



wwPDB EM Validation Summary Report ⓘ

Sep 16, 2026 – 04:31 PM EDT

PDB ID : 8FZF / pdb_00008fzf
EMDB ID : EMD-29624
Title : Cryo-EM structure of an E. coli rotated ribosome complex bound with RF3-ppGpp and p/E-tRNAPhe (Composite state I-C)
Authors : Rybak, M.Y.; Li, L.; Lin, J.; Gagnon, M.G.
Deposited on : 2023-01-28
Resolution : 3.20 Å(reported)
Based on initial model : 7K00

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.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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) : 2.50

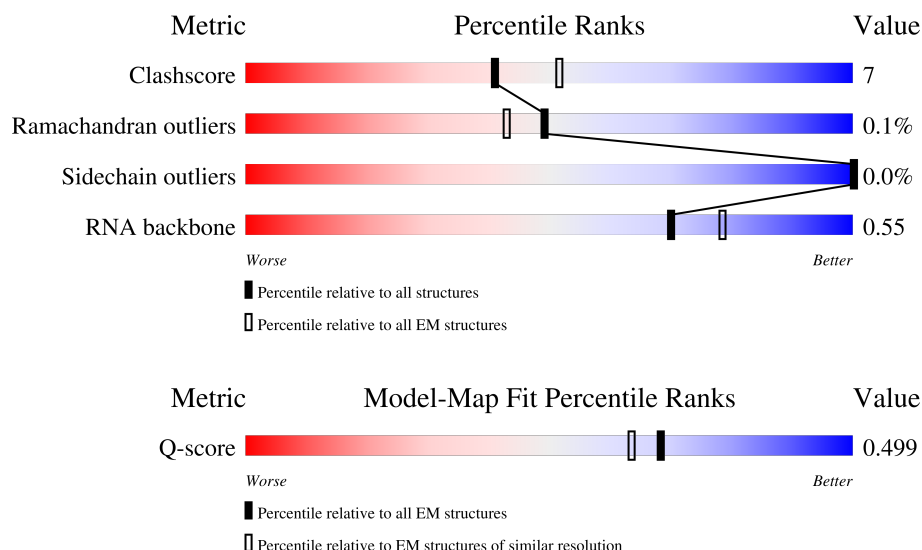
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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 ≥ 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	a	1542	
2	b	241	
3	c	233	

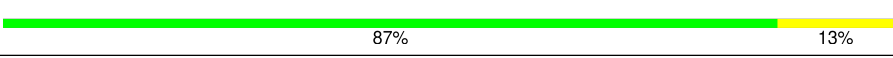
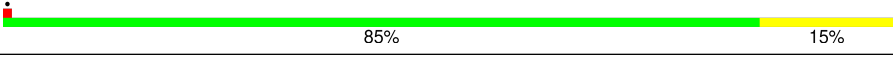
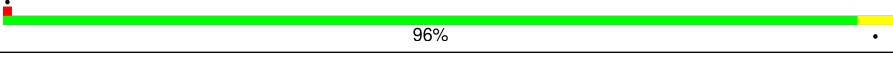
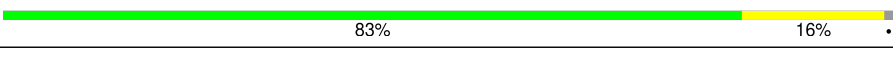
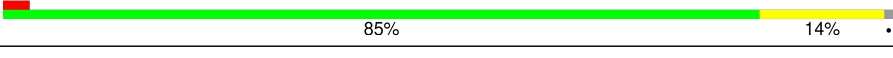
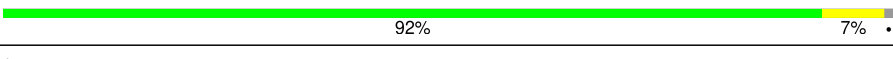
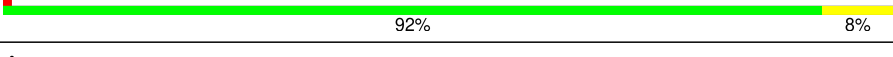
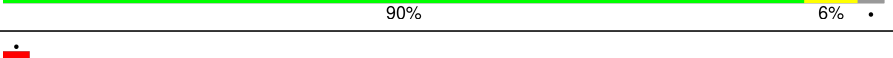
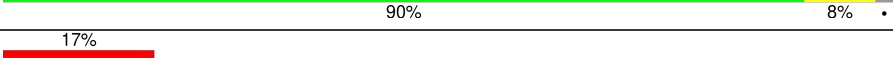
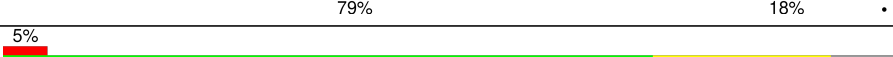
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Mol	Chain	Length	Quality of chain
4	d	206	
5	e	167	
6	f	131	
7	g	156	
8	h	130	
9	i	130	
10	j	103	
11	k	129	
12	l	124	
13	m	118	
14	n	101	
15	o	89	
16	p	82	
17	q	84	
18	r	75	
19	s	92	
20	t	87	
21	u	71	
22	x	76	
23	z	21	
24	v	529	
25	A	2904	
26	B	120	
27	C	273	
28	D	209	

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Mol	Chain	Length	Quality of chain
29	E	201	
30	F	179	
31	G	177	
32	I	165	
33	J	142	
34	L	142	
35	M	123	
36	N	144	
37	O	136	
38	P	127	
39	Q	117	
40	R	115	
41	S	118	
42	T	103	
43	U	110	
44	V	100	
45	W	104	
46	X	94	
47	Y	85	
48	Z	78	
49	1	63	
50	2	59	
51	3	70	
52	4	57	
53	5	55	

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Mol	Chain	Length	Quality of chain
54	6	46	96% .
55	7	65	82% 15%..
56	8	38	82% 18%

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 148897 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 16S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	1528	Total	C	N	O	P	0	0
			32803	14637	6019	10619	1528		

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	b	224	Total	C	N	O	S	0	0
			1754	1110	315	321	8		

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	g	152	Total	C	N	O	S	0	0
			1191	741	230	216	4		

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

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

- Molecule 9 is a protein called Small ribosomal subunit protein uS9.

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	k	117	Total	C	N	O	S	0	0
			877	540	173	161	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	119	IAS	ASN	conflict	UNP A0A0H3PWX2

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	l	121	Total	C	N	O	S	0	0
			942	582	193	162	5		

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

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

- Molecule 14 is a protein called Small ribosomal subunit protein uS14.

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

- Molecule 15 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 16 is a protein called 30S ribosomal protein S16.

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

- Molecule 17 is a protein called Small ribosomal subunit protein uS17.

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

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	r	54	Total	C	N	O	0	0
			446	283	85	78		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	s	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 20 is a protein called 30S ribosomal protein S20.

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

- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	u	55	Total	C	N	O	S	0	0
			460	287	95	77	1		

- Molecule 22 is a RNA chain called p/E phenylalanyl-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace	
22	x	74	Total	C	N	O	P	S	0	0
			1588	713	285	515	73	2		

- Molecule 23 is a RNA chain called F-UAA mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	z	8	Total	C	N	O	P	0	0
			168	76	29	55	8		

- Molecule 24 is a protein called Peptide chain release factor RF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	v	493	Total	C	N	O	S	0	0
			3897	2471	671	735	20		

- Molecule 25 is a RNA chain called 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	A	2899	Total	C	N	O	P	0	0
			62252	27778	11456	20119	2899		

- Molecule 26 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	B	120	Total	C	N	O	P	0	0
			2572	1145	470	837	120		

- Molecule 27 is a protein called 50S ribosomal protein L2.

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

- Molecule 28 is a protein called 50S ribosomal protein L3.

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

- Molecule 29 is a protein called 50S ribosomal protein L4.

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

- Molecule 30 is a protein called 50S ribosomal protein L5.

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

- Molecule 31 is a protein called 50S ribosomal protein L6.

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

- Molecule 32 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	I	131	Total	C	N	O	S	0	0
			988	625	175	183	5		

- Molecule 33 is a protein called 50S ribosomal protein L11.

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

- Molecule 34 is a protein called 50S ribosomal protein L13.

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

- Molecule 35 is a protein called 50S ribosomal protein L14.

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

- Molecule 36 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	N	144	Total	C	N	O	S	0	0
			1052	653	207	190	2		

- Molecule 37 is a protein called 50S ribosomal protein L16.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	82	MS6	MET	conflict	UNP E6BI61

- Molecule 38 is a protein called Large ribosomal subunit protein bL17.

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

- Molecule 39 is a protein called 50S ribosomal protein L18.

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

- Molecule 40 is a protein called 50S ribosomal protein L19.

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

- Molecule 41 is a protein called 50S ribosomal protein L20.

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

- Molecule 42 is a protein called Ribosomal protein L21.

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

- Molecule 43 is a protein called 50S ribosomal protein L22.

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

- Molecule 44 is a protein called 50S ribosomal protein L23.

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

- Molecule 45 is a protein called 50S ribosomal protein L24.

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

- Molecule 46 is a protein called 50S ribosomal protein L25.

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

- Molecule 47 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Y	76	Total	C	N	O	S	0	0
			582	360	117	104	1		

- Molecule 48 is a protein called 50S ribosomal protein L28.

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

- Molecule 49 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	1	61	Total	C	N	O	S	0	0
			495	305	97	92	1		

- Molecule 50 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	2	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 51 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	3	48	Total	C	N	O	S	0	0
			373	232	66	69	6		

- Molecule 52 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	4	55	Total	C	N	O	S	0	0
			434	263	92	78	1		

- Molecule 53 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	5	51	Total	C	N	O	0	0
			417	269	76	72		

- Molecule 54 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	6	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 55 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	7	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

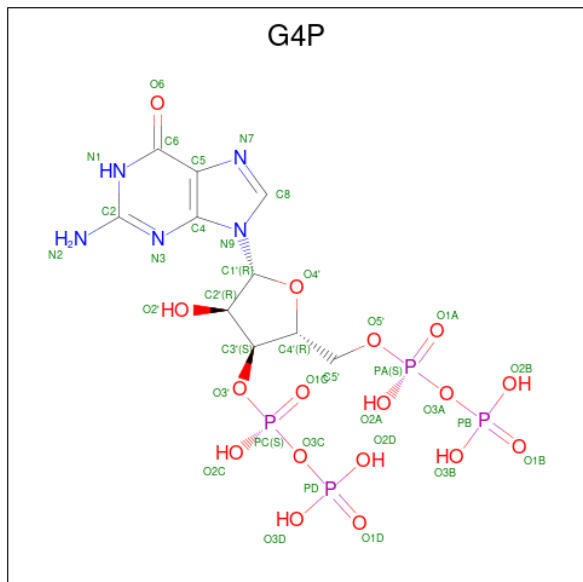
- Molecule 56 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	8	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 57 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
57	a	51	Total	Mg	0
			51	51	
57	x	1	Total	Mg	0
			1	1	
57	A	315	Total	Mg	0
			315	315	
57	B	9	Total	Mg	0
			9	9	
57	C	1	Total	Mg	0
			1	1	
57	D	1	Total	Mg	0
			1	1	
57	E	1	Total	Mg	0
			1	1	
57	P	1	Total	Mg	0
			1	1	
57	S	1	Total	Mg	0
			1	1	
57	4	1	Total	Mg	0
			1	1	
57	6	1	Total	Mg	0
			1	1	
57	7	1	Total	Mg	0
			1	1	

- Molecule 58 is GUANOSINE-5',3'-TETRAPHOSPHATE (CCD ID: G4P) (formula: $C_{10}H_{17}N_5O_{17}P_4$).



Mol	Chain	Residues	Atoms					AltConf
58	v	1	Total	C	N	O	P	0
			36	10	5	17	4	

- Molecule 59 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
59	3	1	Total	Zn	0
			1	1	
59	8	1	Total	Zn	0
			1	1	

- Molecule 60 is water.

Mol	Chain	Residues	Atoms		AltConf
60	a	6	Total	O	0
			6	6	
60	k	1	Total	O	0
			1	1	
60	x	1	Total	O	0
			1	1	
60	A	85	Total	O	0
			85	85	
60	B	2	Total	O	0
			2	2	

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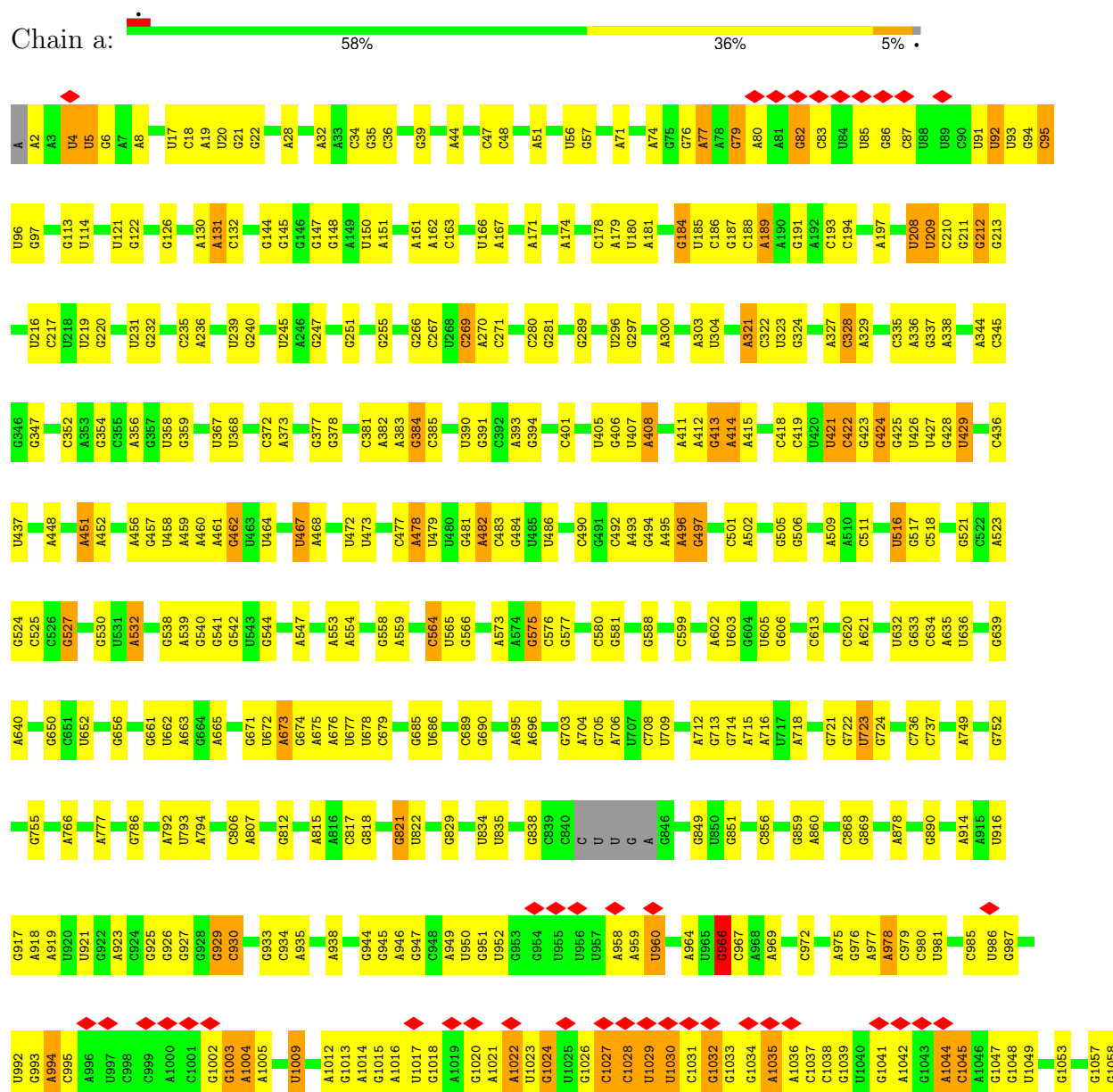
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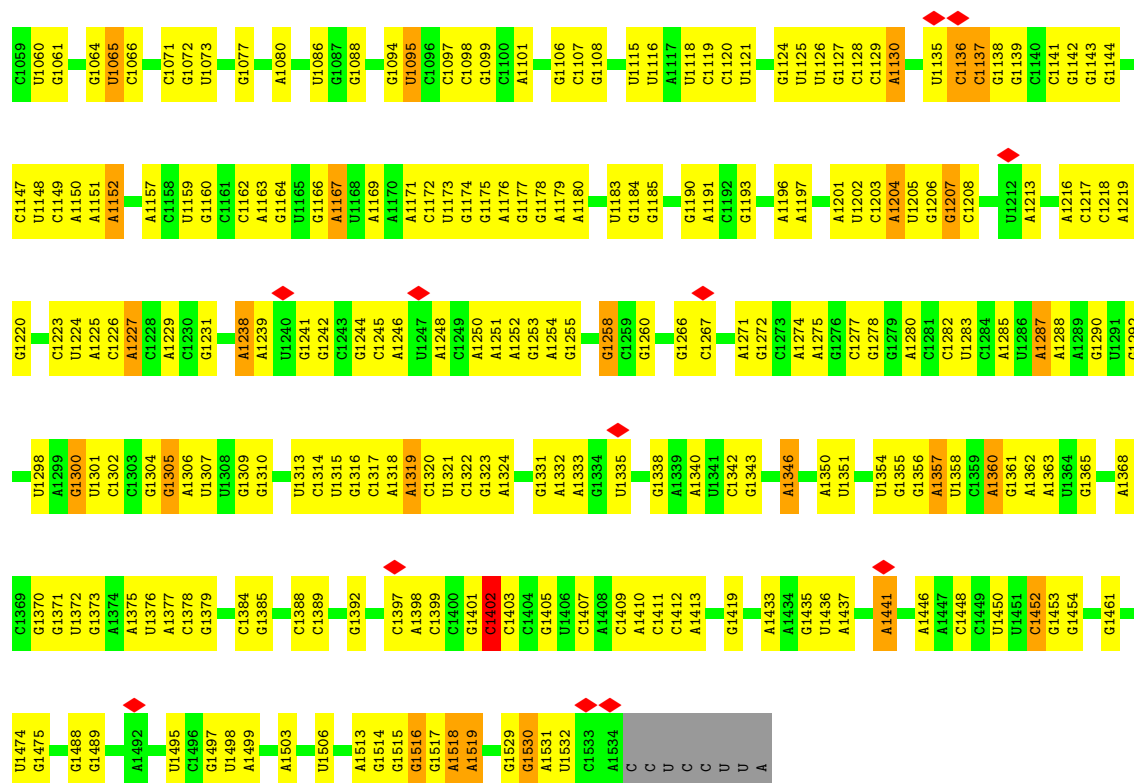
Mol	Chain	Residues	Atoms		AltConf
60	C	1	Total	O	0
			1	1	

3 Residue-property plots

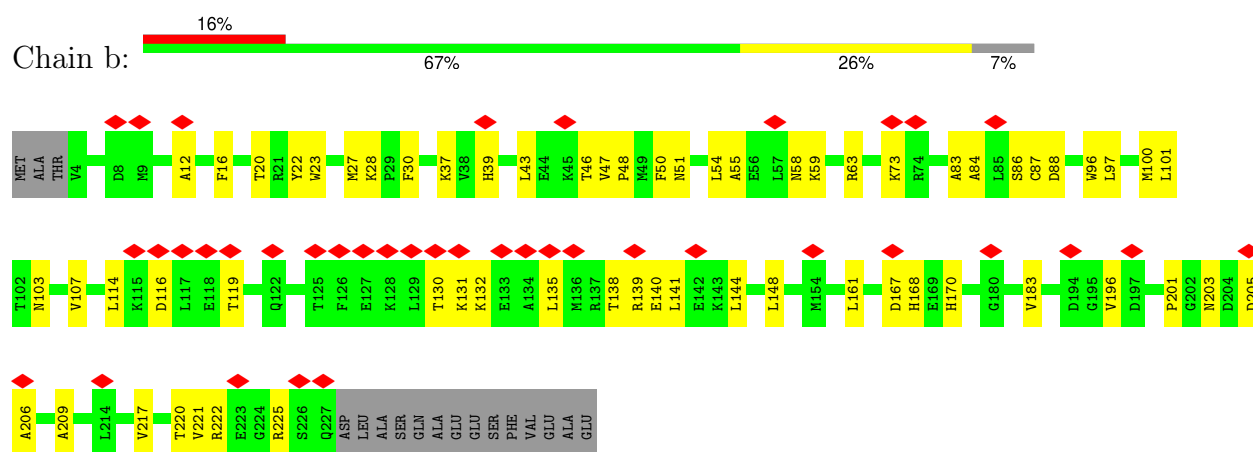
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 16S Ribosomal RNA

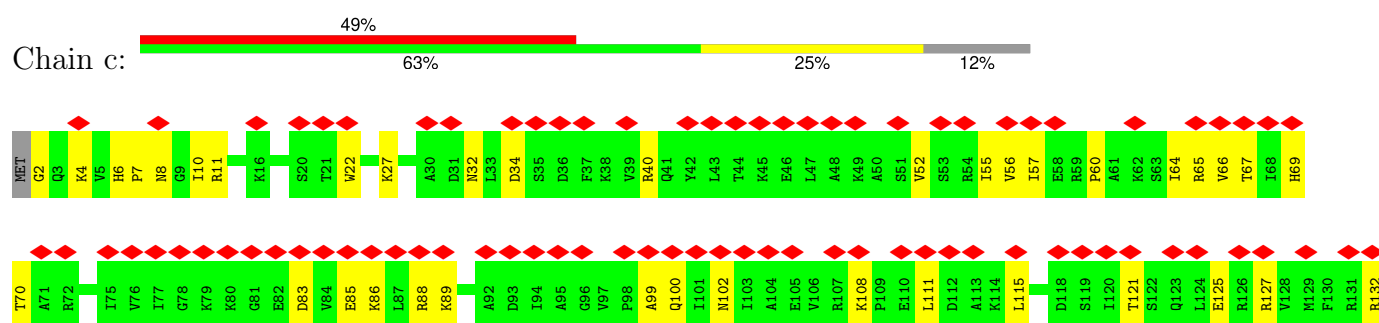


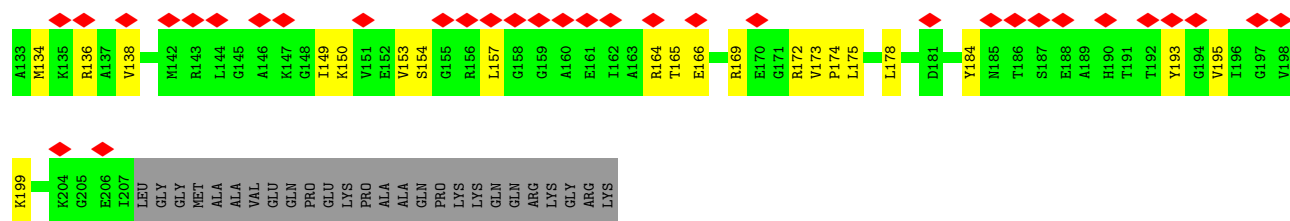


• Molecule 2: 30S ribosomal protein S2

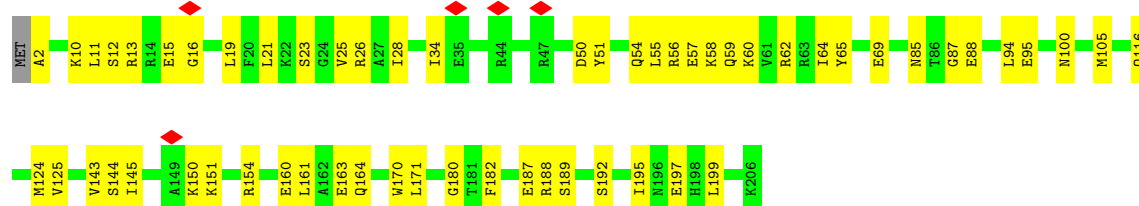


• Molecule 3: 30S ribosomal protein S3





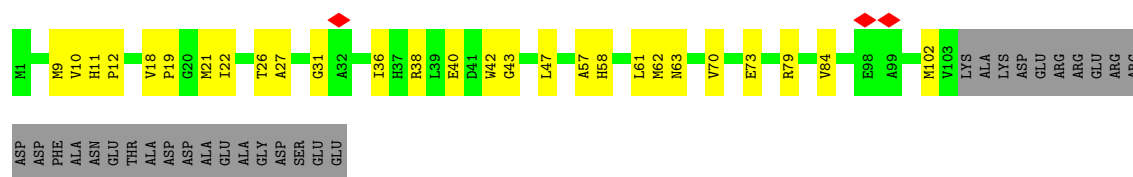
• Molecule 4: 30S ribosomal protein S4



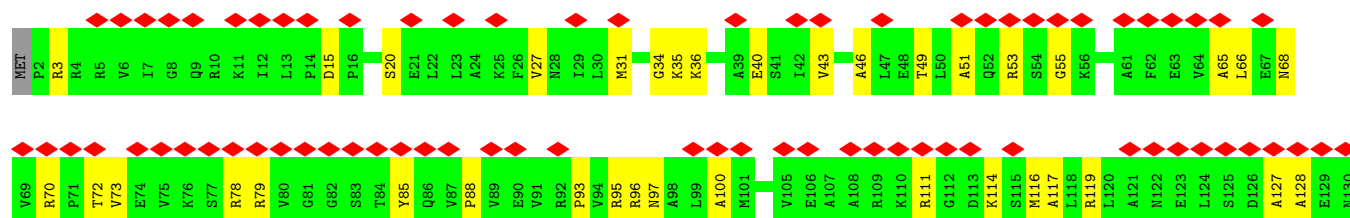
• Molecule 5: 30S ribosomal protein S5



• Molecule 6: 30S ribosomal protein S6

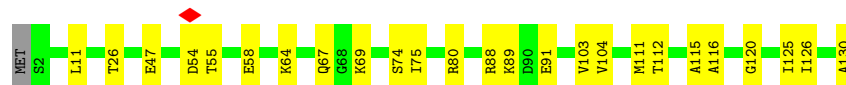
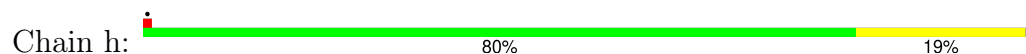


• Molecule 7: 30S ribosomal protein S7

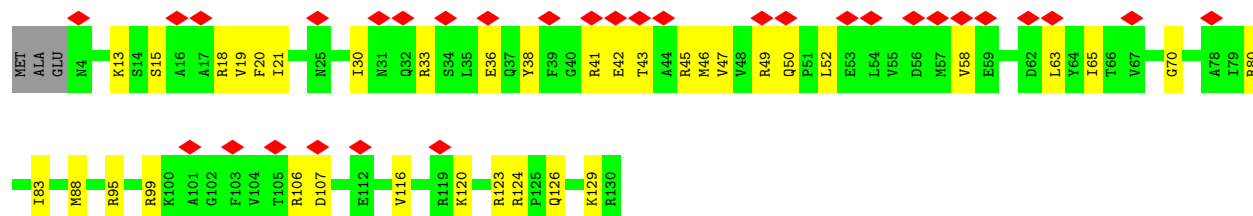




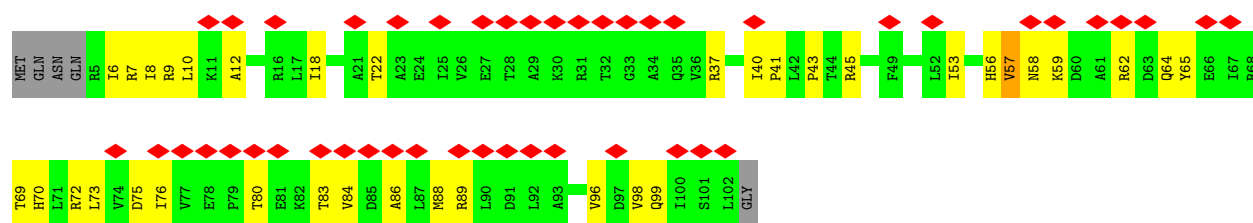
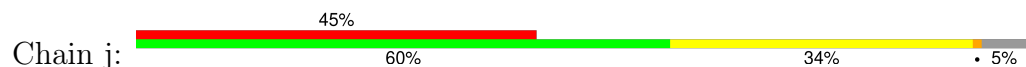
- Molecule 8: 30S ribosomal protein S8



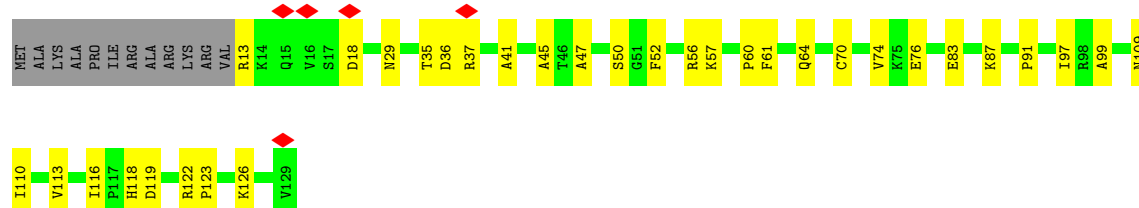
- Molecule 9: Small ribosomal subunit protein uS9



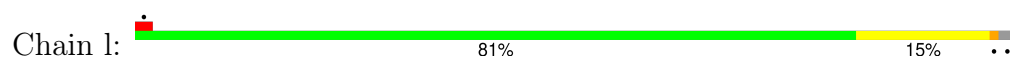
- Molecule 10: 30S ribosomal protein S10

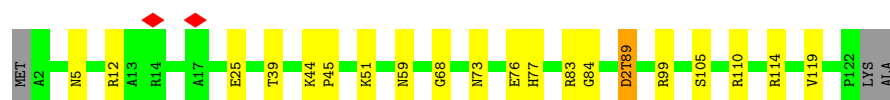


- Molecule 11: 30S ribosomal protein S11

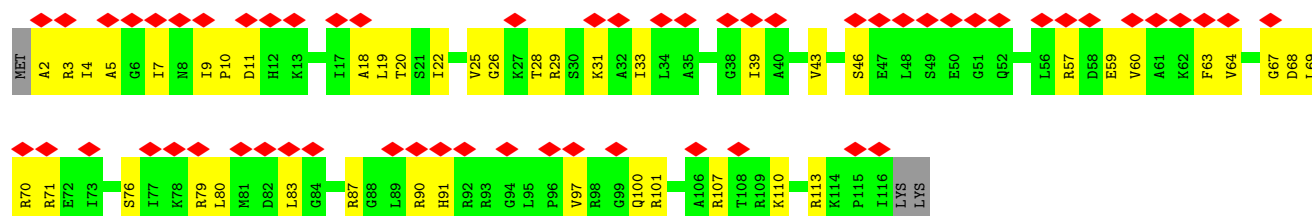


- Molecule 12: 30S ribosomal protein S12

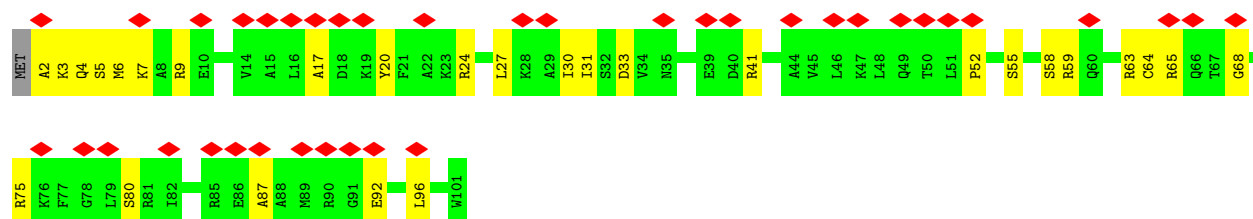




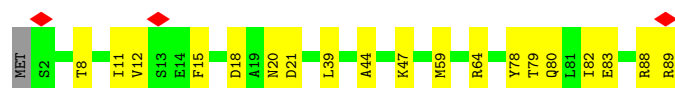
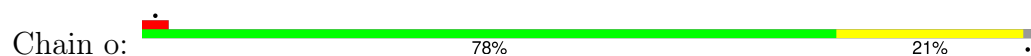
- Molecule 13: 30S ribosomal protein S13



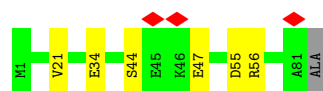
- Molecule 14: Small ribosomal subunit protein uS14



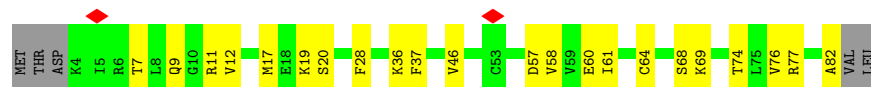
- Molecule 15: Small ribosomal subunit protein uS15



- Molecule 16: 30S ribosomal protein S16



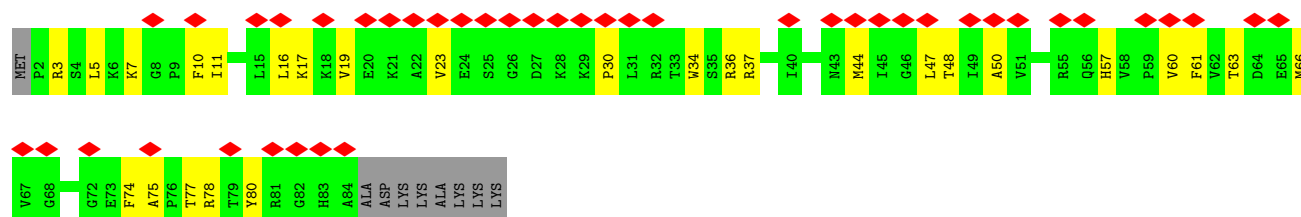
- Molecule 17: Small ribosomal subunit protein uS17



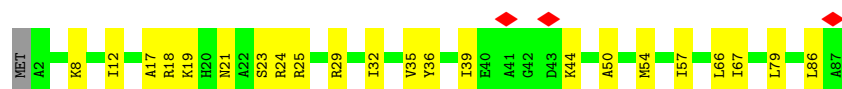
- Molecule 18: 30S ribosomal protein S18



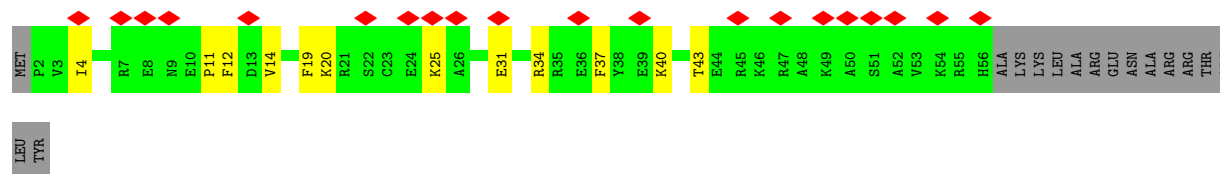
Chain s:



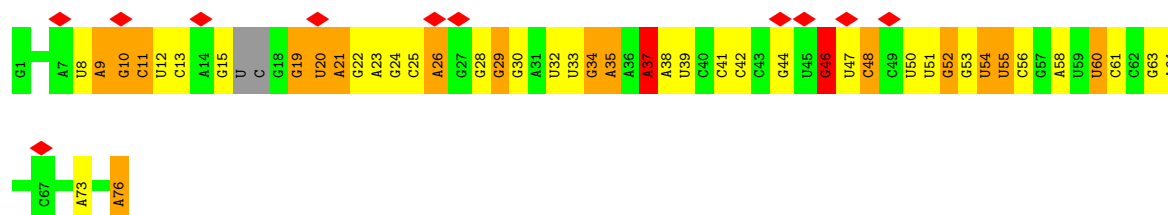
Chain t: 74% 25%



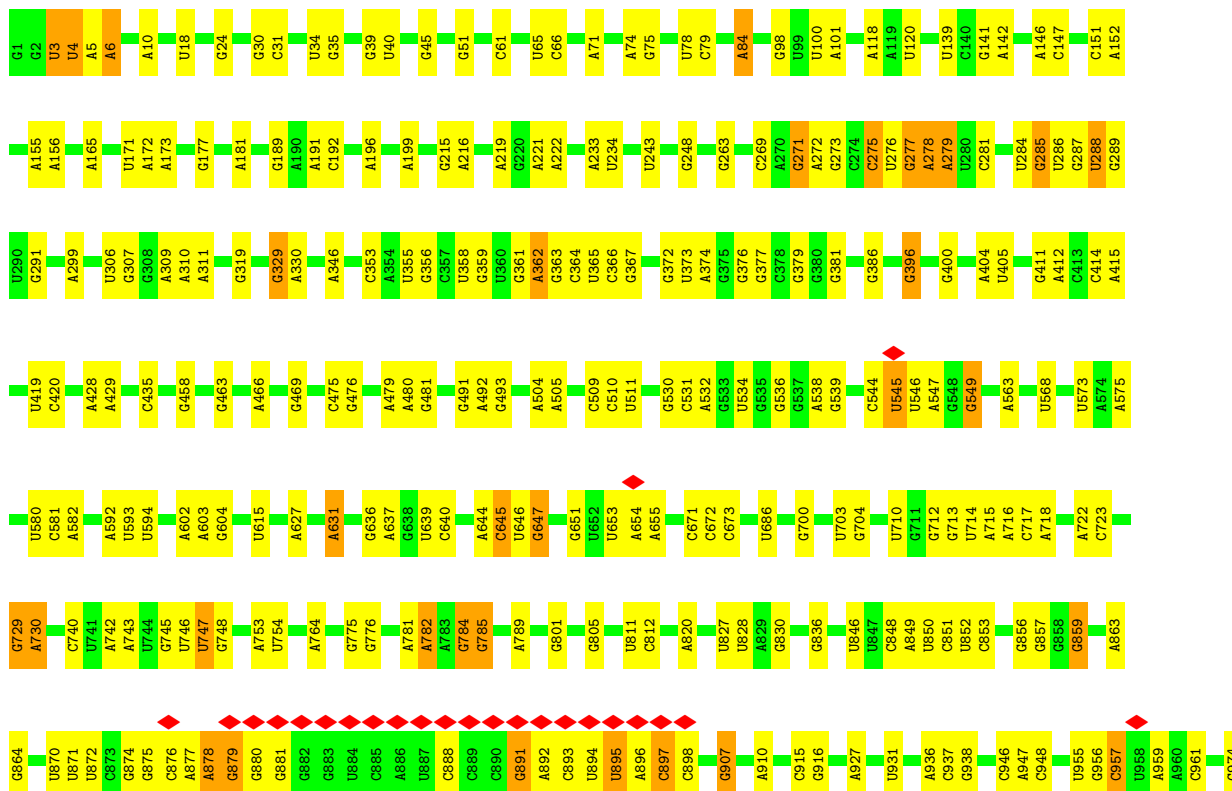
Chain u:



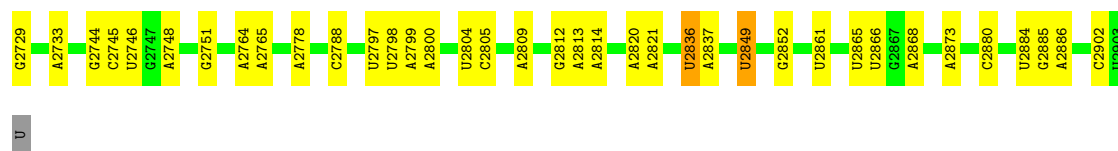
Chain x:



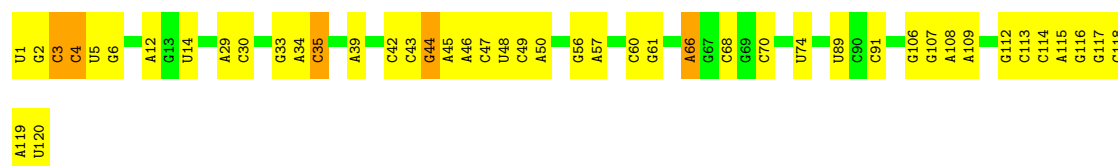
Chain z:



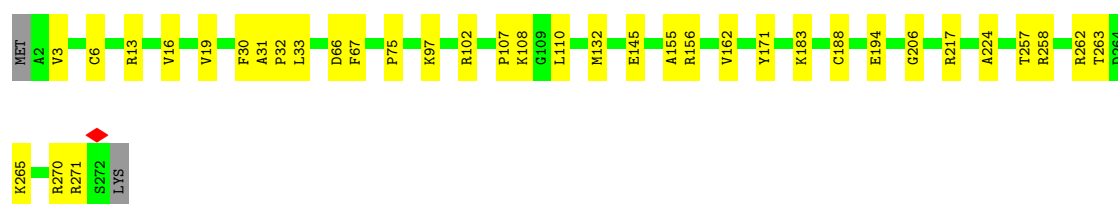
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A2598	G2480	G2361	G2242	G2156	U2075	G1929	U1796	U1497	A1353	U1199	A1086	G976
G2481	G2481	C2364	U2243	G2157	G2093	G1930	U1797	A1505	A1354	U1203	A1088	A981
A2482	G2482	A2377	U2245	C2161	C2096	A1937	C1800	C1507	G1360	G1212	A1090	A983
G2484	G2484	A2381	G2246	A2162	A2097	A1938	A1801	A1508	G1361	A1213	G1091	A990
U2492	G2492	G2382	G2250	A2163	U2098	U1939	A1802	G1674	C1362	A1214	C1092	A993
C2496	G2496	G2383	G2251	C2164	G2100	U1955	A1803	G1675	G1363	G1223	U1094	G993
A2497	G2497	U2384	G2252	U2166	A2101	C1962	A1808	A1515	A1364	U1224	A1096	A996
C2498	G2498	C2385	A2266	U2167	G2102	U1963	A1809	G1524	A1365	G1223	A1097	C1005
C2499	G2499	C2394	G2271	G2168	C2104	C1965	C1816	G1524	C1370	U1224	A1098	
G2502	G2502	G2399	G2271	A2169	U2105	A1966	G1822	G1524	C1370	G1235		
A2503	G2503	G2400	G2279	A2170	U2106	C1967	G1710	A1532	U1379	G1250	C1102	A1009
U2504	G2504	G2401	G2280	A2171	G2107	A1970	A1711	C1533	A1383	G1250	A1103	U1012
G2505	G2505	U2402	A2281	U2172	A2108	U1971	G1715	U1534	A1383	A1253	C1104	C1013
		U2402	G2282	A2173	U2109	G1972	U1716	C1535	C1386	A1254	U1105	
			G2283	C2174	G2110	U1991	A1717	C1536	A1387	U1255	G1106	G1022
			C2283	C2175	U2111	G1992	U1721	G1537	A1392	C1257	U1108	G1026
			A2284	A2176	U2112	U1993	G1727	U1542	U1405	U1262	A1111	G1031
			G2285	G2177	U2113	U1996	U1848	G1543	U1406	U1263	A1112	A1032
			G2286	C2178	G2115	C1996	U1850	A1544	G1410	A1264	U1113	U1033
			G2287	C2179	G2116	G1992	U1851	A1551	U1411	A1265	C1114	
			A2288	C2180	U2117	U1993	U1852	A1552	U1267	U1268	U1038	
			U2291	U2181	A2118	G1996	A1853	A1566	G1416	A1268	U1132	A1039
			U2292	U2182	U2119	A2020	G1857	A1569	G1271	G1271	C1135	C1045
			G2293	A2183	A2119	U2022	A1858	A1570	A1272	A1272	G1138	A1046
			U2305	U2185	G2120	C2023	A1866	A1571	C1278	C1278	U1141	G1047
			G2308	U2186	G2123	A2030	A1872	U1578	A1434	G1281	A1142	G1059
			A2309	U2189	G2124	A2031	C1879	A1583	G1435	U1282	U1060	U1061
			C2310	G2190	G2128	G2032	U1743	U1584	U1438	G1283	G1149	G1062
			U2312	A2191	C2129	A2033	A1745	C1585	A1439	C1150	C1150	G1063
			G2313	U2192	U2130	U2034	U1746	U1440	A1284	A1285	C1153	U1064
			A2314	G2193	U2131	G1884	U1747	U1441	U1442	G1288	A1155	U1065
			G2322	U2195	U2132	C2044	A1754	U1476	A1300	G1300	A1168	U1066
			A2322	U2196	G2133	C2044	A1757	A1477	A1301	A1301	A1169	A1070
			G2325	A2198	G2136	A2051	U1911	G1601	G1452	G1452	C1172	C1072
			A2328	G2204	U2137	A2052	A1912	A1598	C1447	C1295	U	A1073
			U2329	A2211	G2138	C2055	C1914	G1606	G1459	G1296	A	G1074
			A2333	G2216	U2139	G2056	3TD1915	A1608	U1476	A1477	U	C1075
			U2334	G2217	G2140	A2060	A1916	A1618	G1311	G1311	G1177	C1076
			A2335	G2217	A2142	G2061	A1917	A1632	C1315	C1315	C1178	
			G2340	A2225	C2143	C2065	A1918	U1632	G1319	C1319	G1179	C1079
			A2341	G2230	C2145	C2065	A1919	U1636	C1320	C1320	U1180	A1080
			G2345	U2231	C2146	C2065	U1774	U1647	C1493	U1328	U1181	U1081
			C2350	C2232	G2148	G2069	U1775	U1648	A1494	U1328	G1182	U1082
			U2350	U2233	U2149	A2070	A1789		C1495	U1647	U1183	A1084
			G2354	U2234	C2150	C2071	C1925					
			C2359	G2238	U2151	A2072	U1926					
			U2477	G2239	G2152	C2073	A1927					
				U2240	C2153							
					A2154							



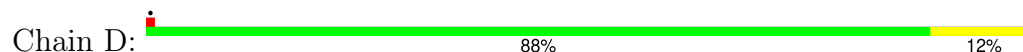
• Molecule 26: 5S Ribosomal RNA



• Molecule 27: 50S ribosomal protein L2



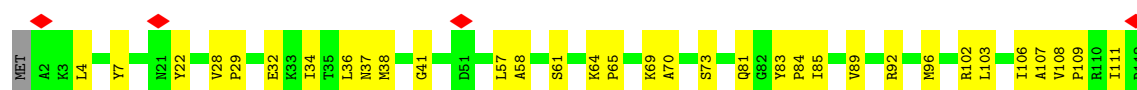
• Molecule 28: 50S ribosomal protein L3

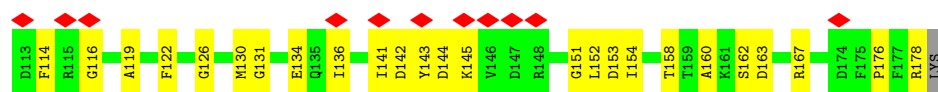


• Molecule 29: 50S ribosomal protein L4

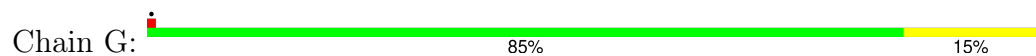


• Molecule 30: 50S ribosomal protein L5

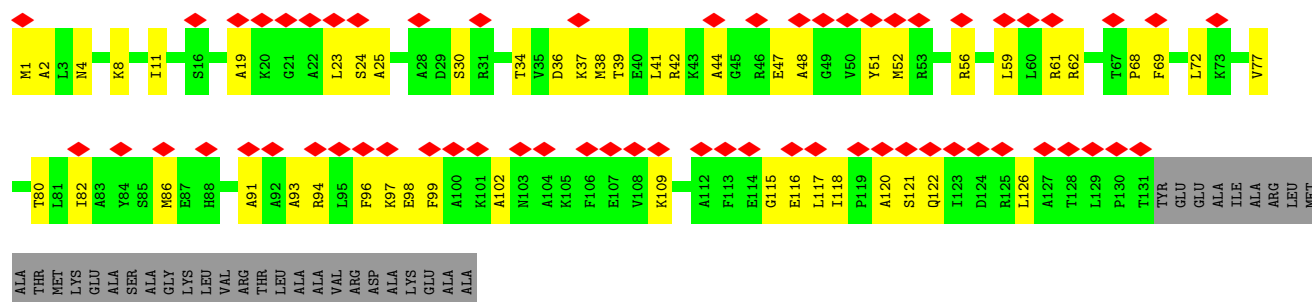




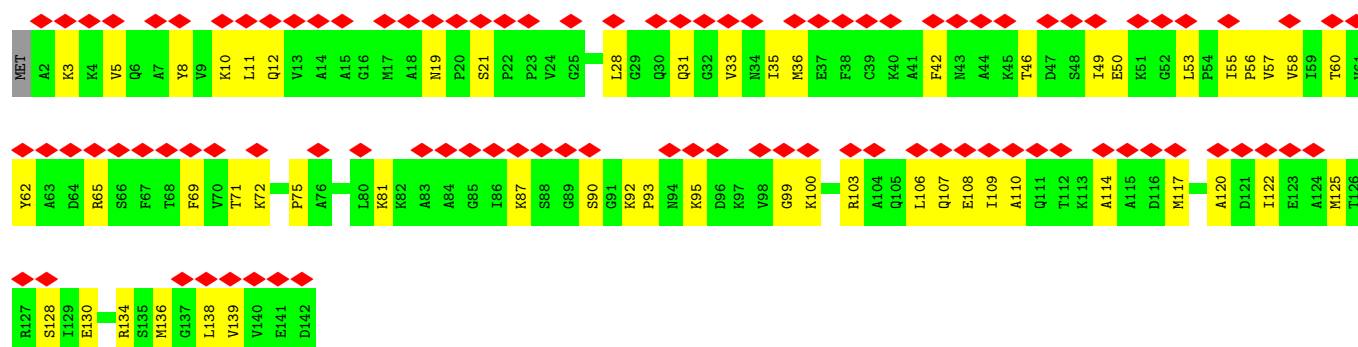
- Molecule 31: 50S ribosomal protein L6



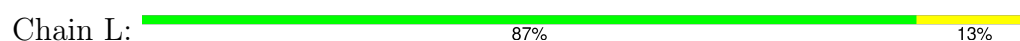
- Molecule 32: 50S ribosomal protein L10



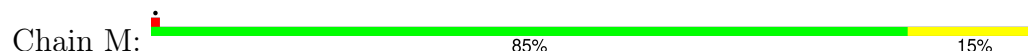
- Molecule 33: 50S ribosomal protein L11

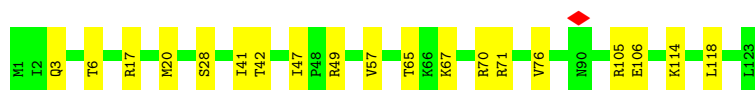


- Molecule 34: 50S ribosomal protein L13



- Molecule 35: 50S ribosomal protein L14

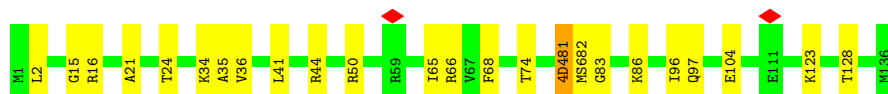
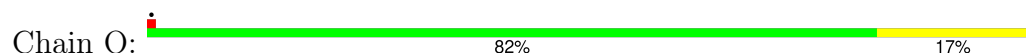




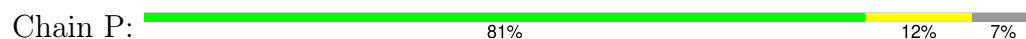
- Molecule 36: 50S ribosomal protein L15



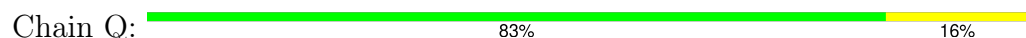
- Molecule 37: 50S ribosomal protein L16



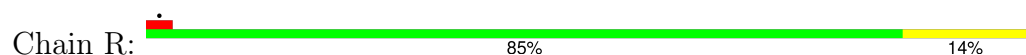
- Molecule 38: Large ribosomal subunit protein bL17



- Molecule 39: 50S ribosomal protein L18



- Molecule 40: 50S ribosomal protein L19



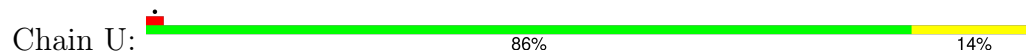
- Molecule 41: 50S ribosomal protein L20



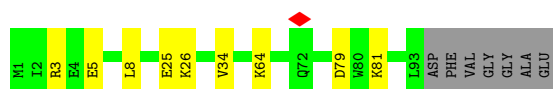
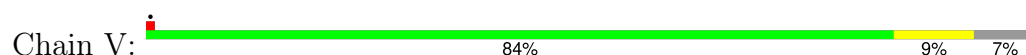
- Molecule 42: Ribosomal protein L21



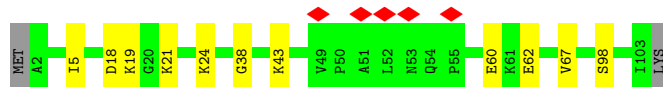
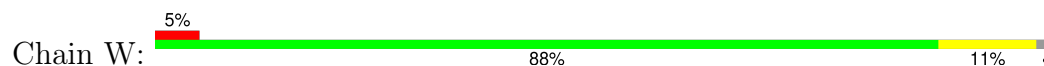
- Molecule 43: 50S ribosomal protein L22



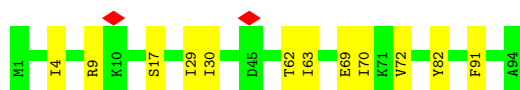
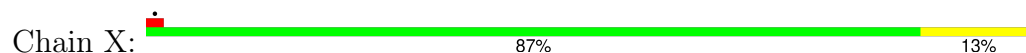
- Molecule 44: 50S ribosomal protein L23



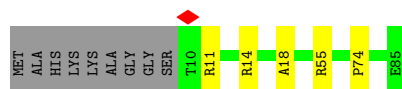
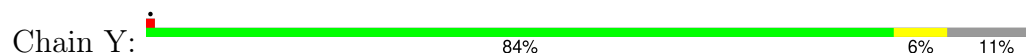
- Molecule 45: 50S ribosomal protein L24



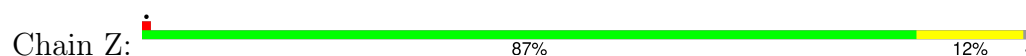
- Molecule 46: 50S ribosomal protein L25



- Molecule 47: 50S ribosomal protein L27



- Molecule 48: 50S ribosomal protein L28



- Molecule 49: 50S ribosomal protein L29

Chain 1:  90% 6% .



- Molecule 50: Large ribosomal subunit protein uL30

Chain 2:  90% 8% .



- Molecule 51: 50S ribosomal protein L31

Chain 3:  17% 59% 10% 31%



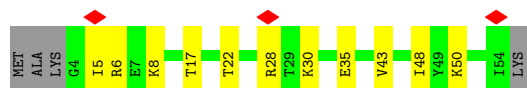
- Molecule 52: 50S ribosomal protein L32

Chain 4:  79% 18% .

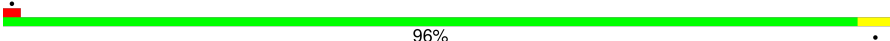


- Molecule 53: Large ribosomal subunit protein bL33

Chain 5:  5% 73% 20% 7%



- Molecule 54: 50S ribosomal protein L34

Chain 6:  96% .

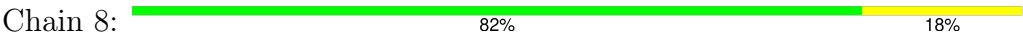


- Molecule 55: 50S ribosomal protein L35

Chain 7:  82% 15% . .



- Molecule 56: 50S ribosomal protein L36



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	33348	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	96000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	28.006	Depositor
Minimum map value	-16.348	Depositor
Average map value	0.001	Depositor
Map value standard deviation	1.015	Depositor
Recommended contour level	3	Depositor
Map size (Å)	435.2, 435.2, 435.2	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85, 0.85, 0.85	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MEQ, 2MG, D2T, PSU, G7M, 4D4, 5MU, OMG, H2U, MS6, 4SU, 4OC, OMU, 1MG, MA6, IAS, 6MZ, 2MA, ZN, 5MC, MIA, 3TD, UR3, MG, G4P, OMC

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	a	0.14	0/36450	0.26	0/56856
2	b	0.15	0/1785	0.40	0/2404
3	c	0.12	0/1651	0.32	0/2225
4	d	0.13	0/1665	0.26	0/2227
5	e	0.15	0/1165	0.34	0/1568
6	f	0.15	0/858	0.39	0/1160
7	g	0.14	0/1206	0.38	0/1617
8	h	0.14	0/989	0.32	0/1326
9	i	0.12	0/1034	0.33	0/1375
10	j	0.13	0/796	0.39	0/1077
11	k	0.14	0/884	0.33	0/1191
12	l	0.16	0/945	0.34	0/1268
13	m	0.12	0/900	0.32	0/1204
14	n	0.11	0/817	0.31	0/1088
15	o	0.16	0/722	0.37	0/964
16	p	0.15	0/653	0.32	0/877
17	q	0.15	0/650	0.35	0/871
18	r	0.13	0/453	0.27	0/609
19	s	0.11	0/680	0.28	0/915
20	t	0.16	0/676	0.36	0/895
21	u	0.12	0/467	0.30	0/620
22	x	0.23	2/1602 (0.1%)	0.31	0/2493
23	z	0.10	0/187	0.27	0/288
24	v	0.30	0/3970	0.49	1/5367 (0.0%)
25	A	0.20	0/69147	0.29	0/107869
26	B	0.16	0/2876	0.28	0/4483
27	C	0.20	0/2121	0.32	0/2852
28	D	0.21	0/1576	0.33	0/2119
29	E	0.18	0/1571	0.27	0/2113
30	F	0.14	0/1434	0.35	0/1926
31	G	0.16	0/1343	0.30	0/1816

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	I	0.14	0/1001	0.41	0/1350
33	J	0.13	0/1046	0.43	0/1410
34	L	0.20	0/1152	0.27	0/1551
35	M	0.19	0/955	0.30	0/1279
36	N	0.19	0/1061	0.28	0/1412
37	O	0.16	0/1073	0.29	0/1433
38	P	0.20	0/958	0.33	0/1281
39	Q	0.15	0/902	0.29	0/1209
40	R	0.19	0/929	0.28	0/1242
41	S	0.22	0/960	0.26	0/1278
42	T	0.19	0/829	0.36	0/1107
43	U	0.20	0/864	0.30	0/1156
44	V	0.18	0/744	0.28	0/994
45	W	0.19	0/787	0.42	2/1051 (0.2%)
46	X	0.15	0/766	0.31	0/1025
47	Y	0.19	0/589	0.29	0/779
48	Z	0.18	0/635	0.26	0/848
49	1	0.15	0/496	0.25	0/660
50	2	0.21	0/453	0.33	0/605
51	3	0.11	0/380	0.29	0/508
52	4	0.20	0/440	0.31	0/588
53	5	0.16	0/424	0.28	0/565
54	6	0.21	0/380	0.29	0/498
55	7	0.19	0/513	0.33	0/676
56	8	0.19	0/303	0.29	0/397
All	All	0.18	2/159913 (0.0%)	0.30	3/238565 (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
37	O	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	x	46	G7M	O3'-P	5.13	1.61	1.56
22	x	8	4SU	O3'-P	5.03	1.61	1.56

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	v	92	HIS	CB-CA-C	-5.77	109.94	116.63
45	W	98	SER	CA-C-N	5.14	131.35	121.54
45	W	98	SER	C-N-CA	5.14	131.35	121.54

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
37	O	81	4D4	Mainchain
37	O	82	MS6	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	a	32803	0	16528	427	0
2	b	1754	0	1782	42	0
3	c	1624	0	1696	45	0
4	d	1643	0	1707	37	0
5	e	1152	0	1196	21	0
6	f	839	0	833	17	0
7	g	1191	0	1245	39	0
8	h	979	0	1031	13	0
9	i	1022	0	1070	24	0
10	j	786	0	828	28	0
11	k	877	0	884	23	0
12	l	942	0	999	14	0
13	m	891	0	952	40	0
14	n	805	0	844	27	0
15	o	714	0	734	12	0
16	p	643	0	661	3	0
17	q	641	0	682	14	0
18	r	446	0	472	11	0
19	s	663	0	688	19	0
20	t	670	0	719	14	0
21	u	460	0	486	8	0
22	x	1588	0	818	38	0
23	z	168	0	86	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	v	3897	0	3881	102	0
25	A	62252	0	31332	454	0
26	B	2572	0	1301	27	0
27	C	2082	0	2154	24	0
28	D	1566	0	1618	20	0
29	E	1552	0	1619	13	0
30	F	1410	0	1444	45	0
31	G	1323	0	1371	15	0
32	I	988	0	1025	37	0
33	J	1032	0	1085	35	0
34	L	1129	0	1162	14	0
35	M	946	0	1023	13	0
36	N	1052	0	1127	6	0
37	O	1075	0	1145	13	0
38	P	945	0	988	11	0
39	Q	892	0	923	12	0
40	R	917	0	962	11	0
41	S	947	0	1019	7	0
42	T	816	0	839	8	0
43	U	857	0	922	9	0
44	V	738	0	807	7	0
45	W	779	0	831	7	0
46	X	753	0	780	8	0
47	Y	582	0	599	4	0
48	Z	625	0	652	5	0
49	1	495	0	526	4	0
50	2	449	0	488	3	0
51	3	373	0	370	6	0
52	4	434	0	445	9	0
53	5	417	0	451	8	0
54	6	377	0	418	2	0
55	7	504	0	572	8	0
56	8	302	0	340	5	0
57	4	1	0	0	0	0
57	6	1	0	0	0	0
57	7	1	0	0	0	0
57	A	315	0	0	0	0
57	B	9	0	0	0	0
57	C	1	0	0	0	0
57	D	1	0	0	0	0
57	E	1	0	0	0	0
57	P	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	S	1	0	0	0	0
57	a	51	0	0	0	0
57	x	1	0	0	0	0
58	v	36	0	11	8	0
59	3	1	0	0	0	0
59	8	1	0	0	0	0
60	A	85	0	0	3	0
60	B	2	0	0	0	0
60	C	1	0	0	0	0
60	a	6	0	0	1	0
60	k	1	0	0	0	0
60	x	1	0	0	0	0
All	All	148897	0	101171	1679	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 1679 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)
22:x:12:U:C4	22:x:23:A:N1	2.18	1.11
58:v:601:G4P:H8	58:v:601:G4P:H5''	1.33	1.09
24:v:98:ASP:O	24:v:101:ARG:N	1.91	1.04
24:v:98:ASP:O	24:v:100:TYR:N	1.93	1.01
1:a:1441:A:H62	1:a:1461:G:N2	1.57	1.01

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	b	222/241 (92%)	195 (88%)	27 (12%)	0	100	100
3	c	204/233 (88%)	191 (94%)	13 (6%)	0	100	100
4	d	203/206 (98%)	200 (98%)	3 (2%)	0	100	100
5	e	154/167 (92%)	145 (94%)	9 (6%)	0	100	100
6	f	101/131 (77%)	95 (94%)	6 (6%)	0	100	100
7	g	150/156 (96%)	144 (96%)	6 (4%)	0	100	100
8	h	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
9	i	125/130 (96%)	118 (94%)	6 (5%)	1 (1%)	16	50
10	j	96/103 (93%)	90 (94%)	5 (5%)	1 (1%)	12	45
11	k	113/129 (88%)	106 (94%)	7 (6%)	0	100	100
12	l	118/124 (95%)	108 (92%)	10 (8%)	0	100	100
13	m	113/118 (96%)	105 (93%)	8 (7%)	0	100	100
14	n	98/101 (97%)	95 (97%)	3 (3%)	0	100	100
15	o	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
16	p	79/82 (96%)	76 (96%)	3 (4%)	0	100	100
17	q	77/84 (92%)	72 (94%)	5 (6%)	0	100	100
18	r	52/75 (69%)	47 (90%)	5 (10%)	0	100	100
19	s	81/92 (88%)	76 (94%)	5 (6%)	0	100	100
20	t	84/87 (97%)	81 (96%)	3 (4%)	0	100	100
21	u	53/71 (75%)	52 (98%)	1 (2%)	0	100	100
24	v	489/529 (92%)	412 (84%)	73 (15%)	4 (1%)	16	50
27	C	269/273 (98%)	256 (95%)	13 (5%)	0	100	100
28	D	206/209 (99%)	198 (96%)	8 (4%)	0	100	100
29	E	199/201 (99%)	196 (98%)	3 (2%)	0	100	100
30	F	175/179 (98%)	163 (93%)	12 (7%)	0	100	100
31	G	174/177 (98%)	164 (94%)	10 (6%)	0	100	100
32	I	129/165 (78%)	103 (80%)	26 (20%)	0	100	100
33	J	139/142 (98%)	121 (87%)	17 (12%)	1 (1%)	18	52
34	L	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
35	M	121/123 (98%)	114 (94%)	7 (6%)	0	100	100
36	N	142/144 (99%)	138 (97%)	4 (3%)	0	100	100
37	O	132/136 (97%)	126 (96%)	5 (4%)	1 (1%)	16	50

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	P	116/127 (91%)	111 (96%)	5 (4%)	0	100	100
39	Q	114/117 (97%)	110 (96%)	4 (4%)	0	100	100
40	R	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
41	S	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
42	T	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
43	U	108/110 (98%)	103 (95%)	5 (5%)	0	100	100
44	V	91/100 (91%)	85 (93%)	6 (7%)	0	100	100
45	W	100/104 (96%)	94 (94%)	6 (6%)	0	100	100
46	X	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
47	Y	74/85 (87%)	72 (97%)	2 (3%)	0	100	100
48	Z	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
49	1	59/63 (94%)	57 (97%)	2 (3%)	0	100	100
50	2	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
51	3	46/70 (66%)	43 (94%)	3 (6%)	0	100	100
52	4	53/57 (93%)	53 (100%)	0	0	100	100
53	5	49/55 (89%)	47 (96%)	2 (4%)	0	100	100
54	6	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
55	7	62/65 (95%)	58 (94%)	3 (5%)	1 (2%)	7	36
56	8	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
All	All	6154/6573 (94%)	5773 (94%)	372 (6%)	9 (0%)	49	79

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
24	v	99	THR
10	j	57	VAL
24	v	18	ILE
24	v	97	GLU
33	J	33	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	
2	b	186/199 (94%)	186 (100%)	0	100	100
3	c	170/190 (90%)	170 (100%)	0	100	100
4	d	172/173 (99%)	172 (100%)	0	100	100
5	e	119/126 (94%)	119 (100%)	0	100	100
6	f	90/112 (80%)	90 (100%)	0	100	100
7	g	125/129 (97%)	125 (100%)	0	100	100
8	h	104/105 (99%)	104 (100%)	0	100	100
9	i	105/107 (98%)	105 (100%)	0	100	100
10	j	86/90 (96%)	86 (100%)	0	100	100
11	k	89/98 (91%)	89 (100%)	0	100	100
12	l	101/103 (98%)	101 (100%)	0	100	100
13	m	93/96 (97%)	93 (100%)	0	100	100
14	n	83/84 (99%)	83 (100%)	0	100	100
15	o	76/77 (99%)	76 (100%)	0	100	100
16	p	65/65 (100%)	65 (100%)	0	100	100
17	q	73/78 (94%)	73 (100%)	0	100	100
18	r	47/65 (72%)	47 (100%)	0	100	100
19	s	72/79 (91%)	72 (100%)	0	100	100
20	t	65/66 (98%)	65 (100%)	0	100	100
21	u	48/61 (79%)	48 (100%)	0	100	100
24	v	421/453 (93%)	420 (100%)	1 (0%)	87	89
27	C	216/218 (99%)	216 (100%)	0	100	100
28	D	163/163 (100%)	163 (100%)	0	100	100
29	E	165/165 (100%)	165 (100%)	0	100	100
30	F	148/150 (99%)	148 (100%)	0	100	100
31	G	137/138 (99%)	137 (100%)	0	100	100
32	I	100/123 (81%)	100 (100%)	0	100	100
33	J	109/110 (99%)	109 (100%)	0	100	100
34	L	116/116 (100%)	116 (100%)	0	100	100
35	M	104/104 (100%)	104 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	N	103/103 (100%)	103 (100%)	0	100	100
37	O	107/107 (100%)	107 (100%)	0	100	100
38	P	98/103 (95%)	98 (100%)	0	100	100
39	Q	86/87 (99%)	86 (100%)	0	100	100
40	R	99/100 (99%)	99 (100%)	0	100	100
41	S	89/90 (99%)	89 (100%)	0	100	100
42	T	84/84 (100%)	84 (100%)	0	100	100
43	U	93/93 (100%)	93 (100%)	0	100	100
44	V	80/84 (95%)	80 (100%)	0	100	100
45	W	83/85 (98%)	83 (100%)	0	100	100
46	X	78/78 (100%)	78 (100%)	0	100	100
47	Y	58/63 (92%)	58 (100%)	0	100	100
48	Z	67/68 (98%)	67 (100%)	0	100	100
49	1	54/55 (98%)	54 (100%)	0	100	100
50	2	48/49 (98%)	48 (100%)	0	100	100
51	3	44/62 (71%)	44 (100%)	0	100	100
52	4	46/48 (96%)	46 (100%)	0	100	100
53	5	46/49 (94%)	46 (100%)	0	100	100
54	6	38/38 (100%)	38 (100%)	0	100	100
55	7	51/52 (98%)	51 (100%)	0	100	100
56	8	34/34 (100%)	34 (100%)	0	100	100
All	All	5134/5375 (96%)	5133 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
24	v	97	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 86 such sidechains are listed below:

Mol	Chain	Res	Type
29	E	97	ASN
39	Q	38	GLN
31	G	20	ASN

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Mol	Chain	Res	Type
34	L	80	HIS
42	T	91	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1526/1542 (98%)	220 (14%)	0
22	x	72/76 (94%)	24 (33%)	0
23	z	7/21 (33%)	1 (14%)	0
25	A	2897/2904 (99%)	376 (12%)	14 (0%)
26	B	119/120 (99%)	11 (9%)	1 (0%)
All	All	4621/4663 (99%)	632 (13%)	15 (0%)

5 of 632 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	4	U
1	a	5	U
1	a	6	G
1	a	8	A
1	a	32	A

5 of 15 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
25	A	1111	A
25	A	2799	A
25	A	1328	A
26	B	3	C
25	A	2191	A

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

47 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
25	PSU	A	2457	25	18,21,22	1.39	3 (16%)	21,30,33	2.14	5 (23%)
1	PSU	a	516	1	18,21,22	1.37	2 (11%)	21,30,33	2.08	4 (19%)
1	2MG	a	1516	1	23,26,27	1.25	3 (13%)	33,38,41	2.15	7 (21%)
1	G7M	a	527	1	23,26,27	1.56	3 (13%)	34,39,42	1.77	5 (14%)
22	PSU	x	39	22	18,21,22	1.34	2 (11%)	21,30,33	2.12	4 (19%)
12	D2T	l	89	12	8,9,10	2.35	1 (12%)	6,11,13	2.23	2 (33%)
25	OMC	A	2498	57,25	19,22,23	0.80	0	25,31,34	0.96	1 (4%)
25	OMG	A	2251	25	23,26,27	1.19	3 (13%)	32,38,41	1.97	5 (15%)
25	PSU	A	2604	25	18,21,22	1.40	4 (22%)	21,30,33	2.03	4 (19%)
25	3TD	A	1915	25	19,22,23	4.26	7 (36%)	23,32,35	1.82	3 (13%)
25	2MG	A	2445	25	23,26,27	1.27	4 (17%)	33,38,41	2.21	8 (24%)
22	PSU	x	55	22	18,21,22	1.40	2 (11%)	21,30,33	2.00	3 (14%)
25	5MU	A	747	25	19,22,23	1.38	4 (21%)	27,32,35	2.21	6 (22%)
1	UR3	a	1498	1	19,22,23	0.98	0	26,32,35	1.74	2 (7%)
25	6MZ	A	1618	25	22,25,26	1.45	5 (22%)	29,36,39	2.27	9 (31%)
1	5MC	a	1407	1	19,22,23	1.63	3 (15%)	26,32,35	1.15	3 (11%)
37	4D4	O	81	37	9,11,12	2.73	3 (33%)	7,13,15	0.92	0
22	MIA	x	37	22	28,31,32	2.37	6 (21%)	38,44,47	2.77	14 (36%)
25	1MG	A	745	25	23,26,27	1.18	3 (13%)	33,39,42	1.74	5 (15%)
25	H2U	A	2449	25	18,21,22	1.04	2 (11%)	19,30,33	1.00	2 (10%)
37	MS6	O	82	37	5,7,8	0.51	0	2,7,9	1.12	0
22	4SU	x	8	22	18,21,22	1.83	5 (27%)	25,30,33	2.34	5 (20%)
25	PSU	A	746	57,25	18,21,22	1.39	3 (16%)	21,30,33	2.06	4 (19%)
11	IAS	k	119	11	6,7,8	0.98	0	3,8,10	1.51	1 (33%)
1	MA6	a	1519	1	23,26,27	1.50	5 (21%)	33,38,41	2.43	14 (42%)
22	PSU	x	32	22	18,21,22	1.37	2 (11%)	21,30,33	2.02	3 (14%)
25	PSU	A	1917	25	18,21,22	1.44	3 (16%)	21,30,33	2.05	3 (14%)
28	MEQ	D	150	28	8,9,10	0.51	0	5,10,12	0.22	0
25	2MG	A	1835	25	23,26,27	1.27	4 (17%)	33,38,41	2.16	6 (18%)
22	G7M	x	46	22	23,26,27	2.37	5 (21%)	34,39,42	3.07	11 (32%)
22	5MU	x	54	22	19,22,23	1.37	5 (26%)	27,32,35	2.00	6 (22%)
25	PSU	A	955	25	18,21,22	1.43	4 (22%)	21,30,33	2.08	3 (14%)
25	G7M	A	2069	25	23,26,27	1.55	3 (13%)	34,39,42	1.72	5 (14%)
1	4OC	a	1402	1	20,23,24	0.76	0	25,32,35	0.94	1 (4%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
25	5MU	A	1939	25	19,22,23	1.37	5 (26%)	27,32,35	2.16	6 (22%)
25	2MA	A	2503	25	22,25,26	1.51	4 (18%)	32,37,40	2.31	8 (25%)
25	PSU	A	1911	25	18,21,22	1.37	2 (11%)	21,30,33	2.05	4 (19%)
25	5MC	A	1962	25	19,22,23	1.43	3 (15%)	26,32,35	1.13	2 (7%)
25	OMU	A	2552	25	19,22,23	1.26	3 (15%)	25,31,34	1.84	5 (20%)
1	2MG	a	966	1	23,26,27	1.25	4 (17%)	33,38,41	2.19	7 (21%)
25	PSU	A	2605	25	18,21,22	1.39	3 (16%)	21,30,33	2.04	4 (19%)
1	5MC	a	967	1	19,22,23	1.62	3 (15%)	26,32,35	1.12	2 (7%)
1	2MG	a	1207	1	23,26,27	1.24	4 (17%)	33,38,41	2.23	8 (24%)
25	PSU	A	2504	25	18,21,22	1.37	3 (16%)	21,30,33	2.01	4 (19%)
25	PSU	A	2580	25	18,21,22	1.41	4 (22%)	21,30,33	2.12	4 (19%)
1	MA6	a	1518	1	23,26,27	1.48	4 (17%)	33,38,41	2.44	14 (42%)
25	6MZ	A	2030	25	22,25,26	1.44	5 (22%)	29,36,39	2.37	10 (34%)

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
25	PSU	A	2457	25	-	0/7/25/26	0/2/2/2
1	PSU	a	516	1	-	0/7/25/26	0/2/2/2
1	2MG	a	1516	1	-	0/9/27/28	0/3/3/3
1	G7M	a	527	1	-	1/7/25/26	0/3/3/3
22	PSU	x	39	22	-	0/7/25/26	0/2/2/2
12	D2T	l	89	12	-	1/7/12/14	-
25	OMC	A	2498	57,25	-	1/9/27/28	0/2/2/2
25	OMG	A	2251	25	-	0/9/27/28	0/3/3/3
25	PSU	A	2604	25	-	0/7/25/26	0/2/2/2
25	3TD	A	1915	25	-	0/7/25/26	0/2/2/2
25	2MG	A	2445	25	-	0/9/27/28	0/3/3/3
22	PSU	x	55	22	-	1/7/25/26	0/2/2/2
25	5MU	A	747	25	-	0/7/25/26	0/2/2/2
1	UR3	a	1498	1	-	0/7/25/26	0/2/2/2
25	6MZ	A	1618	25	-	0/9/27/28	0/3/3/3
1	5MC	a	1407	1	-	0/7/25/26	0/2/2/2
37	4D4	O	81	37	-	8/11/12/14	-
22	MIA	x	37	22	-	4/15/33/34	0/3/3/3
25	1MG	A	745	25	-	0/7/25/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
25	H2U	A	2449	25	-	0/7/38/39	0/2/2/2
37	MS6	O	82	37	-	3/4/6/8	-
22	4SU	x	8	22	-	0/7/25/26	0/2/2/2
25	PSU	A	746	57,25	-	1/7/25/26	0/2/2/2
11	IAS	k	119	11	-	0/7/7/8	-
1	MA6	a	1519	1	-	3/11/29/30	0/3/3/3
22	PSU	x	32	22	-	0/7/25/26	0/2/2/2
25	PSU	A	1917	25	-	1/7/25/26	0/2/2/2
28	MEQ	D	150	28	-	2/8/9/11	-
25	2MG	A	1835	25	-	0/9/27/28	0/3/3/3
22	G7M	x	46	22	-	1/7/25/26	0/3/3/3
22	5MU	x	54	22	-	0/7/25/26	0/2/2/2
25	PSU	A	955	25	-	0/7/25/26	0/2/2/2
25	G7M	A	2069	25	-	3/7/25/26	0/3/3/3
1	4OC	a	1402	1	-	3/9/29/30	0/2/2/2
25	5MU	A	1939	25	-	0/7/25/26	0/2/2/2
25	2MA	A	2503	25	-	0/7/25/26	0/3/3/3
25	PSU	A	1911	25	-	0/7/25/26	0/2/2/2
25	5MC	A	1962	25	-	0/7/25/26	0/2/2/2
25	OMU	A	2552	25	-	1/9/27/28	0/2/2/2
1	2MG	a	966	1	-	2/9/27/28	0/3/3/3
25	PSU	A	2605	25	-	0/7/25/26	0/2/2/2
1	5MC	a	967	1	-	0/7/25/26	0/2/2/2
1	2MG	a	1207	1	-	0/9/27/28	0/3/3/3
25	PSU	A	2504	25	-	0/7/25/26	0/2/2/2
25	PSU	A	2580	25	-	0/7/25/26	0/2/2/2
1	MA6	a	1518	1	-	1/11/29/30	0/3/3/3
25	6MZ	A	2030	25	-	2/9/27/28	0/3/3/3

The worst 5 of 146 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	A	1915	3TD	C6-C5	12.62	1.49	1.35
25	A	1915	3TD	C2-N1	9.92	1.49	1.37
22	x	46	G7M	C8-N7	7.82	1.46	1.33
22	x	37	MIA	C2-S10	-7.34	1.69	1.75
22	x	37	MIA	C13-C14	6.78	1.52	1.32

The worst 5 of 232 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	A	2503	2MA	C5-C4-N3	-8.35	118.38	127.18
22	x	37	MIA	C12-C13-C14	-8.18	112.33	127.01
22	x	46	G7M	CN7-N7-C8	-8.05	112.61	124.79
22	x	37	MIA	C5-C4-N3	-7.97	118.78	127.18
1	a	1207	2MG	C2-N3-C4	7.22	121.03	112.00

There are no chirality outliers.

5 of 39 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	a	1519	MA6	C5-C6-N6-C9
1	a	1519	MA6	N1-C6-N6-C9
22	x	37	MIA	C12-C13-C14-C15
37	O	81	4D4	C-CA-CB-OB
37	O	81	4D4	C-CA-CB-CG

There are no ring outliers.

19 monomers are involved in 32 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
25	A	2457	PSU	1	0
1	a	516	PSU	1	0
1	a	1516	2MG	3	0
12	l	89	D2T	3	0
25	A	2498	OMC	1	0
25	A	1915	3TD	1	0
22	x	37	MIA	2	0
25	A	2449	H2U	1	0
1	a	1519	MA6	2	0
25	A	1917	PSU	1	0
22	x	46	G7M	2	0
22	x	54	5MU	1	0
1	a	1402	4OC	3	0
25	A	2503	2MA	1	0
25	A	2552	OMU	1	0
1	a	966	2MG	2	0
1	a	1207	2MG	1	0
1	a	1518	MA6	4	0
25	A	2030	6MZ	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 387 ligands modelled in this entry, 386 are monoatomic - leaving 1 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
58	G4P	v	601	57	36,38,38	1.50	5 (13%)	56,61,61	2.00	13 (23%)

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
58	G4P	v	601	57	-	5/27/43/43	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	v	601	G4P	C6-N1	-4.37	1.30	1.38
58	v	601	G4P	C5-N7	-3.02	1.33	1.39
58	v	601	G4P	C2-N1	-2.88	1.30	1.37
58	v	601	G4P	C8-N9	-2.43	1.32	1.37
58	v	601	G4P	PA-O3A	-2.34	1.57	1.59

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	v	601	G4P	C5-C4-N3	-7.23	116.89	128.39
58	v	601	G4P	N9-C4-N3	5.76	137.47	125.95
58	v	601	G4P	C2-N3-C4	5.63	121.99	112.30
58	v	601	G4P	C6-C5-N7	3.22	136.15	130.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	v	601	G4P	C5-C6-N1	2.87	120.55	113.25

There are no chirality outliers.

All (5) torsion outliers are listed below:

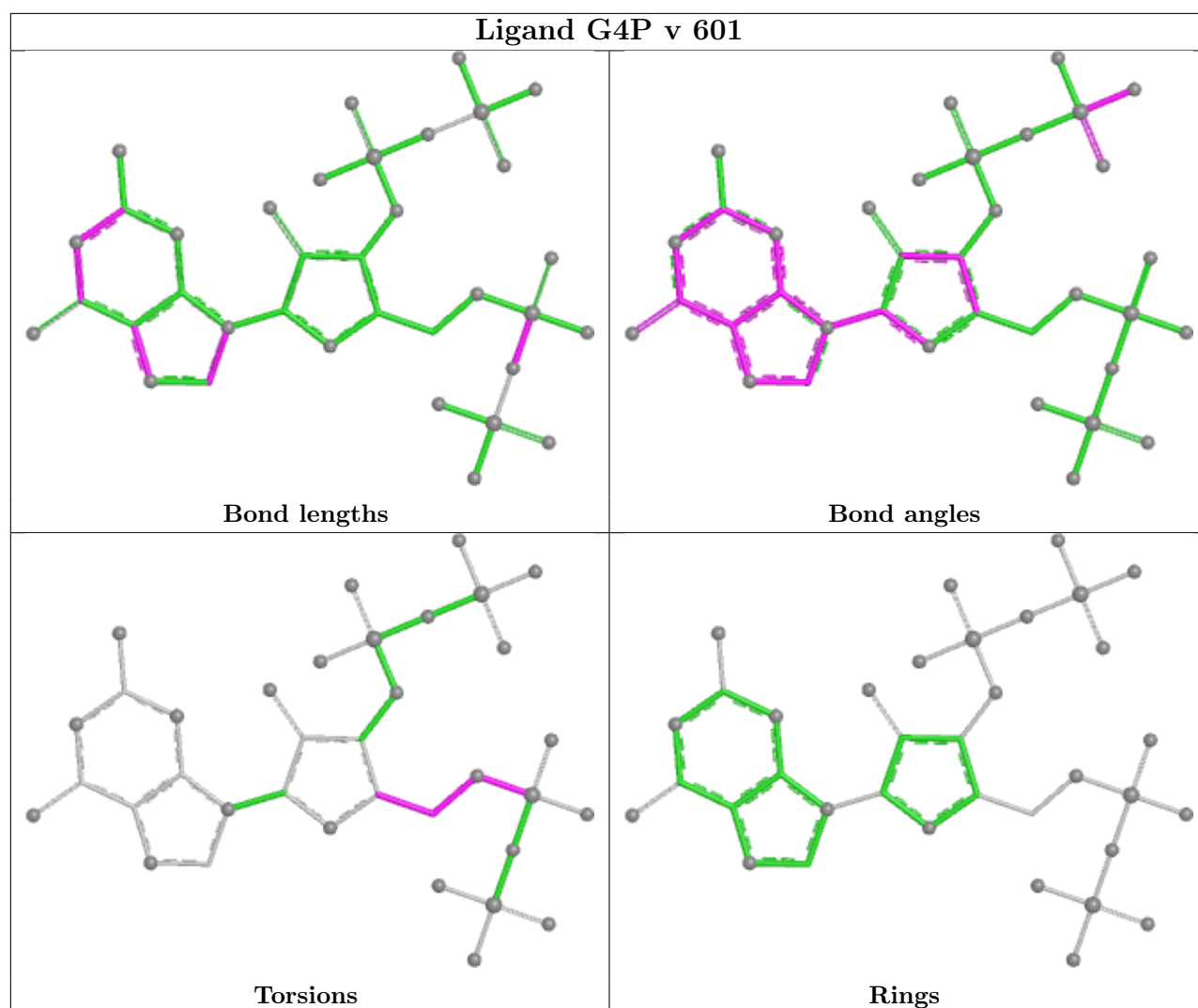
Mol	Chain	Res	Type	Atoms
58	v	601	G4P	C5'-O5'-PA-O3A
58	v	601	G4P	C5'-O5'-PA-O2A
58	v	601	G4P	O4'-C4'-C5'-O5'
58	v	601	G4P	C3'-C4'-C5'-O5'
58	v	601	G4P	C4'-C5'-O5'-PA

There are no ring outliers.

1 monomer is involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
58	v	601	G4P	8	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

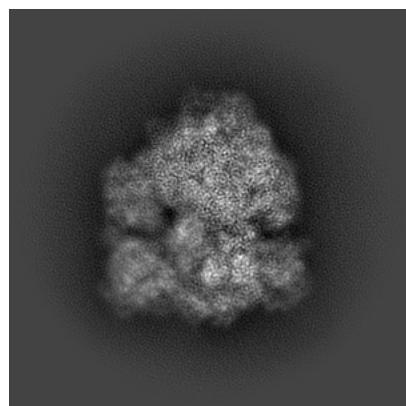
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-29624. These allow visual inspection of the internal detail of the map and identification of artifacts.

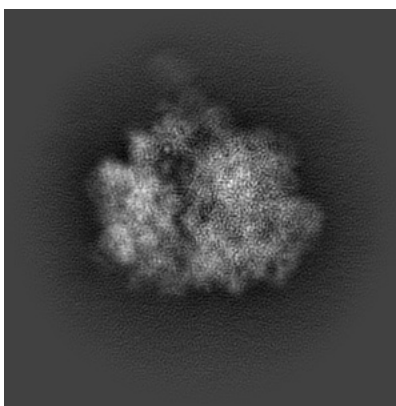
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

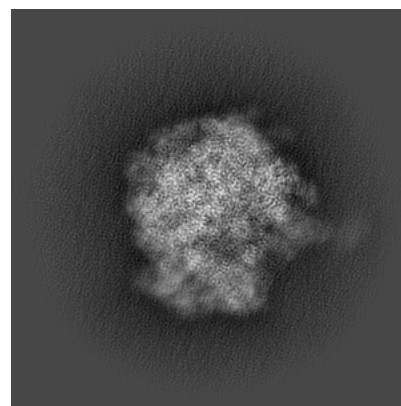
6.1.1 Primary map



X

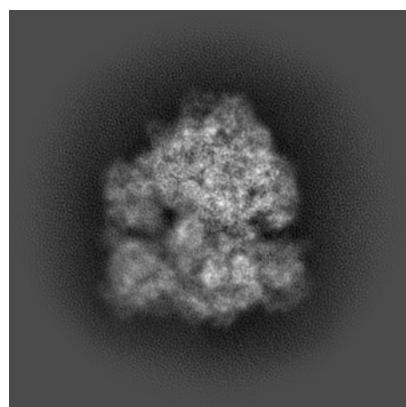


Y

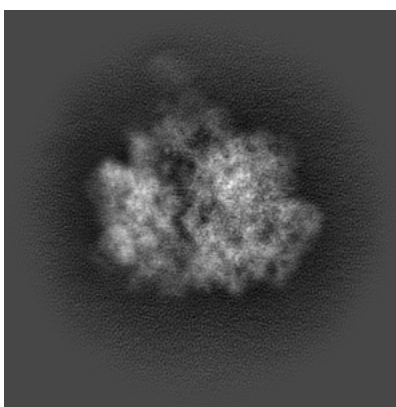


Z

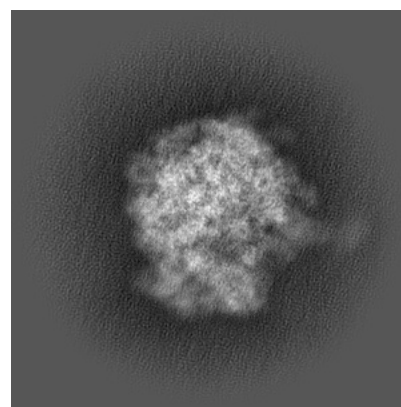
6.1.2 Raw map



X



Y

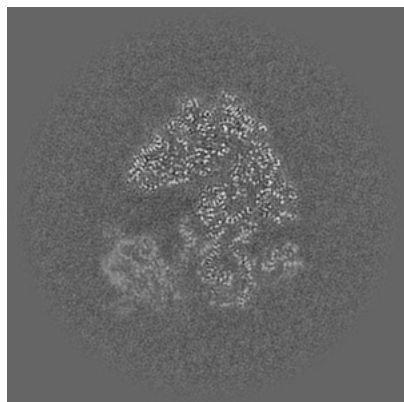


Z

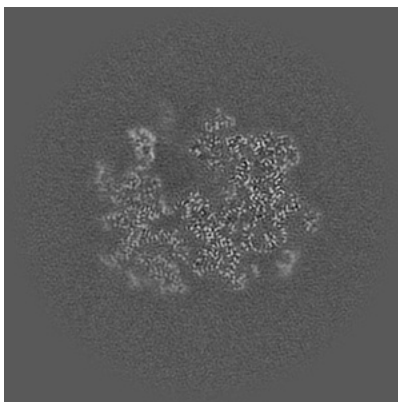
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

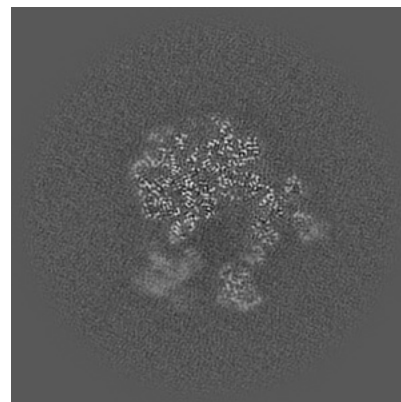
6.2.1 Primary map



X Index: 256

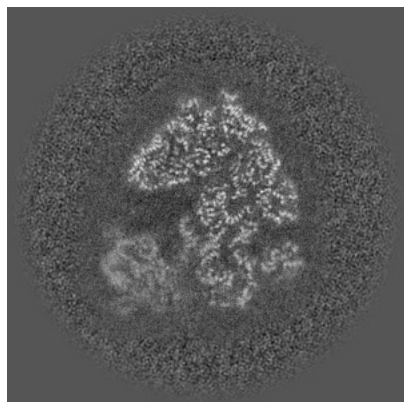


Y Index: 256

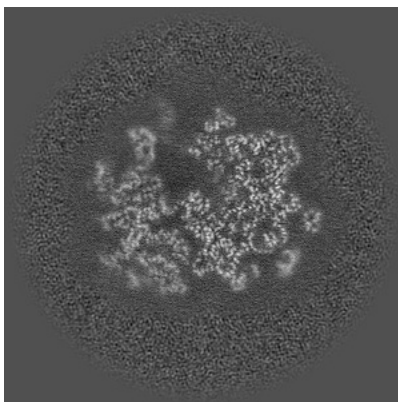


Z Index: 256

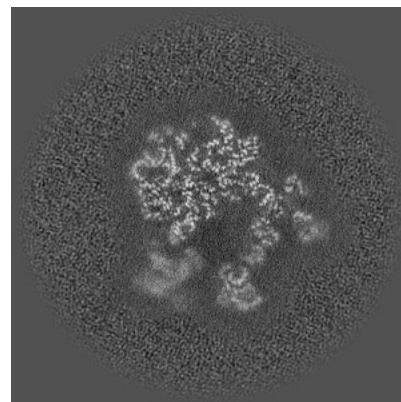
6.2.2 Raw map



X Index: 256



Y Index: 256

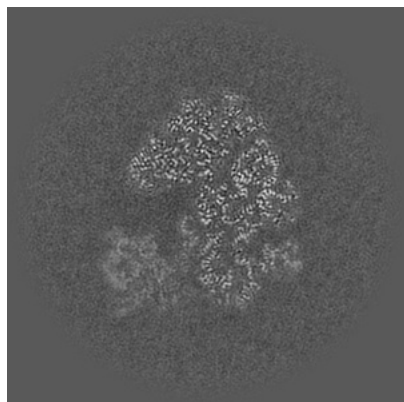


Z Index: 256

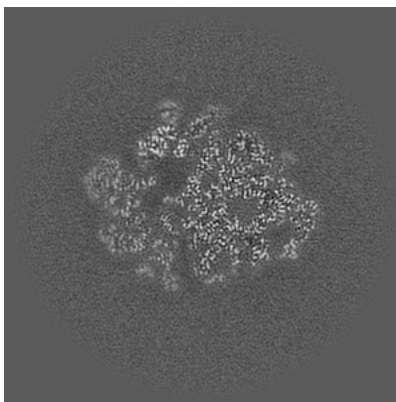
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

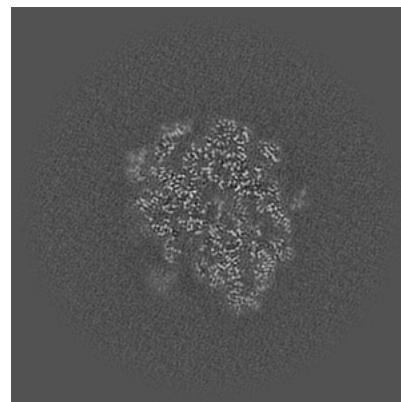
6.3.1 Primary map



X Index: 254

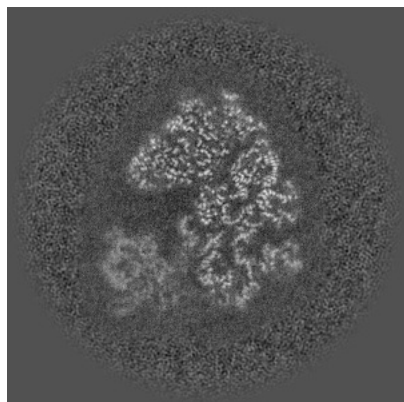


Y Index: 280

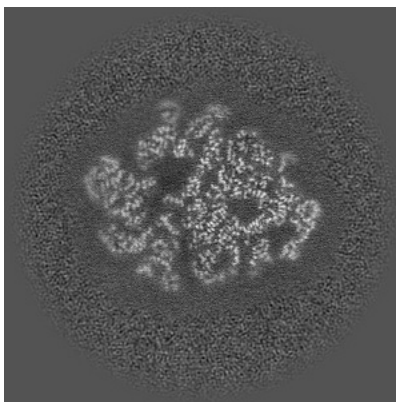


Z Index: 290

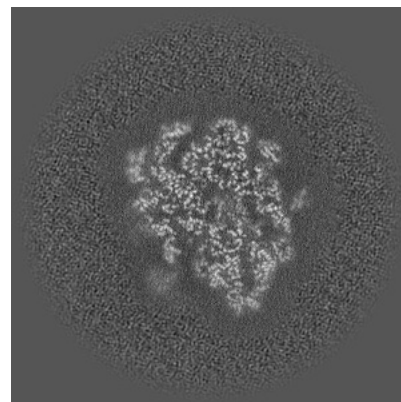
6.3.2 Raw map



X Index: 254



Y Index: 279

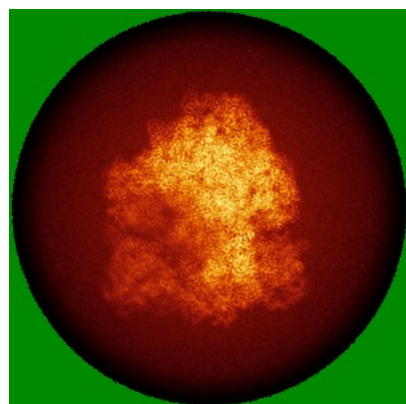


Z Index: 290

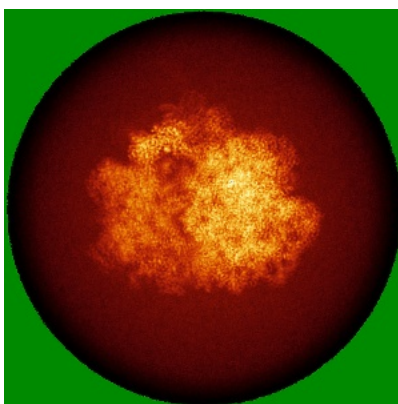
The images above show the largest variance slices of the map in three orthogonal directions.

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

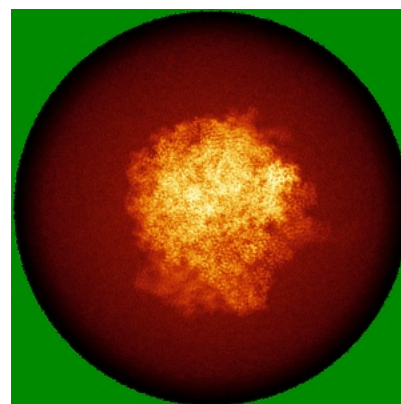
6.4.1 Primary map



X

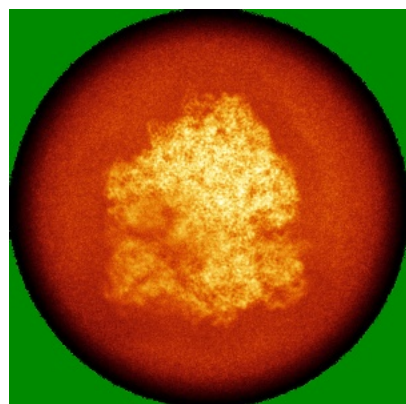


Y

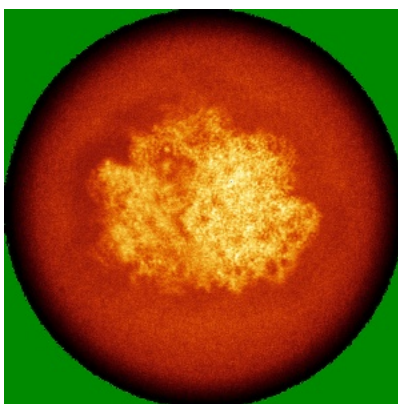


Z

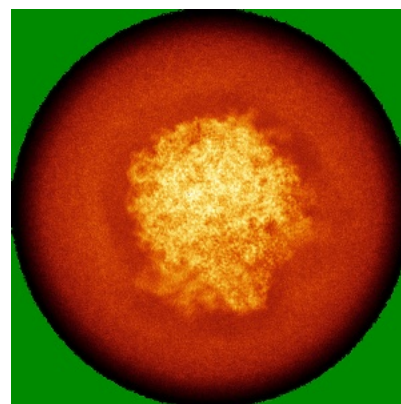
6.4.2 Raw map



X



Y

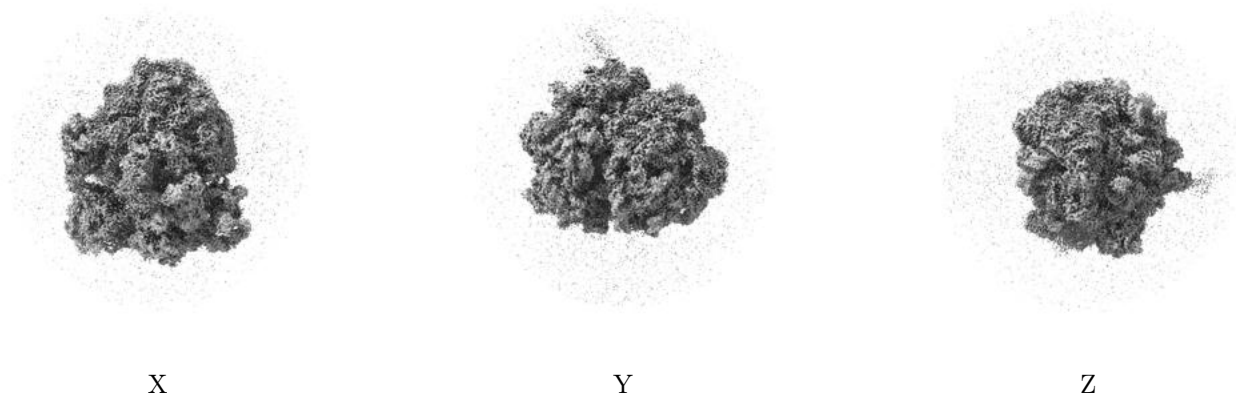


Z

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.

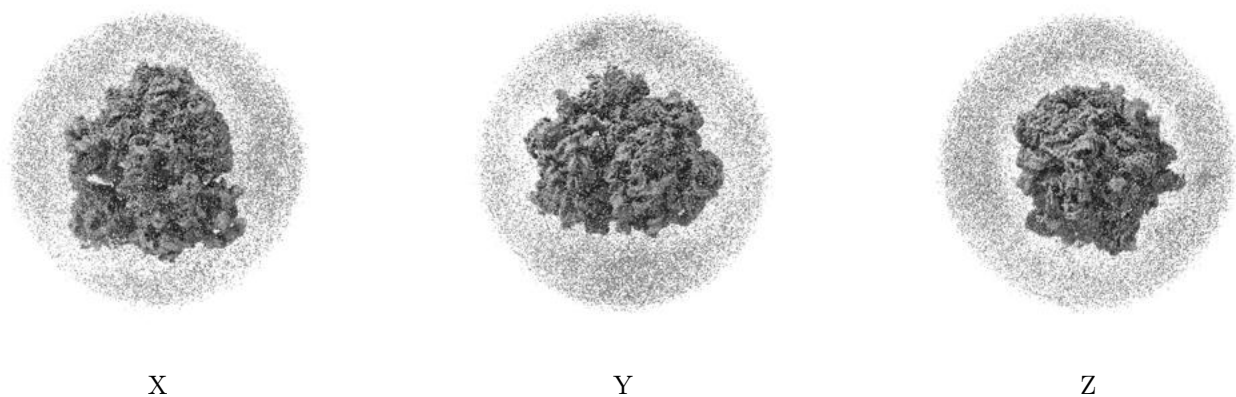
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.0. 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.

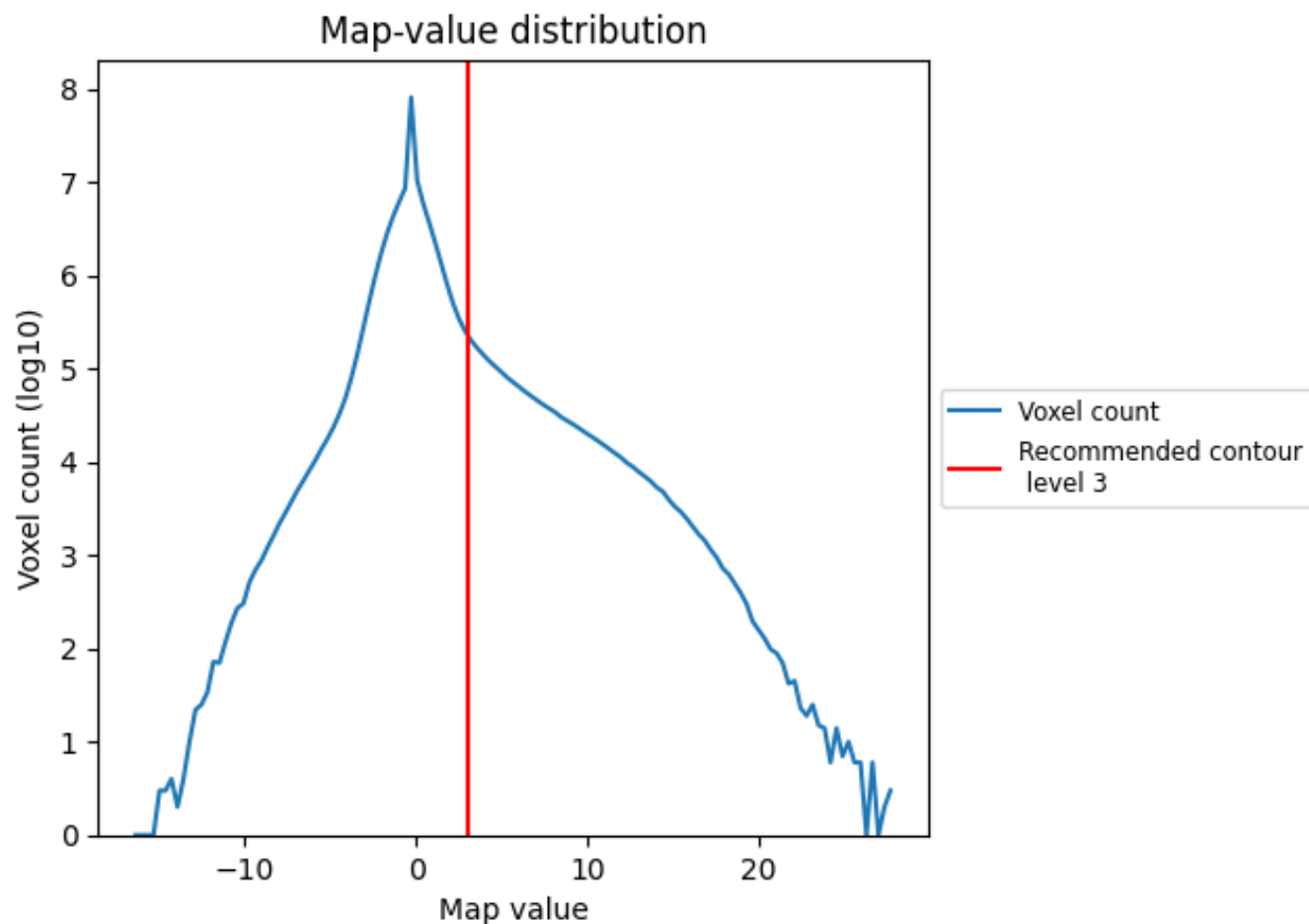
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

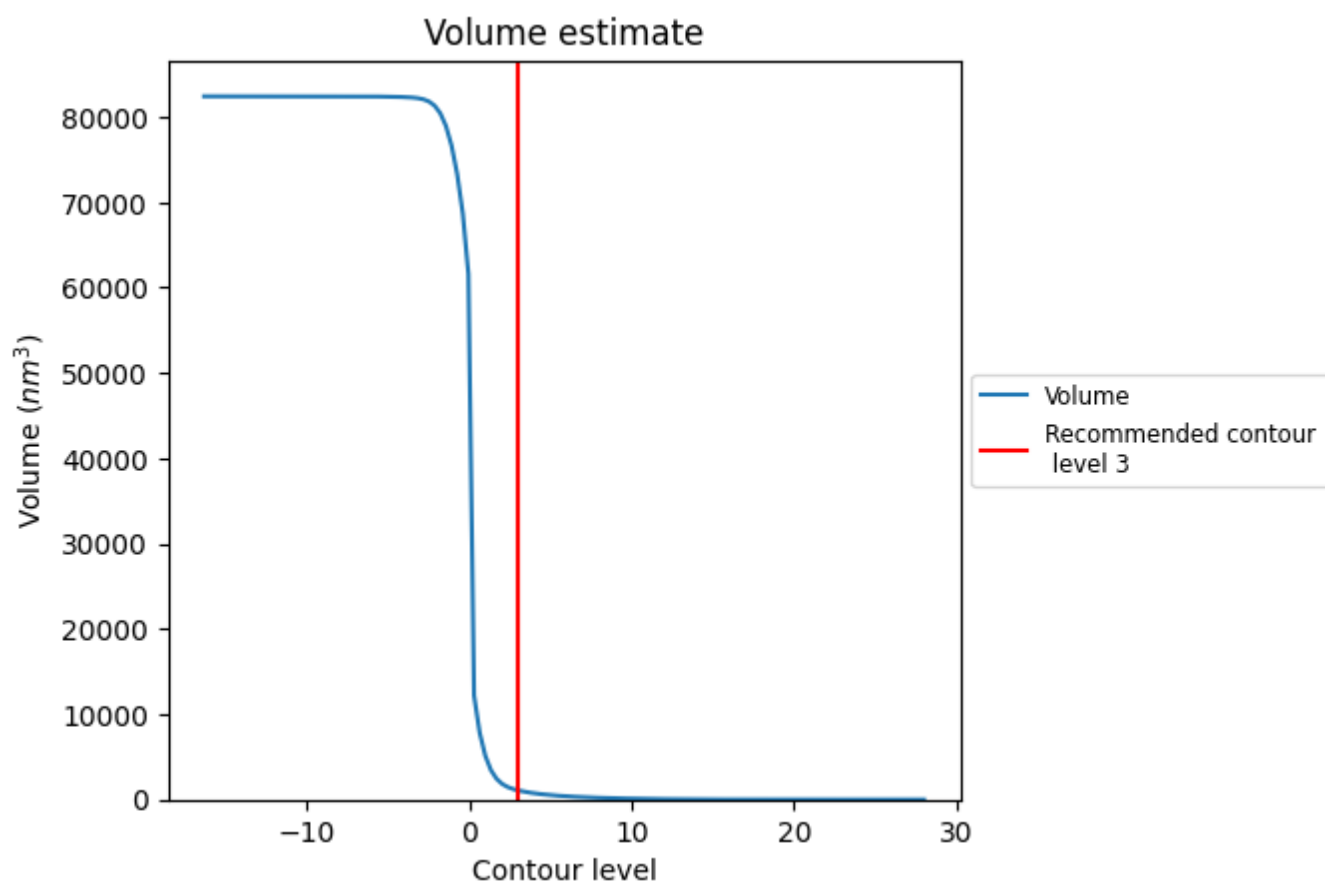
This section contains the results of statistical analysis of the map.

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.

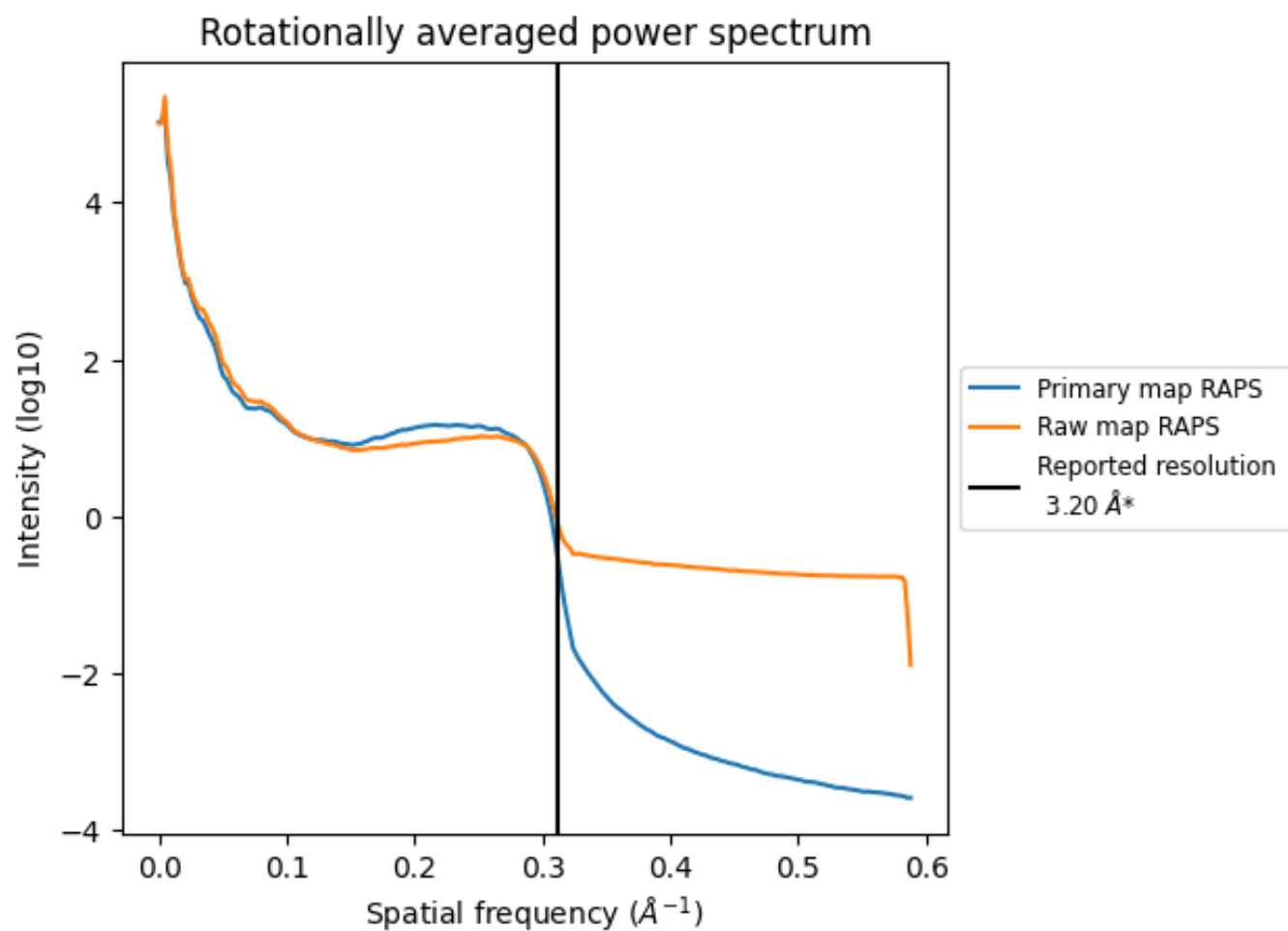
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1076 nm³; this corresponds to an approximate mass of 972 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 ⓘ

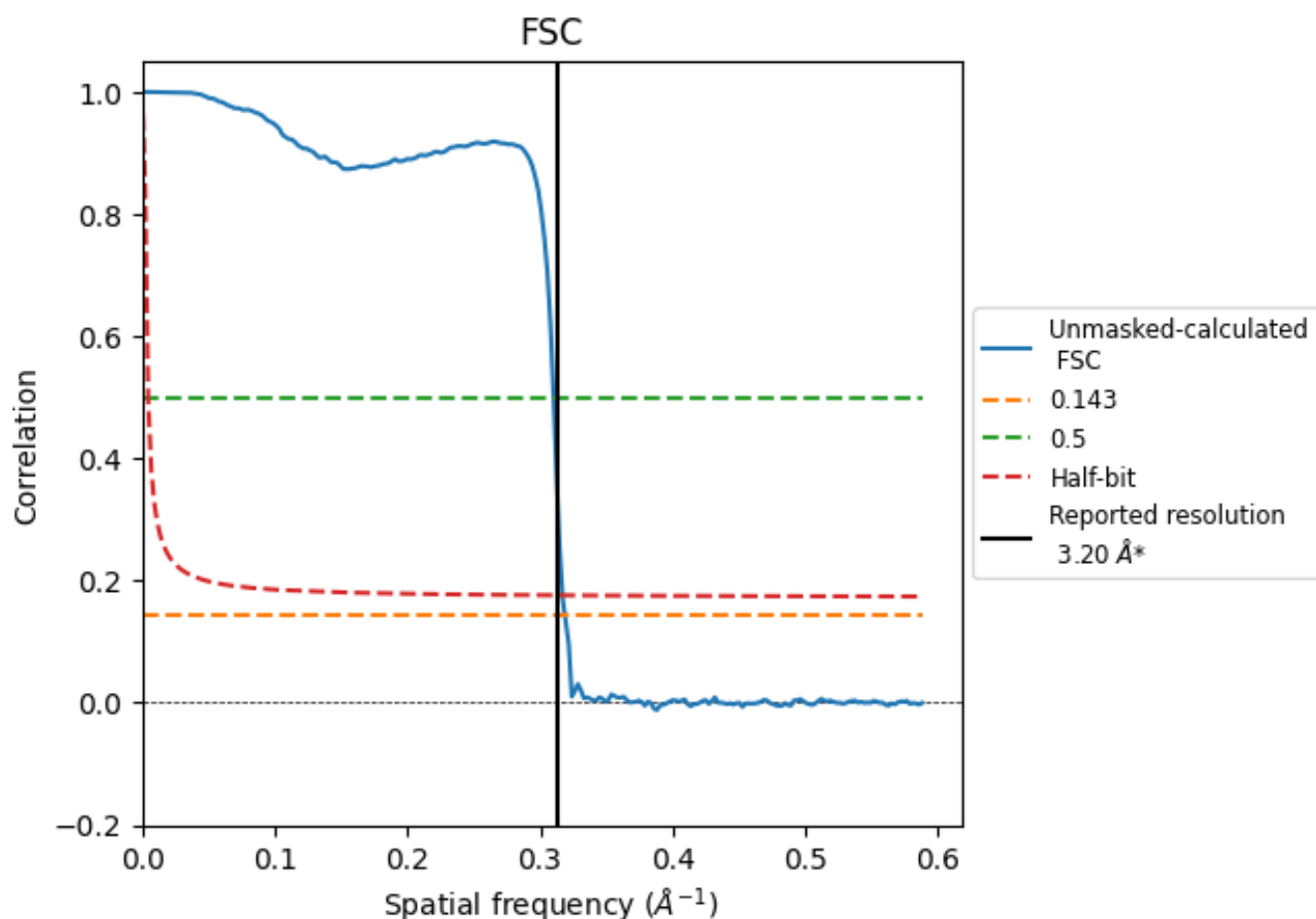


*Reported resolution corresponds to spatial frequency of $0.312 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

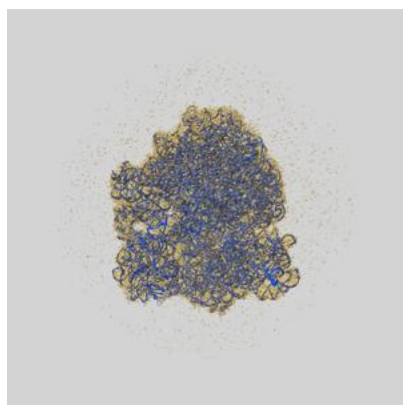
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.14	3.22	3.16

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

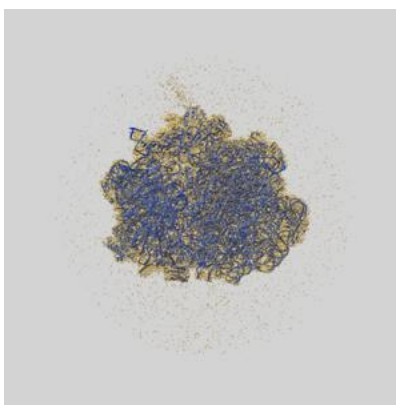
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-29624 and PDB model 8FZF. Per-residue inclusion information can be found in section [3](#) on page [17](#).

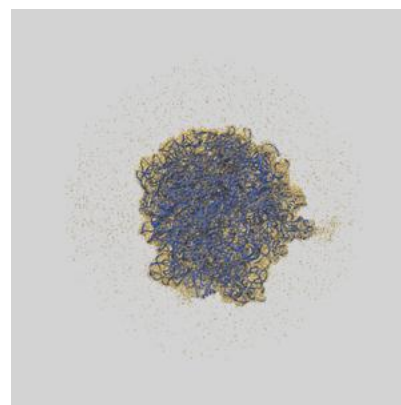
9.1 Map-model overlay [i](#)



X



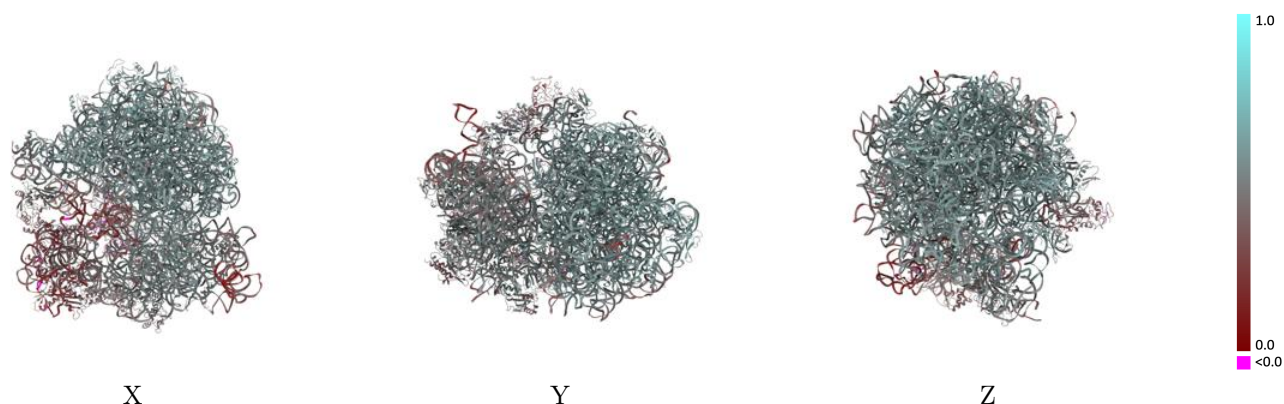
Y



Z

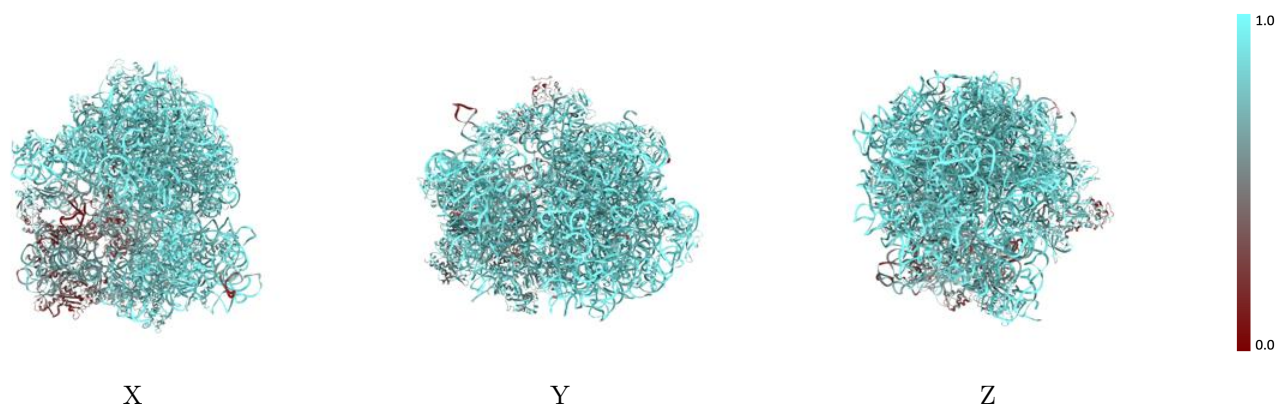
The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



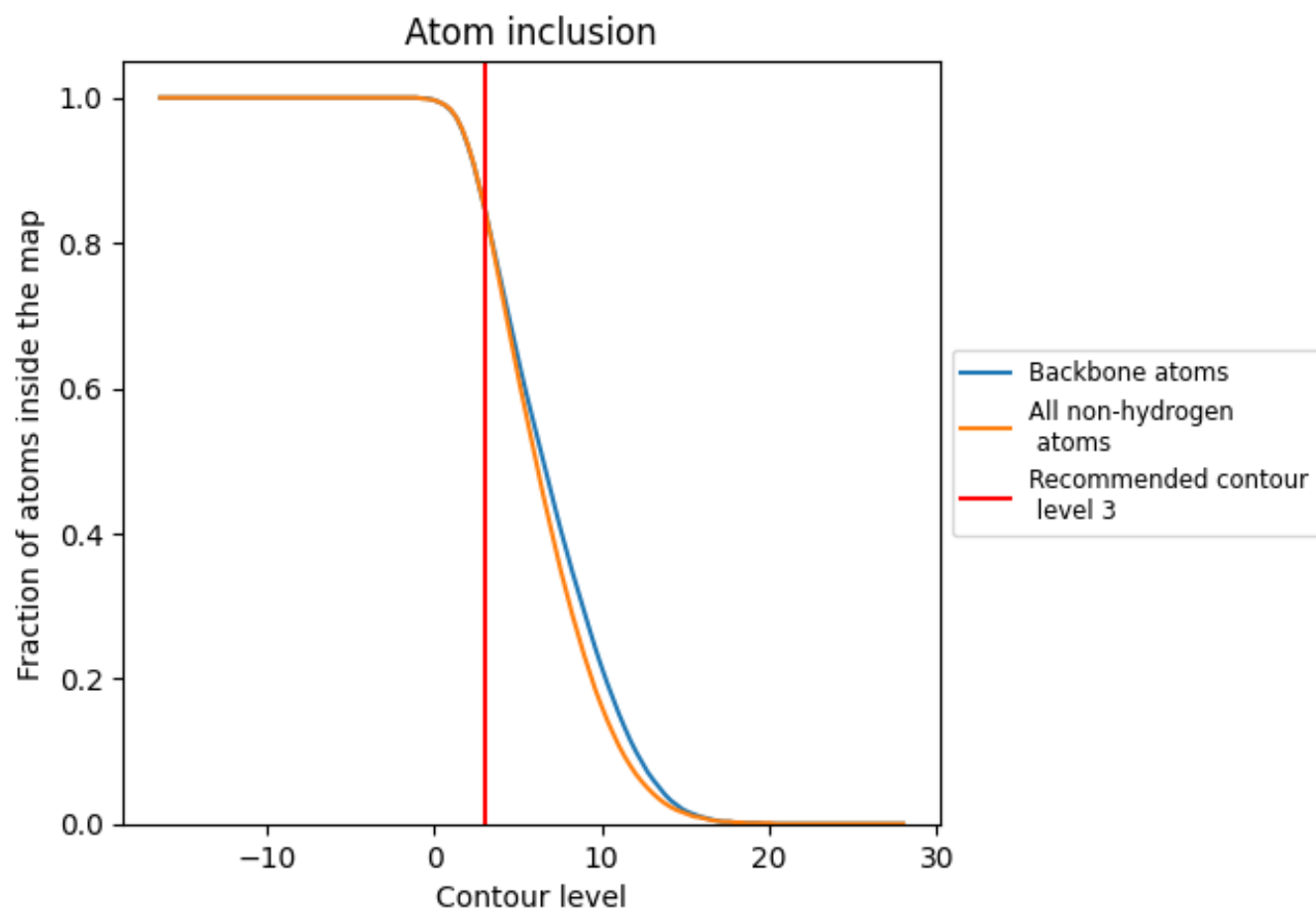
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 85% 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) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8500	 0.4990
1	 0.8780	 0.5530
2	 0.8760	 0.5690
3	 0.5550	 0.4030
4	 0.9260	 0.5790
5	 0.8090	 0.5430
6	 0.9160	 0.5940
7	 0.9110	 0.5860
8	 0.9180	 0.5840
A	 0.9190	 0.5310
B	 0.9170	 0.4930
C	 0.8950	 0.5810
D	 0.8990	 0.5800
E	 0.8650	 0.5670
F	 0.7330	 0.4450
G	 0.8470	 0.5300
I	 0.4290	 0.3140
J	 0.3130	 0.2330
L	 0.9100	 0.5860
M	 0.8570	 0.5760
N	 0.8970	 0.5720
O	 0.8210	 0.5520
P	 0.9420	 0.5920
Q	 0.8620	 0.5310
R	 0.8490	 0.5710
S	 0.9540	 0.5980
T	 0.9250	 0.5730
U	 0.8850	 0.5740
V	 0.8640	 0.5630
W	 0.8660	 0.5430
X	 0.8580	 0.5530
Y	 0.8850	 0.5840
Z	 0.9020	 0.5730
a	 0.8510	 0.4510
b	 0.6130	 0.4070



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Chain	Atom inclusion	Q-score
c	 0.3900	 0.3840
d	 0.8010	 0.4920
e	 0.8080	 0.5130
f	 0.7550	 0.4610
g	 0.3300	 0.2960
h	 0.8200	 0.5080
i	 0.5800	 0.3700
j	 0.4380	 0.3200
k	 0.7320	 0.4910
l	 0.7870	 0.5300
m	 0.4120	 0.3400
n	 0.4930	 0.3780
o	 0.8150	 0.4890
p	 0.8280	 0.5120
q	 0.8180	 0.5150
r	 0.8150	 0.5080
s	 0.4130	 0.2980
t	 0.7880	 0.4880
u	 0.4420	 0.4010
v	 0.9510	 0.5130
x	 0.6210	 0.3410
z	 0.5660	 0.4570