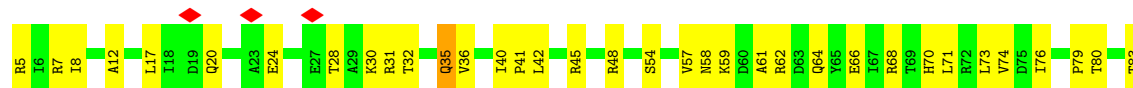


- Molecule 44: 30S ribosomal protein S9





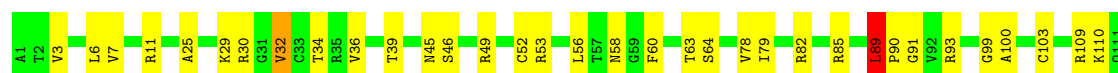
- Molecule 45: 30S ribosomal protein S10



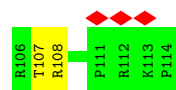
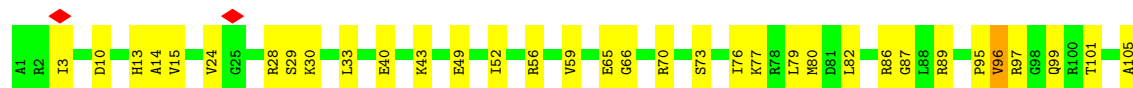
- Molecule 46: 30S ribosomal protein S11



- Molecule 47: 30S ribosomal protein S12



- Molecule 48: 30S ribosomal protein S13

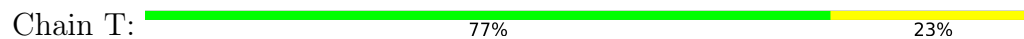


- Molecule 49: 30S ribosomal protein S14





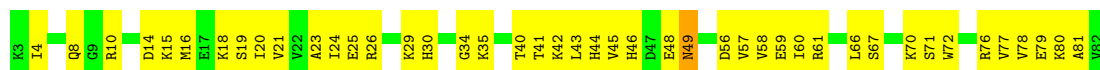
- Molecule 50: 30S ribosomal protein S15



- Molecule 51: 30S ribosomal protein S16



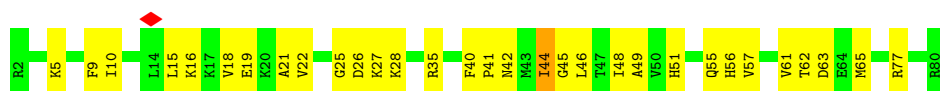
- Molecule 52: 30S ribosomal protein S17



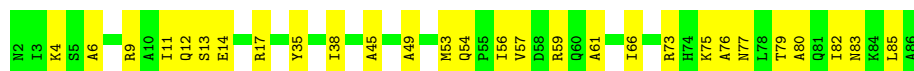
- Molecule 53: 30S ribosomal protein S18



- Molecule 54: 30S ribosomal protein S19

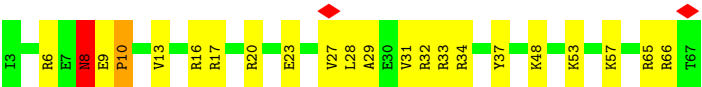


- Molecule 55: 30S ribosomal protein S20



- Molecule 56: 30S ribosomal protein S21





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1163	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 ($e^-/\text{\AA}^2$)	47.6	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	20.281	Depositor
Minimum map value	-12.230	Depositor
Average map value	0.115	Depositor
Map value standard deviation	0.851	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	370.5408, 370.5408, 370.5408	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8271, 0.8271, 0.8271	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	3	0.55	0/36963	0.58	4/57662 (0.0%)
2	1	0.55	0/69796	0.59	21/108888 (0.0%)
3	2	0.55	0/2872	0.57	1/4479 (0.0%)
4	6	0.60	2/1832 (0.1%)	0.75	6/2855 (0.2%)
5	b	0.49	0/2122	0.96	7/2852 (0.2%)
6	c	0.40	0/1586	0.89	5/2134 (0.2%)
7	d	0.36	0/1571	0.82	4/2113 (0.2%)
8	e	0.34	0/1435	0.78	0/1926
9	f	0.29	0/1343	0.72	0/1816
10	g	0.30	0/1122	0.82	2/1515 (0.1%)
11	a	0.26	0/1034	0.69	1/1387 (0.1%)
12	i	0.32	0/1046	0.82	0/1410
13	j	0.39	0/1152	0.86	0/1551
14	k	0.44	0/948	0.96	0/1268
15	l	0.41	0/1054	0.99	2/1403 (0.1%)
16	m	0.42	0/1093	0.85	2/1460 (0.1%)
17	n	0.47	0/974	0.95	0/1301
18	o	0.31	0/902	0.72	2/1209 (0.2%)
19	p	0.39	0/929	0.81	1/1242 (0.1%)
20	q	0.42	0/960	0.74	0/1278
21	r	0.39	0/829	0.83	0/1107
22	s	0.38	0/864	0.81	0/1156
23	t	0.35	0/745	0.80	0/994
24	u	0.34	0/788	0.81	1/1051 (0.1%)
25	v	0.35	0/766	0.80	2/1025 (0.2%)
26	w	0.39	0/582	0.80	0/769
27	x	0.43	0/635	0.76	0/848
28	y	0.28	0/510	0.86	0/677
29	z	0.35	0/453	0.79	0/605
30	B	0.38	0/450	0.86	0/599
31	C	0.31	0/417	0.70	0/554
32	D	0.48	0/380	0.78	0/498
33	E	0.43	0/513	0.97	1/676 (0.1%)
34	F	0.35	0/303	0.88	2/397 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	4	0.57	0/490	0.70	1/763 (0.1%)
36	5	0.58	0/1840	0.61	0/2868
37	G	0.35	0/1736	0.82	7/2338 (0.3%)
38	H	0.27	0/1652	0.71	2/2225 (0.1%)
39	I	0.28	0/1665	0.80	2/2227 (0.1%)
40	J	0.38	0/1170	0.90	1/1573 (0.1%)
41	K	0.40	1/836 (0.1%)	0.91	3/1128 (0.3%)
42	L	0.28	0/1196	0.78	2/1602 (0.1%)
43	M	0.34	0/989	0.84	0/1326
44	N	0.29	0/1034	0.81	2/1375 (0.1%)
45	O	0.35	0/797	0.84	1/1077 (0.1%)
46	P	0.36	0/886	0.82	0/1195
47	Q	0.42	0/969	0.97	2/1300 (0.2%)
48	R	0.33	0/893	0.85	3/1193 (0.3%)
49	S	0.30	0/817	0.81	0/1088
50	T	0.34	0/722	0.81	0/964
51	U	0.33	0/659	0.86	2/884 (0.2%)
52	V	0.37	0/658	0.90	2/881 (0.2%)
53	W	0.41	1/545 (0.2%)	0.81	2/731 (0.3%)
54	X	0.32	0/653	0.93	0/877
55	Y	0.30	0/671	0.72	0/888
56	Z	0.37	0/551	1.01	0/728
All	All	0.50	4/160398 (0.0%)	0.66	96/239936 (0.0%)

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	3	1	4
2	1	1	12
5	b	0	2
6	c	0	2
7	d	0	1
8	e	0	1
10	g	0	1
12	i	0	1
14	k	0	3
15	l	0	4
17	n	0	1
18	o	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
19	p	0	1
25	v	0	1
30	B	0	1
33	E	0	1
35	4	1	0
37	G	0	1
40	J	0	1
44	N	0	1
46	P	0	2
47	Q	0	2
51	U	0	1
52	V	0	2
56	Z	0	1
All	All	3	48

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
41	K	18	VAL	C-N	6.31	1.43	1.33
4	6	13	C	O3'-P	6.28	1.70	1.61
4	6	14	A	P-OP1	5.59	1.60	1.49
53	W	66	LEU	CA-C	-5.50	1.45	1.52

The worst 5 of 96 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	6	13	C	O3'-P-O5'	-19.06	75.40	104.00
1	3	1158	C	C3'-C2'-O2'	13.54	131.01	110.70
1	3	1158	C	C1'-C2'-O2'	11.66	125.89	108.40
4	6	13	C	OP1-P-O3'	11.38	142.15	108.00
2	1	1828	G	N9-C1'-C2'	8.63	124.94	112.00

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	3	1158	C	C2'
2	1	889	C	C2'
35	4	13	A	C4'

5 of 48 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	1	370	G	Sidechain
1	3	1156	G	Sidechain
1	3	1158	C	Sidechain
1	3	1194	U	Sidechain
1	3	800	G	Sidechain

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	3	33012	0	16618	861	0
2	1	62317	0	31346	1381	0
3	2	2568	0	1303	66	0
4	6	1640	0	837	29	0
5	b	2083	0	2157	85	0
6	c	1565	0	1616	51	0
7	d	1552	0	1619	42	0
8	e	1411	0	1447	47	0
9	f	1323	0	1374	28	0
10	g	1111	0	1148	19	0
11	a	1027	0	1092	31	0
12	i	1032	0	1088	25	0
13	j	1129	0	1162	32	0
14	k	939	0	1012	32	0
15	l	1045	0	1117	29	0
16	m	1074	0	1157	30	0
17	n	961	0	1000	32	0
18	o	892	0	923	24	0
19	p	917	0	965	30	0
20	q	947	0	1022	32	0
21	r	816	0	839	22	0
22	s	857	0	922	21	0
23	t	739	0	807	11	0
24	u	780	0	834	18	0
25	v	753	0	780	21	0
26	w	575	0	592	15	0
27	x	625	0	655	21	0
28	y	509	0	543	14	0
29	z	449	0	491	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	B	444	0	461	17	0
31	C	410	0	440	10	0
32	D	377	0	418	9	0
33	E	504	0	574	14	0
34	F	302	0	343	9	0
35	4	436	0	218	10	0
36	5	1647	0	832	31	0
37	G	1705	0	1731	62	0
38	H	1625	0	1699	38	0
39	I	1643	0	1710	56	0
40	J	1157	0	1199	32	0
41	K	818	0	808	22	0
42	L	1182	0	1240	36	0
43	M	979	0	1034	34	0
44	N	1022	0	1070	41	0
45	O	787	0	828	27	0
46	P	870	0	878	39	0
47	Q	955	0	1019	37	0
48	R	884	0	944	45	0
49	S	805	0	847	26	0
50	T	714	0	737	16	0
51	U	649	0	666	19	0
52	V	649	0	691	30	0
53	W	536	0	552	20	0
54	X	638	0	665	26	0
55	Y	665	0	714	21	0
56	Z	545	0	579	18	0
All	All	147596	0	99363	3332	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 14.

The worst 5 of 3332 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)
37:G:159:ALA:HB1	37:G:183:PHE:CE2	1.69	1.25
37:G:71:THR:OG1	37:G:168:GLU:OE2	1.53	1.25
1:3:656:G:H2'	1:3:657:U:H5''	1.32	1.08
1:3:440:C:H2'	1:3:441:A:H4'	1.29	1.08
1:3:1221:G:H2'	1:3:1222:G:H5''	1.34	1.08

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	
5	b	269/271 (99%)	221 (82%)	48 (18%)	0	100	100
6	c	207/209 (99%)	172 (83%)	33 (16%)	2 (1%)	12	43
7	d	199/201 (99%)	167 (84%)	32 (16%)	0	100	100
8	e	175/177 (99%)	144 (82%)	31 (18%)	0	100	100
9	f	174/176 (99%)	154 (88%)	20 (12%)	0	100	100
10	g	147/149 (99%)	131 (89%)	15 (10%)	1 (1%)	18	51
11	a	130/223 (58%)	113 (87%)	17 (13%)	0	100	100
12	i	139/142 (98%)	117 (84%)	22 (16%)	0	100	100
13	j	140/142 (99%)	126 (90%)	13 (9%)	1 (1%)	18	51
14	k	120/122 (98%)	92 (77%)	28 (23%)	0	100	100
15	l	141/143 (99%)	106 (75%)	32 (23%)	3 (2%)	5	31
16	m	134/136 (98%)	109 (81%)	24 (18%)	1 (1%)	18	51
17	n	118/120 (98%)	96 (81%)	22 (19%)	0	100	100
18	o	114/116 (98%)	106 (93%)	8 (7%)	0	100	100
19	p	112/114 (98%)	95 (85%)	17 (15%)	0	100	100
20	q	115/117 (98%)	108 (94%)	7 (6%)	0	100	100
21	r	101/103 (98%)	84 (83%)	17 (17%)	0	100	100
22	s	108/110 (98%)	98 (91%)	10 (9%)	0	100	100
23	t	91/93 (98%)	75 (82%)	16 (18%)	0	100	100
24	u	100/102 (98%)	87 (87%)	13 (13%)	0	100	100
25	v	92/94 (98%)	82 (89%)	9 (10%)	1 (1%)	11	41
26	w	73/75 (97%)	61 (84%)	12 (16%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	x	75/77 (97%)	65 (87%)	10 (13%)	0	100	100
28	y	61/63 (97%)	55 (90%)	5 (8%)	1 (2%)	7	35
29	z	56/58 (97%)	49 (88%)	7 (12%)	0	100	100
30	B	54/56 (96%)	42 (78%)	12 (22%)	0	100	100
31	C	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
32	D	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
33	E	62/64 (97%)	52 (84%)	8 (13%)	2 (3%)	3	24
34	F	36/38 (95%)	25 (69%)	11 (31%)	0	100	100
37	G	216/225 (96%)	187 (87%)	27 (12%)	2 (1%)	14	45
38	H	204/206 (99%)	184 (90%)	20 (10%)	0	100	100
39	I	203/205 (99%)	178 (88%)	25 (12%)	0	100	100
40	J	155/157 (99%)	130 (84%)	25 (16%)	0	100	100
41	K	98/100 (98%)	85 (87%)	13 (13%)	0	100	100
42	L	149/151 (99%)	139 (93%)	10 (7%)	0	100	100
43	M	127/129 (98%)	113 (89%)	14 (11%)	0	100	100
44	N	125/127 (98%)	107 (86%)	18 (14%)	0	100	100
45	O	96/98 (98%)	81 (84%)	15 (16%)	0	100	100
46	P	114/116 (98%)	98 (86%)	16 (14%)	0	100	100
47	Q	121/123 (98%)	93 (77%)	26 (22%)	2 (2%)	7	34
48	R	112/114 (98%)	94 (84%)	18 (16%)	0	100	100
49	S	98/100 (98%)	87 (89%)	10 (10%)	1 (1%)	12	43
50	T	86/88 (98%)	77 (90%)	9 (10%)	0	100	100
51	U	80/82 (98%)	63 (79%)	17 (21%)	0	100	100
52	V	78/80 (98%)	51 (65%)	27 (35%)	0	100	100
53	W	63/65 (97%)	57 (90%)	6 (10%)	0	100	100
54	X	77/79 (98%)	62 (80%)	14 (18%)	1 (1%)	9	38
55	Y	83/85 (98%)	79 (95%)	4 (5%)	0	100	100
56	Z	63/65 (97%)	41 (65%)	18 (29%)	4 (6%)	1	14
All	All	5783/5982 (97%)	4926 (85%)	835 (14%)	22 (0%)	31	62

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
33	E	31	ILE
56	Z	37	TYR
10	g	9	VAL
56	Z	10	PRO
15	l	103	ILE

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	b	216/216 (100%)	214 (99%)	2 (1%)	70	74
6	c	164/164 (100%)	161 (98%)	3 (2%)	51	67
7	d	165/165 (100%)	163 (99%)	2 (1%)	63	72
8	e	148/148 (100%)	148 (100%)	0	100	100
9	f	137/137 (100%)	136 (99%)	1 (1%)	76	77
10	g	114/114 (100%)	113 (99%)	1 (1%)	70	74
11	a	110/174 (63%)	110 (100%)	0	100	100
12	i	109/110 (99%)	109 (100%)	0	100	100
13	j	116/116 (100%)	115 (99%)	1 (1%)	70	74
14	k	103/103 (100%)	101 (98%)	2 (2%)	50	66
15	l	102/102 (100%)	102 (100%)	0	100	100
16	m	109/109 (100%)	108 (99%)	1 (1%)	70	74
17	n	100/100 (100%)	98 (98%)	2 (2%)	48	65
18	o	86/86 (100%)	86 (100%)	0	100	100
19	p	99/99 (100%)	99 (100%)	0	100	100
20	q	89/89 (100%)	88 (99%)	1 (1%)	65	73
21	r	84/84 (100%)	83 (99%)	1 (1%)	63	72
22	s	93/93 (100%)	91 (98%)	2 (2%)	45	63
23	t	80/80 (100%)	79 (99%)	1 (1%)	61	71
24	u	83/83 (100%)	83 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	v	78/78 (100%)	78 (100%)	0	100	100
26	w	57/57 (100%)	57 (100%)	0	100	100
27	x	67/67 (100%)	66 (98%)	1 (2%)	57	69
28	y	55/55 (100%)	55 (100%)	0	100	100
29	z	48/48 (100%)	48 (100%)	0	100	100
30	B	47/47 (100%)	46 (98%)	1 (2%)	47	64
31	C	45/45 (100%)	44 (98%)	1 (2%)	45	63
32	D	38/38 (100%)	38 (100%)	0	100	100
33	E	51/51 (100%)	51 (100%)	0	100	100
34	F	34/34 (100%)	34 (100%)	0	100	100
37	G	180/186 (97%)	177 (98%)	3 (2%)	53	67
38	H	170/170 (100%)	168 (99%)	2 (1%)	63	72
39	I	172/172 (100%)	167 (97%)	5 (3%)	37	58
40	J	119/119 (100%)	119 (100%)	0	100	100
41	K	87/87 (100%)	85 (98%)	2 (2%)	44	63
42	L	124/124 (100%)	122 (98%)	2 (2%)	55	68
43	M	104/104 (100%)	104 (100%)	0	100	100
44	N	105/105 (100%)	104 (99%)	1 (1%)	68	74
45	O	86/86 (100%)	85 (99%)	1 (1%)	63	72
46	P	89/89 (100%)	89 (100%)	0	100	100
47	Q	103/103 (100%)	102 (99%)	1 (1%)	68	74
48	R	92/92 (100%)	91 (99%)	1 (1%)	65	73
49	S	83/83 (100%)	83 (100%)	0	100	100
50	T	76/76 (100%)	76 (100%)	0	100	100
51	U	65/65 (100%)	65 (100%)	0	100	100
52	V	74/74 (100%)	74 (100%)	0	100	100
53	W	56/56 (100%)	56 (100%)	0	100	100
54	X	70/70 (100%)	69 (99%)	1 (1%)	59	70
55	Y	65/65 (100%)	65 (100%)	0	100	100
56	Z	55/55 (100%)	55 (100%)	0	100	100
All	All	4802/4873 (98%)	4760 (99%)	42 (1%)	68	74

5 of 42 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	I	33	ILE
42	L	83	THR
39	I	35	GLN
39	I	186	GLU
44	N	8	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 90 such sidechains are listed below:

Mol	Chain	Res	Type
37	G	176	ASN
43	M	75	GLN
38	H	31	ASN
40	J	131	ASN
47	Q	58	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3	1538/1539 (99%)	282 (18%)	4 (0%)
2	1	2902/2903 (99%)	512 (17%)	10 (0%)
3	2	119/120 (99%)	12 (10%)	0
35	4	19/39 (48%)	5 (26%)	1 (5%)
36	5	76/77 (98%)	15 (19%)	0
4	6	76/77 (98%)	16 (21%)	0
All	All	4730/4755 (99%)	842 (17%)	15 (0%)

5 of 842 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3	5	U
1	3	9	G
1	3	16	A
1	3	31	G
1	3	32	A

5 of 15 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	1	1453	A

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Mol	Chain	Res	Type
2	1	2391	G
2	1	1626	A
35	4	13	A
2	1	2001	C

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

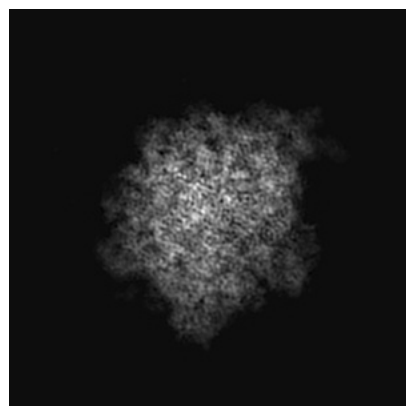
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25415. These allow visual inspection of the internal detail of the map and identification of artifacts.

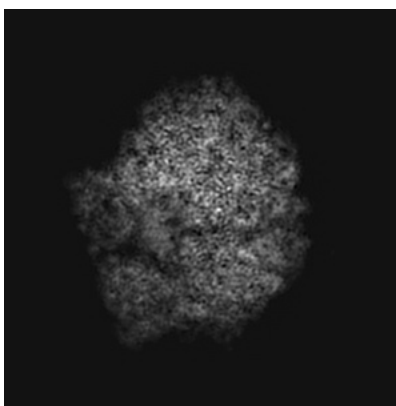
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

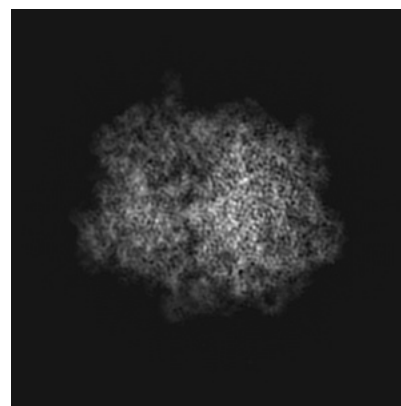
6.1.1 Primary map



X

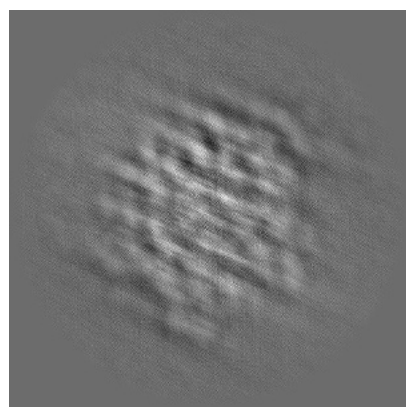


Y

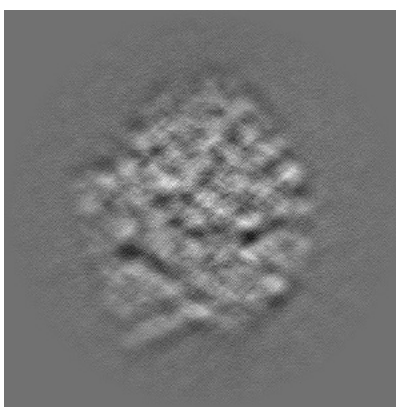


Z

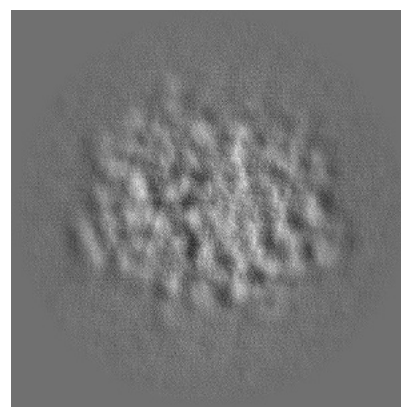
6.1.2 Raw map



X



Y

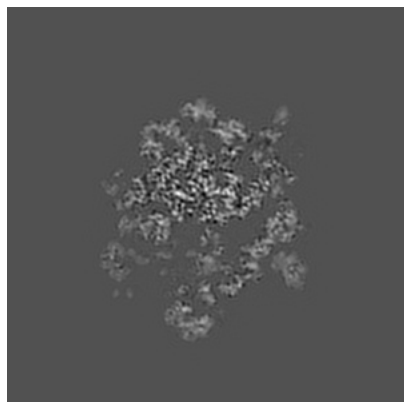


Z

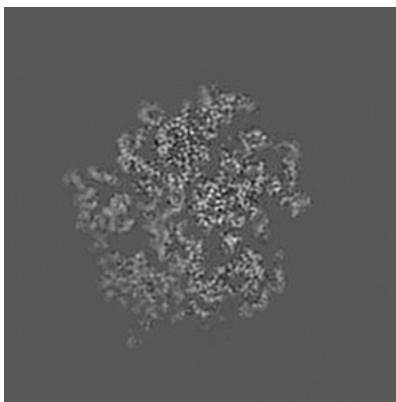
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

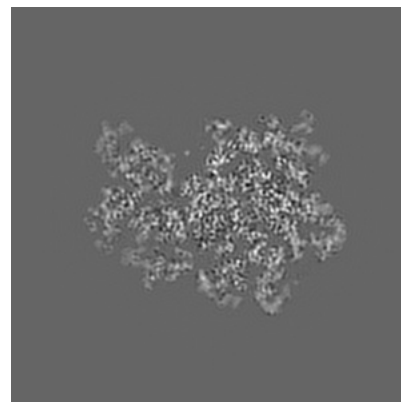
6.2.1 Primary map



X Index: 224

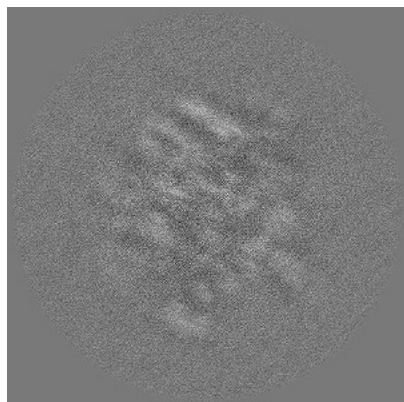


Y Index: 224

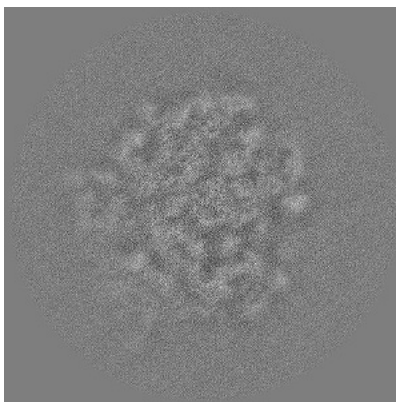


Z Index: 224

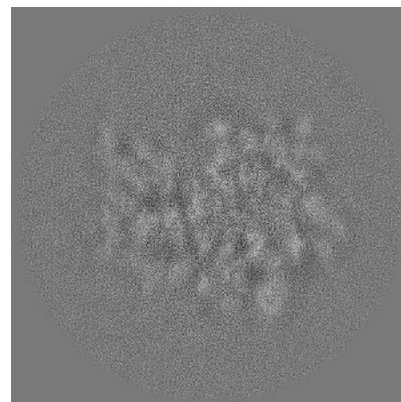
6.2.2 Raw map



X Index: 224



Y Index: 224

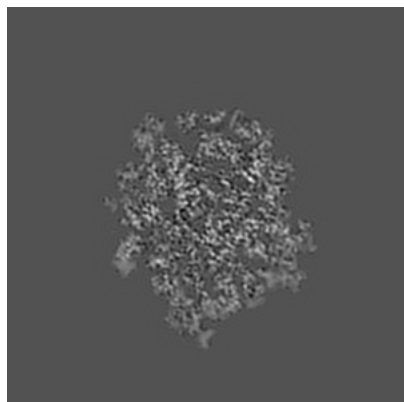


Z Index: 224

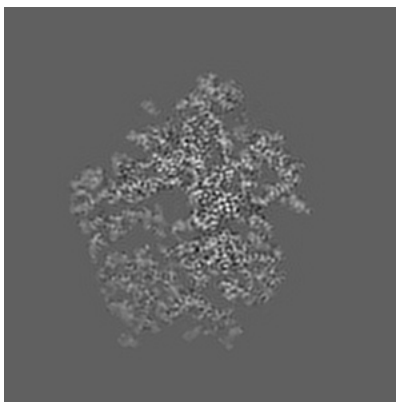
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

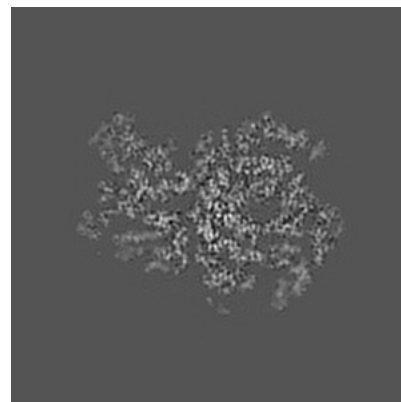
6.3.1 Primary map



X Index: 255

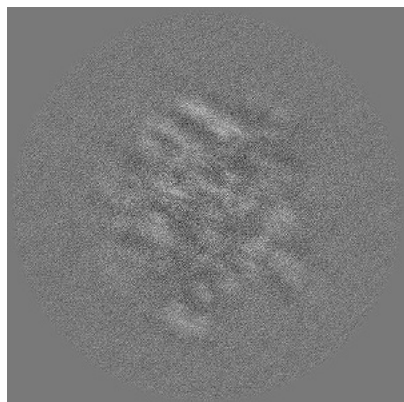


Y Index: 209

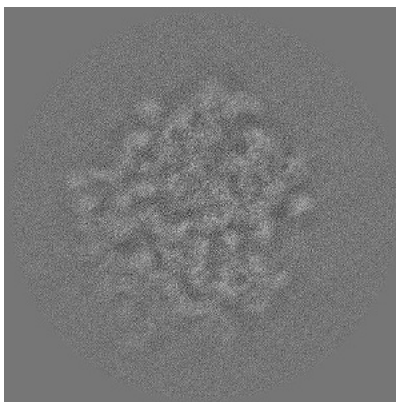


Z Index: 238

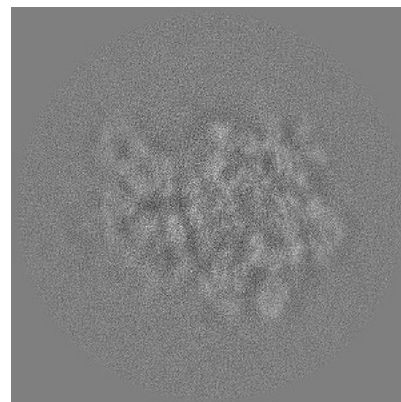
6.3.2 Raw map



X Index: 224



Y Index: 215

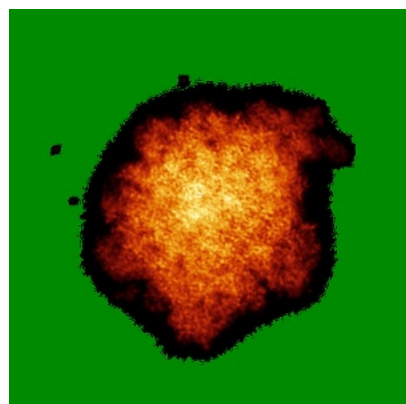


Z Index: 228

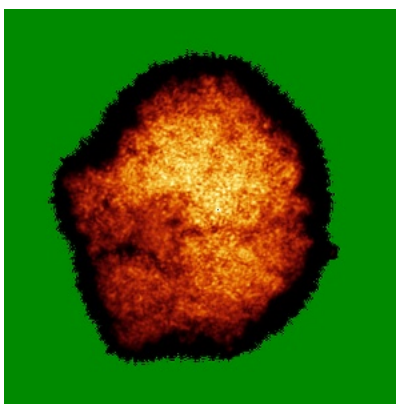
The images above show the largest variance slices of the map in three orthogonal directions.

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

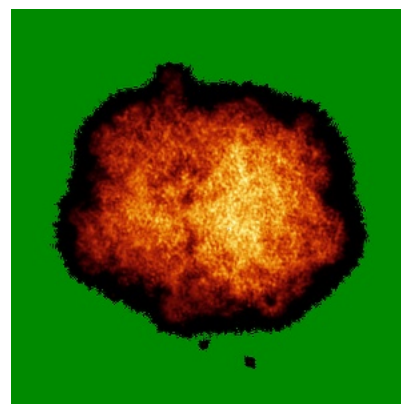
6.4.1 Primary map



X

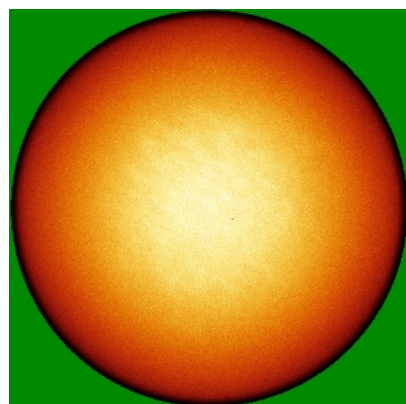


Y

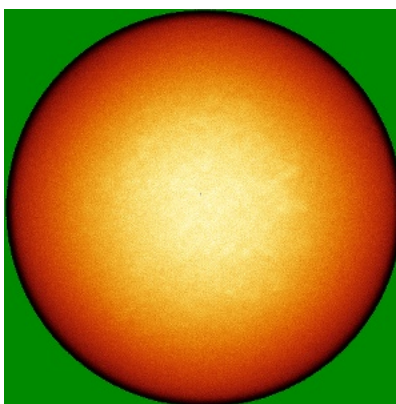


Z

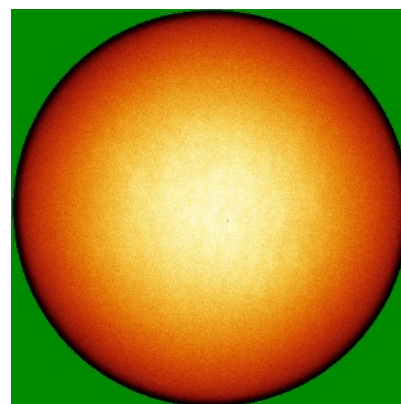
6.4.2 Raw map



X



Y

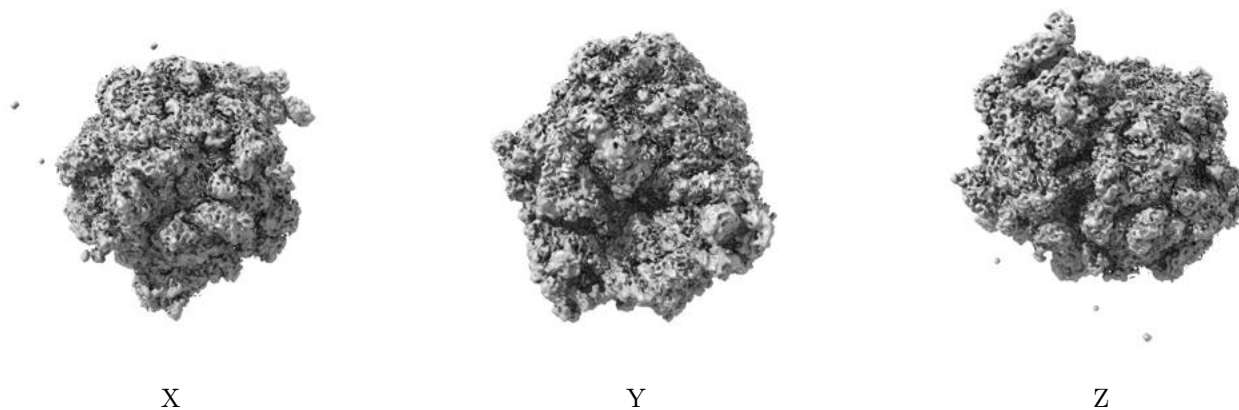


Z

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.

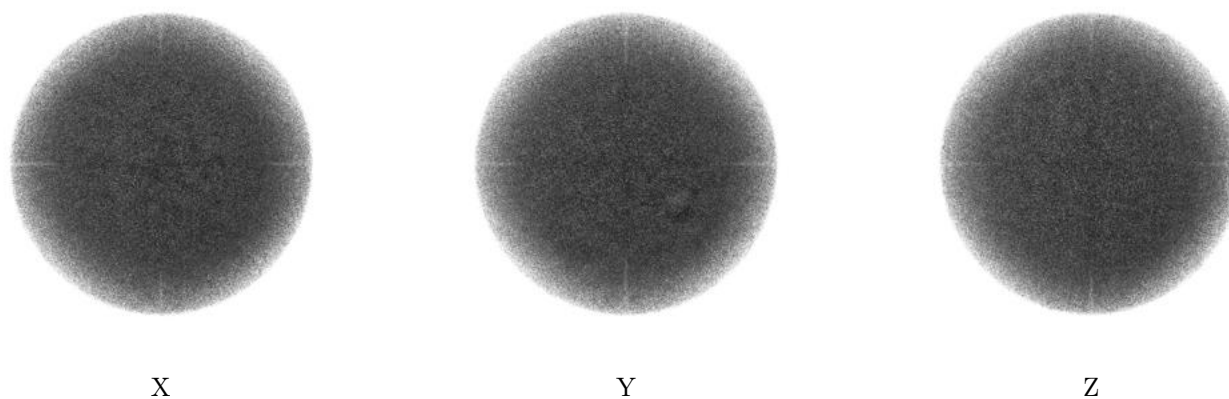
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.5. 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.

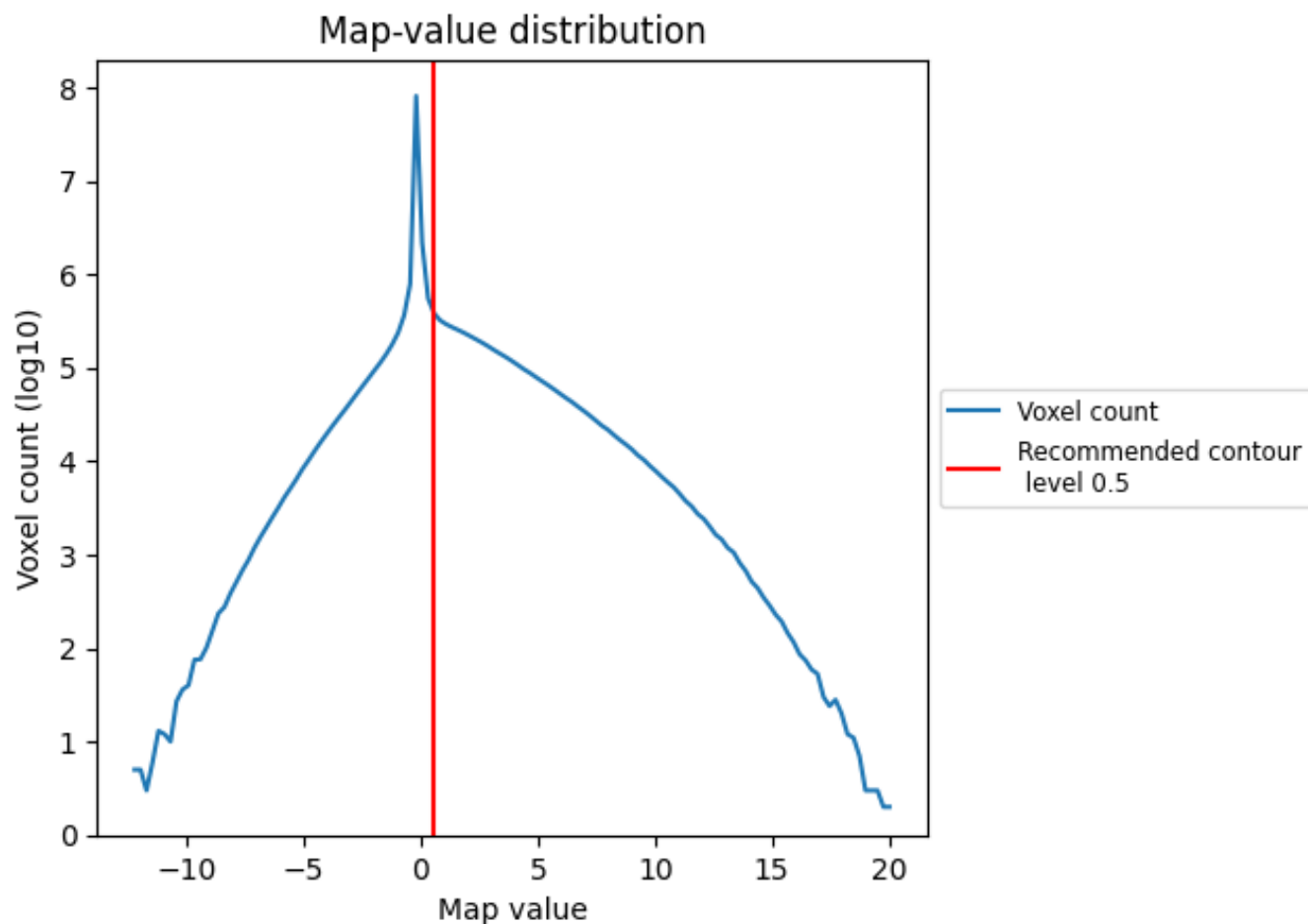
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

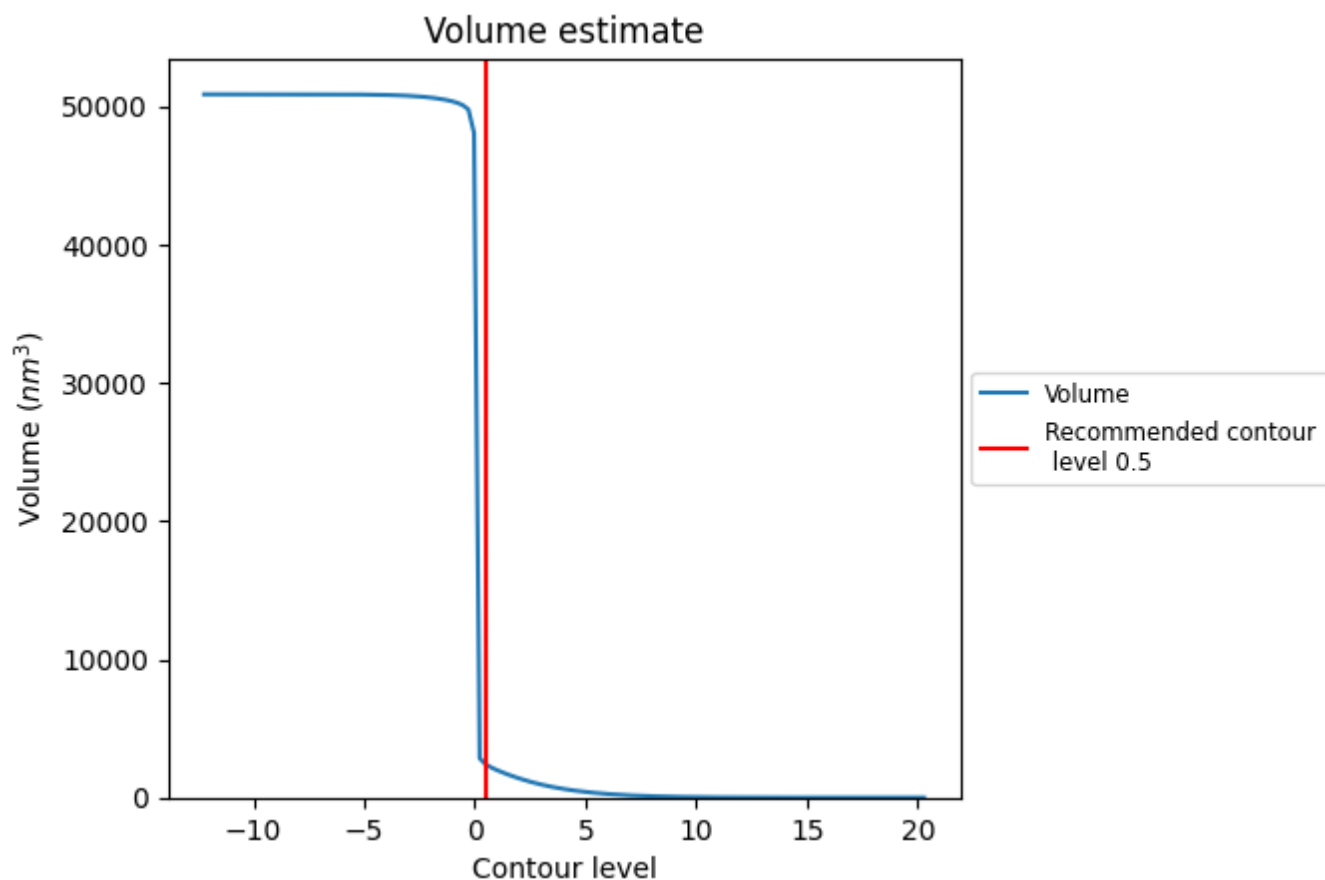
This section contains the results of statistical analysis of the map.

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.

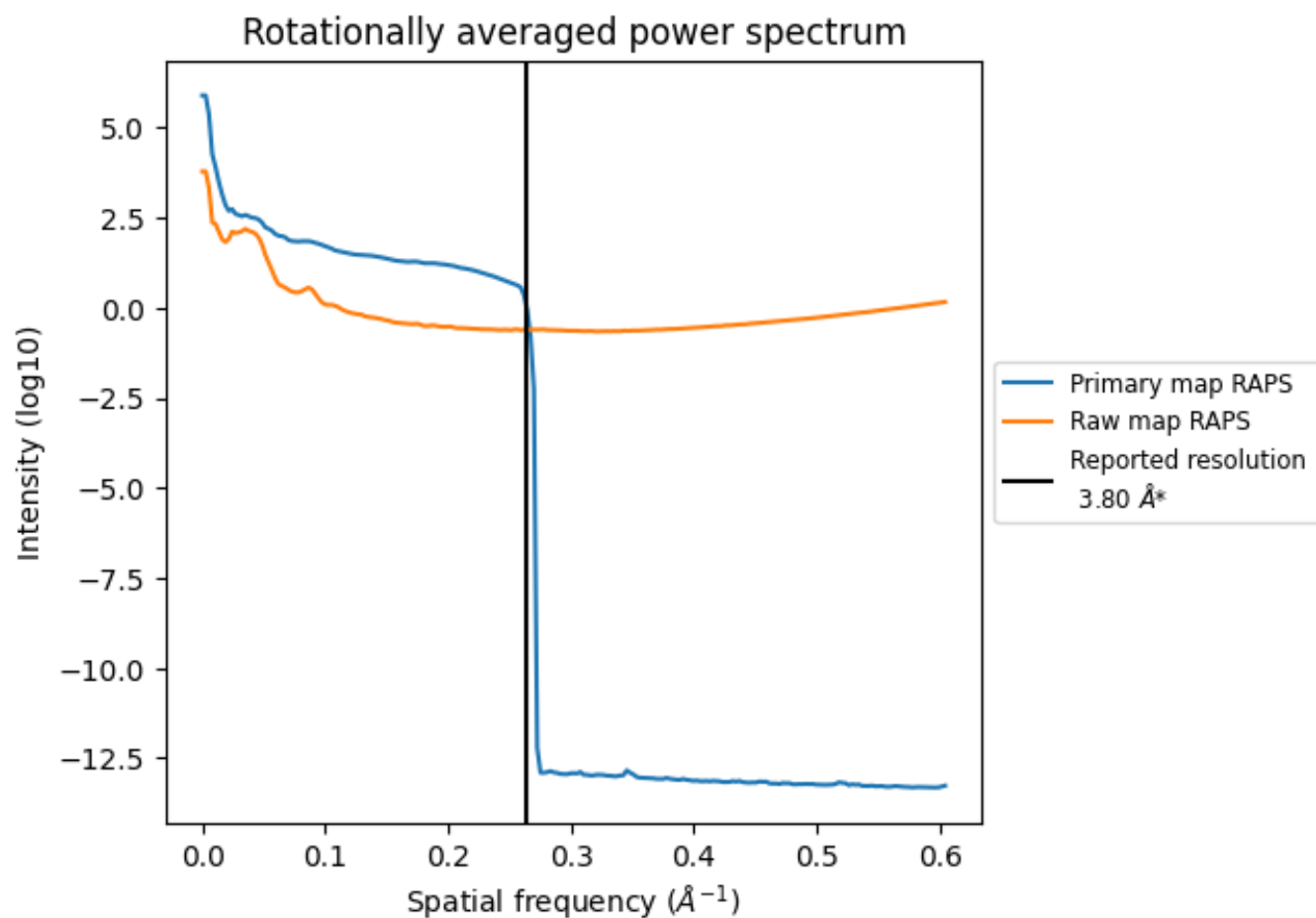
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2398 nm³; this corresponds to an approximate mass of 2166 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 ⓘ

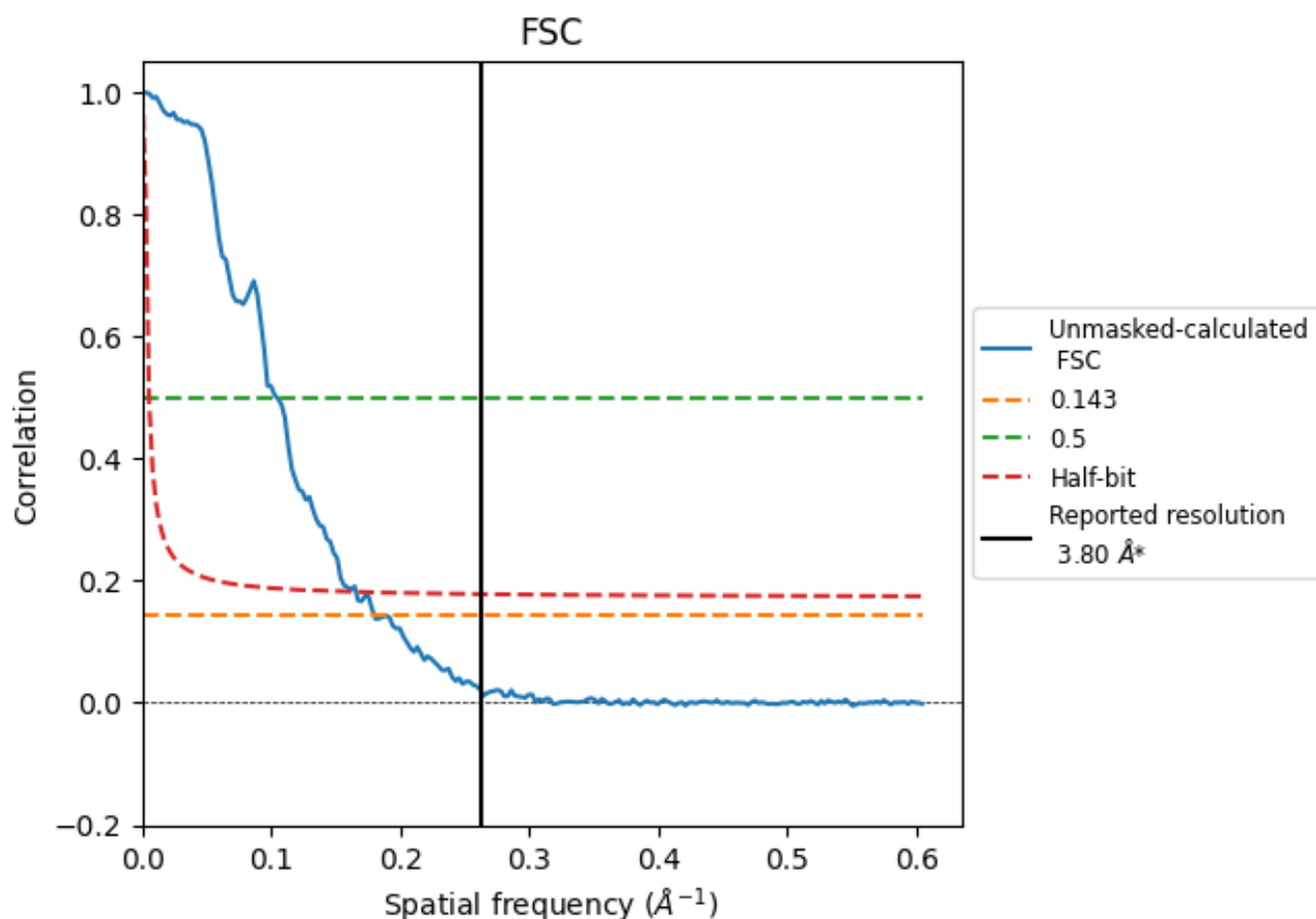


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

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](#)

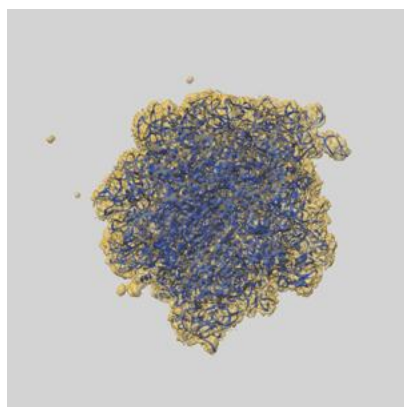
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	5.56	9.61	6.04

*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 5.56 differs from the reported value 3.8 by more than 10 %

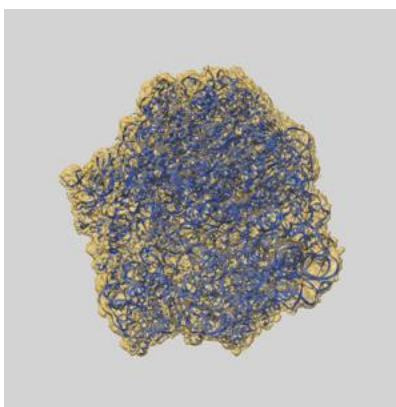
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-25415 and PDB model 7SSW. Per-residue inclusion information can be found in section 3 on page 15.

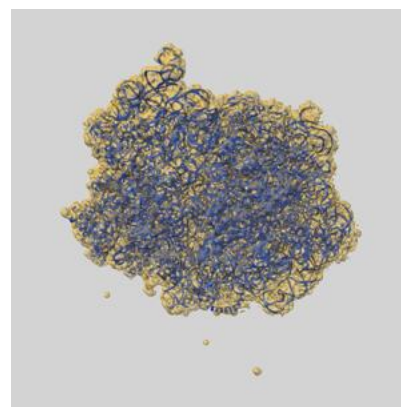
9.1 Map-model overlay [i](#)



X



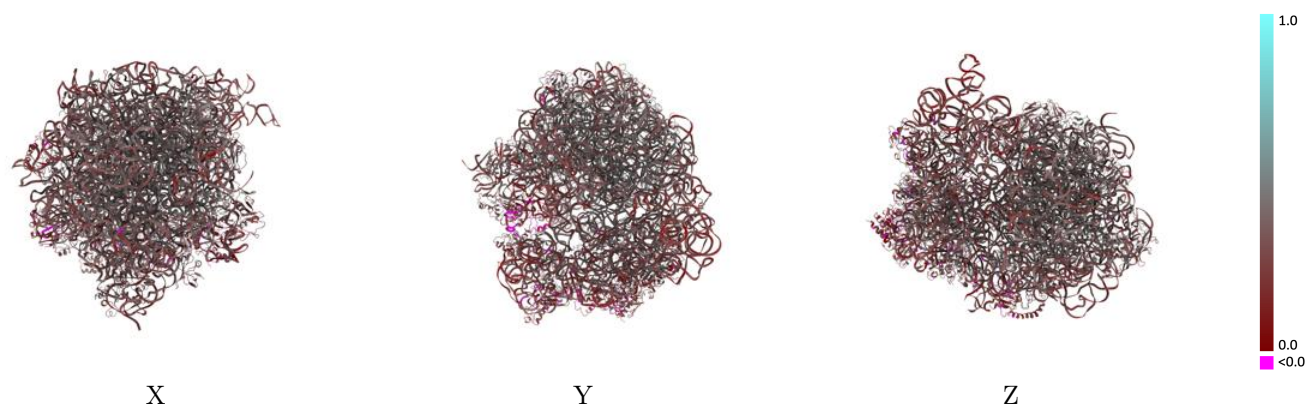
Y



Z

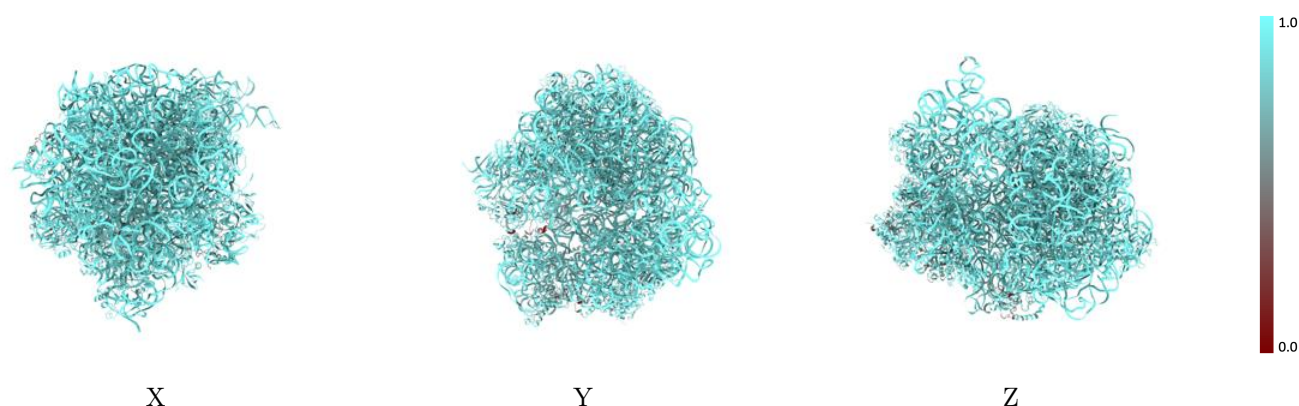
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



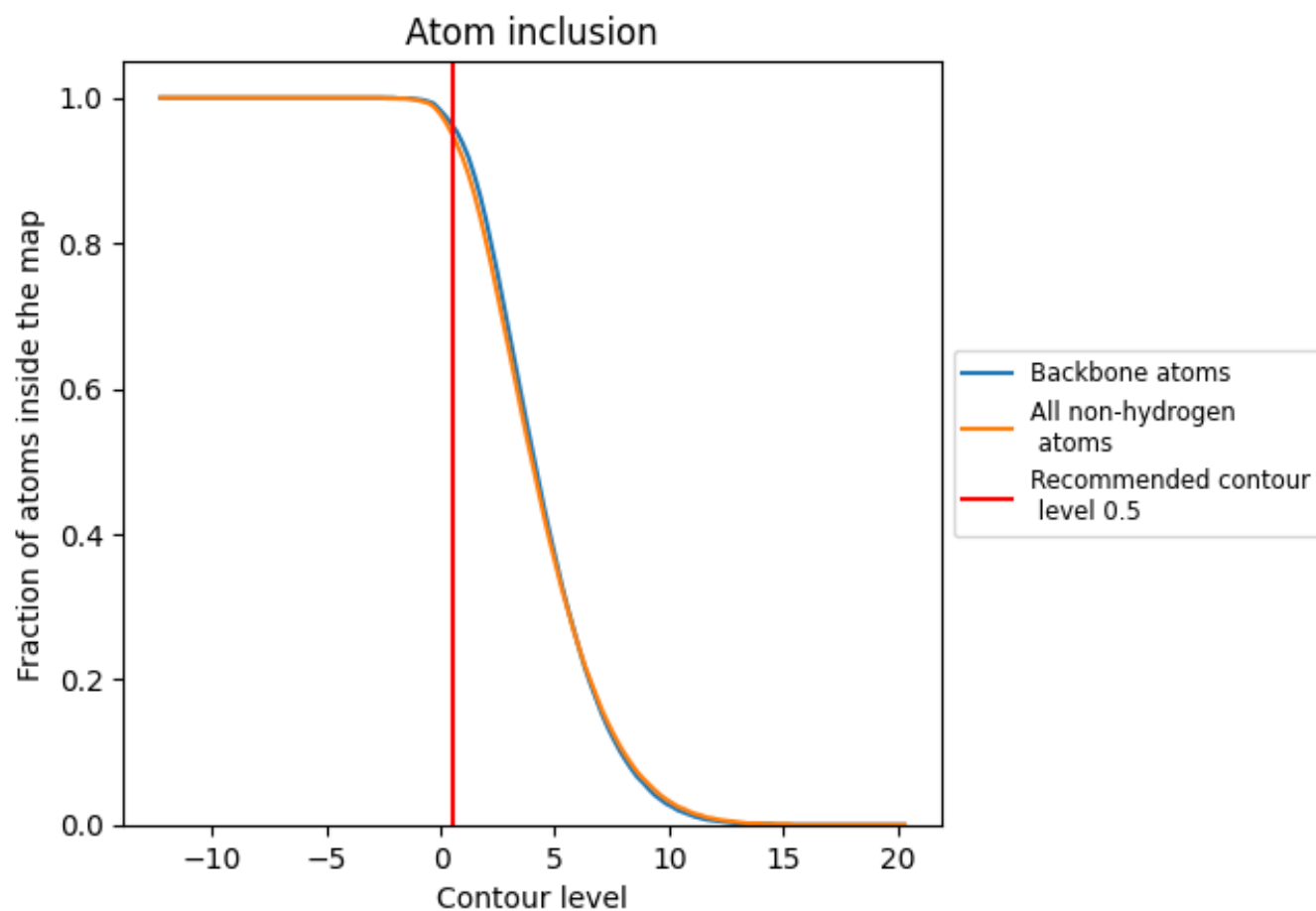
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 95% 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 (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9510	 0.3340
1	 0.9740	 0.3600
2	 0.9830	 0.3210
3	 0.9590	 0.2990
4	 0.8140	 0.1820
5	 0.9480	 0.2540
6	 0.9400	 0.2480
B	 0.9490	 0.4100
C	 0.8580	 0.3160
D	 0.9610	 0.4460
E	 0.9490	 0.4080
F	 0.9620	 0.4150
G	 0.7880	 0.1940
H	 0.7490	 0.2190
I	 0.9220	 0.2890
J	 0.9520	 0.3480
K	 0.9510	 0.3120
L	 0.8070	 0.2400
M	 0.9250	 0.3430
N	 0.8840	 0.2610
O	 0.8320	 0.2450
P	 0.9600	 0.3360
Q	 0.9250	 0.3340
R	 0.8740	 0.2500
S	 0.9250	 0.2820
T	 0.9590	 0.3580
U	 0.9390	 0.3280
V	 0.9180	 0.3250
W	 0.9670	 0.3470
X	 0.9230	 0.2950
Y	 0.9520	 0.3280
Z	 0.8820	 0.2900
a	 0.8750	 0.2070
b	 0.9600	 0.4350
c	 0.9660	 0.4080



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Chain	Atom inclusion	Q-score
d	 0.9430	 0.3930
e	 0.9180	 0.2780
f	 0.9550	 0.3190
g	 0.7000	 0.2240
i	 0.6610	 0.1890
j	 0.9680	 0.4160
k	 0.9570	 0.4030
l	 0.9510	 0.4070
m	 0.9560	 0.3900
n	 0.9640	 0.4230
o	 0.9690	 0.3580
p	 0.9620	 0.4060
q	 0.9570	 0.4060
r	 0.9570	 0.3720
s	 0.9510	 0.3980
t	 0.9490	 0.4030
u	 0.9520	 0.3620
v	 0.9610	 0.3370
w	 0.9480	 0.4200
x	 0.9480	 0.4110
y	 0.9720	 0.3610
z	 0.9540	 0.3900