



## wwPDB EM Validation Summary Report ⓘ

Apr 27, 2026 – 05:08 PM EDT

PDB ID : 11EL / pdb\_000011el  
EMDB ID : EMD-75650  
Title : Chimeric Escherichia coli 70S ribosome containing an evolved 16S rRNA from Vibrio cholerae (VC-ST)  
Authors : Raskar, T.  
Deposited on : 2026-02-19  
Resolution : 3.20 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](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev132  
Mogul : 2022.3.0, CSD as543be (2022)  
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

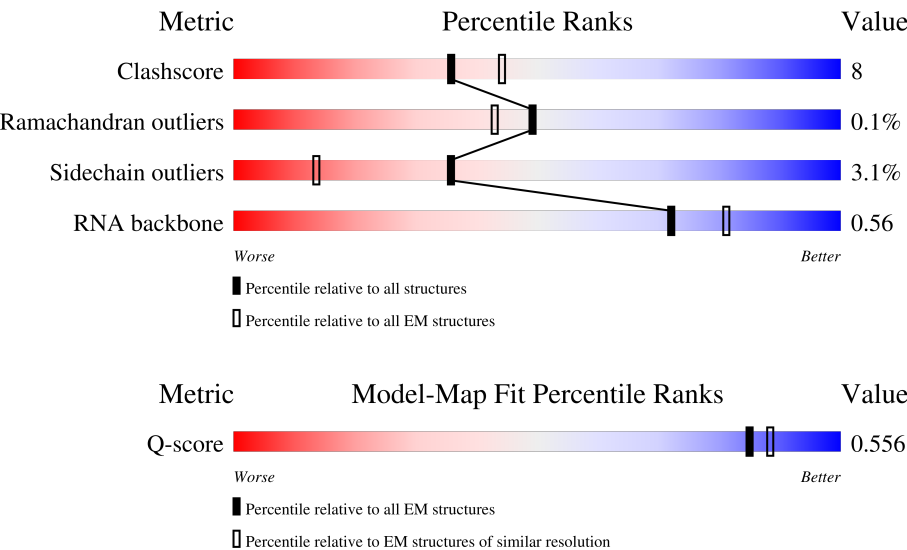


# 1 Overall quality at a glance i

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

The reported resolution of this entry is 3.20 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	15020 ( 2.70 - 3.70 )



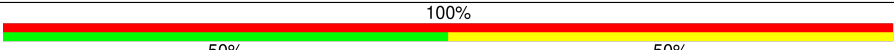
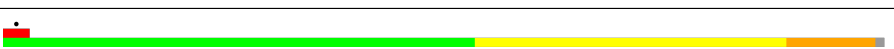

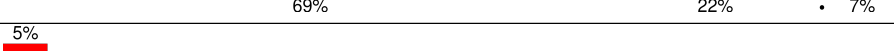
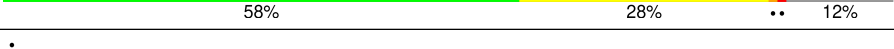


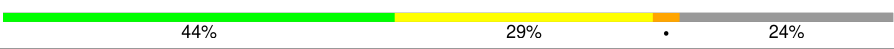


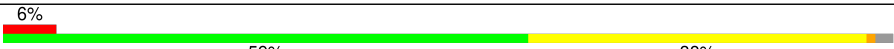


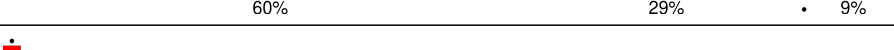








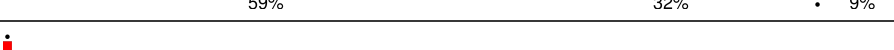
The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey 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	0	55	
2	1	46	
3	2	65	

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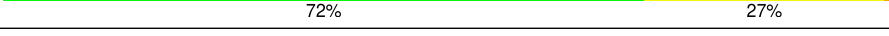

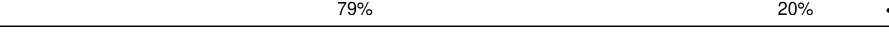
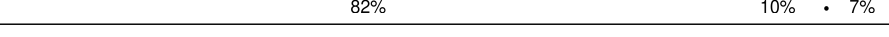

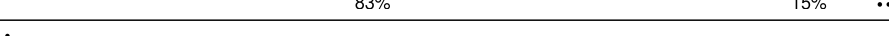


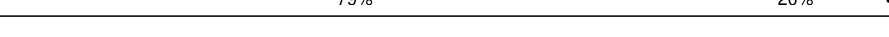

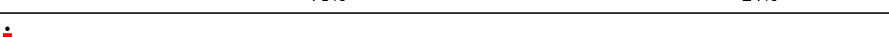






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Mol	Chain	Length	Quality of chain
4	3	38	
5	4	70	
6	5	2	
7	A	1543	
8	B	241	
9	C	233	
10	D	206	
11	E	167	
12	F	135	
13	G	179	
14	H	130	
15	I	130	
16	J	103	
17	K	129	
18	L	124	
19	M	118	
20	N	101	
21	O	89	
22	P	82	
23	Q	84	
24	R	75	
25	S	92	
26	T	87	
27	U	71	
28	a	2904	

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Mol	Chain	Length	Quality of chain
29	b	120	
30	c	273	
31	d	209	
32	e	201	
33	f	179	
34	g	177	
35	h	149	
36	i	142	
37	j	123	
38	k	144	
39	l	136	
40	m	127	
41	n	117	
42	o	115	
43	p	118	
44	q	103	
45	r	110	
46	s	100	
47	t	104	
48	u	94	
49	v	85	
50	w	78	
51	x	63	
52	y	59	
53	z	57	



## 2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 138616 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 L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	0	51	Total	C	N	O	0	0
			417	269	76	72		

- Molecule 2 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 4 is a protein called Large ribosomal subunit protein bL36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 5 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	60	Total	C	N	O	S	0	0
			480	299	90	85	6		

- Molecule 6 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	2	Total	C	N	O	P	0	0
			42	19	8	13	2		



- Molecule 7 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	1520	Total	C	N	O	P	0	0
			32643	14567	5995	10561	1520		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	847	G	U	conflict	GB 3166933093

- Molecule 8 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	224	Total	C	N	O	S	0	0
			1753	1109	315	321	8		

- Molecule 9 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 10 is a protein called Small ribosomal subunit protein uS4.

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

- Molecule 11 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	156	Total	C	N	O	S	0	0
			1152	717	217	212	6		

- Molecule 12 is a protein called Small ribosomal subunit protein bS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	103	Total	C	N	O	S	0	0
			839	530	151	151	7		

- Molecule 13 is a protein called Small ribosomal subunit protein uS7.



Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	153	Total	C	N	O	S	0	0
			1203	750	231	218	4		

- Molecule 14 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 15 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 16 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	J	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 17 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	K	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 18 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	L	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 19 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	M	115	Total	C	N	O	S	0	0
			891	552	179	157	3		

- Molecule 20 is a protein called Small ribosomal subunit protein uS14.



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

- Molecule 21 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 22 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	P	81	Total	C	N	O	S	0	0
			643	403	127	112	1		

- Molecule 23 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Q	79	Total	C	N	O	S	0	0
			641	406	120	112	3		

- Molecule 24 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	R	66	Total	C	N	O	S	0	0
			544	345	102	96	1		

- Molecule 25 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	S	84	Total	C	N	O	S	0	0
			668	427	127	112	2		

- Molecule 26 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	T	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 27 is a protein called Small ribosomal subunit protein bS21.



Mol	Chain	Residues	Atoms					AltConf	Trace
27	U	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

- Molecule 28 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	2753	Total	C	N	O	P	0	0
			59130	26384	10897	19096	2753		

- Molecule 29 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	119	Total	C	N	O	P	0	0
			2549	1135	466	829	119		

- Molecule 30 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 31 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	209	Total	C	N	O	S	0	0
			1566	980	288	294	4		

- Molecule 32 is a protein called Large ribosomal subunit protein uL4.

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

- Molecule 33 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 34 is a protein called Large ribosomal subunit protein uL6.



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

- Molecule 35 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	41	Total	C	N	O	S	0	0
			303	194	54	54	1		

- Molecule 36 is a protein called Large ribosomal subunit protein uL13.

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

- Molecule 37 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	j	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 38 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	k	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 39 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	l	136	Total	C	N	O	S	0	0
			1075	686	205	177	7		

- Molecule 40 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	m	118	Total	C	N	O	S	0	0
			945	585	194	161	5		

- Molecule 41 is a protein called Large ribosomal subunit protein uL18.



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

- Molecule 42 is a protein called Large ribosomal subunit protein bL19.

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

- Molecule 43 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	p	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 44 is a protein called Large ribosomal subunit protein bL21.

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

- Molecule 45 is a protein called Large ribosomal subunit protein uL22.

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

- Molecule 46 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	s	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 47 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	t	102	Total	C	N	O	0	0
			779	492	146	141		

- Molecule 48 is a protein called Large ribosomal subunit protein bL25.



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

- Molecule 49 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	v	78	Total	C	N	O	S	0	0
			586	362	116	107	1		

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

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

- Molecule 51 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	x	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 52 is a protein called 50S ribosomal protein L30.

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

- Molecule 53 is a protein called 50S ribosomal protein L32.

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

- Molecule 54 is ZINC ION (CCD ID: ZN) (formula: Zn).

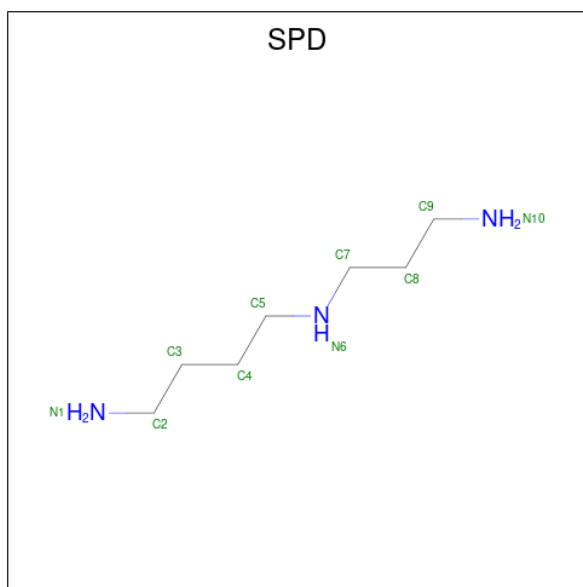
Mol	Chain	Residues	Atoms		AltConf
54	3	1	Total	Zn	0
			1	1	
54	4	1	Total	Zn	0
			1	1	

- Molecule 55 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).



Mol	Chain	Residues	Atoms		AltConf
55	A	90	Total	Mg	0
			90	90	
55	D	1	Total	Mg	0
			1	1	
55	N	1	Total	Mg	0
			1	1	
55	a	207	Total	Mg	0
			207	207	
55	b	5	Total	Mg	0
			5	5	
55	c	1	Total	Mg	0
			1	1	
55	m	1	Total	Mg	0
			1	1	
55	p	1	Total	Mg	0
			1	1	
55	z	1	Total	Mg	0
			1	1	

- Molecule 56 is SPERMIDINE (CCD ID: SPD) (formula:  $C_7H_{19}N_3$ ).



Mol	Chain	Residues	Atoms			AltConf
56	A	1	Total	C	N	0
			10	7	3	
56	A	1	Total	C	N	0
			10	7	3	
56	a	1	Total	C	N	0
			10	7	3	

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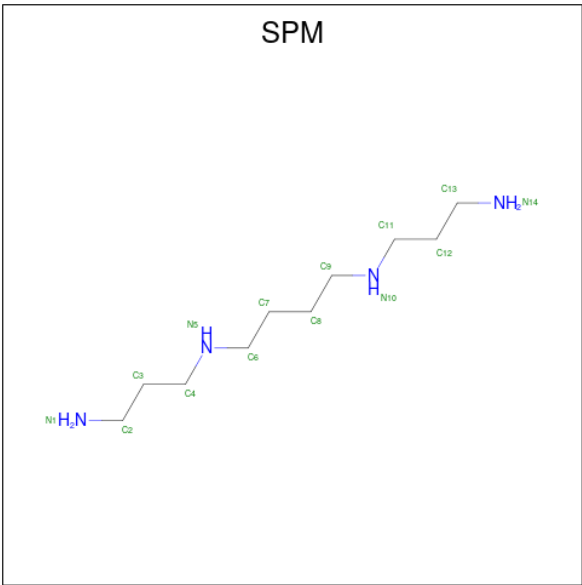


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Mol	Chain	Residues	Atoms			AltConf
56	a	1	Total	C	N	0
			10	7	3	
56	a	1	Total	C	N	0
			10	7	3	
56	a	1	Total	C	N	0
			10	7	3	
56	a	1	Total	C	N	0
			10	7	3	
56	a	1	Total	C	N	0
			10	7	3	
56	a	1	Total	C	N	0
			10	7	3	
56	a	1	Total	C	N	0
			10	7	3	
56	a	1	Total	C	N	0
			10	7	3	
56	a	1	Total	C	N	0
			10	7	3	
56	a	1	Total	C	N	0
			10	7	3	

- Molecule 57 is SPERMINE (CCD ID: SPM) (formula: C<sub>10</sub>H<sub>26</sub>N<sub>4</sub>).





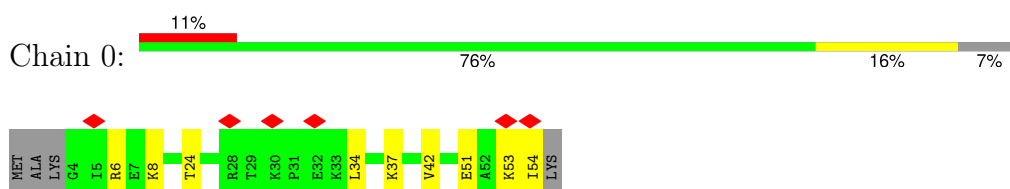
Mol	Chain	Residues	Atoms			AltConf
57	a	1	Total	C	N	0
			14	10	4	



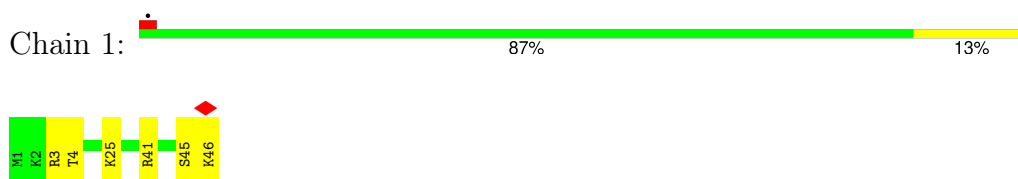
### 3 Residue-property plots [i](#)

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.

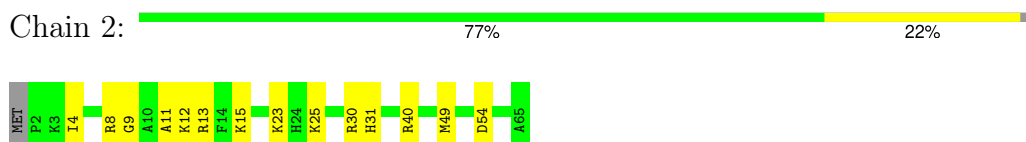
- Molecule 1: 50S ribosomal protein L33



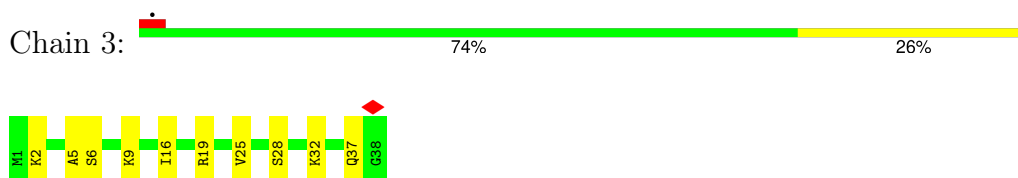
- Molecule 2: Large ribosomal subunit protein bL34



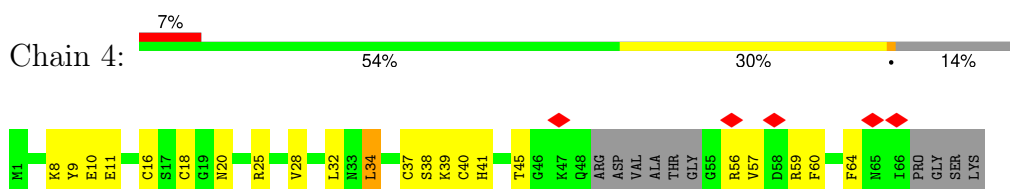
- Molecule 3: 50S ribosomal protein L35



- Molecule 4: Large ribosomal subunit protein bL36A



- Molecule 5: 50S ribosomal protein L31

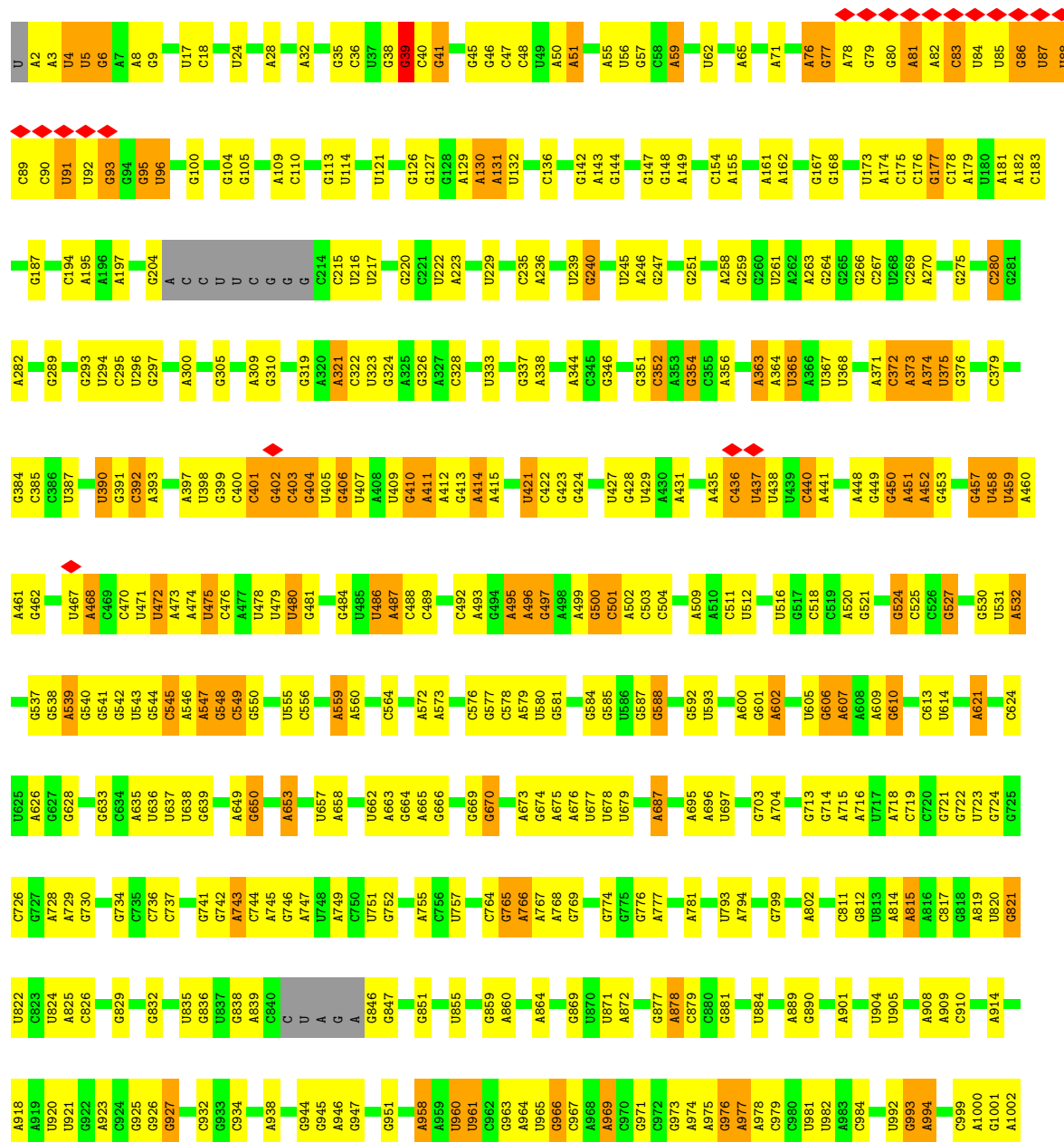




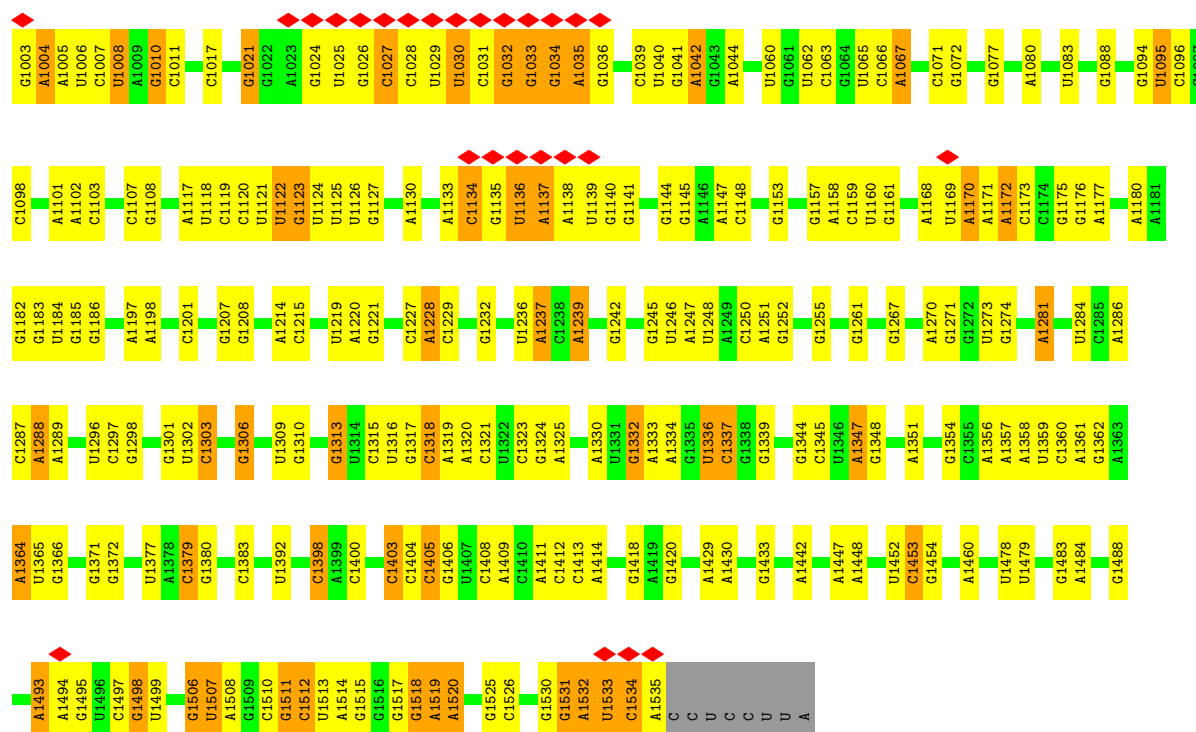
- Molecule 6: E-site tRNA



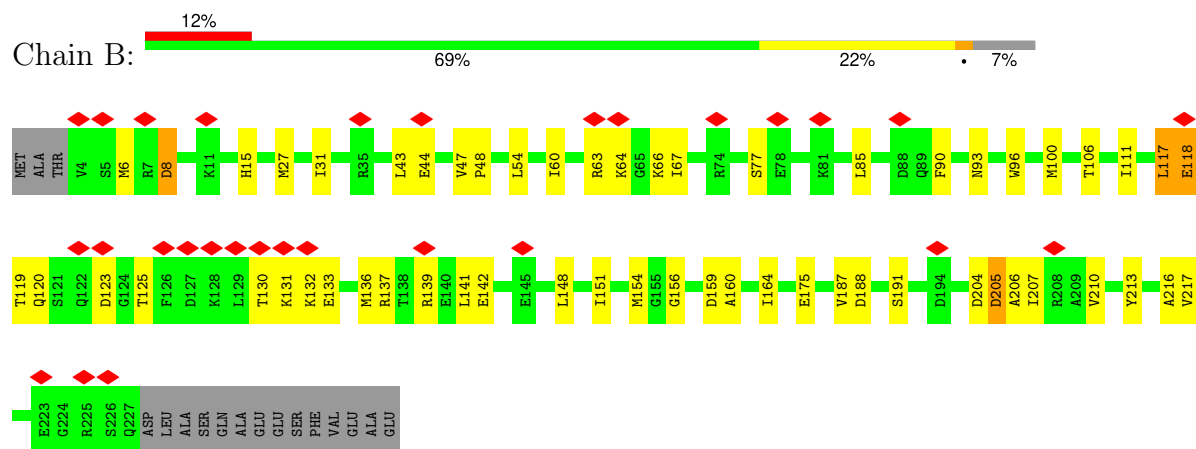
- Molecule 7: 16S ribosomal RNA



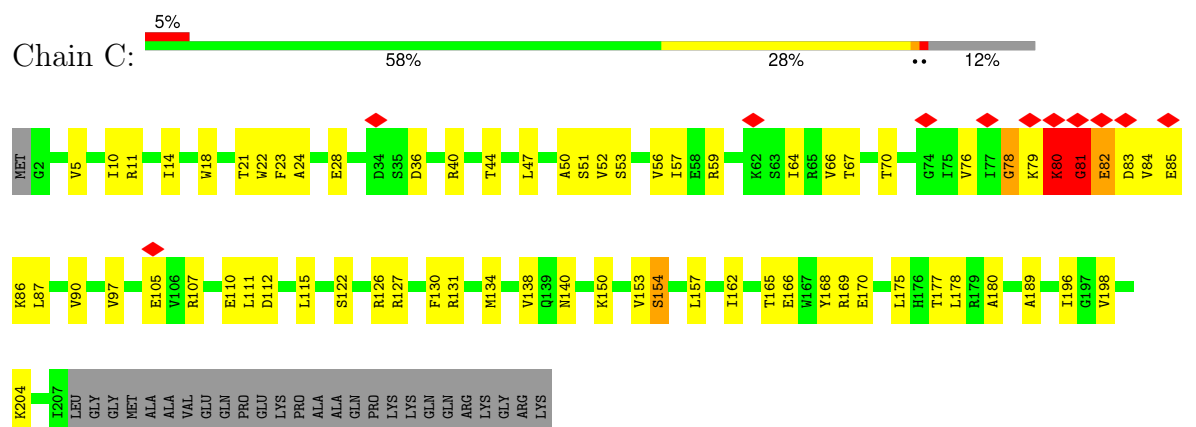




• Molecule 8: Small ribosomal subunit protein uS2

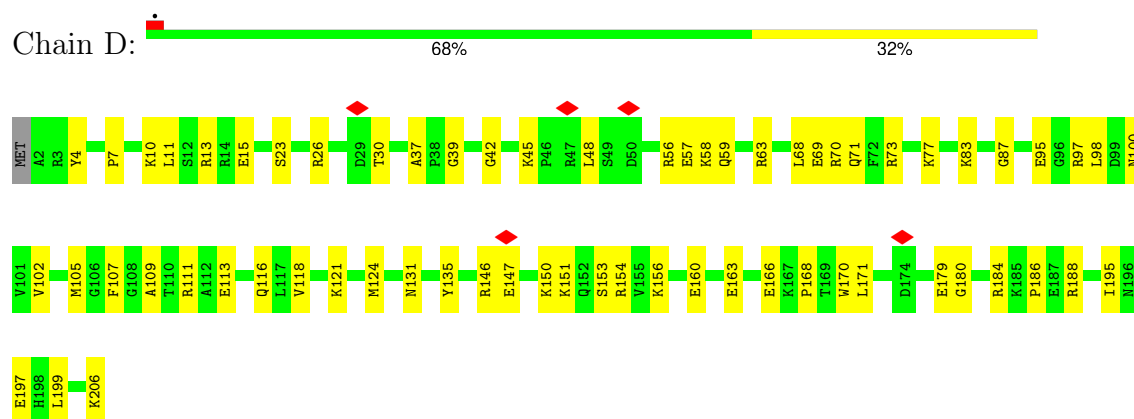


• Molecule 9: Small ribosomal subunit protein uS3

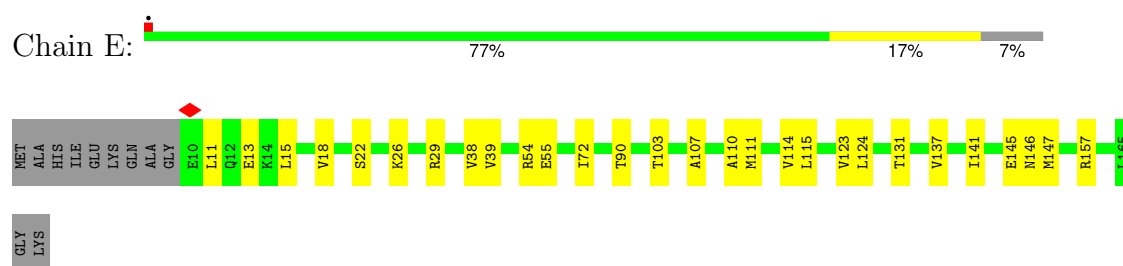




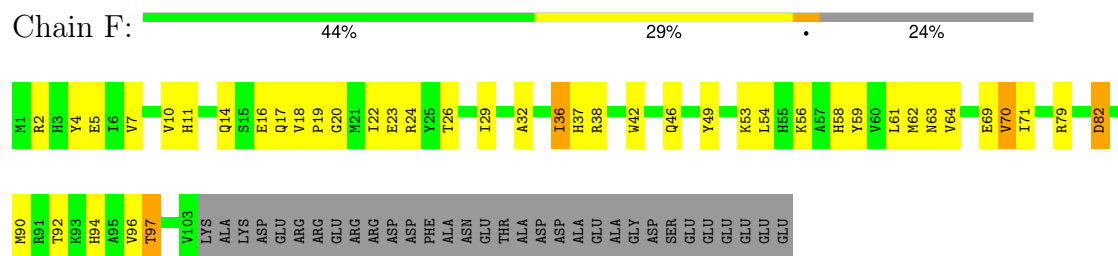
- Molecule 10: Small ribosomal subunit protein uS4



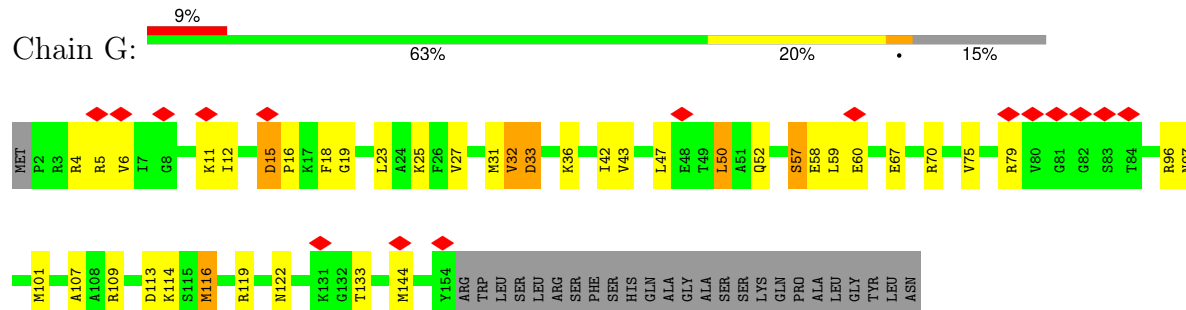
- Molecule 11: Small ribosomal subunit protein uS5



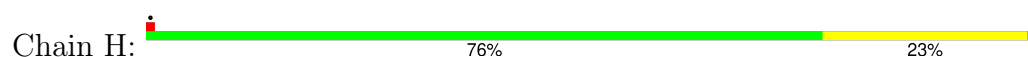
- Molecule 12: Small ribosomal subunit protein bS6



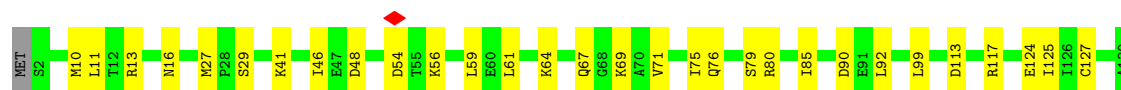
- Molecule 13: Small ribosomal subunit protein uS7



- Molecule 14: Small ribosomal subunit protein uS8



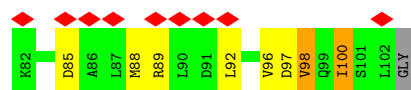
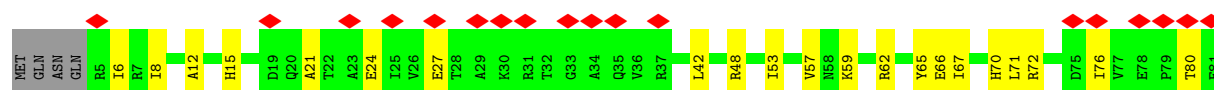




- Molecule 15: Small ribosomal subunit protein uS9



- Molecule 16: Small ribosomal subunit protein uS10



- Molecule 17: 30S ribosomal protein S11



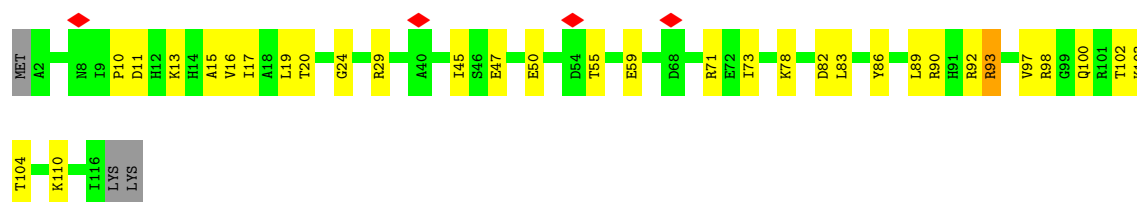
- Molecule 18: Small ribosomal subunit protein uS12



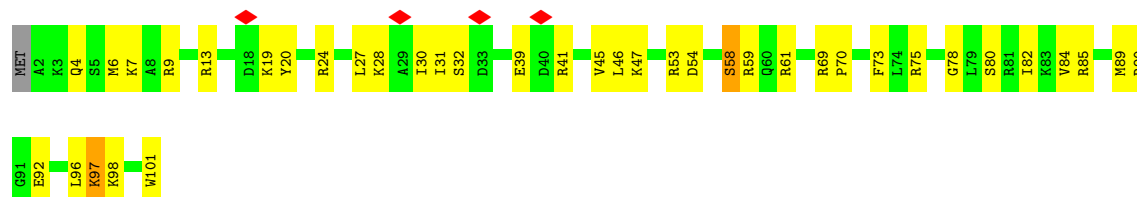
- Molecule 19: Small ribosomal subunit protein uS13



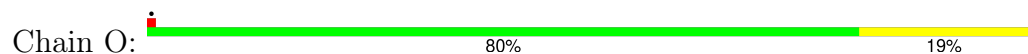




- Molecule 20: Small ribosomal subunit protein uS14



- Molecule 21: Small ribosomal subunit protein uS15



- Molecule 22: Small ribosomal subunit protein bS16



- Molecule 23: Small ribosomal subunit protein uS17

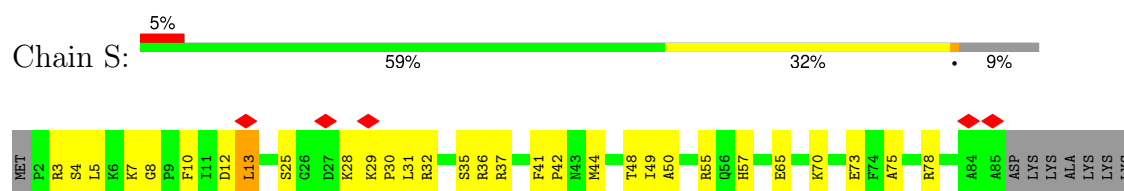


- Molecule 24: Small ribosomal subunit protein bS18

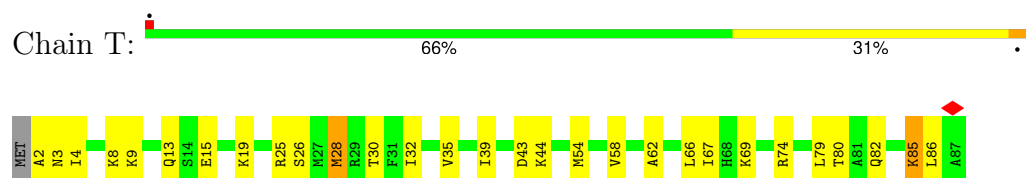


- Molecule 25: Small ribosomal subunit protein uS19

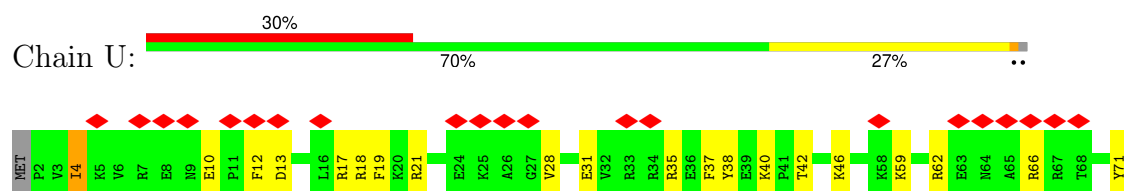




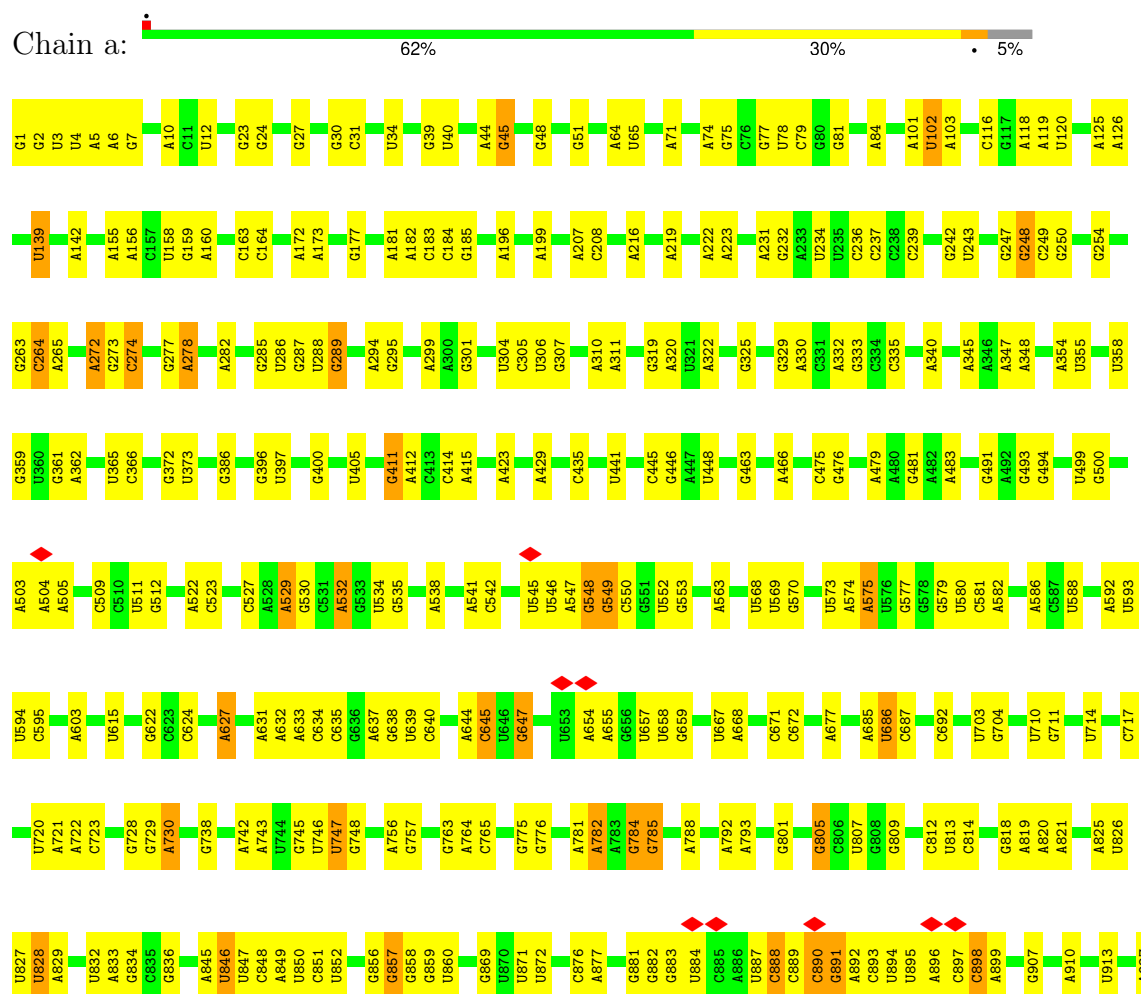
- Molecule 26: Small ribosomal subunit protein bS20



- Molecule 27: Small ribosomal subunit protein bS21



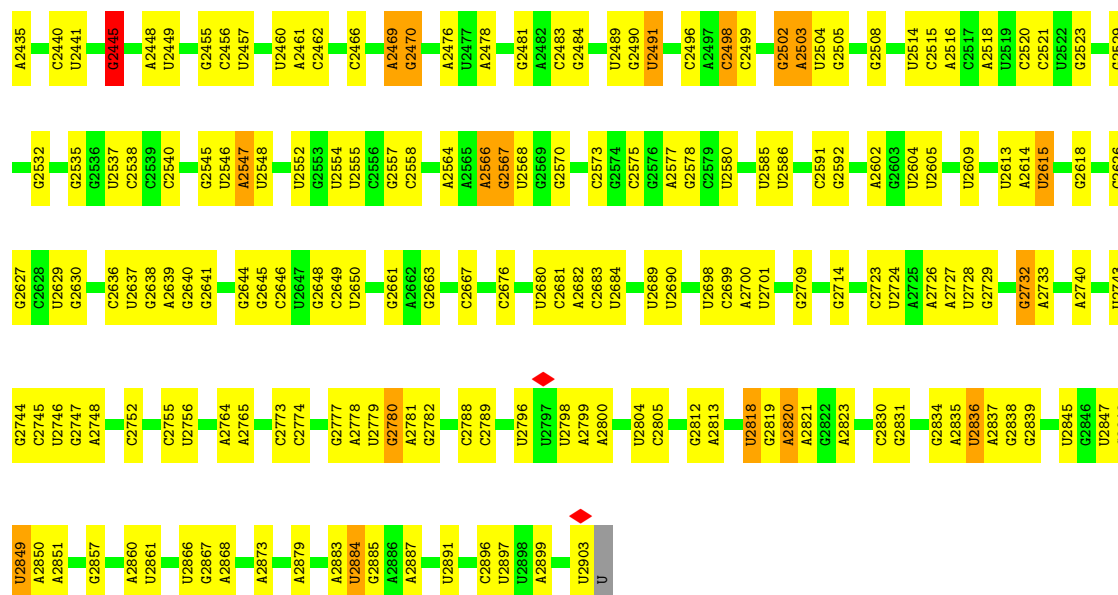
- Molecule 28: 23S ribosomal RNA





A2225	A2322	A2071	U1971	A1853	G1731	U1584	U1476	A1385	G1245	G1115	A
C2226	G2325	U2076	G1972	A1854	C1732	C1585	A1477	A1366	G1248	G1116	G
U2233	C2326	U2077	G1980	U1855	G1733	U1589	G1482	A1367	G1249	G1122	A
G2234	U2327	U2079	A1981	U1856	A1735	A1590	G1483	U1378	G1250	G1125	U
G2238	A2328	U2092	U1982	G1857	U1736	A1591	U1484	U1379	A1253	A1126	G
G2239	U2329	U2093	U1991	A1858	G1737	C1592	U1485	A1383	A1254	A1127	U
A2244	C2330	G2093	U1992	U1864	G1738	A1597	U1486	A1384	U1255	G1128	G
U2245	A2331	A2095	G1993	A1864	A1739	A1598	U1487	A1385	G1256	A1129	G
U2246	G2332	C2096	G1996	G1870	G1743	A1871	C1493	A1387	U1263	G1130	C
U2247	A2333	A2097	C1997	A1872	A1746	A1608	A1494	A1392	G1266	U1132	U
A2248	U2334	U2098	C1997	G1873	U1747	A1607	A1496	A1393	U1267	A1134	G
G2249	G2335	U	C2000	C1874	G1760	G1613	U1497	A1395	A1268	C1135	A
U2249	A2336	G	C2006	G1875	C1760	A1618	C1498	U1396	A1269	G1138	C
G2250	U2340	G	C2006	G1875	C1760	A1618	C1499	U1396	C1270	G1138	G
G2251	U2343	C	U2011	U1880	C1764	G1622	G1500	A1403	G1271	U1141	C
C2261	G2344	C	G2012	C1881	A1773	U1506	U1506	C1404	A1272	U1141	A
U2262	U2345	U	A2013	U1882	G1773	C1626	C1507	U1405	U1273	A1142	C
C2263	U2346	U	A2014	G1884	U1779	A1636	A1508	U1406	G1278	G1149	C
G	A2347	A	A2015	G1884	U1779	U1629	A1509	A1413	C1279	C1150	A
A2266	C2359	U	C2021	A1901	U1782	A1630	G1510	C1414	G1280	A1155	U
G2271	G2360	G	U2022	C1905	A1783	U1636	A1515	U1415	G1281	A1155	C
C2272	U2361	U	G2023	G1906	A1784	A1637	A1515	G1416	U1282	A1155	C
G2273	C2362	U	G2024	G1907	A1786	G1637	G1519	C1417	G1168	A1169	U
G2279	G2363	A	C2025	U1911	U1794	G1645	G1524	G1418	G1288	G1170	U
A2281	U2364	G	U2026	U1912	A1795	C1646	G1524	A1419	G1292	G1171	A
G2282	C2365	G	G2027	A1912	C1795	U1647	G1527	A1420	C1293	C1172	A
C2283	U2366	U	U2028	A1913	U1996	U1648	A1528	G1421	U1294	U	A
A2284	C2367	C	G2029	C1914	G1797	G1649	A1529	A1427	C1295	U	G
C2285	G2374	A	A2030	3TD1915	U1798	G1649	G1529	G1428	G1296	A	A
G2286	U2375	G	A2031	A1916	G1799	G1667	A1532	G1429	G1300	G1177	A
A2287	A2376	U	C2032	U1917	C1800	A1668	A1532	G1430	A1301	C1178	A
G2288	U2377	U	A2033	A1901	A1801	A1669	C1533	A1431	G1306	U1181	C
U2291	G2383	A	U2034	A1928	A1802	G1674	U1534	G1432	C1307	G1182	U
U2292	U2384	G	G2038	G1929	A1803	G1674	A1535	A1433	U1181	G1182	A
G	C2385	G	U2039	U1931	U1808	G1682	C1536	A1434	G1311	G1186	A
U2296	G2389	U	C2043	A1932	A1809	U1683	G1537	G1435	G1187	G1187	U
A2297	U2392	U	G2043	G1933	A1809	C1684	U1538	G1441	C1315	U1188	G
U2298	U2393	C	U2043	G1933	G1813	C1685	U1539	U1442	G1319	G1197	C





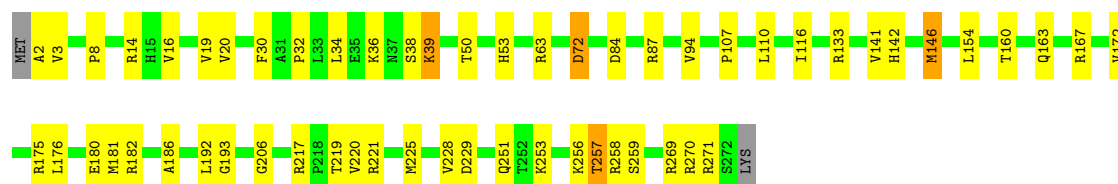
• Molecule 29: 5S ribosomal RNA

Chain b: 72% 24%



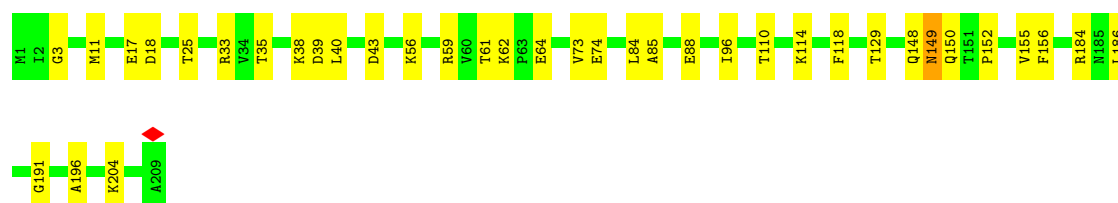
• Molecule 30: 50S ribosomal protein L2

Chain c: 78% 19%



• Molecule 31: 50S ribosomal protein L3

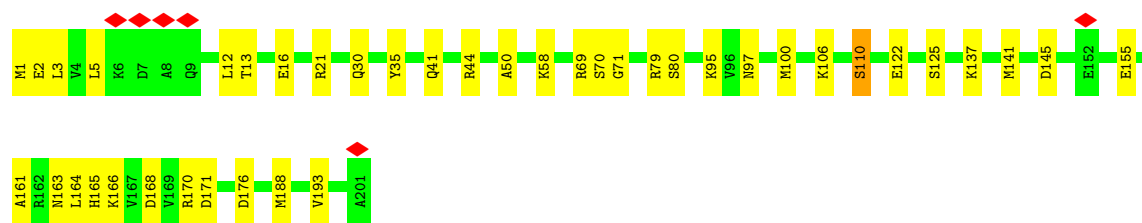
Chain d: 82% 17%



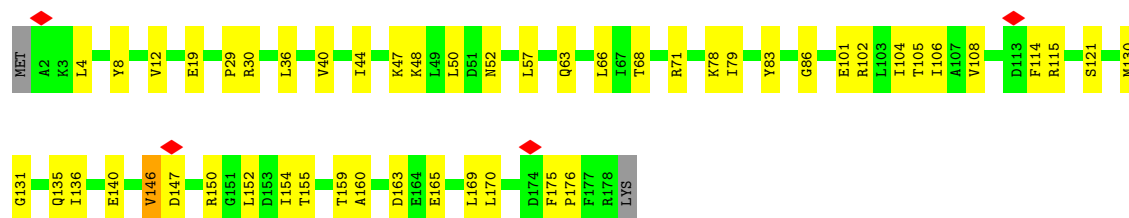
• Molecule 32: Large ribosomal subunit protein uL4

Chain e: 80% 20%

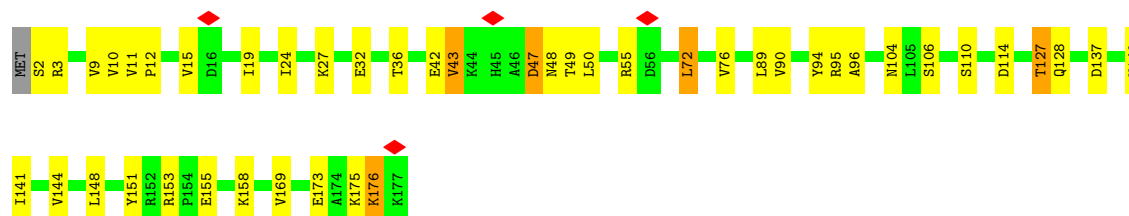




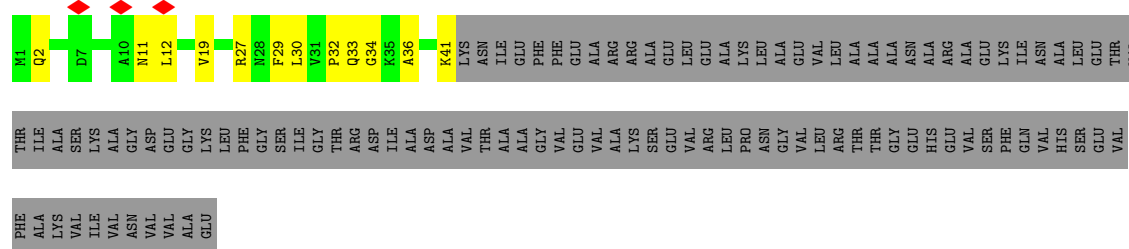
- Molecule 33: Large ribosomal subunit protein uL5



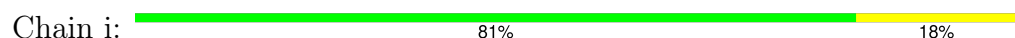
- Molecule 34: Large ribosomal subunit protein uL6



- Molecule 35: Large ribosomal subunit protein bL9

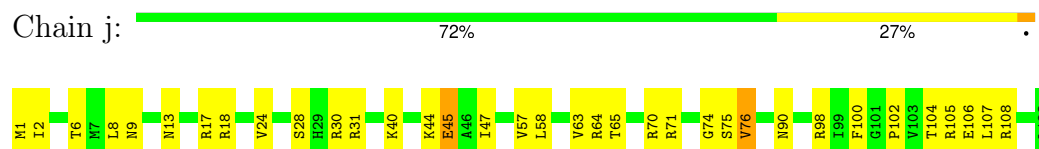


- Molecule 36: Large ribosomal subunit protein uL13

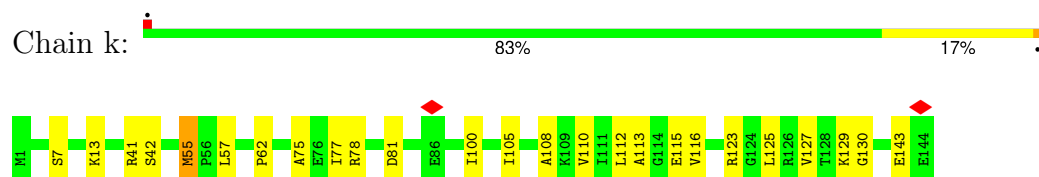


- Molecule 37: Large ribosomal subunit protein uL14

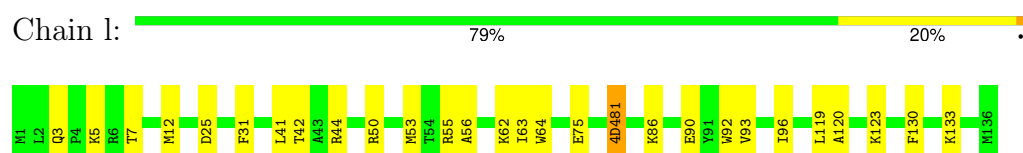




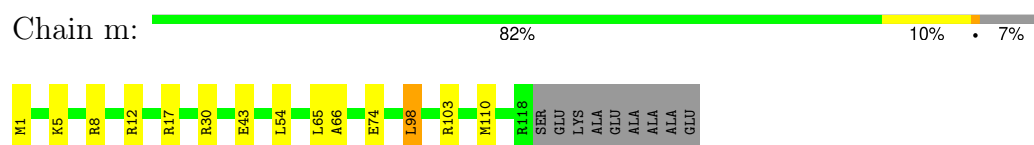
- Molecule 38: Large ribosomal subunit protein uL15



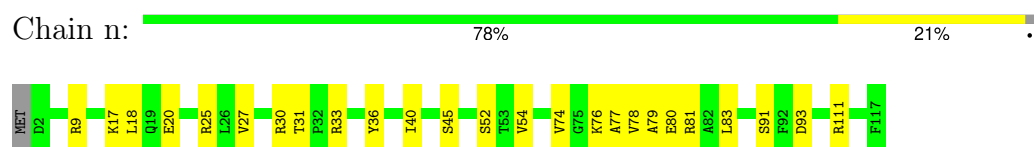
- Molecule 39: Large ribosomal subunit protein uL16



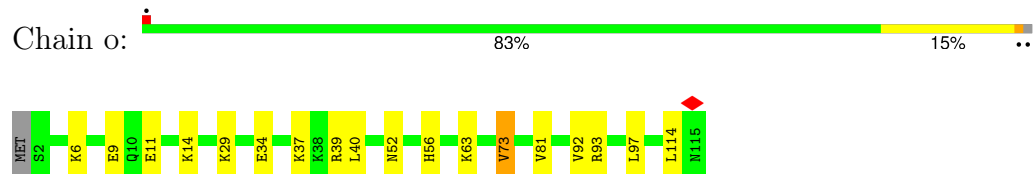
- Molecule 40: Large ribosomal subunit protein bL17



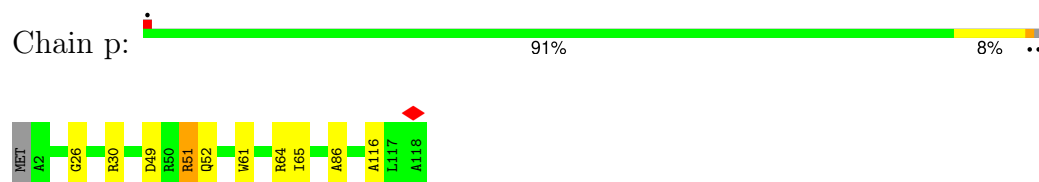
- Molecule 41: Large ribosomal subunit protein uL18



- Molecule 42: Large ribosomal subunit protein bL19




- Molecule 43: 50S ribosomal protein L20





- Molecule 44: Large ribosomal subunit protein bL21

Chain q:  80% 18%



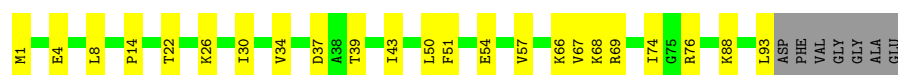
- Molecule 45: Large ribosomal subunit protein uL22

Chain r:  79% 20%



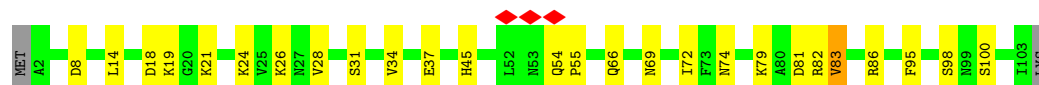
- Molecule 46: 50S ribosomal protein L23

Chain s:  70% 23% 7%




- Molecule 47: 50S ribosomal protein L24

Chain t:  73% 24%



- Molecule 48: Large ribosomal subunit protein bL25

Chain u:  77% 22%




- Molecule 49: 50S ribosomal protein L27

Chain v:  68% 24% 8%



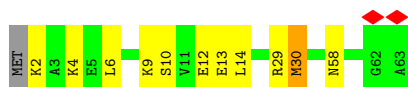
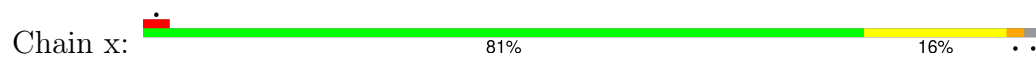
- Molecule 50: 50S ribosomal protein L28

Chain w:  86% 13%

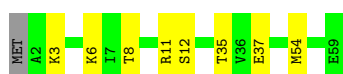
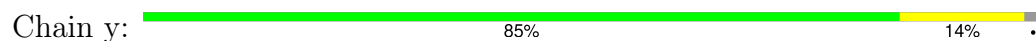




- Molecule 51: Large ribosomal subunit protein uL29



- Molecule 52: 50S ribosomal protein L30



- Molecule 53: 50S ribosomal protein L32





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	577128	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	27.798	Depositor
Minimum map value	-18.382	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2.5	Depositor
Map size (Å)	425.984, 425.984, 425.984	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.832, 0.832, 0.832	Depositor



## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MS6, SPD, D2T, 6MZ, MA6, OMC, SPM, MEQ, OMG, 5MU, G7M, 2MA, H2U, 2MG, OMU, 5MC, 3TD, MG, 4OC, 4D4, UR3, 1MG, ZN, PSU

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	0	0.17	0/424	0.30	0/565
2	1	0.36	0/380	0.30	0/498
3	2	0.32	0/513	0.32	0/676
4	3	0.32	0/303	0.31	0/397
5	4	0.19	0/488	0.39	0/649
6	5	0.10	0/46	0.09	0/69
7	A	0.31	2/36275 (0.0%)	0.34	2/56582 (0.0%)
8	B	0.19	0/1784	0.36	0/2403
9	C	0.26	0/1651	0.41	0/2225
10	D	0.22	0/1665	0.37	0/2227
11	E	0.29	0/1165	0.34	0/1568
12	F	0.24	0/858	0.41	0/1160
13	G	0.18	0/1219	0.33	0/1635
14	H	0.27	0/989	0.29	0/1326
15	I	0.21	0/1034	0.41	0/1375
16	J	0.20	0/796	0.40	0/1077
17	K	0.25	0/893	0.39	0/1205
18	L	0.28	0/960	0.35	0/1286
19	M	0.19	0/900	0.34	0/1204
20	N	0.23	0/817	0.39	0/1088
21	O	0.27	0/722	0.32	0/964
22	P	0.28	0/653	0.47	0/877
23	Q	0.26	0/650	0.49	0/871
24	R	0.25	0/553	0.33	0/742
25	S	0.20	0/685	0.33	0/922
26	T	0.26	0/676	0.35	0/895
27	U	0.17	0/597	0.27	0/792
28	a	0.36	0/65651	0.31	0/102413
29	b	0.27	0/2850	0.25	0/4444
30	c	0.36	0/2121	0.33	0/2852
31	d	0.34	0/1576	0.31	0/2119



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
32	e	0.27	0/1571	0.30	0/2113
33	f	0.20	0/1434	0.35	0/1926
34	g	0.21	0/1343	0.42	0/1816
35	h	0.22	0/306	0.48	0/413
36	i	0.30	0/1152	0.28	0/1551
37	j	0.34	0/955	0.30	0/1279
38	k	0.31	0/1062	0.32	0/1413
39	l	0.31	0/1073	0.30	0/1433
40	m	0.33	0/958	0.33	0/1281
41	n	0.22	0/902	0.35	0/1209
42	o	0.32	0/929	0.31	0/1242
43	p	0.35	0/960	0.28	0/1278
44	q	0.29	0/829	0.29	0/1107
45	r	0.30	0/864	0.28	0/1156
46	s	0.27	0/744	0.37	0/994
47	t	0.23	0/787	0.39	0/1051
48	u	0.26	0/766	0.29	0/1025
49	v	0.33	0/593	0.33	0/785
50	w	0.32	0/635	0.26	0/848
51	x	0.22	0/502	0.33	0/667
52	y	0.31	0/453	0.34	0/605
53	z	0.32	0/450	0.35	0/599
All	All	0.32	2/149162 (0.0%)	0.33	2/222897 (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
9	C	0	5
23	Q	0	1
34	g	0	1
39	l	0	1
All	All	0	8

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	39	G	C2-N2	-11.28	1.11	1.34
7	A	39	G	C6-N1	8.22	1.55	1.39



All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	39	G	N1-C2-N2	-28.51	30.68	116.20
7	A	39	G	N3-C2-N2	-10.54	88.27	119.90

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	C	78	GLY	Peptide
9	C	80	LYS	Mainchain,Peptide
9	C	81	GLY	Peptide
9	C	82	GLU	Peptide
23	Q	16	LYS	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	0	417	0	451	4	0
2	1	377	0	418	6	0
3	2	504	0	572	14	0
4	3	302	0	340	7	0
5	4	480	0	478	19	0
6	5	42	0	23	0	0
7	A	32643	0	16433	452	0
8	B	1753	0	1780	39	0
9	C	1624	0	1696	51	0
10	D	1643	0	1707	49	0
11	E	1152	0	1196	20	0
12	F	839	0	833	33	0
13	G	1203	0	1254	29	0
14	H	979	0	1031	20	0
15	I	1022	0	1070	46	0
16	J	786	0	828	20	0
17	K	877	0	887	33	0
18	L	957	0	1017	29	0
19	M	891	0	952	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	N	805	0	844	36	0
21	O	714	0	734	13	0
22	P	643	0	661	27	0
23	Q	641	0	682	22	0
24	R	544	0	565	15	0
25	S	668	0	693	25	0
26	T	670	0	719	21	0
27	U	589	0	629	18	0
28	a	59130	0	29769	514	0
29	b	2549	0	1291	19	0
30	c	2082	0	2154	40	0
31	d	1566	0	1618	25	0
32	e	1552	0	1619	27	0
33	f	1410	0	1444	37	0
34	g	1323	0	1371	26	0
35	h	303	0	327	10	0
36	i	1129	0	1162	22	0
37	j	946	0	1023	23	0
38	k	1053	0	1129	17	0
39	l	1075	0	1145	18	0
40	m	945	0	989	8	0
41	n	892	0	923	15	0
42	o	917	0	962	15	0
43	p	947	0	1019	8	0
44	q	816	0	839	11	0
45	r	857	0	922	16	0
46	s	738	0	807	17	0
47	t	779	0	831	16	0
48	u	753	0	780	18	0
49	v	586	0	596	14	0
50	w	625	0	652	7	0
51	x	501	0	531	11	0
52	y	449	0	488	5	0
53	z	444	0	458	13	0
54	3	1	0	0	0	0
54	4	1	0	0	0	0
55	A	90	0	0	0	0
55	D	1	0	0	0	0
55	N	1	0	0	0	0
55	a	207	0	0	0	0
55	b	5	0	0	0	0
55	c	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
55	m	1	0	0	0	0
55	p	1	0	0	0	0
55	z	1	0	0	0	0
56	A	20	0	36	2	0
56	a	140	0	266	15	0
57	a	14	0	26	1	0
All	All	138616	0	93670	1767	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 8.

The worst 5 of 1767 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)
9:C:80:LYS:O	9:C:82:GLU:N	1.70	1.24
7:A:76:A:N6	7:A:93:G:H1	1.49	1.09
28:a:627:A:OP1	38:k:78:ARG:NH2	2.02	0.91
24:R:42:SER:HB2	24:R:52:GLN:HG3	1.55	0.89
5:4:16:CYS:SG	5:4:37:CYS:HB3	2.16	0.86

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	0	49/55 (89%)	48 (98%)	1 (2%)	0	100	100
2	1	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
3	2	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
4	3	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
5	4	56/70 (80%)	55 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	B	222/241 (92%)	207 (93%)	15 (7%)	0	100	100
9	C	204/233 (88%)	191 (94%)	11 (5%)	2 (1%)	12	45
10	D	203/206 (98%)	186 (92%)	17 (8%)	0	100	100
11	E	154/167 (92%)	151 (98%)	3 (2%)	0	100	100
12	F	101/135 (75%)	94 (93%)	7 (7%)	0	100	100
13	G	151/179 (84%)	139 (92%)	12 (8%)	0	100	100
14	H	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
15	I	125/130 (96%)	119 (95%)	6 (5%)	0	100	100
16	J	96/103 (93%)	91 (95%)	4 (4%)	1 (1%)	12	45
17	K	115/129 (89%)	108 (94%)	7 (6%)	0	100	100
18	L	120/124 (97%)	113 (94%)	7 (6%)	0	100	100
19	M	113/118 (96%)	108 (96%)	5 (4%)	0	100	100
20	N	98/101 (97%)	94 (96%)	4 (4%)	0	100	100
21	O	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
22	P	79/82 (96%)	70 (89%)	9 (11%)	0	100	100
23	Q	77/84 (92%)	73 (95%)	4 (5%)	0	100	100
24	R	64/75 (85%)	59 (92%)	5 (8%)	0	100	100
25	S	82/92 (89%)	80 (98%)	2 (2%)	0	100	100
26	T	84/87 (97%)	84 (100%)	0	0	100	100
27	U	68/71 (96%)	66 (97%)	2 (3%)	0	100	100
30	c	269/273 (98%)	265 (98%)	4 (2%)	0	100	100
31	d	206/209 (99%)	200 (97%)	5 (2%)	1 (0%)	24	59
32	e	199/201 (99%)	196 (98%)	3 (2%)	0	100	100
33	f	175/179 (98%)	170 (97%)	5 (3%)	0	100	100
34	g	174/177 (98%)	157 (90%)	16 (9%)	1 (1%)	21	56
35	h	39/149 (26%)	34 (87%)	5 (13%)	0	100	100
36	i	140/142 (99%)	139 (99%)	1 (1%)	0	100	100
37	j	121/123 (98%)	116 (96%)	5 (4%)	0	100	100
38	k	142/144 (99%)	139 (98%)	3 (2%)	0	100	100
39	l	132/136 (97%)	130 (98%)	2 (2%)	0	100	100
40	m	116/127 (91%)	109 (94%)	7 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	n	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
42	o	112/115 (97%)	107 (96%)	5 (4%)	0	100	100
43	p	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
44	q	101/103 (98%)	96 (95%)	5 (5%)	0	100	100
45	r	108/110 (98%)	105 (97%)	3 (3%)	0	100	100
46	s	91/100 (91%)	86 (94%)	5 (6%)	0	100	100
47	t	100/104 (96%)	93 (93%)	7 (7%)	0	100	100
48	u	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
49	v	76/85 (89%)	73 (96%)	3 (4%)	0	100	100
50	w	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
51	x	60/63 (95%)	57 (95%)	3 (5%)	0	100	100
52	y	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
53	z	54/57 (95%)	53 (98%)	1 (2%)	0	100	100
All	All	5483/5913 (93%)	5243 (96%)	235 (4%)	5 (0%)	49	79

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	C	81	GLY
31	d	149	ASN
16	J	57	VAL
34	g	47	ASP
9	C	80	LYS

### 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	0	46/49 (94%)	43 (94%)	3 (6%)	15	47
2	1	38/38 (100%)	38 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	2	51/52 (98%)	51 (100%)	0	100	100
4	3	34/34 (100%)	33 (97%)	1 (3%)	37	67
5	4	55/62 (89%)	54 (98%)	1 (2%)	51	74
8	B	186/199 (94%)	180 (97%)	6 (3%)	34	65
9	C	170/190 (90%)	166 (98%)	4 (2%)	43	70
10	D	172/173 (99%)	169 (98%)	3 (2%)	53	75
11	E	119/126 (94%)	117 (98%)	2 (2%)	53	75
12	F	90/116 (78%)	83 (92%)	7 (8%)	11	41
13	G	126/147 (86%)	116 (92%)	10 (8%)	11	40
14	H	104/105 (99%)	103 (99%)	1 (1%)	68	80
15	I	105/107 (98%)	98 (93%)	7 (7%)	15	47
16	J	86/90 (96%)	83 (96%)	3 (4%)	32	64
17	K	90/99 (91%)	86 (96%)	4 (4%)	25	59
18	L	102/103 (99%)	100 (98%)	2 (2%)	48	72
19	M	93/96 (97%)	87 (94%)	6 (6%)	15	47
20	N	83/84 (99%)	79 (95%)	4 (5%)	23	56
21	O	76/77 (99%)	76 (100%)	0	100	100
22	P	65/65 (100%)	64 (98%)	1 (2%)	57	76
23	Q	73/78 (94%)	68 (93%)	5 (7%)	14	46
24	R	57/65 (88%)	54 (95%)	3 (5%)	20	53
25	S	72/79 (91%)	71 (99%)	1 (1%)	59	77
26	T	65/66 (98%)	61 (94%)	4 (6%)	16	49
27	U	60/61 (98%)	58 (97%)	2 (3%)	33	65
30	c	216/218 (99%)	208 (96%)	8 (4%)	30	63
31	d	163/163 (100%)	157 (96%)	6 (4%)	30	63
32	e	165/165 (100%)	163 (99%)	2 (1%)	63	79
33	f	148/150 (99%)	145 (98%)	3 (2%)	48	72
34	g	137/138 (99%)	129 (94%)	8 (6%)	18	51
35	h	32/114 (28%)	32 (100%)	0	100	100
36	i	116/116 (100%)	114 (98%)	2 (2%)	53	75
37	j	104/104 (100%)	98 (94%)	6 (6%)	18	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	k	103/103 (100%)	100 (97%)	3 (3%)	37	67
39	l	107/107 (100%)	105 (98%)	2 (2%)	50	73
40	m	98/103 (95%)	96 (98%)	2 (2%)	48	72
41	n	86/87 (99%)	86 (100%)	0	100	100
42	o	99/100 (99%)	98 (99%)	1 (1%)	68	80
43	p	89/90 (99%)	88 (99%)	1 (1%)	65	79
44	q	84/84 (100%)	79 (94%)	5 (6%)	17	50
45	r	93/93 (100%)	92 (99%)	1 (1%)	65	79
46	s	80/84 (95%)	77 (96%)	3 (4%)	29	62
47	t	83/85 (98%)	81 (98%)	2 (2%)	43	70
48	u	78/78 (100%)	75 (96%)	3 (4%)	29	62
49	v	58/63 (92%)	57 (98%)	1 (2%)	53	75
50	w	67/68 (98%)	67 (100%)	0	100	100
51	x	54/55 (98%)	52 (96%)	2 (4%)	30	63
52	y	48/49 (98%)	48 (100%)	0	100	100
53	z	47/48 (98%)	45 (96%)	2 (4%)	26	59
All	All	4573/4826 (95%)	4430 (97%)	143 (3%)	36	66

5 of 143 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	k	7	SER
39	l	25	ASP
46	s	37	ASP
17	K	46	THR
16	J	100	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
47	t	45	HIS
48	u	49	ASN
52	y	20	HIS
21	O	40	GLN
17	K	119	ASN



### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
28	a	2748/2904 (94%)	324 (11%)	0
29	b	118/120 (98%)	13 (11%)	0
6	5	1/2 (50%)	1 (100%)	0
7	A	1517/1543 (98%)	310 (20%)	17 (1%)
All	All	4384/4569 (95%)	648 (14%)	17 (0%)

5 of 648 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
6	5	76	A
7	A	3	A
7	A	4	U
7	A	5	U
7	A	6	G

5 of 17 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	A	1035	A
7	A	1533	U
7	A	500	G
7	A	548	G
7	A	606	G

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

39 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
39	MS6	l	82	39	5,7,8	0.62	0	2,7,9	1.17	0
28	G7M	a	2069	28	23,26,27	0.64	0	34,39,42	0.96	1 (2%)
7	PSU	A	516	7,55	18,21,22	1.16	3 (16%)	21,30,33	2.01	5 (23%)



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
28	PSU	a	2580	28	18,21,22	1.26	4 (22%)	21,30,33	2.12	5 (23%)
7	MA6	A	1519	7	23,26,27	2.58	5 (21%)	33,38,41	2.84	7 (21%)
28	5MU	a	1939	28	19,22,23	1.33	4 (21%)	27,32,35	2.25	6 (22%)
7	5MC	A	967	7	19,22,23	1.41	2 (10%)	26,32,35	1.11	1 (3%)
28	PSU	a	2604	28	18,21,22	1.20	3 (16%)	21,30,33	2.03	4 (19%)
28	2MA	a	2503	28,55	22,25,26	1.31	4 (18%)	32,37,40	2.02	7 (21%)
31	MEQ	d	150	31	8,9,10	0.89	0	5,10,12	0.56	0
28	6MZ	a	1618	28	22,25,26	1.14	2 (9%)	29,36,39	2.28	9 (31%)
28	PSU	a	746	28,55	18,21,22	1.13	3 (16%)	21,30,33	1.94	3 (14%)
28	6MZ	a	2030	28	22,25,26	1.16	2 (9%)	29,36,39	2.37	10 (34%)
28	PSU	a	2457	28	18,21,22	1.22	4 (22%)	21,30,33	2.17	5 (23%)
28	5MU	a	747	28	19,22,23	1.33	4 (21%)	27,32,35	2.24	7 (25%)
28	OMC	a	2498	28,55	19,22,23	1.11	1 (5%)	25,31,34	1.22	2 (8%)
18	D2T	L	89	18	8,9,10	2.70	1 (12%)	6,11,13	1.43	1 (16%)
7	2MG	A	1517	7	23,26,27	0.85	1 (4%)	33,38,41	2.28	12 (36%)
28	PSU	a	2605	28	18,21,22	1.26	3 (16%)	21,30,33	2.01	4 (19%)
28	PSU	a	955	28	18,21,22	1.23	3 (16%)	21,30,33	2.03	4 (19%)
28	H2U	a	2449	28	18,21,22	0.64	0	19,30,33	1.11	1 (5%)
28	PSU	a	2504	28	18,21,22	1.14	3 (16%)	21,30,33	2.03	4 (19%)
7	2MG	A	1208	7	23,26,27	0.80	0	33,38,41	2.16	9 (27%)
28	OMU	a	2552	28	19,22,23	1.24	3 (15%)	25,31,34	1.98	6 (24%)
39	4D4	l	81	39	9,11,12	0.89	0	7,13,15	1.63	2 (28%)
7	MA6	A	1520	7	23,26,27	2.56	5 (21%)	33,38,41	2.81	7 (21%)
7	4OC	A	1403	7	20,23,24	2.35	4 (20%)	25,32,35	0.99	1 (4%)
7	UR3	A	1499	7	19,22,23	3.79	6 (31%)	26,32,35	4.61	10 (38%)
28	PSU	a	1917	28	18,21,22	1.10	2 (11%)	21,30,33	1.91	4 (19%)
28	3TD	a	1915	28	19,22,23	1.19	3 (15%)	23,32,35	1.92	3 (13%)
28	OMG	a	2251	28	23,26,27	0.85	2 (8%)	32,38,41	1.96	10 (31%)
7	5MC	A	1408	7	19,22,23	1.62	2 (10%)	26,32,35	1.10	3 (11%)
7	2MG	A	966	7	23,26,27	0.80	0	33,38,41	2.25	12 (36%)
7	G7M	A	527	7	23,26,27	0.58	0	34,39,42	0.95	2 (5%)
28	2MG	a	2445	28	23,26,27	0.93	2 (8%)	33,38,41	2.22	13 (39%)
28	2MG	a	1835	28	23,26,27	0.87	1 (4%)	33,38,41	2.30	13 (39%)
28	PSU	a	1911	28	18,21,22	1.07	3 (16%)	21,30,33	2.03	4 (19%)
28	1MG	a	745	28	23,26,27	1.13	1 (4%)	33,39,42	1.81	6 (18%)



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
28	5MC	a	1962	28	19,22,23	1.55	2 (10%)	26,32,35	1.23	3 (11%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
39	MS6	l	82	39	-	4/4/6/8	-
28	G7M	a	2069	28	-	0/7/25/26	0/3/3/3
7	PSU	A	516	7,55	-	0/7/25/26	0/2/2/2
28	PSU	a	2580	28	-	2/7/25/26	0/2/2/2
7	MA6	A	1519	7	-	0/11/29/30	0/3/3/3
28	5MU	a	1939	28	-	0/7/25/26	0/2/2/2
7	5MC	A	967	7	-	0/7/25/26	0/2/2/2
28	PSU	a	2604	28	-	0/7/25/26	0/2/2/2
28	2MA	a	2503	28,55	-	1/7/25/26	0/3/3/3
31	MEQ	d	150	31	-	2/8/9/11	-
28	6MZ	a	1618	28	-	2/9/27/28	0/3/3/3
28	PSU	a	746	28,55	-	1/7/25/26	0/2/2/2
28	6MZ	a	2030	28	-	1/9/27/28	0/3/3/3
28	PSU	a	2457	28	-	0/7/25/26	0/2/2/2
28	5MU	a	747	28	-	0/7/25/26	0/2/2/2
28	OMC	a	2498	28,55	-	0/9/27/28	0/2/2/2
18	D2T	L	89	18	-	1/7/12/14	-
7	2MG	A	1517	7	-	0/9/27/28	0/3/3/3
28	PSU	a	2605	28	-	0/7/25/26	0/2/2/2
28	PSU	a	955	28	-	0/7/25/26	0/2/2/2
28	H2U	a	2449	28	-	1/7/38/39	0/2/2/2
28	PSU	a	2504	28	-	2/7/25/26	0/2/2/2
7	2MG	A	1208	7	-	0/9/27/28	0/3/3/3
28	OMU	a	2552	28	-	2/9/27/28	0/2/2/2
39	4D4	l	81	39	-	2/11/12/14	-
7	MA6	A	1520	7	-	2/11/29/30	0/3/3/3
7	4OC	A	1403	7	-	1/9/29/30	0/2/2/2
7	UR3	A	1499	7	-	0/7/25/26	0/2/2/2
28	PSU	a	1917	28	-	0/7/25/26	0/2/2/2
28	3TD	a	1915	28	-	2/7/25/26	0/2/2/2
28	OMG	a	2251	28	-	0/9/27/28	0/3/3/3
7	5MC	A	1408	7	-	1/7/25/26	0/2/2/2

Continued on next page...



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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	2MG	A	966	7	-	2/9/27/28	0/3/3/3
7	G7M	A	527	7	-	2/7/25/26	0/3/3/3
28	2MG	a	2445	28	-	2/9/27/28	0/3/3/3
28	2MG	a	1835	28	-	2/9/27/28	0/3/3/3
28	PSU	a	1911	28	-	0/7/25/26	0/2/2/2
28	1MG	a	745	28	-	0/7/25/26	0/3/3/3
28	5MC	a	1962	28	-	0/7/25/26	0/2/2/2

The worst 5 of 88 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	1499	UR3	C2-N1	13.61	1.57	1.38
7	A	1403	4OC	O2-C2	8.31	1.39	1.23
7	A	1520	MA6	C5-N7	7.60	1.53	1.39
7	A	1519	MA6	C5-N7	7.57	1.52	1.39
18	L	89	D2T	CB-CA	-6.99	1.52	1.54

The worst 5 of 206 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	1499	UR3	C4-N3-C2	-14.64	112.80	124.58
7	A	1499	UR3	C6-N1-C2	-13.94	110.41	121.80
7	A	1519	MA6	C4-N9-C8	13.71	120.13	105.74
7	A	1520	MA6	C4-N9-C8	13.49	119.90	105.74
7	A	1499	UR3	C5-C4-N3	7.79	125.30	115.04

There are no chirality outliers.

5 of 35 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	966	2MG	O4'-C4'-C5'-O5'
7	A	1520	MA6	O4'-C4'-C5'-O5'
28	a	1915	3TD	O4'-C4'-C5'-O5'
39	l	82	MS6	CA-CB-CG-SD
7	A	527	G7M	C3'-C4'-C5'-O5'

There are no ring outliers.

9 monomers are involved in 11 short contacts:



Mol	Chain	Res	Type	Clashes	Symm-Clashes
28	a	2503	2MA	1	0
31	d	150	MEQ	1	0
28	a	2030	6MZ	3	0
18	L	89	D2T	1	0
28	a	955	PSU	1	0
7	A	1403	4OC	1	0
28	a	1915	3TD	1	0
28	a	2251	OMG	1	0
28	a	2445	2MG	1	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 327 ligands modelled in this entry, 310 are monoatomic - leaving 17 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
56	SPD	a	6208	-	9,9,9	0.25	0	8,8,8	0.26	0
57	SPM	a	6221	-	13,13,13	0.35	0	12,12,12	0.94	0
56	SPD	a	6214	-	9,9,9	0.28	0	8,8,8	0.24	0
56	SPD	a	6215	-	9,9,9	0.27	0	8,8,8	0.31	0
56	SPD	a	6210	-	9,9,9	0.27	0	8,8,8	0.30	0
56	SPD	a	6209	-	9,9,9	0.25	0	8,8,8	0.21	0
56	SPD	a	6216	-	9,9,9	0.29	0	8,8,8	0.31	0
56	SPD	a	6220	-	9,9,9	0.28	0	8,8,8	0.32	0
56	SPD	a	6218	-	9,9,9	0.26	0	8,8,8	0.43	0
56	SPD	a	6219	-	9,9,9	0.27	0	8,8,8	0.34	0
56	SPD	a	6213	-	9,9,9	0.25	0	8,8,8	0.26	0
56	SPD	A	1692	7	9,9,9	0.26	0	8,8,8	0.19	0
56	SPD	a	6212	-	9,9,9	0.28	0	8,8,8	0.29	0
56	SPD	a	6211	-	9,9,9	0.25	0	8,8,8	0.22	0
56	SPD	A	1691	-	9,9,9	0.25	0	8,8,8	0.26	0



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
56	SPD	a	6217	-	9,9,9	0.25	0	8,8,8	0.25	0
56	SPD	a	6207	-	9,9,9	0.28	0	8,8,8	0.23	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
56	SPD	a	6208	-	-	3/7/7/7	-
57	SPM	a	6221	-	-	2/11/11/11	-
56	SPD	a	6214	-	-	3/7/7/7	-
56	SPD	a	6215	-	-	4/7/7/7	-
56	SPD	a	6210	-	-	1/7/7/7	-
56	SPD	a	6209	-	-	2/7/7/7	-
56	SPD	a	6216	-	-	3/7/7/7	-
56	SPD	a	6220	-	-	1/7/7/7	-
56	SPD	a	6218	-	-	6/7/7/7	-
56	SPD	a	6219	-	-	1/7/7/7	-
56	SPD	a	6213	-	-	0/7/7/7	-
56	SPD	A	1692	7	-	2/7/7/7	-
56	SPD	a	6212	-	-	2/7/7/7	-
56	SPD	a	6211	-	-	4/7/7/7	-
56	SPD	A	1691	-	-	2/7/7/7	-
56	SPD	a	6217	-	-	2/7/7/7	-
56	SPD	a	6207	-	-	4/7/7/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 42 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
56	A	1691	SPD	C3-C4-C5-N6
56	a	6207	SPD	C3-C4-C5-N6
56	a	6207	SPD	N6-C7-C8-C9
56	a	6208	SPD	N6-C7-C8-C9
56	a	6216	SPD	C3-C4-C5-N6



There are no ring outliers.

10 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
56	a	6208	SPD	3	0
57	a	6221	SPM	1	0
56	a	6214	SPD	3	0
56	a	6215	SPD	1	0
56	a	6216	SPD	1	0
56	a	6218	SPD	2	0
56	a	6212	SPD	1	0
56	a	6211	SPD	2	0
56	A	1691	SPD	2	0
56	a	6217	SPD	2	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
7	A	3
28	a	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	a	1914:C	O3'	1915:3TD	P	4.24
1	A	1402:G	O3'	1403:4OC	P	2.92
1	A	1498:G	O3'	1499:UR3	P	2.91
1	A	1518:G	O3'	1519:MA6	P	2.83



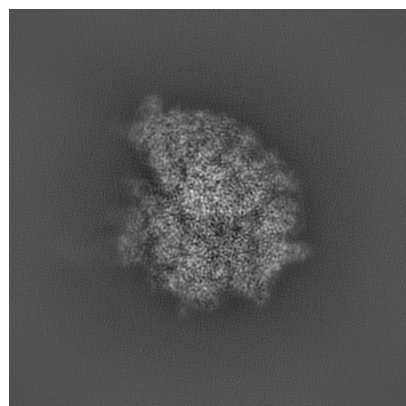
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-75650. These allow visual inspection of the internal detail of the map and identification of artifacts.

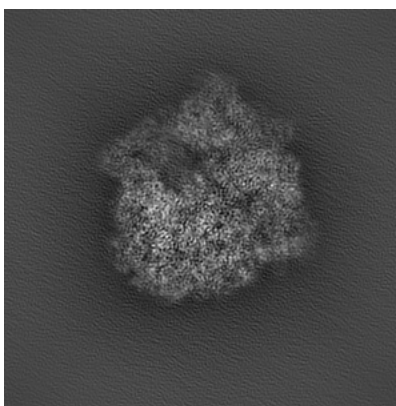
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

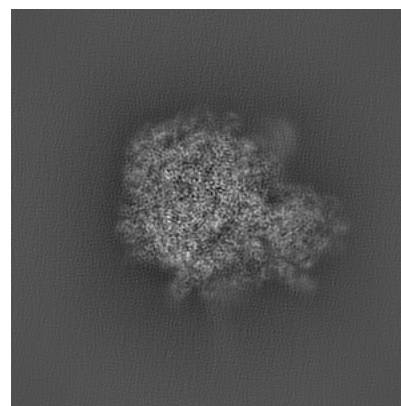
#### 6.1.1 Primary map



X

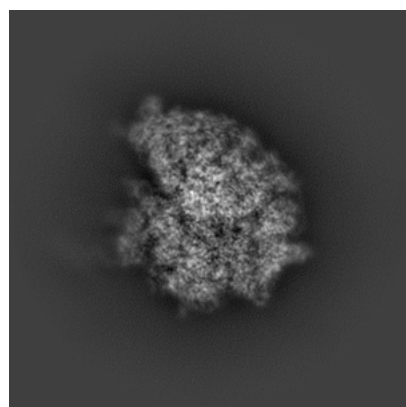


Y

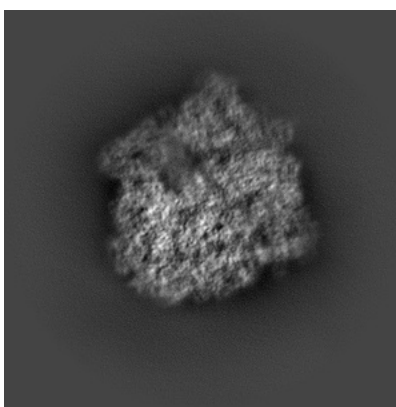


Z

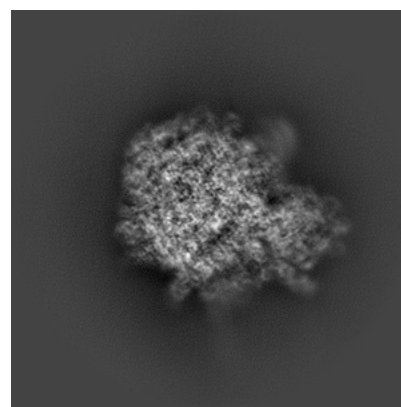
#### 6.1.2 Raw map



X



Y



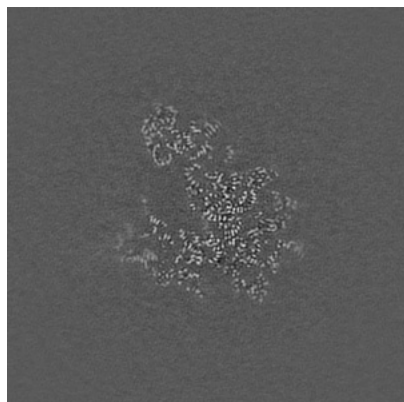
Z

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

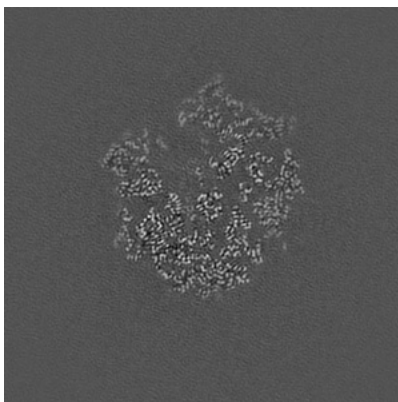


## 6.2 Central slices [i](#)

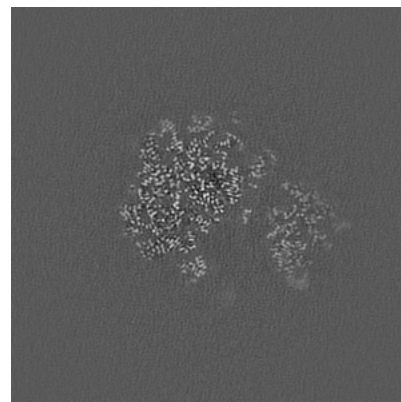
### 6.2.1 Primary map



X Index: 256

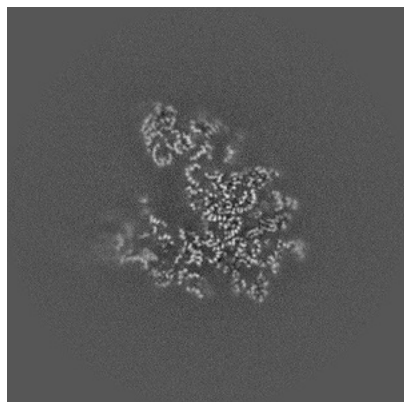


Y Index: 256

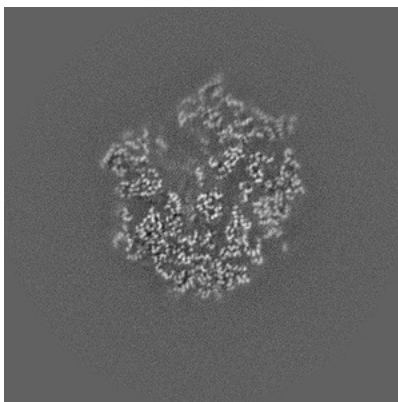


Z Index: 256

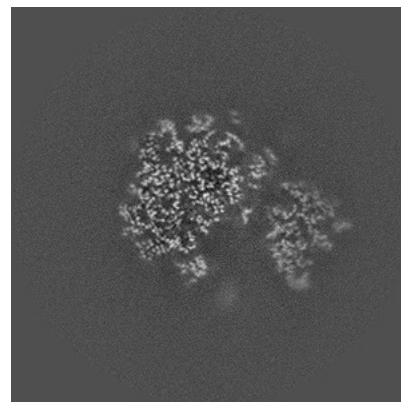
### 6.2.2 Raw map



X Index: 256



Y Index: 256



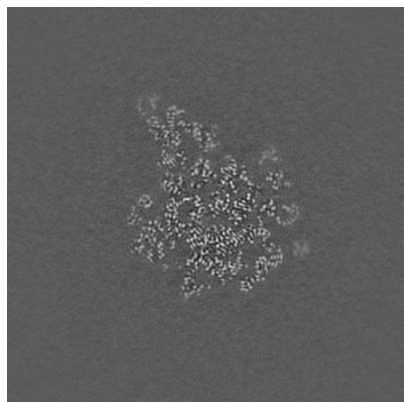
Z Index: 256

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

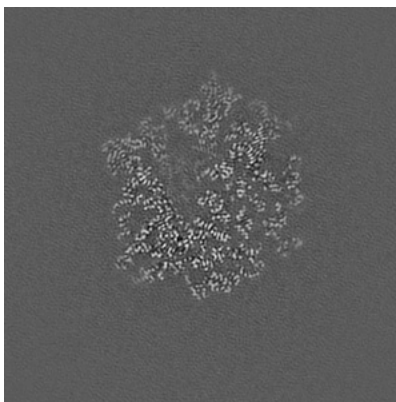


## 6.3 Largest variance slices [i](#)

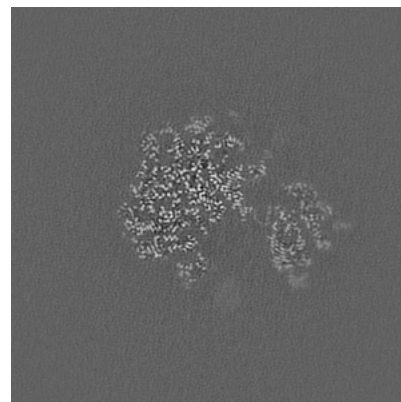
### 6.3.1 Primary map



X Index: 234

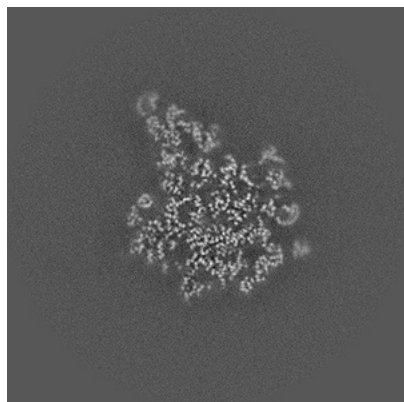


Y Index: 247

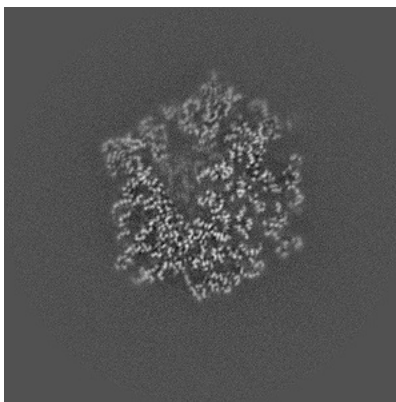


Z Index: 253

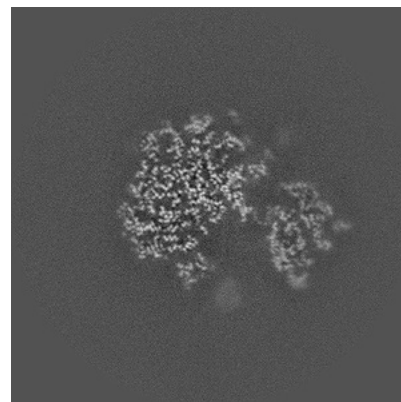
### 6.3.2 Raw map



X Index: 234



Y Index: 247



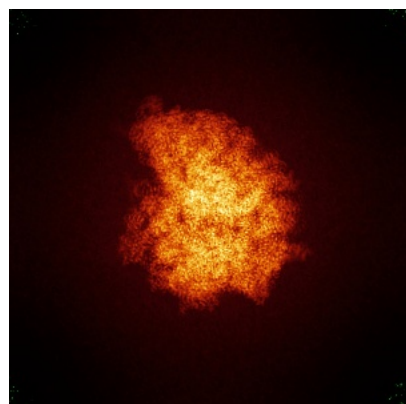
Z Index: 253

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

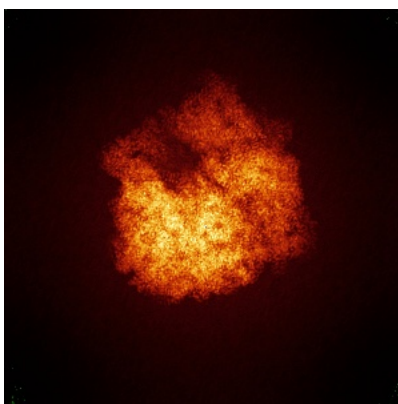


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

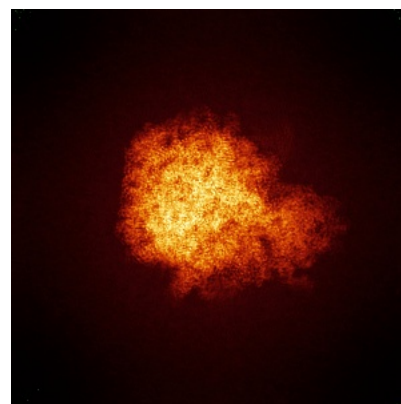
### 6.4.1 Primary map



X

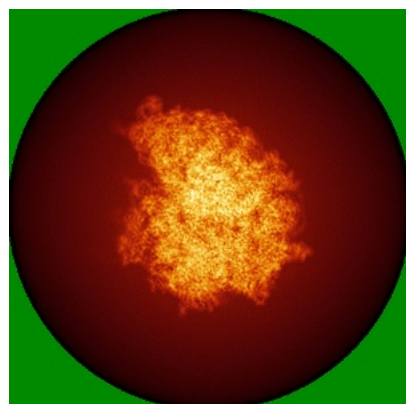


Y

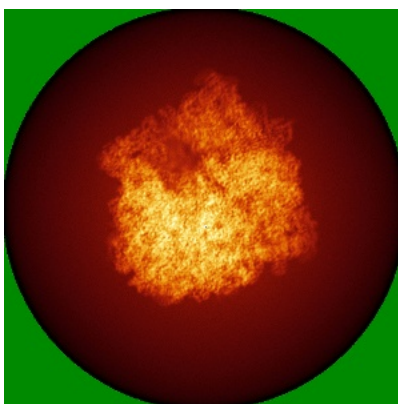


Z

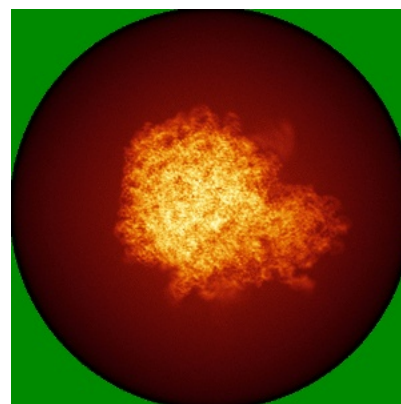
### 6.4.2 Raw map



X



Y



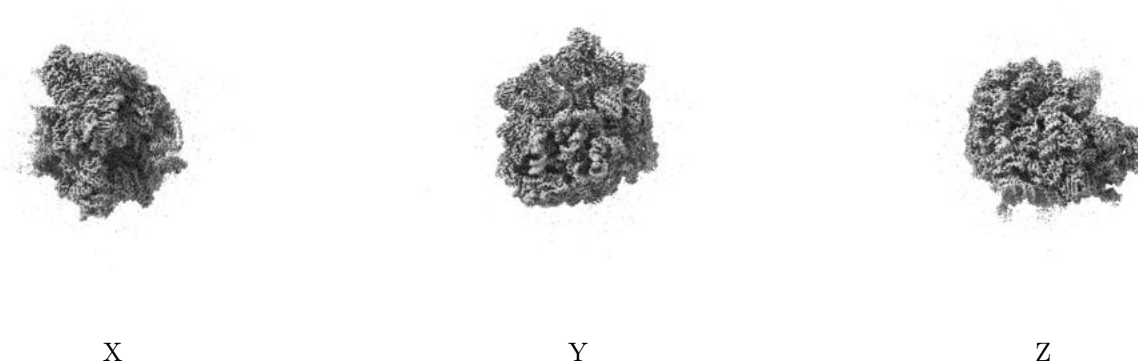
Z

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.



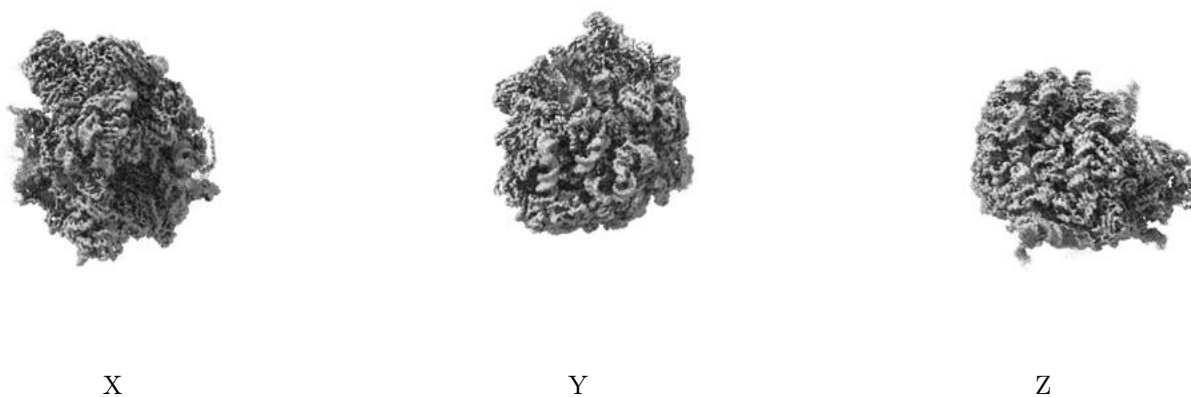
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



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

## 6.6 Mask visualisation [i](#)

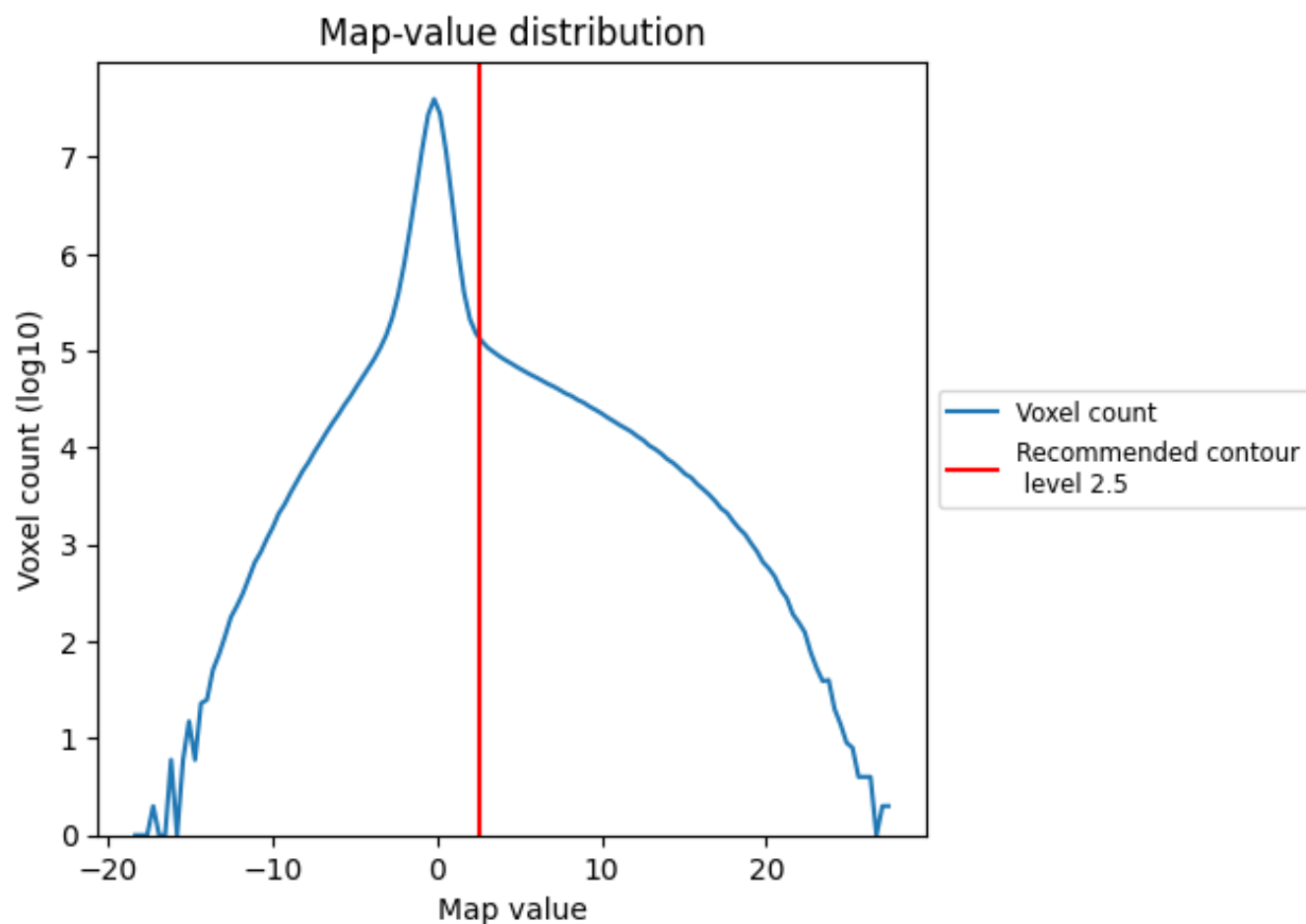
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

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

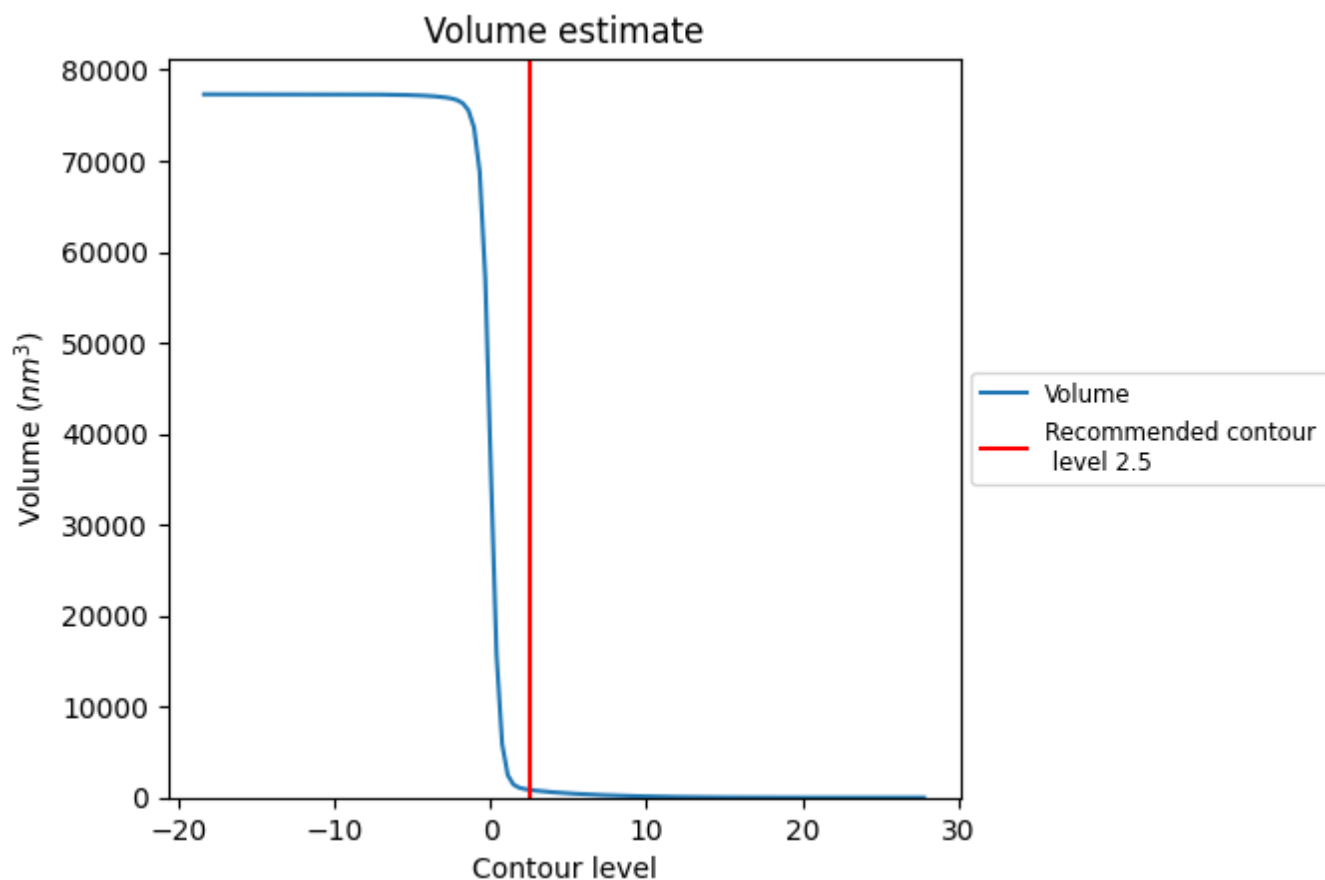
### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.



## 7.2 Volume estimate [i](#)

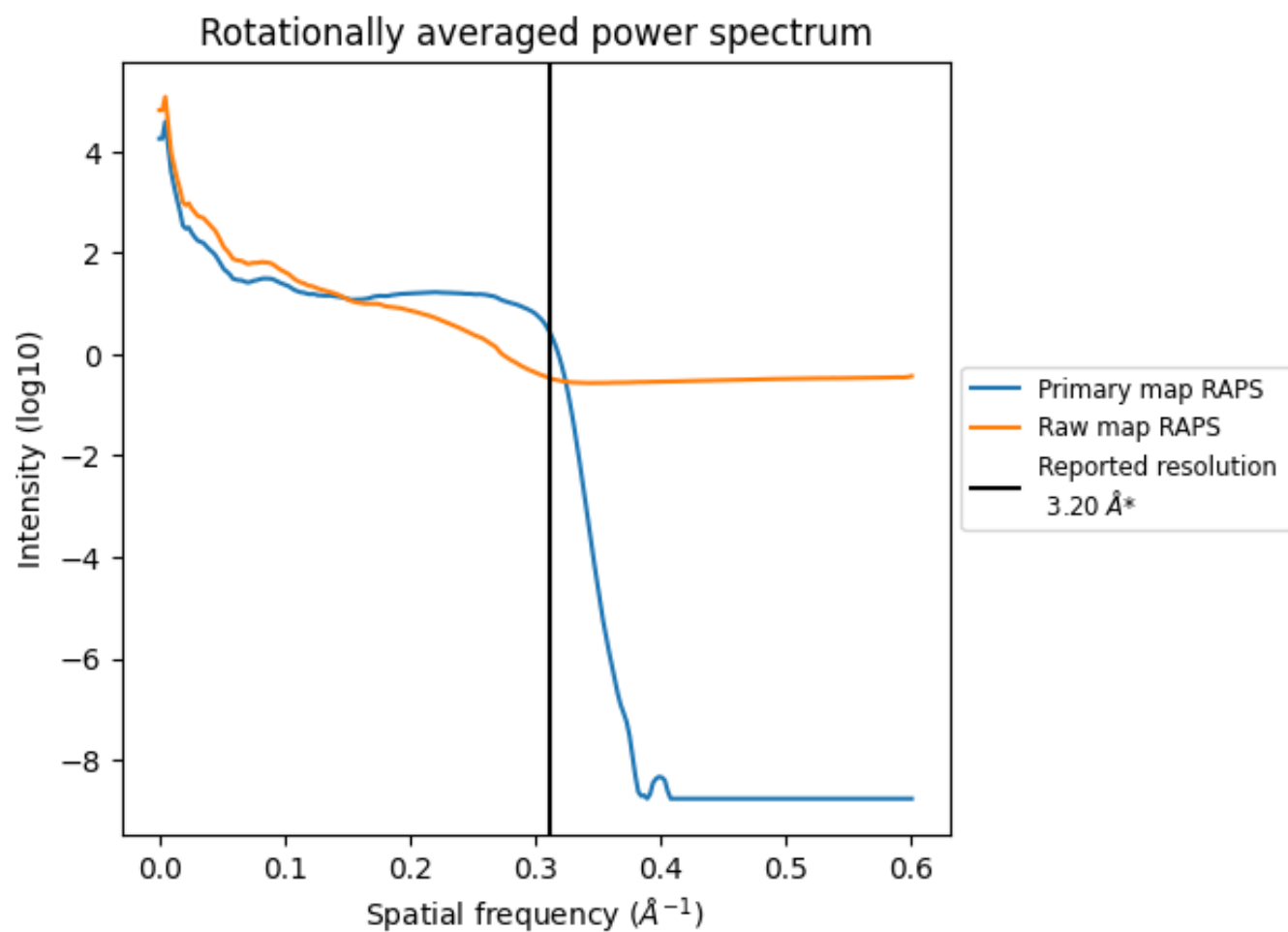


The volume at the recommended contour level is 852 nm<sup>3</sup>; this corresponds to an approximate mass of 769 kDa.

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 ⓘ



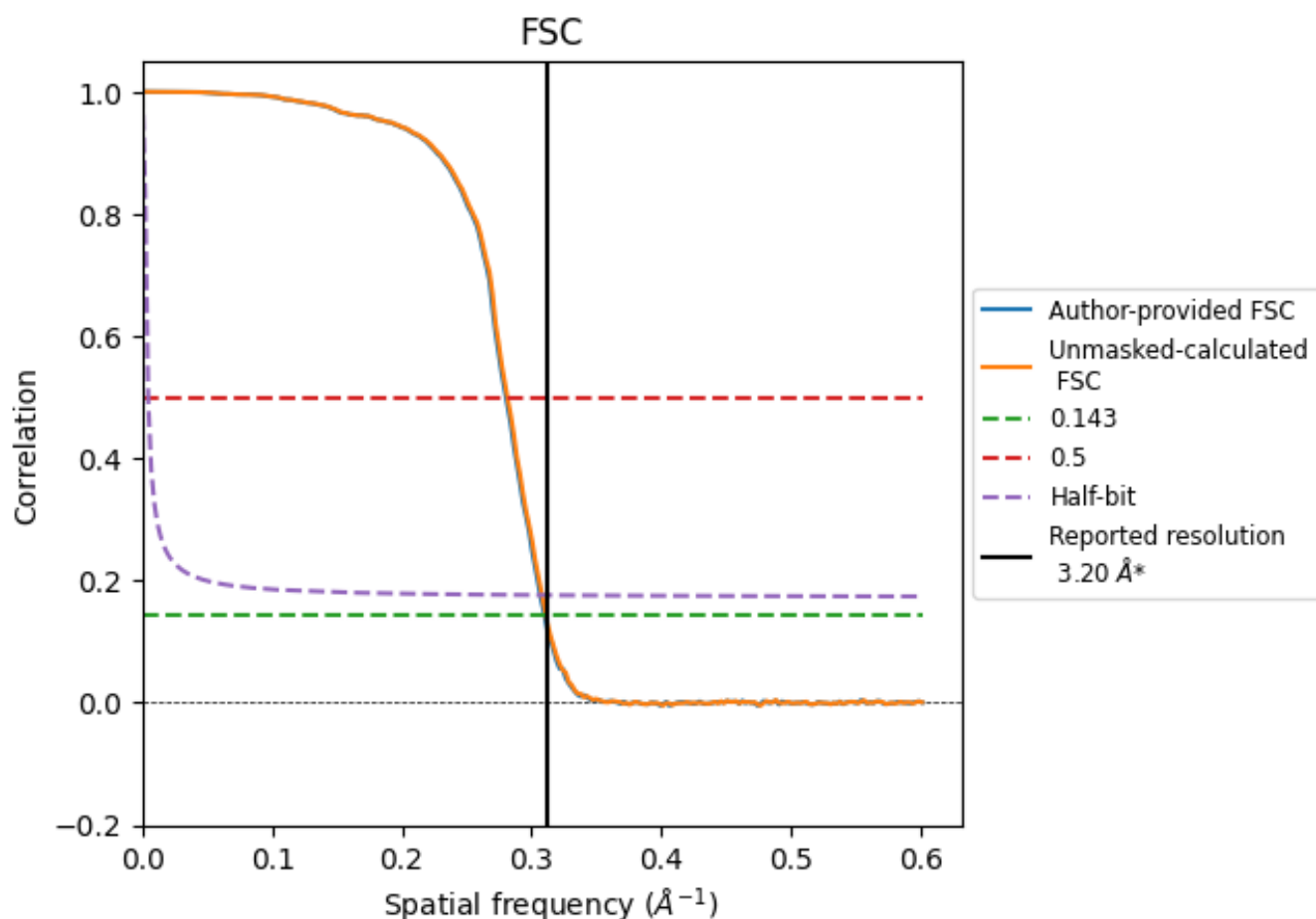
\*Reported resolution corresponds to spatial frequency of 0.312 Å<sup>-1</sup>



## 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 0.312 Å<sup>-1</sup>



## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.23	3.57	3.26
Unmasked-calculated*	3.21	3.55	3.25

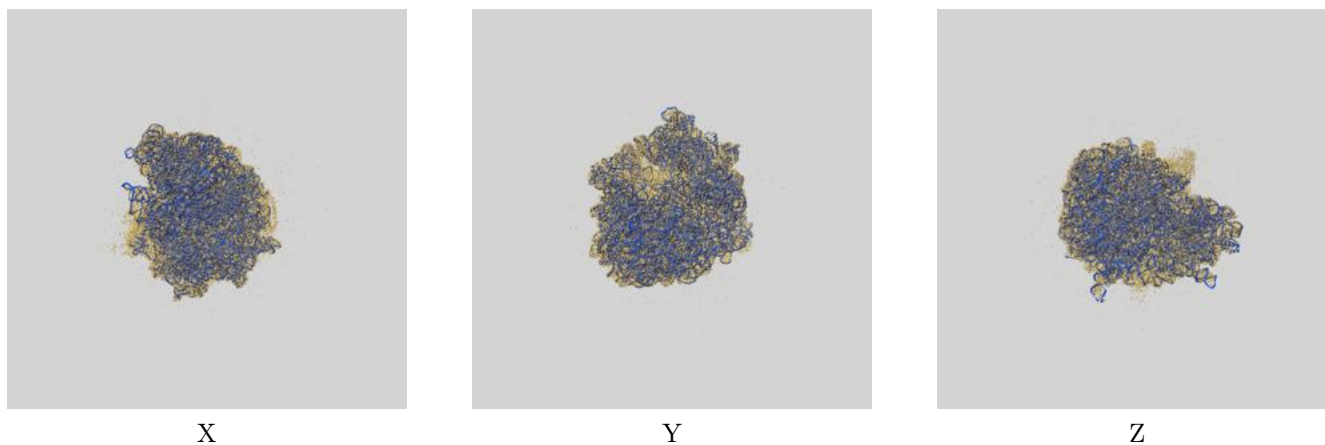
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.



## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-75650 and PDB model 11EL. Per-residue inclusion information can be found in section [3](#) on page [16](#).

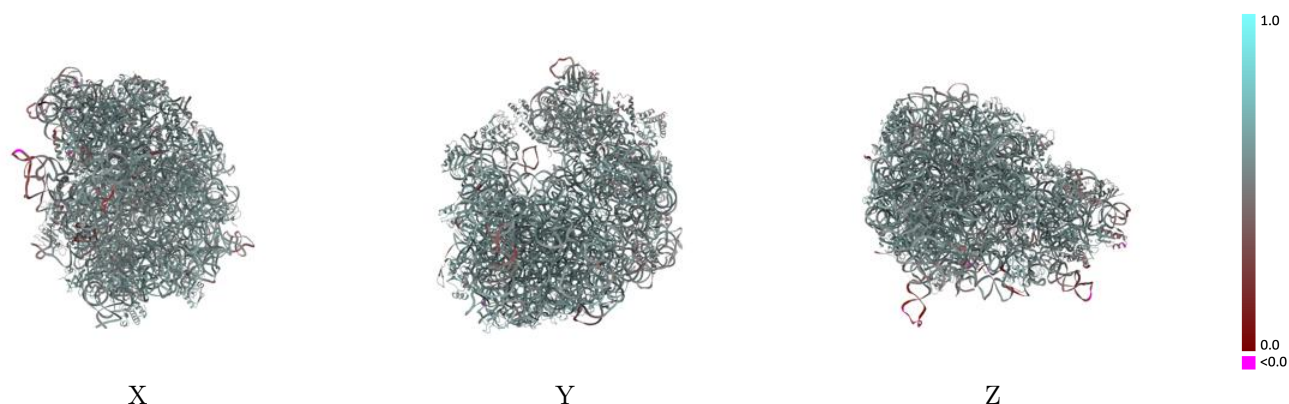
### 9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 2.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

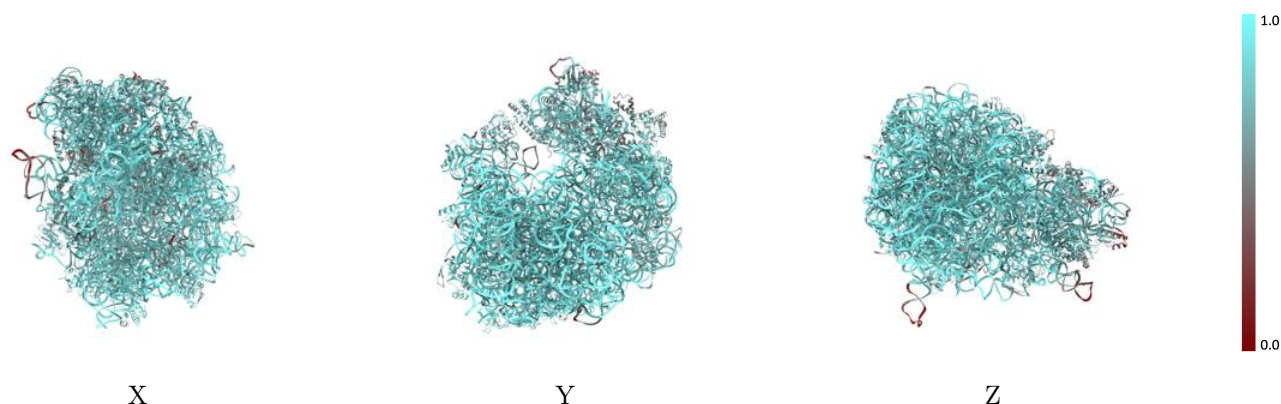


## 9.2 Q-score mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

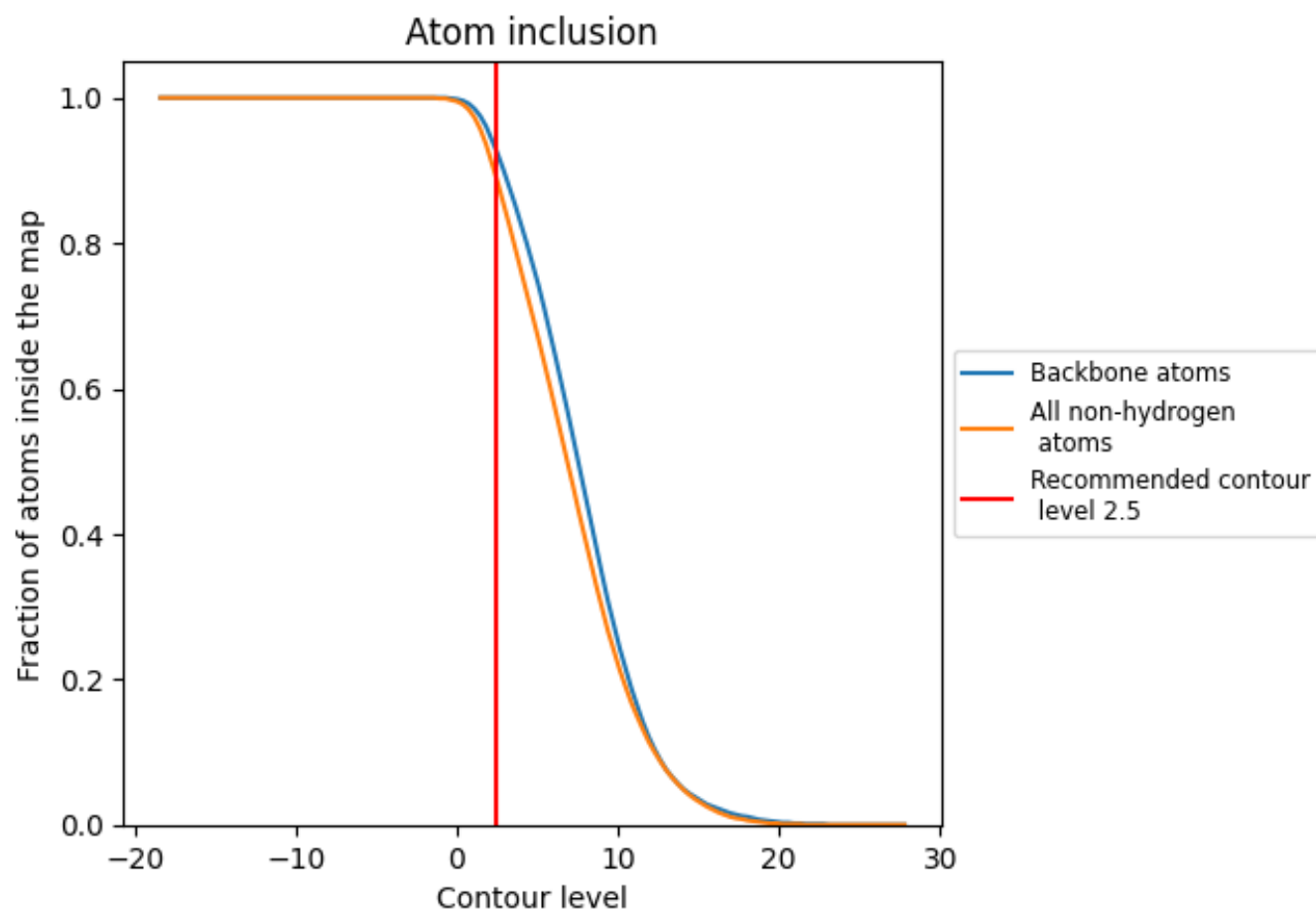
## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (2.5).



## 9.4 Atom inclusion [i](#)









































































At the recommended contour level, 92% of all backbone atoms, 89% 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 (2.5) and Q-score for the entire model and for each chain.







































Chain	Atom inclusion	Q-score
All	 0.8870	 0.5560
0	 0.6410	 0.5560
1	 0.9010	 0.5960
2	 0.9080	 0.6030
3	 0.8980	 0.6060
4	 0.7060	 0.5010
5	 0.0950	 0.4890
A	 0.8930	 0.5350
B	 0.6420	 0.5180
C	 0.7500	 0.5470
D	 0.7570	 0.5480
E	 0.8580	 0.5740
F	 0.8200	 0.5440
G	 0.6670	 0.5000
H	 0.8440	 0.5760
I	 0.6920	 0.5260
J	 0.5860	 0.4920
K	 0.8430	 0.5570
L	 0.8840	 0.5780
M	 0.7650	 0.5410
N	 0.7470	 0.5370
O	 0.8590	 0.5700
P	 0.6840	 0.4320
Q	 0.8160	 0.5460
R	 0.8300	 0.5520
S	 0.7640	 0.5240
T	 0.8260	 0.5500
U	 0.5080	 0.4940
a	 0.9370	 0.5660
b	 0.9170	 0.5490
c	 0.9250	 0.5990
d	 0.9050	 0.5950
e	 0.8200	 0.5700
f	 0.7500	 0.5370
g	 0.7800	 0.5310



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*Continued from previous page...*

Chain	Atom inclusion	Q-score
h	 0.7370	 0.5180
i	 0.9050	 0.5950
j	 0.9010	 0.5910
k	 0.8790	 0.5830
l	 0.8880	 0.5840
m	 0.9010	 0.5920
n	 0.8300	 0.5670
o	 0.8910	 0.5960
p	 0.8930	 0.5910
q	 0.8700	 0.5930
r	 0.8640	 0.5840
s	 0.8410	 0.5700
t	 0.8200	 0.5700
u	 0.8540	 0.5800
v	 0.9000	 0.5910
w	 0.8950	 0.5860
x	 0.7950	 0.5500
y	 0.8580	 0.5820
z	 0.8880	 0.5870