



wwPDB EM Validation Summary Report ⓘ

Jun 24, 2026 – 06:40 PM EDT

PDB ID : 9ZNI / pdb_00009zni
EMDB ID : EMD-74448
Title : Cryo-EM structure of the Methanosarcina acetivorans 70S ribosome in complex with SriC and SriD
Authors : Nissley, A.J.; Cate, J.H.D.
Deposited on : 2025-12-12
Resolution : 2.89 Å(reported)
Based on initial model : .

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:

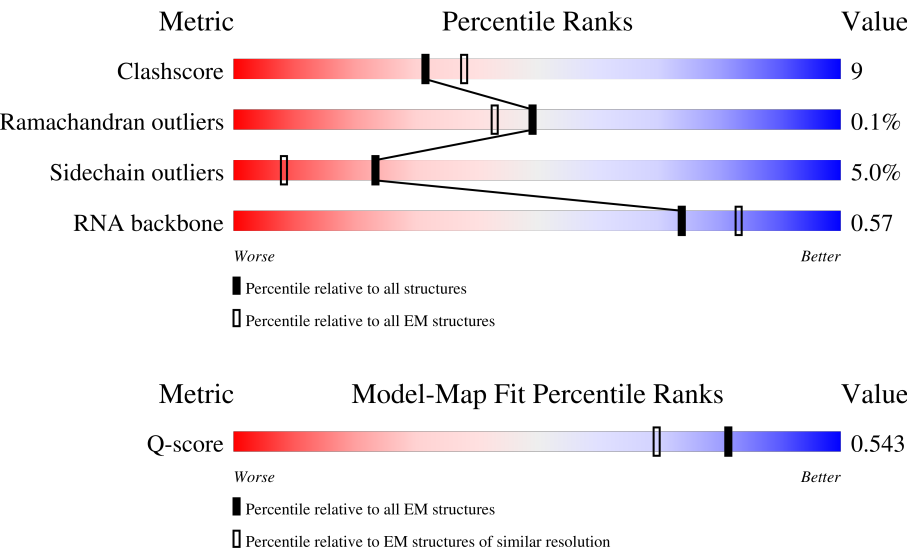
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
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 i

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

The reported resolution of this entry is 2.89 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	12148 (2.39 - 3.39)

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	59%31%7%
2	2	133	53%38%5%5%
3	3	1478	50%39%7%

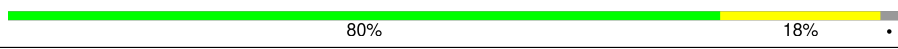
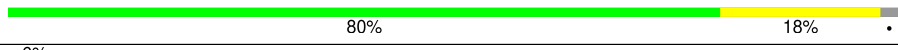
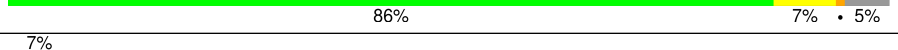
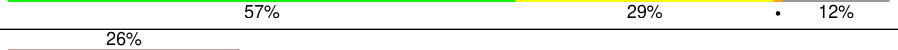
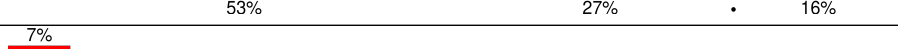
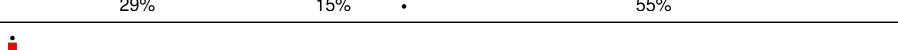
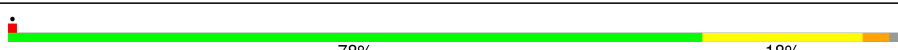
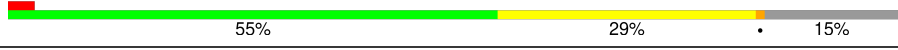
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Mol	Chain	Length	Quality of chain
4	6	281	
5	7	274	
6	AA	238	
7	AB	337	
8	AC	253	
9	AD	165	
10	AE	176	
11	AF	120	
12	AG	143	
13	AH	132	
14	AI	140	
15	AJ	196	
16	AK	173	
17	AL	174	
18	AM	126	
19	AN	151	
20	AO	61	
21	AP	97	
22	AQ	151	
23	AR	82	
24	AS	119	
25	AT	62	
26	AU	67	
27	AV	153	
28	AW	99	

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Mol	Chain	Length	Quality of chain
29	AX	89	
30	AY	129	
31	AZ	56	
32	Aa	51	
33	Ab	49	
34	Ac	92	
35	Ad	94	
36	BA	203	
37	BB	225	
38	BC	318	
39	BD	218	
40	BE	235	
41	BF	209	
42	BG	136	
43	BH	189	
44	BI	130	
45	BJ	134	
46	BK	125	
47	BL	102	
48	BM	126	
49	BN	142	
50	BO	162	
51	BP	50	
52	BQ	152	
53	BR	109	

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Mol	Chain	Length	Quality of chain
54	BS	64	
55	BT	136	
56	BU	149	
57	BV	56	
58	BW	101	
59	BX	62	
60	BY	76	
61	BZ	57	

2 Entry composition

There are 63 unique types of molecules in this entry. The entry contains 150576 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 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2711	Total	C	N	O	P	0	0
			58043	25909	10576	18847	2711		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	1	A	-	insertion	GB 470469544
1	2	A	-	insertion	GB 470469544
1	3	U	-	insertion	GB 470469544
1	4	U	-	insertion	GB 470469544
1	403	G	U	conflict	GB 470469544
1	408	U	C	conflict	GB 470469544
1	2716	U	C	conflict	GB 470469544
1	2721	A	G	conflict	GB 470469544
1	2904	A	-	insertion	GB 470469544

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	127	Total	C	N	O	P	0	0
			2697	1204	476	890	127		

- Molecule 3 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	1427	Total	C	N	O	P	0	0
			30583	13638	5572	9946	1427		

- Molecule 4 is a protein called CBS domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	6	281	Total	C	N	O	S	0	0
			2186	1374	381	420	11		

- Molecule 5 is a protein called CBS domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	7	257	Total	C	N	O	S	0	0
			1996	1250	353	383	10		

- Molecule 6 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AA	235	Total	C	N	O	S	0	0
			1779	1112	343	317	7		

- Molecule 7 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AB	335	Total	C	N	O	S	0	0
			2583	1631	472	473	7		

- Molecule 8 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AC	252	Total	C	N	O	S	0	0
			1929	1208	368	352	1		

- Molecule 9 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AD	159	Total	C	N	O	S	0	0
			1241	781	228	225	7		

- Molecule 10 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AE	171	Total	C	N	O	S	0	0
			1329	849	229	246	5		

- Molecule 11 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AF	106	Total	C	N	O	S	0	0
			779	490	133	154	2		

- Molecule 12 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AG	139	Total	C	N	O	S	0	0
			1092	687	201	200	4		

- Molecule 13 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AH	132	Total	C	N	O	S	0	0
			998	623	185	181	9		

- Molecule 14 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AI	139	Total	C	N	O	S	0	0
			1048	638	203	201	6		

- Molecule 15 is a protein called Large ribosomal subunit protein eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AJ	195	Total	C	N	O	S	0	0
			1584	981	328	271	4		

- Molecule 16 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AK	161	Total	C	N	O	S	0	0
			1277	803	245	220	9		

- Molecule 17 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AL	172	Total	C	N	O	S	0	0
			1341	845	240	255	1		

- Molecule 18 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AM	125	Total	C	N	O	S	0	0
			953	603	172	176	2		

- Molecule 19 is a protein called Large ribosomal subunit protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AN	147	Total	C	N	O	S	0	0
			1159	717	236	203	3		

- Molecule 20 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	AO	56	Total	C	N	O	0	0
			447	284	78	85		

- Molecule 21 is a protein called Large ribosomal subunit protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AP	96	Total	C	N	O	S	0	0
			765	475	146	140	4		

- Molecule 22 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AQ	149	Total	C	N	O	S	0	0
			1149	718	213	209	9		

- Molecule 23 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AR	79	Total	C	N	O	S	0	0
			633	405	105	117	6		

- Molecule 24 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AS	115	Total	C	N	O	S	0	0
			880	545	166	164	5		

- Molecule 25 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AT	60	Total	C	N	O	S	0	0
			484	307	85	84	8		

- Molecule 26 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AU	65	Total	C	N	O	S	0	0
			515	310	101	103	1		

- Molecule 27 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AV	153	Total	C	N	O	S	0	0
			1236	779	230	221	6		

- Molecule 28 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AW	84	Total	C	N	O	S	0	0
			605	383	100	118	4		

- Molecule 29 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AX	84	Total	C	N	O	S	0	0
			685	437	128	117	3		

- Molecule 30 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AY	126	Total	C	N	O	S	0	0
			981	617	188	174	2		

- Molecule 31 is a protein called Large ribosomal subunit protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AZ	55	Total	C	N	O	S	0	0
			436	264	91	74	7		

- Molecule 32 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Aa	50	Total	C	N	O	S	0	0
			430	267	100	62	1		

- Molecule 33 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Ab	43	Total	C	N	O	S	0	0
			348	212	73	58	5		

- Molecule 34 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Ac	91	Total	C	N	O	S	0	0
			750	475	150	118	7		

- Molecule 35 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Ad	89	Total	C	N	O	S	0	0
			699	437	139	117	6		

- Molecule 36 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BA	178	Total	C	N	O	S	0	0
			1426	895	258	265	8		

- Molecule 37 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BB	188	Total	C	N	O	S	0	0
			1476	933	260	278	5		

- Molecule 38 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BC	142	Total	C	N	O	S	0	0
			1085	686	193	199	7		

- Molecule 39 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BD	160	Total	C	N	O	S	0	0
			1288	815	238	230	5		

- Molecule 40 is a protein called Small ribosomal subunit protein eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BE	228	Total	C	N	O	S	0	0
			1796	1131	327	333	5		

- Molecule 41 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BF	201	Total	C	N	O	S	0	0
			1527	966	273	281	7		

- Molecule 42 is a protein called Small ribosomal subunit protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BG	125	Total	C	N	O	S	0	0
			935	594	169	168	4		

- Molecule 43 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BH	175	Total	C	N	O	S	0	0
			1363	851	253	256	3		

- Molecule 44 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BI	129	Total	C	N	O	S	0	0
			980	628	166	182	4		

- Molecule 45 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BJ	132	Total	C	N	O	S	0	0
			1001	622	188	188	3		

- Molecule 46 is a protein called Small ribosomal subunit protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BK	124	Total	C	N	O	S	0	0
			954	582	195	173	4		

- Molecule 47 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BL	38	Total	C	N	O	S	0	0
			302	194	57	50	1		

- Molecule 48 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BM	123	Total	C	N	O	S	0	0
			910	560	180	166	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BM	116	IAS	ASP	conflict	UNP Q8TRR0

- Molecule 49 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BN	139	Total	C	N	O	S	0	0
			1057	662	202	188	5		

- Molecule 50 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BO	138	Total	C	N	O	S	0	0
			1071	670	207	192	2		

- Molecule 51 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BP	46	Total	C	N	O	S	0	0
			382	238	76	63	5		

- Molecule 52 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BQ	150	Total	C	N	O	S	0	0
			1206	766	218	217	5		

- Molecule 53 is a protein called Small ribosomal subunit protein uS17A.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BR	107	Total	C	N	O	S	0	0
			831	522	149	153	7		

- Molecule 54 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BS	58	Total	C	N	O	S	0	0
			476	302	86	87	1		

- Molecule 55 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	BT	121	Total	C	N	O	S	0	0
			968	609	180	176	3		

- Molecule 56 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BU	148	Total	C	N	O	S	0	0
			1154	734	203	213	4		

- Molecule 57 is a protein called Putative zinc finger domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	BV	52	Total	C	N	O	S	0	0
			394	247	70	69	8		

- Molecule 58 is a protein called Small ribosomal subunit protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	BW	89	Total	C	N	O	S	0	0
			729	458	130	137	4		

- Molecule 59 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	BX	61	Total	C	N	O	S	0	0
			474	293	86	91	4		

- Molecule 60 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	BY	50	Total	C	N	O	S	0	0
			374	227	72	71	4		

- Molecule 61 is a protein called DUF5350 family protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	BZ	57	Total	C	N	O	S	0	0
			452	283	97	71	1		

- Molecule 62 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
62	1	239	Total	Mg	0
			239	239	
62	2	1	Total	Mg	0
			1	1	
62	3	64	Total	Mg	0
			64	64	
62	7	1	Total	Mg	0
			1	1	
62	AA	1	Total	Mg	0
			1	1	
62	AB	2	Total	Mg	0
			2	2	
62	AH	1	Total	Mg	0
			1	1	
62	AI	2	Total	Mg	0
			2	2	
62	AZ	1	Total	Mg	0
			1	1	
62	BF	1	Total	Mg	0
			1	1	
62	BM	1	Total	Mg	0
			1	1	

- Molecule 63 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
63	AT	1	Total	Zn	0
			1	1	
63	AZ	1	Total	Zn	0
			1	1	

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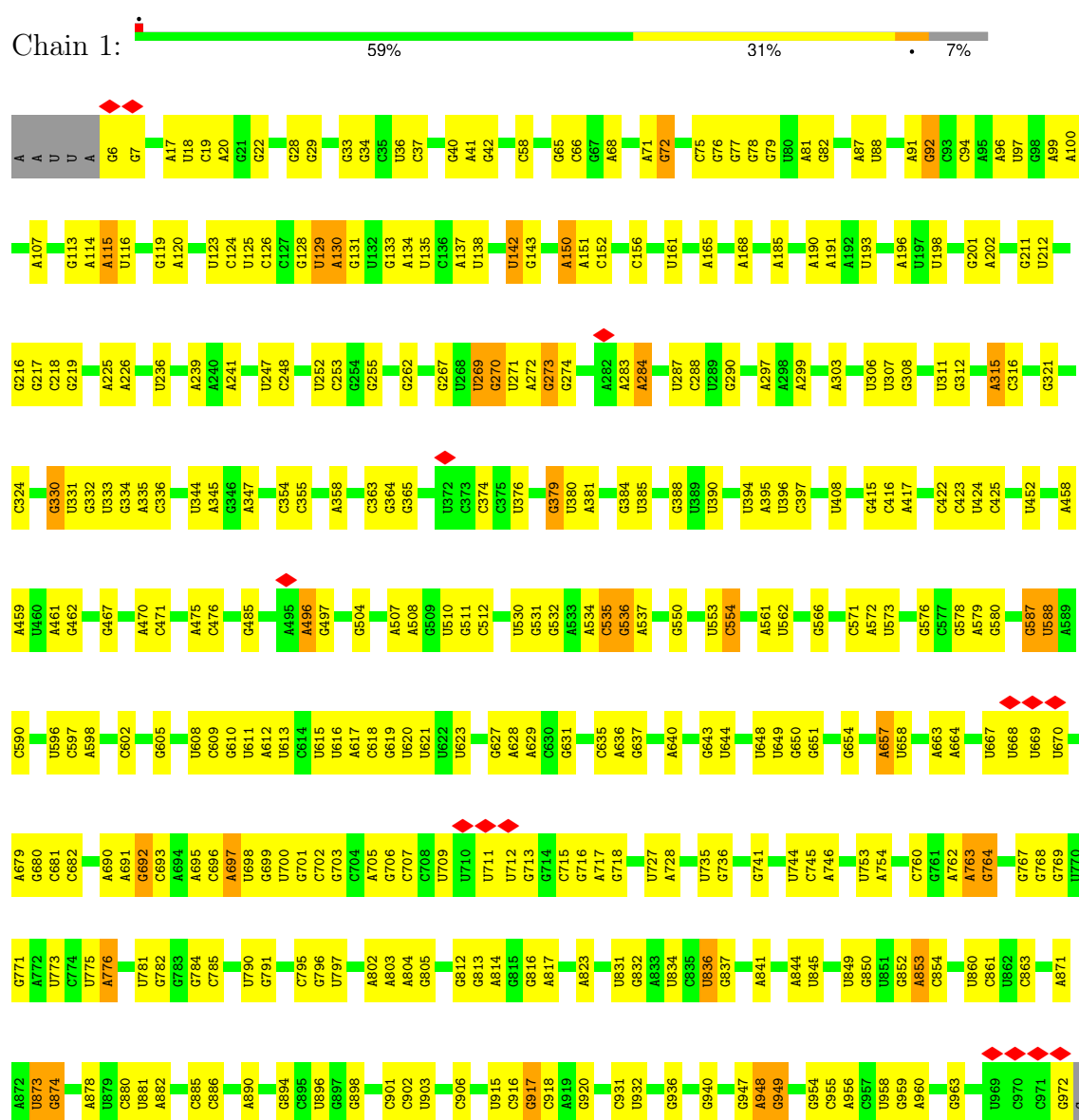
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Mol	Chain	Residues	Atoms		AltConf
63	Ab	1	Total 1	Zn 1	0
63	Ac	1	Total 1	Zn 1	0
63	Ad	1	Total 1	Zn 1	0
63	BF	1	Total 1	Zn 1	0
63	BP	1	Total 1	Zn 1	0
63	BR	1	Total 1	Zn 1	0
63	BV	2	Total 2	Zn 2	0
63	BX	1	Total 1	Zn 1	0

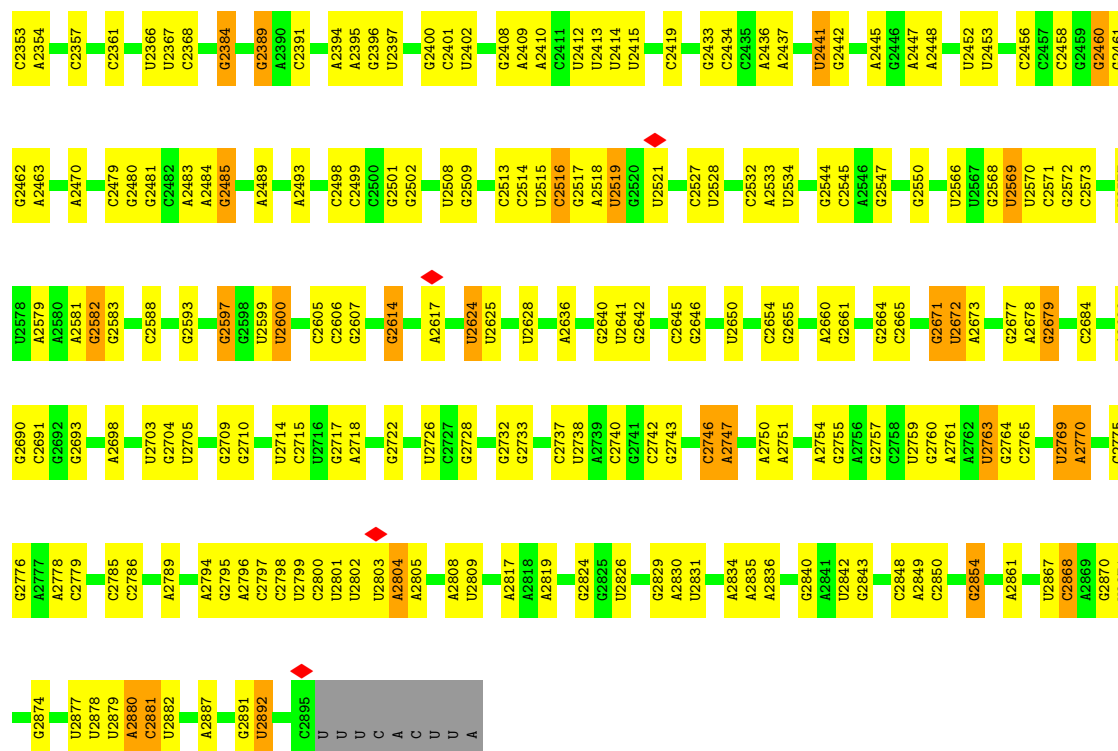
3 Residue-property plots

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.

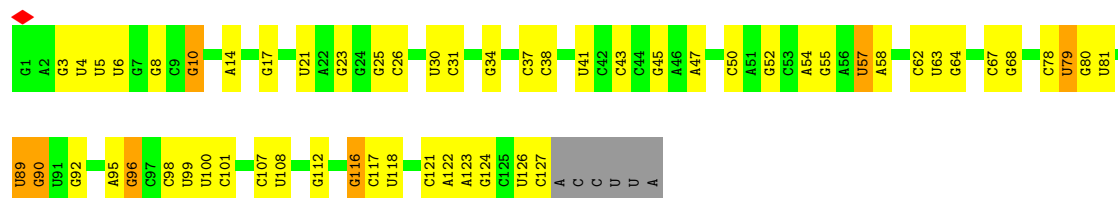
• Molecule 1: 23S rRNA



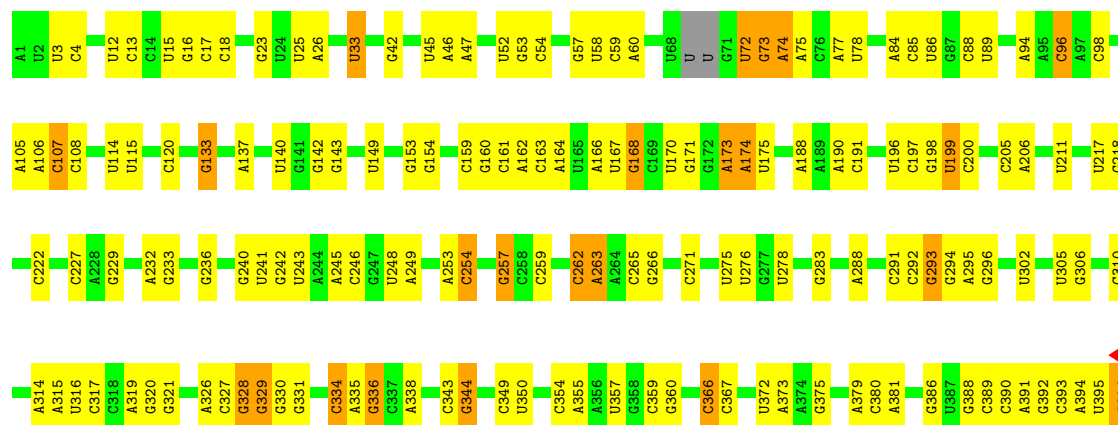
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U2249	U2104	G1997	A1906	G1804	C1666	C1529	G1438	A1318	U1227	U	A1075	G
G2250	G2105	G1998	G1910	G1804	G1667	A1530	C1443	A1319	G1228	A	A1076	G
G2251	U2000	A1999	A1911	U1811	A1668	C1534	U1444	G1320	C1229	G	A1077	G
U2256	G2108	A2006	A1914	A1812	A1671	C1534	A1445	C1321	C1231	U	C1077	A
U2257	U2111	G2007	A1915	A1813	C1672	C1549	A1446	C1322	G1235	U	C1078	A
C2261	G2112	U2016	A1926	G1816	A1673	A1557	C1449	A1329	G1235	A	G1081	A
U2262	U2117	G2017	C1927	A1820	A1679	A1558	G1450	C1330	A1238	G	C1082	C
G2263	G2118	U2018	A1928	A1822	A1683	A1561	G1459	C1331	A1239	A	A1091	C
G2264	U2109	C2019	A1928	A1823	C1684	C1563	U1459	C1341	C1243	G	A1092	C
A2271	G2123	C2020	G1931	A1823	C1685	C1563	G1462	G1342	C1246	A	G1093	C
G2279	U	C2021	G1932	A1826	C1686	G1574	A1463	A1344	C1249	G	G1094	C
U2288	G	U2022	G1933	A1826	C1686	A1575	G1464	A1345	C1250	C	U095	C
C2289	C	G2028	G1934	U1830	G1693	G1576	G1468	U1347	U1250	U	C991	C
G2293	U	U2047	U1936	A1831	C1706	A1577	G1468	C1348	U1253	C	G1002	C
C2297	U	U2048	A	G1835	C1707	G1578	A1472	A1355	U1253	C	G996	C
U2301	G	C2049	C	A1836	U1708	C1579	A1473	U1356	U1257	C	U997	C
A2302	U	U2050	U	U1837	G1711	C1580	A1474	U1356	C1258	U	C998	C
U2305	U	A2051	A	G1839	C1718	U1582	A1478	A1363	U1263	C	A1001	C
C2307	U	G2054	G	C1840	A1718	A1584	A1478	A1367	A1264	A	C1002	C
A2308	U	C2055	A	C1844	A1722	U1585	A1479	A1368	C1265	A	U1110	C
C2309	U	C2056	C	U1848	G1730	G1586	A1482	G1369	U1270	G	A1111	C
U2313	U	A2057	U	U1848	G1730	U1586	A1482	C1370	A1270	G	U1112	C
G2314	U	G2066	U	G1851	G1737	U1587	A1488	A1371	A1270	G	G1113	C
C2319	U	C2067	U	G1852	C1738	C1588	A1488	C1384	G1271	U	U1116	C
C2320	U	C2068	U	A1856	A1740	A1590	U1489	U1385	G1272	G	U1117	C
G2321	U	C2069	U	A1861	A1741	A1590	U1491	G1386	A1274	G	A1118	C
A2324	U	U2070	U	A1862	U1742	A1591	G1500	G1388	A1275	A	A1124	C
C2325	U	C2071	U	C1866	U1743	A1592	G1501	G1389	U1276	A	A1125	C
A2326	U	G2074	U	C1866	A1744	G1502	A1501	A1394	U1277	C	A1126	C
C2327	U	G2075	U	A1869	A1752	U1503	A1502	C1400	G1283	C	C1130	C
C2328	U	A2080	U	A1870	C1754	U1504	U1504	C1400	G1284	C	G1131	C
G2329	U	A2085	U	C1872	G1759	G1506	G1506	C1408	G1288	C	C1132	C
U2330	U	G2086	U	C1873	C1775	C1507	G	U1409	U1291	C	C1133	C
C2332	U	C2087	U	A1879	U1776	G	U	C1410	U1292	C	A1136	C
A2333	U	C2088	U	G1880	G1777	A1513	U	G1412	G1293	C	A1137	C
C2336	U	C2089	U	U1881	C1777	A1514	U	C1413	U1294	C	A1143	C
A2341	U	C2090	U	C1882	U1780	U1515	A1514	A1414	G1295	C	G1144	C
C2342	U	U2093	U	C1883	A1781	C1515	U1515	A1415	G1300	C	C1146	C
G2343	U	C2094	U	A1884	G1782	U1519	C1519	A1424	G1304	C	A1147	C
A2349	U	C2095	U	G1885	A1783	G1520	G1520	C1426	U1209	C	G	C
U2349	U	C2097	U	A1893	C1787	U1521	U1521	G1428	U1211	C	U	C
G2247	U	C2098	U	A1894	A1788	G1658	C1524	G1431	U1212	C	G	C
G2247	U	U2099	U	U1903	G1793	U1659	A1525	G1432	A1223	C	A	C
G2247	U	A1995	U	C1904	G1793	C1660	A1525	A1433	A1225	C	A	C

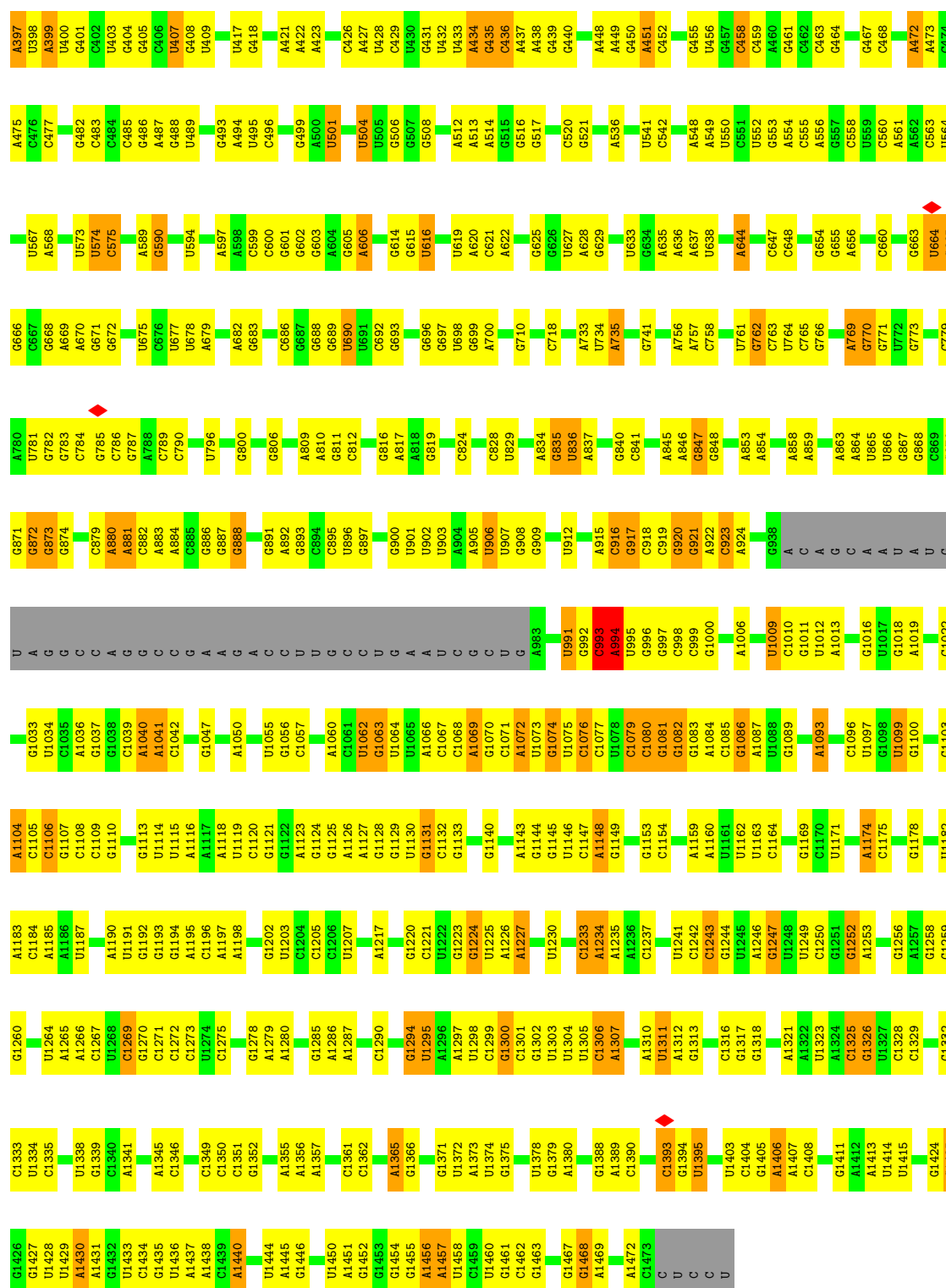


• Molecule 2: 5S rRNA

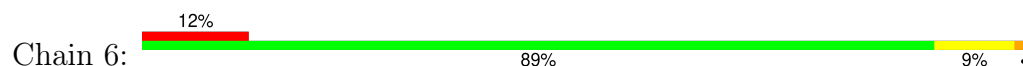


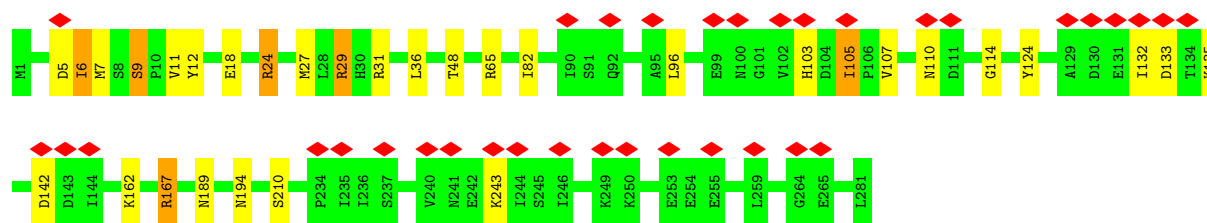
• Molecule 3: 16S rRNA



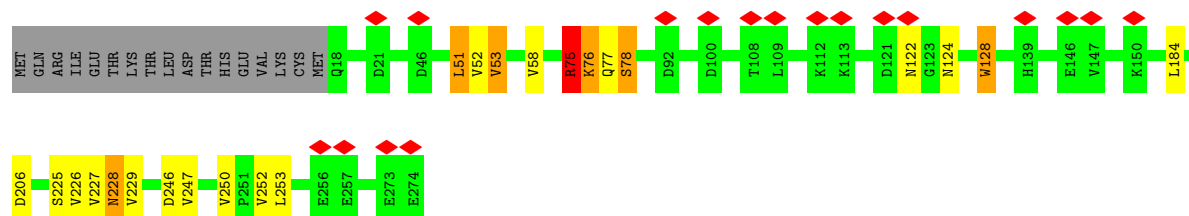
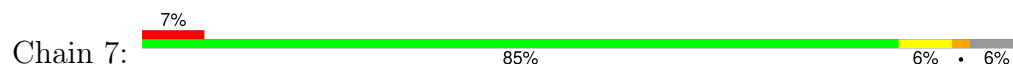


• Molecule 4: CBS domain-containing protein

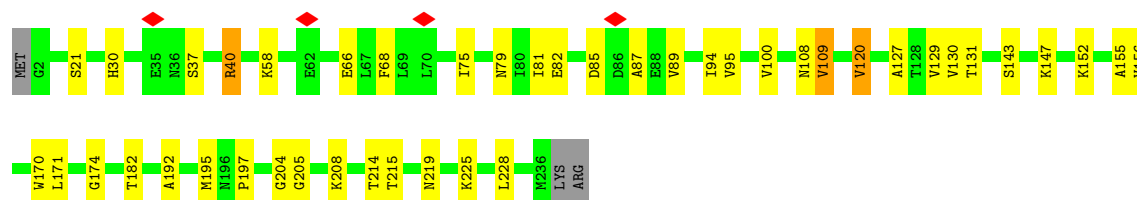
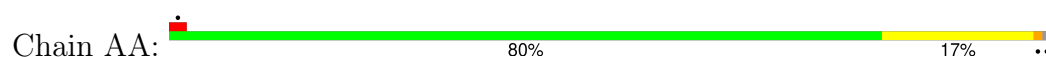




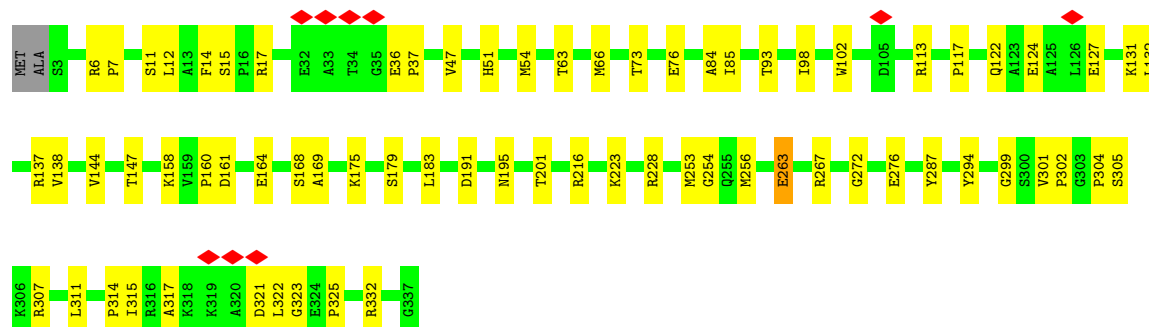
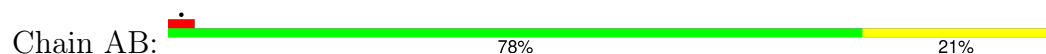
• Molecule 5: CBS domain-containing protein



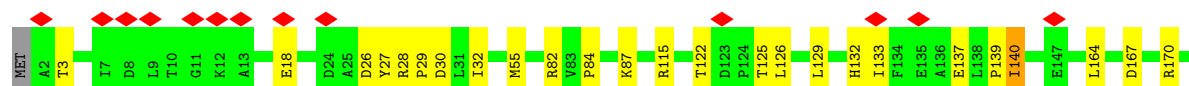
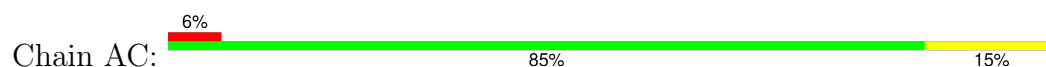
• Molecule 6: Large ribosomal subunit protein uL2

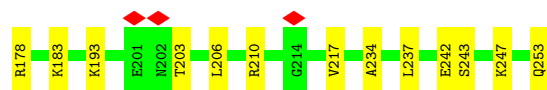


• Molecule 7: Large ribosomal subunit protein uL3

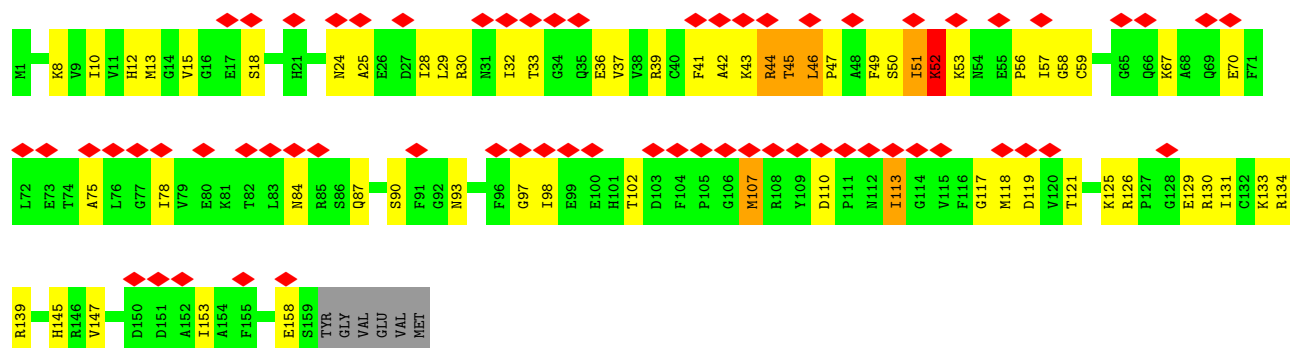
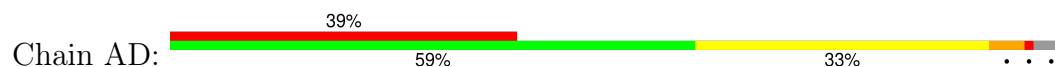


• Molecule 8: Large ribosomal subunit protein uL4

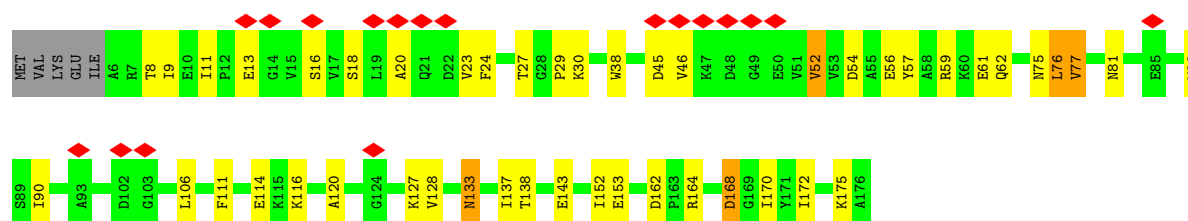




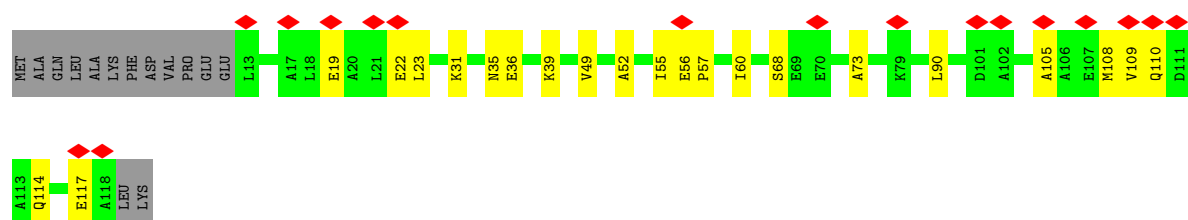
- Molecule 9: Large ribosomal subunit protein uL5



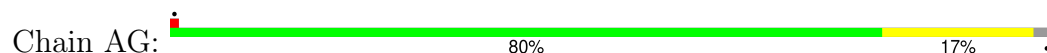
- Molecule 10: Large ribosomal subunit protein uL6



- Molecule 11: Large ribosomal subunit protein eL8

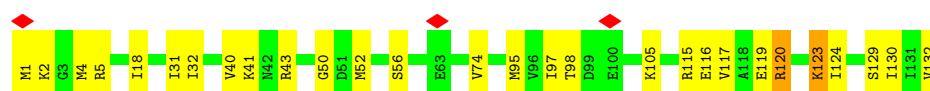


- Molecule 12: Large ribosomal subunit protein uL13



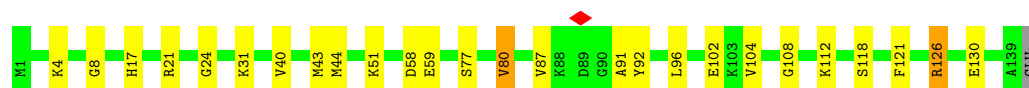
- Molecule 13: Large ribosomal subunit protein uL14

Chain AH:  79% 20%



- Molecule 14: Large ribosomal subunit protein uL15

Chain AI:  81% 17%



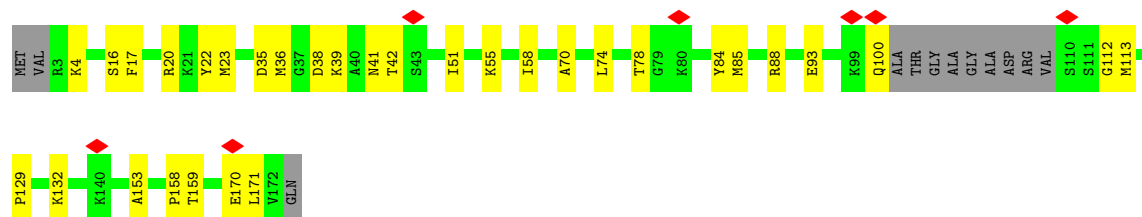
- Molecule 15: Large ribosomal subunit protein eL15

Chain AJ:  87% 12%



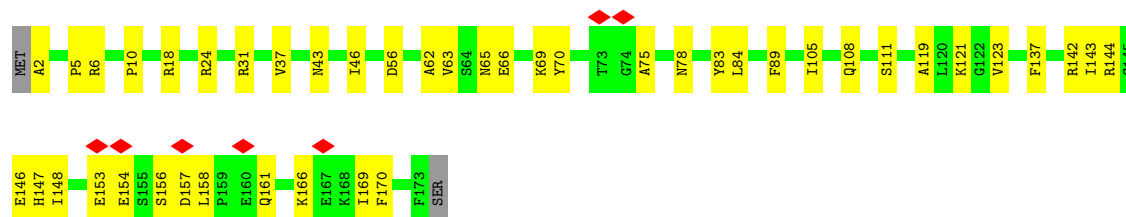
- Molecule 16: Large ribosomal subunit protein uL16

Chain AK:  75% 18% 7%



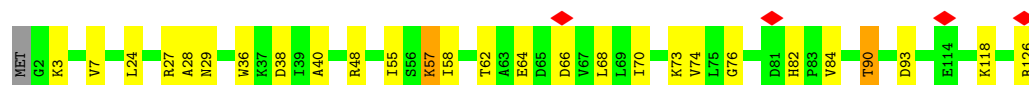
- Molecule 17: Large ribosomal subunit protein uL18

Chain AL:  74% 25%



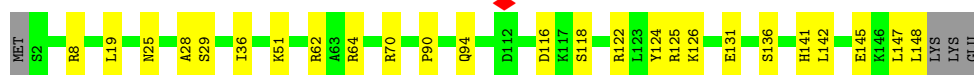
- Molecule 18: Large ribosomal subunit protein eL18

Chain AM:  78% 20%



- Molecule 19: Large ribosomal subunit protein eL19

Chain AN:  81% 17% .



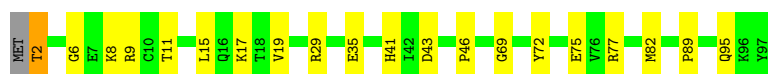
- Molecule 20: Large ribosomal subunit protein eL20

Chain AO:  13% 72% 20% 8%



- Molecule 21: Large ribosomal subunit protein eL21

Chain AP:  78% 20% ..



- Molecule 22: Large ribosomal subunit protein uL22

Chain AQ:  82% 17% .



- Molecule 23: Large ribosomal subunit protein uL23

Chain AR:  77% 20% .



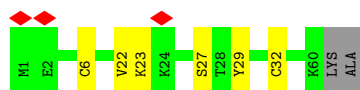
- Molecule 24: Large ribosomal subunit protein uL24

Chain AS:  76% 19% ..

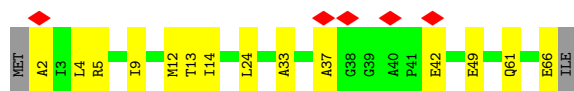
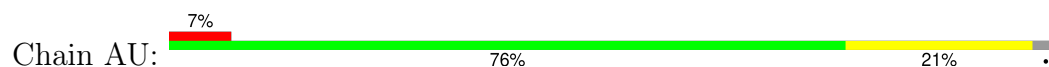


- Molecule 25: Large ribosomal subunit protein eL24

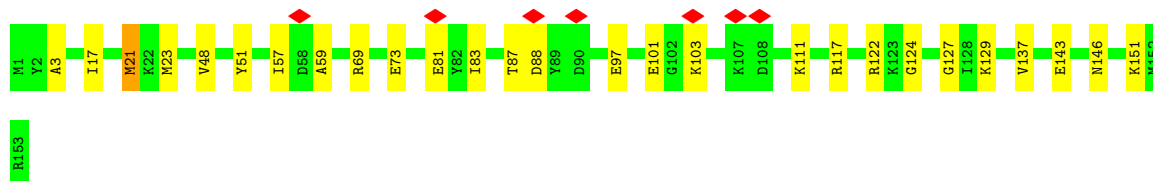
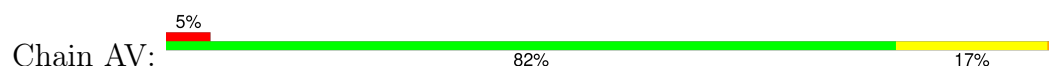
Chain AT:  5% 87% 10% .



- Molecule 26: Large ribosomal subunit protein uL29



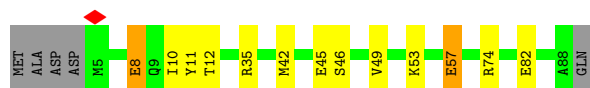
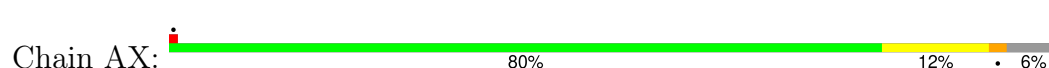
- Molecule 27: Large ribosomal subunit protein uL30



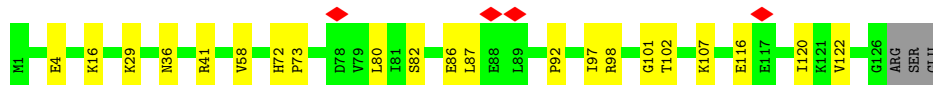
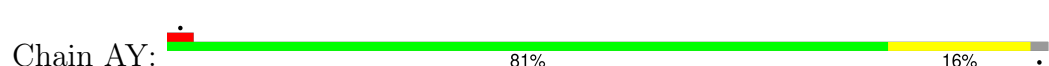
- Molecule 28: Large ribosomal subunit protein eL30



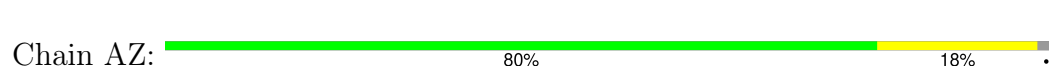
- Molecule 29: Large ribosomal subunit protein eL31



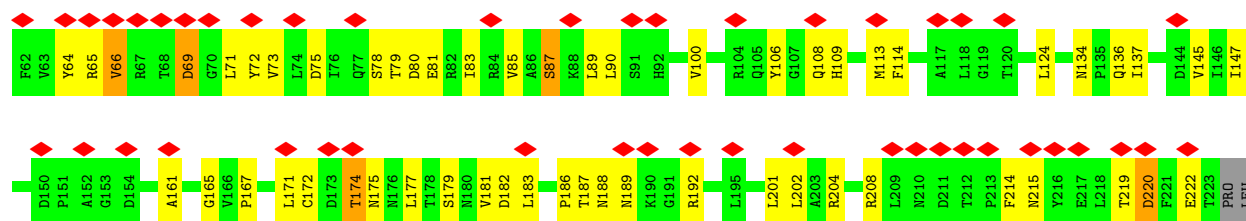
- Molecule 30: Large ribosomal subunit protein eL32



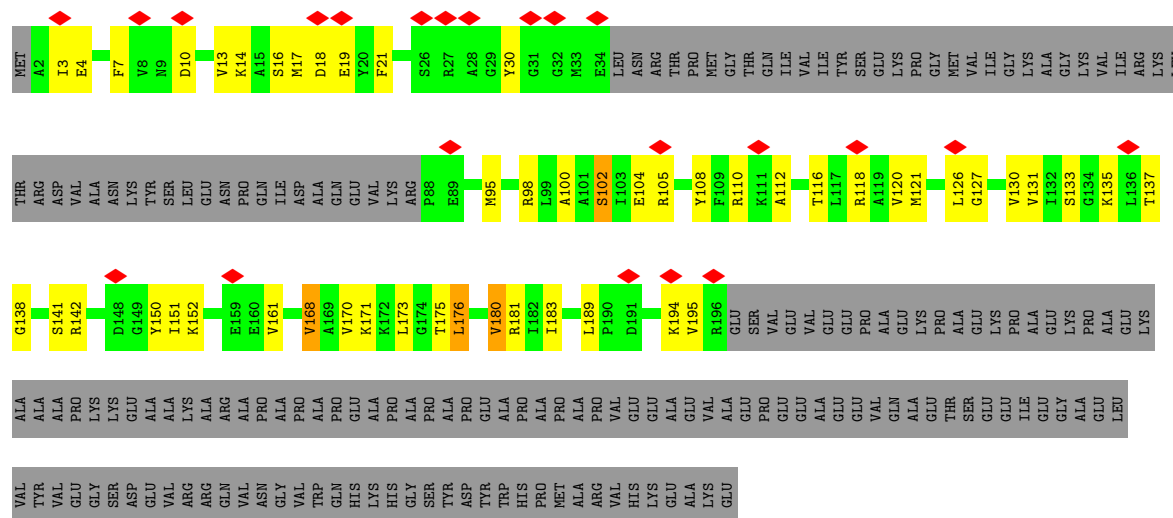
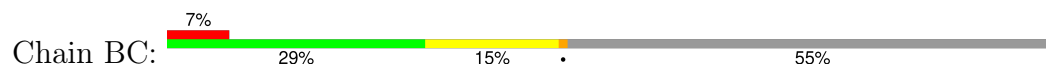
- Molecule 31: Large ribosomal subunit protein eL37



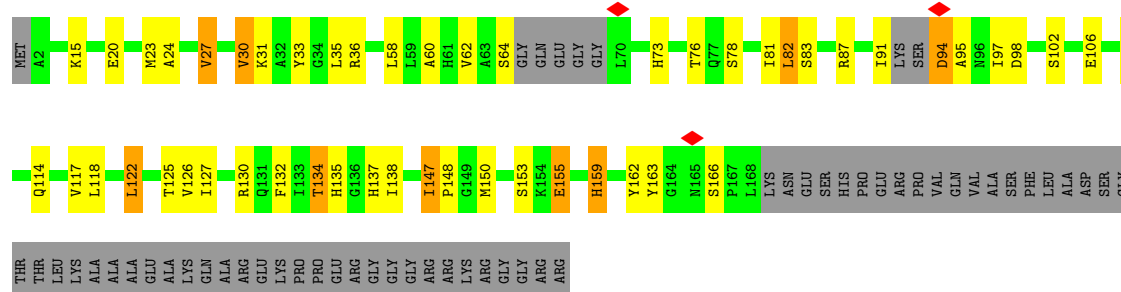
- | MET | ALA | GLU | LYS | PRO | LEU | GLU | LYS | ALA | VAL | THR | GLY | SER | ILE | PRO | SER | GLU | SER | GLU | ASP | THR | ALA | SER | HIS | LYS | GLU | GLY | SER | THR |
|-----|
| S36 | L37 | V38 | S39 | I40 | D41 | E42 | Y43 | L44 | A45 | A46 | G47 | I50 | G51 | T52 | Q53 | Q54 | K55 | T56 | Q57 | D58 | M59 | M60 | C61 | | | | | |



• Molecule 38: Small ribosomal subunit protein uS3



• Molecule 39: Small ribosomal subunit protein uS4



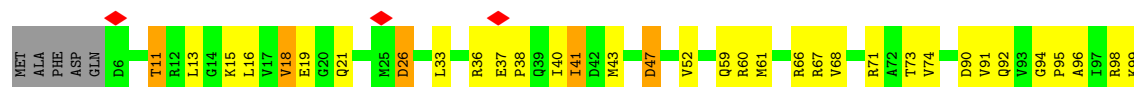
• Molecule 40: Small ribosomal subunit protein eS4





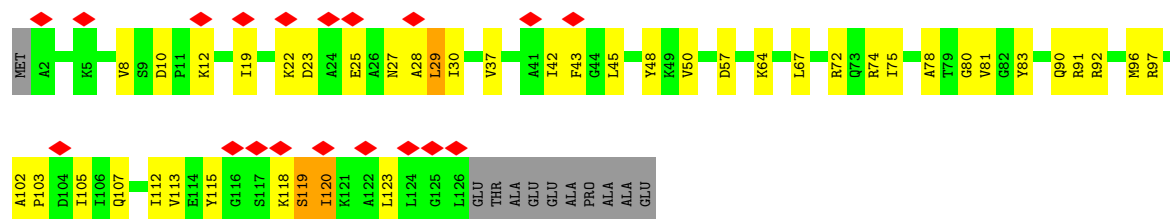
- Molecule 41: Small ribosomal subunit protein uS5

Chain BF: 66% 27%



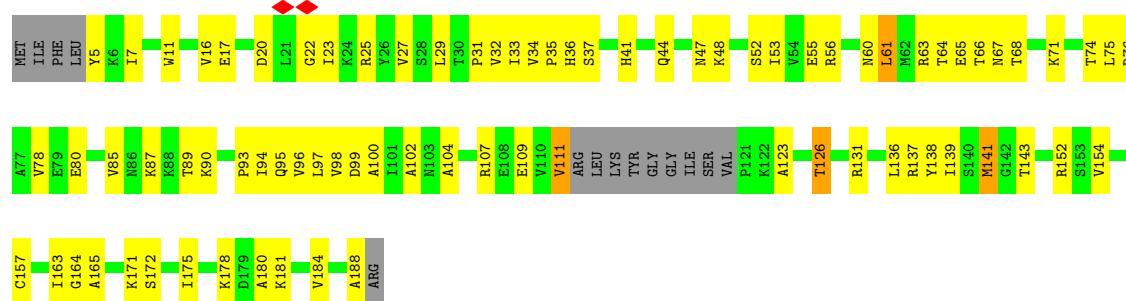
- Molecule 42: Small ribosomal subunit protein eS6

Chain BG: 14% 60% 29% 8%



- Molecule 43: Small ribosomal subunit protein uS7

Chain BH: 50% 40% 7%

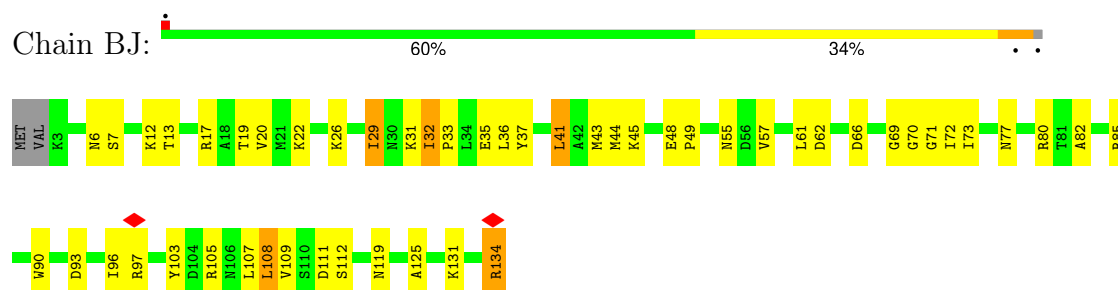


- Molecule 44: Small ribosomal subunit protein uS8

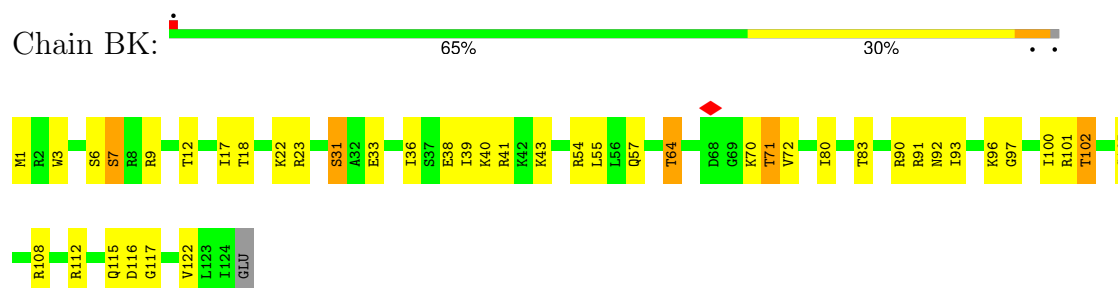
Chain BI: 78% 18%



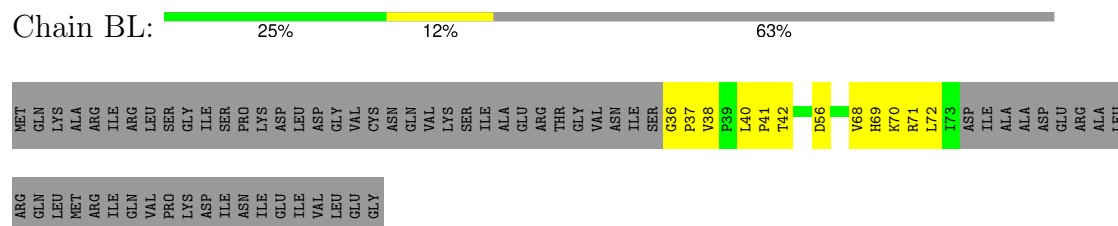
- Molecule 45: Small ribosomal subunit protein uS9



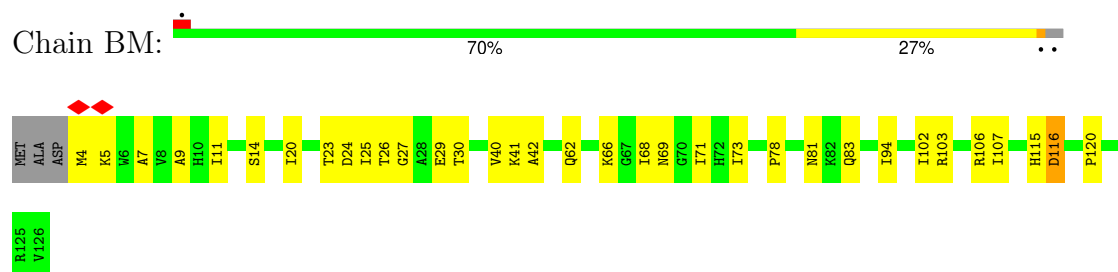
- Molecule 46: Small ribosomal subunit protein eS8



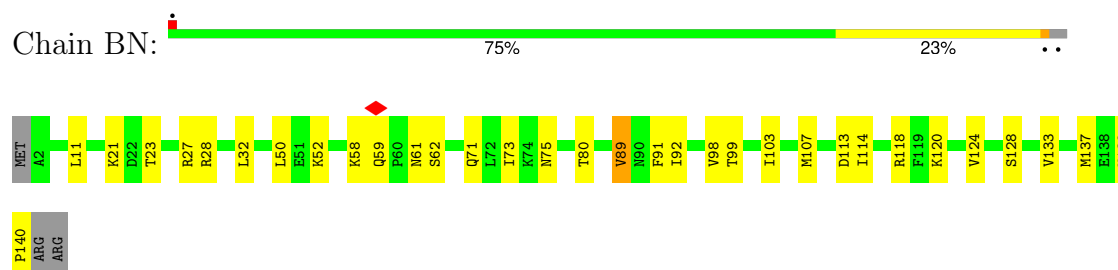
- Molecule 47: Small ribosomal subunit protein uS10



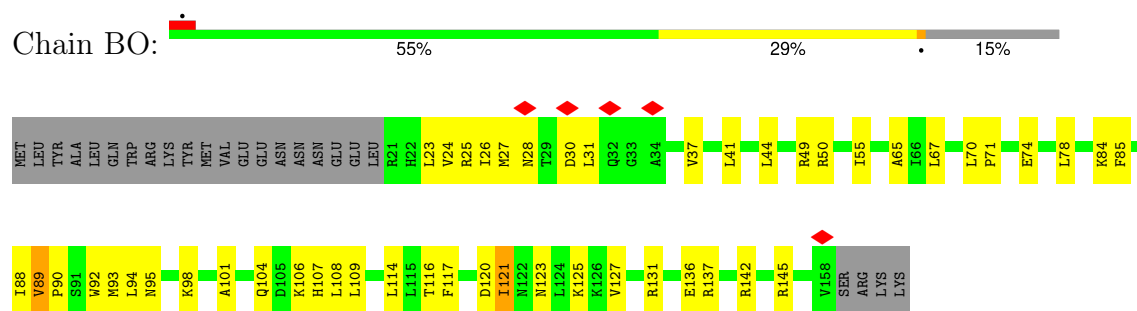
- Molecule 48: Small ribosomal subunit protein uS11



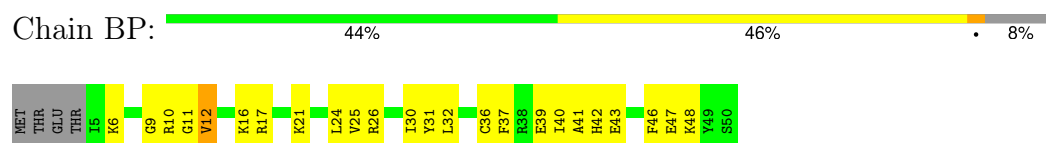
- Molecule 49: Small ribosomal subunit protein uS12



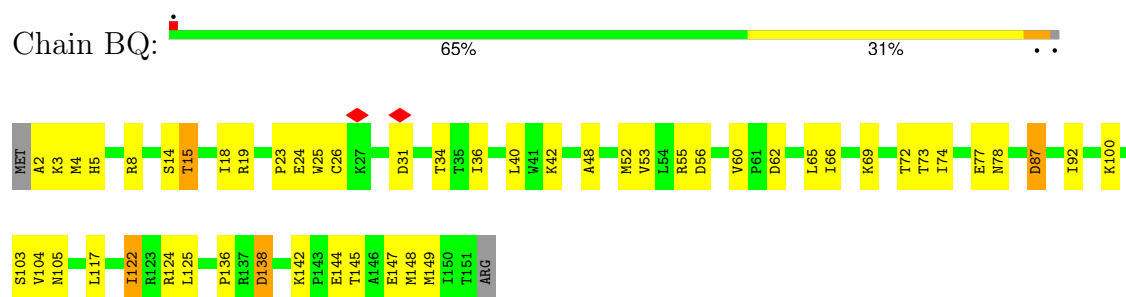
- Molecule 50: Small ribosomal subunit protein uS13



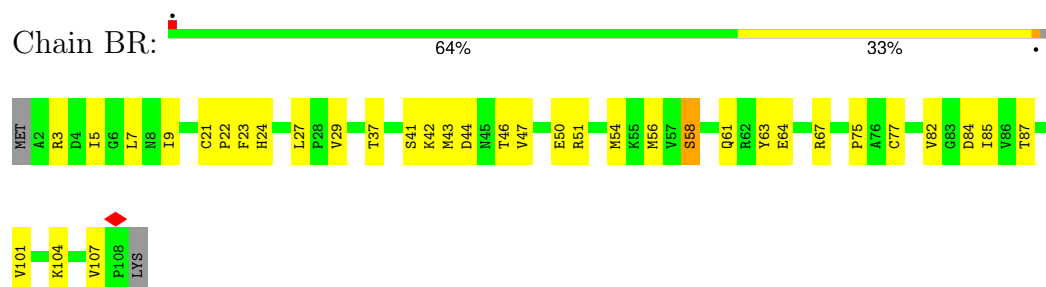
- Molecule 51: Small ribosomal subunit protein uS14



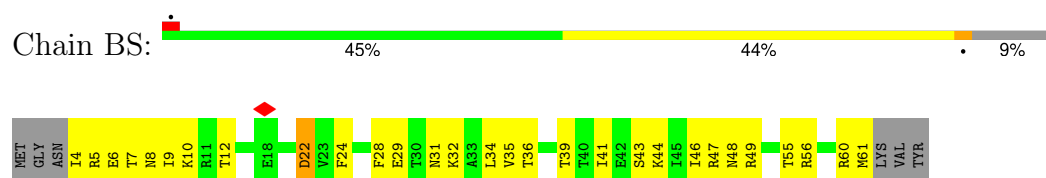
- Molecule 52: Small ribosomal subunit protein uS15



- Molecule 53: Small ribosomal subunit protein uS17A

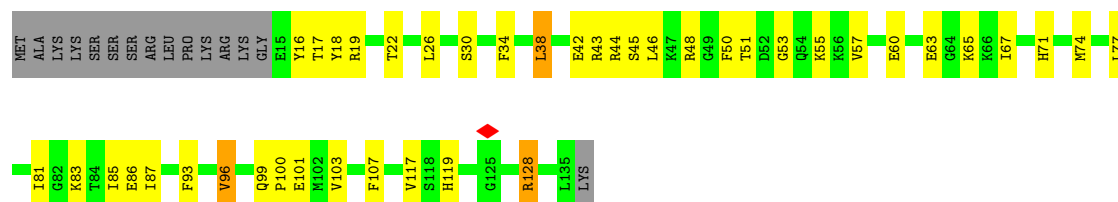


- Molecule 54: Small ribosomal subunit protein eS17

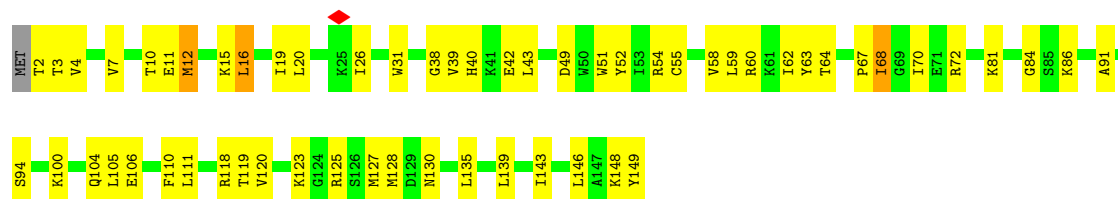


- Molecule 55: Small ribosomal subunit protein uS19

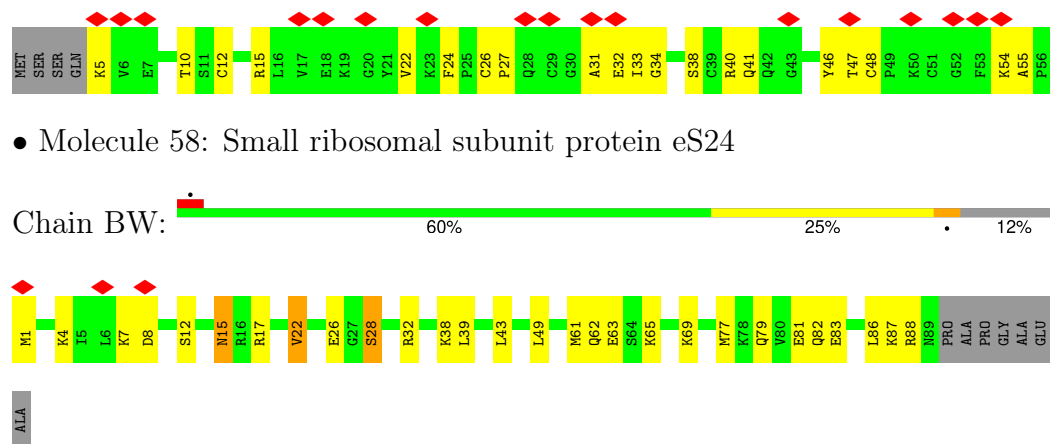




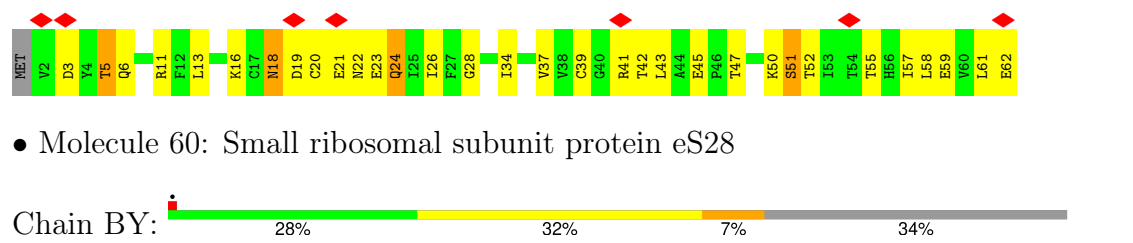
- Molecule 56: Small ribosomal subunit protein eS19



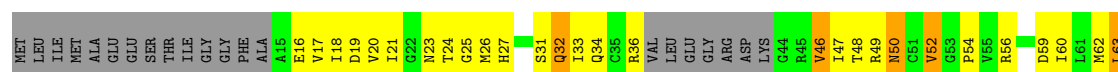
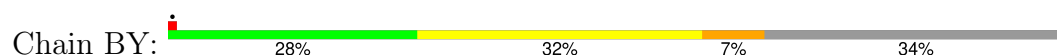
- Molecule 57: Putative zinc finger domain-containing protein



- Molecule 58: Small ribosomal subunit protein eS24

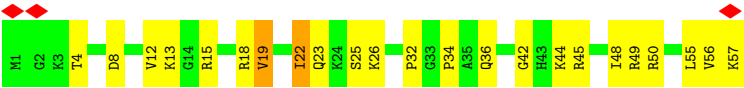


- Molecule 60: Small ribosomal subunit protein eS28





• Molecule 61: DUF5350 family protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	5477	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)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.734	Depositor
Minimum map value	-0.247	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.040	Depositor
Recommended contour level	0.142	Depositor
Map size (Å)	423.1168, 423.1168, 423.1168	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8264, 0.8264, 0.8264	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: OMU, MA6, ZN, 5MC, OMG, 6MZ, 5MU, MG, IAS

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	0.29	0/64866	0.32	0/101141
2	2	0.23	0/3011	0.31	0/4689
3	3	0.28	0/34118	0.35	3/53210 (0.0%)
4	6	0.79	0/2211	1.35	5/2992 (0.2%)
5	7	0.76	0/2020	1.29	0/2731
6	AA	0.26	0/1821	0.38	0/2462
7	AB	0.26	0/2632	0.38	0/3552
8	AC	0.25	0/1963	0.36	0/2654
9	AD	0.31	0/1261	0.57	0/1697
10	AE	0.29	0/1350	0.46	0/1816
11	AF	0.21	0/784	0.32	0/1055
12	AG	0.26	0/1107	0.35	0/1484
13	AH	0.25	0/1009	0.38	0/1355
14	AI	0.30	0/1061	0.45	0/1413
15	AJ	0.31	0/1616	0.39	0/2166
16	AK	0.23	0/1300	0.36	0/1741
17	AL	0.26	0/1367	0.40	0/1845
18	AM	0.23	0/966	0.36	0/1302
19	AN	0.24	0/1173	0.35	0/1558
20	AO	0.21	0/454	0.34	0/602
21	AP	0.28	0/779	0.34	0/1042
22	AQ	0.24	0/1169	0.36	0/1564
23	AR	0.27	0/641	0.42	0/856
24	AS	0.23	0/889	0.33	0/1189
25	AT	0.24	0/493	0.27	0/652
26	AU	0.23	0/517	0.43	0/695
27	AV	0.26	0/1258	0.38	0/1692
28	AW	0.20	0/610	0.42	0/825
29	AX	0.25	0/697	0.36	0/937
30	AY	0.26	0/997	0.35	0/1333
31	AZ	0.30	0/443	0.39	0/583
32	Aa	0.26	0/439	0.33	0/585

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Ab	0.23	0/350	0.45	0/461
34	Ac	0.24	0/767	0.34	0/1017
35	Ad	0.22	0/712	0.34	0/950
36	BA	0.25	0/1444	0.45	0/1947
37	BB	0.21	0/1504	0.39	0/2045
38	BC	0.22	0/1102	0.39	0/1477
39	BD	0.24	0/1309	0.34	0/1757
40	BE	0.25	0/1822	0.37	0/2451
41	BF	0.24	0/1552	0.40	0/2105
42	BG	0.27	0/948	0.46	0/1273
43	BH	0.21	0/1380	0.42	0/1858
44	BI	0.33	0/996	0.39	0/1343
45	BJ	0.23	0/1013	0.44	0/1364
46	BK	0.25	0/962	0.37	0/1288
47	BL	0.24	0/312	0.33	0/425
48	BM	0.26	0/915	0.42	0/1230
49	BN	0.24	0/1071	0.32	0/1438
50	BO	0.35	0/1085	0.61	0/1458
51	BP	0.24	0/388	0.44	0/510
52	BQ	0.30	0/1227	0.40	0/1654
53	BR	0.28	0/846	0.39	0/1144
54	BS	0.22	0/481	0.45	0/645
55	BT	0.45	0/987	0.66	0/1319
56	BU	0.27	0/1177	0.50	0/1586
57	BV	0.19	0/402	0.34	0/539
58	BW	0.23	0/736	0.35	0/983
59	BX	0.22	0/479	0.40	0/645
60	BY	0.18	0/374	0.42	0/500
61	BZ	0.24	0/459	0.38	0/603
All	All	0.30	0/161822	0.41	8/239433 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
4	6	0	3
5	7	0	1
15	AJ	0	1
44	BI	0	1
45	BJ	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
48	BM	0	1
50	BO	0	2
55	BT	0	1
All	All	0	11

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	6	29	ARG	NE-CZ-NH2	7.84	126.26	119.20
3	3	994	A	O3'-P-O5'	-6.21	94.69	104.00
3	3	993	C	C2'-C3'-O3'	6.08	118.62	109.50
4	6	24	ARG	NE-CZ-NH2	6.04	124.64	119.20
4	6	29	ARG	CD-NE-CZ	6.03	132.85	124.40

There are no chirality outliers.

5 of 11 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	6	167	ARG	Sidechain
4	6	24	ARG	Sidechain
4	6	9	SER	Peptide
5	7	75	ARG	Sidechain
15	AJ	177	ARG	Sidechain

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	58043	0	29263	582	0
2	2	2697	0	1371	41	0
3	3	30583	0	15425	494	0
4	6	2186	0	2304	11	0
5	7	1996	0	2061	9	0
6	AA	1779	0	1804	32	0
7	AB	2583	0	2674	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	AC	1929	0	1989	29	0
9	AD	1241	0	1272	58	0
10	AE	1329	0	1375	31	0
11	AF	779	0	820	12	0
12	AG	1092	0	1142	21	0
13	AH	998	0	1059	21	0
14	AI	1048	0	1038	16	0
15	AJ	1584	0	1625	20	0
16	AK	1277	0	1318	21	0
17	AL	1341	0	1341	29	0
18	AM	953	0	1009	20	0
19	AN	1159	0	1233	14	0
20	AO	447	0	457	10	0
21	AP	765	0	777	13	0
22	AQ	1149	0	1186	18	0
23	AR	633	0	662	12	0
24	AS	880	0	935	15	0
25	AT	484	0	497	3	0
26	AU	515	0	524	12	0
27	AV	1236	0	1269	19	0
28	AW	605	0	643	15	0
29	AX	685	0	723	8	0
30	AY	981	0	1033	17	0
31	AZ	436	0	443	7	0
32	Aa	430	0	467	5	0
33	Ab	348	0	369	5	0
34	Ac	750	0	791	10	0
35	Ad	699	0	730	6	0
36	BA	1426	0	1477	45	0
37	BB	1476	0	1482	50	0
38	BC	1085	0	1098	38	0
39	BD	1288	0	1331	30	0
40	BE	1796	0	1878	50	0
41	BF	1527	0	1581	46	0
42	BG	935	0	988	36	0
43	BH	1363	0	1415	59	0
44	BI	980	0	1008	15	0
45	BJ	1001	0	1034	53	0
46	BK	954	0	1021	33	0
47	BL	302	0	314	9	0
48	BM	910	0	936	31	0
49	BN	1057	0	1104	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	BO	1071	0	1127	36	0
51	BP	382	0	384	19	0
52	BQ	1206	0	1280	50	0
53	BR	831	0	852	22	0
54	BS	476	0	499	28	0
55	BT	968	0	980	26	0
56	BU	1154	0	1185	48	0
57	BV	394	0	388	15	0
58	BW	729	0	762	19	0
59	BX	474	0	481	24	0
60	BY	374	0	386	23	0
61	BZ	452	0	502	21	0
62	1	239	0	0	0	0
62	2	1	0	0	0	0
62	3	64	0	0	0	0
62	7	1	0	0	0	0
62	AA	1	0	0	0	0
62	AB	2	0	0	0	0
62	AH	1	0	0	0	0
62	AI	2	0	0	0	0
62	AZ	1	0	0	0	0
62	BF	1	0	0	0	0
62	BM	1	0	0	0	0
63	AT	1	0	0	0	0
63	AZ	1	0	0	0	0
63	Ab	1	0	0	0	0
63	Ac	1	0	0	0	0
63	Ad	1	0	0	0	0
63	BF	1	0	0	0	0
63	BP	1	0	0	0	0
63	BR	1	0	0	0	0
63	BV	2	0	0	0	0
63	BX	1	0	0	0	0
All	All	150576	0	107122	2208	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 9.

The worst 5 of 2208 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)
3:3:1371:G:H1	3:3:1414:U:H3	1.07	0.97
27:AV:21:MET:HE1	27:AV:51:TYR:HB2	1.60	0.84
3:3:1103:G:N7	54:BS:44:LYS:NZ	2.24	0.84
43:BH:22:GLY:H	60:BY:62:MET:HE1	1.43	0.84
46:BK:1:MET:HE3	46:BK:3:TRP:HB2	1.58	0.83

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	
4	6	279/281 (99%)	257 (92%)	21 (8%)	1 (0%)	30	59
5	7	255/274 (93%)	244 (96%)	11 (4%)	0	100	100
6	AA	233/238 (98%)	228 (98%)	4 (2%)	1 (0%)	30	59
7	AB	333/337 (99%)	322 (97%)	11 (3%)	0	100	100
8	AC	250/253 (99%)	244 (98%)	5 (2%)	1 (0%)	30	59
9	AD	157/165 (95%)	147 (94%)	9 (6%)	1 (1%)	21	51
10	AE	169/176 (96%)	165 (98%)	4 (2%)	0	100	100
11	AF	104/120 (87%)	103 (99%)	1 (1%)	0	100	100
12	AG	137/143 (96%)	137 (100%)	0	0	100	100
13	AH	130/132 (98%)	128 (98%)	2 (2%)	0	100	100
14	AI	137/140 (98%)	134 (98%)	3 (2%)	0	100	100
15	AJ	193/196 (98%)	191 (99%)	2 (1%)	0	100	100
16	AK	157/173 (91%)	151 (96%)	6 (4%)	0	100	100
17	AL	170/174 (98%)	167 (98%)	3 (2%)	0	100	100
18	AM	123/126 (98%)	122 (99%)	1 (1%)	0	100	100
19	AN	145/151 (96%)	142 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	AO	54/61 (88%)	52 (96%)	2 (4%)	0	100	100
21	AP	94/97 (97%)	91 (97%)	3 (3%)	0	100	100
22	AQ	147/151 (97%)	145 (99%)	2 (1%)	0	100	100
23	AR	77/82 (94%)	76 (99%)	1 (1%)	0	100	100
24	AS	113/119 (95%)	112 (99%)	1 (1%)	0	100	100
25	AT	58/62 (94%)	58 (100%)	0	0	100	100
26	AU	63/67 (94%)	61 (97%)	2 (3%)	0	100	100
27	AV	151/153 (99%)	149 (99%)	2 (1%)	0	100	100
28	AW	82/99 (83%)	81 (99%)	1 (1%)	0	100	100
29	AX	82/89 (92%)	80 (98%)	2 (2%)	0	100	100
30	AY	124/129 (96%)	119 (96%)	4 (3%)	1 (1%)	16	44
31	AZ	53/56 (95%)	48 (91%)	5 (9%)	0	100	100
32	Aa	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
33	Ab	41/49 (84%)	41 (100%)	0	0	100	100
34	Ac	89/92 (97%)	88 (99%)	1 (1%)	0	100	100
35	Ad	87/94 (93%)	84 (97%)	3 (3%)	0	100	100
36	BA	176/203 (87%)	166 (94%)	10 (6%)	0	100	100
37	BB	186/225 (83%)	176 (95%)	10 (5%)	0	100	100
38	BC	138/318 (43%)	131 (95%)	7 (5%)	0	100	100
39	BD	154/218 (71%)	149 (97%)	5 (3%)	0	100	100
40	BE	226/235 (96%)	210 (93%)	16 (7%)	0	100	100
41	BF	199/209 (95%)	179 (90%)	20 (10%)	0	100	100
42	BG	123/136 (90%)	116 (94%)	6 (5%)	1 (1%)	16	44
43	BH	171/189 (90%)	156 (91%)	15 (9%)	0	100	100
44	BI	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
45	BJ	130/134 (97%)	126 (97%)	4 (3%)	0	100	100
46	BK	122/125 (98%)	116 (95%)	6 (5%)	0	100	100
47	BL	36/102 (35%)	35 (97%)	1 (3%)	0	100	100
48	BM	119/126 (94%)	116 (98%)	3 (2%)	0	100	100
49	BN	137/142 (96%)	127 (93%)	10 (7%)	0	100	100
50	BO	136/162 (84%)	129 (95%)	7 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	BP	44/50 (88%)	41 (93%)	3 (7%)	0	100	100
52	BQ	148/152 (97%)	144 (97%)	4 (3%)	0	100	100
53	BR	105/109 (96%)	102 (97%)	3 (3%)	0	100	100
54	BS	56/64 (88%)	55 (98%)	1 (2%)	0	100	100
55	BT	119/136 (88%)	118 (99%)	1 (1%)	0	100	100
56	BU	146/149 (98%)	140 (96%)	6 (4%)	0	100	100
57	BV	50/56 (89%)	48 (96%)	2 (4%)	0	100	100
58	BW	87/101 (86%)	83 (95%)	4 (5%)	0	100	100
59	BX	59/62 (95%)	55 (93%)	4 (7%)	0	100	100
60	BY	46/76 (60%)	40 (87%)	5 (11%)	1 (2%)	5	20
61	BZ	55/57 (96%)	49 (89%)	6 (11%)	0	100	100
All	All	7430/8196 (91%)	7142 (96%)	281 (4%)	7 (0%)	49	77

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
42	BG	28	ALA
30	AY	4	GLU
9	AD	52	LYS
4	6	12	TYR
8	AC	82	ARG

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	
4	6	252/252 (100%)	239 (95%)	13 (5%)	21	52
5	7	228/245 (93%)	213 (93%)	15 (7%)	15	43
6	AA	185/188 (98%)	181 (98%)	4 (2%)	45	77
7	AB	276/277 (100%)	269 (98%)	7 (2%)	42	74
8	AC	197/198 (100%)	194 (98%)	3 (2%)	57	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	AD	135/140 (96%)	121 (90%)	14 (10%)	7	23
10	AE	143/148 (97%)	132 (92%)	11 (8%)	12	35
11	AF	79/91 (87%)	76 (96%)	3 (4%)	29	64
12	AG	115/119 (97%)	115 (100%)	0	100	100
13	AH	109/109 (100%)	104 (95%)	5 (5%)	24	57
14	AI	107/108 (99%)	102 (95%)	5 (5%)	23	56
15	AJ	165/166 (99%)	163 (99%)	2 (1%)	63	86
16	AK	134/141 (95%)	131 (98%)	3 (2%)	45	77
17	AL	141/143 (99%)	137 (97%)	4 (3%)	38	72
18	AM	103/104 (99%)	99 (96%)	4 (4%)	28	63
19	AN	119/123 (97%)	113 (95%)	6 (5%)	22	53
20	AO	49/54 (91%)	49 (100%)	0	100	100
21	AP	85/86 (99%)	84 (99%)	1 (1%)	63	86
22	AQ	122/124 (98%)	122 (100%)	0	100	100
23	AR	70/73 (96%)	67 (96%)	3 (4%)	26	60
24	AS	97/100 (97%)	94 (97%)	3 (3%)	35	69
25	AT	53/54 (98%)	52 (98%)	1 (2%)	50	79
26	AU	55/57 (96%)	53 (96%)	2 (4%)	31	65
27	AV	134/134 (100%)	131 (98%)	3 (2%)	45	77
28	AW	66/78 (85%)	64 (97%)	2 (3%)	36	70
29	AX	74/78 (95%)	71 (96%)	3 (4%)	27	61
30	AY	103/106 (97%)	103 (100%)	0	100	100
31	AZ	48/49 (98%)	47 (98%)	1 (2%)	47	77
32	Aa	47/48 (98%)	43 (92%)	4 (8%)	10	31
33	Ab	37/40 (92%)	37 (100%)	0	100	100
34	Ac	81/82 (99%)	81 (100%)	0	100	100
35	Ad	73/76 (96%)	71 (97%)	2 (3%)	39	73
36	BA	157/173 (91%)	145 (92%)	12 (8%)	12	36
37	BB	164/193 (85%)	151 (92%)	13 (8%)	11	34
38	BC	111/250 (44%)	100 (90%)	11 (10%)	7	24
39	BD	136/178 (76%)	119 (88%)	17 (12%)	4	15

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	BE	204/209 (98%)	192 (94%)	12 (6%)	18	48
41	BF	163/170 (96%)	149 (91%)	14 (9%)	10	30
42	BG	96/103 (93%)	90 (94%)	6 (6%)	16	45
43	BH	147/159 (92%)	140 (95%)	7 (5%)	23	55
44	BI	104/105 (99%)	94 (90%)	10 (10%)	8	26
45	BJ	105/107 (98%)	99 (94%)	6 (6%)	18	49
46	BK	104/105 (99%)	94 (90%)	10 (10%)	8	26
47	BL	34/89 (38%)	33 (97%)	1 (3%)	37	71
48	BM	91/93 (98%)	89 (98%)	2 (2%)	45	77
49	BN	109/112 (97%)	100 (92%)	9 (8%)	10	32
50	BO	112/135 (83%)	107 (96%)	5 (4%)	24	58
51	BP	40/44 (91%)	39 (98%)	1 (2%)	42	74
52	BQ	136/138 (99%)	130 (96%)	6 (4%)	25	59
53	BR	94/96 (98%)	90 (96%)	4 (4%)	26	60
54	BS	52/57 (91%)	49 (94%)	3 (6%)	18	49
55	BT	105/118 (89%)	94 (90%)	11 (10%)	6	22
56	BU	122/123 (99%)	114 (93%)	8 (7%)	15	43
57	BV	44/48 (92%)	43 (98%)	1 (2%)	44	76
58	BW	80/87 (92%)	72 (90%)	8 (10%)	7	24
59	BX	55/56 (98%)	49 (89%)	6 (11%)	6	20
60	BY	41/62 (66%)	33 (80%)	8 (20%)	1	5
61	BZ	47/47 (100%)	44 (94%)	3 (6%)	16	44
All	All	6335/6848 (92%)	6017 (95%)	318 (5%)	23	53

5 of 318 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
45	BJ	108	LEU
56	BU	10	THR
46	BK	71	THR
52	BQ	15	THR
58	BW	86	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 58 such sidechains are listed below:

Mol	Chain	Res	Type
26	AU	62	HIS
58	BW	89	ASN
36	BA	106	ASN
54	BS	48	ASN
48	BM	83	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2704/2904 (93%)	341 (12%)	11 (0%)
2	2	126/133 (94%)	16 (12%)	3 (2%)
3	3	1424/1478 (96%)	237 (16%)	16 (1%)
All	All	4254/4515 (94%)	594 (13%)	30 (0%)

5 of 594 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	58	C
1	1	68	A
1	1	71	A
1	1	72	G
1	1	82	G

5 of 30 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	3	173	A
3	3	1325	C
3	3	769	A
3	3	1436	U
3	3	1080	C

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

9 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
3	6MZ	3	1438	62,3	22,25,26	0.41	0	29,36,39	0.71	1 (3%)
3	MA6	3	1456	3	23,26,27	0.28	0	33,38,41	0.67	1 (3%)
1	OMU	1	2567	1,62	19,22,23	0.21	0	25,31,34	0.46	0
48	IAS	BM	116	48	6,7,8	1.44	1 (16%)	3,8,10	0.91	0
3	5MU	3	1222	3	19,22,23	0.26	0	27,32,35	0.42	0
1	5MC	1	2516	1	19,22,23	0.88	1 (5%)	26,32,35	0.62	1 (3%)
1	5MC	1	2514	1,62	19,22,23	0.77	1 (5%)	26,32,35	0.49	0
1	OMG	1	2568	1	23,26,27	0.32	0	32,38,41	0.48	0
3	MA6	3	1457	3	23,26,27	0.27	0	33,38,41	0.72	1 (3%)

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
3	6MZ	3	1438	62,3	-	0/9/27/28	0/3/3/3
3	MA6	3	1456	3	-	0/11/29/30	0/3/3/3
1	OMU	1	2567	1,62	-	0/9/27/28	0/2/2/2
48	IAS	BM	116	48	-	2/7/7/8	-
3	5MU	3	1222	3	-	0/7/25/26	0/2/2/2
1	5MC	1	2516	1	-	4/7/25/26	0/2/2/2
1	5MC	1	2514	1,62	-	0/7/25/26	0/2/2/2
1	OMG	1	2568	1	-	0/9/27/28	0/3/3/3
3	MA6	3	1457	3	-	2/11/29/30	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2516	5MC	C5-C4	-3.54	1.41	1.44
1	1	2514	5MC	C5-C4	-3.10	1.41	1.44
48	BM	116	IAS	CB-CG	2.46	1.56	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	3	1457	MA6	C2-N1-C6	2.84	118.78	111.83
3	3	1456	MA6	C2-N1-C6	2.84	118.76	111.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	2516	5MC	C5-C6-N1	-2.10	121.03	123.31
3	3	1438	6MZ	C9-N6-C6	2.06	124.76	122.85

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	3	1457	MA6	O4'-C4'-C5'-O5'
1	1	2516	5MC	C2'-C1'-N1-C6
3	3	1457	MA6	C3'-C4'-C5'-O5'
1	1	2516	5MC	C2'-C1'-N1-C2
1	1	2516	5MC	O4'-C1'-N1-C6

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	3	1456	MA6	1	0
48	BM	116	IAS	1	0
1	1	2516	5MC	2	0
1	1	2568	OMG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 325 ligands modelled in this entry, 325 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

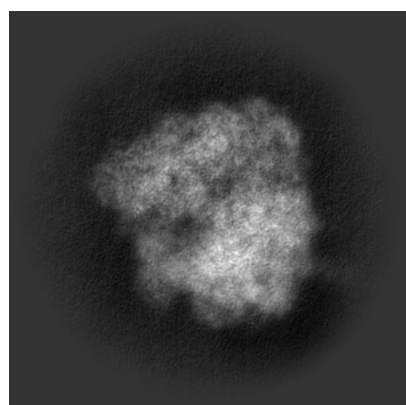
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-74448. These allow visual inspection of the internal detail of the map and identification of artifacts.

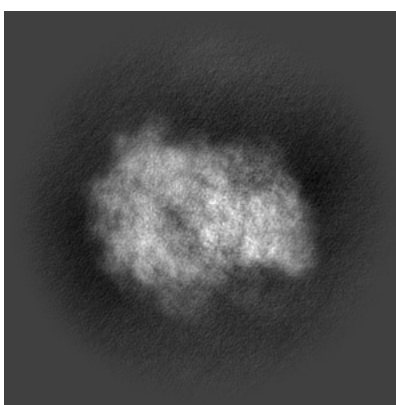
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

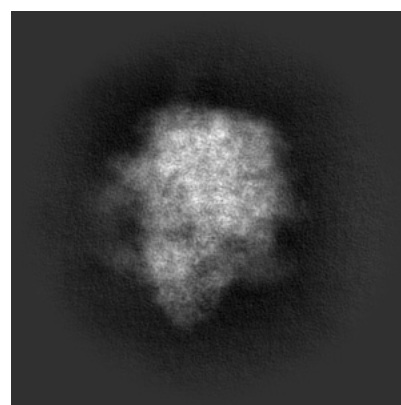
6.1.1 Primary map



X



Y

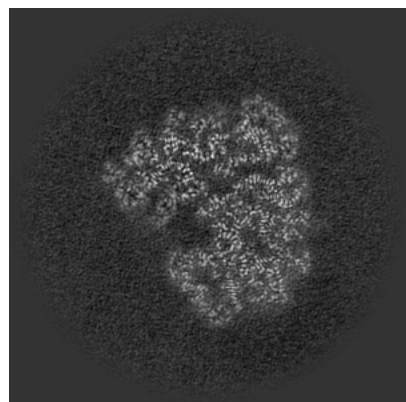


Z

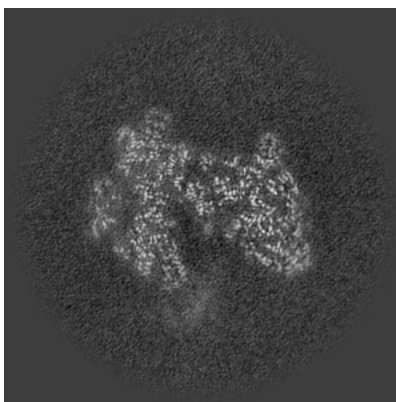
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

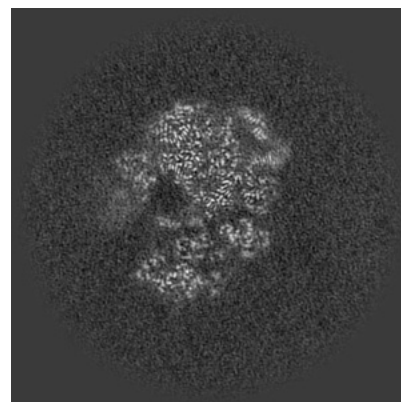
6.2.1 Primary map



X Index: 256



Y Index: 256

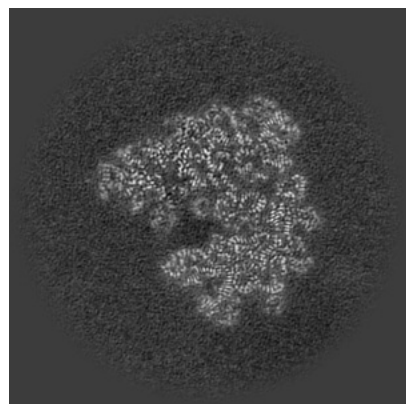


Z Index: 256

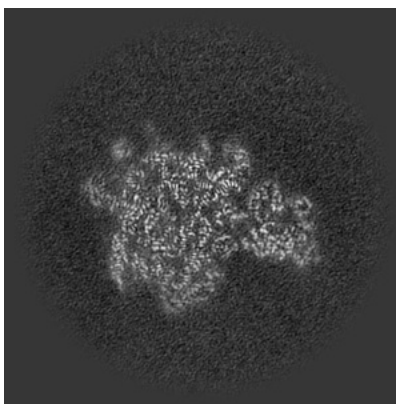
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

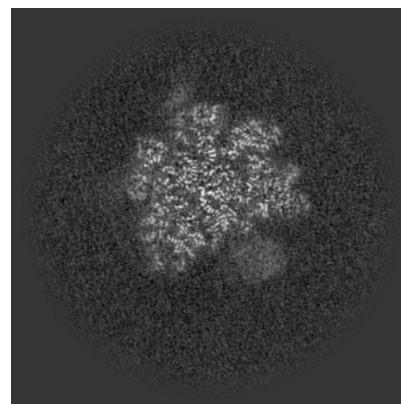
6.3.1 Primary map



X Index: 240



Y Index: 312

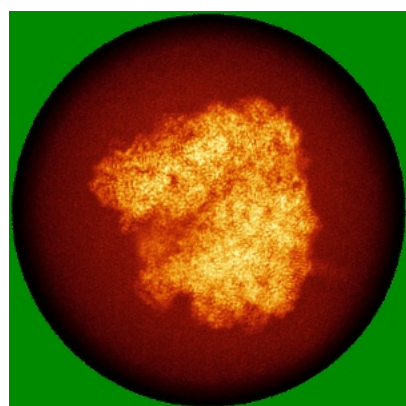


Z Index: 188

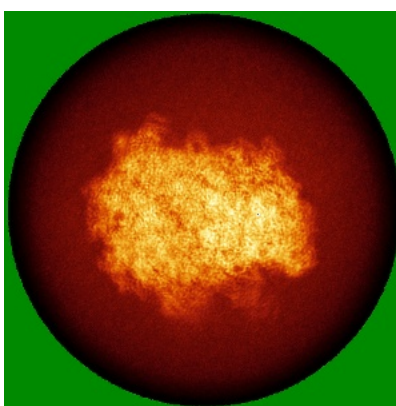
The images above show the largest variance slices of the map in three orthogonal directions.

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

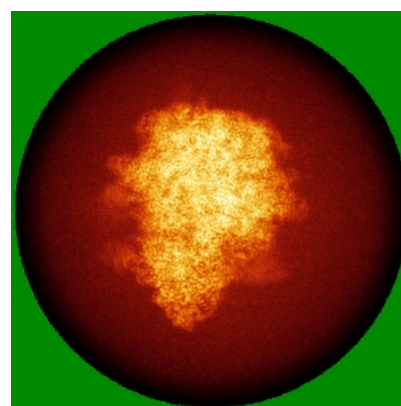
6.4.1 Primary map



X



Y

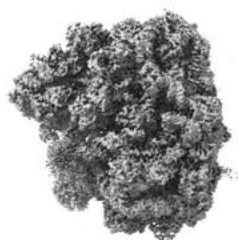


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.142. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

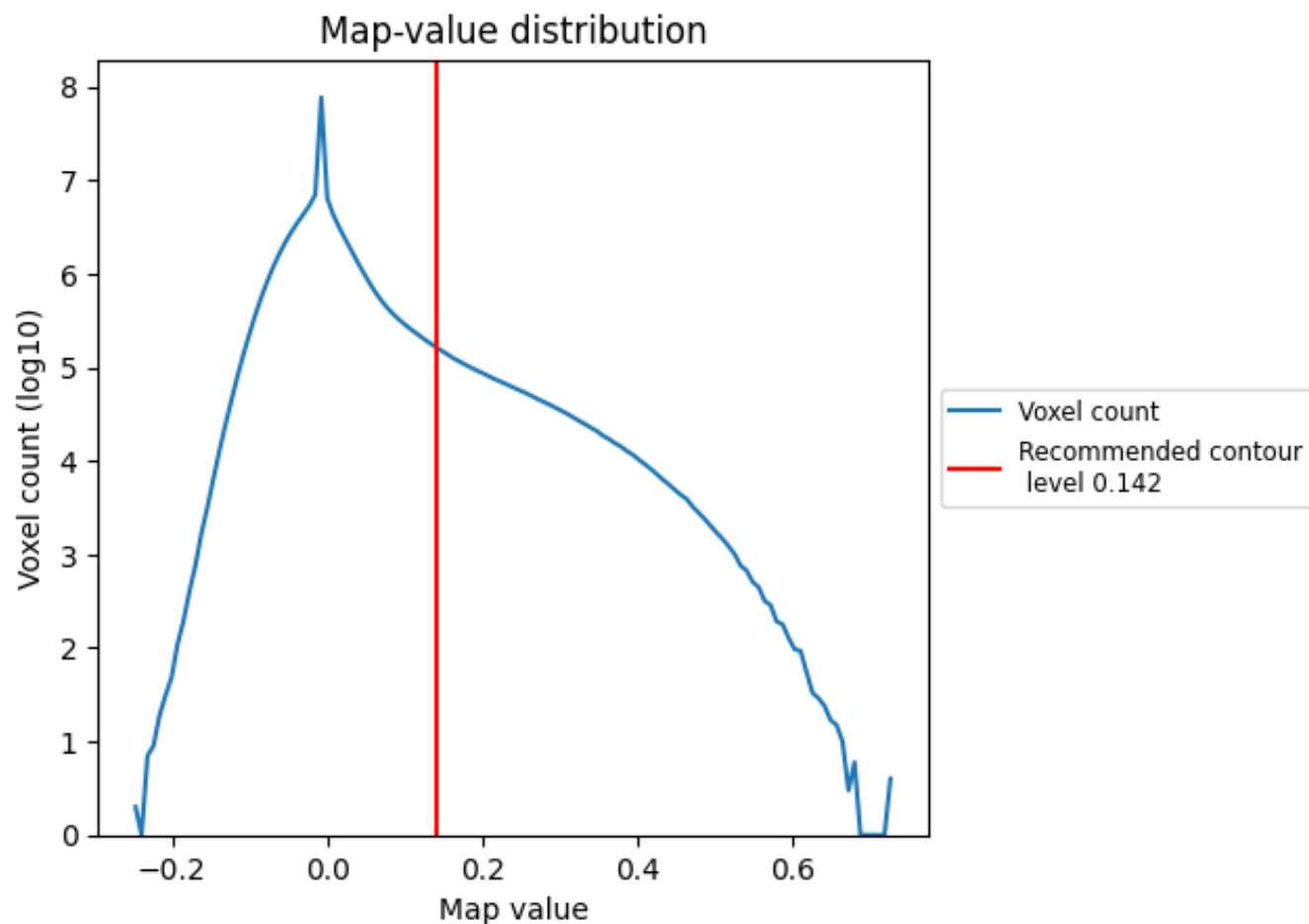
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

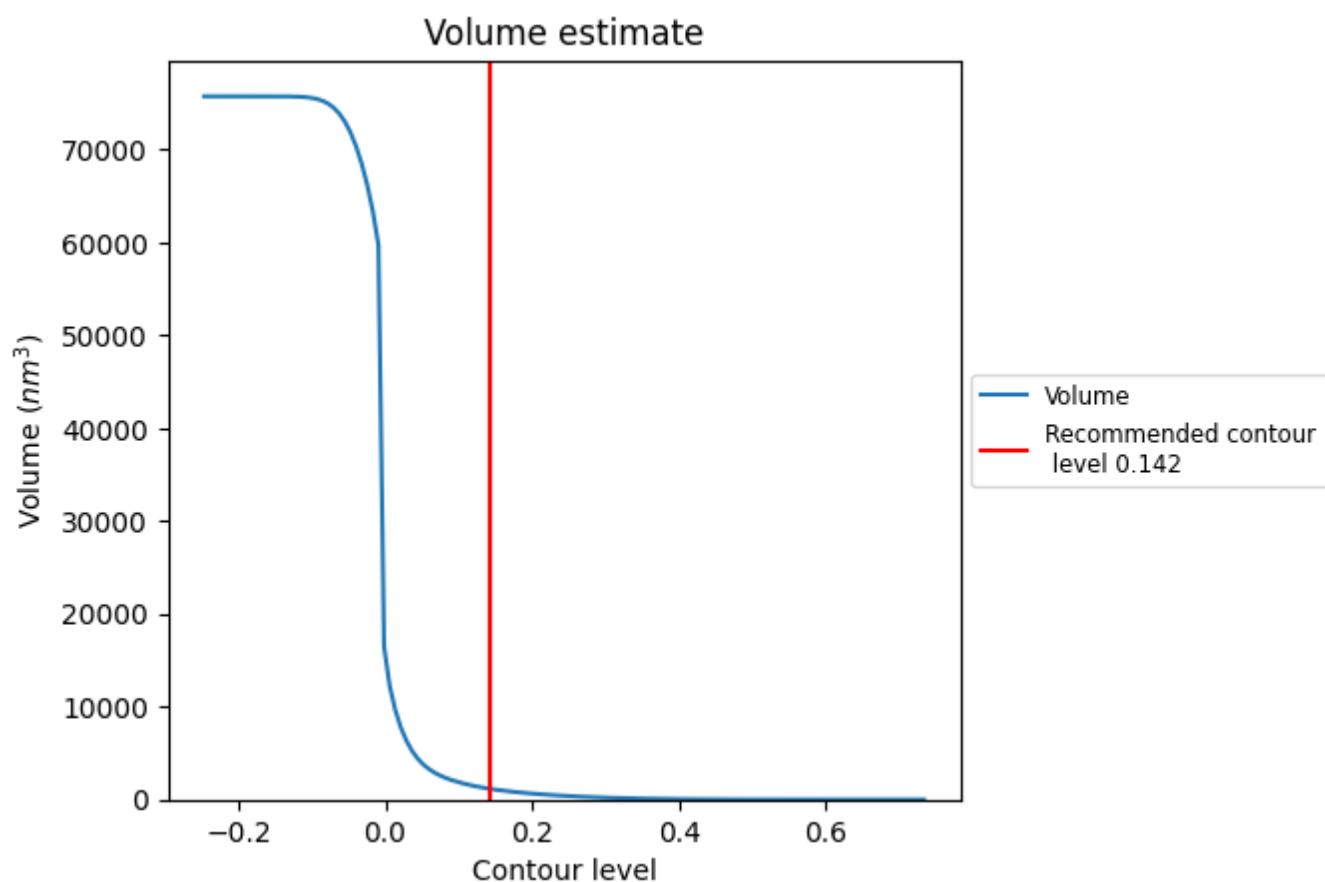
This section contains the results of statistical analysis of the map.

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.

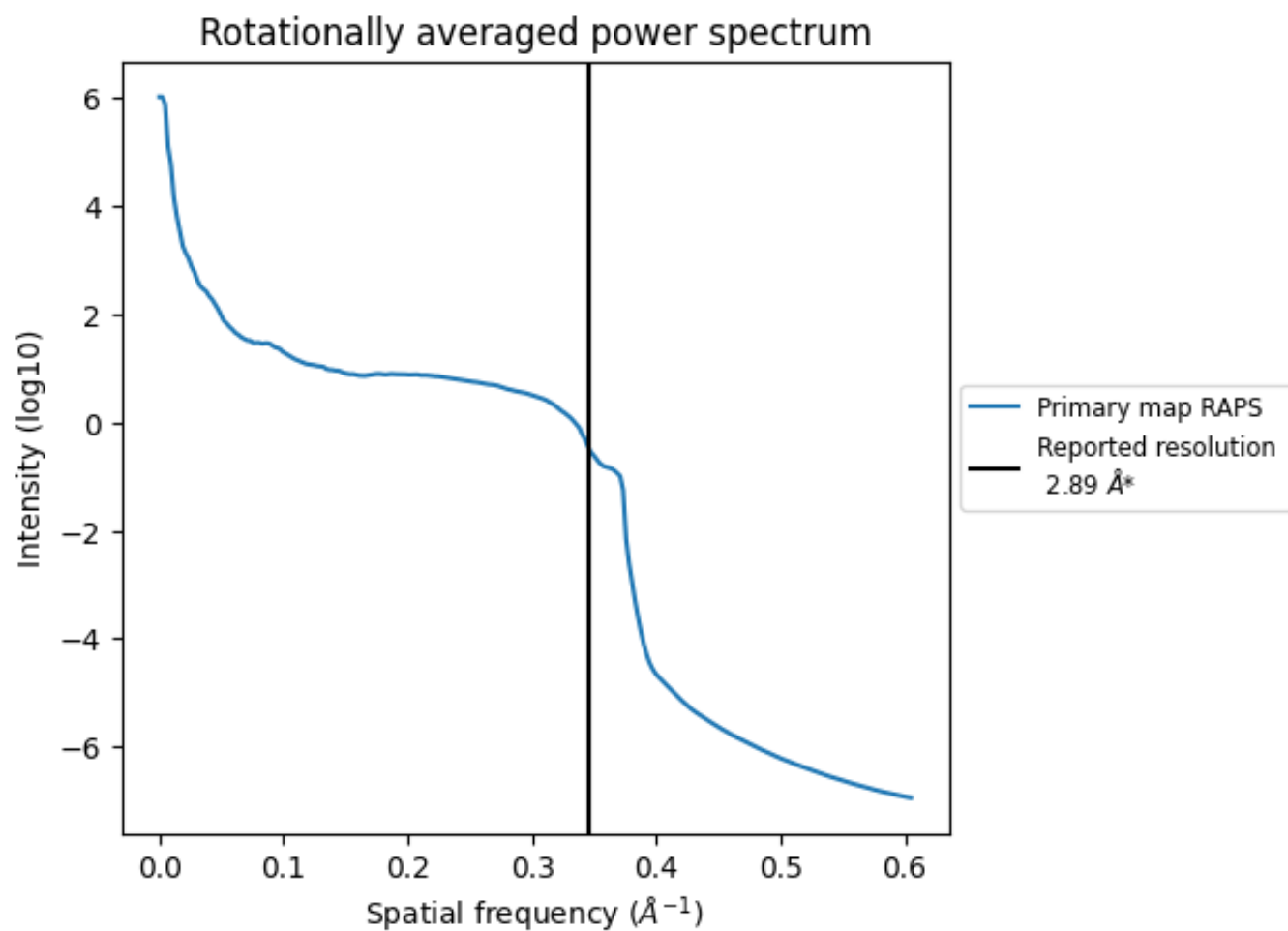
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1167 nm³; this corresponds to an approximate mass of 1054 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 0.346 Å⁻¹

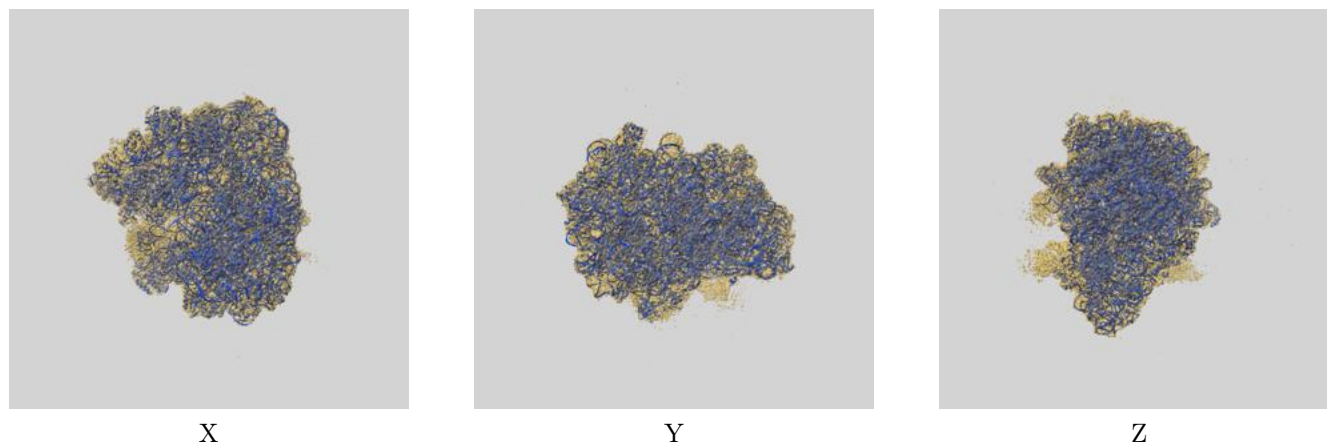
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

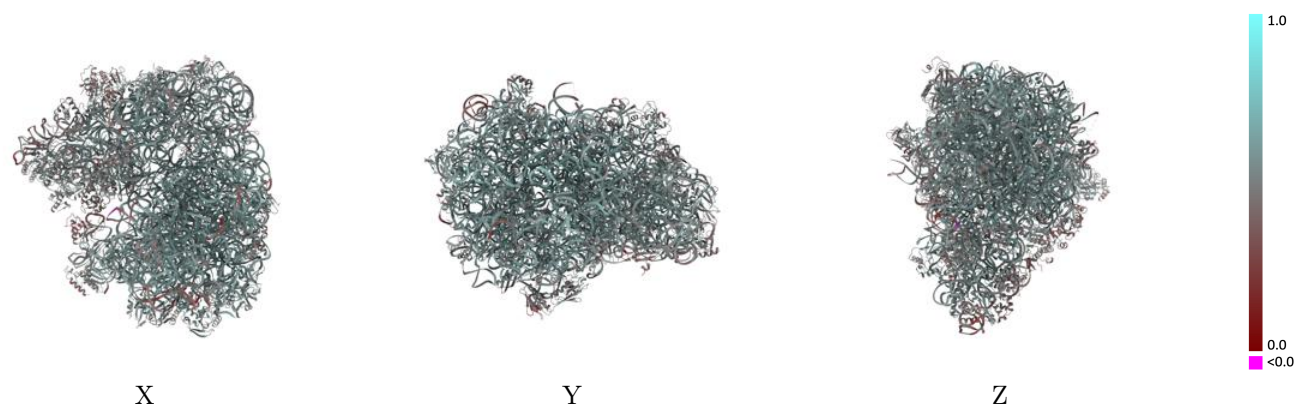
This section contains information regarding the fit between EMDB map EMD-74448 and PDB model 9ZNI. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



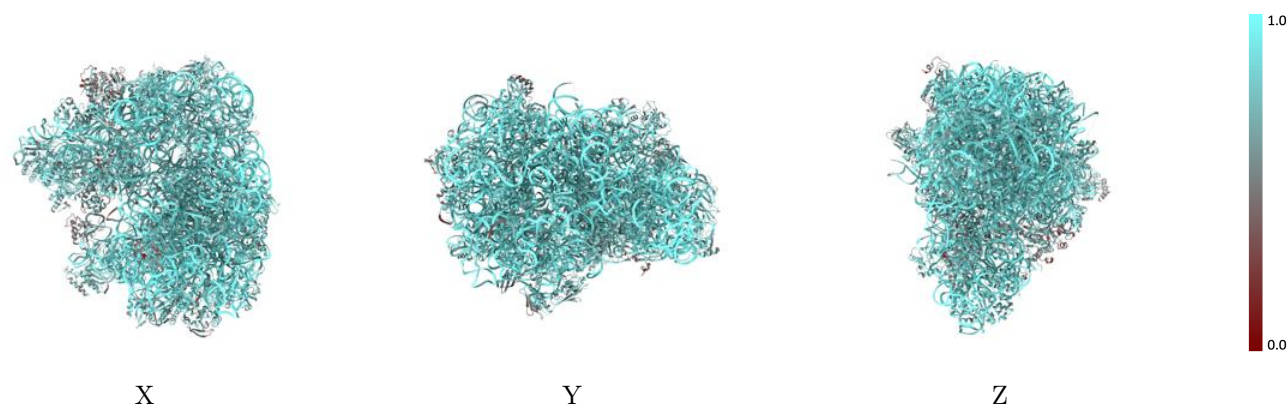
The images above show the 3D surface view of the map at the recommended contour level 0.142 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



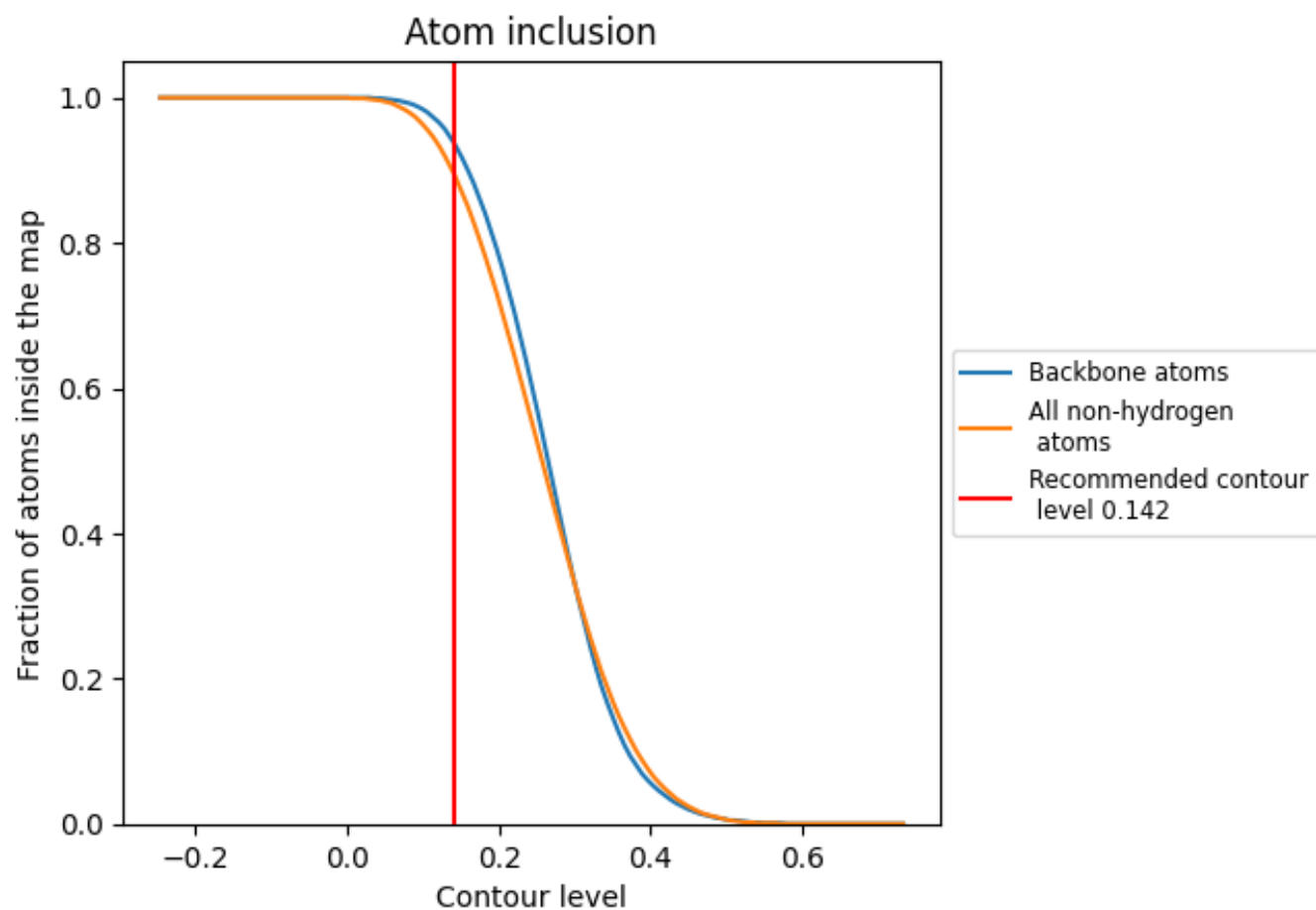
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.142).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 89% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.142) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8930	 0.5430
1	 0.9600	 0.5710
2	 0.9280	 0.4940
3	 0.9640	 0.5450
6	 0.6700	 0.4750
7	 0.7020	 0.4800
AA	 0.8590	 0.5750
AB	 0.8450	 0.5580
AC	 0.7990	 0.5580
AD	 0.4850	 0.3520
AE	 0.7030	 0.4750
AF	 0.6370	 0.4920
AG	 0.8340	 0.5540
AH	 0.7940	 0.5590
AI	 0.8170	 0.5450
AJ	 0.9120	 0.5810
AK	 0.8010	 0.5430
AL	 0.7630	 0.4940
AM	 0.7940	 0.5360
AN	 0.8670	 0.5500
AO	 0.6950	 0.5060
AP	 0.8940	 0.5730
AQ	 0.8510	 0.5490
AR	 0.8190	 0.5370
AS	 0.8040	 0.5410
AT	 0.8610	 0.5750
AU	 0.7750	 0.4940
AV	 0.8120	 0.5460
AW	 0.7340	 0.4780
AX	 0.8890	 0.5660
AY	 0.8480	 0.5610
AZ	 0.9530	 0.6080
Aa	 0.9020	 0.5680
Ab	 0.7460	 0.4930
Ac	 0.8600	 0.5690



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Chain	Atom inclusion	Q-score
Ad	 0.8520	 0.5670
BA	 0.7090	 0.4630
BB	 0.5140	 0.4420
BC	 0.6510	 0.4700
BD	 0.8400	 0.4990
BE	 0.8080	 0.5080
BF	 0.8060	 0.5190
BG	 0.6960	 0.4570
BH	 0.7920	 0.4770
BI	 0.8650	 0.5380
BJ	 0.8290	 0.4950
BK	 0.8810	 0.5410
BL	 0.8910	 0.5240
BM	 0.8200	 0.5180
BN	 0.8270	 0.5370
BO	 0.7890	 0.4890
BP	 0.8780	 0.5510
BQ	 0.8140	 0.5180
BR	 0.8480	 0.5370
BS	 0.7830	 0.4630
BT	 0.8120	 0.5200
BU	 0.8370	 0.4970
BV	 0.5430	 0.4830
BW	 0.7580	 0.4770
BX	 0.6550	 0.4910
BY	 0.8020	 0.4580
BZ	 0.8280	 0.4940