



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 08:17 AM UTC

PDB ID : 6DZI / pdb_00006dzi
EMDB ID : EMD-8932
Title : Cryo-EM Structure of Mycobacterium smegmatis 70S C(minus) ribosome 70S-MPY complex
Authors : Sharma, M.R.; Li, Y.; Korripella, R.; Yang, Y.; Kaushal, P.S.; Lin, Q.; Wade, J.T.; Gray, A.G.; Derbyshire, K.M.; Agrawal, R.K.; Ojha, A.
Deposited on : 2018-07-05
Resolution : 3.46 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

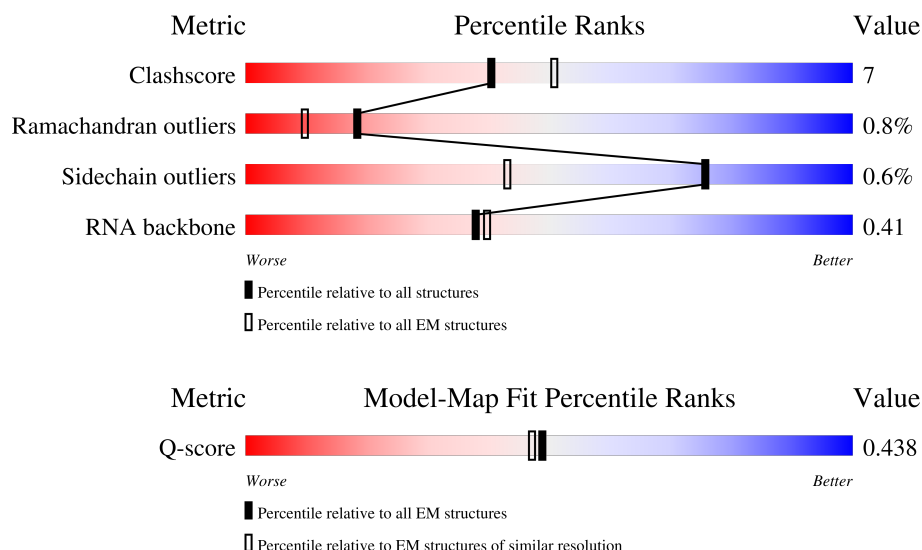
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.46 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.



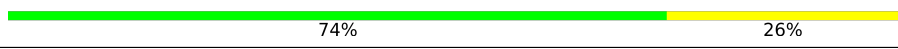
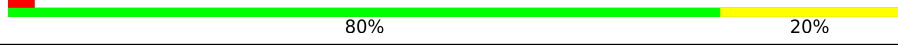
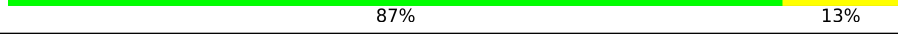
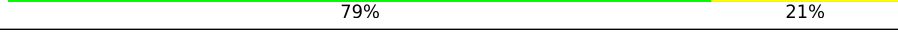
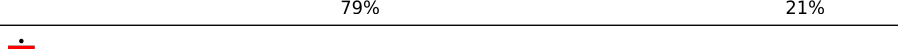
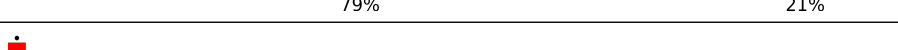
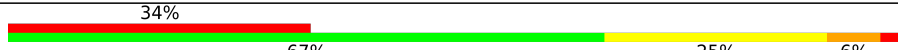
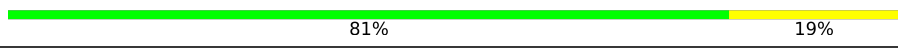
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13788 (2.96 - 3.96)

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	h	1511	
2	j	32	
3	k	208	

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Mol	Chain	Length	Quality of chain
4	l	200	
5	m	180	
6	n	96	
7	p	155	
8	q	131	
9	4	126	
10	s	99	
11	t	115	
12	u	122	
13	v	116	
14	x	88	
15	z	113	
16	5	94	
17	6	82	
18	7	85	
19	8	228	
20	r	84	
21	Y	103	
22	9	100	
23	A	3119	
24	B	118	
25	C	275	
26	D	214	
27	E	209	
28	F	182	

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Mol	Chain	Length	Quality of chain
29	G	176	
30	H	151	
31	I	126	
32	J	133	
33	K	146	
34	L	122	
35	M	145	
36	N	136	
37	O	118	
38	P	126	
39	Q	113	
40	R	124	
41	S	100	
42	T	114	
43	U	97	
44	V	105	
45	W	192	
46	X	79	
47	Z	64	
48	a	59	
49	b	54	
50	c	53	
51	d	46	
52	e	63	
53	f	37	

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Mol	Chain	Length	Quality of chain
54	g	82	
55	y	77	
56	3	23	

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 150868 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	h	1511	Total	C	N	O	P	0	0
			32439	14448	5930	10550	1511		

- Molecule 2 is a protein called CONSERVED PROTEIN DOMAIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	j	32	Total	C	N	O	S	0	0
			280	172	71	36	1		

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	k	208	Total	C	N	O	S	0	0
			1660	1036	322	298	4		

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	l	200	Total	C	N	O	S	0	0
			1641	1028	316	295	2		

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	m	180	Total	C	N	O	S	0	0
			1296	812	245	235	4		

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	n	96	Total	C	N	O	S	0	0
			771	486	138	145	2		

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	p	155	Total	C	N	O	S	0	0
			1232	768	241	221	2		

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	q	131	Total	C	N	O	S	0	0
			1010	633	189	187	1		

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	4	126	Total	C	N	O	0	0
			994	630	194	170		

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	s	99	Total	C	N	O	S	0	0
			788	495	146	144	3		

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	t	115	Total	C	N	O	S	0	0
			855	528	170	156	1		

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	u	122	Total	C	N	O	S	0	0
			958	594	197	165	2		

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	v	116	Total	C	N	O	S	0	0
			935	572	191	169	3		

- Molecule 14 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	x	88	Total	C	N	O	0	0
			720	449	147	124		

- Molecule 15 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	z	113	Total	C	N	O	0	0
			891	570	162	159		

- Molecule 16 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	5	94	Total	C	N	O	S	0	0
			748	469	142	135	2		

- Molecule 17 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	6	82	Total	C	N	O	S	0	0
			662	425	124	112	1		

- Molecule 18 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	7	85	Total	C	N	O	0	0
			660	402	139	119		

- Molecule 19 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	8	228	Total	C	N	O	S	0	0
			1793	1132	322	330	9		

- Molecule 20 is a protein called 30S ribosomal protein S18 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	r	84	Total	C	N	O	S	0	0
			659	408	131	116	4		

- Molecule 21 is a protein called Ribosome hibernation promoting factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Y	103	Total	C	N	O	S	0	0
			861	529	175	155	2		

- Molecule 22 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	9	100	Total	C	N	O	S	0	0
			819	497	183	138	1		

- Molecule 23 is a RNA chain called 23 S rRNA (3119-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
23	A	3119	Total	C	N	O	P	0	0
			66981	29854	12313	21695	3119		

- Molecule 24 is a RNA chain called 5S RNA (118-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
24	B	118	Total	C	N	O	P	0	0
			2522	1126	468	810	118		

- Molecule 25 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	C	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

- Molecule 26 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	D	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 27 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	E	209	Total	C	N	O	S	0	0
			1569	969	295	303	2		

- Molecule 28 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	F	182	Total	C	N	O	S	0	0
			1445	907	271	261	6		

- Molecule 29 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	G	176	Total	C	N	O	S	0	0
			1348	845	249	253	1		

- Molecule 30 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	H	151	Total	C	N	O	S	0	0
			1119	695	209	214	1		

- Molecule 31 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	I	126	Total	C	N	O	S	0	0
			918	580	156	180	2		

- Molecule 32 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	J	133	Total	C	N	O	S	0	0
			990	625	175	187	3		

- Molecule 33 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	K	146	Total	C	N	O	S	0	0
			1130	722	207	200	1		

- Molecule 34 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	L	122	Total	C	N	O	S	0	0
			938	586	179	170	3		

- Molecule 35 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	M	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

- Molecule 36 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	N	136	Total	C	N	O	S	0	0
			1092	690	213	187	2		

- Molecule 37 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	O	118	Total	C	N	O	S	0	0
			928	583	180	163	2		

- Molecule 38 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	P	126	Total	C	N	O		0	0
			956	586	199	171			

- Molecule 39 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Q	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 40 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	R	124	Total	C	N	O		0	0
			988	613	203	172			

- Molecule 41 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	S	100	Total	C	N	O		0	0
			754	478	137	139			

- Molecule 42 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	T	114	Total	C	N	O	0	0
			873	543	171	159		

- Molecule 43 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	U	97	Total	C	N	O	0	0
			756	479	138	139		

- Molecule 44 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	V	97	Total	C	N	O	S	0	0
			732	456	137	137	2		

- Molecule 45 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	W	192	Total	C	N	O	0	0
			1428	881	255	292		

- Molecule 46 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	X	79	Total	C	N	O	0	0
			586	361	123	102		

- Molecule 47 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Z	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

- Molecule 48 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	a	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 49 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	b	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 50 is a protein called 50S ribosomal protein L33 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	c	53	Total	C	N	O	S	0	0
			456	281	97	78			

- Molecule 51 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	d	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 52 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	e	63	Total	C	N	O	S	0	0
			502	302	115	85			

- Molecule 53 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	f	37	Total	C	N	O	S	0	0
			299	181	66	47	5		

- Molecule 54 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	g	75	Total	C	N	O	S	0	0
			593	379	103	110	1		

- Molecule 55 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	y	77	Total	C	N	O	S	0	0
			617	377	132	106	2		

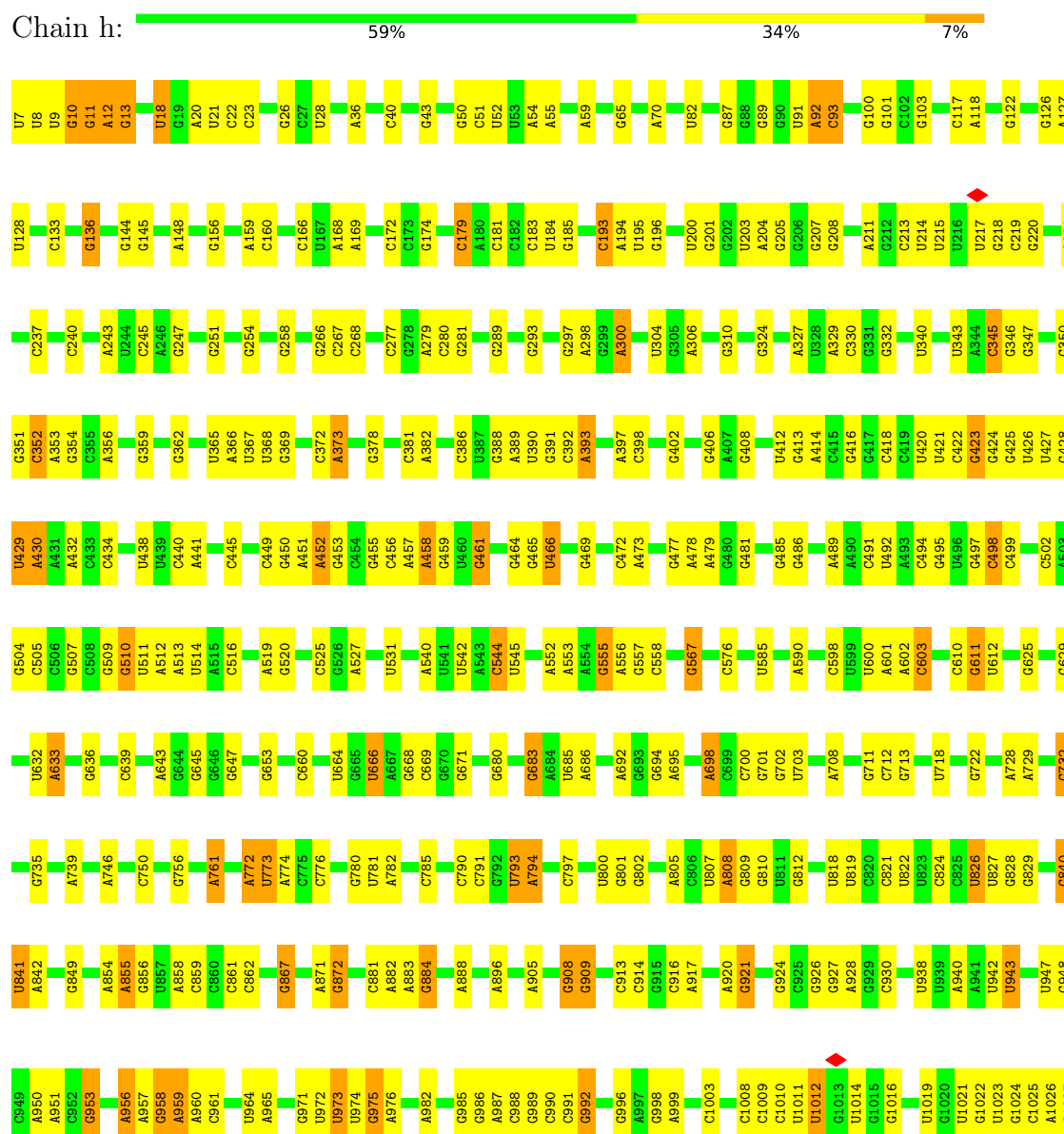
- Molecule 56 is a protein called Uncharacterized protein.

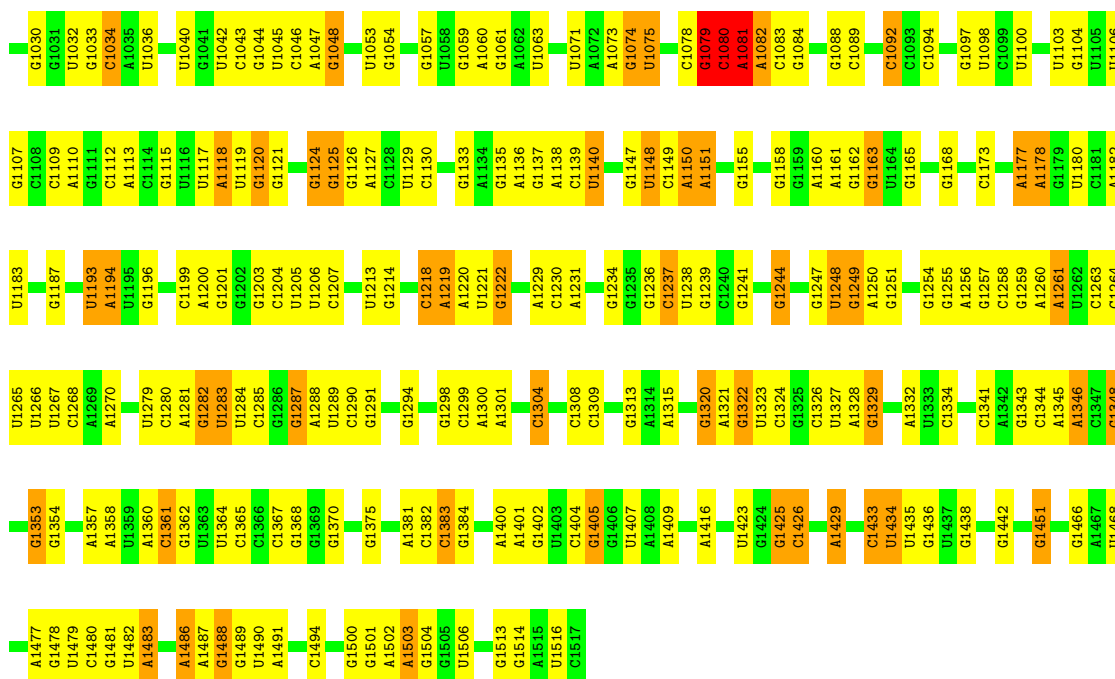
Mol	Chain	Residues	Atoms				AltConf	Trace
56	3	23	Total	C	N	O	0	0
			189	111	50	28		

3 Residue-property plots

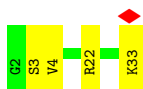
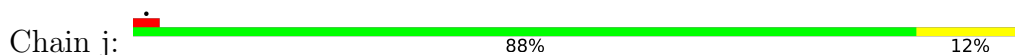
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

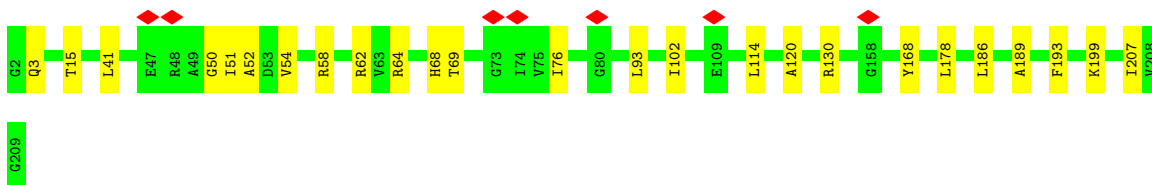
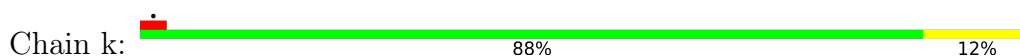




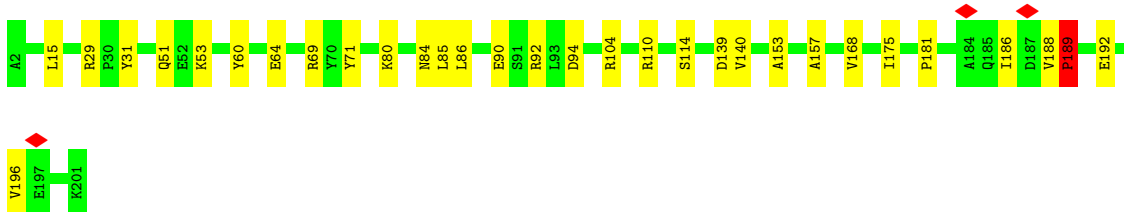
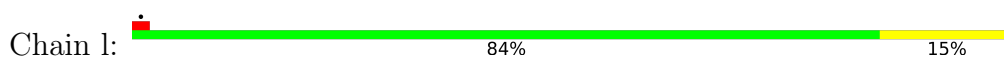
• Molecule 2: CONSERVED PROTEIN DOMAIN



• Molecule 3: 30S ribosomal protein S3

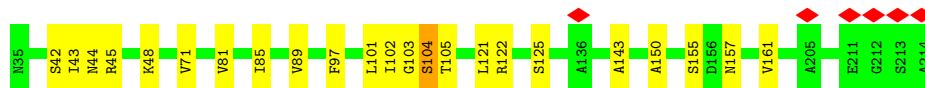


• Molecule 4: 30S ribosomal protein S4



• Molecule 5: 30S ribosomal protein S5

Chain m:  87% 12%



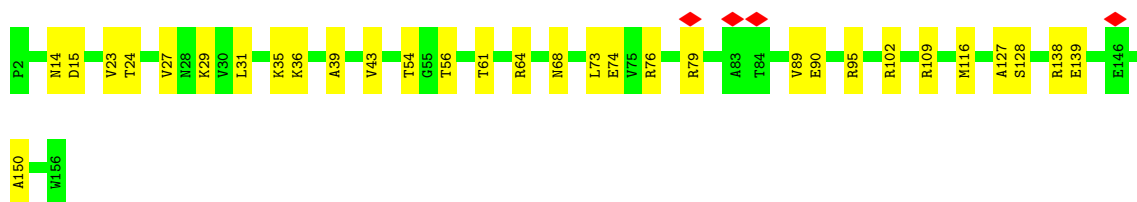
- Molecule 6: 30S ribosomal protein S6

Chain n:  74% 26%



- Molecule 7: 30S ribosomal protein S7

Chain p:  80% 20%



- Molecule 8: 30S ribosomal protein S8

Chain q:  80% 19%



- Molecule 9: 30S ribosomal protein S9

Chain 4:  78% 21%



- Molecule 10: 30S ribosomal protein S10

Chain s:  87% 13%

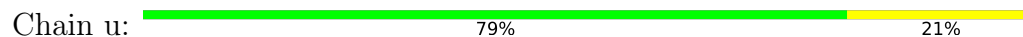


- Molecule 11: 30S ribosomal protein S11

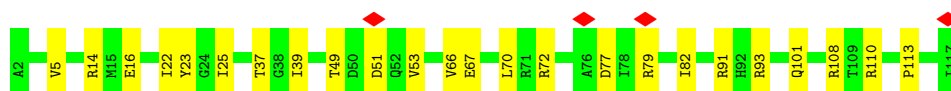
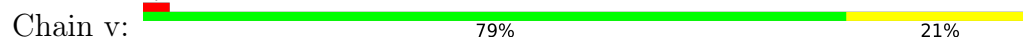
Chain t:  79% 21%



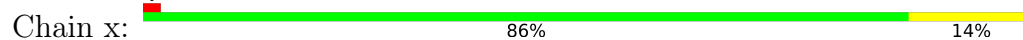
- Molecule 12: 30S ribosomal protein S12



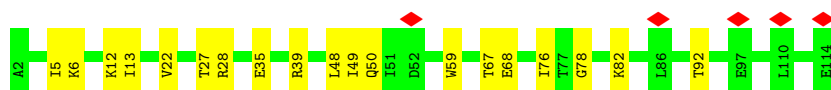
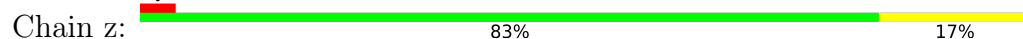
- Molecule 13: 30S ribosomal protein S13



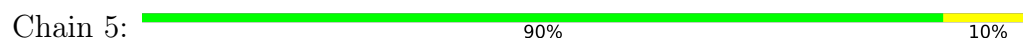
- Molecule 14: 30S ribosomal protein S15



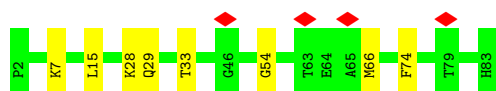
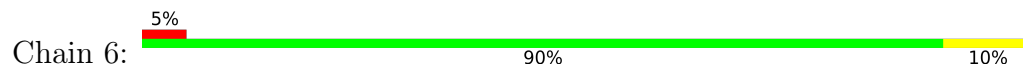
- Molecule 15: 30S ribosomal protein S16



- Molecule 16: 30S ribosomal protein S17



- Molecule 17: 30S ribosomal protein S19



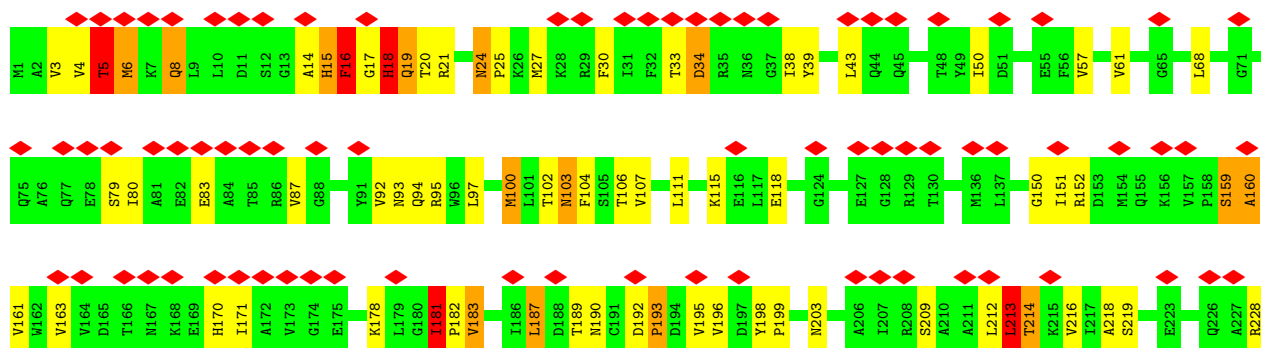
- Molecule 18: 30S ribosomal protein S20

Chain 7:  82% 16% .



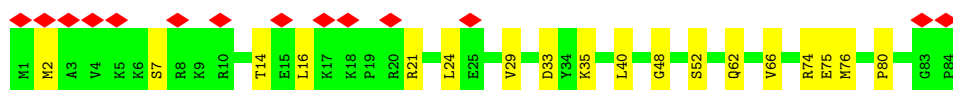
- Molecule 19: 30S ribosomal protein S2

Chain 8:  34% 67% 25% 6% .



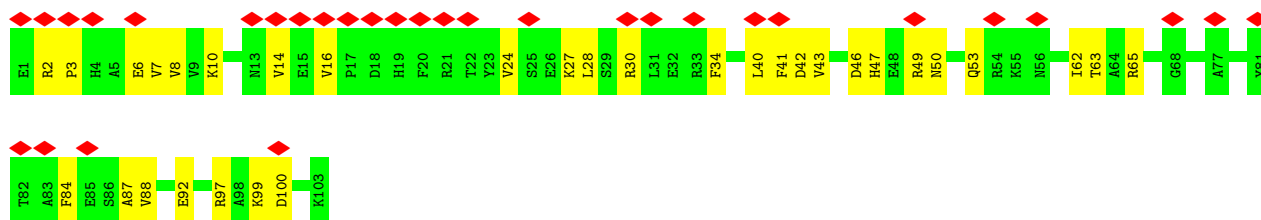
- Molecule 20: 30S ribosomal protein S18 1

Chain r:  17% 79% 21%



- Molecule 21: Ribosome hibernation promoting factor

Chain Y:  30% 69% 31%



- Molecule 22: 30S ribosomal protein S14

Chain 9:  77% 23%



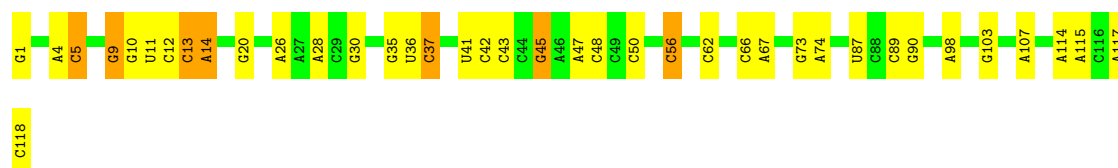
- Molecule 23: 23 S rRNA (3119-MER)

Chain A:  64% 29% 6%

U1544	C1440	C1287	A1195	C1103	U995	A897	U641	U544	U444	U337	G250	C126	A2
G1545	C1445	C1290	U1199	C1104	U996	A898	G642	G551	U445	C338	A251	G127	A3
G1546	C1445	C1291	U1200	C1105	G997	G899	G643	G552	G446	U339	A255	G128	U7
C1548	C1445	U1292	G1201	G1107	C996	A904	G644	G553	U448	C341	C259	U136	A11
G1549	C1449	U1293	A1202	C1112	C1001	U905	G645	G554	U449	C342	A265	G137	A11
G1550	C1451	U1294	A1203	C1113	C1002	A907	G646	G555	G450	U343	U266	A138	U19
U1551	C1456	G1302	A1204	C1114	C1003	A908	G647	G556	U451	G348	G267	U139	G20
A1552	C1457	G1303	A1205	C1115	C1004	A909	U654	G561	C455	G351	G271	A148	G23
C1553	C1457	U1303	A1206	C1116	C1005	A909	G655	G562	U452	G352	A271	C150	G24
U1554	C1462	A1504	G1207	C1117	C1006	C910	G655	U563	C460	G352	A272	A151	A25
A1555	C1462	G1305	U1208	U1117	C1007	U911	U658	G564	G467	A355	A273	A159	C28
A1556	C1465	U1320	G1209	A1118	C1008	U915	U661	A565	C467	G356	A279	A160	C29
G1557	C1468	U1321	U1212	G1121	A1011	G916	G662	A566	C472	U357	U279	U161	U30
A1558	C1468	U1325	A1213	C1125	C1012	G920	A663	A567	C473	G358	A282	A162	U31
U1560	C1478	G1332	U1214	U1126	G1013	G920	A664	G568	C474	A361	U285	U163	G32
C1562	C1479	U1337	A1215	C1127	A1014	G924	G665	G569	C475	A362	G286	A164	C43
A1563	A1480	G1338	U1216	A1127	C1015	U925	A666	C574	C476	A363	A287	A180	U47
A1564	C1482	G1339	G1129	G1128	A1025	U926	A667	G578	U482	U370	A288	G183	G48
A1565	G1483	G1340	C1130	C1131	C1027	C927	C676	G579	G483	A364	C290	A195	A49
A1566	G1484	G1343	U1223	G1140	U1028	G933	G679	G585	C484	G369	A289	G188	U56
C1567	A1493	A1344	G1224	U1141	C1029	A934	G683	A588	C485	U376	G292	A195	A57
A1568	G1494	G1345	G1225	G1142	C1030	A935	G684	A589	C486	C377	G293	A198	G58
A1569	G1495	A1352	C1227	G1143	U1034	A940	G685	A590	C487	A370	G298	A203	G59
C1570	A1499	G1353	U1228	A1144	U1034	U942	A696	A591	C488	A381	G299	G204	A60
C1571	A1500	G1359	A1229	G1148	G1038	U943	G697	A592	C489	A382	G300	A204	A63
G1572	C1501	U1362	G1230	U1151	C1046	A944	C697	C593	C490	U383	U301	G210	A71
U1573	G1507	A1362	U1234	U1152	A1047	U946	U700	A594	C491	G384	U302	U211	G72
A1574	A1508	G1365	U1235	G1153	A1048	U947	A701	A595	C492	U385	U304	A212	A81
C1576	U1509	U1370	G1238	U1157	G1049	C948	G706	A596	C493	G389	G305	G213	A82
C1577	U1511	G1371	G1239	G1157	U1058	U954	G707	C603	C494	G390	U306	G214	C83
G1578	A1518	C1376	G1240	G1162	G1059	U959	G708	C604	C505	G391	G314	A215	U84
C1579	A1522	A1377	A1244	A1163	U1060	G960	G713	G605	C506	U393	U315	A216	G85
A1580	G1523	U1380	A1245	G1165	G1061	U961	U714	C610	C508	A404	U316	A220	G84
C1581	U1529	G1381	G1251	G1173	G1063	C964	A715	C614	C512	A412	U317	A221	G85
C1582	G1530	G1386	G1252	U1178	U1075	U965	A721	U617	C513	G413	U318	A222	C95
U1584	C1531	U1387	C1253	U1179	A1076	C969	G724	C618	C514	G417	U319	A223	G96
U1585	U1538	U1388	C1258	G1180	G1077	G970	G725	C619	U515	C417	C323	A227	U97
C1586	G1532	U1389	U1259	U1183	C1079	G971	A726	G620	U516	A428	U324	A228	U98
G1587	U1534	C1404	C1260	U1184	U1080	A972	A727	A625	C517	U428	U325	U229	G99
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G1589	C1536	A1415	G1270	G1186	U1084	G974	A731	A634	C530	G434	C328	U231	A108
U1590	U1537	A1416	A1271	G1187	G1085	U975	A736	A635	C531	G435	U329	G232	U109
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G1592	A1539	C1435	A1275	C1190	A1091	A978	A738	U636	C533	G437	C332	A241	A115
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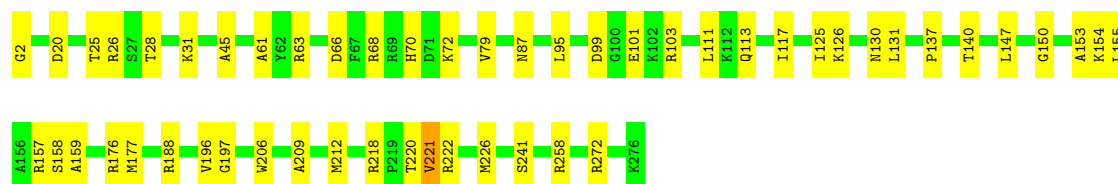
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Chain B:  67% 27% 6%



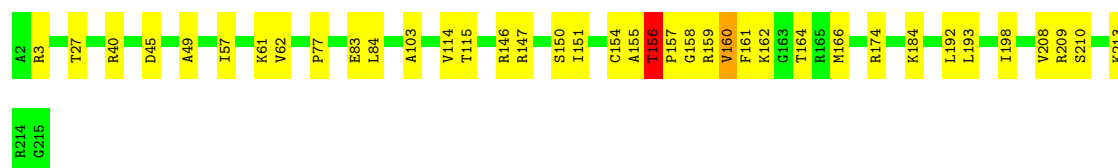
- Molecule 25: 50S ribosomal protein L2

Chain C:  81% 19%



- Molecule 26: 50S ribosomal protein L3

Chain D:  82% 17%



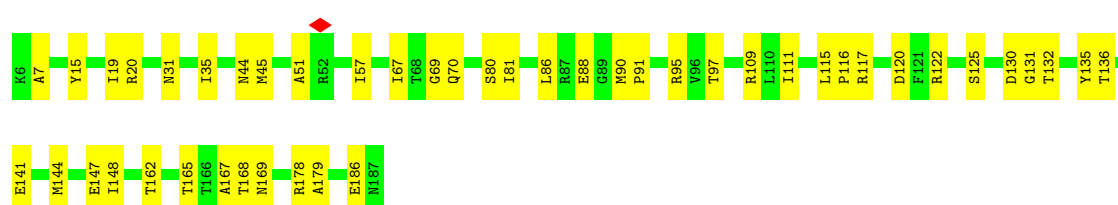
- Molecule 27: 50S ribosomal protein L4

Chain E:  88% 12%



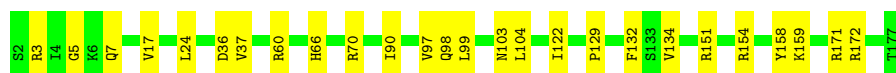
- Molecule 28: 50S ribosomal protein L5

Chain F:  75% 25%



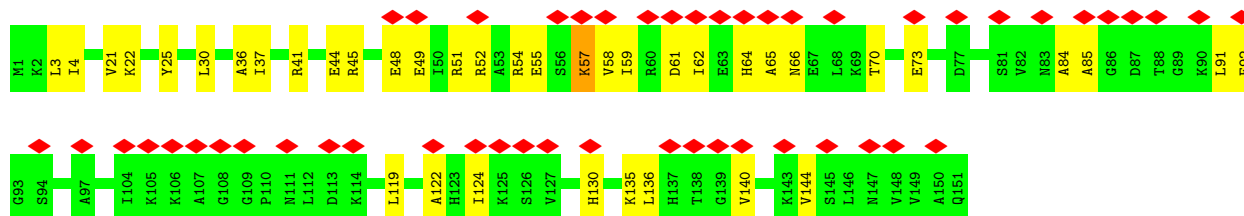
- Molecule 29: 50S ribosomal protein L6

Chain G:  85% 15%



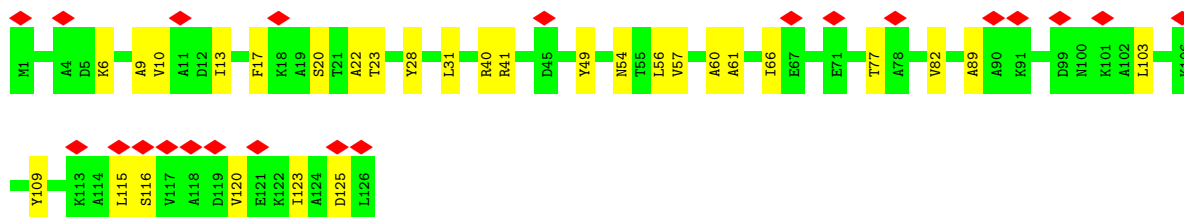
- Molecule 30: 50S ribosomal protein L9

Chain H: 33% 74% 25%



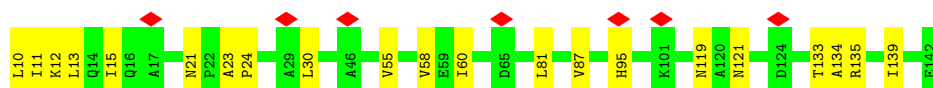
- Molecule 31: 50S ribosomal protein L10

Chain I: 17% 77% 23%



- Molecule 32: 50S ribosomal protein L11

Chain J: 5% 84% 16%



- Molecule 33: 50S ribosomal protein L13

Chain K: 93% 7%



- Molecule 34: 50S ribosomal protein L14

Chain L: 77% 23%



- Molecule 35: 50S ribosomal protein L15

Chain M: 87% 13%



- Molecule 36: 50S ribosomal protein L16

Chain N: 88% 12%



- Molecule 37: 50S ribosomal protein L17

Chain O: 86% 14%



- Molecule 38: 50S ribosomal protein L18

Chain P: 88% 12%



- Molecule 39: 50S ribosomal protein L19

Chain Q: 81% 18% .



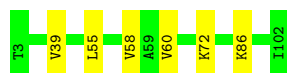
- Molecule 40: 50S ribosomal protein L20

Chain R: 86% 14%



- Molecule 41: 50S ribosomal protein L21

Chain S: 94% 6%

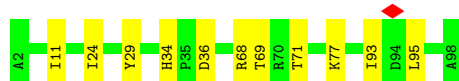
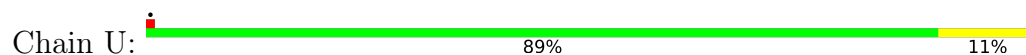


- Molecule 42: 50S ribosomal protein L22

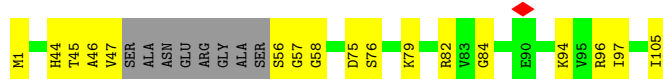
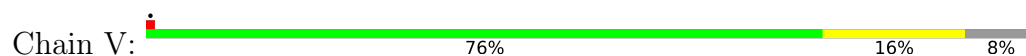
Chain T: 87% 13%



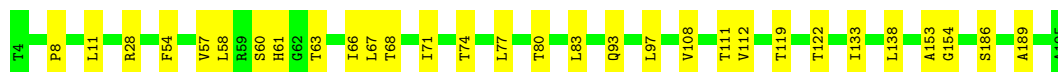
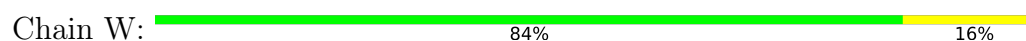
- Molecule 43: 50S ribosomal protein L23



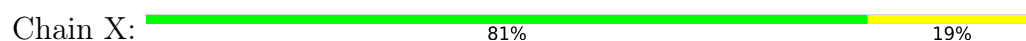
- Molecule 44: 50S ribosomal protein L24



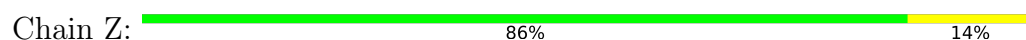
- Molecule 45: 50S ribosomal protein L25



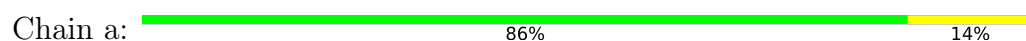
- Molecule 46: 50S ribosomal protein L27



- Molecule 47: 50S ribosomal protein L29



- Molecule 48: 50S ribosomal protein L30

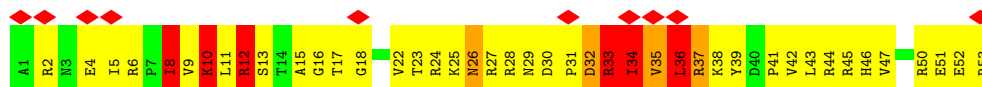


- Molecule 49: 50S ribosomal protein L32

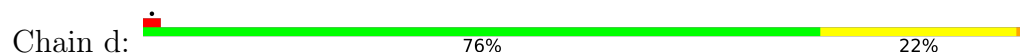




- Molecule 50: 50S ribosomal protein L33 2



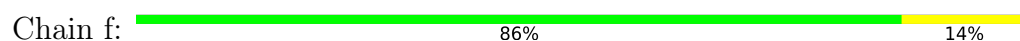
- Molecule 51: 50S ribosomal protein L34



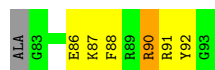
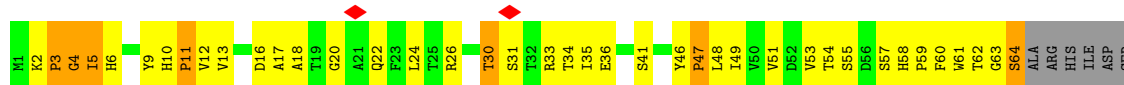
- Molecule 52: 50S ribosomal protein L35



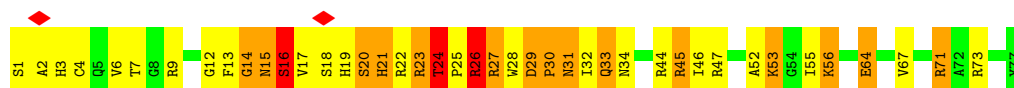
- Molecule 53: 50S ribosomal protein L36



- Molecule 54: 50S ribosomal protein L31



- Molecule 55: 50S ribosomal protein L28



- Molecule 56: Uncharacterized protein

Chain 3:  61% 35% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	66840	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 ($e^-/\text{\AA}^2$)	67.10	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.313	Depositor
Minimum map value	-0.175	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	485.78003, 485.78003, 485.78003	wwPDB
Map dimensions	454, 454, 454	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	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	h	0.34	0/36309	0.43	9/56657 (0.0%)
2	j	0.56	0/280	0.66	0/359
3	k	0.31	0/1684	0.50	0/2261
4	l	0.32	0/1672	0.55	0/2251
5	m	0.36	0/1312	0.55	0/1772
6	n	0.37	0/782	0.54	0/1059
7	p	0.30	0/1252	0.56	0/1690
8	q	0.39	0/1025	0.53	0/1385
9	4	0.30	0/1012	0.57	0/1362
10	s	0.31	0/802	0.50	0/1086
11	t	0.39	0/873	0.55	0/1180
12	u	0.42	0/969	0.64	0/1294
13	v	0.31	0/942	0.55	0/1260
14	x	0.45	0/729	0.52	0/977
15	z	0.36	0/908	0.64	0/1226
16	5	0.37	0/759	0.55	0/1016
17	6	0.31	0/680	0.53	0/915
18	7	0.42	0/663	0.52	0/882
19	8	0.50	0/1822	1.51	40/2457 (1.6%)
20	r	0.38	0/665	0.60	0/889
21	Y	0.34	0/875	0.56	0/1169
22	9	0.32	0/830	0.54	0/1106
23	A	0.57	0/75001	0.51	11/117027 (0.0%)
24	B	0.44	0/2821	0.43	0/4396
25	C	0.74	1/2153 (0.0%)	0.68	3/2895 (0.1%)
26	D	0.74	0/1609	0.75	3/2165 (0.1%)
27	E	0.64	0/1592	0.57	0/2153
28	F	0.45	0/1467	0.55	0/1973
29	G	0.47	0/1369	0.60	0/1848
30	H	0.40	0/1129	0.65	0/1524
31	I	0.29	0/925	0.50	0/1246
32	J	0.32	0/1006	0.58	0/1364
33	K	0.67	0/1157	0.58	0/1567
34	L	0.73	0/946	0.63	0/1268

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	M	0.65	0/1091	0.65	0/1457
36	N	0.67	0/1118	0.62	0/1506
37	O	0.75	0/945	0.64	0/1267
38	P	0.55	0/966	0.58	0/1298
39	Q	0.74	1/921 (0.1%)	0.72	2/1236 (0.2%)
40	R	0.83	0/1000	0.63	0/1341
41	S	0.63	0/764	0.55	0/1030
42	T	0.74	0/887	0.62	0/1204
43	U	0.62	0/766	0.57	0/1030
44	V	0.48	0/738	0.58	0/987
45	W	0.49	0/1443	0.55	0/1970
46	X	0.75	0/595	0.59	0/798
47	Z	0.57	0/534	0.57	0/713
48	a	0.69	0/477	0.56	0/640
49	b	0.69	0/427	0.78	0/572
50	c	0.57	0/463	1.16	4/621 (0.6%)
51	d	0.86	0/380	0.90	3/500 (0.6%)
52	e	0.70	0/507	0.59	0/672
53	f	0.77	0/303	0.55	0/401
54	g	0.45	0/613	1.02	2/835 (0.2%)
55	y	0.56	0/629	1.09	7/843 (0.8%)
56	3	0.76	0/191	0.73	1/247 (0.4%)
All	All	0.52	2/163778 (0.0%)	0.54	85/244847 (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
4	l	0	1
19	8	0	10
26	D	0	1
32	J	0	1
45	W	0	1
All	All	0	14

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	Q	50	GLN	CA-CB	-10.13	1.35	1.53
25	C	45	ALA	CA-C	-5.51	1.45	1.52

The worst 5 of 85 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	8	187	LEU	CA-C-N	16.06	144.38	121.42
19	8	187	LEU	C-N-CA	16.06	144.38	121.42
54	g	90	ARG	N-CA-C	-12.06	97.28	112.72
19	8	18	HIS	CA-C-N	10.36	141.60	122.02
19	8	18	HIS	C-N-CA	10.36	141.60	122.02

There are no chirality outliers.

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
19	8	24	ASN	Peptide
19	8	4	VAL	Peptide
19	8	5	THR	Peptide
19	8	8	GLN	Peptide
4	l	189	PRO	Peptide

5.2 Too-close contacts [i](#)

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	h	32439	0	16321	272	0
2	j	280	0	342	3	0
3	k	1660	0	1707	36	0
4	l	1641	0	1668	18	0
5	m	1296	0	1360	18	0
6	n	771	0	797	29	0
7	p	1232	0	1281	30	0
8	q	1010	0	1042	27	0
9	4	994	0	1050	37	0
10	s	788	0	819	13	0
11	t	855	0	863	15	0
12	u	958	0	1045	20	0
13	v	935	0	986	18	0
14	x	720	0	760	9	0
15	z	891	0	935	14	0
16	5	748	0	795	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	6	662	0	677	5	0
18	7	660	0	712	18	0
19	8	1793	0	1839	61	0
20	r	659	0	717	17	0
21	Y	861	0	862	25	0
22	9	819	0	866	17	0
23	A	66981	0	33700	396	0
24	B	2522	0	1285	15	0
25	C	2110	0	2165	45	0
26	D	1587	0	1630	32	0
27	E	1569	0	1607	18	0
28	F	1445	0	1476	40	0
29	G	1348	0	1399	20	0
30	H	1119	0	1165	54	0
31	I	918	0	959	20	0
32	J	990	0	1021	18	0
33	K	1130	0	1167	7	0
34	L	938	0	1000	22	0
35	M	1078	0	1151	26	0
36	N	1092	0	1128	10	0
37	O	928	0	972	17	0
38	P	956	0	991	12	0
39	Q	907	0	938	13	0
40	R	988	0	1038	13	0
41	S	754	0	802	4	0
42	T	873	0	909	12	0
43	U	756	0	802	10	0
44	V	732	0	782	20	0
45	W	1428	0	1443	17	0
46	X	586	0	601	10	0
47	Z	531	0	541	8	0
48	a	474	0	500	6	0
49	b	423	0	460	23	0
50	c	456	0	474	109	0
51	d	377	0	411	12	0
52	e	502	0	541	32	0
53	f	299	0	324	6	0
54	g	593	0	568	105	0
55	y	617	0	625	77	0
56	3	189	0	205	15	0
All	All	150868	0	102224	1615	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 7.

The worst 5 of 1615 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)
55:y:14:GLY:HA3	55:y:28:TRP:CZ3	1.28	1.66
54:g:35:ILE:CD1	54:g:49:ILE:HG23	1.12	1.58
19:8:16:PHE:CD2	19:8:203:ASN:ND2	1.72	1.54
7:p:61:THR:CB	7:p:64:ARG:NH2	1.69	1.50
55:y:14:GLY:CA	55:y:28:TRP:CZ3	1.97	1.47

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	j	30/32 (94%)	29 (97%)	1 (3%)	0	100	100
3	k	206/208 (99%)	182 (88%)	24 (12%)	0	100	100
4	l	198/200 (99%)	178 (90%)	19 (10%)	1 (0%)	24	57
5	m	178/180 (99%)	154 (86%)	22 (12%)	2 (1%)	11	42
6	n	94/96 (98%)	86 (92%)	8 (8%)	0	100	100
7	p	153/155 (99%)	146 (95%)	7 (5%)	0	100	100
8	q	129/131 (98%)	113 (88%)	16 (12%)	0	100	100
9	4	124/126 (98%)	111 (90%)	12 (10%)	1 (1%)	16	49
10	s	97/99 (98%)	89 (92%)	8 (8%)	0	100	100
11	t	113/115 (98%)	100 (88%)	13 (12%)	0	100	100
12	u	120/122 (98%)	102 (85%)	18 (15%)	0	100	100
13	v	114/116 (98%)	100 (88%)	14 (12%)	0	100	100
14	x	86/88 (98%)	81 (94%)	5 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	z	111/113 (98%)	98 (88%)	13 (12%)	0	100	100
16	5	92/94 (98%)	86 (94%)	6 (6%)	0	100	100
17	6	80/82 (98%)	77 (96%)	3 (4%)	0	100	100
18	7	83/85 (98%)	82 (99%)	1 (1%)	0	100	100
19	8	226/228 (99%)	196 (87%)	23 (10%)	7 (3%)	3	25
20	r	82/84 (98%)	75 (92%)	7 (8%)	0	100	100
21	Y	101/103 (98%)	87 (86%)	14 (14%)	0	100	100
22	9	98/100 (98%)	91 (93%)	7 (7%)	0	100	100
25	C	273/275 (99%)	232 (85%)	41 (15%)	0	100	100
26	D	212/214 (99%)	182 (86%)	28 (13%)	2 (1%)	14	46
27	E	207/209 (99%)	192 (93%)	15 (7%)	0	100	100
28	F	180/182 (99%)	165 (92%)	14 (8%)	1 (1%)	21	53
29	G	174/176 (99%)	157 (90%)	17 (10%)	0	100	100
30	H	149/151 (99%)	139 (93%)	10 (7%)	0	100	100
31	I	124/126 (98%)	117 (94%)	6 (5%)	1 (1%)	16	49
32	J	131/133 (98%)	116 (88%)	15 (12%)	0	100	100
33	K	144/146 (99%)	135 (94%)	9 (6%)	0	100	100
34	L	120/122 (98%)	109 (91%)	11 (9%)	0	100	100
35	M	143/145 (99%)	120 (84%)	21 (15%)	2 (1%)	9	38
36	N	134/136 (98%)	119 (89%)	15 (11%)	0	100	100
37	O	116/118 (98%)	107 (92%)	9 (8%)	0	100	100
38	P	124/126 (98%)	116 (94%)	8 (6%)	0	100	100
39	Q	111/113 (98%)	94 (85%)	15 (14%)	2 (2%)	6	34
40	R	122/124 (98%)	117 (96%)	5 (4%)	0	100	100
41	S	98/100 (98%)	93 (95%)	5 (5%)	0	100	100
42	T	112/114 (98%)	105 (94%)	7 (6%)	0	100	100
43	U	95/97 (98%)	81 (85%)	14 (15%)	0	100	100
44	V	93/105 (89%)	87 (94%)	6 (6%)	0	100	100
45	W	190/192 (99%)	169 (89%)	20 (10%)	1 (0%)	24	57
46	X	77/79 (98%)	69 (90%)	8 (10%)	0	100	100
47	Z	62/64 (97%)	62 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	a	57/59 (97%)	54 (95%)	3 (5%)	0	100	100
49	b	52/54 (96%)	47 (90%)	4 (8%)	1 (2%)	6	33
50	c	51/53 (96%)	26 (51%)	15 (29%)	10 (20%)	0	1
51	d	44/46 (96%)	40 (91%)	4 (9%)	0	100	100
52	e	61/63 (97%)	56 (92%)	5 (8%)	0	100	100
53	f	35/37 (95%)	31 (89%)	4 (11%)	0	100	100
54	g	71/82 (87%)	50 (70%)	16 (22%)	5 (7%)	1	10
55	y	75/77 (97%)	56 (75%)	8 (11%)	11 (15%)	0	3
56	3	21/23 (91%)	18 (86%)	3 (14%)	0	100	100
All	All	6173/6298 (98%)	5524 (90%)	602 (10%)	47 (1%)	18	49

5 of 47 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	m	103	GLY
19	8	16	PHE
19	8	25	PRO
19	8	161	VAL
26	D	156	THR

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	j	30/30 (100%)	30 (100%)	0	100	100
3	k	170/170 (100%)	170 (100%)	0	100	100
4	l	175/175 (100%)	175 (100%)	0	100	100
5	m	127/127 (100%)	126 (99%)	1 (1%)	73	77
6	n	85/85 (100%)	84 (99%)	1 (1%)	63	74
7	p	131/131 (100%)	131 (100%)	0	100	100
8	q	107/107 (100%)	106 (99%)	1 (1%)	70	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	4	102/102 (100%)	101 (99%)	1 (1%)	68	76
10	s	89/89 (100%)	89 (100%)	0	100	100
11	t	89/89 (100%)	88 (99%)	1 (1%)	65	75
12	u	103/103 (100%)	103 (100%)	0	100	100
13	v	99/99 (100%)	99 (100%)	0	100	100
14	x	76/76 (100%)	75 (99%)	1 (1%)	61	73
15	z	92/92 (100%)	92 (100%)	0	100	100
16	5	80/80 (100%)	80 (100%)	0	100	100
17	6	73/73 (100%)	73 (100%)	0	100	100
18	7	69/69 (100%)	68 (99%)	1 (1%)	59	72
19	8	191/191 (100%)	184 (96%)	7 (4%)	30	57
20	r	70/70 (100%)	70 (100%)	0	100	100
21	Y	91/91 (100%)	91 (100%)	0	100	100
22	9	85/85 (100%)	85 (100%)	0	100	100
25	C	215/215 (100%)	215 (100%)	0	100	100
26	D	160/160 (100%)	160 (100%)	0	100	100
27	E	169/169 (100%)	169 (100%)	0	100	100
28	F	151/151 (100%)	151 (100%)	0	100	100
29	G	148/148 (100%)	148 (100%)	0	100	100
30	H	116/116 (100%)	115 (99%)	1 (1%)	70	76
31	I	89/89 (100%)	89 (100%)	0	100	100
32	J	102/102 (100%)	102 (100%)	0	100	100
33	K	119/119 (100%)	118 (99%)	1 (1%)	73	77
34	L	100/100 (100%)	100 (100%)	0	100	100
35	M	112/112 (100%)	112 (100%)	0	100	100
36	N	114/114 (100%)	114 (100%)	0	100	100
37	O	97/97 (100%)	97 (100%)	0	100	100
38	P	93/93 (100%)	93 (100%)	0	100	100
39	Q	100/100 (100%)	100 (100%)	0	100	100
40	R	97/97 (100%)	97 (100%)	0	100	100
41	S	81/81 (100%)	81 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	T	90/90 (100%)	89 (99%)	1 (1%)	65	75
43	U	83/83 (100%)	83 (100%)	0	100	100
44	V	81/86 (94%)	80 (99%)	1 (1%)	63	74
45	W	155/155 (100%)	155 (100%)	0	100	100
46	X	58/58 (100%)	58 (100%)	0	100	100
47	Z	58/58 (100%)	58 (100%)	0	100	100
48	a	52/52 (100%)	52 (100%)	0	100	100
49	b	43/43 (100%)	42 (98%)	1 (2%)	44	65
50	c	49/49 (100%)	45 (92%)	4 (8%)	10	35
51	d	35/35 (100%)	35 (100%)	0	100	100
52	e	53/53 (100%)	52 (98%)	1 (2%)	50	68
53	f	35/35 (100%)	35 (100%)	0	100	100
54	g	64/70 (91%)	62 (97%)	2 (3%)	35	61
55	y	64/64 (100%)	58 (91%)	6 (9%)	8	31
56	3	18/18 (100%)	18 (100%)	0	100	100
All	All	5135/5146 (100%)	5103 (99%)	32 (1%)	76	80

5 of 32 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
55	y	33	GLN
55	y	45	ARG
19	8	212	LEU
19	8	39	TYR
55	y	53	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
50	c	46	HIS
54	g	58	HIS
55	y	21	HIS
25	C	38	HIS
21	Y	58	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	h	1510/1511 (99%)	391 (25%)	0
23	A	3118/3119 (99%)	771 (24%)	32 (1%)
24	B	117/118 (99%)	23 (19%)	1 (0%)
All	All	4745/4748 (99%)	1185 (24%)	33 (0%)

5 of 1185 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	h	9	U
1	h	10	G
1	h	11	G
1	h	12	A
1	h	13	G

5 of 33 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
23	A	2350	G
23	A	2384	C
24	B	10	G
23	A	1002	C
23	A	974	G

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

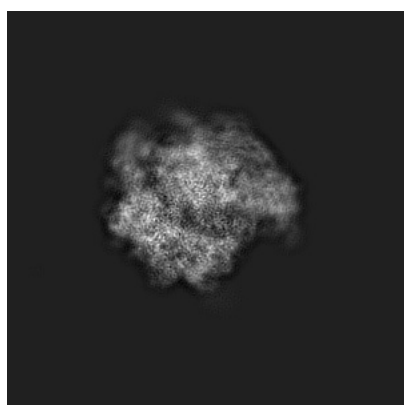
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8932. These allow visual inspection of the internal detail of the map and identification of artifacts.

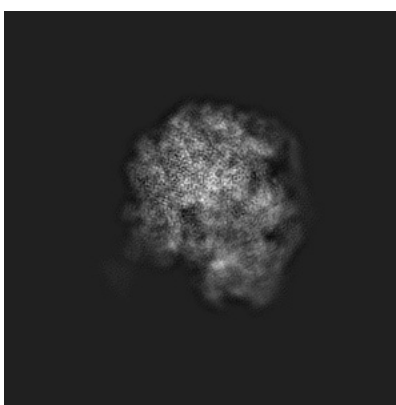
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

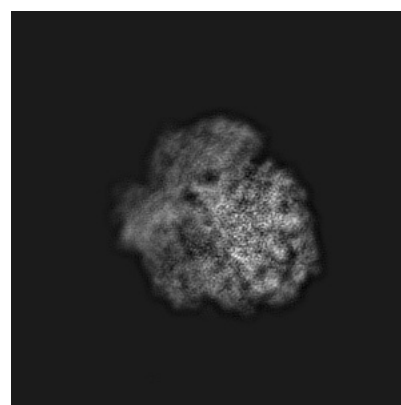
6.1.1 Primary map



X



Y

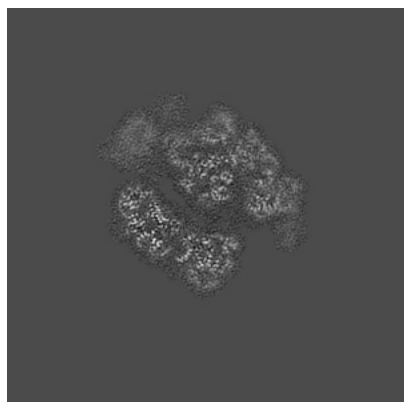


Z

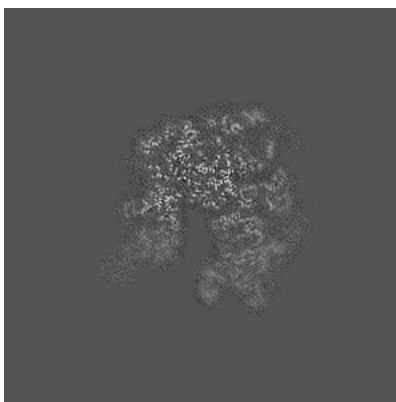
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

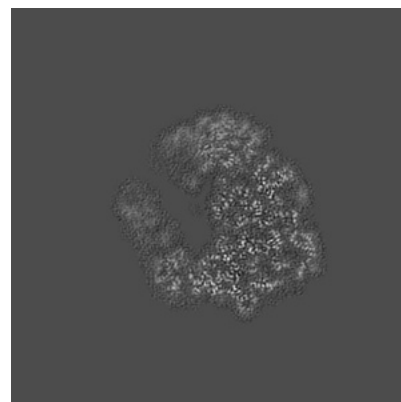
6.2.1 Primary map



X Index: 227



Y Index: 227

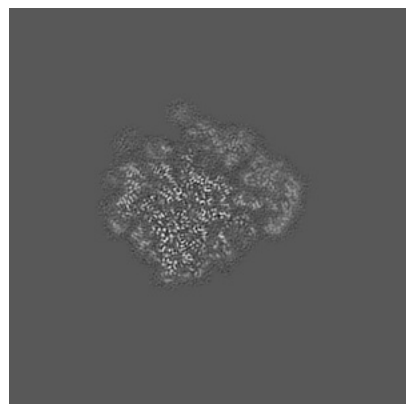


Z Index: 227

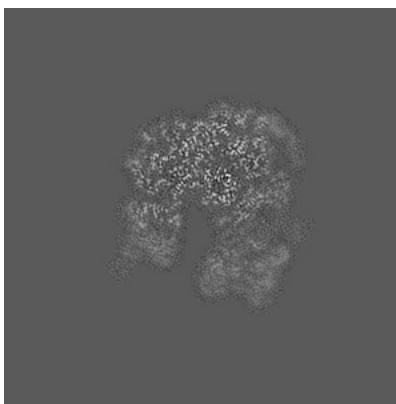
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

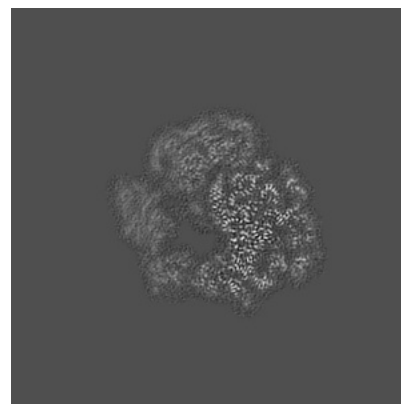
6.3.1 Primary map



X Index: 255



Y Index: 216

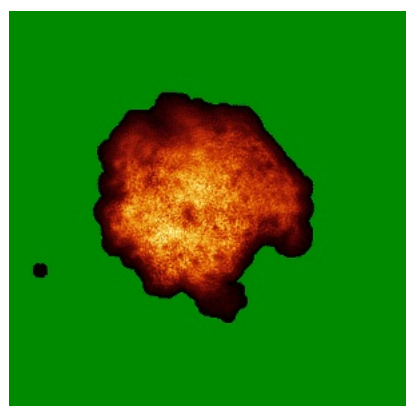


Z Index: 238

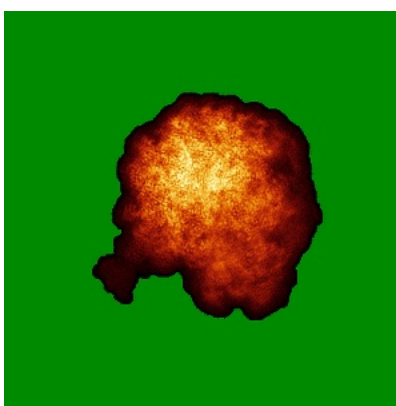
The images above show the largest variance slices of the map in three orthogonal directions.

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

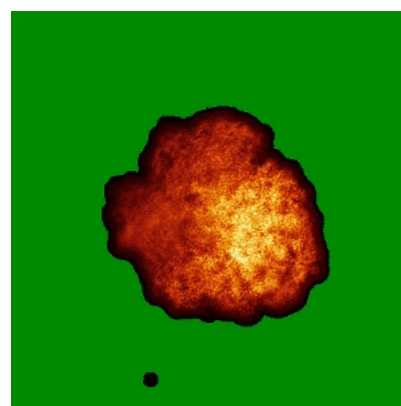
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views

This section was not generated.

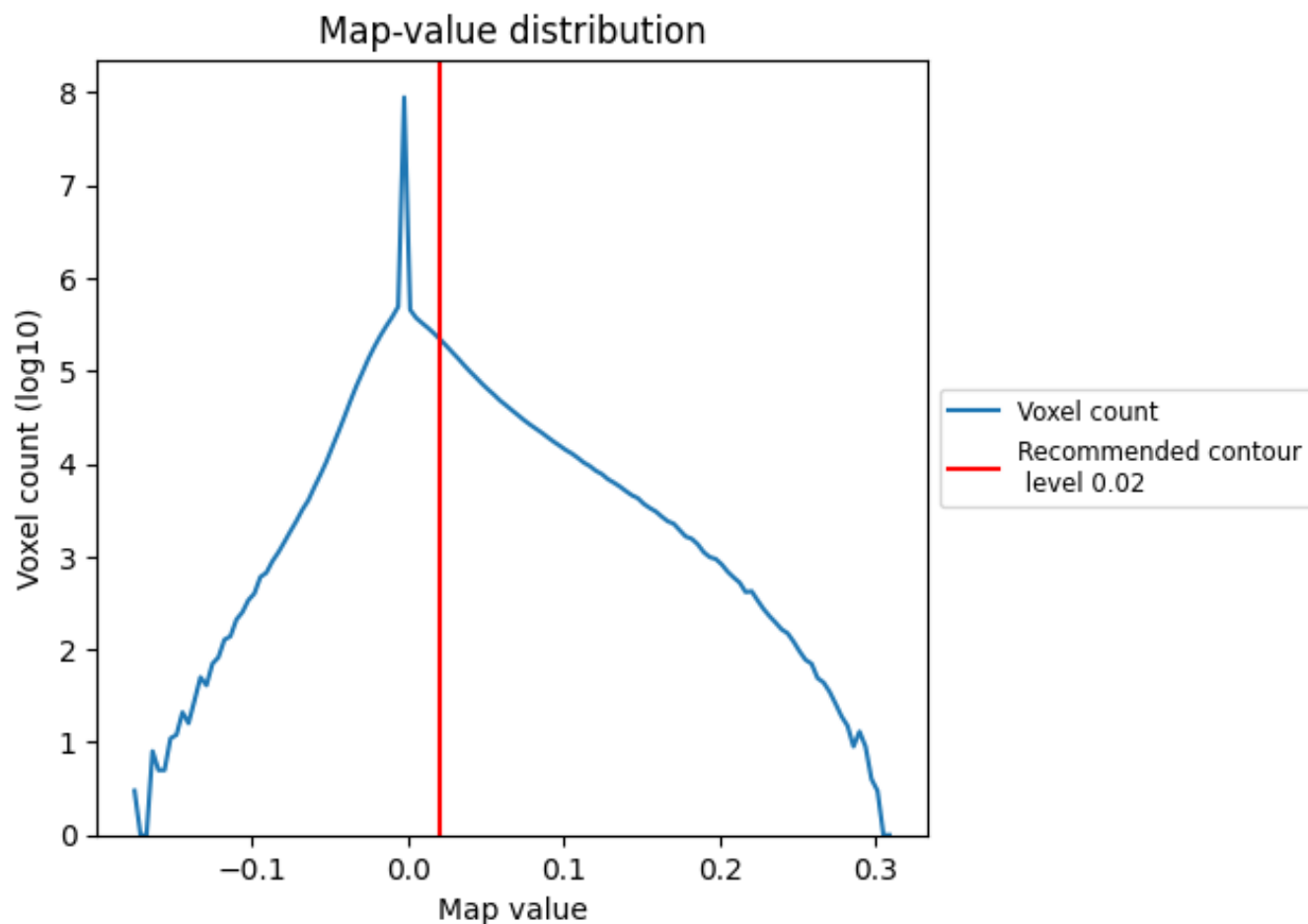
6.6 Mask visualisation

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

7 Map analysis [i](#)

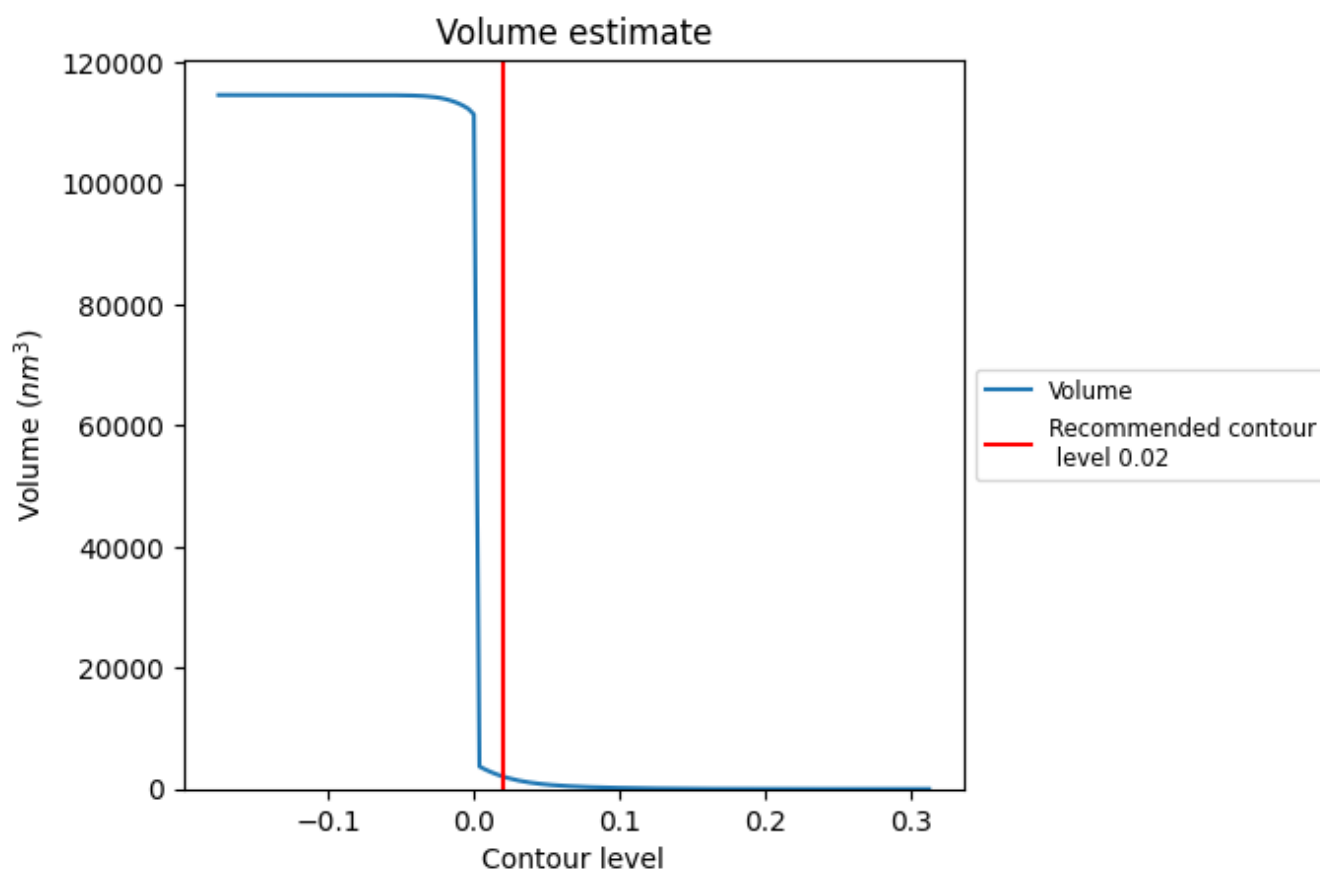
This section contains the results of statistical analysis of the map.

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.

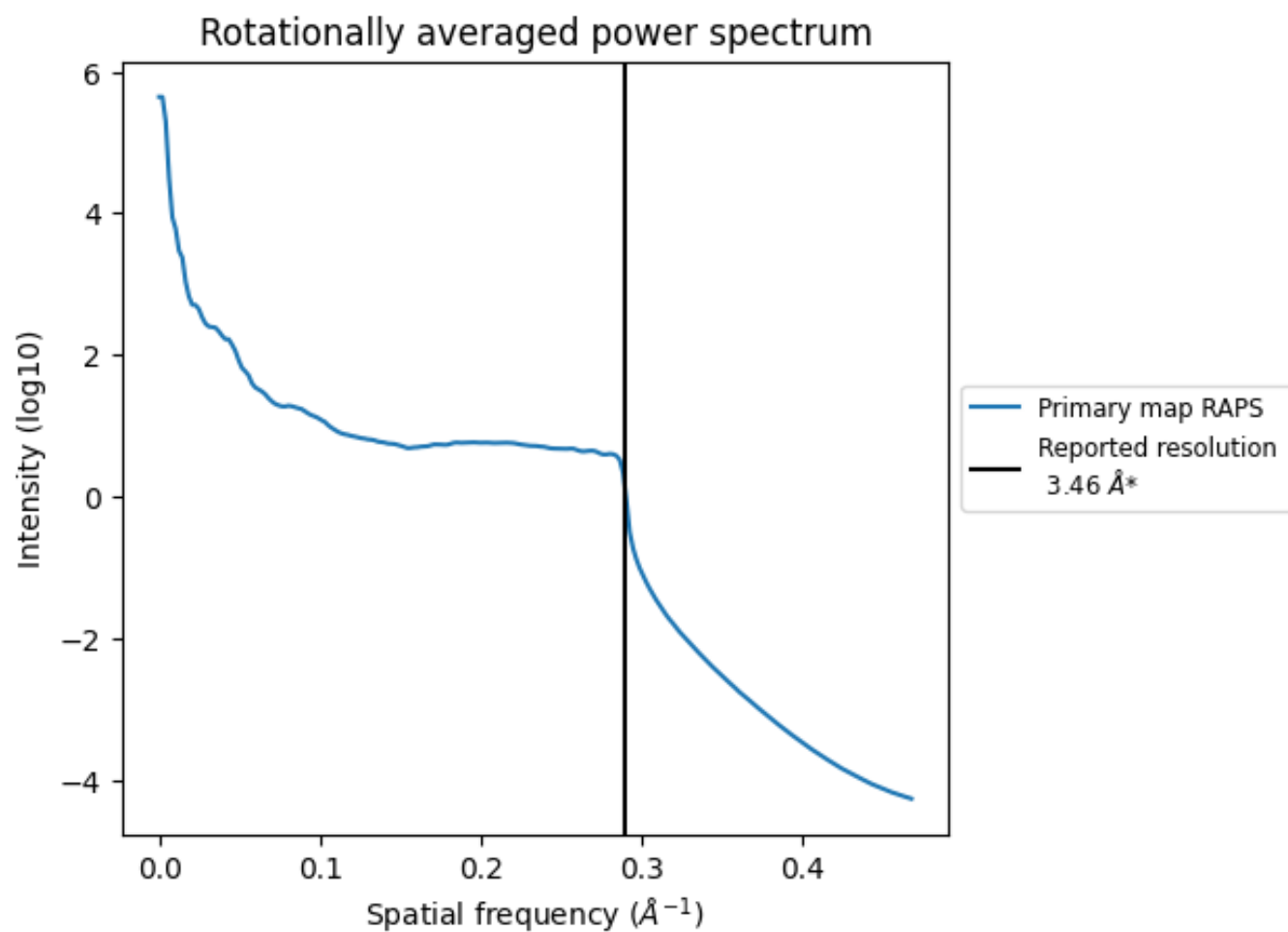
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2059 nm³; this corresponds to an approximate mass of 1860 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 ⓘ

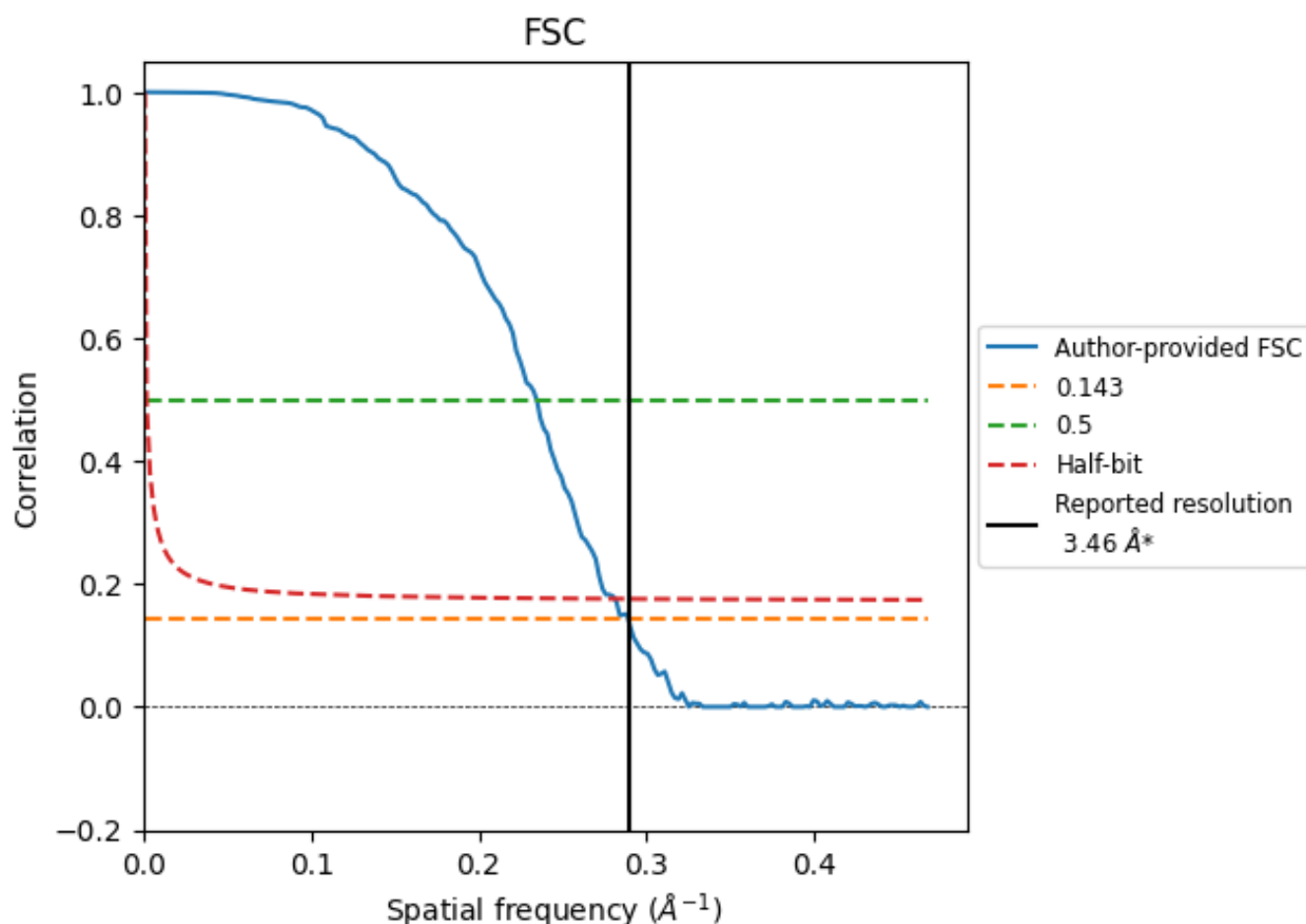


*Reported resolution corresponds to spatial frequency of 0.289 Å⁻¹

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 0.289 Å⁻¹

8.2 Resolution estimates [i](#)

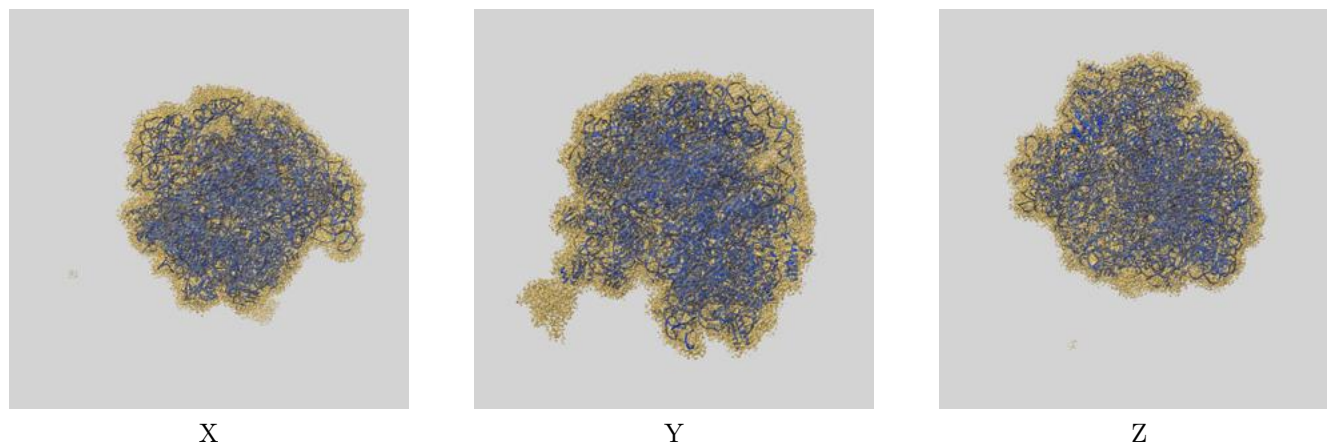
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.46	-	-
Author-provided FSC curve	3.46	4.27	3.56
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

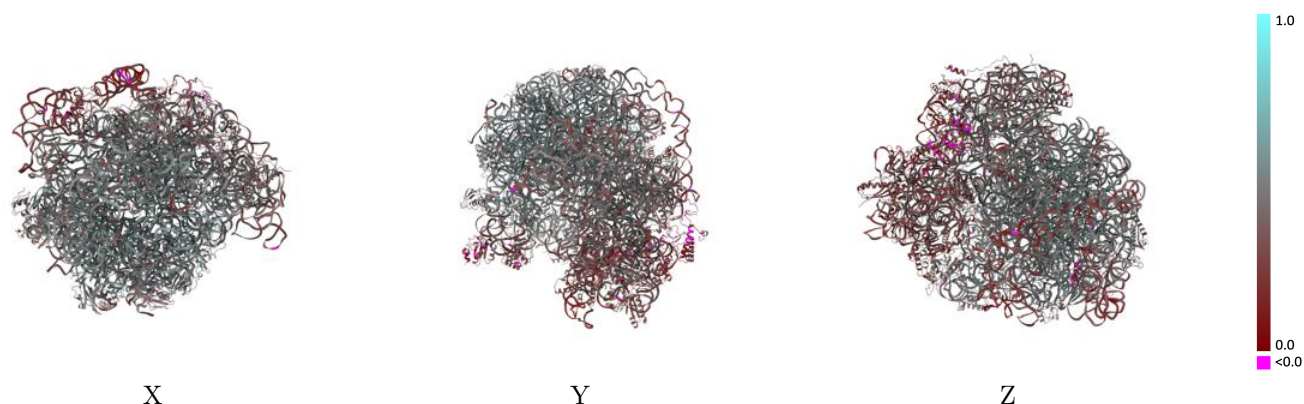
This section contains information regarding the fit between EMDB map EMD-8932 and PDB model 6DZI. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

9.1 Map-model overlay [i](#)



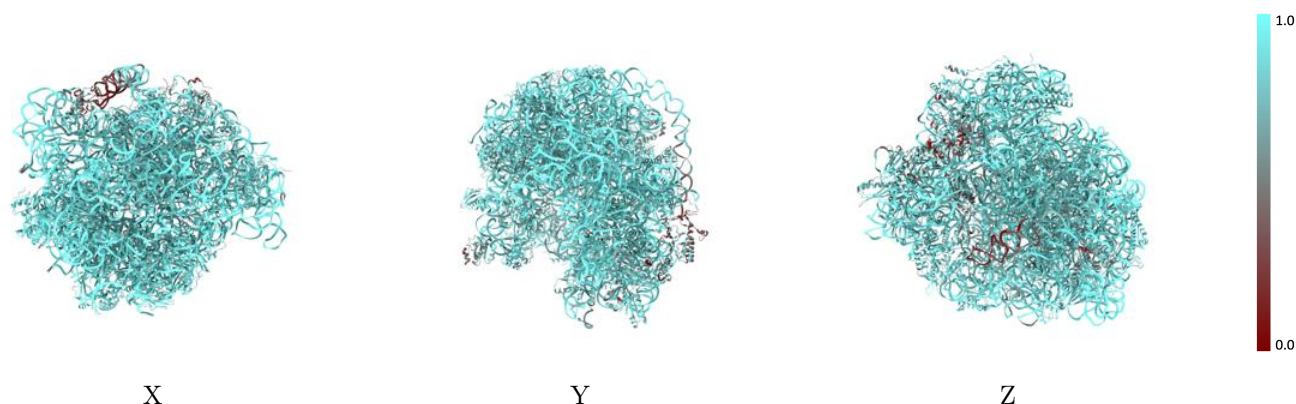
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



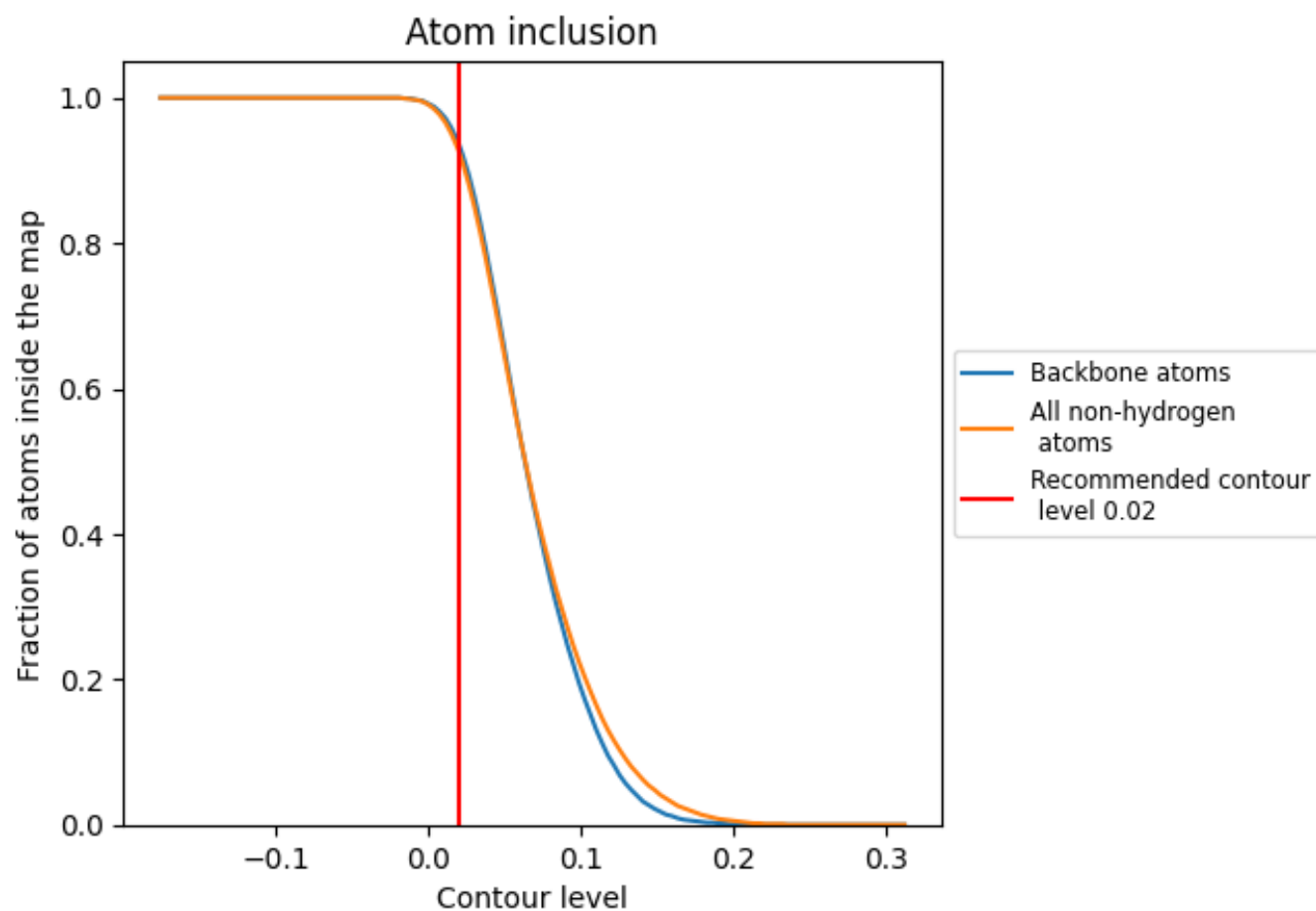
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 93% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9280	 0.4380
3	 0.9110	 0.5190
4	 0.8930	 0.3240
5	 0.8730	 0.4370
6	 0.7960	 0.3270
7	 0.8870	 0.3630
8	 0.5220	 0.1690
9	 0.8690	 0.3250
A	 0.9620	 0.4760
B	 0.9830	 0.4620
C	 0.8920	 0.5100
D	 0.9330	 0.5100
E	 0.9210	 0.4830
F	 0.9160	 0.4010
G	 0.9260	 0.4290
H	 0.5670	 0.2940
I	 0.6280	 0.2350
J	 0.7940	 0.2780
K	 0.9380	 0.5090
L	 0.8930	 0.5020
M	 0.9290	 0.4940
N	 0.9110	 0.5050
O	 0.9250	 0.5030
P	 0.9470	 0.4560
Q	 0.8920	 0.4730
R	 0.9120	 0.5060
S	 0.9500	 0.5090
T	 0.9110	 0.4950
U	 0.9110	 0.4620
V	 0.9030	 0.4270
W	 0.8950	 0.4510
X	 0.9330	 0.5160
Y	 0.5180	 0.2720
Z	 0.9330	 0.4440
a	 0.9350	 0.4990



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Chain	Atom inclusion	Q-score
b	 0.9350	 0.4940
c	 0.7620	 0.3500
d	 0.9000	 0.5200
e	 0.9150	 0.5140
f	 0.9370	 0.5230
g	 0.8480	 0.2800
h	 0.9640	 0.4050
j	 0.7820	 0.4360
k	 0.8210	 0.3330
l	 0.8410	 0.3100
m	 0.8560	 0.3790
n	 0.8550	 0.3930
p	 0.8080	 0.3130
q	 0.9250	 0.4160
r	 0.7210	 0.3310
s	 0.8310	 0.3250
t	 0.8560	 0.4150
u	 0.8750	 0.4180
v	 0.8500	 0.3210
x	 0.8850	 0.4130
y	 0.8740	 0.4340
z	 0.8540	 0.3830