



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 10:15 AM UTC

PDB ID : 8W2N / pdb_00008w2n
EMDB ID : EMD-43752
Title : E. coli 70S ribosome with unmodified Lys-tRNA^{Pro}(GGG) in the P/P conformation on a slippery CCC-C codon and Elongation Factor P bound (uL1 in the open conformation)
Authors : Kimbrough, E.M.; Dunham, C.M.; Nguyen, H.A.
Deposited on : 2024-02-20
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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
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

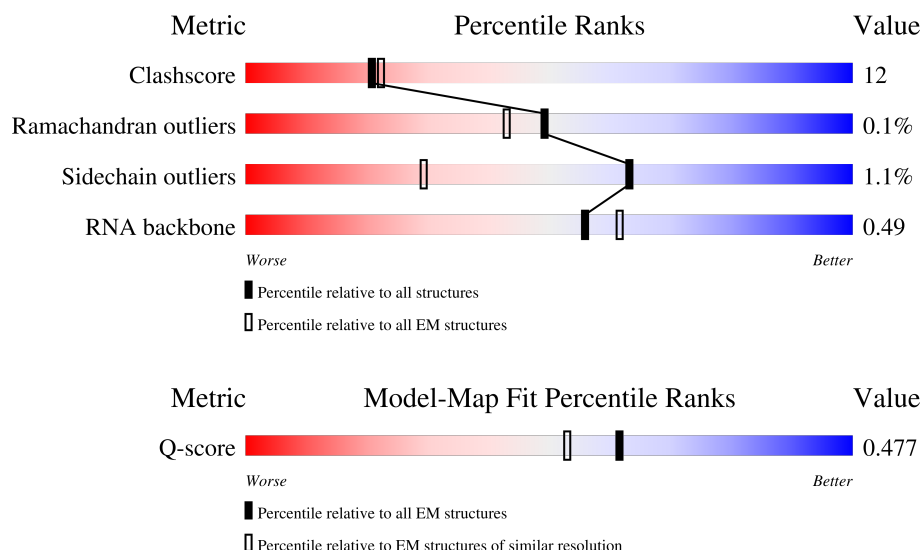
1 Overall quality at a glance

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.



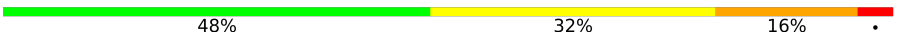
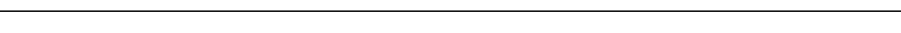
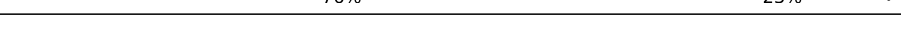
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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	1	2904	
2	2	1540	
3	3	120	

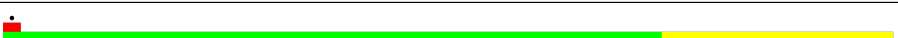
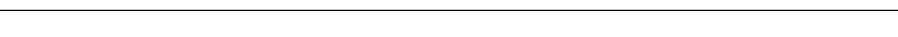
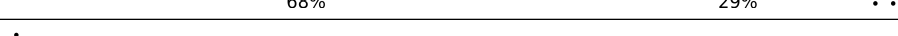
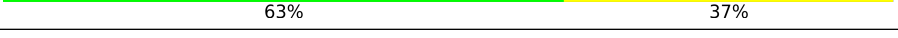
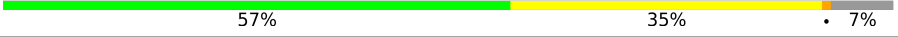
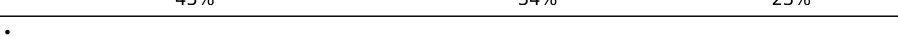
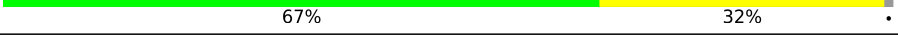
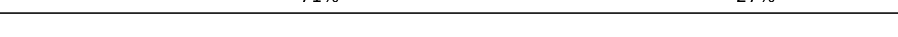
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Mol	Chain	Length	Quality of chain
4	4	18	
5	5	77	
6	6	188	
7	B	273	
8	C	209	
9	D	201	
10	E	179	
11	F	177	
12	G	149	
13	J	142	
14	K	123	
15	L	144	
16	M	136	
17	N	127	
18	O	117	
19	P	115	
20	Q	118	
21	R	103	
22	S	110	
23	T	100	
24	U	104	
25	V	94	
26	W	84	
27	X	78	
28	Y	63	

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Mol	Chain	Length	Quality of chain
29	Z	59	
30	a	70	
31	b	57	
32	c	55	
33	d	46	
34	e	65	
35	f	38	
36	g	241	
37	h	233	
38	i	206	
39	j	167	
40	k	135	
41	l	179	
42	m	130	
43	n	130	
44	o	103	
45	p	129	
46	q	124	
47	r	118	
48	s	101	
49	t	89	
50	u	82	
51	v	84	
52	w	75	
53	x	92	

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Mol	Chain	Length	Quality of chain
54	y	87	76% 23%
55	z	71	23% 68% 31%

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 145329 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 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2815	Total	C	N	O	P	0	0
			60445	26964	11140	19526	2815		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 1914786293
1	887	A	U	conflict	GB 1914786293
1	1847	G	A	conflict	GB 1914786293
1	2069	A	G	conflict	GB 1914786293

- Molecule 2 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	1532	Total	C	N	O	P	0	0
			32887	14674	6033	10648	1532		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	120	Total	C	N	O	P	0	0
			2569	1144	468	837	120		

- Molecule 4 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	6	Total	C	N	O	P	0	0
			125	56	21	42	6		

- Molecule 5 is a RNA chain called tRNA^{ProL} (GGG).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	77	Total	C	N	O	P	0	0
			1648	733	297	541	77		

- Molecule 6 is a protein called Elongation factor P.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	188	Total	C	N	O	S	0	0
			1461	928	242	286	5		

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

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

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

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

- Molecule 9 is a protein called 50S ribosomal protein L4.

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

- Molecule 10 is a protein called 50S ribosomal protein L5.

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

- Molecule 11 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F	175	Total	C	N	O	S	0	0
			1313	826	241	244	2		

- Molecule 12 is a protein called 50S ribosomal protein L9.

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	N	119	Total	C	N	O	S	0	0
			951	588	195	163	5		

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	T	94	Total	C	N	O	S	0	0
			746	470	140	134	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	U	103	Total	C	N	O		0	0
			788	498	148	142			

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Z	58	Total	C	N	O	S	0	0
			448	281	87	78	2		

- Molecule 30 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	a	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 31 is a protein called 50S ribosomal protein L32.

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

- Molecule 32 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	c	52	Total	C	N	O	0	0
			426	275	78	73		

- Molecule 33 is a protein called 50S ribosomal protein L34.

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

- Molecule 34 is a protein called 50S ribosomal protein L35.

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

- Molecule 35 is a protein called 50S ribosomal protein L36.

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

- Molecule 36 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	g	225	Total	C	N	O	S	0	0
			1760	1113	316	323	8		

- Molecule 37 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	h	208	Total	C	N	O	S	0	0
			1636	1036	307	290	3		

- Molecule 38 is a protein called 30S ribosomal protein S4.

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

- Molecule 39 is a protein called 30S ribosomal protein S5.

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

- Molecule 40 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	k	104	Total	C	N	O	S	0	0
			848	536	153	152	7		

- Molecule 41 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	l	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 42 is a protein called 30S ribosomal protein S8.

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

- Molecule 43 is a protein called 30S ribosomal protein S9.

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

- Molecule 44 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	o	99	Total	C	N	O	S	0	0
			790	495	151	143	1		

- Molecule 45 is a protein called 30S ribosomal protein S11.

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

- Molecule 46 is a protein called 30S ribosomal protein S12.

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

- Molecule 47 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	r	116	Total	C	N	O	S	0	0
			900	558	181	158	3		

- Molecule 48 is a protein called 30S ribosomal protein S14.

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

- Molecule 49 is a protein called 30S ribosomal protein S15.

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

- Molecule 50 is a protein called 30S ribosomal protein S16.

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

- Molecule 51 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	v	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 52 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	w	66	Total	C	N	O	S	0	0
			544	344	102	97	1		

- Molecule 53 is a protein called 30S ribosomal protein S19.

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

- Molecule 54 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	y	86	Total	C	N	O	S	0	0
			669	414	138	114	3		

- Molecule 55 is a protein called 30S ribosomal protein S21.

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

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
56	1	290	Total	Mg	0
			290	290	
56	2	138	Total	Mg	0
			138	138	
56	3	10	Total	Mg	0
			10	10	
56	B	3	Total	Mg	0
			3	3	
56	C	2	Total	Mg	0
			2	2	
56	D	4	Total	Mg	0
			4	4	
56	E	1	Total	Mg	0
			1	1	
56	J	1	Total	Mg	0
			1	1	
56	L	2	Total	Mg	0
			2	2	
56	M	1	Total	Mg	0
			1	1	
56	P	2	Total	Mg	0
			2	2	
56	Q	2	Total	Mg	0
			2	2	
56	R	2	Total	Mg	0
			2	2	
56	S	1	Total	Mg	0
			1	1	
56	T	1	Total	Mg	0
			1	1	
56	Z	2	Total	Mg	0
			2	2	

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Mol	Chain	Residues	Atoms		AltConf
56	b	2	Total 2	Mg 2	0
56	d	1	Total 1	Mg 1	0
56	e	3	Total 3	Mg 3	0
56	f	2	Total 2	Mg 2	0
56	i	3	Total 3	Mg 3	0
56	j	2	Total 2	Mg 2	0
56	l	2	Total 2	Mg 2	0
56	m	2	Total 2	Mg 2	0
56	q	1	Total 1	Mg 1	0
56	y	1	Total 1	Mg 1	0

- Molecule 57 is water.

Mol	Chain	Residues	Atoms		AltConf
57	1	508	Total 508	O 508	0
57	2	395	Total 395	O 395	0
57	3	17	Total 17	O 17	0
57	5	5	Total 5	O 5	0
57	C	1	Total 1	O 1	0
57	D	2	Total 2	O 2	0
57	E	7	Total 7	O 7	0
57	F	3	Total 3	O 3	0
57	G	4	Total 4	O 4	0

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Mol	Chain	Residues	Atoms		AltConf
57	J	2	Total 2	O 2	0
57	L	1	Total 1	O 1	0
57	N	1	Total 1	O 1	0
57	O	1	Total 1	O 1	0
57	P	2	Total 2	O 2	0
57	T	1	Total 1	O 1	0
57	V	2	Total 2	O 2	0
57	W	1	Total 1	O 1	0
57	X	1	Total 1	O 1	0
57	Y	8	Total 8	O 8	0
57	Z	1	Total 1	O 1	0
57	a	2	Total 2	O 2	0
57	c	2	Total 2	O 2	0
57	g	10	Total 10	O 10	0
57	h	11	Total 11	O 11	0
57	i	1	Total 1	O 1	0
57	k	5	Total 5	O 5	0
57	l	9	Total 9	O 9	0
57	m	5	Total 5	O 5	0
57	n	4	Total 4	O 4	0
57	p	2	Total 2	O 2	0

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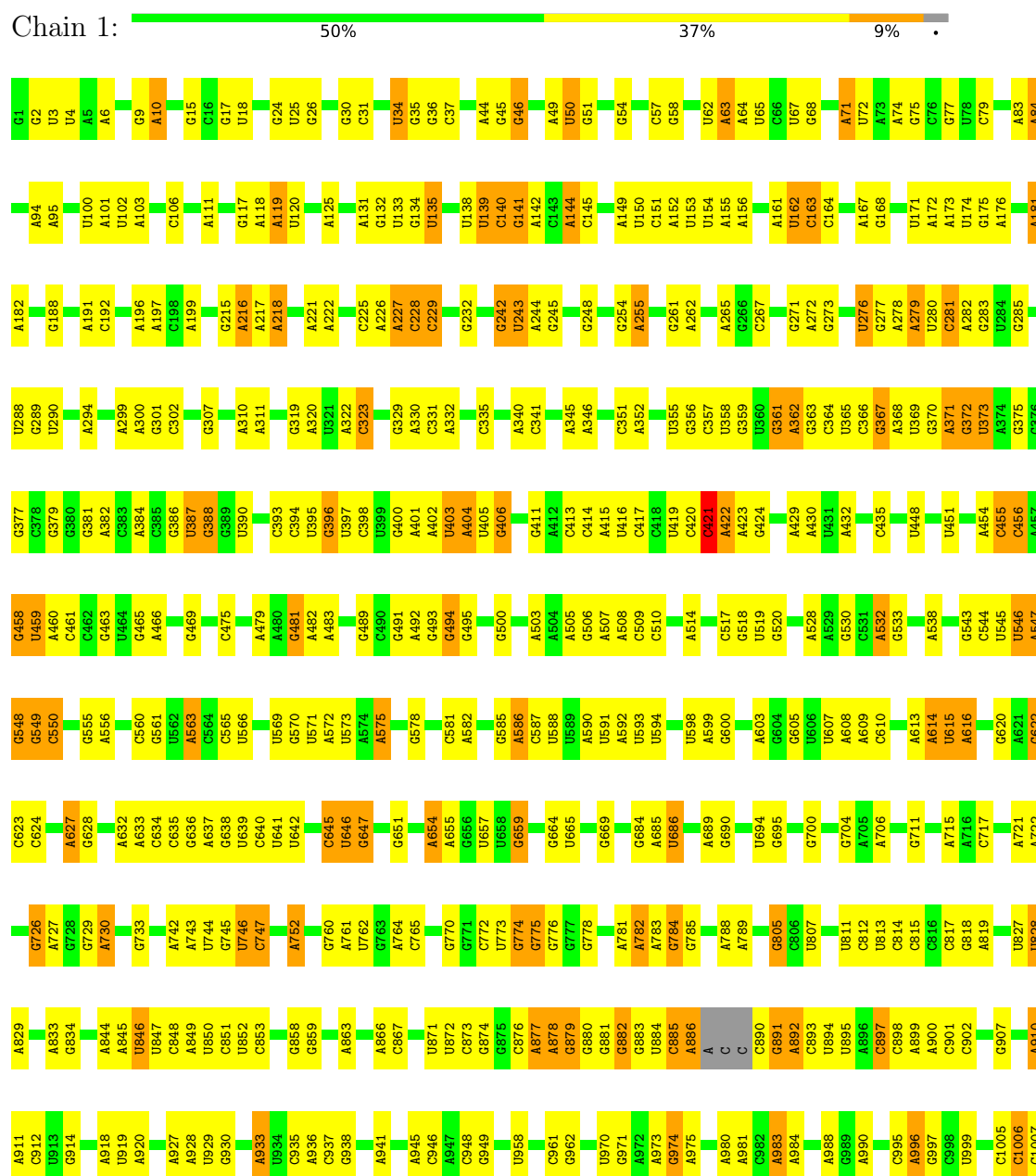
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Mol	Chain	Residues	Atoms		AltConf
57	q	3	Total 3	O 3	0
57	r	6	Total 6	O 6	0
57	s	1	Total 1	O 1	0
57	t	5	Total 5	O 5	0
57	u	1	Total 1	O 1	0
57	v	3	Total 3	O 3	0
57	w	6	Total 6	O 6	0
57	x	5	Total 5	O 5	0
57	y	3	Total 3	O 3	0
57	z	7	Total 7	O 7	0

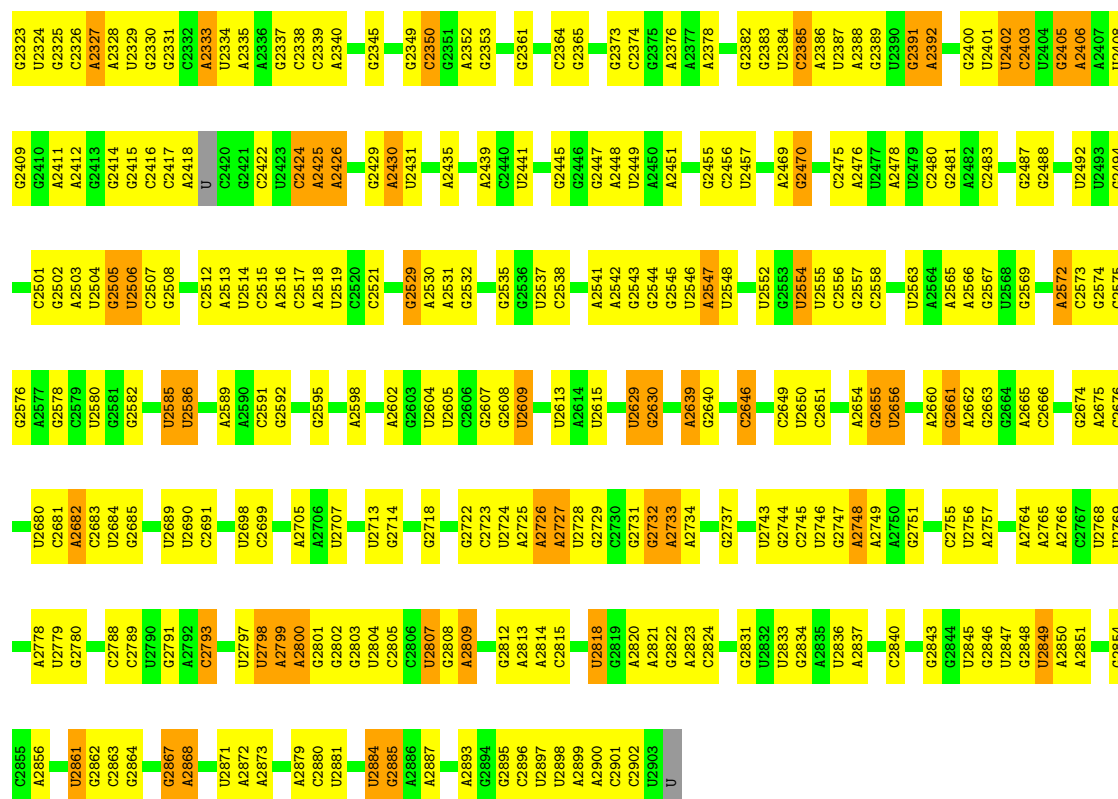
3 Residue-property plots

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: 23S ribosomal RNA

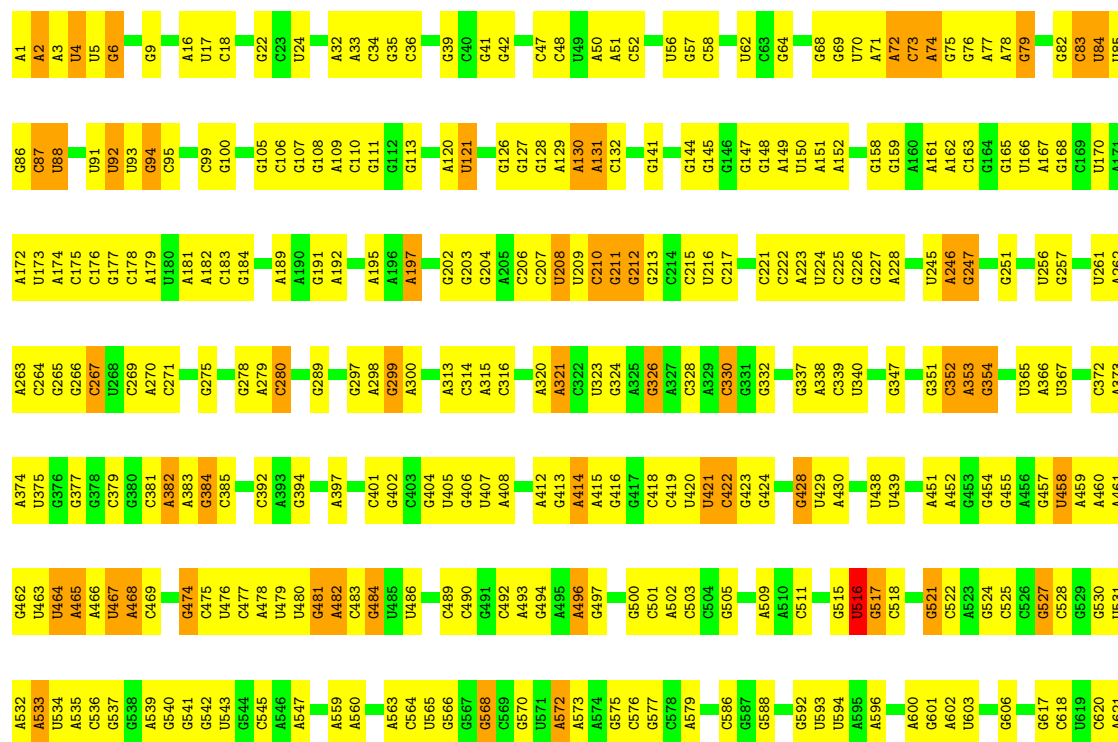


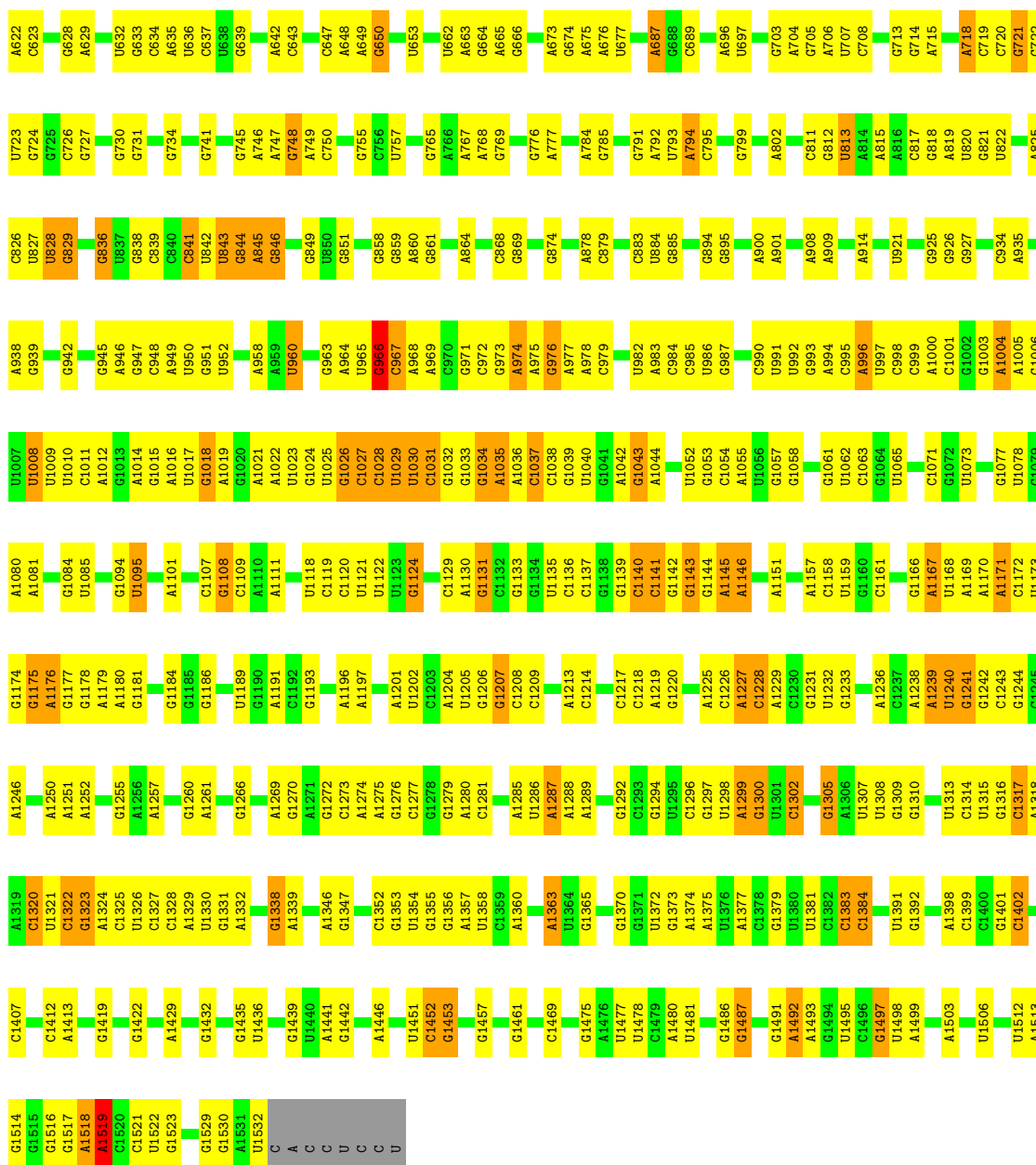
U2244	A2020	G1907	G1799	G1722	U1599	U1523	A1433	G1343	G1250	G1160	U1081	A1008
U2245	C2021	A1913	C1800	A1722	C1600	G1524	A1434	U1344	A1253	G1169	U1082	A1009
A2246	U2022	G1914	A1801	G1723	C1607	A1528	C1437	C1345	A1254	C1170	A1083	A1010
A2247	C2023	G1915	A1802	G1724	A1608	G1529	C1437	U1352	U1255	G1171	A1084	G1011
U2248	G2024	A1916	A1803	U1725	A1614	A1532	G1441	C1357	G1256	U1173	A1086	U1012
G2250	U2026	U1917	A1808	C1727	A1614	A1532	U1442	U1357	U1263	U1174	G1087	C1013
G2251	G2027	A1918	A1809	C1728	A1618	C1533	U1443	A1359	U1264	U1175	A1088	A1014
C2252	A2030	C1920	C1816	U1729	G1618	U1534	U1444	A1365	A1265	U1176	A1089	U1019
C2263	A2031	C1920	G1817	C1730	G1619	C1535	U1445	A1367	A1266	U1177	A1090	A1020
C2264	G2032	U1923	U1818	G1731	U1621	C1536	C1446	A1368	A1268	C1178	G1092	G1022
	A2033	U1923	A1819	G1732	G1622	G1537	U1447	G1368	A1269	U1179	G1093	U1023
		U1928	G1826	C1733	G1622	U1539	U1448	G1369	C1270	U1180	U1094	G1024
	A2037	A1928	G1826	G1734	G1627	G1540	A1453	G1371	A1271	U1180	A1095	G1025
	G2038	G1929	A1829	A1735	G1628	C1541	U1458	U1379	A1272	U1183	A1096	G1026
	U2039	G1930	A1829	U1736	G1628	U1542	G1459	U1380	A1272	U1184	U1097	A1027
	G2040	U1932	C1830	G1737	U1542	G1543	U1460	G1385	A1275	G1185	A1098	A1028
	U2041	G1933	G1831	G1738	A1632	G1543	U1461	U1387	A1285	U1188	G1099	A1032
	A2042	C1933	C1832	U1742	U1636	A1551	A1469	A1392	G1283	U1188	U1100	U1033
	C2043	A1936	C1833	G1743	A1637	A1552	U1470	A1395	A1285	G1193	C1102	
	A2051	A1937	G1840	U1746	G1645	C1558	A1471	U1396	G1295	G1193	A1103	A1039
	G2052	A1938	U1841	U1747	C1646	U1559	G1471	U1397	C1296	C1196	C1104	A1040
	A2053	U1939	G1842	U1751	U1647	G1560	G1475	C1398	G1296	C1197	U1105	G1041
	A2054	C1941	C1843	U1752	U1648	G1561	U1476	C1399	G1300	U1198	G1106	G1042
	C2055	U1942	G1847	G1753	G1651	U1562	U1477	U1400	A1301	U1199	C1043	C1043
	U2056	U1943	A1848	G1754	A1652	C1564	U1478	U1401	A1302	C1200	U1108	C1044
	A2060	U1955	U1856	G1756	G1653	C1565	G1482	G1407	C1306	G1210	G1110	A1046
	G2061	U1956	G1857	A1757	A1655	A1566	U1483	U1408	A1307	G1211	A1111	G1047
	A2062	C1957	A1858	U1758	G1656	A1569	U1484	U1409	A1204	A1214	G1112	A1048
	C2063	C1958	C1760	A1759	G1667	A1570	U1485	U1410	G1205	G1212	U1130	A1054
	G2064	G1964	C1764	C1765	G1674	A1571	U1486	U1411	G1206	G1223	U1132	G1064
	C2065	G1964	G1862	U1765	A1675	A1572	U1487	U1412	G1224	U1225	A1134	U1065
	A2069	G1967	U1864	U1766	A1676	C1574	C1488	G1416	U1316	G1227	G1135	U1066
	G2070	G1968	U1865	G1766	A1676	C1574	C1489	C1417	G1317	G1227	G1136	A1067
	A2071	A1969	C1870	A1773	A1679	C1577	A1490	U1407	U1318	G1227	G1139	G1068
	C2072	U1970	A1871	G1776	G1680	U1578	G1491	U1408	C1319	A1214	C1140	A1069
	G2073	G1972	A1872	G1776	G1681	A1579	A1494	U1409	A1320	G1220	U1141	A1070
	A2078	A1987	G1873	U1779	U1683	C1581	A1495	U1411	A1321	G1223	A1142	G1071
	U2079	U1991	C1874	A1780	U1683	C1582	U1497	G1416	A1322	G1224	A1143	A1073
	C2086	U1992	C1881	A1783	U1693	C1583	C1498	C1417	G1324	G1225	G1136	C1072
	G2087	U1993	U1882	A1784	G1695	U1584	A1504	C1417	U1326	G1227	G1139	G1074
	U2092	C1996	U1883	A1787	G1695	C1585	A1505	A1419	A1327	G1227	G1139	C1075
	G2093	C1997	A1884	G1788	G1699	G1587	U1506	A1420	A1328	A1230	C1140	C1076
	C2096	C2006	G1888	A1789	U1709	G1588	C1507	G1421	U1329	G1236	G1141	C1077
	A2097	G2006	G1888	C1790	U1710	A1590	A1508	G1422	C1330	A1237	A1143	A1073
	U2098	G2010	G1896	A1791	U1711	C1592	G1510	G1425	G1334	U1240	G1149	G1074
	G2100	A1900	A1901	A1794	U1712	C1593	U1513	C1428	G1338	A1241	C1150	C1075
	A2101	C2103	A1901	C1795	A1713	U1594	G1514	G1429	G1339	A1247	C1153	C1076
	G2102	U2015	G1715	U1796	G1714	U1597	A1515	G1430	U1340	G1248	U1159	U1078
	C2103	U2016	G1715	G1797	G1715	A1597	G1516	A1431	G1341	G1249		G1079
	C2104	C2104	G1906	U1798	U1716	A1598	G1516	G1432	A1342			A1080



• Molecule 2: 16S ribosomal RNA

Chain 2: 50% 41% 8%





• Molecule 3: 5S mRNA



• Molecule 4: mRNA





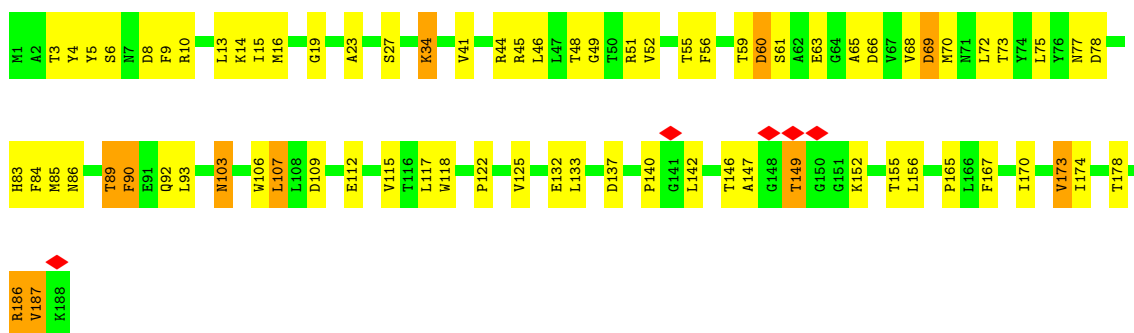
• Molecule 5: tRNA^{ProL} (GGG)

Chain 5: 48% 32% 16%



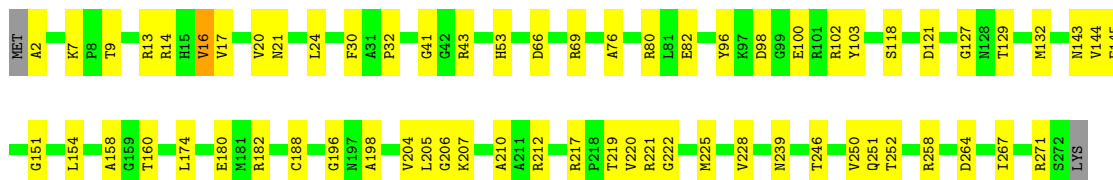
• Molecule 6: Elongation factor P

Chain 6: 60% 35% 6%



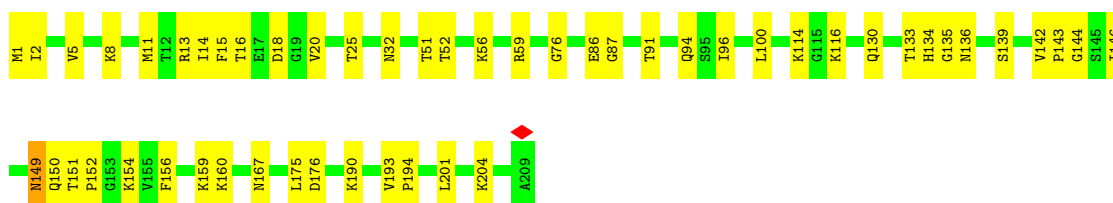
• Molecule 7: 50S ribosomal protein L2

Chain B: 75% 23%



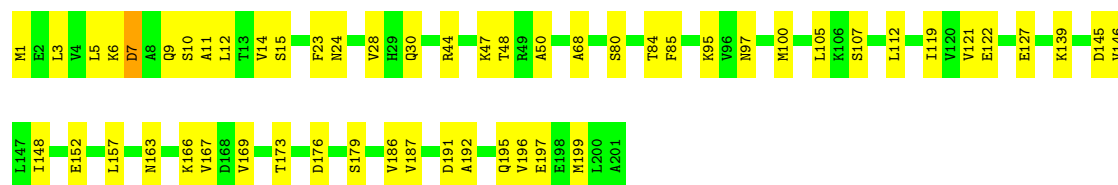
• Molecule 8: 50S ribosomal protein L3

Chain C: 75% 24%



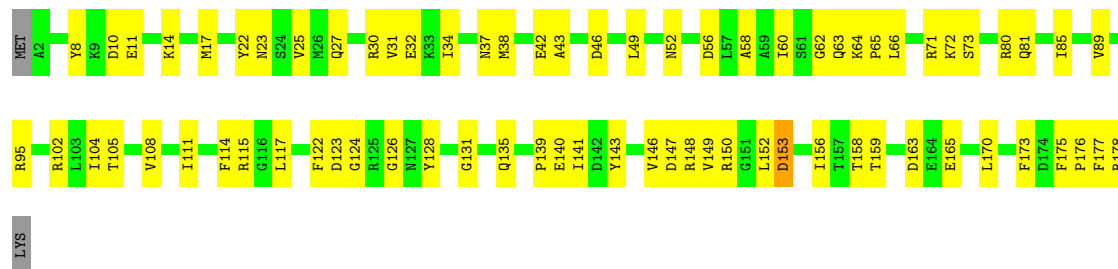
• Molecule 9: 50S ribosomal protein L4

Chain D: 73% 26%



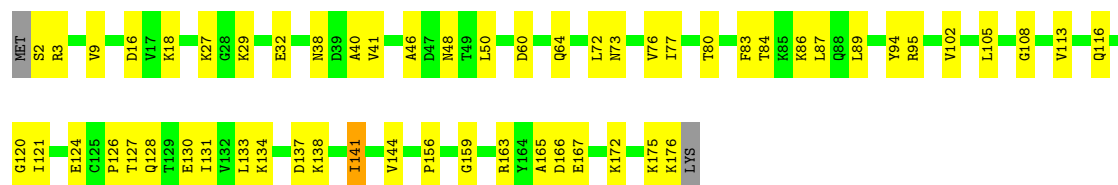
- Molecule 10: 50S ribosomal protein L5

Chain E: 58% 40% ..



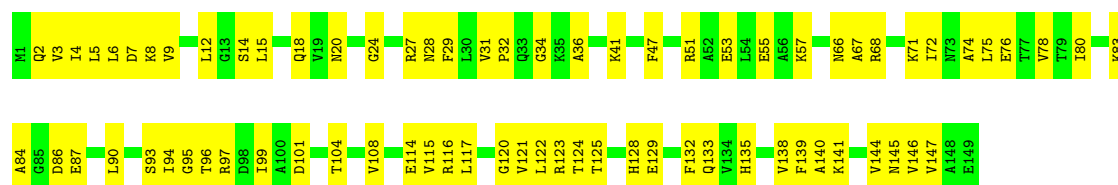
- Molecule 11: 50S ribosomal protein L6

Chain F: 67% 31% ..



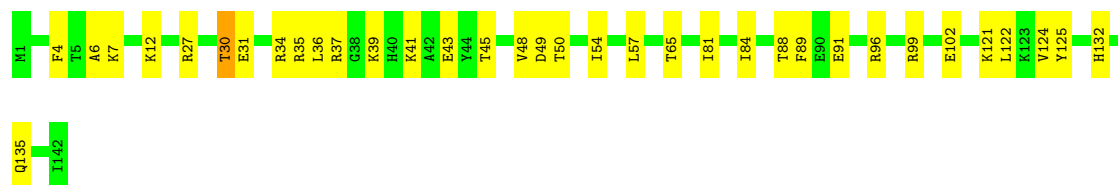
- Molecule 12: 50S ribosomal protein L9

Chain G: 50% 50%



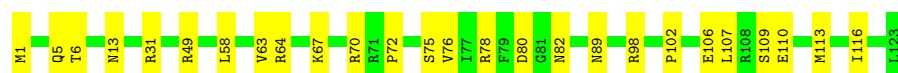
- Molecule 13: 50S ribosomal protein L13

Chain J: 75% 24%



- Molecule 14: 50S ribosomal protein L14

Chain K:  79% 21%



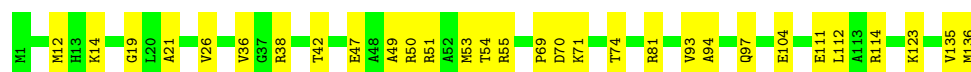
- Molecule 15: 50S ribosomal protein L15

Chain L:  74% 26%



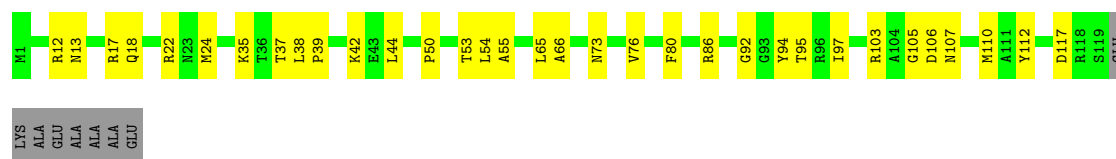
- Molecule 16: 50S ribosomal protein L16

Chain M:  78% 22%



- Molecule 17: 50S ribosomal protein L17

Chain N:  68% 26% 6%



- Molecule 18: 50S ribosomal protein L18

Chain O:  76% 23%



- Molecule 19: 50S ribosomal protein L19

Chain P:  73% 24% ..



- Molecule 20: 50S ribosomal protein L20

Chain Q:  74% 25% ..



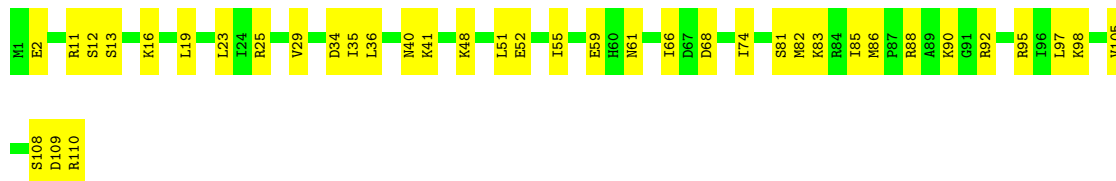
- Molecule 21: 50S ribosomal protein L21

Chain R:  67% 33%



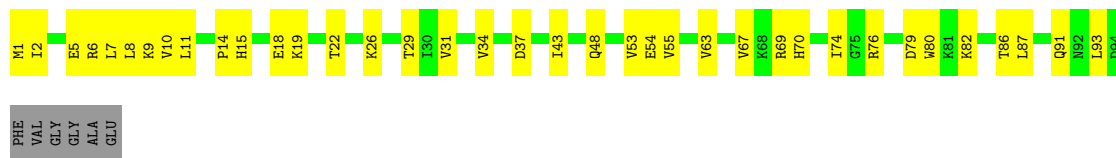
- Molecule 22: 50S ribosomal protein L22

Chain S:  65% 35%



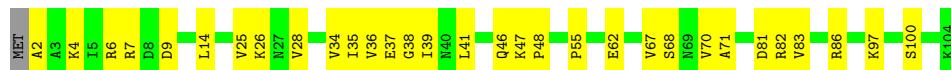
- Molecule 23: 50S ribosomal protein L23

Chain T:  57% 37% 6%



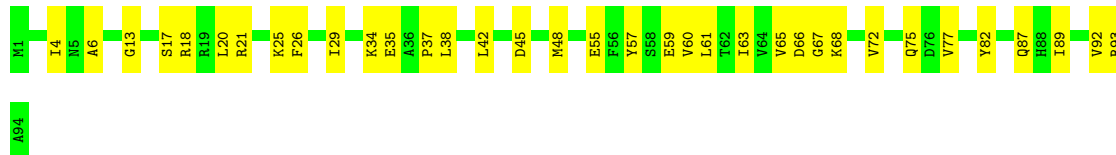
- Molecule 24: 50S ribosomal protein L24

Chain U:  69% 30%



- Molecule 25: 50S ribosomal protein L25

Chain V:  63% 37%



- Molecule 26: 50S ribosomal protein L27

Chain W:  64% 26% 10%



- Molecule 27: 50S ribosomal protein L28

Chain X: 



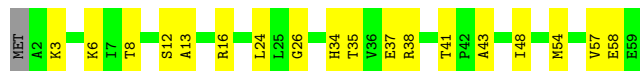
- Molecule 28: 50S ribosomal protein L29

Chain Y: 



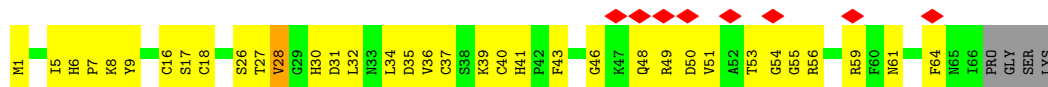
- Molecule 29: 50S ribosomal protein L30

Chain Z: 



- Molecule 30: 50S ribosomal protein L31

Chain a: 



- Molecule 31: 50S ribosomal protein L32

Chain b: 



- Molecule 32: 50S ribosomal protein L33

Chain c: 



- Molecule 33: 50S ribosomal protein L34

Chain d: 



- Molecule 34: 50S ribosomal protein L35

Chain e: 68% 29%



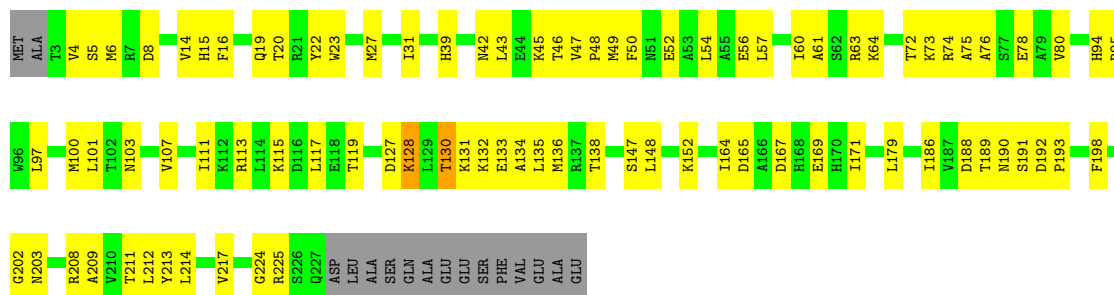
- Molecule 35: 50S ribosomal protein L36

Chain f: 63% 37%



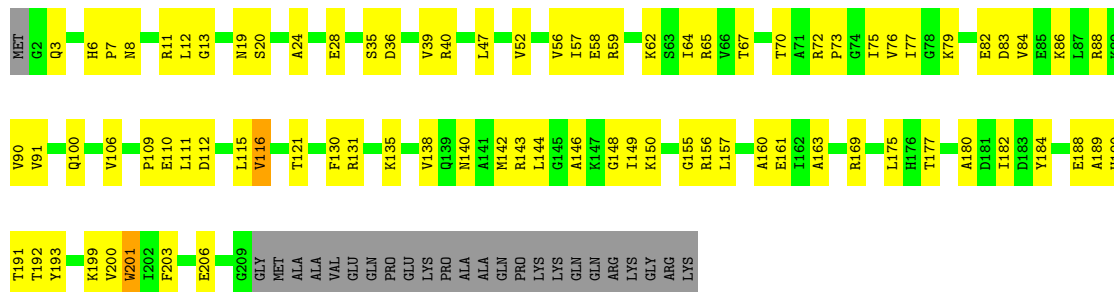
- Molecule 36: 30S ribosomal protein S2

Chain g: 57% 35% 7%



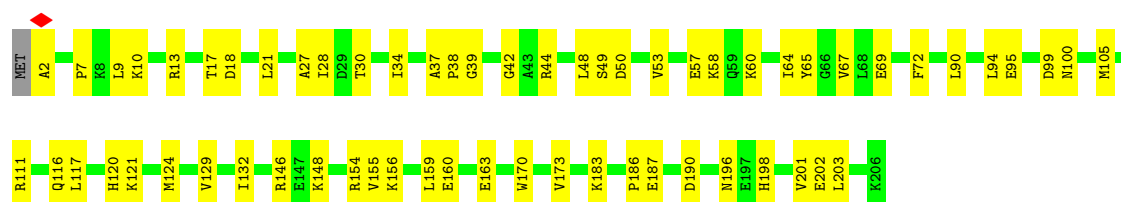
- Molecule 37: 30S ribosomal protein S3

Chain h: 54% 35% 11%

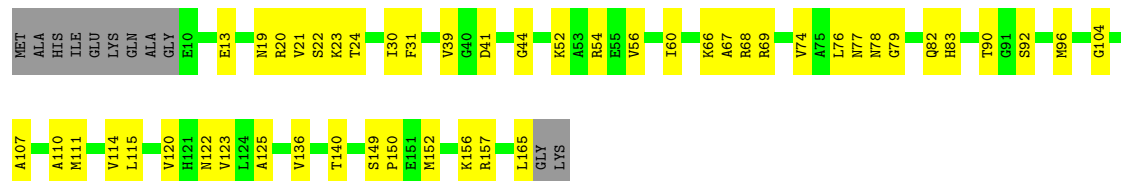


- Molecule 38: 30S ribosomal protein S4

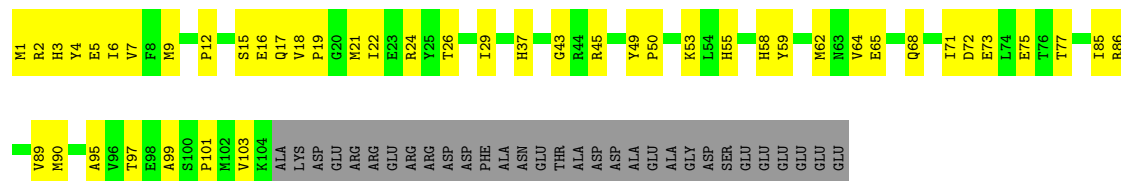
Chain i: 69% 30%



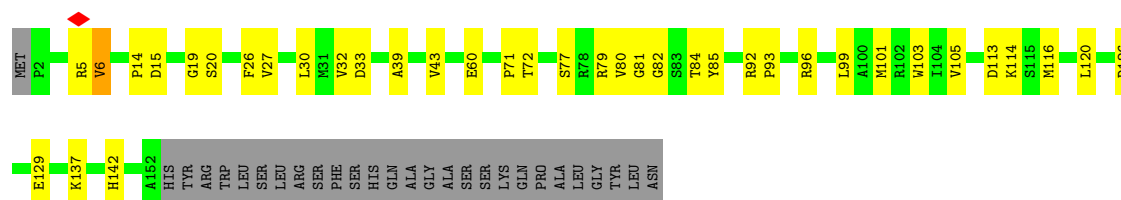
- Molecule 39: 30S ribosomal protein S5



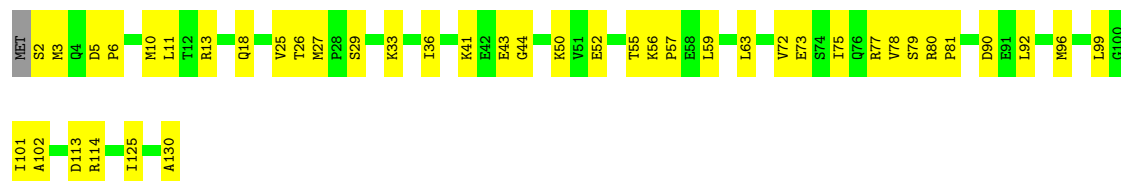
- Molecule 40: 30S ribosomal protein S6



- Molecule 41: 30S ribosomal protein S7

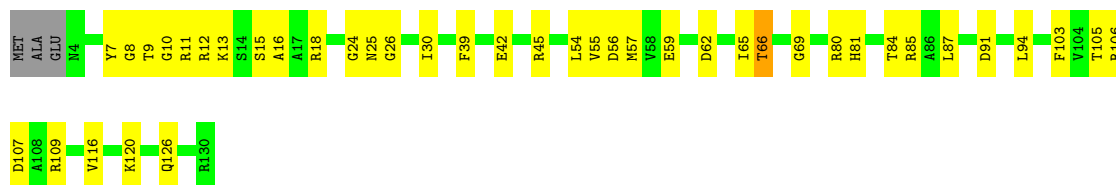


- Molecule 42: 30S ribosomal protein S8



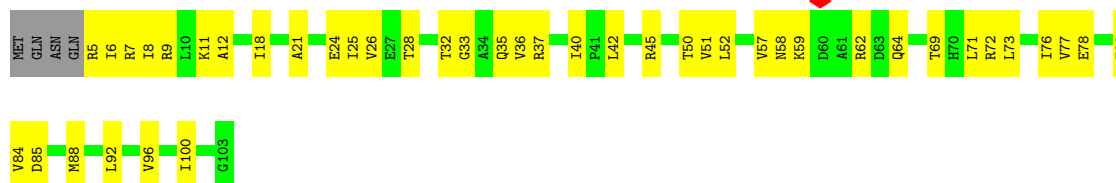
- Molecule 43: 30S ribosomal protein S9

Chain n:  66% 31% ..



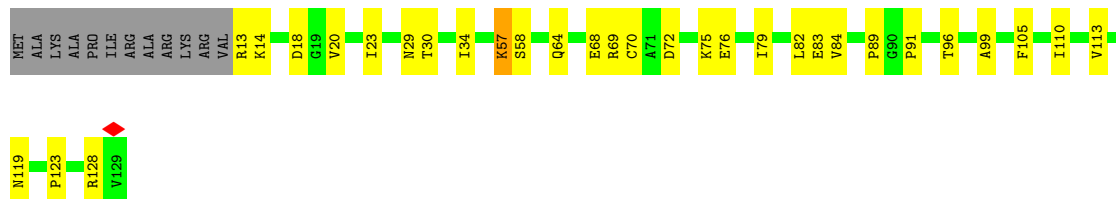
- Molecule 44: 30S ribosomal protein S10

Chain o:  54% 42% .



- Molecule 45: 30S ribosomal protein S11

Chain p:  67% 23% 9% .



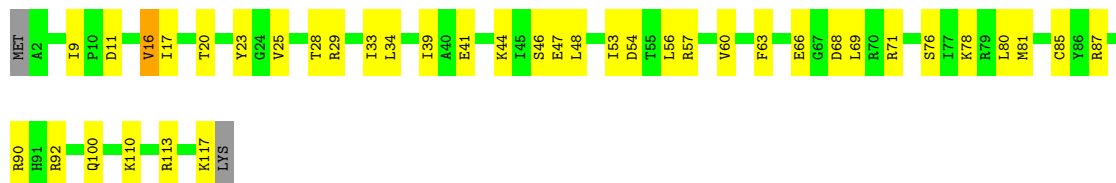
- Molecule 46: 30S ribosomal protein S12

Chain q:  71% 27% ..



- Molecule 47: 30S ribosomal protein S13

Chain r:  65% 32% ..



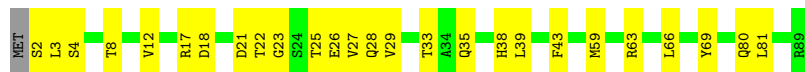
- Molecule 48: 30S ribosomal protein S14

Chain s:  69% 29% ..



- Molecule 49: 30S ribosomal protein S15

Chain t:  70% 29% .



- Molecule 50: 30S ribosomal protein S16

Chain u:  60% 40%



- Molecule 51: 30S ribosomal protein S17

Chain v:  56% 39% 5%



- Molecule 52: 30S ribosomal protein S18

Chain w:  5% 40% 48% 12%



- Molecule 53: 30S ribosomal protein S19

Chain x:  58% 33% 10%



- Molecule 54: 30S ribosomal protein S20

Chain y:  76% 23% .



• Molecule 55: 30S ribosomal protein S21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	74503	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	56.07	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.031	Depositor
Minimum map value	-0.019	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.00251	Depositor
Map size ($\text{\AA}$)	547.328, 547.328, 547.328	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.069, 1.069, 1.069	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 5MC, 4OC, MA6, PSU, UR3, MG, G7M, 0TD, 2MG, KEO

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	1	0.74	1/67700 (0.0%)	0.47	7/105611 (0.0%)
2	2	0.62	0/36543	0.42	1/57001 (0.0%)
3	3	0.60	0/2872	0.46	0/4478
4	4	0.53	0/138	0.65	0/212
5	5	0.49	0/1841	0.64	3/2870 (0.1%)
6	6	0.90	1/1470 (0.1%)	1.06	6/1992 (0.3%)
7	B	0.82	2/2121 (0.1%)	0.68	0/2852
8	C	0.75	0/1586	0.70	1/2134 (0.0%)
9	D	0.66	0/1571	0.57	0/2113
10	E	0.54	0/1434	0.60	0/1926
11	F	0.54	0/1333	0.58	0/1805
12	G	0.38	0/1122	0.58	0/1515
13	J	0.67	0/1152	0.62	0/1551
14	K	0.76	0/955	0.62	0/1279
15	L	0.77	0/1062	0.80	2/1413 (0.1%)
16	M	0.66	0/1093	0.58	0/1460
17	N	0.81	0/964	0.70	1/1289 (0.1%)
18	O	0.55	0/902	0.62	1/1209 (0.1%)
19	P	0.80	1/929 (0.1%)	0.70	1/1242 (0.1%)
20	Q	0.93	2/960 (0.2%)	0.66	1/1278 (0.1%)
21	R	0.75	1/829 (0.1%)	0.61	0/1107
22	S	0.69	0/864	0.61	0/1156
23	T	0.62	0/752	0.59	0/1005
24	U	0.55	0/796	0.55	0/1062
25	V	0.64	0/766	0.59	0/1025
26	W	0.71	0/589	0.62	0/779
27	X	0.74	0/635	0.61	0/848
28	Y	0.53	0/502	0.55	0/667
29	Z	0.68	0/452	0.57	0/605
30	a	0.28	0/531	0.49	0/709
31	b	0.68	0/450	0.64	0/599
32	c	0.71	0/433	0.60	0/576

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	d	0.78	0/380	0.59	0/498
34	e	0.86	0/513	0.72	0/676
35	f	0.79	0/303	0.72	0/397
36	g	0.37	0/1791	0.52	0/2413
37	h	0.59	1/1663 (0.1%)	0.66	0/2241
38	i	0.50	0/1665	0.56	0/2227
39	j	0.63	0/1165	0.59	0/1568
40	k	0.49	0/867	0.53	0/1171
41	l	0.57	0/1195	0.63	0/1602
42	m	0.66	0/989	0.56	0/1326
43	n	0.55	0/1034	0.61	0/1375
44	o	0.50	0/800	0.56	0/1082
45	p	0.59	1/893 (0.1%)	0.58	0/1205
46	q	0.60	0/960	0.61	0/1286
47	r	0.52	0/909	0.59	0/1215
48	s	0.62	0/817	0.57	0/1088
49	t	0.61	0/722	0.55	0/964
50	u	0.63	0/659	0.73	2/884 (0.2%)
51	v	0.54	0/657	0.55	0/881
52	w	0.53	0/553	0.55	0/743
53	x	0.46	0/680	0.57	0/915
54	y	0.51	0/675	0.49	0/895
55	z	0.27	0/597	0.47	0/792
All	All	0.68	10/155834 (0.0%)	0.51	26/232812 (0.0%)

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	143	ASN	CA-C	-7.59	1.46	1.53
1	1	2102	G	C1'-N9	-7.38	1.36	1.48
20	Q	25	TYR	CA-C	-6.36	1.44	1.52
6	6	77	ASN	CA-C	-6.12	1.45	1.52
20	Q	48	ARG	CA-C	-5.88	1.44	1.52

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	C	149	ASN	N-CA-C	10.53	125.08	109.59
6	6	149	THR	N-CA-C	9.82	121.58	111.07
15	L	36	LYS	N-CA-C	9.01	131.70	113.31
5	5	2	G	C4'-C3'-O3'	8.30	121.85	109.40
6	6	60	ASP	N-CA-C	8.23	121.98	109.23

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	60445	0	30406	1004	0
2	2	32887	0	16565	590	0
3	3	2569	0	1301	40	0
4	4	125	0	66	2	0
5	5	1648	0	834	24	0
6	6	1461	0	1421	52	0
7	B	2082	0	2154	47	0
8	C	1565	0	1616	47	0
9	D	1552	0	1619	41	0
10	E	1410	0	1444	63	0
11	F	1313	0	1358	38	0
12	G	1111	0	1148	58	0
13	J	1129	0	1162	37	0
14	K	946	0	1023	24	0
15	L	1053	0	1128	31	0
16	M	1074	0	1157	21	0
17	N	951	0	994	21	0
18	O	892	0	923	19	0
19	P	917	0	962	24	0
20	Q	947	0	1019	22	0
21	R	816	0	839	27	0
22	S	857	0	922	27	0
23	T	746	0	811	27	0
24	U	788	0	844	23	0
25	V	753	0	780	25	0
26	W	582	0	599	17	0
27	X	625	0	652	16	0
28	Y	501	0	531	15	0
29	Z	448	0	488	15	0
30	a	522	0	524	28	0
31	b	444	0	458	16	0
32	c	426	0	464	15	0
33	d	377	0	418	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	e	504	0	572	19	0
35	f	302	0	343	12	0
36	g	1760	0	1787	61	0
37	h	1636	0	1710	64	0
38	i	1643	0	1706	43	0
39	j	1152	0	1196	42	0
40	k	848	0	846	35	0
41	l	1181	0	1238	29	0
42	m	979	0	1031	33	0
43	n	1022	0	1070	36	0
44	o	790	0	831	37	0
45	p	877	0	887	25	0
46	q	957	0	1017	30	0
47	r	900	0	965	31	0
48	s	805	0	844	26	0
49	t	714	0	734	25	0
50	u	649	0	666	33	0
51	v	648	0	691	28	0
52	w	544	0	560	31	0
53	x	663	0	688	25	0
54	y	669	0	719	17	0
55	z	589	0	629	19	0
56	1	290	0	0	0	0
56	2	138	0	0	0	0
56	3	10	0	0	0	0
56	B	3	0	0	0	0
56	C	2	0	0	0	0
56	D	4	0	0	0	0
56	E	1	0	0	0	0
56	J	1	0	0	0	0
56	L	2	0	0	0	0
56	M	1	0	0	0	0
56	P	2	0	0	0	0
56	Q	2	0	0	0	0
56	R	2	0	0	0	0
56	S	1	0	0	0	0
56	T	1	0	0	0	0
56	Z	2	0	0	0	0
56	b	2	0	0	0	0
56	d	1	0	0	0	0
56	e	3	0	0	0	0
56	f	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	i	3	0	0	0	0
56	j	2	0	0	0	0
56	l	2	0	0	0	0
56	m	2	0	0	0	0
56	q	1	0	0	0	0
56	y	1	0	0	0	0
57	1	508	0	0	44	0
57	2	395	0	0	36	0
57	3	17	0	0	1	0
57	5	5	0	0	2	0
57	C	1	0	0	0	0
57	D	2	0	0	3	0
57	E	7	0	0	0	0
57	F	3	0	0	0	0
57	G	4	0	0	0	0
57	J	2	0	0	0	0
57	L	1	0	0	0	0
57	N	1	0	0	0	0
57	O	1	0	0	0	0
57	P	2	0	0	0	0
57	T	1	0	0	0	0
57	V	2	0	0	1	0
57	W	1	0	0	0	0
57	X	1	0	0	0	0
57	Y	8	0	0	1	0
57	Z	1	0	0	3	0
57	a	2	0	0	1	0
57	c	2	0	0	0	0
57	g	10	0	0	0	0
57	h	11	0	0	3	0
57	i	1	0	0	0	0
57	k	5	0	0	0	0
57	l	9	0	0	0	0
57	m	5	0	0	0	0
57	n	4	0	0	0	0
57	p	2	0	0	2	0
57	q	3	0	0	0	0
57	r	6	0	0	1	0
57	s	1	0	0	0	0
57	t	5	0	0	1	0
57	u	1	0	0	4	0
57	v	3	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	w	6	0	0	0	0
57	x	5	0	0	0	0
57	y	3	0	0	0	0
57	z	7	0	0	2	0
All	All	145329	0	97360	2856	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 12.

The worst 5 of 2856 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)
1:1:2799:A:H5''	57:1:3407:HOH:O	1.32	1.22
29:Z:3:LYS:HE2	57:Z:201:HOH:O	1.46	1.14
51:v:75:LEU:HD11	57:v:101:HOH:O	1.62	0.98
50:u:14:ARG:HG2	57:u:101:HOH:O	1.63	0.98
46:q:72:HIS:HB3	46:q:99:ARG:HH22	1.29	0.96

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	
6	6	185/188 (98%)	167 (90%)	16 (9%)	2 (1%)	11	43
7	B	269/273 (98%)	243 (90%)	26 (10%)	0	100	100
8	C	207/209 (99%)	184 (89%)	23 (11%)	0	100	100
9	D	199/201 (99%)	189 (95%)	10 (5%)	0	100	100
10	E	175/179 (98%)	161 (92%)	14 (8%)	0	100	100
11	F	173/177 (98%)	161 (93%)	12 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	G	147/149 (99%)	133 (90%)	14 (10%)	0	100	100
13	J	140/142 (99%)	134 (96%)	6 (4%)	0	100	100
14	K	121/123 (98%)	110 (91%)	11 (9%)	0	100	100
15	L	142/144 (99%)	127 (89%)	15 (11%)	0	100	100
16	M	134/136 (98%)	123 (92%)	11 (8%)	0	100	100
17	N	117/127 (92%)	108 (92%)	9 (8%)	0	100	100
18	O	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
19	P	112/115 (97%)	108 (96%)	4 (4%)	0	100	100
20	Q	115/118 (98%)	112 (97%)	3 (3%)	0	100	100
21	R	101/103 (98%)	92 (91%)	9 (9%)	0	100	100
22	S	108/110 (98%)	106 (98%)	2 (2%)	0	100	100
23	T	92/100 (92%)	87 (95%)	5 (5%)	0	100	100
24	U	101/104 (97%)	95 (94%)	6 (6%)	0	100	100
25	V	92/94 (98%)	82 (89%)	10 (11%)	0	100	100
26	W	74/84 (88%)	67 (90%)	7 (10%)	0	100	100
27	X	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
28	Y	60/63 (95%)	58 (97%)	2 (3%)	0	100	100
29	Z	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
30	a	64/70 (91%)	54 (84%)	10 (16%)	0	100	100
31	b	54/57 (95%)	50 (93%)	4 (7%)	0	100	100
32	c	50/55 (91%)	45 (90%)	5 (10%)	0	100	100
33	d	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
34	e	62/65 (95%)	53 (86%)	9 (14%)	0	100	100
35	f	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
36	g	223/241 (92%)	198 (89%)	24 (11%)	1 (0%)	30	62
37	h	206/233 (88%)	189 (92%)	17 (8%)	0	100	100
38	i	203/206 (98%)	191 (94%)	12 (6%)	0	100	100
39	j	154/167 (92%)	144 (94%)	10 (6%)	0	100	100
40	k	102/135 (76%)	96 (94%)	6 (6%)	0	100	100
41	l	149/179 (83%)	141 (95%)	8 (5%)	0	100	100
42	m	127/130 (98%)	122 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	n	125/130 (96%)	116 (93%)	9 (7%)	0	100	100
44	o	97/103 (94%)	86 (89%)	11 (11%)	0	100	100
45	p	115/129 (89%)	106 (92%)	9 (8%)	0	100	100
46	q	120/124 (97%)	112 (93%)	8 (7%)	0	100	100
47	r	114/118 (97%)	103 (90%)	11 (10%)	0	100	100
48	s	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
49	t	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
50	u	80/82 (98%)	72 (90%)	8 (10%)	0	100	100
51	v	78/84 (93%)	76 (97%)	2 (3%)	0	100	100
52	w	64/75 (85%)	59 (92%)	5 (8%)	0	100	100
53	x	81/92 (88%)	75 (93%)	6 (7%)	0	100	100
54	y	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
55	z	68/71 (96%)	66 (97%)	2 (3%)	0	100	100
All	All	5793/6100 (95%)	5374 (93%)	416 (7%)	3 (0%)	49	79

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	6	165	PRO
6	6	187	VAL
36	g	128	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	
6	6	154/154 (100%)	139 (90%)	15 (10%)	8	32
7	B	216/218 (99%)	215 (100%)	1 (0%)	81	85
8	C	164/164 (100%)	164 (100%)	0	100	100
9	D	165/165 (100%)	164 (99%)	1 (1%)	78	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	E	148/150 (99%)	147 (99%)	1 (1%)	76	83
11	F	136/138 (99%)	134 (98%)	2 (2%)	57	76
12	G	114/114 (100%)	114 (100%)	0	100	100
13	J	116/116 (100%)	115 (99%)	1 (1%)	70	81
14	K	104/104 (100%)	104 (100%)	0	100	100
15	L	103/103 (100%)	101 (98%)	2 (2%)	50	73
16	M	109/109 (100%)	108 (99%)	1 (1%)	70	81
17	N	99/103 (96%)	98 (99%)	1 (1%)	68	80
18	O	86/87 (99%)	85 (99%)	1 (1%)	63	79
19	P	99/100 (99%)	95 (96%)	4 (4%)	28	61
20	Q	89/90 (99%)	87 (98%)	2 (2%)	45	71
21	R	84/84 (100%)	84 (100%)	0	100	100
22	S	93/93 (100%)	93 (100%)	0	100	100
23	T	81/84 (96%)	81 (100%)	0	100	100
24	U	84/85 (99%)	83 (99%)	1 (1%)	63	79
25	V	78/78 (100%)	77 (99%)	1 (1%)	61	78
26	W	58/62 (94%)	57 (98%)	1 (2%)	53	75
27	X	67/68 (98%)	67 (100%)	0	100	100
28	Y	54/55 (98%)	54 (100%)	0	100	100
29	Z	48/49 (98%)	48 (100%)	0	100	100
30	a	59/62 (95%)	58 (98%)	1 (2%)	53	75
31	b	47/48 (98%)	46 (98%)	1 (2%)	47	71
32	c	47/49 (96%)	47 (100%)	0	100	100
33	d	38/38 (100%)	38 (100%)	0	100	100
34	e	51/52 (98%)	50 (98%)	1 (2%)	48	72
35	f	34/34 (100%)	33 (97%)	1 (3%)	37	67
36	g	187/199 (94%)	186 (100%)	1 (0%)	81	85
37	h	171/190 (90%)	168 (98%)	3 (2%)	51	74
38	i	172/173 (99%)	171 (99%)	1 (1%)	78	84
39	j	119/126 (94%)	119 (100%)	0	100	100
40	k	91/116 (78%)	91 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	l	124/147 (84%)	121 (98%)	3 (2%)	43	70
42	m	104/105 (99%)	104 (100%)	0	100	100
43	n	105/107 (98%)	103 (98%)	2 (2%)	50	73
44	o	86/90 (96%)	86 (100%)	0	100	100
45	p	90/99 (91%)	90 (100%)	0	100	100
46	q	102/103 (99%)	101 (99%)	1 (1%)	68	80
47	r	94/96 (98%)	91 (97%)	3 (3%)	34	65
48	s	83/84 (99%)	82 (99%)	1 (1%)	63	79
49	t	76/77 (99%)	76 (100%)	0	100	100
50	u	65/65 (100%)	65 (100%)	0	100	100
51	v	74/78 (95%)	74 (100%)	0	100	100
52	w	57/65 (88%)	57 (100%)	0	100	100
53	x	72/79 (91%)	72 (100%)	0	100	100
54	y	65/66 (98%)	64 (98%)	1 (2%)	57	76
55	z	60/61 (98%)	60 (100%)	0	100	100
All	All	4822/4982 (97%)	4767 (99%)	55 (1%)	63	79

5 of 55 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
19	P	53	ARG
30	a	28	VAL
54	y	30	THR
46	q	80	ILE
19	P	60	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 88 such sidechains are listed below:

Mol	Chain	Res	Type
38	i	74	ASN
46	q	29	GLN
38	i	152	GLN
43	n	75	GLN
48	s	49	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2811/2904 (96%)	522 (18%)	46 (1%)
2	2	1530/1540 (99%)	260 (16%)	6 (0%)
3	3	119/120 (99%)	22 (18%)	0
4	4	5/18 (27%)	1 (20%)	0
5	5	76/77 (98%)	24 (31%)	4 (5%)
All	All	4541/4659 (97%)	829 (18%)	56 (1%)

5 of 829 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	10	A
1	1	15	G
1	1	34	U
1	1	35	G
1	1	36	G

5 of 56 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	1801	A
5	5	72	G
1	1	2190	G
5	5	18	G
2	2	1109	C

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

13 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	$\# Z > 2$
2	PSU	2	516	2	18,21,22	1.06	1 (5%)	21,30,33	2.03	4 (19%)
2	4OC	2	1402	2	20,23,24	2.92	8 (40%)	25,32,35	1.14	3 (12%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	2MG	2	1207	2	23,26,27	2.74	8 (34%)	33,38,41	2.14	10 (30%)
2	2MG	2	1516	2	23,26,27	2.60	8 (34%)	33,38,41	2.45	11 (33%)
2	MA6	2	1519	2	23,26,27	1.74	6 (26%)	33,38,41	3.01	12 (36%)
2	G7M	2	527	2	23,26,27	3.51	11 (47%)	34,39,42	1.86	7 (20%)
2	MA6	2	1518	2	23,26,27	1.70	5 (21%)	33,38,41	2.93	12 (36%)
2	5MC	2	967	2	19,22,23	3.45	8 (42%)	26,32,35	1.07	2 (7%)
6	KEO	6	34	6	16,18,19	0.74	0	15,21,23	1.54	1 (6%)
46	0TD	q	89	46	8,9,10	2.55	2 (25%)	6,11,13	1.24	0
2	5MC	2	1407	2	19,22,23	3.29	8 (42%)	26,32,35	1.06	1 (3%)
2	2MG	2	966	2	23,26,27	2.82	8 (34%)	33,38,41	2.17	7 (21%)
2	UR3	2	1498	2	19,22,23	2.48	5 (26%)	26,32,35	1.58	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
2	PSU	2	516	2	-	2/7/25/26	0/2/2/2
2	4OC	2	1402	2	-	2/9/29/30	0/2/2/2
2	2MG	2	1207	2	-	0/9/27/28	0/3/3/3
2	2MG	2	1516	2	-	0/9/27/28	0/3/3/3
2	MA6	2	1519	2	-	2/11/29/30	0/3/3/3
2	G7M	2	527	2	-	2/7/25/26	0/3/3/3
2	MA6	2	1518	2	-	0/11/29/30	0/3/3/3
2	5MC	2	967	2	-	2/7/25/26	0/2/2/2
6	KEO	6	34	6	-	8/19/20/22	-
46	0TD	q	89	46	-	2/7/12/14	-
2	5MC	2	1407	2	-	0/7/25/26	0/2/2/2
2	2MG	2	966	2	-	0/9/27/28	0/3/3/3
2	UR3	2	1498	2	-	0/7/25/26	0/2/2/2

The worst 5 of 78 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	527	G7M	C8-N7	10.30	1.50	1.33
2	2	967	5MC	C6-C5	8.49	1.48	1.34
2	2	1407	5MC	C6-C5	8.37	1.48	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	966	2MG	C2-N3	7.26	1.45	1.32
2	2	1207	2MG	C2-N3	6.82	1.45	1.32

The worst 5 of 73 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1519	MA6	N1-C6-N6	-10.22	104.41	116.86
2	2	1518	MA6	N1-C6-N6	-10.08	104.58	116.86
2	2	1516	2MG	C2-N3-C4	6.63	120.29	112.00
2	2	1518	MA6	C5-C6-N6	6.54	135.69	125.33
2	2	1519	MA6	C5-C6-N6	6.50	135.62	125.33

There are no chirality outliers.

5 of 20 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	2	516	PSU	O4'-C1'-C5-C4
2	2	516	PSU	O4'-C1'-C5-C6
2	2	967	5MC	O4'-C4'-C5'-O5'
2	2	967	5MC	C3'-C4'-C5'-O5'
2	2	1519	MA6	O4'-C4'-C5'-O5'

There are no ring outliers.

7 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	2	516	PSU	1	0
2	2	1402	4OC	1	0
2	2	1207	2MG	2	0
2	2	1519	MA6	1	0
2	2	1518	MA6	2	0
6	6	34	KEO	3	0
2	2	966	2MG	1	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 481 ligands modelled in this entry, 481 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

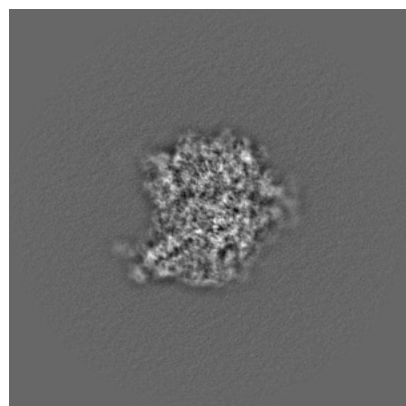
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43752. These allow visual inspection of the internal detail of the map and identification of artifacts.

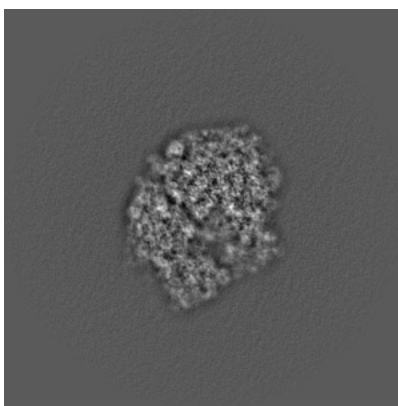
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

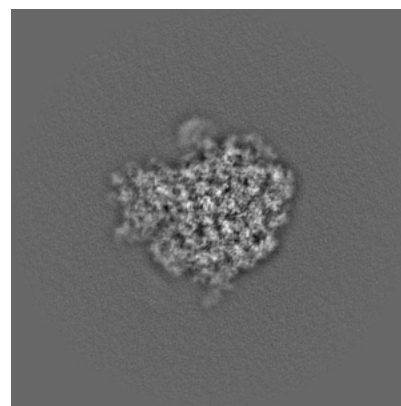
6.1.1 Primary map



X

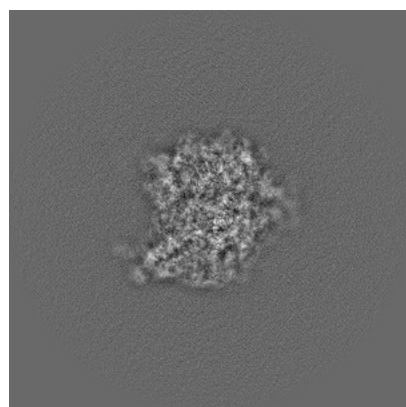


Y

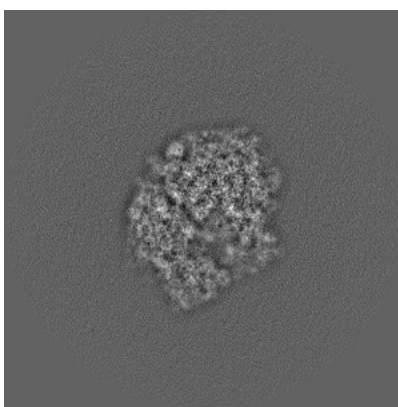


Z

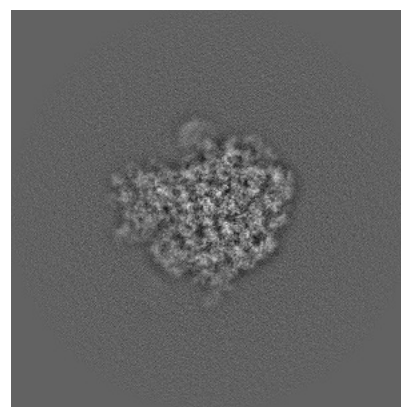
6.1.2 Raw map



X



Y

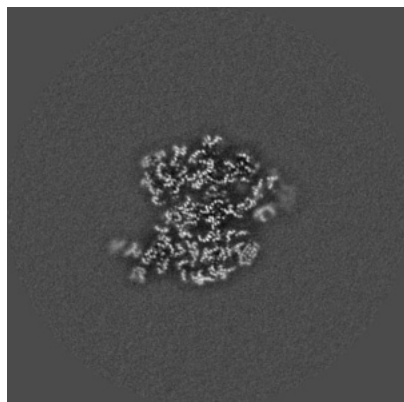


Z

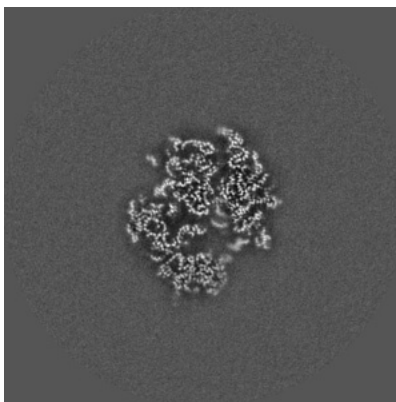
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

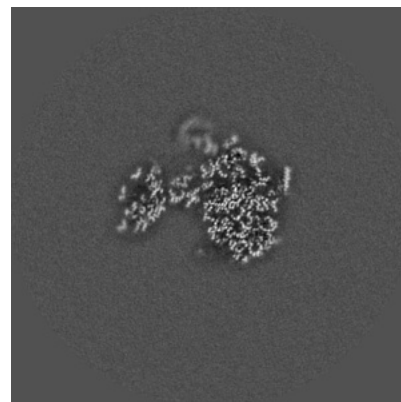
6.2.1 Primary map



X Index: 256

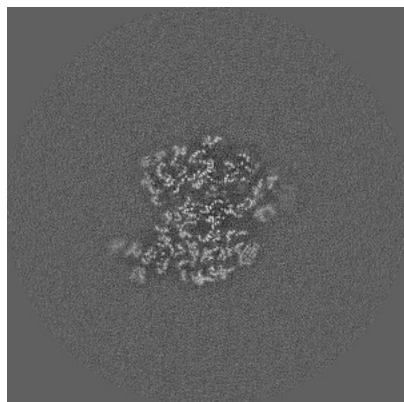


Y Index: 256

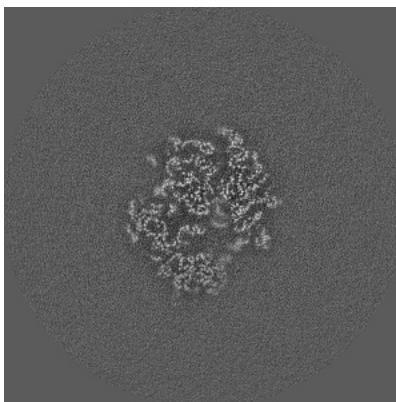


Z Index: 256

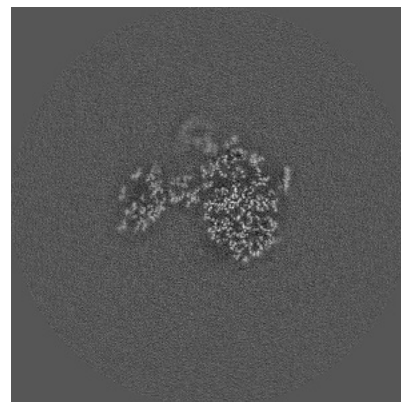
6.2.2 Raw map



X Index: 256



Y Index: 256

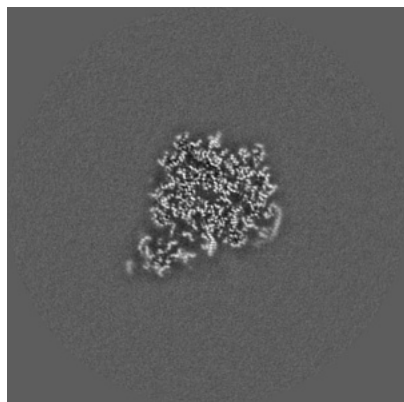


Z Index: 256

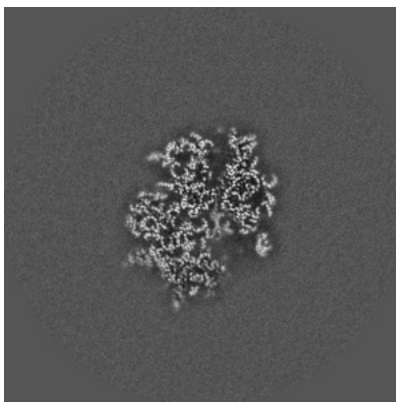
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

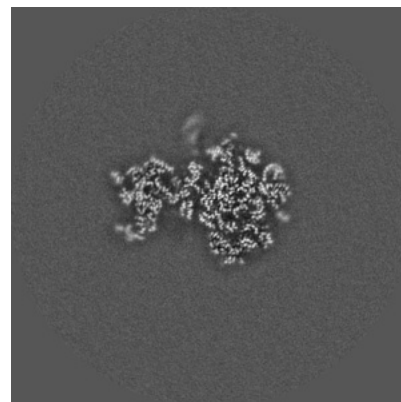
6.3.1 Primary map



X Index: 283

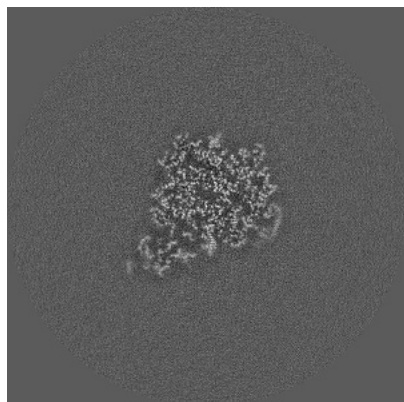


Y Index: 263

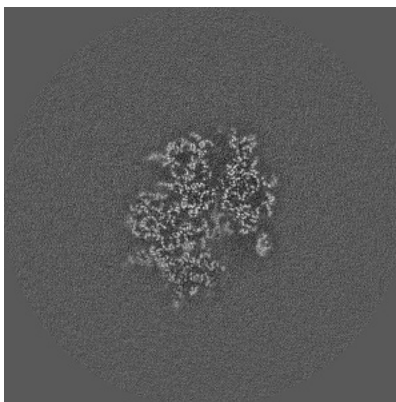


Z Index: 241

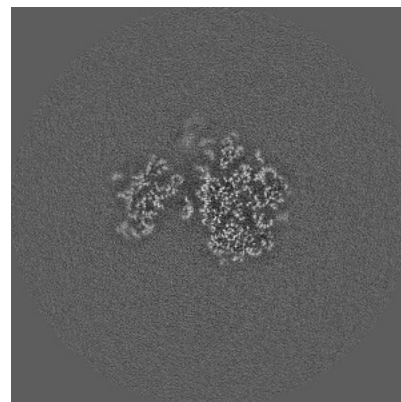
6.3.2 Raw map



X Index: 283



Y Index: 263

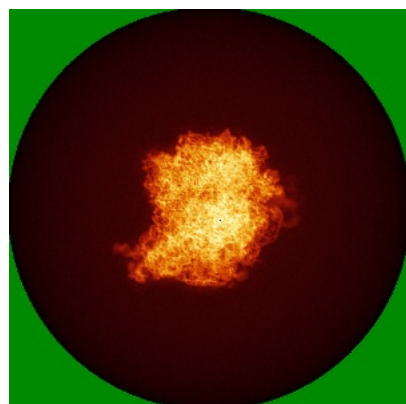


Z Index: 247

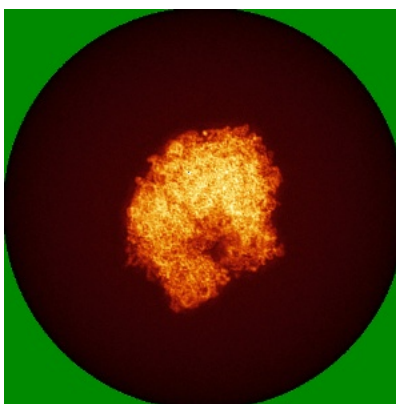
The images above show the largest variance slices of the map in three orthogonal directions.

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

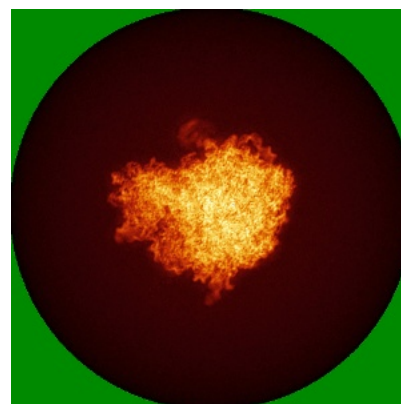
6.4.1 Primary map



X

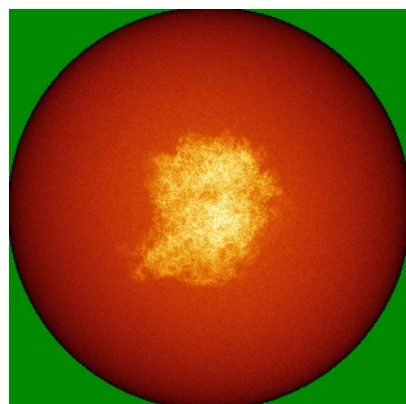


Y

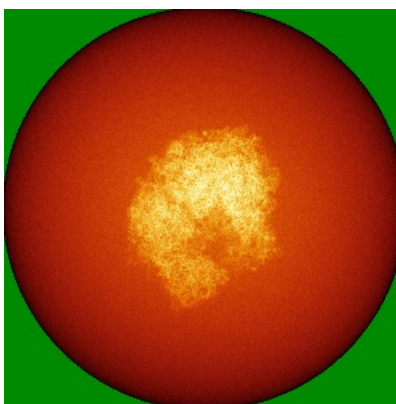


Z

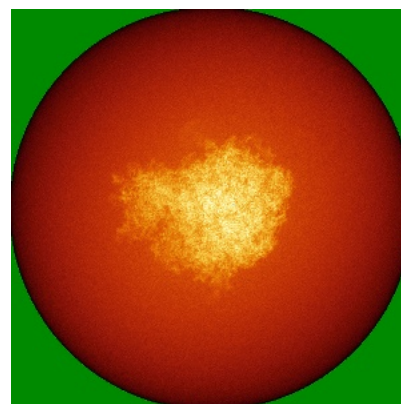
6.4.2 Raw map



X



Y

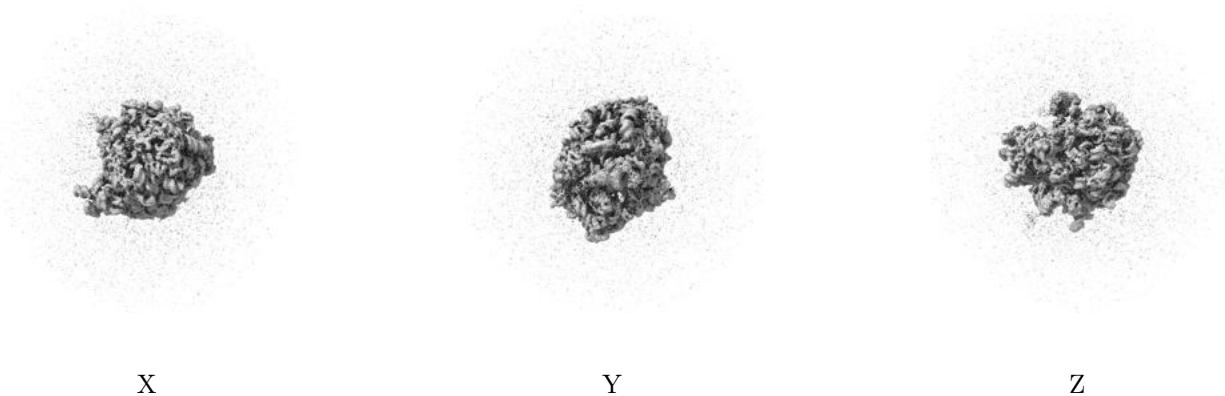


Z

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

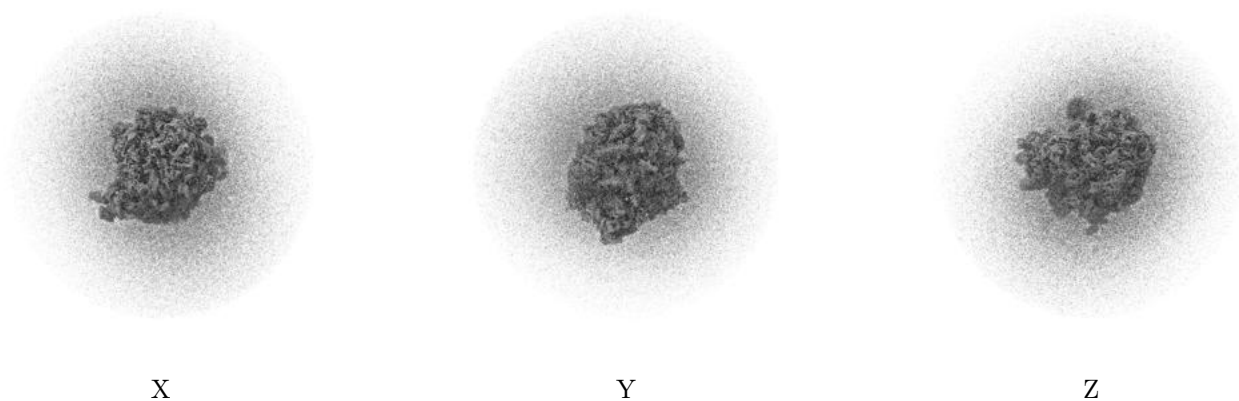
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00251. 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.

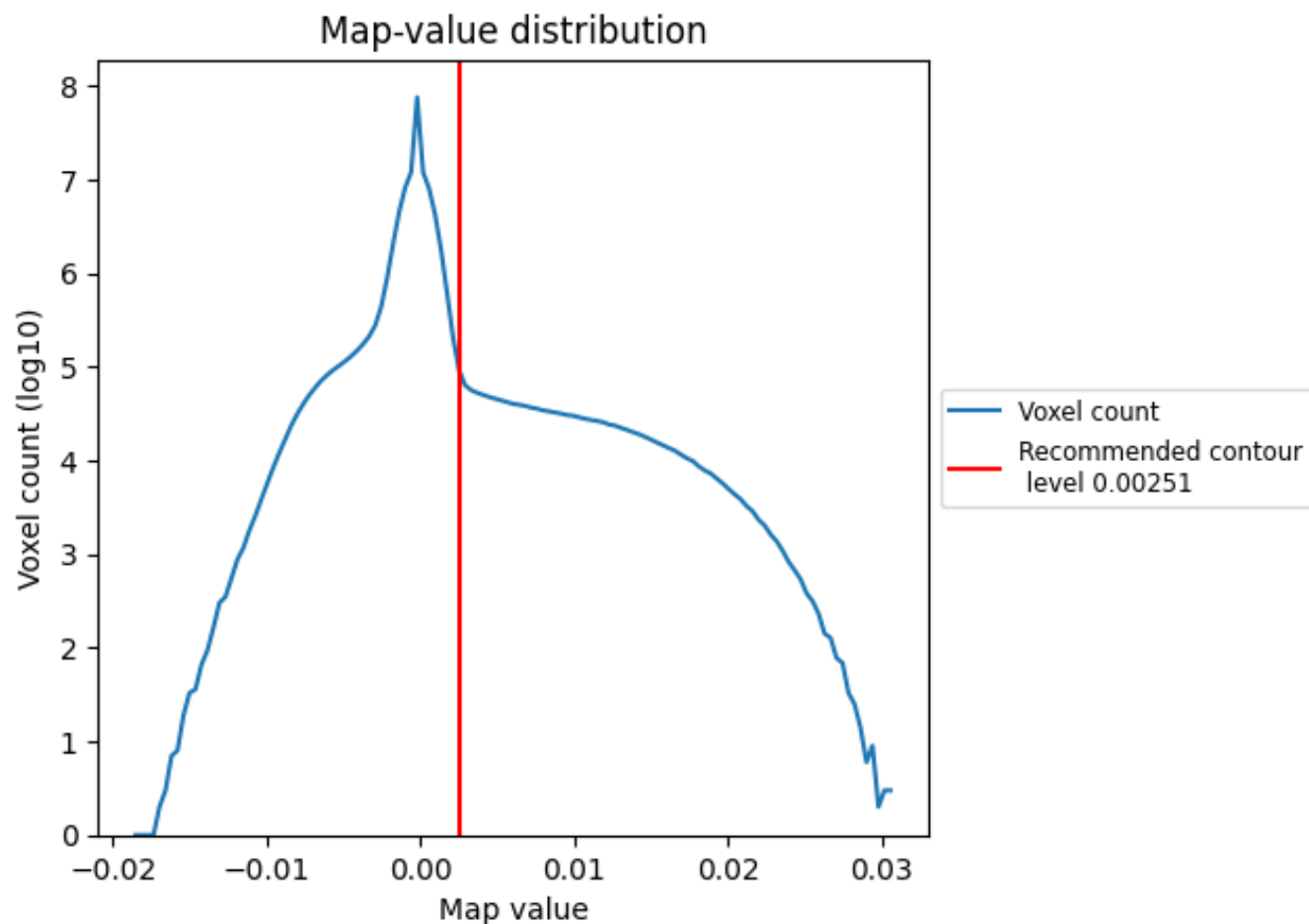
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

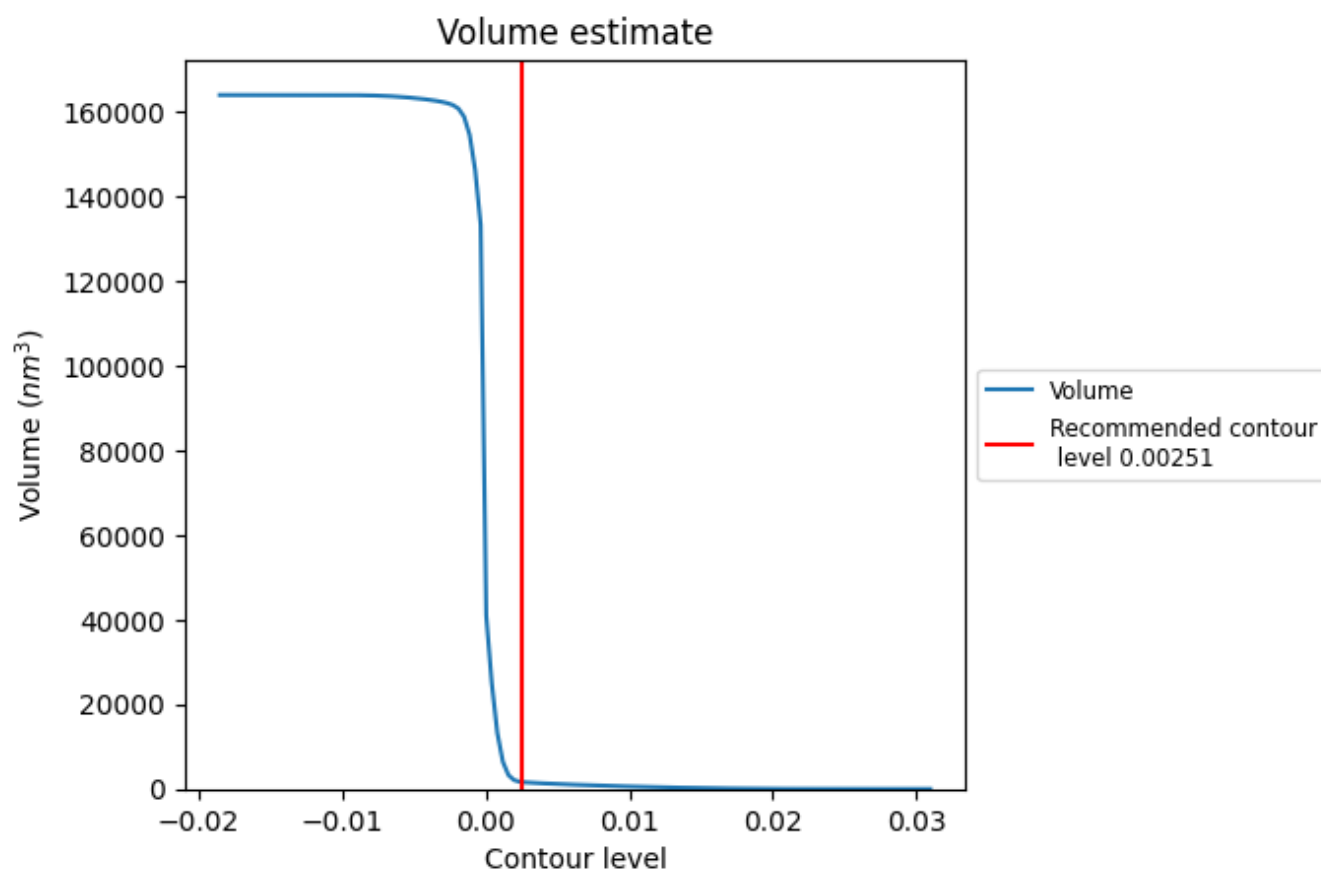
This section contains the results of statistical analysis of the map.

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.

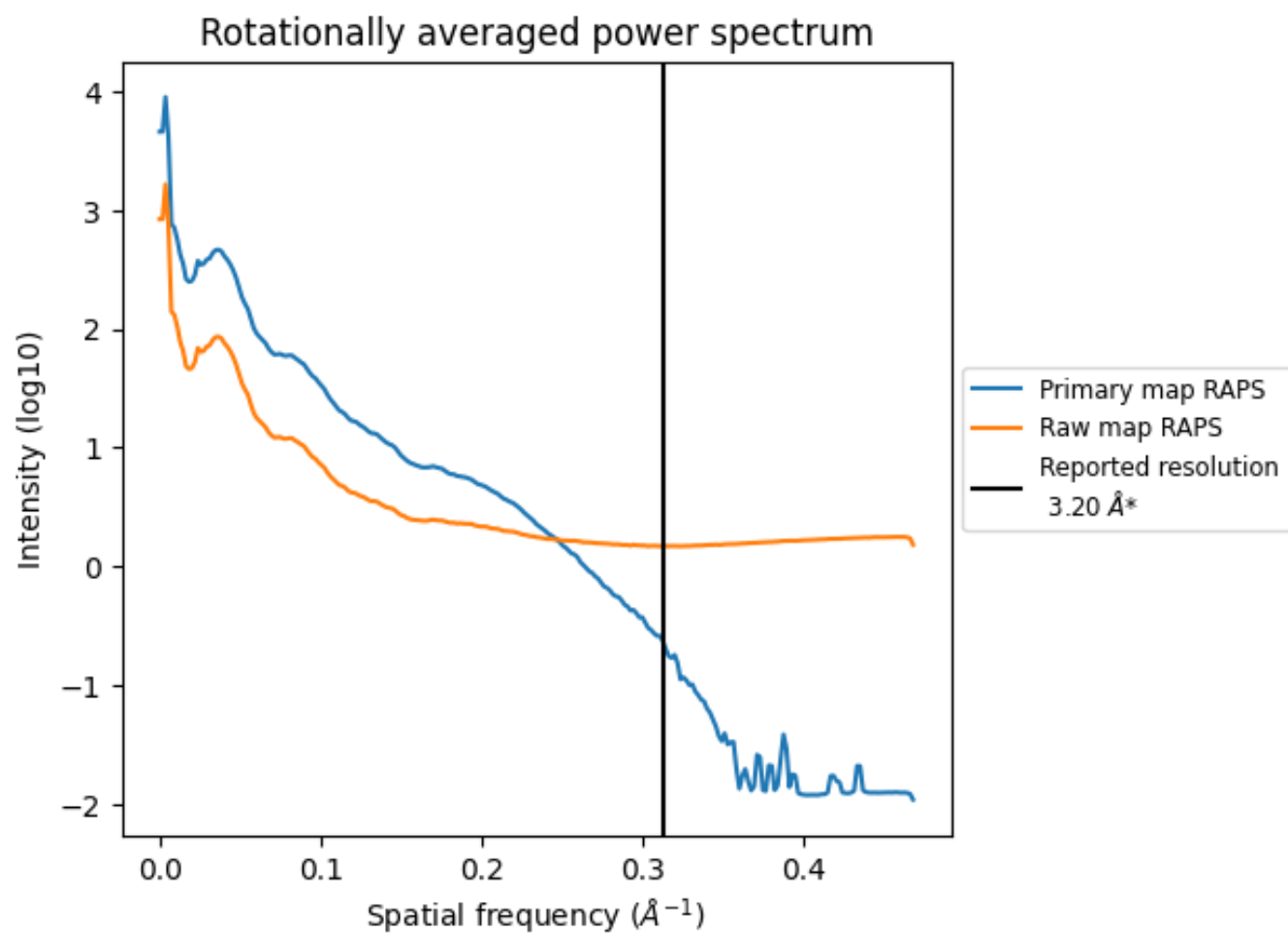
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1650 nm³; this corresponds to an approximate mass of 1491 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 ⓘ

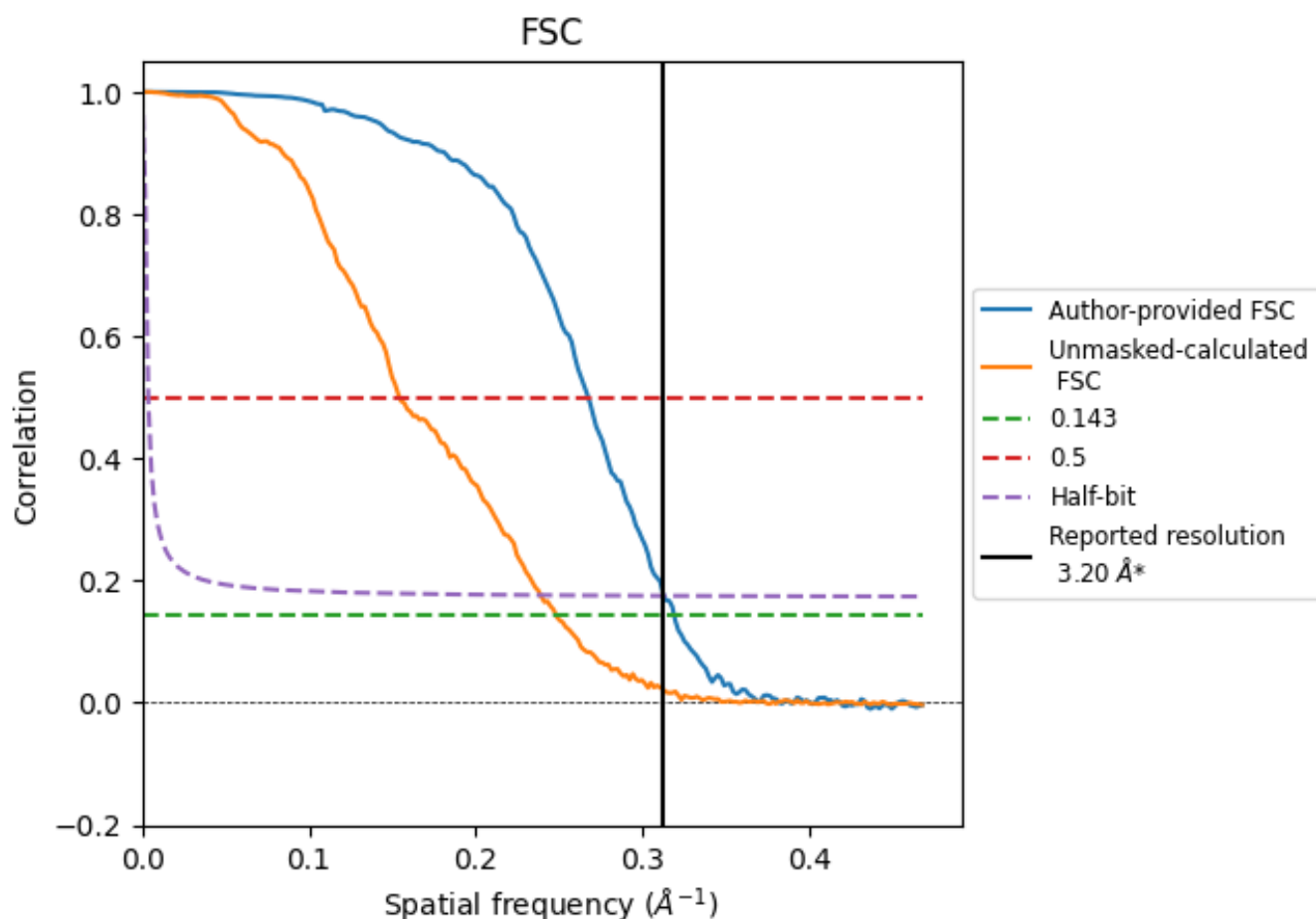


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

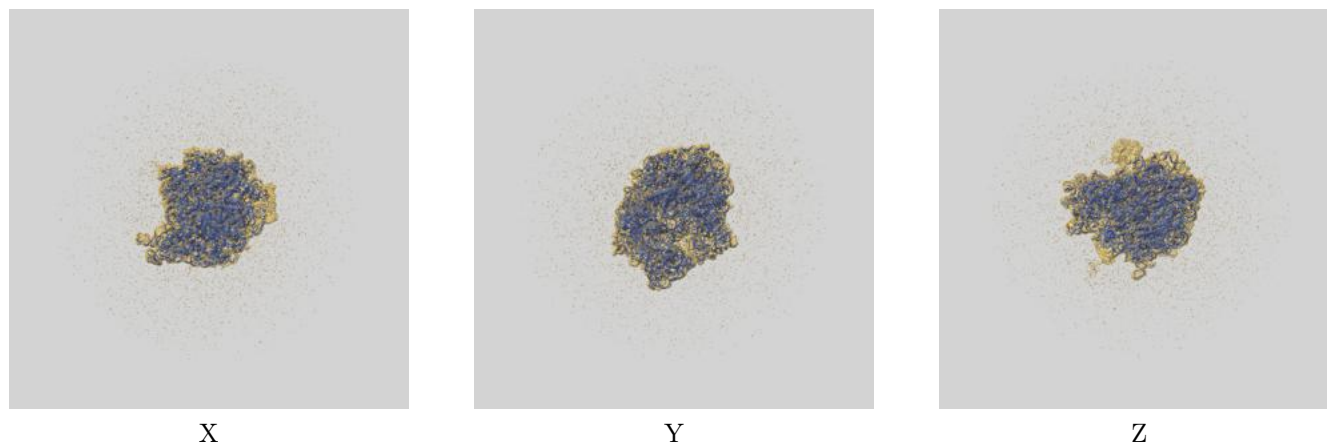
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.13	3.74	3.20
Unmasked-calculated*	4.03	6.48	4.19

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.03 differs from the reported value 3.2 by more than 10 %

9 Map-model fit [i](#)

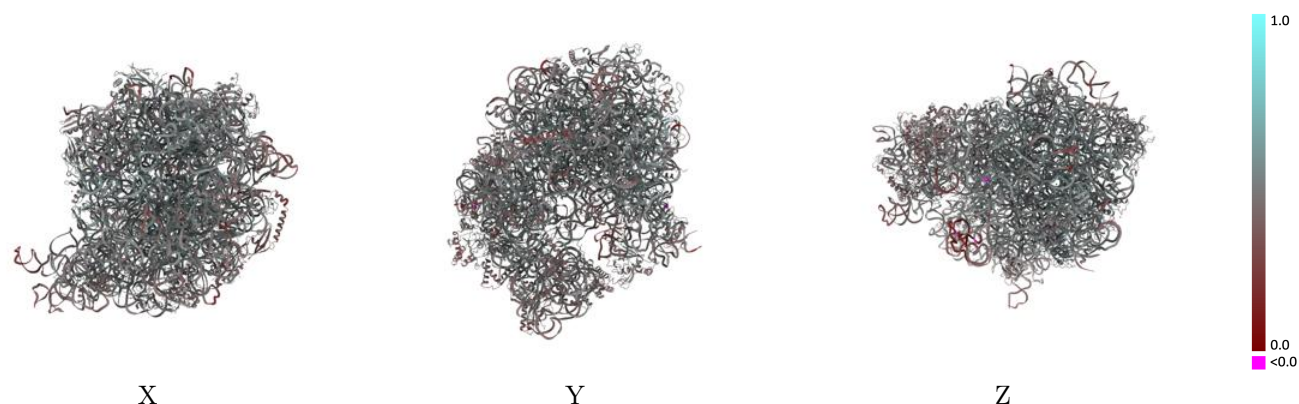
This section contains information regarding the fit between EMDB map EMD-43752 and PDB model 8W2N. Per-residue inclusion information can be found in [section 3](#) on [page 18](#).

9.1 Map-model overlay [i](#)



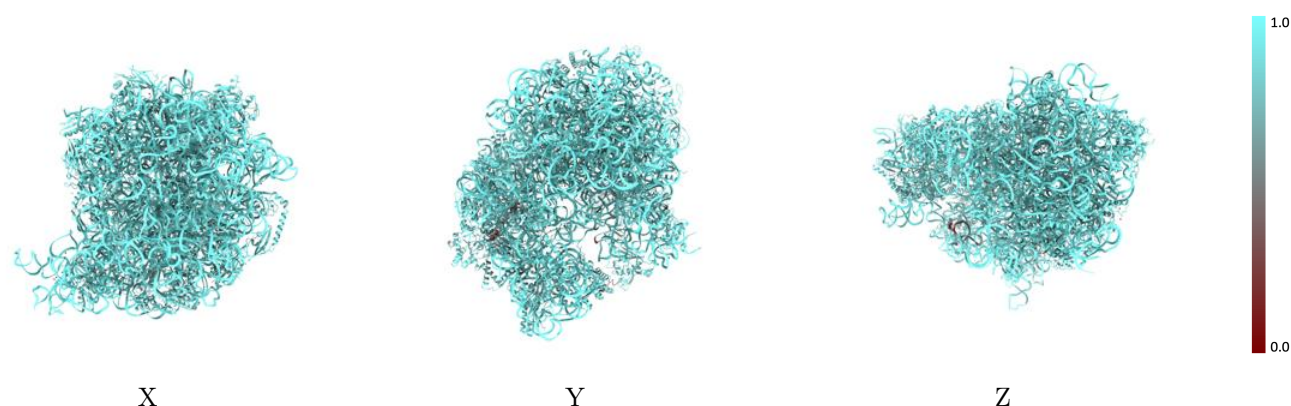
The images above show the 3D surface view of the map at the recommended contour level 0.00251 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



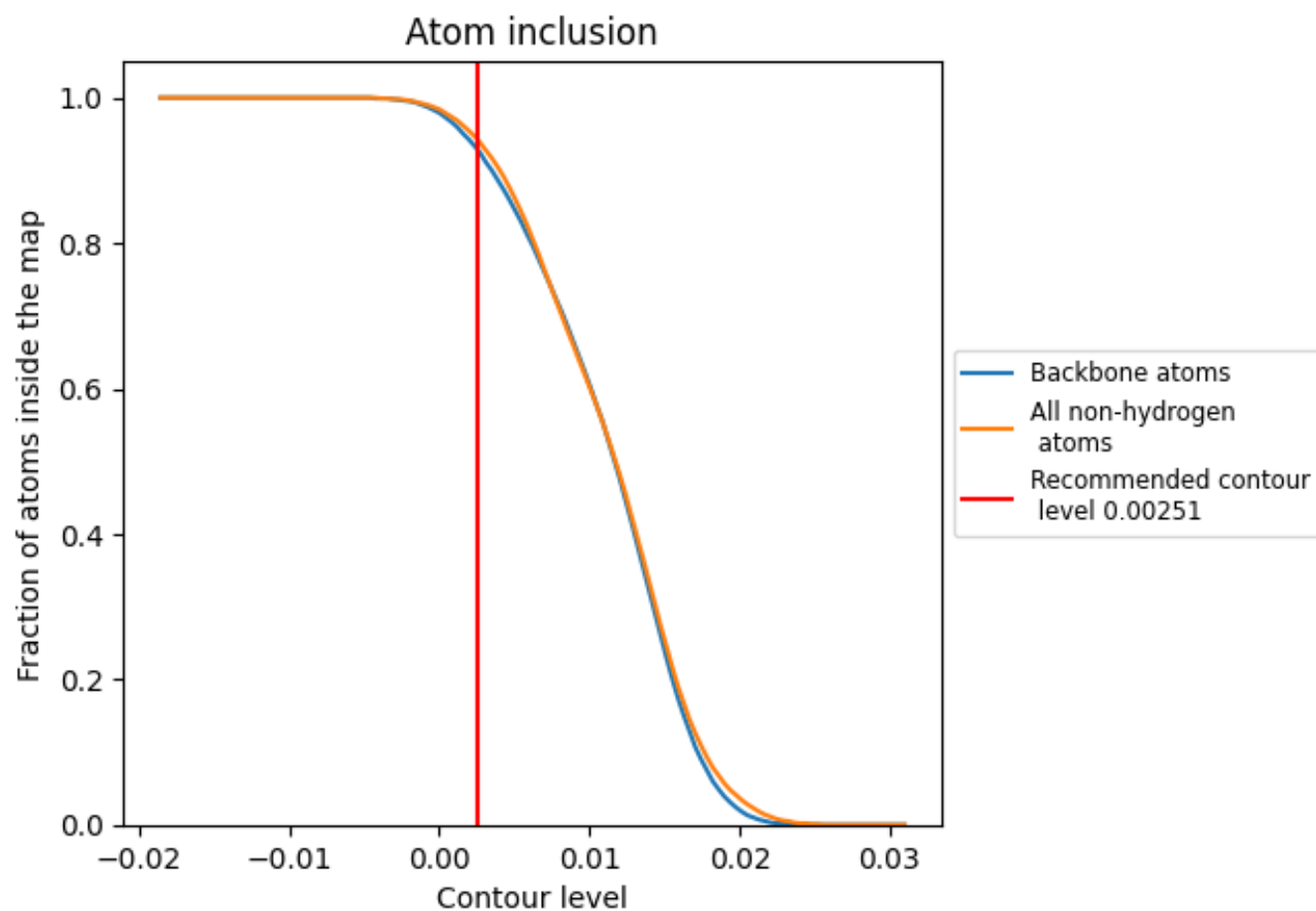
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.00251).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 94% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.00251) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9440	 0.4770
1	 0.9800	 0.4850
2	 0.9850	 0.4700
3	 0.9820	 0.4600
4	 0.9200	 0.5050
5	 0.9730	 0.4610
6	 0.7960	 0.4400
B	 0.8890	 0.5260
C	 0.8960	 0.5140
D	 0.8940	 0.4920
E	 0.8710	 0.4300
F	 0.9260	 0.4540
G	 0.9110	 0.3870
J	 0.8950	 0.5020
K	 0.8860	 0.5130
L	 0.8790	 0.5070
M	 0.8990	 0.5090
N	 0.8840	 0.5100
O	 0.8970	 0.4590
P	 0.8940	 0.5130
Q	 0.8750	 0.4930
R	 0.9120	 0.5100
S	 0.8730	 0.5020
T	 0.8500	 0.4830
U	 0.8940	 0.4790
V	 0.9240	 0.4850
W	 0.8780	 0.5180
X	 0.8770	 0.5010
Y	 0.8900	 0.4320
Z	 0.9130	 0.4980
a	 0.7460	 0.4060
b	 0.8880	 0.5120
c	 0.8900	 0.4850
d	 0.8510	 0.5170
e	 0.8460	 0.5240



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Chain	Atom inclusion	Q-score
f	 0.8060	 0.4940
g	 0.8260	 0.4160
h	 0.8930	 0.4670
i	 0.8450	 0.4480
j	 0.8820	 0.4830
k	 0.9010	 0.4470
l	 0.8820	 0.4350
m	 0.8930	 0.4880
n	 0.8650	 0.4510
o	 0.8560	 0.4480
p	 0.8990	 0.4700
q	 0.8730	 0.4960
r	 0.8840	 0.4410
s	 0.8540	 0.4580
t	 0.8850	 0.4520
u	 0.8770	 0.4890
v	 0.8860	 0.4620
w	 0.8130	 0.4280
x	 0.8810	 0.4530
y	 0.8440	 0.4250
z	 0.5600	 0.4060