



wwPDB EM Validation Summary Report ⓘ

Mar 23, 2026 – 11:25 AM UTC

PDB ID : 8CD1 / pdb_00008cd1
EMDB ID : EMD-16566
Title : 70S-PHIKZ014
Authors : Gerovac, M.; Vogel, J.
Deposited on : 2023-01-29
Resolution : 3.00 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:

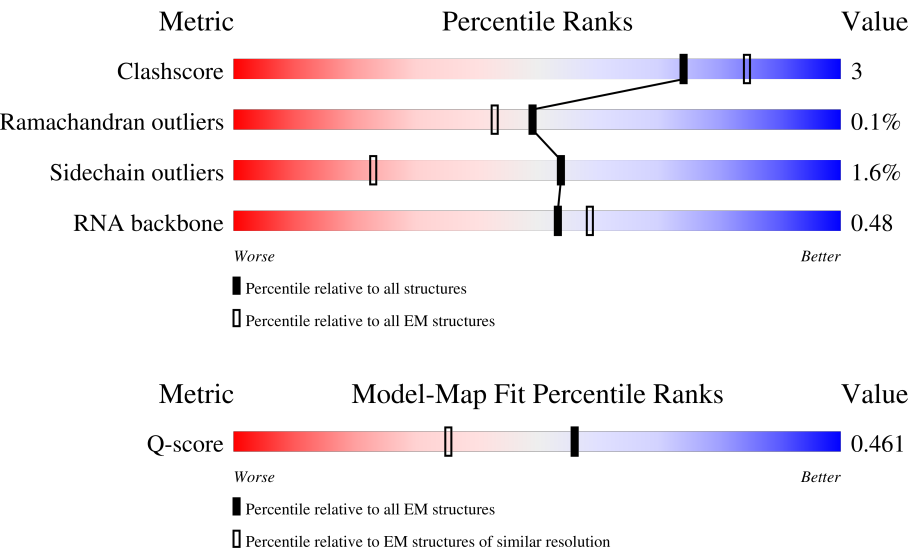
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.00 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	14081 (2.50 - 3.50)

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

Mol	Chain	Length	Quality of chain
1	2	60	
2	4	44	
3	5	64	

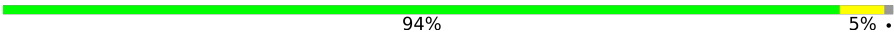











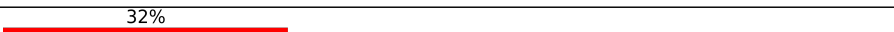

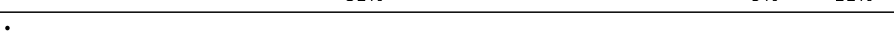

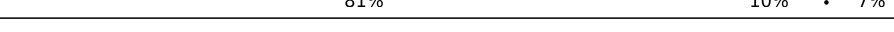

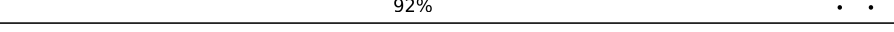






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Mol	Chain	Length	Quality of chain
4	6	38	
5	A	2888	
6	B	120	
7	C	273	
8	D	211	
9	Dt	76	
10	E	200	
11	F	179	
12	G	177	
13	H	148	
14	J	142	
15	K	122	
16	L	144	
17	Le	71	
18	M	137	
19	N	129	
20	O	116	
21	P	116	
22	Q	118	
23	R	103	
24	S	110	
25	T	99	
26	U	104	
27	V	204	
28	W	85	

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Mol	Chain	Length	Quality of chain
29	X	78	
30	Y	63	
31	Z	58	
32	a	1526	
33	b	246	
34	c	228	
35	d	206	
36	e	166	
37	f	139	
38	g	156	
39	h	130	
40	i	130	
41	j	103	
42	k	129	
43	l	123	
44	m	118	
45	n	101	
46	o	89	
47	p	83	
48	q	88	
49	r	76	
50	s	91	
51	t	91	
52	u	71	
53	v	370	

2 Entry composition

There are 54 unique types of molecules in this entry. The entry contains 144789 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	53	Total	C	N	O	S	0	0
			423	254	90	78	1		

- Molecule 2 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	4	44	Total	C	N	O	S	1	0
			376	228	91	55	2		

- Molecule 3 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	5	63	Total	C	N	O	S	0	0
			506	314	108	81	3		

- Molecule 4 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	6	38	Total	C	N	O	S	0	0
			303	184	69	46	4		

- Molecule 5 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A	2883	Total	C	N	O	P	0	0
			61859	27600	11347	20030	2882		

- Molecule 6 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B	120	Total	C	N	O	P	0	0
			2555	1141	455	839	120		

- Molecule 7 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C	271	Total	C	N	O	S	0	0
			2048	1258	422	362	6		

- Molecule 8 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D	207	Total	C	N	O	S	0	0
			1549	960	297	287	5		

- Molecule 9 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Dt	76	Total	C	N	O	P	0	0
			1623	723	290	534	76		

- Molecule 10 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	199	Total	C	N	O	S	0	0
			1509	948	281	278	2		

- Molecule 11 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F	174	Total	C	N	O	S	0	0
			1288	811	228	246	3		

- Molecule 12 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	173	Total	C	N	O	S	0	0
			1294	815	238	239	2		

- Molecule 13 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	H	78	Total	C	N	O	0	0
			577	363	104	110		

- Molecule 14 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	J	141	Total	C	N	O	S	0	0
			1122	713	205	201	3		

- Molecule 15 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	K	120	Total	C	N	O	S	0	0
			922	576	178	162	6		

- Molecule 16 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L	143	Total	C	N	O	S	0	0
			1055	648	213	192	2		

- Molecule 17 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Le	68	Total	C	N	O	S	0	0
			531	334	95	96	6		

- Molecule 18 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	135	Total	C	N	O	S	0	0
			1069	679	209	178	3		

- Molecule 19 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	118	Total	C	N	O	S	0	0
			945	590	190	160	5		

- Molecule 20 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	O	115	Total	C	N	O	S	0	0
			881	544	174	161	2		

- Molecule 21 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	P	113	Total	C	N	O	S	0	0
			891	563	168	159	1		

- Molecule 22 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Q	117	Total	C	N	O	S	0	0
			936	592	196	148			

- Molecule 23 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	R	102	Total	C	N	O	S	0	0
			801	509	154	136	2		

- Molecule 24 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	S	109	Total	C	N	O	S	0	0
			825	510	160	152	3		

- Molecule 25 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	T	92	Total	C	N	O	S	0	0
			701	449	124	128			

- Molecule 26 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	U	103	Total	C	N	O	S	0	0
			800	503	152	143	2		

- Molecule 27 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	V	188	Total	C	N	O	S	0	0
			1396	887	254	253	2		

- Molecule 28 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	W	76	Total	C	N	O	0	0
			575	364	111	100		

- Molecule 29 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	X	77	Total	C	N	O	S	0
			626	389	134	101	2	0

- Molecule 30 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	Y	59	Total	C	N	O	S	0
			473	291	94	87	1	0

- Molecule 31 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	Z	57	Total	C	N	O	S	0
			445	277	87	79	2	0

- Molecule 32 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	a	1526	Total	C	N	O	P	0
			32744	14606	6011	10602	1525	0

- Molecule 33 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	b	234	Total	C	N	O	S	0
			1821	1145	329	337	10	0

- Molecule 34 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	c	205	Total	C	N	O	S	0
			1627	1028	307	287	5	0

- Molecule 35 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	d	205	Total	C	N	O	S	0	0
			1603	991	311	296	5		

- Molecule 36 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	e	156	Total	C	N	O	S	0	0
			1145	720	209	210	6		

- Molecule 37 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	f	105	Total	C	N	O	S	0	0
			853	531	158	159	5		

- Molecule 38 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	g	154	Total	C	N	O	S	0	0
			1190	747	227	211	5		

- Molecule 39 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	h	129	Total	C	N	O	S	0	0
			982	618	173	185	6		

- Molecule 40 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	i	127	Total	C	N	O	S	0	0
			1010	625	203	181	1		

- Molecule 41 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	j	96	Total	C	N	O	S	0	0
			765	479	143	142	1		

- Molecule 42 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	k	115	Total	C	N	O	S	0	0
			838	517	163	156	2		

- Molecule 43 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	l	121	Total	C	N	O	S	0	0
			949	582	196	167	4		

- Molecule 44 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	m	110	Total	C	N	O	S	0	0
			859	524	174	157	4		

- Molecule 45 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	n	98	Total	C	N	O	S	0	0
			777	479	163	132	3		

- Molecule 46 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	o	86	Total	C	N	O	S	0	0
			686	425	134	126	1		

- Molecule 47 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	p	78	Total	C	N	O	0	0
			610	381	121	108		

- Molecule 48 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	q	76	Total	C	N	O	S	0	0
			619	387	120	110	2		

- Molecule 49 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	r	71	Total	C	N	O	S	0	0
			566	361	107	97	1		

- Molecule 50 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	s	80	Total	C	N	O	S	0	0
			635	405	121	106	3		

- Molecule 51 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	t	85	Total	C	N	O	S	0	0
			654	404	135	113	2		

- Molecule 52 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	u	62	Total	C	N	O	S	0	0
			519	320	112	86	1		

- Molecule 53 is a protein called PHIKZ014.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	v	271	Total	C	N	O	S	0	0
			2262	1436	410	409	7		

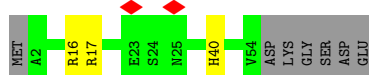
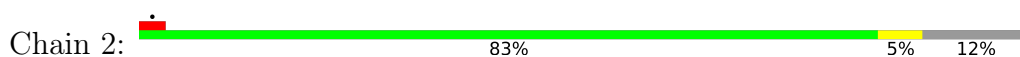
- Molecule 54 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
54	A	150	Total	Mg	0
			150	150	
54	C	1	Total	Mg	0
			1	1	
54	D	1	Total	Mg	0
			1	1	
54	P	1	Total	Mg	0
			1	1	
54	U	1	Total	Mg	0
			1	1	
54	a	17	Total	Mg	0
			17	17	

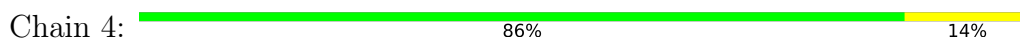
3 Residue-property plots [i](#)

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.

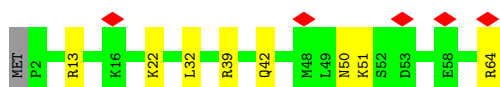
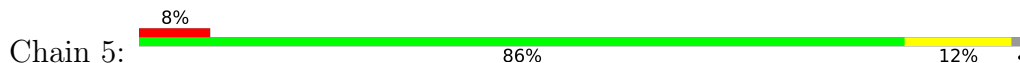
- Molecule 1: 50S ribosomal protein L32



- Molecule 2: 50S ribosomal protein L34



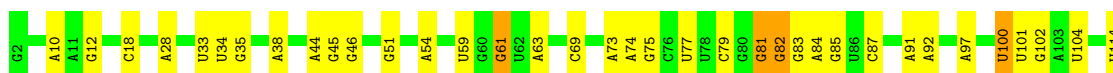
- Molecule 3: 50S ribosomal protein L35



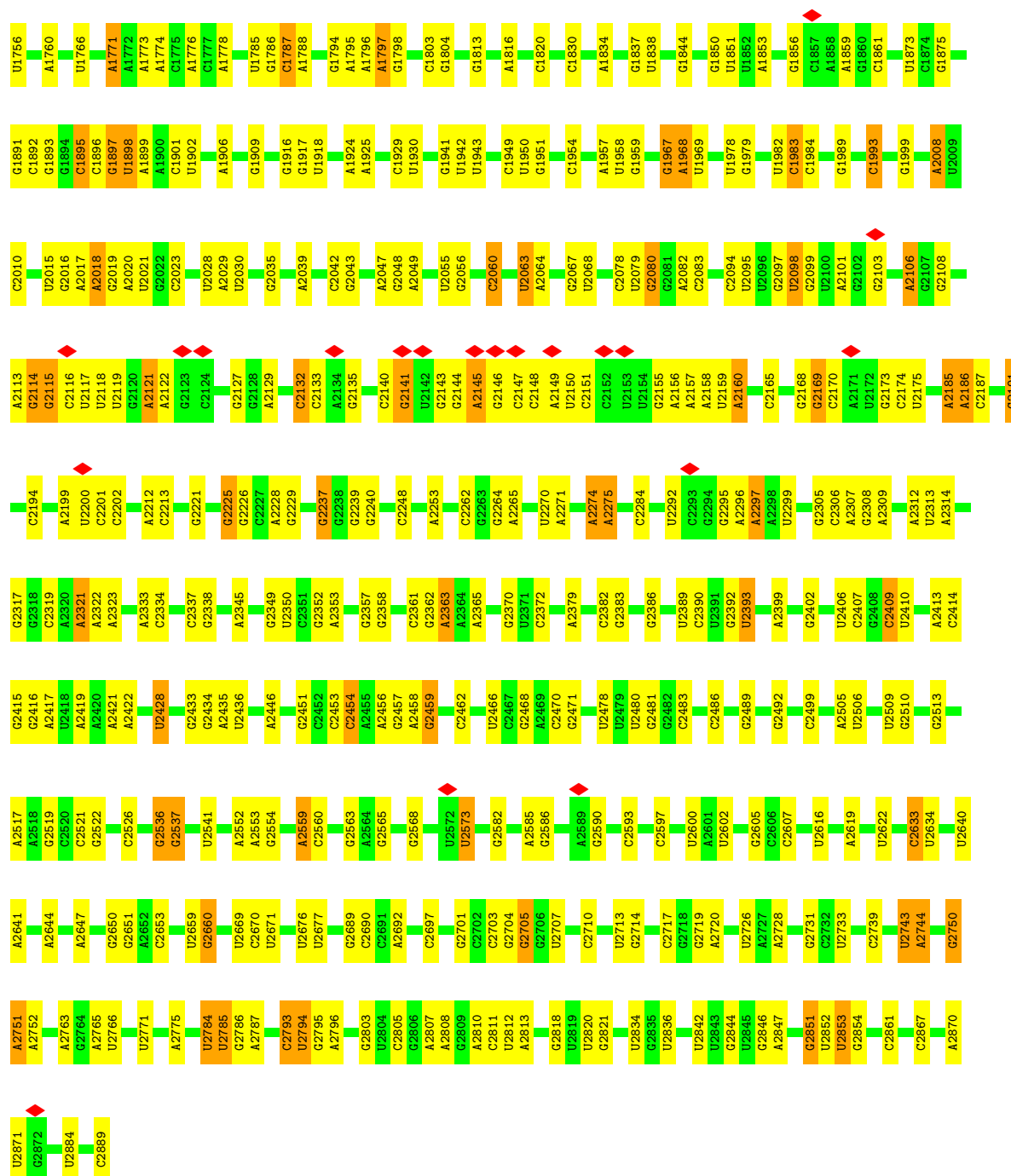
- Molecule 4: 50S ribosomal protein L36



- Molecule 5: 23S rRNA

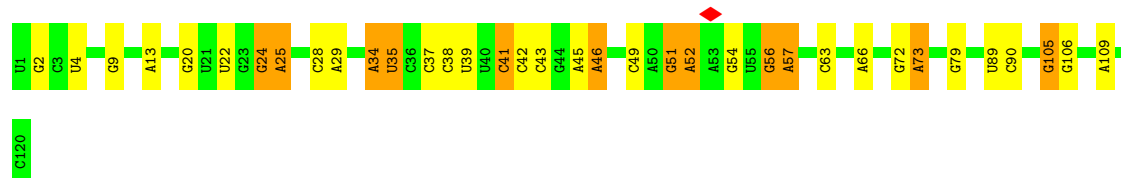


U1637	U1638	G1639	G1653	A1654	G1657	G1663	G1664	G1671	G1672	C1673	U1683	C1684	G1685	G1686	G1689	A1690	C1698	A1704	G1705	U1708	G1709	A1710	A1711	A1714	U1715	U1716	U1717	U1720	C1721	U1724	U1731	G1732	U1735	A1741	A1742	U1745	U1746	C1747	G1748	A1749	G1750	G1751								
U1522	U	U	A1526	G1527	A1528	A1534	A1535	G1536	U1537	U1540	U1541	G1542	A1556	A1557	G1558	A1559	A1560	U1573	U1574	C1575	A1576	G1577	A1580	C1589	C1597	A1598	A1599	C1600	C1601	G1602	G1603	A1604	C1605	A1606	C1607	A1608	G1609	U1614	C1615	G1616	U1626	A1627	C1628	C1629	G1634	A1635	C1636			
A1380	U1381	A1382	C1385	C1386	A1390	U1402	A1403	C1404	G1408	A1414	C1415	G1422	G1423	C1424	U1434	U1440	U1441	G1442	U1445	G1446	U1447	C1448	C1449	U1453	U1454	G1469	C1474	U1480	A1481	U1484	C1494	A1495	A1496	G1497	G1508	A1509	U1510	G1511	A1512	C1513	G1514	A1515	G1516							
G1251	A1252	G1253	A1256	G1257	G1258	A1259	C1260	A1261	A1262	U1263	G1270	A1273	C1276	A1281	C1282	G1283	A1287	A1288	C1301	C1310	C1311	U1316	G1321	G1325	U1339	G1348	C1349	U1350	G1351	A1352	A1353	A1354	A1355	C1363	G1364	A1365	U1366	G1367	A1370	C1373	U1378	A1379								
C1125	G1128	C1132	A1133	A1142	C1143	C1144	G1145	A1146	A1147	G1148	C1149	G1154	U1162	U1163	A1164	U1167	G1168	A1169	C1170	G1171	A1191	A1192	G1193	U1198	G1199	A1214	U1218	G1223	A1224	G1225	G1226	U1227	A1228	G1232	A1233	A1234	C1238	G1239	A1240	A1241	U1242	G1243	C1244	A1249	U1250					
U908	C911	C912	C920	C921	G922	A931	A935	C936	A949	A950	C951	G952	U953	C954	A963	A964	A965	G966	A971	C972	A973	A974	C977	A978	G979	A980	G983	A986	A990	A999	U1002	U1003	U1009	A1010	A1011	G1012	U1013	U1016	A1017	U1023	G1024	U1025								
G1031	A1036	G1037	A1047	G1048	G1049	U1050	U1051	G1052	U1055	U1056	A1057	G1058	A1059	A1060	G1061	C1062	A1063	G1064	C1065	C1066	A1067	C1068	A1076	G1077	A1078	A1079	A1080	G1081	G1082	U1084	A1085	A1086	U1087	G1088	G1089	C1090	G1097	G1100	A1101	G1114	G1115	A1116	A1117	G1118	A1119	U1120	G1121	U1122	A1123	A1124
U792	A793	U793	A794	G795	C802	U817	G824	C827	G833	U834	A835	U836	U840	C841	U842	G843	G844	G845	G846	G847	U848	A850	G853	C854	A855	U866	G870	G871	G872	U873	C874	U876	C877	C878	C879	G880	A881	C882	U883	U884	A885	A889	A899	C904						
C535	U536	U537	G538	U539	U540	A541	U544	C547	C550	A553	U557	U558	A562	U563	A564	A565	U566	G567	G568	G575	A576	A586	G589	A593	G594	A599	C600	G601	G602	U603	A604	U610	A611	G618	C619	G620	A621	A622	G626	A627	G628	U629	U635	A636						
U642	U	U	A645	G646	U647	G654	G659	A660	G671	G672	C673	U676	U680	C681	G687	C688	A708	G716	A720	A724	G735	U736	U737	G738	G743	G747	G748	A754	C755	G765	G766	A767	G768	U769	A771	A772	A773	G774	G775	A783	G784									
A413	A414	G415	G416	U428	C431	A434	C435	A438	A444	A445	U446	C447	A448	G456	A457	G458	G459	G460	A461	A462	A463	G464	G465	C466	A470	A471	G472	A481	G485	A496	A499	C500	G503	G509	G514	A519	A520	G521	C522	A523	G524	U525	A534							
U322	G323	A324	U325	A334	C335	G336	C337	G338	U342	U347	U348	U349	G350	A351	A352	G353	U354	G355	A356	A357	A358	U359	A361	C374	A375	C376	G377	A380	A381	U385	U386	G387	U390	G391	A395	U396	G397	G398	G399	A304	A305	U202	G205	A314	U315	A316	G317	U318	G321	
C1115	A1118	A1119	U1120	G1125	A1126	A1127	A1131	G1137	A1138	U1139	A1140	A1141	C1142	C1143	U1144	A1145	G1146	G1147	U1149	U1150	A1160	A1161	C1163	C1164	U1166	C1172	A1173	G1177	A1181	C1184	G1194	A1195	A1196	A1199	U1202	G205	G215	A216	A217	A218	A219	G220								
A221	A222	A227	C228	C229	G230	A233	U234	U240	A241	G242	U243	A244	G245	U246	G247	C248	C249	G252	A255	G259	A265	G266	C267	U271	A272	A273	U281	U285	A288	G289	A293	A294	C299	A303	A304	A305	G306	A314	U315	A316	G317	U318	A219	G220						




• Molecule 6: 5S rRNA

Chain B: 70% 20% 10%



- Molecule 7: 50S ribosomal protein L2

Chain C:  89% 11% .




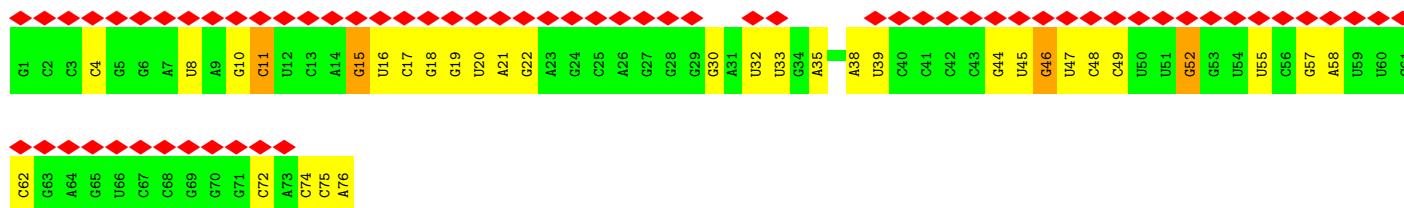
- Molecule 8: 50S ribosomal protein L3

Chain D:  86% 12% .

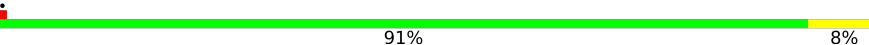


- Molecule 9: tRNA

Chain Dt:  87% 57% 38% 5%




- Molecule 10: 50S ribosomal protein L4

Chain E:  91% 8%



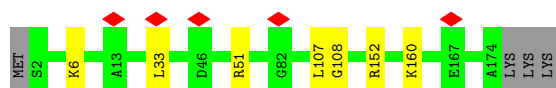
- Molecule 11: 50S ribosomal protein L5

Chain F:  84% 12% . .



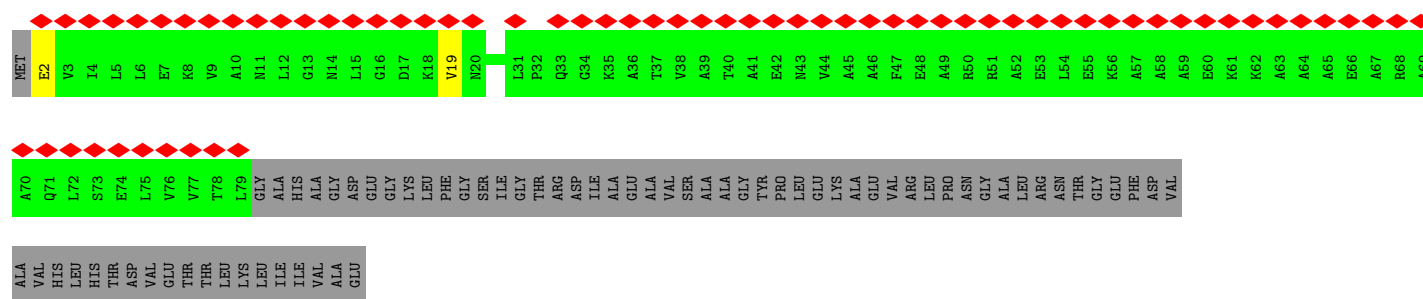
- Molecule 12: 50S ribosomal protein L6

Chain G:  94% . .




- Molecule 13: 50S ribosomal protein L9

Chain H: 




- Molecule 14: 50S ribosomal protein L13

Chain J: 



- Molecule 15: 50S ribosomal protein L14

Chain K: 




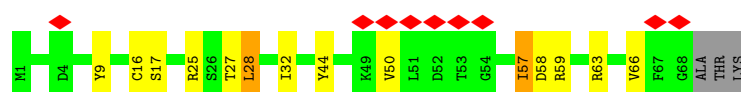
- Molecule 16: 50S ribosomal protein L15

Chain L: 



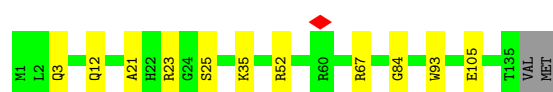
- Molecule 17: 50S ribosomal protein L31

Chain Le: 




- Molecule 18: 50S ribosomal protein L16

Chain M: 



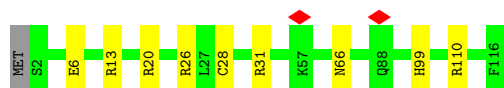
- Molecule 19: 50S ribosomal protein L17

Chain N:  78% 13% 9%




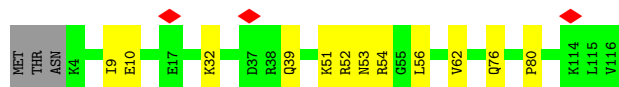
- Molecule 20: 50S ribosomal protein L18

Chain O:  91% 8% .




- Molecule 21: 50S ribosomal protein L19

Chain P:  87% 10% .



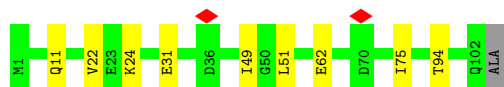
- Molecule 22: 50S ribosomal protein L20

Chain Q:  90% 9% .



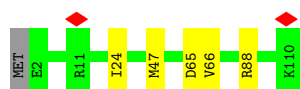
- Molecule 23: 50S ribosomal protein L21

Chain R:  90% 9% .




- Molecule 24: Large ribosomal subunit protein uL22

Chain S:  95% 5% .

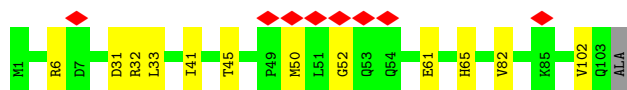
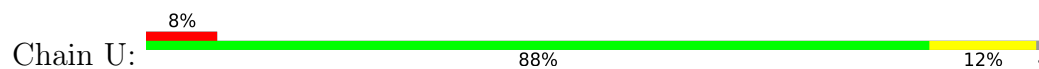


- Molecule 25: 50S ribosomal protein L23

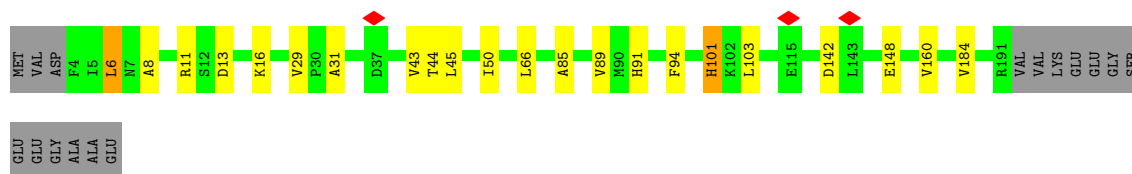
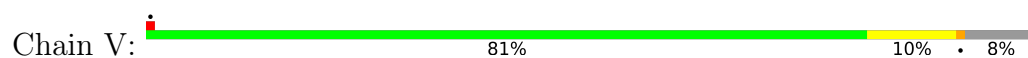
Chain T:  83% 10% 7%



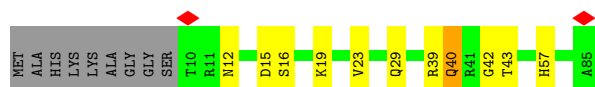
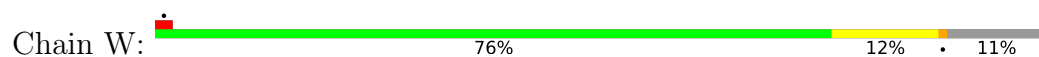
- Molecule 26: 50S ribosomal protein L24



- Molecule 27: 50S ribosomal protein L25



- Molecule 28: 50S ribosomal protein L27



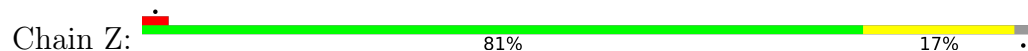
- Molecule 29: 50S ribosomal protein L28



- Molecule 30: 50S ribosomal protein L29

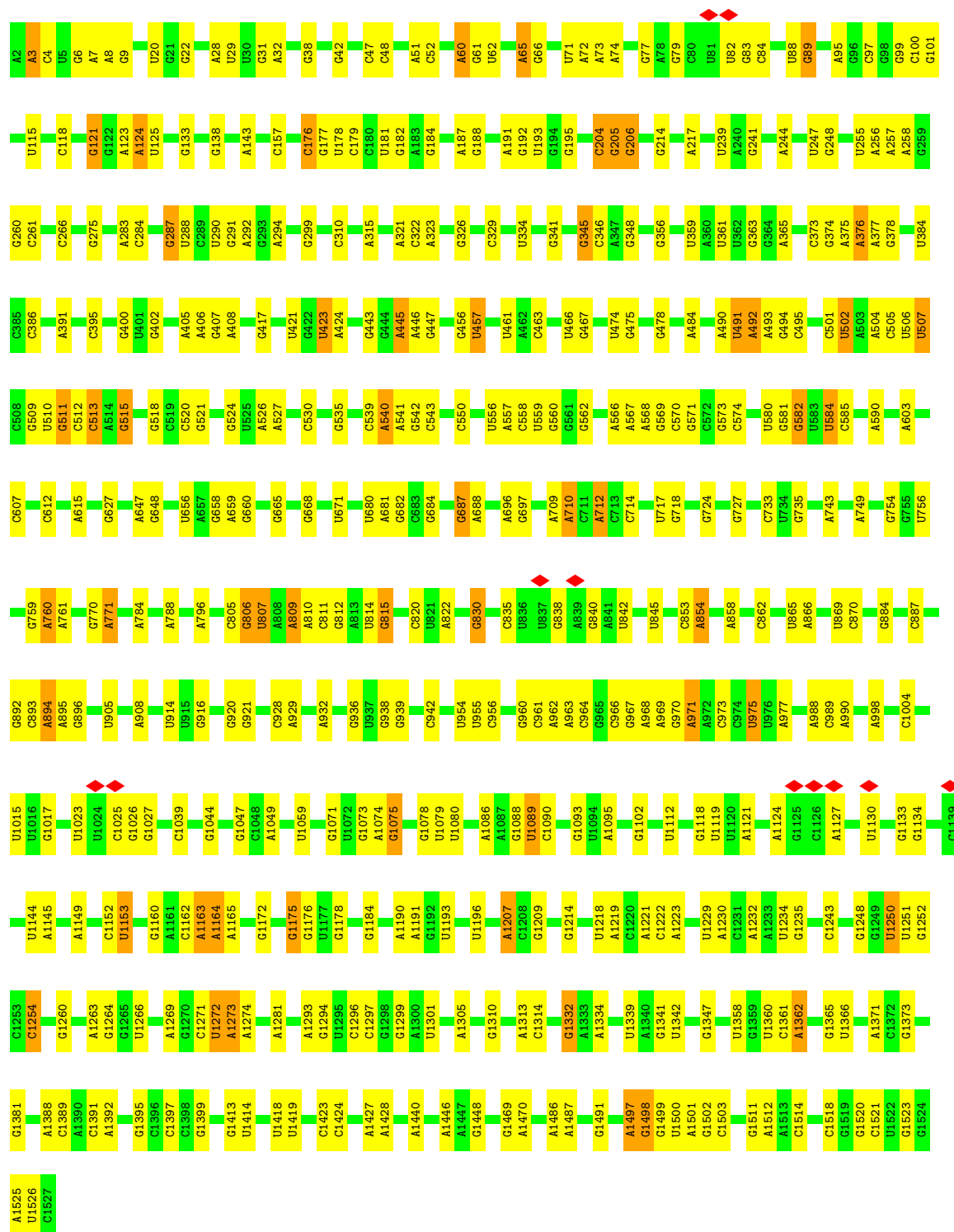


- Molecule 31: 50S ribosomal protein L30

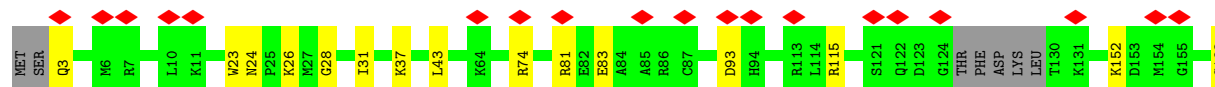
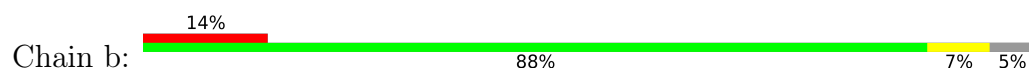


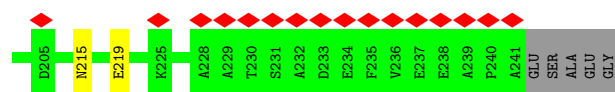
- Molecule 32: 16S rRNA



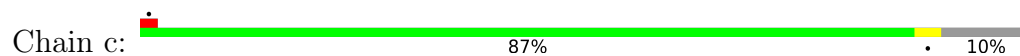


• Molecule 33: 30S ribosomal protein S2

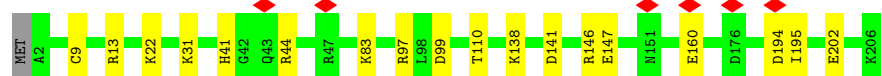




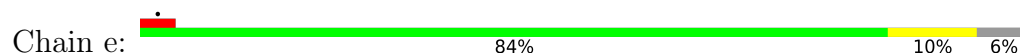
- Molecule 34: 30S ribosomal protein S3



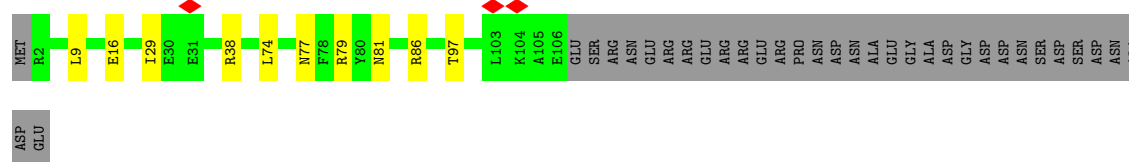
- Molecule 35: 30S ribosomal protein S4



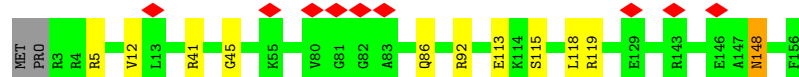
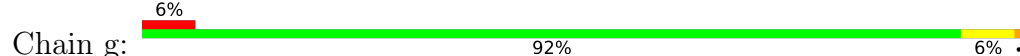
- Molecule 36: 30S ribosomal protein S5



- Molecule 37: 30S ribosomal protein S6



- Molecule 38: 30S ribosomal protein S7

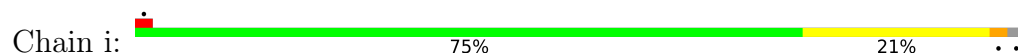


- Molecule 39: 30S ribosomal protein S8

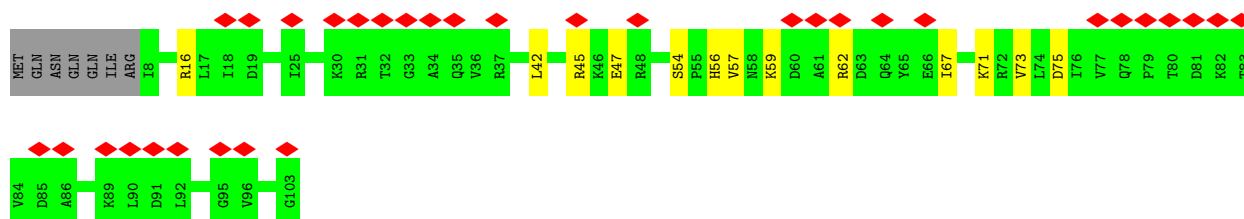
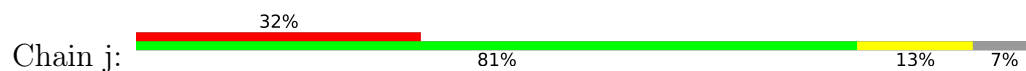




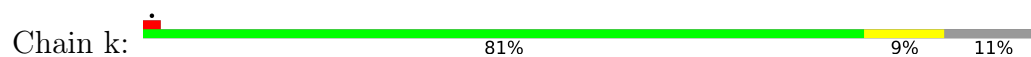
- Molecule 40: 30S ribosomal protein S9



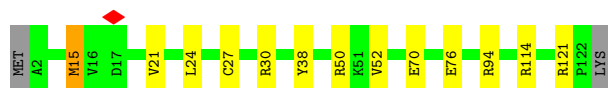
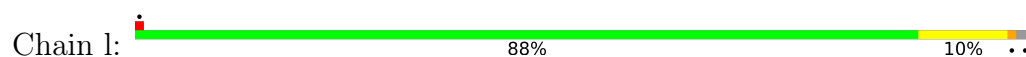
- Molecule 41: 30S ribosomal protein S10



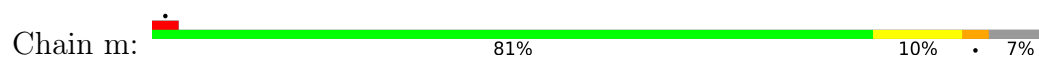
- Molecule 42: 30S ribosomal protein S11



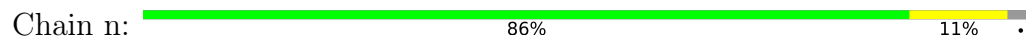
- Molecule 43: 30S ribosomal protein S12



- Molecule 44: 30S ribosomal protein S13



- Molecule 45: 30S ribosomal protein S14





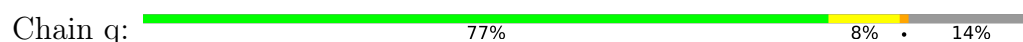
- Molecule 46: 30S ribosomal protein S15



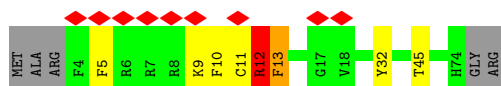
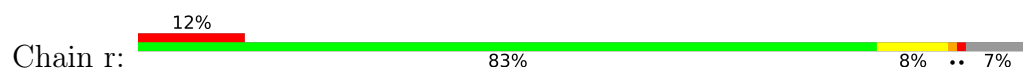
- Molecule 47: 30S ribosomal protein S16



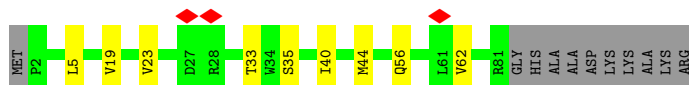
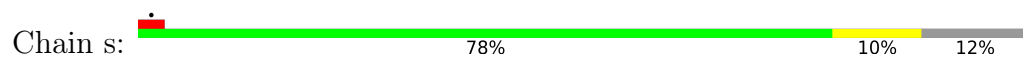
- Molecule 48: 30S ribosomal protein S17



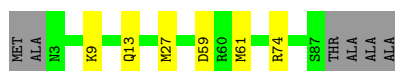
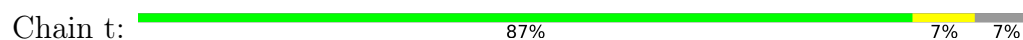
- Molecule 49: 30S ribosomal protein S18



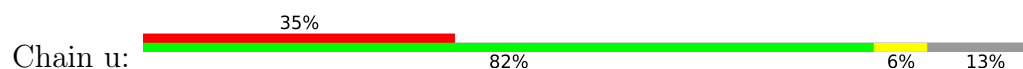
- Molecule 50: 30S ribosomal protein S19

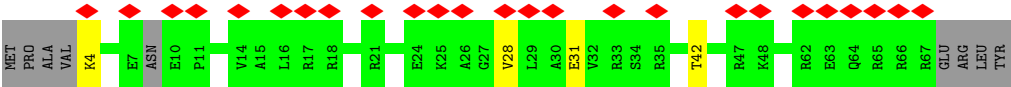


- Molecule 51: 30S ribosomal protein S20

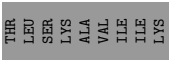
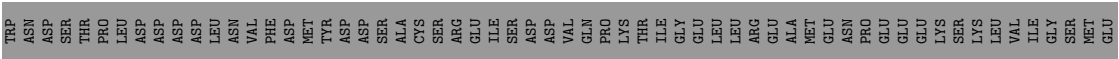
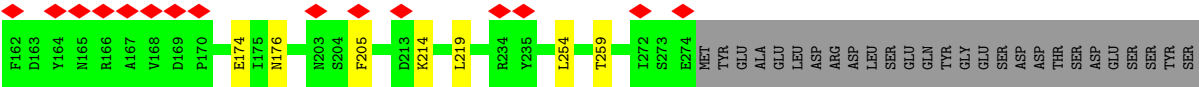
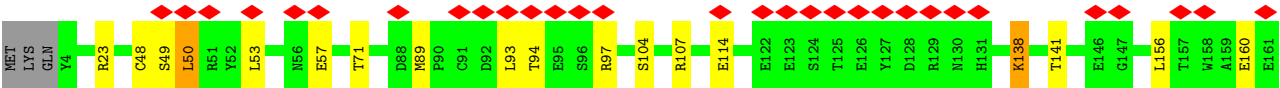


- Molecule 52: 30S ribosomal protein S21





• Molecule 53: PHIKZ014



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	169672	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 ($e^-/\text{\AA}^2$)	88.28	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	26.120	Depositor
Minimum map value	-7.773	Depositor
Average map value	-0.008	Depositor
Map value standard deviation	0.894	Depositor
Recommended contour level	3.46	Depositor
Map size (Å)	544.512, 544.512, 544.512	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0635, 1.0635, 1.0635	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	2	0.15	0/429	0.36	0/572
2	4	0.18	0/379	0.43	0/496
3	5	0.15	0/511	0.40	0/668
4	6	0.18	0/304	0.35	0/399
5	A	0.13	0/69275	0.31	2/108063 (0.0%)
6	B	0.12	0/2855	0.31	0/4447
7	C	0.17	0/2084	0.39	0/2800
8	D	0.17	0/1572	0.42	0/2118
9	Dt	0.17	0/1813	0.47	0/2823
10	E	0.15	0/1529	0.38	0/2060
11	F	0.22	0/1304	0.46	0/1766
12	G	0.17	0/1311	0.39	0/1767
13	H	0.15	0/580	0.39	0/781
14	J	0.18	0/1148	0.38	0/1549
15	K	0.19	0/931	0.40	0/1247
16	L	0.16	0/1067	0.40	0/1422
17	Le	0.23	0/542	0.41	0/728
18	M	0.19	0/1089	0.37	0/1456
19	N	0.17	0/960	0.40	0/1282
20	O	0.15	0/888	0.37	0/1183
21	P	0.17	0/900	0.40	0/1203
22	Q	0.17	0/946	0.44	0/1257
23	R	0.18	0/814	0.40	0/1091
24	S	0.16	0/829	0.39	0/1104
25	T	0.17	0/710	0.40	0/953
26	U	0.21	0/808	0.46	0/1079
27	V	0.16	0/1419	0.41	0/1925
28	W	0.22	0/583	0.56	0/774
29	X	0.17	0/637	0.42	0/849
30	Y	0.43	0/474	0.71	2/632 (0.3%)
31	Z	0.16	0/449	0.36	0/602
32	a	0.12	0/36667	0.29	0/57202

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	b	0.16	0/1849	0.37	0/2486
34	c	0.16	0/1656	0.41	0/2232
35	d	0.14	0/1622	0.38	0/2171
36	e	0.19	0/1159	0.43	0/1559
37	f	0.15	0/867	0.32	0/1167
38	g	0.15	0/1207	0.39	0/1616
39	h	0.18	0/993	0.39	0/1332
40	i	0.18	0/1022	0.41	0/1365
41	j	0.19	0/775	0.38	0/1046
42	k	0.15	0/854	0.36	0/1159
43	l	0.18	0/963	0.40	0/1292
44	m	0.16	0/867	0.39	0/1165
45	n	0.16	0/787	0.38	0/1048
46	o	0.14	0/693	0.35	0/926
47	p	0.16	0/621	0.34	0/837
48	q	0.17	0/627	0.40	0/844
49	r	0.23	0/575	2.14	3/771 (0.4%)
50	s	0.16	0/649	0.38	0/874
51	t	0.16	0/661	0.43	0/881
52	u	0.15	0/524	0.40	0/689
53	v	0.17	0/2323	0.38	0/3138
All	All	0.14	0/157101	0.35	7/234896 (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
5	A	1	0
8	D	0	1
23	R	0	1
49	r	0	1
All	All	1	3

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	r	12	ARG	O-C-N	-56.99	31.82	123.00
49	r	12	ARG	CA-C-N	-8.67	104.98	121.54
49	r	12	ARG	C-N-CA	-8.67	104.98	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1895	C	C1'-C2'-O2'	6.80	118.59	108.40
5	A	1895	C	C3'-C2'-O2'	6.69	120.73	110.70

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	A	1897	G	C1'

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	D	151	THR	Peptide
23	R	51	LEU	Peptide
49	r	12	ARG	Mainchain

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	2	423	0	420	4	0
2	4	376	0	421	4	0
3	5	506	0	569	6	0
4	6	303	0	341	2	0
5	A	61859	0	31109	266	0
6	B	2555	0	1294	16	0
7	C	2048	0	2097	21	0
8	D	1549	0	1560	19	0
9	Dt	1623	0	821	10	0
10	E	1509	0	1563	13	0
11	F	1288	0	1254	15	0
12	G	1294	0	1344	4	0
13	H	577	0	606	1	0
14	J	1122	0	1148	10	0
15	K	922	0	992	12	0
16	L	1055	0	1096	5	0
17	Le	531	0	532	10	0
18	M	1069	0	1139	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	N	945	0	989	11	0
20	O	881	0	920	10	0
21	P	891	0	950	8	0
22	Q	936	0	1025	11	0
23	R	801	0	830	8	0
24	S	825	0	885	3	0
25	T	701	0	735	5	0
26	U	800	0	864	5	0
27	V	1396	0	1415	14	0
28	W	575	0	598	11	0
29	X	626	0	649	2	0
30	Y	473	0	502	29	0
31	Z	445	0	472	7	0
32	a	32744	0	16477	153	0
33	b	1821	0	1847	10	0
34	c	1627	0	1657	6	0
35	d	1603	0	1624	15	0
36	e	1145	0	1192	12	0
37	f	853	0	828	6	0
38	g	1190	0	1227	5	0
39	h	982	0	1036	10	0
40	i	1010	0	1052	22	0
41	j	765	0	801	9	0
42	k	838	0	830	8	0
43	l	949	0	996	10	0
44	m	859	0	898	9	0
45	n	777	0	818	8	0
46	o	686	0	709	4	0
47	p	610	0	612	3	0
48	q	619	0	659	6	0
49	r	566	0	577	32	0
50	s	635	0	662	6	0
51	t	654	0	699	5	0
52	u	519	0	548	4	0
53	v	2262	0	2213	12	0
54	A	150	0	0	0	0
54	C	1	0	0	0	0
54	D	1	0	0	0	0
54	P	1	0	0	0	0
54	U	1	0	0	0	0
54	a	17	0	0	0	0
All	All	144789	0	97102	723	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 3.

The worst 5 of 723 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)
49:r:9:LYS:O	49:r:12:ARG:CB	1.66	1.40
49:r:5:PHE:CE2	49:r:9:LYS:CE	2.11	1.31
49:r:11:CYS:C	49:r:12:ARG:HA	1.60	1.27
49:r:5:PHE:CE2	49:r:9:LYS:HE3	1.73	1.22
49:r:9:LYS:O	49:r:12:ARG:HB3	1.24	1.13

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	2	51/60 (85%)	49 (96%)	2 (4%)	0	100	100
2	4	43/44 (98%)	42 (98%)	1 (2%)	0	100	100
3	5	61/64 (95%)	54 (88%)	7 (12%)	0	100	100
4	6	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
7	C	269/273 (98%)	255 (95%)	14 (5%)	0	100	100
8	D	205/211 (97%)	184 (90%)	21 (10%)	0	100	100
10	E	197/200 (98%)	190 (96%)	7 (4%)	0	100	100
11	F	172/179 (96%)	155 (90%)	17 (10%)	0	100	100
12	G	171/177 (97%)	164 (96%)	7 (4%)	0	100	100
13	H	76/148 (51%)	76 (100%)	0	0	100	100
14	J	139/142 (98%)	134 (96%)	5 (4%)	0	100	100
15	K	118/122 (97%)	111 (94%)	7 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	L	141/144 (98%)	130 (92%)	11 (8%)	0	100	100
17	Le	66/71 (93%)	59 (89%)	6 (9%)	1 (2%)	8	35
18	M	133/137 (97%)	132 (99%)	1 (1%)	0	100	100
19	N	116/129 (90%)	105 (90%)	11 (10%)	0	100	100
20	O	113/116 (97%)	108 (96%)	5 (4%)	0	100	100
21	P	111/116 (96%)	104 (94%)	7 (6%)	0	100	100
22	Q	115/118 (98%)	109 (95%)	6 (5%)	0	100	100
23	R	100/103 (97%)	93 (93%)	7 (7%)	0	100	100
24	S	107/110 (97%)	107 (100%)	0	0	100	100
25	T	90/99 (91%)	84 (93%)	5 (6%)	1 (1%)	11	43
26	U	101/104 (97%)	94 (93%)	7 (7%)	0	100	100
27	V	186/204 (91%)	173 (93%)	13 (7%)	0	100	100
28	W	74/85 (87%)	57 (77%)	17 (23%)	0	100	100
29	X	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
30	Y	57/63 (90%)	54 (95%)	2 (4%)	1 (2%)	6	31
31	Z	55/58 (95%)	54 (98%)	1 (2%)	0	100	100
33	b	230/246 (94%)	214 (93%)	16 (7%)	0	100	100
34	c	203/228 (89%)	188 (93%)	15 (7%)	0	100	100
35	d	203/206 (98%)	190 (94%)	13 (6%)	0	100	100
36	e	154/166 (93%)	141 (92%)	13 (8%)	0	100	100
37	f	103/139 (74%)	98 (95%)	5 (5%)	0	100	100
38	g	152/156 (97%)	147 (97%)	5 (3%)	0	100	100
39	h	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
40	i	125/130 (96%)	110 (88%)	14 (11%)	1 (1%)	16	50
41	j	94/103 (91%)	88 (94%)	6 (6%)	0	100	100
42	k	113/129 (88%)	110 (97%)	3 (3%)	0	100	100
43	l	119/123 (97%)	111 (93%)	8 (7%)	0	100	100
44	m	108/118 (92%)	103 (95%)	5 (5%)	0	100	100
45	n	96/101 (95%)	91 (95%)	5 (5%)	0	100	100
46	o	84/89 (94%)	83 (99%)	1 (1%)	0	100	100
47	p	76/83 (92%)	73 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	q	74/88 (84%)	72 (97%)	2 (3%)	0	100	100
49	r	67/76 (88%)	65 (97%)	1 (2%)	1 (2%)	8	35
50	s	78/91 (86%)	71 (91%)	7 (9%)	0	100	100
51	t	83/91 (91%)	83 (100%)	0	0	100	100
52	u	58/71 (82%)	56 (97%)	1 (2%)	1 (2%)	7	32
53	v	269/370 (73%)	264 (98%)	5 (2%)	0	100	100
All	All	5794/6327 (92%)	5463 (94%)	325 (6%)	6 (0%)	49	80

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
25	T	71	ARG
30	Y	10	VAL
40	i	28	ILE
49	r	13	PHE
17	Le	66	VAL

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	
1	2	46/52 (88%)	46 (100%)	0	100	100
2	4	38/37 (103%)	37 (97%)	1 (3%)	40	72
3	5	54/55 (98%)	53 (98%)	1 (2%)	50	76
4	6	33/34 (97%)	33 (100%)	0	100	100
7	C	206/213 (97%)	205 (100%)	1 (0%)	81	89
8	D	157/162 (97%)	156 (99%)	1 (1%)	78	88
10	E	155/158 (98%)	155 (100%)	0	100	100
11	F	124/153 (81%)	119 (96%)	5 (4%)	28	62
12	G	133/141 (94%)	132 (99%)	1 (1%)	73	86
13	H	55/107 (51%)	55 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	J	118/119 (99%)	115 (98%)	3 (2%)	42	72
15	K	100/102 (98%)	100 (100%)	0	100	100
16	L	104/106 (98%)	104 (100%)	0	100	100
17	Le	59/61 (97%)	56 (95%)	3 (5%)	21	55
18	M	108/110 (98%)	108 (100%)	0	100	100
19	N	97/104 (93%)	96 (99%)	1 (1%)	68	84
20	O	86/87 (99%)	86 (100%)	0	100	100
21	P	94/98 (96%)	93 (99%)	1 (1%)	65	83
22	Q	87/88 (99%)	86 (99%)	1 (1%)	65	83
23	R	82/86 (95%)	82 (100%)	0	100	100
24	S	86/87 (99%)	86 (100%)	0	100	100
25	T	73/82 (89%)	70 (96%)	3 (4%)	27	61
26	U	88/88 (100%)	84 (96%)	4 (4%)	24	59
27	V	143/164 (87%)	136 (95%)	7 (5%)	22	56
28	W	56/61 (92%)	54 (96%)	2 (4%)	31	65
29	X	65/67 (97%)	64 (98%)	1 (2%)	57	80
30	Y	52/55 (94%)	44 (85%)	8 (15%)	2	13
31	Z	48/49 (98%)	48 (100%)	0	100	100
33	b	191/202 (95%)	190 (100%)	1 (0%)	81	89
34	c	165/187 (88%)	165 (100%)	0	100	100
35	d	166/174 (95%)	165 (99%)	1 (1%)	78	88
36	e	114/124 (92%)	114 (100%)	0	100	100
37	f	88/119 (74%)	87 (99%)	1 (1%)	65	83
38	g	116/122 (95%)	113 (97%)	3 (3%)	40	72
39	h	108/109 (99%)	107 (99%)	1 (1%)	70	85
40	i	104/106 (98%)	99 (95%)	5 (5%)	23	57
41	j	85/92 (92%)	83 (98%)	2 (2%)	43	73
42	k	84/98 (86%)	84 (100%)	0	100	100
43	l	105/107 (98%)	104 (99%)	1 (1%)	68	84
44	m	92/99 (93%)	85 (92%)	7 (8%)	12	41
45	n	78/82 (95%)	78 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	o	73/75 (97%)	73 (100%)	0	100	100
47	p	61/65 (94%)	60 (98%)	1 (2%)	55	79
48	q	70/79 (89%)	69 (99%)	1 (1%)	59	80
49	r	56/64 (88%)	56 (100%)	0	100	100
50	s	69/78 (88%)	69 (100%)	0	100	100
51	t	67/70 (96%)	67 (100%)	0	100	100
52	u	51/60 (85%)	51 (100%)	0	100	100
53	v	242/335 (72%)	232 (96%)	10 (4%)	27	61
All	All	4732/5173 (92%)	4654 (98%)	78 (2%)	54	79

5 of 78 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
41	j	67	ILE
53	v	89	MET
44	m	40	ASN
44	m	108	THR
53	v	214	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 37 such sidechains are listed below:

Mol	Chain	Res	Type
42	k	64	GLN
51	t	20	HIS
44	m	76	ASN
48	q	34	HIS
22	Q	44	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
32	a	1525/1526 (99%)	301 (19%)	0
5	A	2880/2888 (99%)	707 (24%)	49 (1%)
6	B	119/120 (99%)	26 (21%)	2 (1%)
9	Dt	75/76 (98%)	23 (30%)	0
All	All	4599/4610 (99%)	1057 (22%)	51 (1%)

5 of 1057 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	A	10	A
5	A	33	U
5	A	34	U
5	A	35	G
5	A	44	A

5 of 51 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	A	1448	C
5	A	1891	G
6	B	34	A
5	A	1627	A
5	A	1710	A

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](#)

Of 171 ligands modelled in this entry, 171 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
49	r	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	r	11:CYS	C	12:ARG	N	3.53

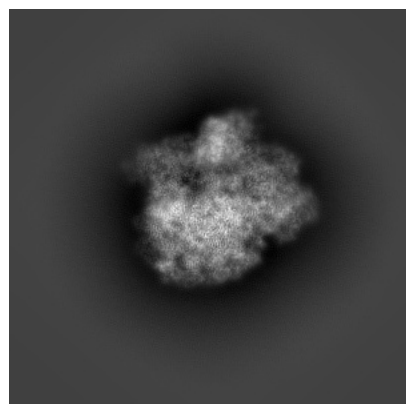
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16566. These allow visual inspection of the internal detail of the map and identification of artifacts.

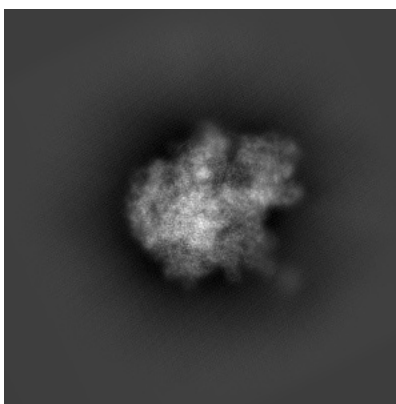
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

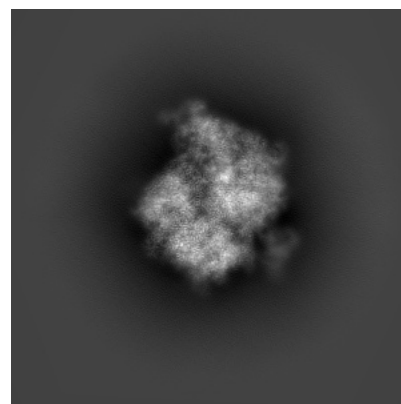
6.1.1 Primary map



X

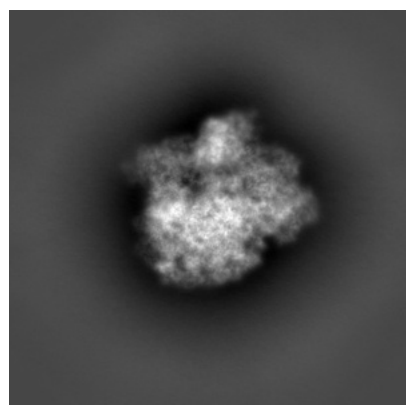


Y

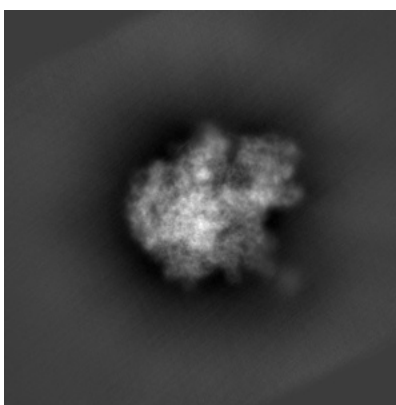


Z

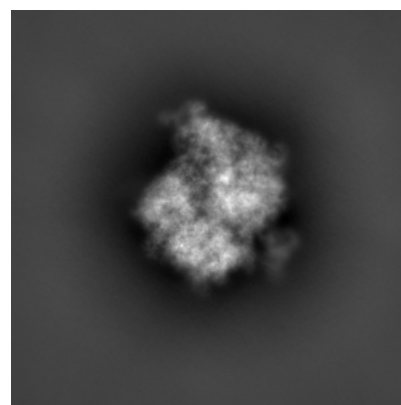
6.1.2 Raw map



X



Y

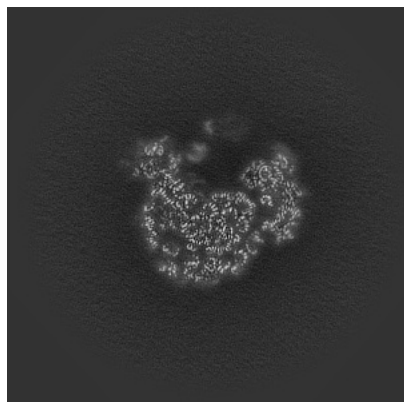


Z

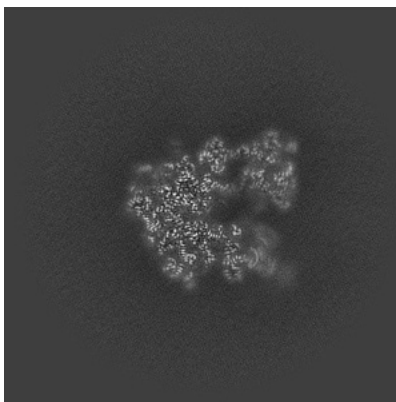
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

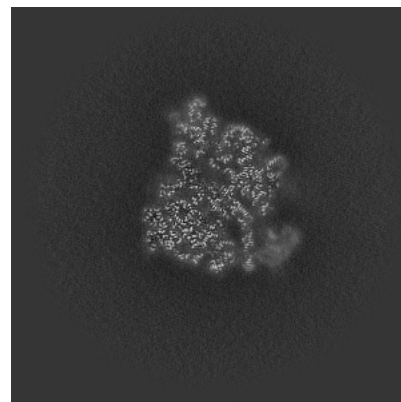
6.2.1 Primary map



X Index: 256

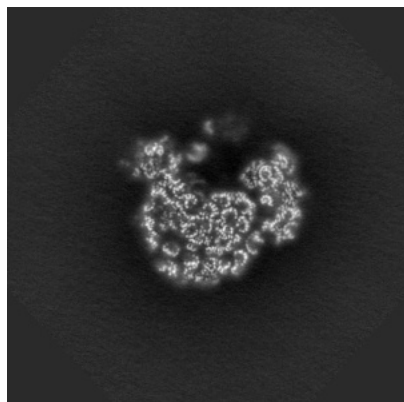


Y Index: 256

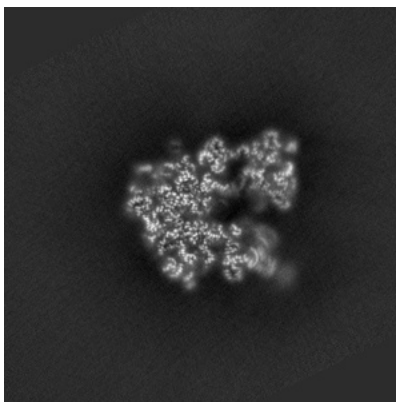


Z Index: 256

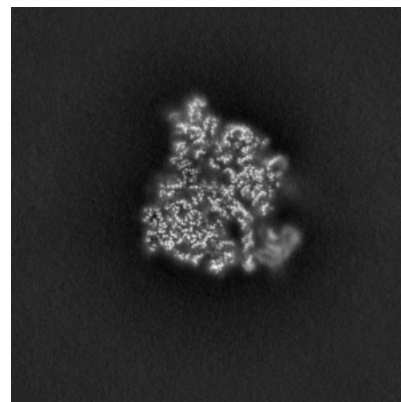
6.2.2 Raw map



X Index: 256



Y Index: 256

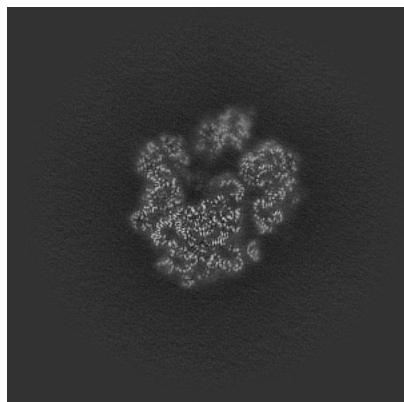


Z Index: 256

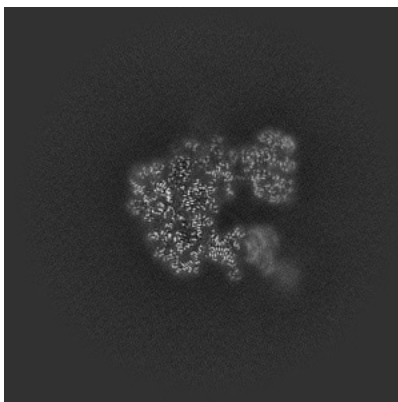
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

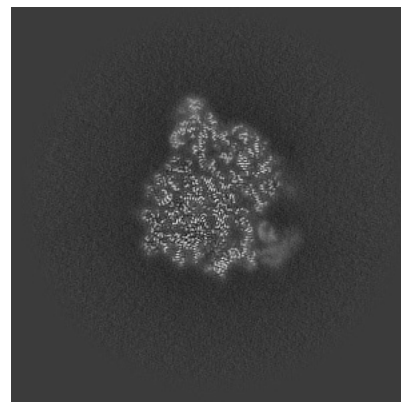
6.3.1 Primary map



X Index: 268

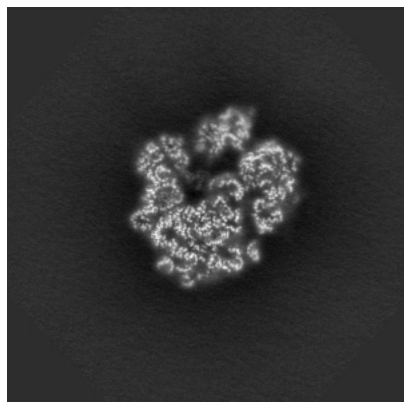


Y Index: 267

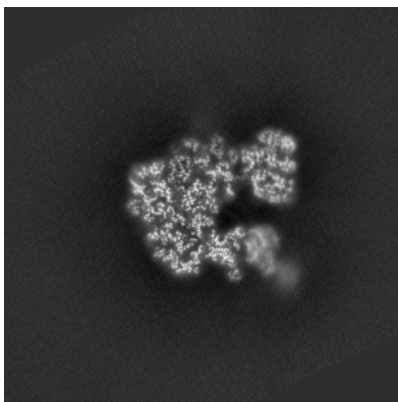


Z Index: 250

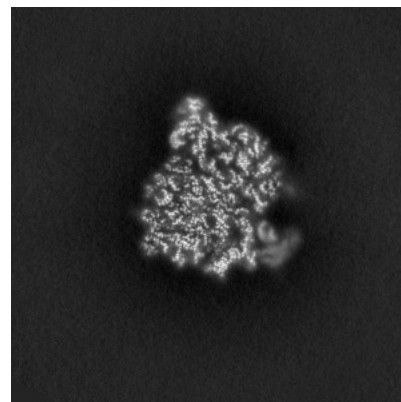
6.3.2 Raw map



X Index: 269



Y Index: 267

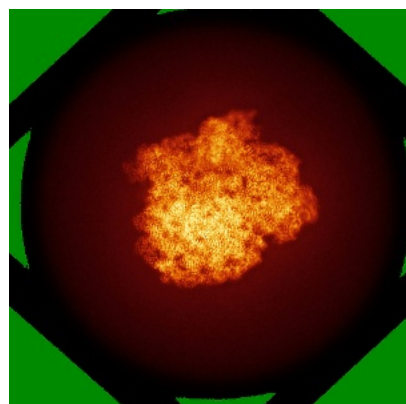


Z Index: 250

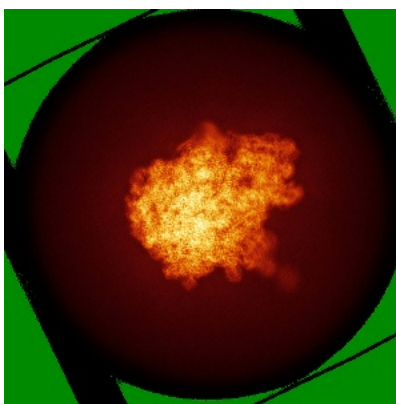
The images above show the largest variance slices of the map in three orthogonal directions.

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

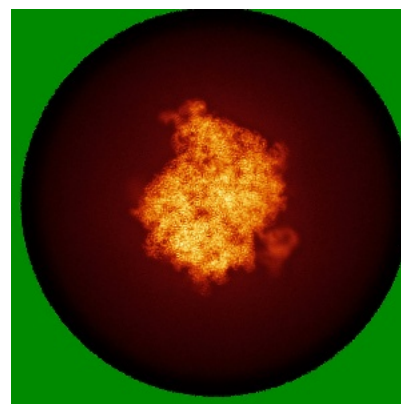
6.4.1 Primary map



X

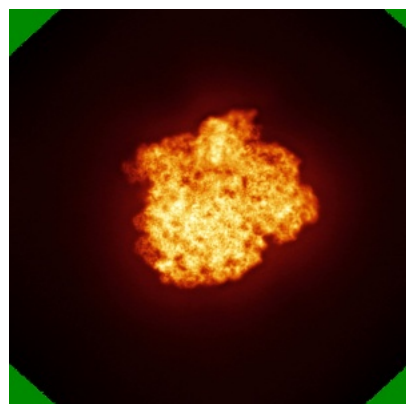


Y

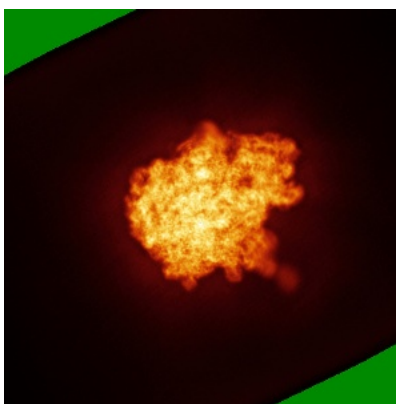


Z

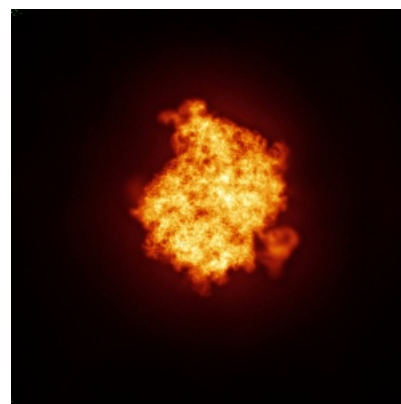
6.4.2 Raw map



X



Y

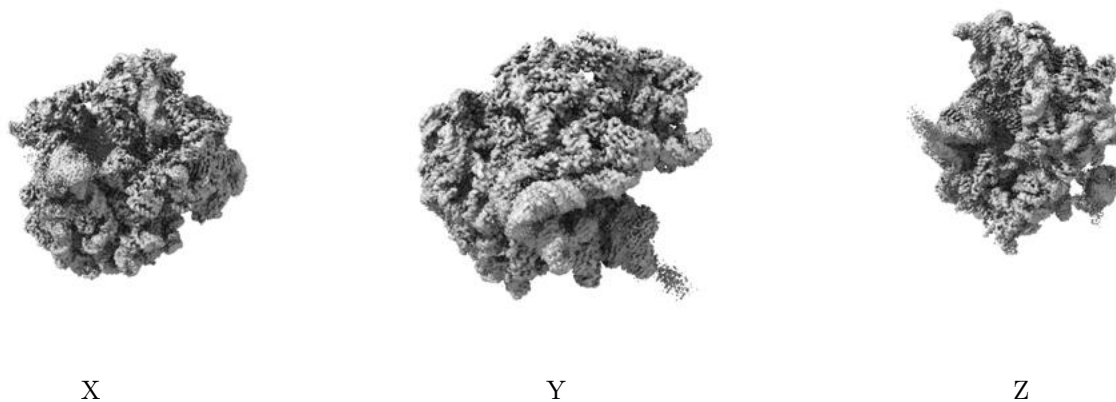


Z

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.

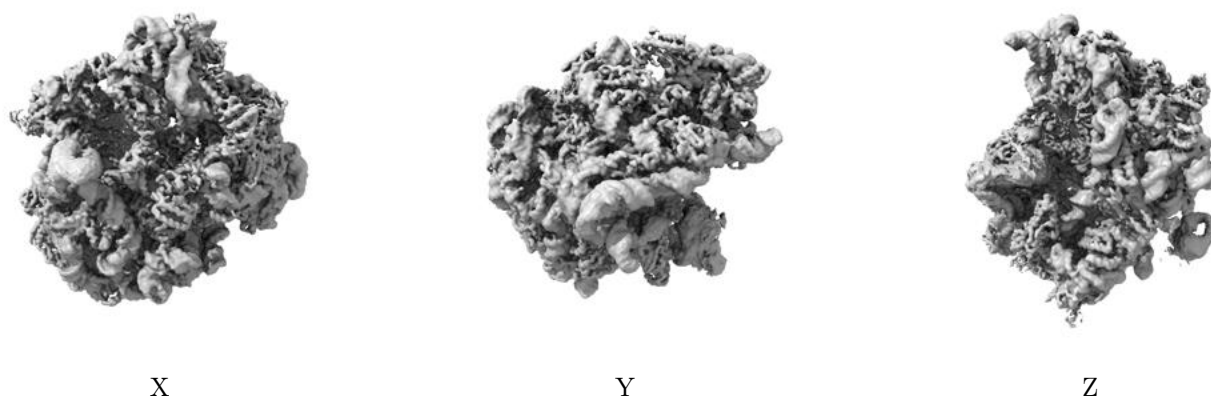
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.46. 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.

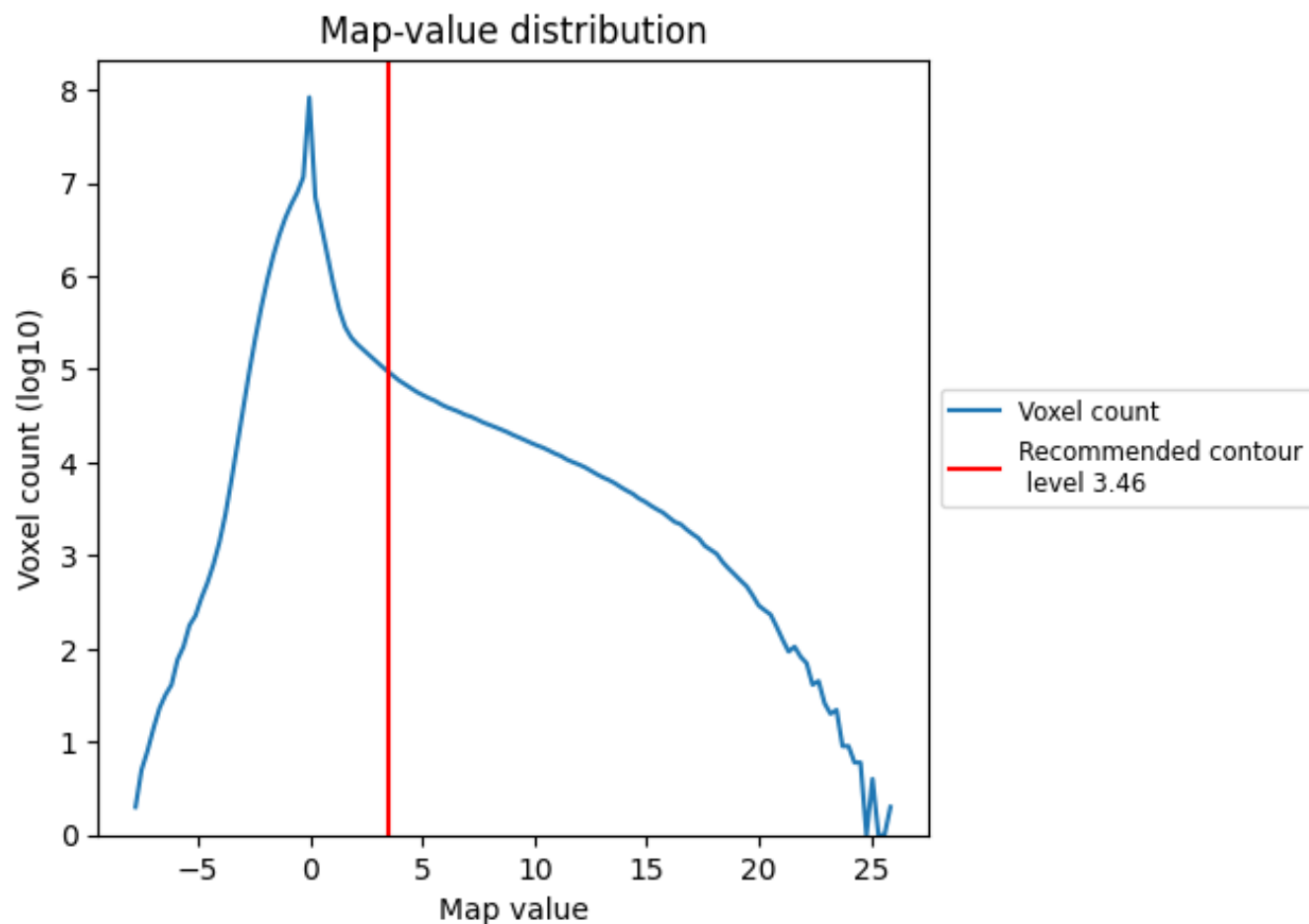
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

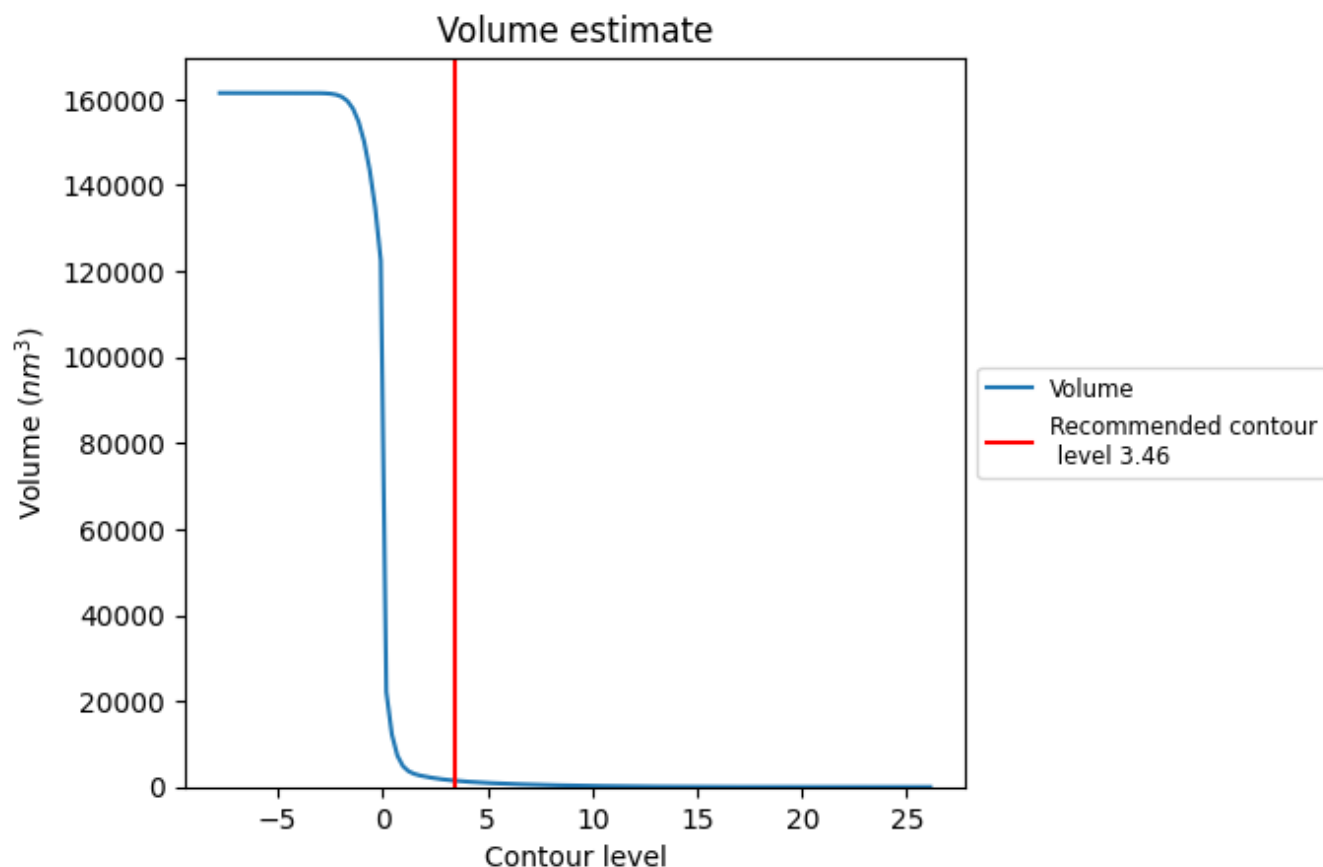
This section contains the results of statistical analysis of the map.

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.

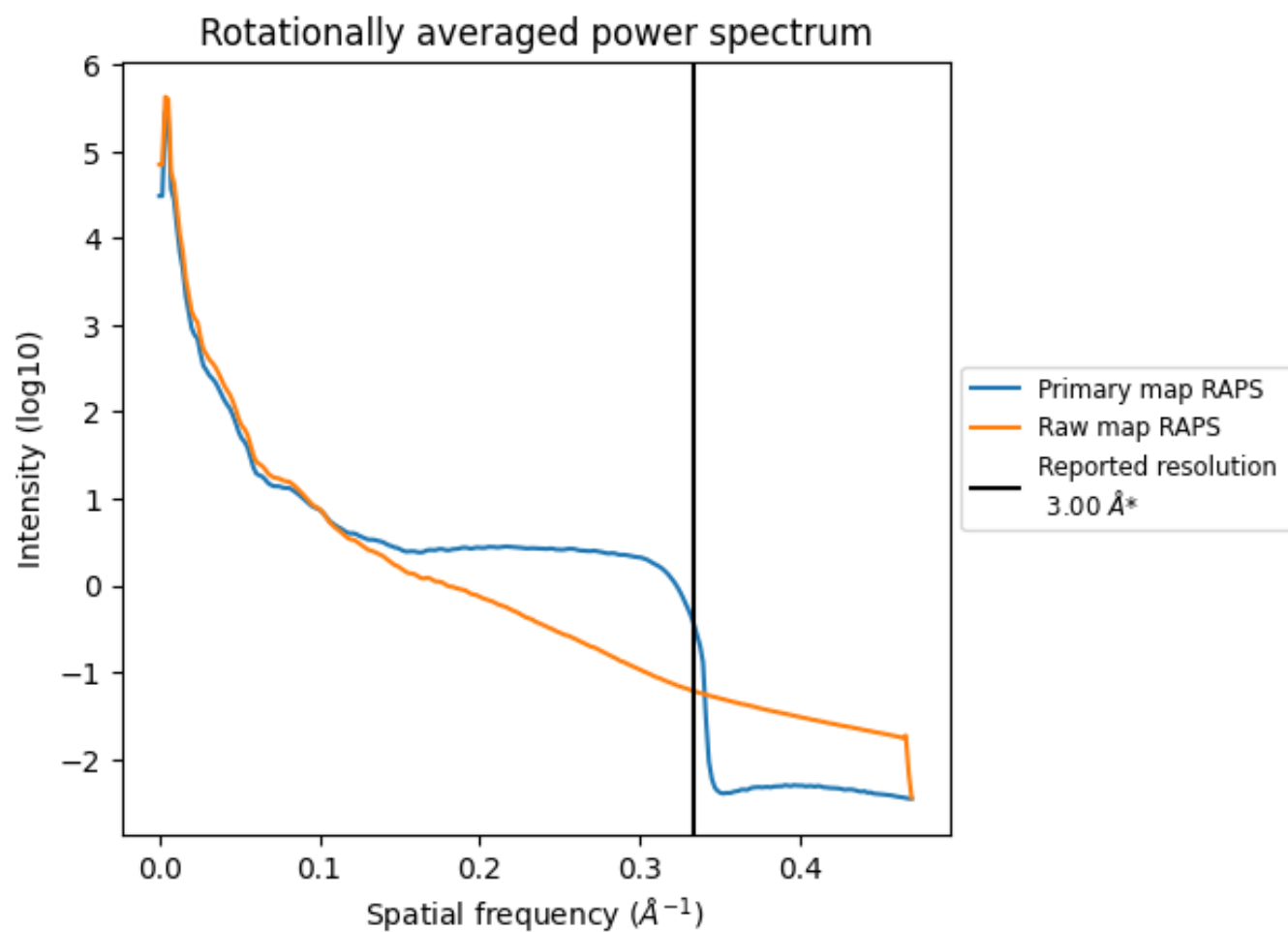
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1459 nm^3 ; this corresponds to an approximate mass of 1318 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 ⓘ

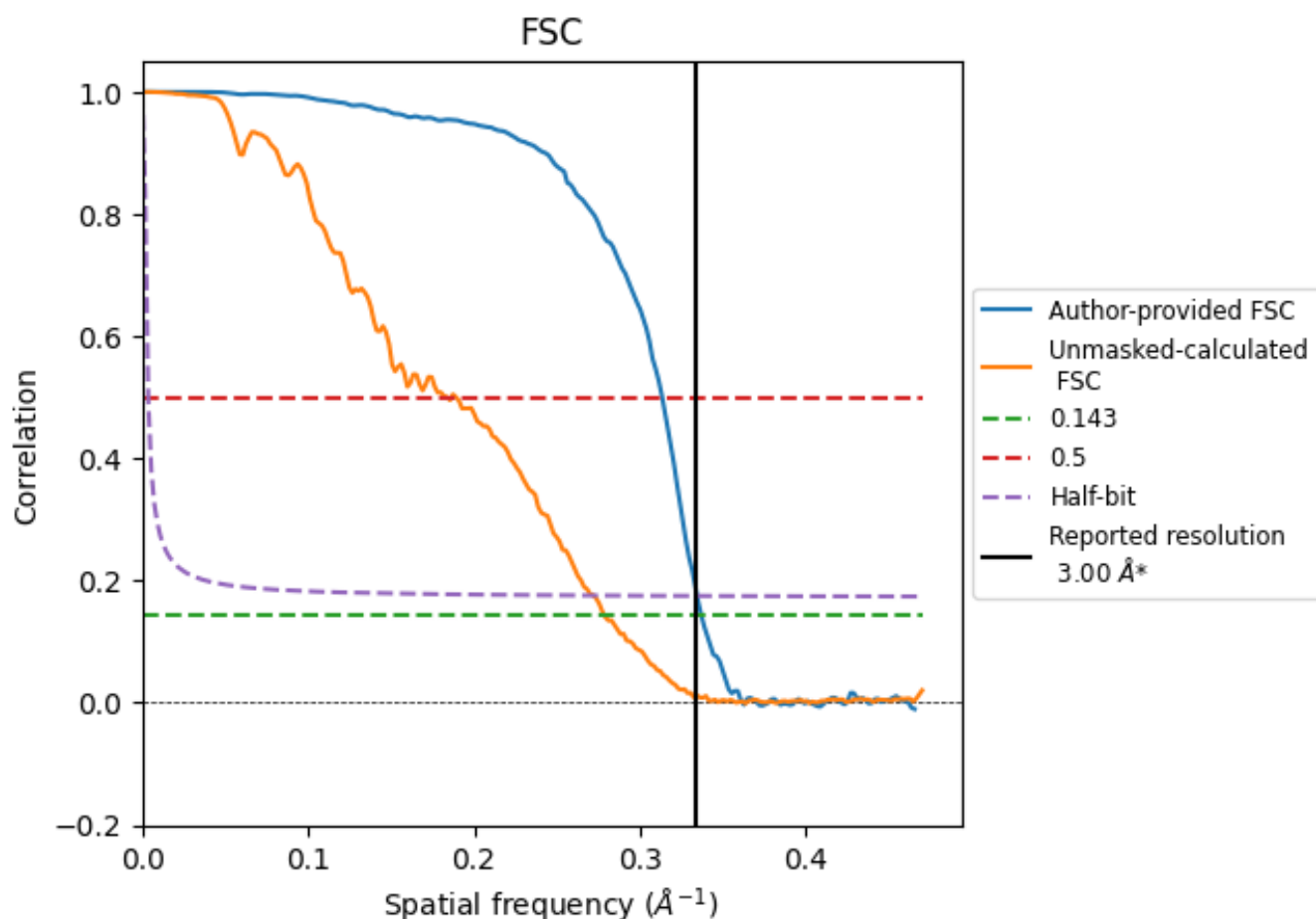


*Reported resolution corresponds to spatial frequency of 0.333 \AA^{-1}

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.333 \AA^{-1}

8.2 Resolution estimates [i](#)

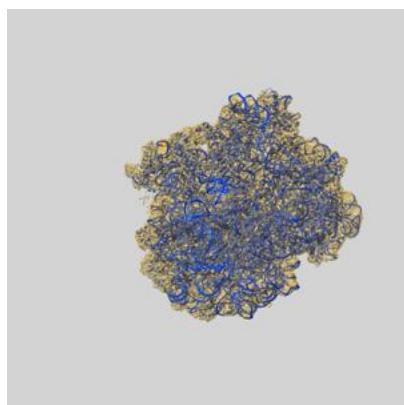
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	2.97	3.19	2.99
Unmasked-calculated*	3.59	5.44	3.68

*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 3.59 differs from the reported value 3.0 by more than 10 %

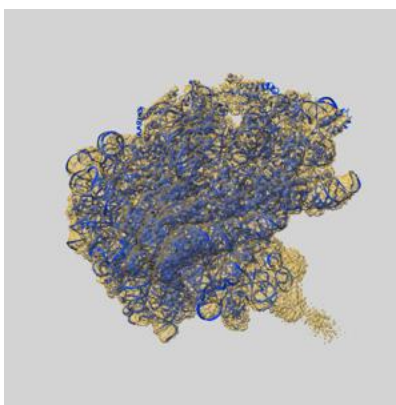
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-16566 and PDB model 8CD1. Per-residue inclusion information can be found in section [3](#) on page [13](#).

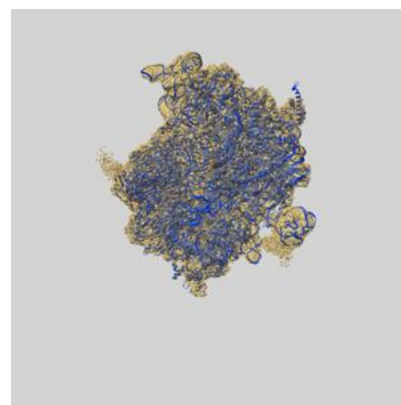
9.1 Map-model overlay [i](#)



X



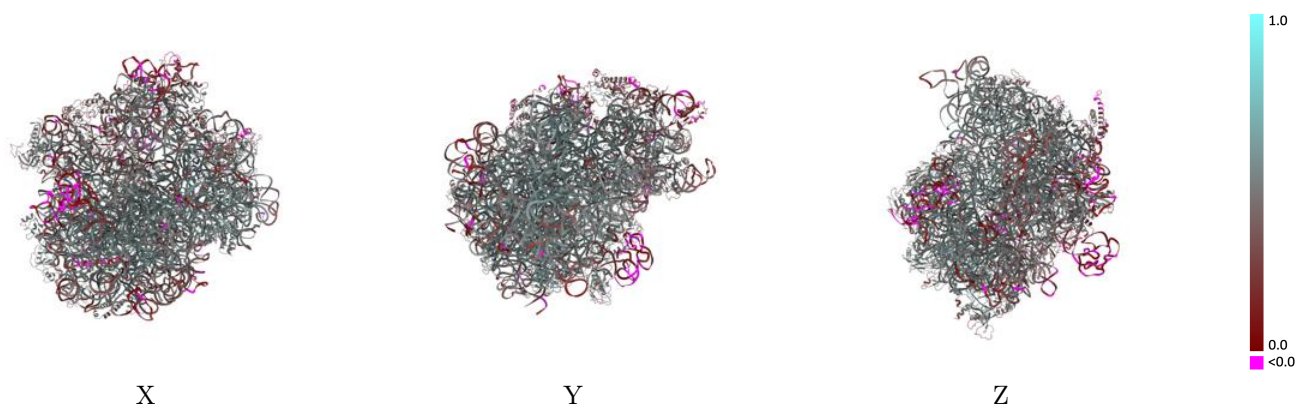
Y



Z

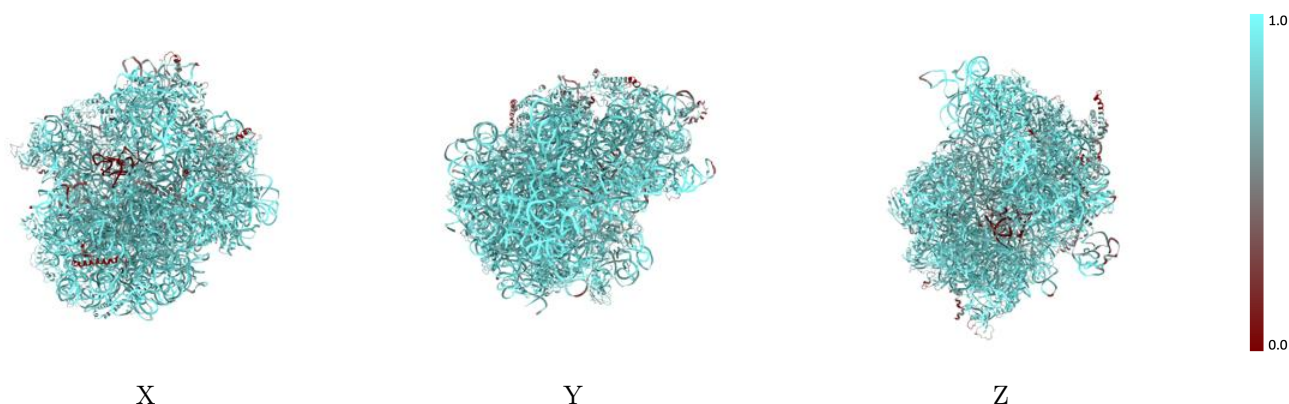
The images above show the 3D surface view of the map at the recommended contour level 3.46 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



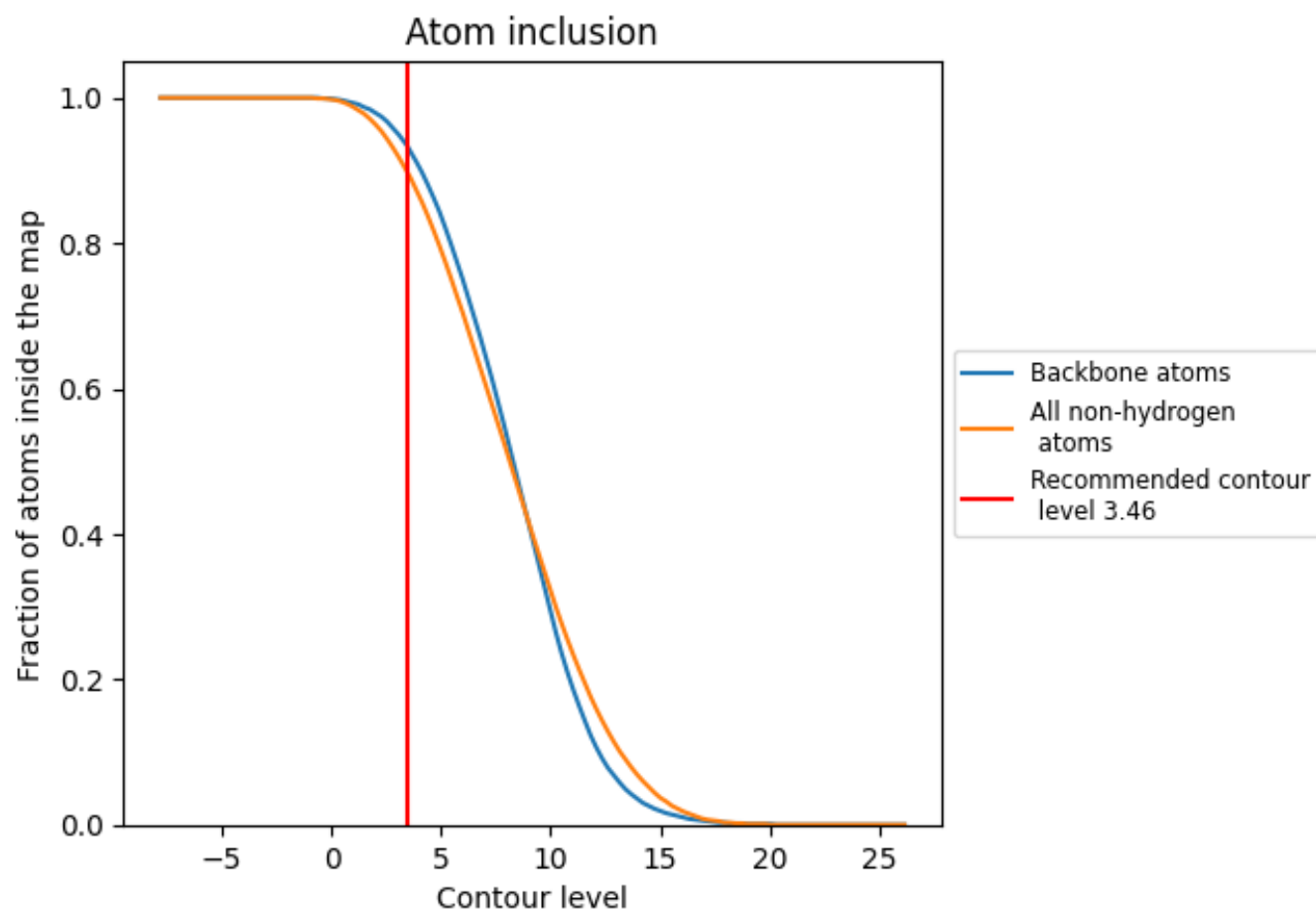
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.46).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 90% 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 (3.46) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8980	 0.4610
2	 0.8800	 0.5090
4	 0.9330	 0.5560
5	 0.6800	 0.4950
6	 0.8960	 0.5200
A	 0.9400	 0.4550
B	 0.9300	 0.4200
C	 0.9020	 0.5320
D	 0.8950	 0.5120
Dt	 0.1470	 0.3840
E	 0.8990	 0.5220
F	 0.7810	 0.3700
G	 0.8210	 0.4400
H	 0.1530	 0.2090
J	 0.9060	 0.5310
K	 0.8330	 0.4870
L	 0.8800	 0.4960
Le	 0.7180	 0.3440
M	 0.8750	 0.5400
N	 0.9200	 0.5360
O	 0.8660	 0.4610
P	 0.8550	 0.4940
Q	 0.9290	 0.5520
R	 0.8940	 0.5230
S	 0.8790	 0.5210
T	 0.9020	 0.5250
U	 0.8180	 0.4650
V	 0.8200	 0.4580
W	 0.8750	 0.5090
X	 0.9000	 0.5260
Y	 0.8850	 0.4640
Z	 0.9140	 0.5280
a	 0.9630	 0.4840
b	 0.6390	 0.3340
c	 0.8060	 0.4230



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Chain	Atom inclusion	Q-score
d	 0.8360	 0.4510
e	 0.8150	 0.4450
f	 0.7900	 0.4050
g	 0.7650	 0.3770
h	 0.8740	 0.4970
i	 0.8530	 0.4170
j	 0.5110	 0.1420
k	 0.8480	 0.4720
l	 0.8320	 0.4750
m	 0.7860	 0.3550
n	 0.8650	 0.4270
o	 0.8730	 0.4910
p	 0.9250	 0.5130
q	 0.8600	 0.4860
r	 0.8000	 0.4290
s	 0.8260	 0.3850
t	 0.8990	 0.5050
u	 0.4290	 0.3630
v	 0.6920	 0.4530