



wwPDB EM Validation Summary Report ⓘ

Nov 4, 2024 – 02:24 AM JST

PDB ID : 6IP5
EMDB ID : EMD-9701
Title : Cryo-EM structure of the CMV-stalled human 80S ribosome (Structure ii)
Authors : Yokoyama, T.; Shigematsu, H.; Shirouzu, M.; Imataka, H.; Ito, T.
Deposited on : 2018-11-02
Resolution : 3.90 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.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

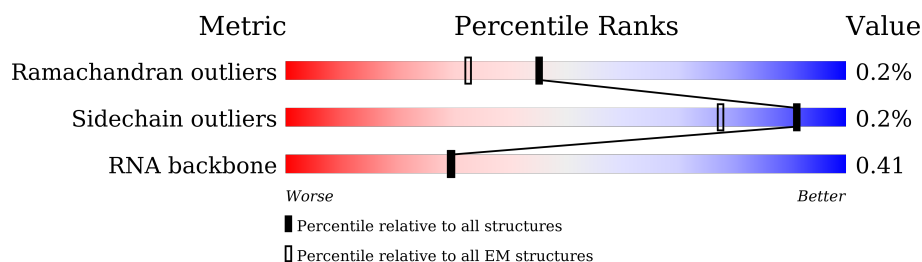
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 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.



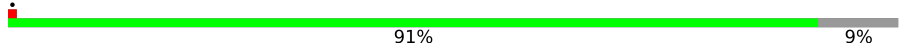

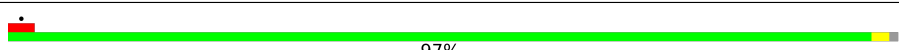
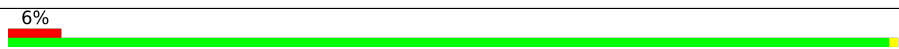
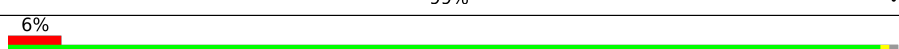
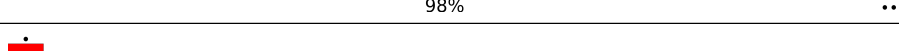
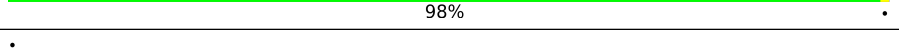

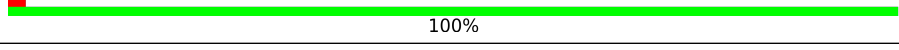
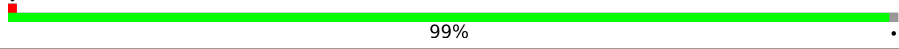

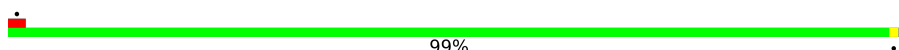
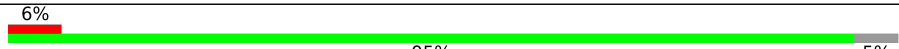

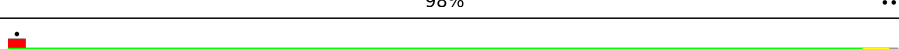
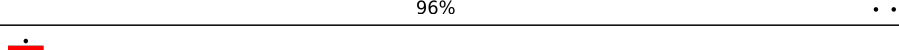

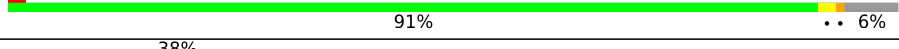


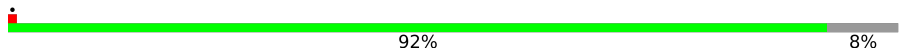
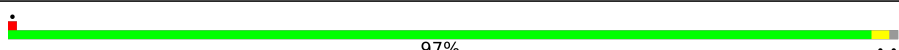

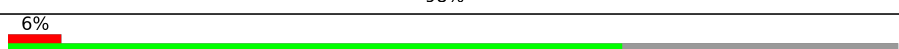
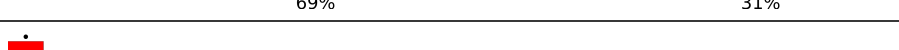
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	1A	5070	
2	1B	121	
3	1C	157	
4	1D	257	
5	1E	403	
6	1F	427	
7	1G	297	
8	1H	288	

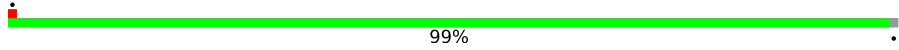
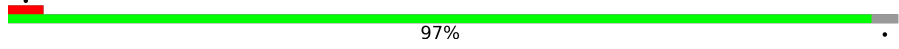
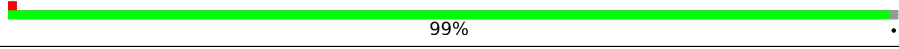
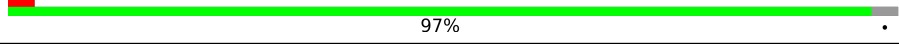

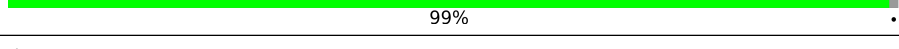
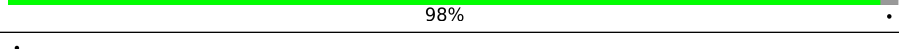
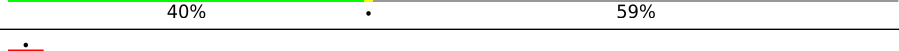
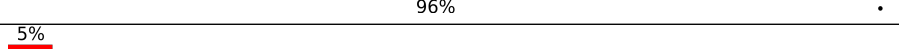
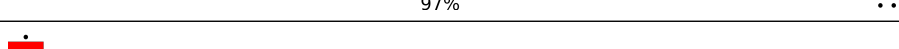
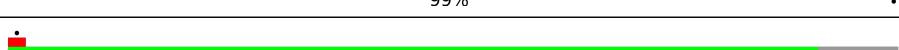
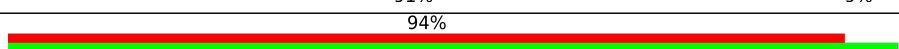
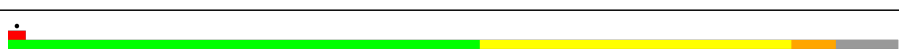

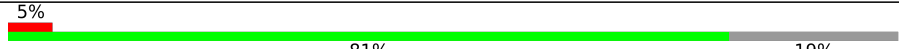
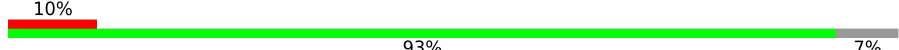
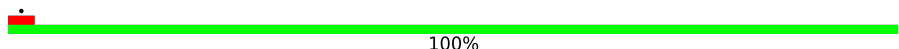

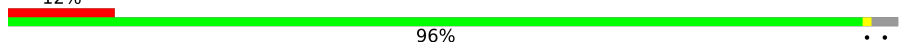
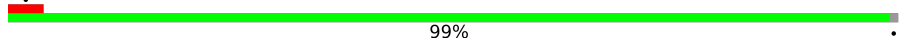
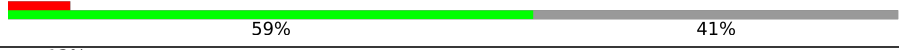
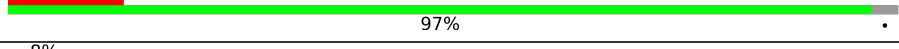

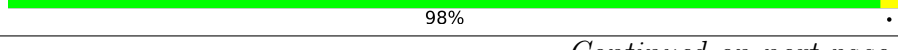

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Mol	Chain	Length	Quality of chain
9	2A	248	
10	2B	266	
11	2C	192	
12	2D	214	
13	2E	178	
14	2F	211	
15	2G	215	
16	2H	204	
17	2I	203	
18	2J	184	
19	2K	188	
20	2L	196	
21	2M	176	
22	2N	160	
23	2O	128	
24	2P	140	
25	2Q	157	
26	2R	156	
27	2S	145	
28	2T	136	
29	2U	148	
30	2V	159	
31	2W	115	
32	2X	125	
33	2Y	135	

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Mol	Chain	Length	Quality of chain
34	2Z	110	 99%
35	2a	117	 97%
36	2b	123	 99%
37	2c	105	 97%
38	2d	97	 88% 11%
39	2e	70	 99%
40	2f	51	 98%
41	2g	128	 40% 59%
42	2h	25	 96%
43	2i	106	 97%
44	2j	92	 99%
45	2k	137	 91% 9%
46	2l	217	 94% 100%
47	2m	1869	 53% 35% 5% 7%
48	2n	295	 75% 25%
49	2o	264	 81% 19%
50	2p	243	 93% 7%
51	2q	263	 100%
52	2r	204	 90% 8%
53	2s	194	 96%
54	2t	208	 99%
55	2u	165	 59% 41%
56	2v	158	 97%
57	2w	145	 67% 33%
58	2x	146	 98%

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Mol	Chain	Length	Quality of chain
59	2y	135	
60	2z	152	
61	20	145	
62	21	119	
63	3A	83	
64	3B	143	
65	3C	115	
66	3D	69	
67	3E	56	
68	3F	317	
69	3G	293	
70	3H	249	
71	3I	194	
72	3J	132	
73	3K	151	
74	3L	151	
75	3M	130	
76	3N	133	
77	3O	125	
78	3P	84	
79	3Q	59	
80	3R	156	
81	zv	6	
82	zx	17	
83	zu	75	

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Mol	Chain	Length	Quality of chain
83	zy	75	<div><div></div><div>69%</div><div>28%</div><div></div></div>

2 Entry composition

There are 83 unique types of molecules in this entry. The entry contains 220009 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 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1A	3717	Total	C	N	O	P	0	0
			79676	35480	14585	25895	3716		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1B	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	1C	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 4 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	1D	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	1E	402	Total	C	N	O	S	0	0
			3238	2060	608	556	14		

- Molecule 6 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	1F	368	Total	C	N	O	S	0	0
			2927	1840	583	489	15		

- Molecule 7 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	1G	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

- Molecule 8 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	1H	237	Total	C	N	O	S	0	0
			1913	1228	363	318	4		

- Molecule 9 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	2A	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 10 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	2B	241	Total	C	N	O	S	0	0
			1927	1228	371	324	4		

- Molecule 11 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	2C	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 12 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	2D	213	Total	C	N	O	S	0	0
			1711	1082	329	285	15		

- Molecule 13 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	2E	176	Total	C	N	O	S	0	0
			1410	888	263	253	6		

- Molecule 14 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	2F	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		

- Molecule 15 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	2G	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 16 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	2H	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 17 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	2I	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

- Molecule 18 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	2J	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 19 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	2K	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 20 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	2L	187	Total	C	N	O	S	0	0
			1566	971	336	250	9		

- Molecule 21 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	2M	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

- Molecule 22 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	2N	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 23 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	2O	101	Total	C	N	O	S	0	0
			825	529	144	150	2		

- Molecule 24 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	2P	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 25 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	2Q	124	Total	C	N	O	S	0	0
			1015	634	207	170	4		

- Molecule 26 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	2R	119	Total	C	N	O	S	0	0
			976	625	184	166	1		

- Molecule 27 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	2S	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 28 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	2T	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 29 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	2U	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	2V	109	Total	C	N	O	S	0	0
			876	546	189	137	4		

- Molecule 31 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	2W	98	Total	C	N	O	S	0	0
			764	485	135	138	6		

- Molecule 32 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	2X	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 33 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	2Y	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 34 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	2Z	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 35 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	2a	113	Total	C	N	O	S	0	0
			895	560	183	146	6		

- Molecule 36 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	2b	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 37 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	2c	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 38 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	2d	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 39 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	2e	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 40 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	2f	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 41 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	2g	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 42 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	2h	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 43 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	2i	105	Total	C	N	O	S	0	0
			862	542	175	139	6		

- Molecule 44 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	2j	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 45 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	2k	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 46 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	2l	217	Total	C	N	O	S	0	0
			1741	1113	312	307	9		

- Molecule 47 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	2m	1742	Total	C	N	O	P	0	0
			36900	16458	6595	12106	1741		

- Molecule 48 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	2n	221	Total	C	N	O	S	0	0
			1741	1106	305	322	8		

- Molecule 49 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	2o	214	Total	C	N	O	S	0	0
			1738	1103	310	311	14		

- Molecule 50 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	2p	227	Total	C	N	O	S	0	0
			1765	1125	317	315	8		

- Molecule 51 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	2q	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 52 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	2r	187	Total	C	N	O	S	0	0
			1479	924	282	266	7		

- Molecule 53 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	2s	189	Total	C	N	O	S	0	0
			1521	969	280	271	1		

- Molecule 54 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	2t	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 55 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	2u	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 56 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	2v	153	Total	C	N	O	S	0	0
			1247	793	234	214	6		

- Molecule 57 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	2w	97	Total	C	N	O	S	0	0
			804	505	155	138	6		

- Molecule 58 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	2x	146	Total	C	N	O	S	0	0
			1158	736	218	200	4		

- Molecule 59 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	2y	132	Total	C	N	O	S	0	0
			1072	673	199	195	5		

- Molecule 60 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	2z	150	Total	C	N	O	S	0	0
			1235	776	250	208	1		

- Molecule 61 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	20	143	Total	C	N	O	S	0	0
			1112	697	214	198	3		

- Molecule 62 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	21	104	Total	C	N	O	S	0	0
			821	514	155	148	4		

- Molecule 63 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	3A	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 64 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	3B	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 65 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	3C	107	Total	C	N	O	S	0	0
			847	528	176	138	5		

- Molecule 66 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	3D	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 67 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	3E	53	Total	C	N	O	S	0	0
			445	278	90	72	5		

- Molecule 68 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	3F	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 69 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	3G	222	Total	C	N	O	S	0	0
			1725	1115	298	302	10		

- Molecule 70 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	3H	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 71 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	3I	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 72 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	3J	122	Total	C	N	O	S	0	0
			952	596	169	179	8		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
3J	52	GLN	LEU	conflict	UNP P25398
3J	69	LEU	CYS	conflict	UNP P25398
3J	99	ASN	LYS	conflict	UNP P25398

- Molecule 73 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	3K	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 74 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	3L	140	Total	C	N	O	S	0	0
			1049	642	204	197	6		

- Molecule 75 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	3M	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 76 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	3N	131	Total	C	N	O	S	0	0
			1065	673	209	178	5		

- Molecule 77 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	3O	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 78 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	3P	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 79 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	3Q	58	Total	C	N	O	S	0	0
			459	284	100	74	1		

- Molecule 80 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	3R	67	Total	C	N	O	S	0	0
			548	346	102	93	7		

- Molecule 81 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	zv	6	Total	C	N	O	P	0	0
			123	55	19	43	6		

- Molecule 82 is a protein called nascent peptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	zx	17	Total	C	N	O	S	0	0
			129	86	20	22	1		

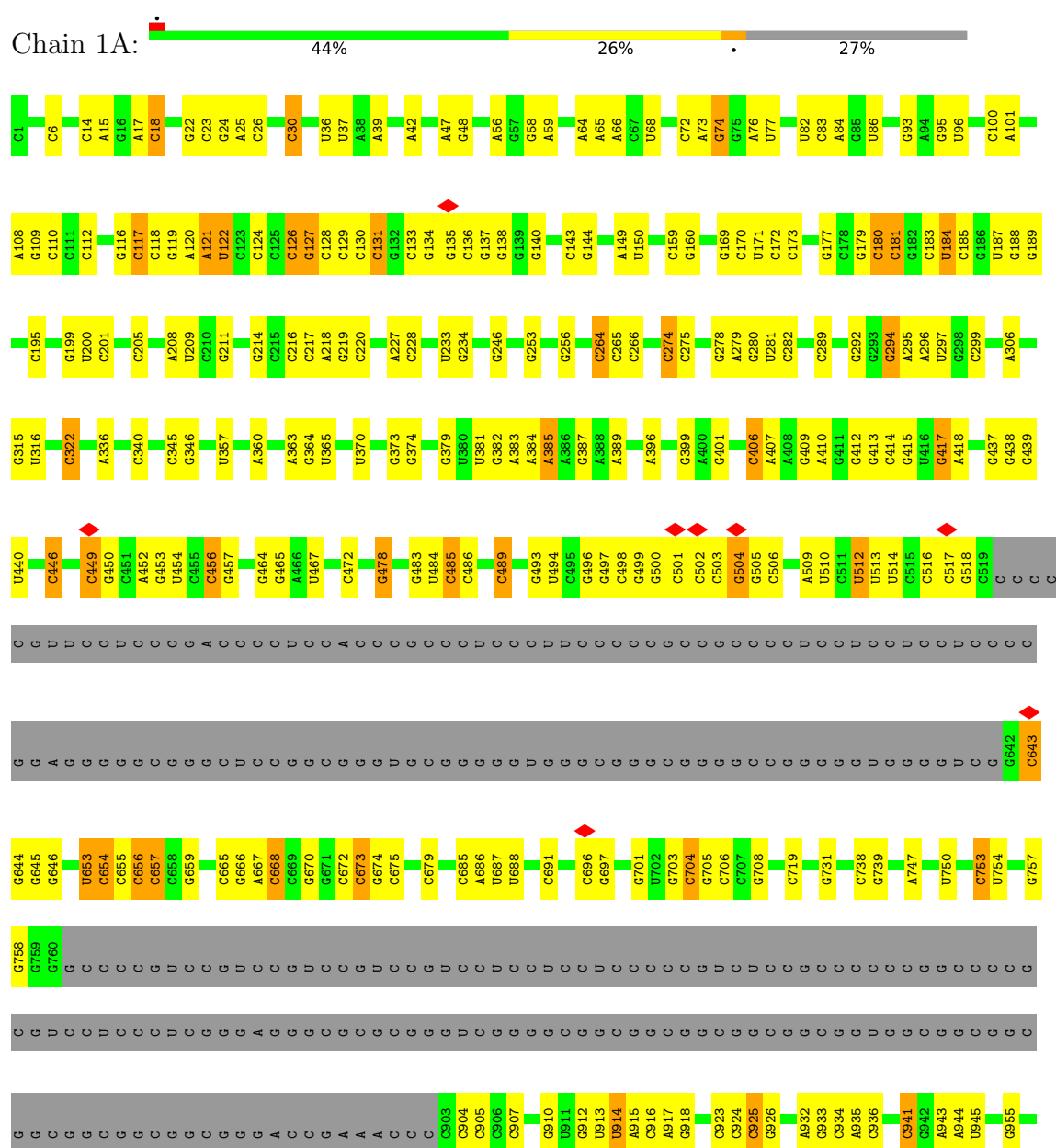
- Molecule 83 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	zy	75	Total 1599	C 713	N 284	O 528	P 74	0	0
83	zu	75	Total 1599	C 713	N 284	O 528	P 74	0	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.

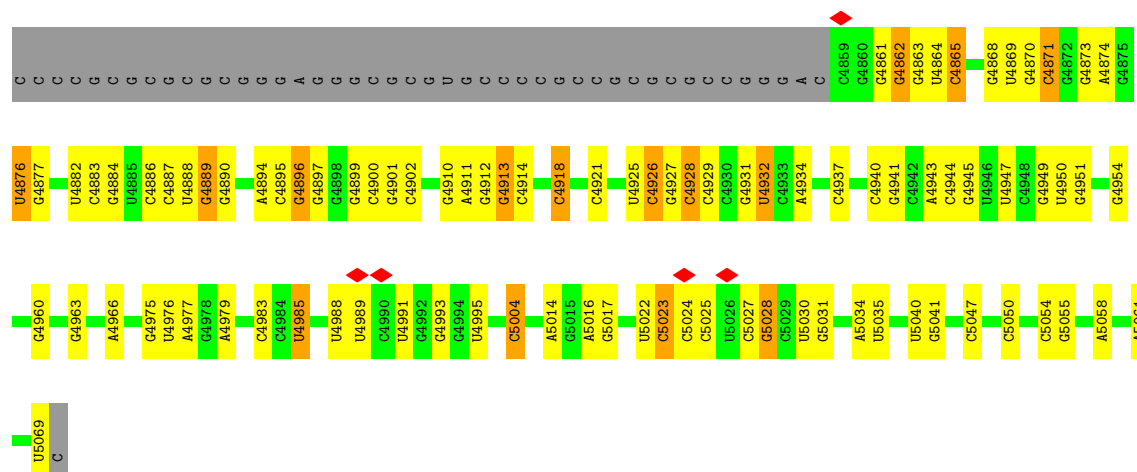
• Molecule 1: 28S ribosomal RNA



C2084	C2085	C1993	C1994	C1915	U1771	C1694	U1582	U1440	A1326	G	U	C1099	G	G	G959
G2085	G2086	C1994	C1995	U1918	C1772	G1697	U1588	C1441	A1326	G	C	U1100	G	G	A960
G2087	G2088	C1995	G1919	C1698	A1775	C1698	U1588	C1442	A1333	G1234	G	C	G	G	G961
G2089	G2090	C1996	G1920	A1776	A1776	A1699	U1591	G1444	A1333	G1235	G	U	G	G	G962
G2091	G2092	A1998	C1921	G1700	A1776	G1700	G1592	U1445	G1338	C1239	G	C	U	U	G963
G2092	G2093	A1999	G1922	A1701	A1701	A1701	U1596	C1446	C1344	G1240	G	C	U	U	A964
A2093	A2094	C2002	G1929	C1702	C1702	C1702	U1597	C1447	C1344	G1241	G	C	U	U	G965
A2095	A2096	G2003	A1930	C1704	C1704	C1704	G1597	G1457	A1354	G1242	C1167	A	C	C	A966
G2096	G2097	C2003	C1931	G1705	A1787	G1705	A1501	G1458	A1354	C1243	G1168	C	C	C	G967
G2098	G2099	A1932	A1932	A1706	U1792	C1707	C1607	C1468	G1358	C1244	G1171	C	C	C	G968
G2100	G2101	G2005	C1933	G1708	U1792	G1708	G1603	C1468	G1359	C1245	G1172	U	C	C	G969
G2102	G2103	C2006	C1934	A	C	A	G1609	C1472	G1360	C1252	G1173	C	C	C	G970
G2104	G2105	C2007	C1935	C	C	C	C1610	C1472	C1365	G1253	G1173	C	C	C	U971
A2106	A2107	U2008	C1936	C	C	C	C1611	G1482	C1366	A1254	G1178	U	G	G	C977
G2108	G2109	C2009	C1937	C	C	C	C1612	C1483	C1367	A1255	U1179	C	G	G	C981
G2110	G2111	A2010	A1938	C	C	C	C1614	U1494	G1370	G1261	U1180	C	G	G	U982
G2112	G2113	C2012	G1940	C1714	C1714	C1714	A1621	A1497	A1372	A1263	C1181	C	C	C	C983
G2114	G2115	G1945	G1945	A1719	A1719	A1719	G1624	A1498	A1372	G1264	C1182	C	C	C	C984
G2116	G2117	C2016	G1948	C1720	C1720	C1720	G1625	C1501	G1377	G1265	C1183	G	C	C	C985
G2118	G2119	U1949	G1949	G1724	G1724	G1724	A1631	C1505	C1378	G1266	C1184	C	C	C	C988
G2120	G2121	C2017	C1953	U1726	U1726	U1726	A1632	C1505	C1379	G1267	C1187	C	C	C	C989
G2122	G2123	U1953	U1953	C1731	C1731	C1731	A1634	U1513	C1380	G1268	C1188	C	C	C	C991
G2124	G2125	C2018	C2018	C1734	C1734	C1734	G1641	C1517	U1381	G1269	C1189	C	C	C	C992
G2126	G2127	U1959	U1959	U1735	U1735	U1735	U1649	A1518	A1387	G1271	C1190	C	C	C	C993
G2128	G2129	A2025	A2025	G1836	G1836	G1836	A1650	C1519	G1394	C1272	C1191	C	C	C	C994
G2130	G2131	C2026	C2026	A1837	A1837	A1837	A1655	C1520	A1397	G1273	C1192	C	C	C	C995
G2132	G2133	U1960	U1960	G1842	G1842	G1842	G1656	A1523	A1398	G1274	C1193	C	C	C	C996
G2134	G2135	C2027	C2027	A1843	A1843	A1843	U1657	A1524	G1399	C1275	C1196	C	C	C	C
G2136	G2137	U1970	U1970	G1851	G1851	G1851	G1658	A1525	C1402	C1276	C1197	C	C	C	C
G2138	G2139	C2031	C2031	U1852	U1852	U1852	U1659	A1534	G1403	C1277	C1198	C	C	C	C
G2140	G2141	U1965	U1965	G1853	G1853	G1853	U1660	C1546	G1404	C1278	C1199	C	C	C	C
G2142	G2143	C2033	C2033	G1854	G1854	G1854	U1661	A1547	U1279	C1279	C1201	C	C	C	C
G2144	G2145	G2034	G2034	G1855	G1855	G1855	C1662	G1548	G1405	C1280	C1202	C	C	C	C
G2146	G2147	U1970	U1970	G1869	G1869	G1869	C1663	G1549	U1410	G1281	C1203	C	C	C	C
G2148	G2149	C2038	C2038	C1881	C1881	C1881	U1671	A1564	C1411	G1282	C1204	C	C	C	C
G2150	G2151	A2040	A2040	U1756	U1756	U1756	C1676	C1566	C1412	U1283	C1205	C	C	C	C
G2152	G2153	C2039	C2039	G1758	G1758	G1758	U1677	A1565	C1413	U1284	C1206	C	C	C	C
G2154	G2155	U1973	U1973	G1759	G1759	G1759	C1678	C1566	C1414	U1285	C1207	C	C	C	C
G2156	G2157	C2044	C2044	C1761	C1761	C1761	U1678	G1567	C1415	C1286	C1208	C	C	C	C
G2158	G2159	G2046	G2046	C1762	C1762	C1762	G1681	A1574	C1416	G1287	C1209	C	C	C	C
G2160	G2161	C2047	C2047	C1763	C1763	C1763	U1682	A1575	C1417	C1288	C1210	C	C	C	C
G2162	G2163	U1980	U1980	A1765	A1765	A1765	U1683	G1576	A1420	G1289	C1211	C	C	C	C
G2164	G2165	C1985	C1985	A1766	A1766	A1766	G1688	G1577	C1301	U1290	C1212	C	C	C	C
G2166	G2167	U1986	U1986	A1767	A1767	A1767	U1689	G1578	U1302	U1291	C1213	C	C	C	C
G2168	G2169	C2062	C2062	U1906	U1906	U1906	G1691	C1579	U1303	G1292	C1214	C	C	C	C
A2069	A2070	G1988	G1988	G1912	G1912	G1912	C1691	C1580	C1304	U1293	C1215	C	C	C	C
A2071	A2072	C2066	C2066	C1912	C1912	C1912	C1691	C1580	C1304	U1294	C1216	C	C	C	C
A2073	A2074	G1989	G1989	C1912	C1912	C1912	C1691	C1580	C1304	U1295	C1217	C	C	C	C
A2075	A2076	C2067	C2067	C1912	C1912	C1912	C1691	C1580	C1304	U1296	C1218	C	C	C	C
A2077	A2078	G1990	G1990	C1912	C1912	C1912	C1691	C1580	C1304	U1297	C1219	C	C	C	C
A2079	A2080	C2068	C2068	C1912	C1912	C1912	C1691	C1580	C1304	U1298	C1220	C	C	C	C
A2081	A2082	G1991	G1991	C1912	C1912	C1912	C1691	C1580	C1304	U1299	C1221	C	C	C	C
A2083	A2084	C2069	C2069	C1912	C1912	C1912	C1691	C1580	C1304	U1300	C1222	C	C	C	C
A2085	A2086	G1992	G1992	C1912	C1912	C1912	C1691	C1580	C1304	U1301	C1223	C	C	C	C
A2087	A2088	C2070	C2070	C1912	C1912	C1912	C1691	C1580	C1304	U1302	C1224	C	C	C	C
A2089	A2090	G1993	G1993	C1912	C1912	C1912	C1691	C1580	C1304	U1303	C1225	C	C	C	C
A2091	A2092	C2071	C2071	C1912	C1912	C1912	C1691	C1580	C1304	U1304	C1226	C	C	C	C
A2093	A2094	G1994	G1994	C1912	C1912	C1912	C1691	C1580	C1304	U1305	C1227	C	C	C	C
A2095	A2096	C2072	C2072	C1912	C1912	C1912	C1691	C1580	C1304	U1306	C1228	C	C	C	C
A2097	A2098	G1995	G1995	C1912	C1912	C1912	C1691	C1580	C1304	U1307	C1229	C	C	C	C
A2099	A2100	C2073	C2073	C1912	C1912	C1912	C1691	C1580	C1304	U1308	C1230	C	C	C	C
A2101	A2102	G1996	G1996	C1912	C1912	C1912	C1691	C1580	C1304	U1309	C1231	C	C	C	C
A2103	A2104	C2074	C2074	C1912	C1912	C1912	C1691	C1580	C1304	U1310	C1232	C	C	C	C
A2105	A2106	G1997	G1997	C1912	C1912	C1912	C1691	C1580	C1304	U1311	C1233	C	C	C	C
A2107	A2108	C2075	C2075	C1912	C1912	C1912	C1691	C1580	C1304	U1312	C1234	C	C	C	C
A2109	A2110	G1998	G1998	C1912	C1912	C1912	C1691	C1580	C1304	U1313	C1235	C	C	C	C
A2111	A2112	C2076	C2076	C1912	C1912	C1912	C1691	C1580	C1304	U1314	C1236	C	C	C	C
A2113	A2114	G1999	G1999	C1912	C1912	C1912	C1691	C1580	C1304	U1315	C1237	C	C	C	C
A2115	A2116	C2077	C2077	C1912	C1912	C1912	C1691	C1580	C1304	U1316	C1238	C	C	C	C
A2117	A2118	G2000	G2000	C1912	C1912	C1912	C1691	C1580	C1304	U1317	C1239	C	C	C	C
A2119	A2120	C2078	C2078	C1912	C1912	C1912	C1691	C1580	C1304	U1318	C1240	C	C	C	C
A2121	A2122	G2001	G2001	C1912	C1912	C1912	C1691	C1580	C1304	U1319	C1241	C	C	C	C
A2123	A2124	C2079	C2079	C1912	C1912	C1912	C1691	C1580	C1304	U1320	C1242	C	C	C	C
A2125	A2126	G2002	G2002	C1912	C1912	C1912	C1691	C1580	C1304	U1321	C1243	C	C	C	C
A2127	A2128	C2080	C2080	C1912	C1912	C1912	C1691	C1580	C1304	U1322	C1244	C	C	C	C
A2129	A2130	G2003	G2003	C1912	C1912	C1912	C1691	C1580	C1304	U1323	C1245	C	C	C	C
A2131	A2132	C2081	C2081	C1912	C1912	C1912	C1691	C1580	C1304	U1324	C1246	C	C	C	C
A2133	A2134	G2004	G2004	C1912	C1912	C1912	C1691	C1580	C1304	U1325	C1247	C	C	C	C
A2135	A2136	C2082	C2082	C1912	C1912	C1912	C1691	C1580	C1304	U1326	C1248	C	C	C	C
A2137	A2138	G2005	G2005	C1912	C1912	C1912	C1691	C1580	C1304	U1327	C1249	C	C	C	C
A2139	A2140	C2083	C2083	C1912	C1912	C1912	C1691	C1580	C1304	U1328	C1250	C	C	C	C
A2141	A2142	G2006	G2006	C1912	C1912	C1912	C1691	C1580	C1304	U1329	C1251	C	C	C	C
A2143	A2144	C2084	C2084	C1912	C1912	C1912	C1691	C1580	C1304	U1330	C1252	C	C	C	C
A2145	A2146	G2007	G2007	C1912	C1912	C1912	C1691	C1580	C1304	U1331	C1253	C	C	C	C
A2147	A2148	C2085	C2085	C1912	C1912	C1912	C1691	C1580	C1304	U1332	C1254	C	C	C	C
A2149	A2150	G2008	G2008	C1912	C1912	C1912	C1691	C1580	C1304	U1333	C1255	C	C	C	C
A2151	A2152	C2086	C2086	C1912	C1912	C1912	C1691	C1580	C1304	U1334	C1256	C	C	C	C
A2153	A2154	G2009	G2009	C1912	C1912	C1912	C1691	C1580	C1304	U1335	C1257	C	C	C	C
A2155	A2156	C2087	C2087	C1912	C1912	C1912	C1691	C1580	C1304	U1336	C1258	C	C	C	C
A2157	A2158	G2010	G2010	C1912	C1912	C1912	C1691	C1580	C1304	U1337	C1259	C	C	C	C
A2159	A2160	C2088	C2088	C1912	C1912	C1912	C1691	C1580	C1304	U1338	C1260	C	C	C	C
A2161	A2162	G2011	G2011	C1912	C1912	C1912	C1691	C1580	C1304	U1339	C1261	C			

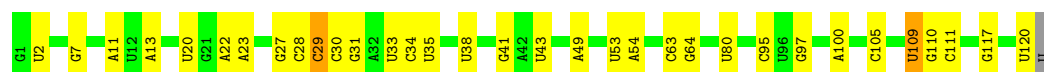






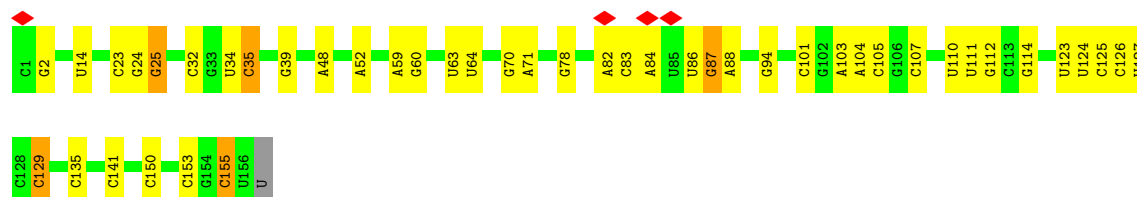
• Molecule 2: 5S ribosomal RNA

Chain 1B: 72% 26% ..



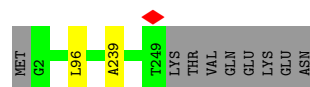
• Molecule 3: 5.8S ribosomal RNA

Chain 1C: 71% 25% ..



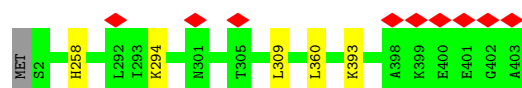
• Molecule 4: 60S ribosomal protein L8

Chain 1D: 96% ..



• Molecule 5: 60S ribosomal protein L3

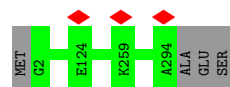
Chain 1E: 99% .



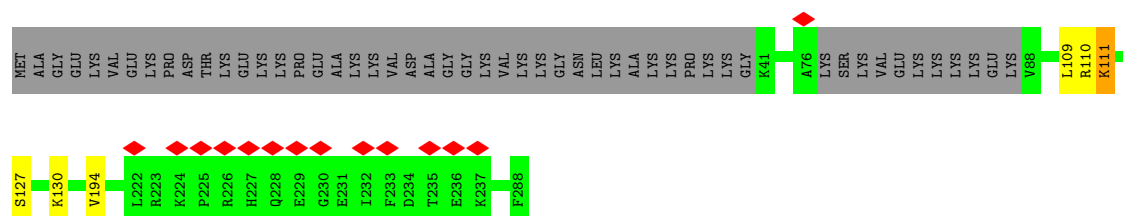
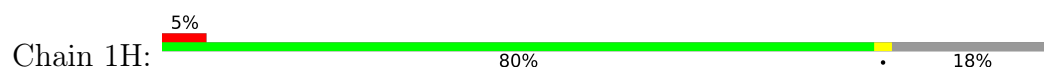
• Molecule 6: 60S ribosomal protein L4

Chain 1F: 86% 14%

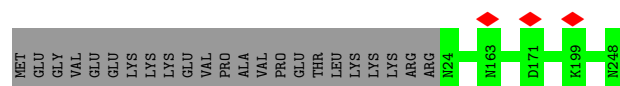
- Molecule 7: 60S ribosomal protein L5



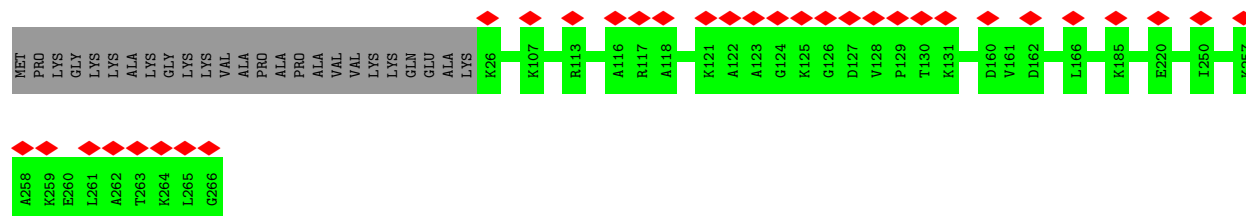
- Molecule 8: 60S ribosomal protein L6



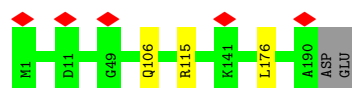
- Molecule 9: 60S ribosomal protein L7



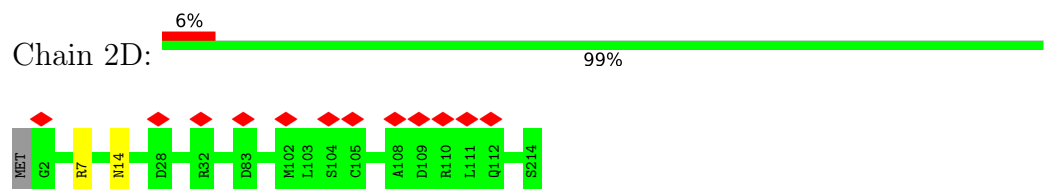
- Molecule 10: 60S ribosomal protein L7a



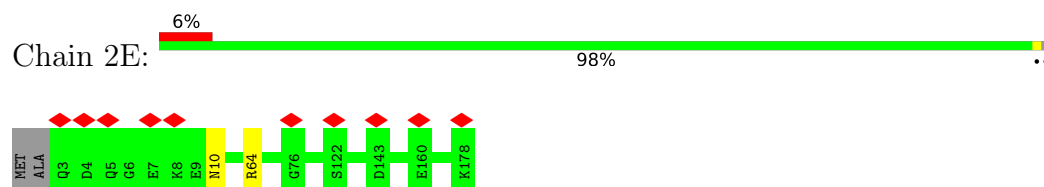
- Molecule 11: 60S ribosomal protein L9



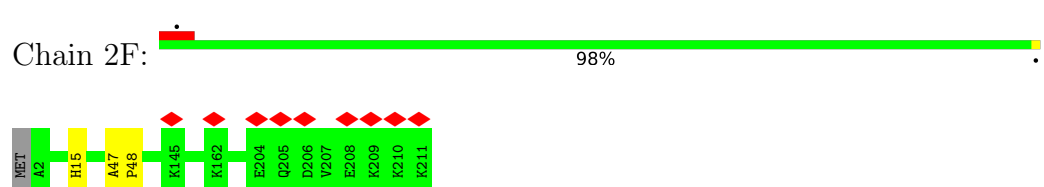
- Molecule 12: 60S ribosomal protein L10-like



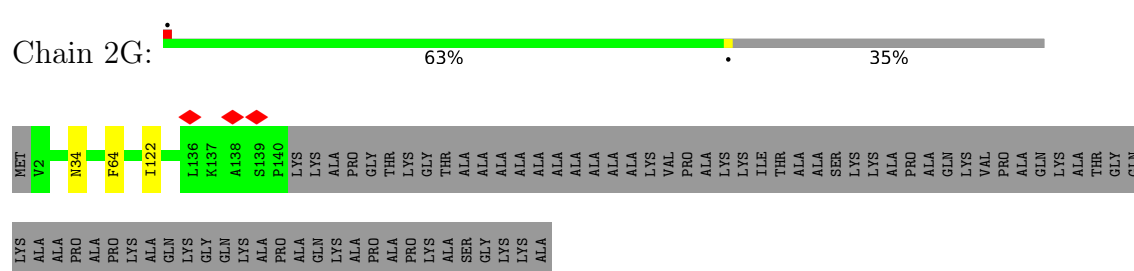
- Molecule 13: 60S ribosomal protein L11



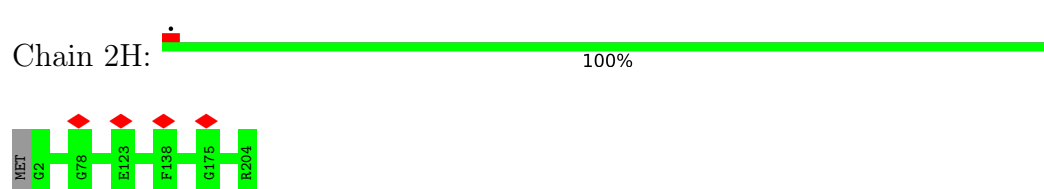
- Molecule 14: 60S ribosomal protein L13



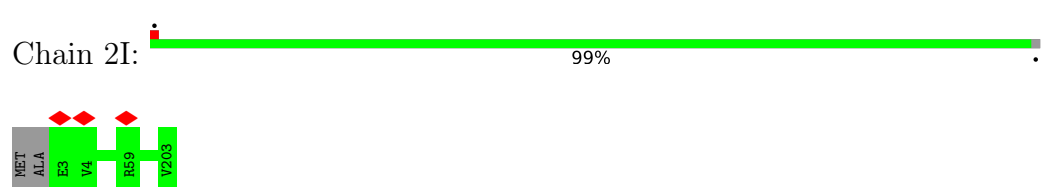
- Molecule 15: 60S ribosomal protein L14




- Molecule 16: 60S ribosomal protein L15

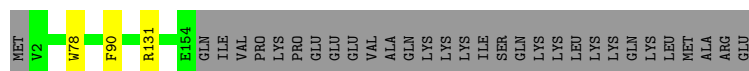


- Molecule 17: 60S ribosomal protein L13a



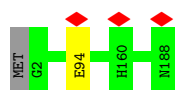
- Molecule 18: 60S ribosomal protein L17

Chain 2J:  82% 17%



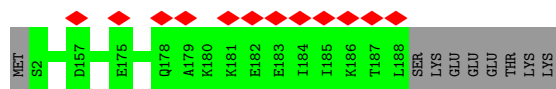
- Molecule 19: 60S ribosomal protein L18

Chain 2K:  99%



- Molecule 20: 60S ribosomal protein L19

Chain 2L:  95% 5% 6%



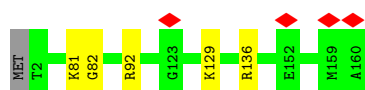
- Molecule 21: 60S ribosomal protein L18a

Chain 2M:  98%




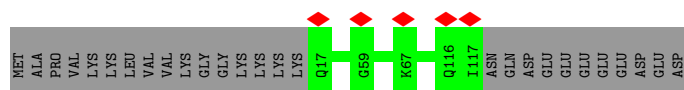
- Molecule 22: 60S ribosomal protein L21

Chain 2N:  96%



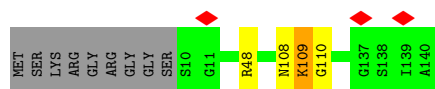
- Molecule 23: 60S ribosomal protein L22

Chain 2O:  79% 21%

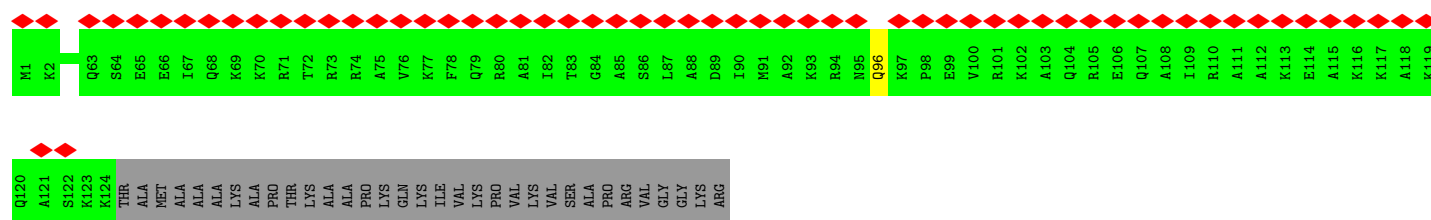
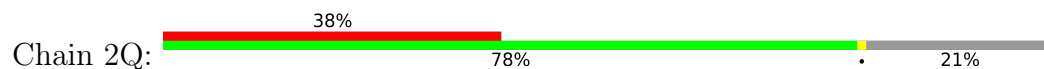


- Molecule 24: 60S ribosomal protein L23

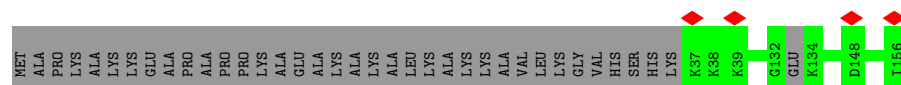
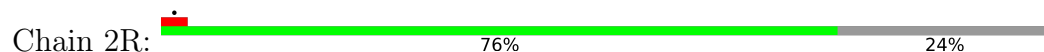
Chain 2P:  91% 6%



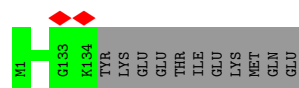
- Chain 2Q:



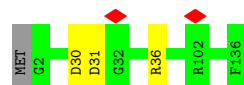
- Chain 2R:



- Chain 2S:



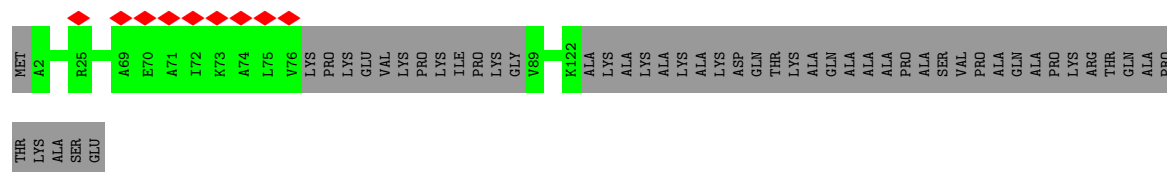
- Chain 2T:




- Chain 2U:

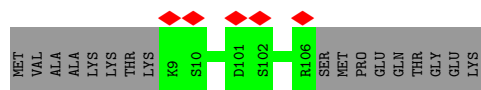


- Chain 2V:




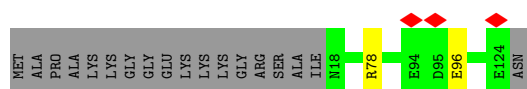
- Molecule 31: 60S ribosomal protein L30

Chain 2W:  85% 15%



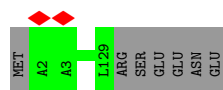
- Molecule 32: 60S ribosomal protein L31

Chain 2X:  84% 14%



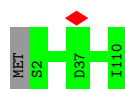
- Molecule 33: 60S ribosomal protein L32

Chain 2Y:  95% 5%



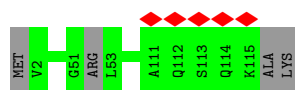
- Molecule 34: 60S ribosomal protein L35a

Chain 2Z:  99%



- Molecule 35: 60S ribosomal protein L34

Chain 2a:  97%



- Molecule 36: 60S ribosomal protein L35

Chain 2b:  99%

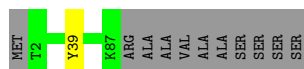
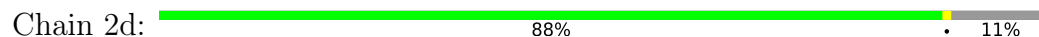


- Molecule 37: 60S ribosomal protein L36

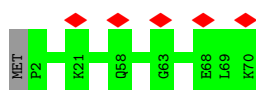
Chain 2c:  97%



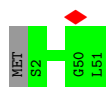
- Molecule 38: 60S ribosomal protein L37



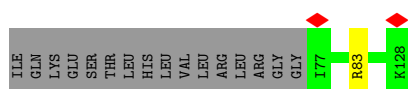
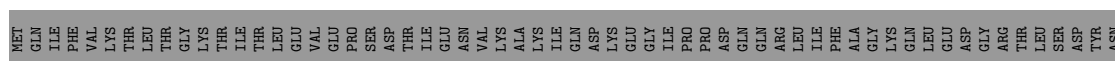
- Molecule 39: 60S ribosomal protein L38



- Molecule 40: 60S ribosomal protein L39



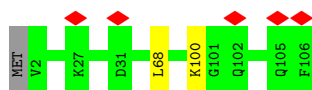
- Molecule 41: Ubiquitin-60S ribosomal protein L40



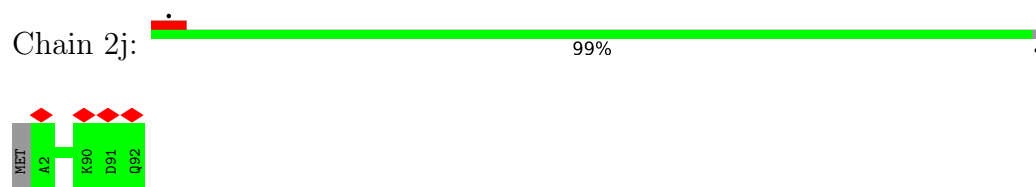
- Molecule 42: 60S ribosomal protein L41



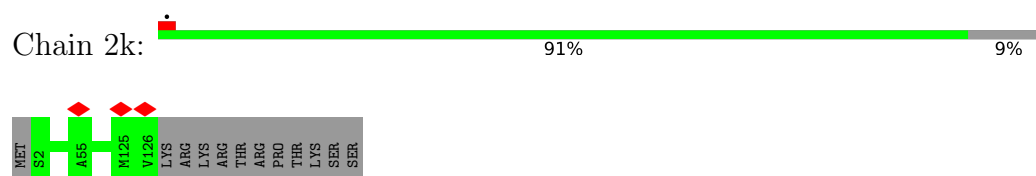
- Molecule 43: 60S ribosomal protein L36a



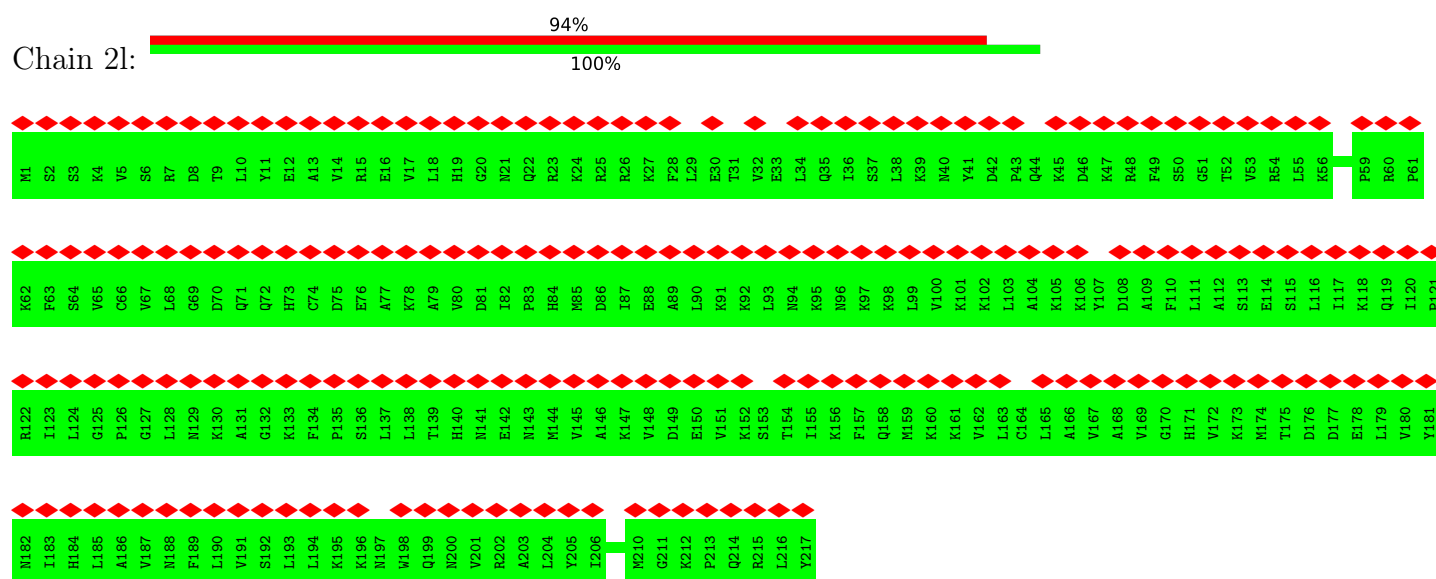
- Molecule 44: 60S ribosomal protein L37a



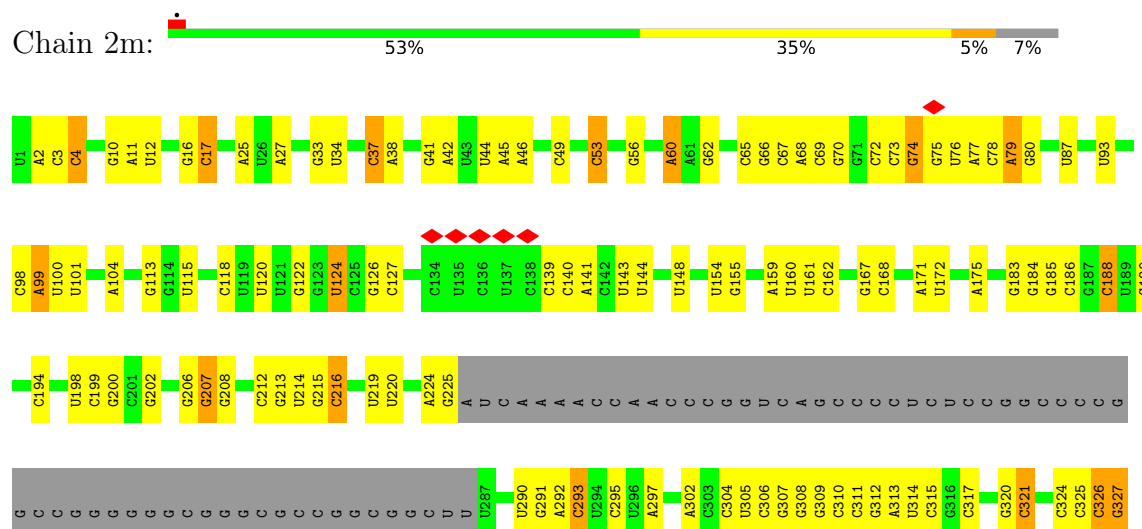
- Molecule 45: 60S ribosomal protein L28



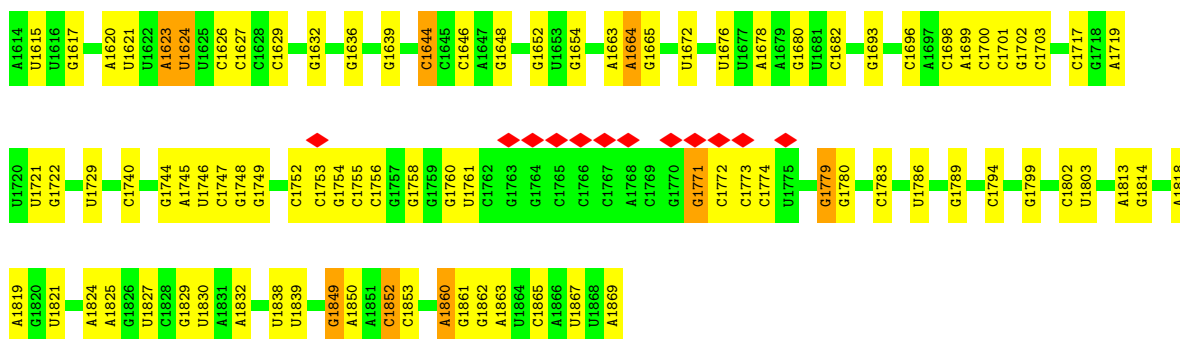
- Molecule 46: 60S ribosomal protein L10a



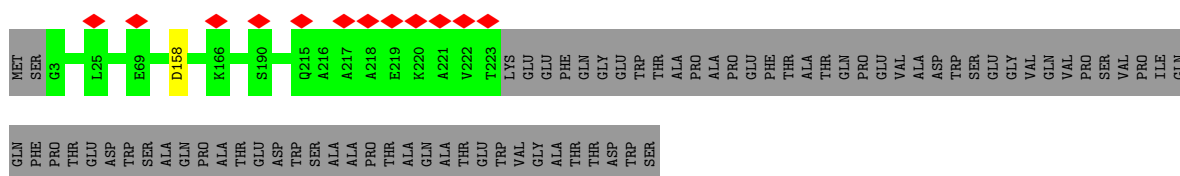
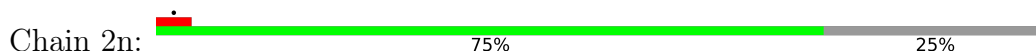
- Molecule 47: 18S ribosomal RNA



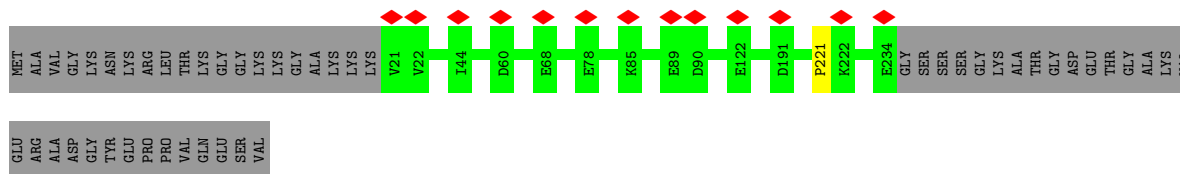
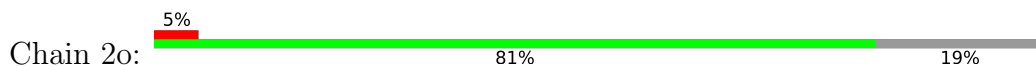




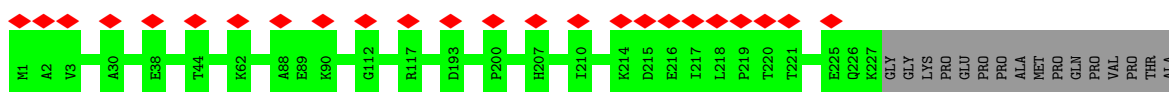
• Molecule 48: 40S ribosomal protein SA



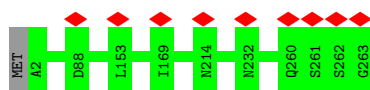
• Molecule 49: 40S ribosomal protein S3a



• Molecule 50: 40S ribosomal protein S3

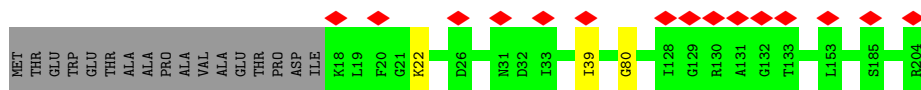


• Molecule 51: 40S ribosomal protein S4, X isoform

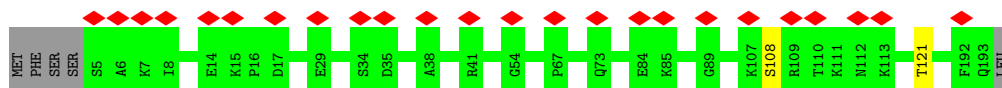


• Molecule 52: 40S ribosomal protein S5

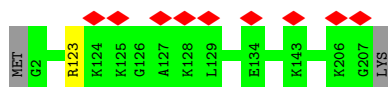




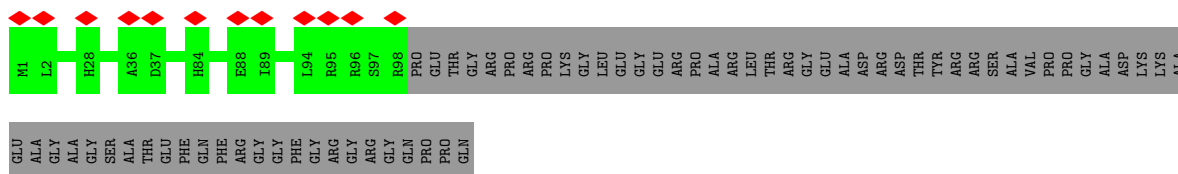
- Molecule 53: 40S ribosomal protein S7



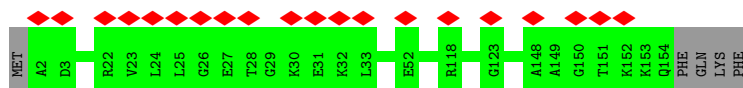
- Molecule 54: 40S ribosomal protein S8



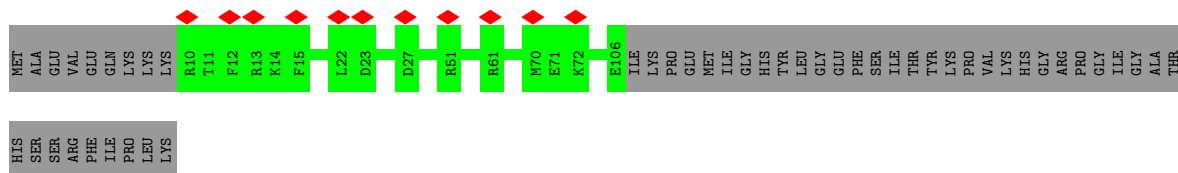
- Molecule 55: 40S ribosomal protein S10



- Molecule 56: 40S ribosomal protein S11



- Molecule 57: 40S ribosomal protein S15

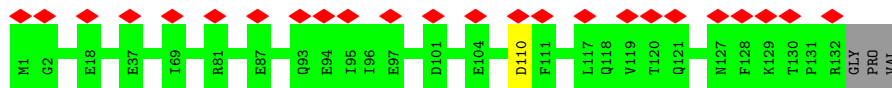


- Molecule 58: 40S ribosomal protein S16

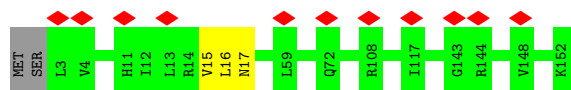




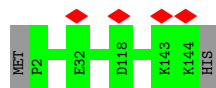
- Molecule 59: 40S ribosomal protein S17



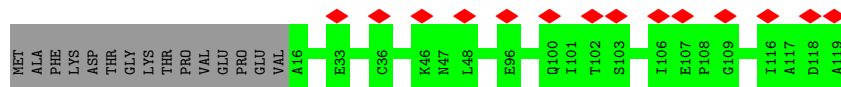
- Molecule 60: 40S ribosomal protein S18



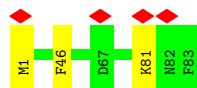
- Molecule 61: 40S ribosomal protein S19



- Molecule 62: 40S ribosomal protein S20



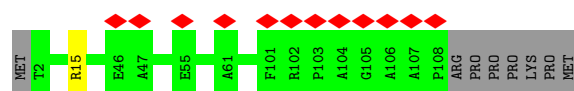
- Molecule 63: 40S ribosomal protein S21



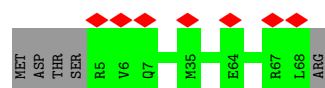
- Molecule 64: 40S ribosomal protein S23



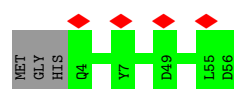
- Molecule 65: 40S ribosomal protein S26



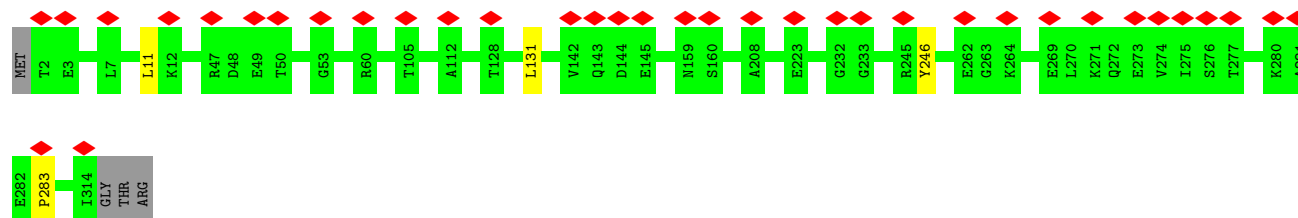
- Chain 3D:  10% 93% 7%

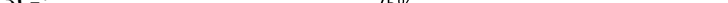


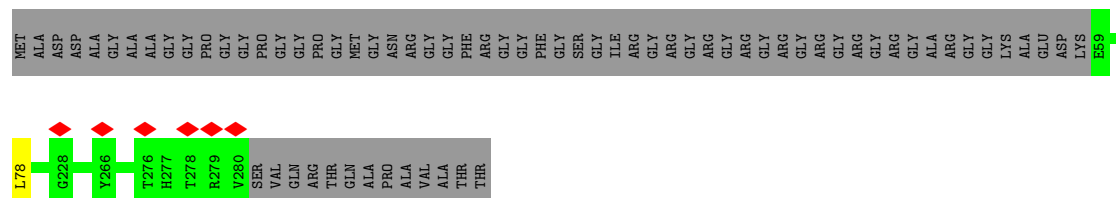
- Chain 3E: 



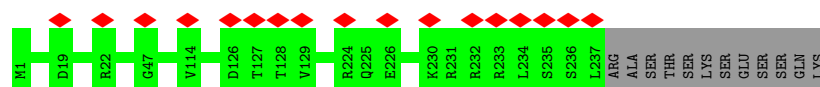
- Chain 3F:  11% 97% ..



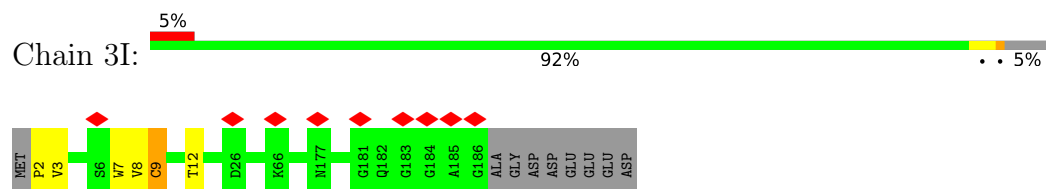
- Chain 3G:  75% 24%



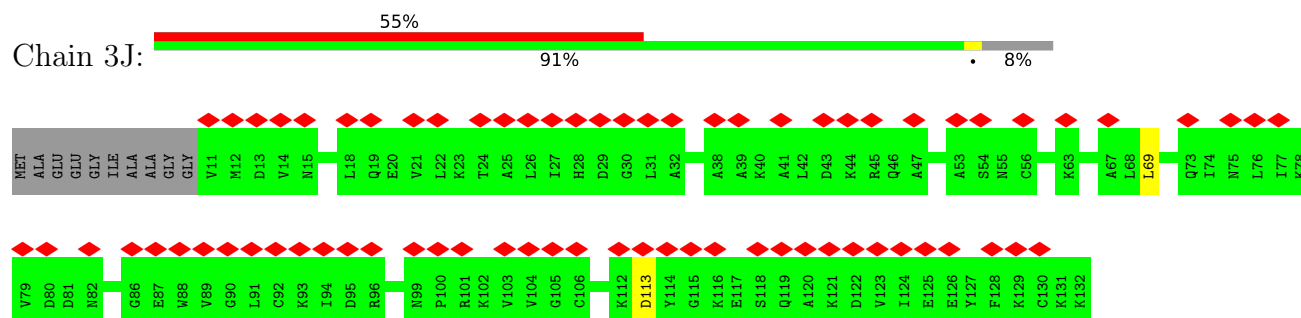
- Chain 3H: 



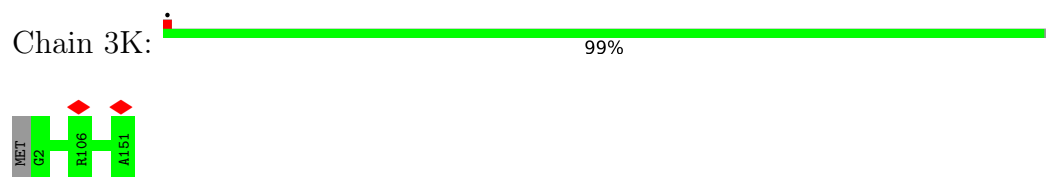
- Molecule 71: 40S ribosomal protein S9



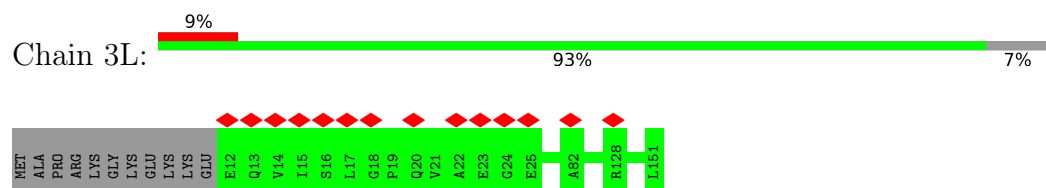
- Molecule 72: 40S ribosomal protein S12



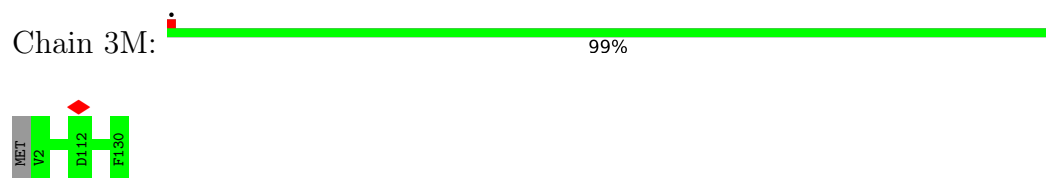
- Molecule 73: 40S ribosomal protein S13



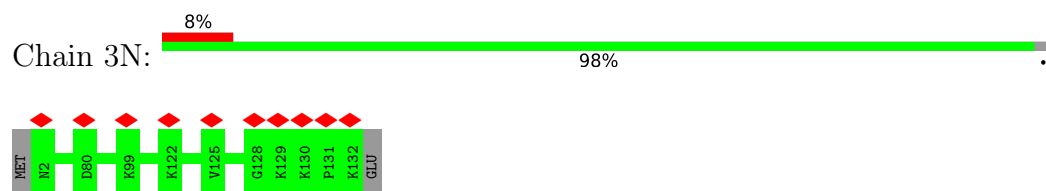
- Molecule 74: 40S ribosomal protein S14



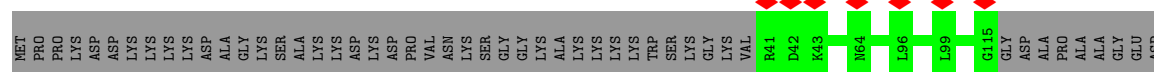
- Molecule 75: 40S ribosomal protein S15a



- Molecule 76: 40S ribosomal protein S24

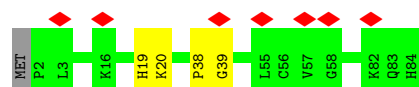


- Molecule 77: 40S ribosomal protein S25

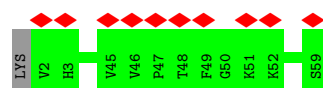


ALA

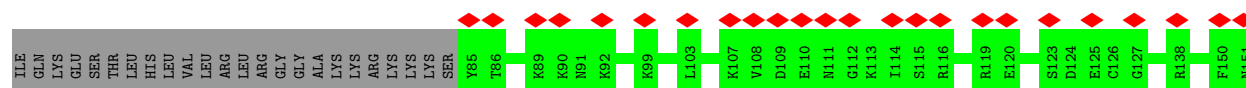
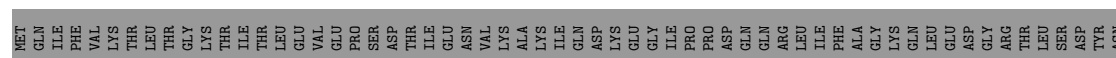
- Molecule 78: 40S ribosomal protein S27



- Molecule 79: 40S ribosomal protein S30



- Molecule 80: Ubiquitin-40S ribosomal protein S27a

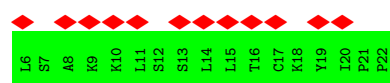


LYS
PRO
GLU
ASP
LYS

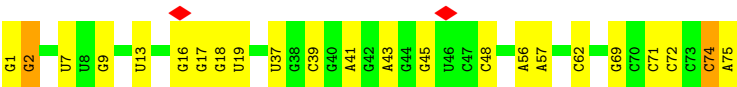
- Molecule 81: mRNA



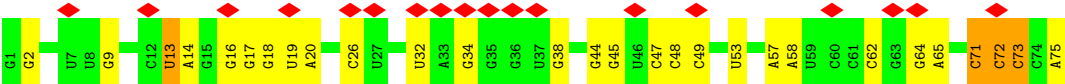
- Molecule 82: nascent peptide



- Molecule 83: P-site tRNA



• Molecule 83: P-site tRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	40295	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	33557	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.241	Depositor
Minimum map value	-0.107	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	625.8, 625.8, 625.8	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.49, 1.49, 1.49	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	1A	0.79	3/89129 (0.0%)	1.27	864/139038 (0.6%)
2	1B	0.79	0/2858	1.21	12/4455 (0.3%)
3	1C	0.76	0/3701	1.17	13/5766 (0.2%)
4	1D	0.42	0/1936	0.64	1/2596 (0.0%)
5	1E	0.41	0/3306	0.62	2/4424 (0.0%)
6	1F	0.40	0/2981	0.62	0/4002
7	1G	0.38	0/2428	0.59	0/3252
8	1H	0.38	0/1951	0.73	0/2618
9	2A	0.44	0/1905	0.61	0/2539
10	2B	0.37	0/1960	0.60	0/2637
11	2C	0.37	0/1537	0.65	0/2066
12	2D	0.40	0/1751	0.61	0/2340
13	2E	0.36	0/1433	0.63	0/1915
14	2F	0.37	0/1732	0.62	0/2315
15	2G	0.43	0/1161	0.59	0/1554
16	2H	0.47	0/1746	0.64	0/2338
17	2I	0.42	0/1682	0.58	0/2250
18	2J	0.41	0/1268	0.59	0/1701
19	2K	0.39	0/1537	0.58	0/2052
20	2L	0.37	0/1582	0.58	0/2091
21	2M	0.43	0/1493	0.60	1/2003 (0.0%)
22	2N	0.39	0/1326	0.61	1/1770 (0.1%)
23	2O	0.37	0/839	0.57	0/1126
24	2P	0.41	0/993	0.63	0/1332
25	2Q	0.38	0/1030	0.62	0/1364
26	2R	0.34	0/992	0.55	0/1330
27	2S	0.39	0/1132	0.59	0/1504
28	2T	0.39	0/1130	0.59	0/1507
29	2U	0.41	0/1191	0.60	0/1591
30	2V	0.33	0/889	0.59	0/1175
31	2W	0.38	0/774	0.55	0/1038
32	2X	0.43	0/903	0.60	0/1216
33	2Y	0.43	0/1071	0.57	0/1429
34	2Z	0.45	0/895	0.65	0/1198

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	2a	0.40	0/904	0.61	0/1203
36	2b	0.33	0/1023	0.54	0/1351
37	2c	0.33	0/843	0.57	0/1115
38	2d	0.40	0/720	0.61	0/952
39	2e	0.35	0/575	0.68	0/761
40	2f	0.39	0/454	0.59	0/599
41	2g	0.35	0/435	0.58	0/575
42	2h	0.35	0/231	0.50	0/294
43	2i	0.43	0/876	0.65	0/1156
44	2j	0.41	0/718	0.59	0/953
45	2k	0.38	0/1017	0.58	0/1364
46	2l	0.28	0/1769	0.62	0/2371
47	2m	0.73	1/41243 (0.0%)	1.29	424/64257 (0.7%)
48	2n	0.37	0/1778	0.60	0/2416
49	2o	0.35	0/1765	0.60	0/2362
50	2p	0.36	0/1793	0.61	0/2414
51	2q	0.36	0/2118	0.61	0/2849
52	2r	0.33	0/1500	0.61	0/2015
53	2s	0.34	0/1544	0.63	0/2068
54	2t	0.36	0/1715	0.60	0/2287
55	2u	0.35	0/851	0.66	0/1147
56	2v	0.40	0/1268	0.61	0/1696
57	2w	0.34	0/815	0.73	0/1087
58	2x	0.36	0/1177	0.64	0/1575
59	2y	0.33	0/1086	0.63	1/1457 (0.1%)
60	2z	0.35	0/1253	0.71	0/1676
61	20	0.33	0/1131	0.55	0/1515
62	21	0.37	0/831	0.66	0/1115
63	3A	0.35	0/643	0.59	0/860
64	3B	0.37	0/1116	0.63	0/1490
65	3C	0.36	0/863	0.59	0/1159
66	3D	0.32	0/508	0.71	0/680
67	3E	0.37	0/455	0.57	0/603
68	3F	0.34	0/2493	0.68	2/3394 (0.1%)
69	3G	0.39	0/1762	0.60	0/2381
70	3H	0.32	0/1946	0.64	0/2590
71	3I	0.37	0/1550	0.66	0/2069
72	3J	0.31	0/962	0.66	1/1290 (0.1%)
73	3K	0.39	0/1232	0.62	0/1656
74	3L	0.34	0/1062	0.64	0/1425
75	3M	0.41	0/1051	0.64	0/1406
76	3N	0.36	0/1083	0.55	0/1438
77	3O	0.33	0/604	0.69	0/810

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	3P	0.35	0/665	0.64	0/891
79	3Q	0.32	0/465	0.53	0/612
80	3R	0.32	0/560	0.62	0/745
81	zv	0.54	0/135	1.53	2/207 (1.0%)
82	zx	0.38	0/131	0.55	0/176
83	zu	0.47	0/1786	1.20	14/2784 (0.5%)
83	zy	0.56	0/1786	1.21	17/2784 (0.6%)
All	All	0.64	4/236533 (0.0%)	1.07	1355/347612 (0.4%)

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	1D	0	1
5	1E	0	1
8	1H	0	4
11	2C	0	2
12	2D	0	1
14	2F	0	2
15	2G	0	2
18	2J	0	1
19	2K	0	1
22	2N	0	2
24	2P	0	2
25	2Q	0	1
28	2T	0	2
32	2X	0	1
38	2d	0	1
43	2i	0	1
49	2o	0	1
53	2s	0	1
58	2x	0	3
60	2z	0	2
63	3A	0	2
64	3B	0	4
68	3F	0	1
71	3I	0	5
72	3J	0	1
78	3P	0	1
All	All	0	46

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	2m	99	A	N7-C5	-5.88	1.35	1.39
1	1A	3903	A	N9-C4	-5.37	1.34	1.37
1	1A	3824	A	N9-C4	-5.27	1.34	1.37
1	1A	3617	G	C8-N7	-5.08	1.27	1.30

The worst 5 of 1355 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1A	184	U	N1-C2-O2	14.54	132.98	122.80
1	1A	485	C	C2-N1-C1'	14.13	134.35	118.80
1	1A	4303	C	N1-C2-O2	13.73	127.14	118.90
1	1A	969	C	N1-C2-O2	13.62	127.07	118.90
47	2m	1553	C	N1-C2-O2	13.59	127.05	118.90

There are no chirality outliers.

5 of 46 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	1D	239	ALA	Peptide
5	1E	258	HIS	Peptide
8	1H	109	LEU	Peptide
8	1H	110	ARG	Peptide
8	1H	111	LYS	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	1D	246/257 (96%)	221 (90%)	25 (10%)	0	100	100
5	1E	400/403 (99%)	353 (88%)	45 (11%)	2 (0%)	25	60
6	1F	366/427 (86%)	328 (90%)	37 (10%)	1 (0%)	37	70
7	1G	291/297 (98%)	260 (89%)	31 (11%)	0	100	100
8	1H	233/288 (81%)	196 (84%)	35 (15%)	2 (1%)	14	48
9	2A	223/248 (90%)	199 (89%)	24 (11%)	0	100	100
10	2B	239/266 (90%)	205 (86%)	34 (14%)	0	100	100
11	2C	188/192 (98%)	163 (87%)	25 (13%)	0	100	100
12	2D	211/214 (99%)	181 (86%)	30 (14%)	0	100	100
13	2E	174/178 (98%)	155 (89%)	19 (11%)	0	100	100
14	2F	208/211 (99%)	181 (87%)	26 (12%)	1 (0%)	25	60
15	2G	137/215 (64%)	125 (91%)	12 (9%)	0	100	100
16	2H	201/204 (98%)	187 (93%)	14 (7%)	0	100	100
17	2I	199/203 (98%)	188 (94%)	11 (6%)	0	100	100
18	2J	151/184 (82%)	135 (89%)	16 (11%)	0	100	100
19	2K	185/188 (98%)	174 (94%)	11 (6%)	0	100	100
20	2L	185/196 (94%)	176 (95%)	9 (5%)	0	100	100
21	2M	173/176 (98%)	147 (85%)	26 (15%)	0	100	100
22	2N	157/160 (98%)	134 (85%)	21 (13%)	2 (1%)	10	41
23	2O	99/128 (77%)	89 (90%)	10 (10%)	0	100	100
24	2P	129/140 (92%)	112 (87%)	15 (12%)	2 (2%)	8	37
25	2Q	122/157 (78%)	108 (88%)	14 (12%)	0	100	100
26	2R	115/156 (74%)	107 (93%)	8 (7%)	0	100	100
27	2S	132/145 (91%)	121 (92%)	11 (8%)	0	100	100
28	2T	133/136 (98%)	121 (91%)	11 (8%)	1 (1%)	16	51
29	2U	145/148 (98%)	133 (92%)	12 (8%)	0	100	100
30	2V	105/159 (66%)	94 (90%)	11 (10%)	0	100	100
31	2W	96/115 (84%)	89 (93%)	7 (7%)	0	100	100
32	2X	105/125 (84%)	92 (88%)	13 (12%)	0	100	100
33	2Y	126/135 (93%)	117 (93%)	9 (7%)	0	100	100
34	2Z	107/110 (97%)	98 (92%)	9 (8%)	0	100	100
35	2a	109/117 (93%)	103 (94%)	6 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	2b	120/123 (98%)	116 (97%)	4 (3%)	0	100	100
37	2c	100/105 (95%)	95 (95%)	5 (5%)	0	100	100
38	2d	84/97 (87%)	70 (83%)	14 (17%)	0	100	100
39	2e	67/70 (96%)	58 (87%)	9 (13%)	0	100	100
40	2f	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
41	2g	50/128 (39%)	44 (88%)	6 (12%)	0	100	100
42	2h	22/25 (88%)	21 (96%)	1 (4%)	0	100	100
43	2i	103/106 (97%)	92 (89%)	11 (11%)	0	100	100
44	2j	89/92 (97%)	79 (89%)	10 (11%)	0	100	100
45	2k	123/137 (90%)	116 (94%)	7 (6%)	0	100	100
46	2l	215/217 (99%)	176 (82%)	39 (18%)	0	100	100
48	2n	219/295 (74%)	196 (90%)	22 (10%)	1 (0%)	25	60
49	2o	212/264 (80%)	192 (91%)	20 (9%)	0	100	100
50	2p	225/243 (93%)	193 (86%)	32 (14%)	0	100	100
51	2q	260/263 (99%)	230 (88%)	30 (12%)	0	100	100
52	2r	185/204 (91%)	161 (87%)	22 (12%)	2 (1%)	12	45
53	2s	187/194 (96%)	161 (86%)	26 (14%)	0	100	100
54	2t	204/208 (98%)	185 (91%)	19 (9%)	0	100	100
55	2u	96/165 (58%)	85 (88%)	11 (12%)	0	100	100
56	2v	151/158 (96%)	135 (89%)	16 (11%)	0	100	100
57	2w	95/145 (66%)	76 (80%)	19 (20%)	0	100	100
58	2x	144/146 (99%)	120 (83%)	24 (17%)	0	100	100
59	2y	130/135 (96%)	113 (87%)	17 (13%)	0	100	100
60	2z	148/152 (97%)	124 (84%)	23 (16%)	1 (1%)	19	54
61	20	141/145 (97%)	127 (90%)	14 (10%)	0	100	100
62	21	102/119 (86%)	86 (84%)	16 (16%)	0	100	100
63	3A	81/83 (98%)	70 (86%)	10 (12%)	1 (1%)	11	43
64	3B	139/143 (97%)	120 (86%)	16 (12%)	3 (2%)	5	32
65	3C	105/115 (91%)	95 (90%)	10 (10%)	0	100	100
66	3D	62/69 (90%)	49 (79%)	13 (21%)	0	100	100
67	3E	51/56 (91%)	47 (92%)	4 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
68	3F	311/317 (98%)	263 (85%)	47 (15%)	1 (0%)	37	70
69	3G	220/293 (75%)	200 (91%)	19 (9%)	1 (0%)	25	60
70	3H	235/249 (94%)	205 (87%)	30 (13%)	0	100	100
71	3I	183/194 (94%)	156 (85%)	25 (14%)	2 (1%)	12	45
72	3J	120/132 (91%)	99 (82%)	21 (18%)	0	100	100
73	3K	148/151 (98%)	133 (90%)	15 (10%)	0	100	100
74	3L	138/151 (91%)	117 (85%)	21 (15%)	0	100	100
75	3M	127/130 (98%)	112 (88%)	15 (12%)	0	100	100
76	3N	129/133 (97%)	119 (92%)	10 (8%)	0	100	100
77	3O	73/125 (58%)	55 (75%)	18 (25%)	0	100	100
78	3P	81/84 (96%)	67 (83%)	11 (14%)	3 (4%)	2	23
79	3Q	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
80	3R	65/156 (42%)	54 (83%)	11 (17%)	0	100	100
82	zx	15/17 (88%)	11 (73%)	4 (27%)	0	100	100
All	All	11549/12922 (89%)	10211 (88%)	1312 (11%)	26 (0%)	45	75

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	1F	111	TRP
8	1H	111	LYS
24	2P	110	GLY
60	2z	17	ASN
64	3B	109	GLY

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	1D	190/199 (96%)	190 (100%)	0	100	100
5	1E	348/349 (100%)	348 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	1F	306/348 (88%)	305 (100%)	1 (0%)	91	92
7	1G	246/250 (98%)	246 (100%)	0	100	100
8	1H	210/252 (83%)	209 (100%)	1 (0%)	86	90
9	2A	194/215 (90%)	194 (100%)	0	100	100
10	2B	203/223 (91%)	203 (100%)	0	100	100
11	2C	169/171 (99%)	168 (99%)	1 (1%)	84	88
12	2D	180/181 (99%)	179 (99%)	1 (1%)	84	88
13	2E	148/149 (99%)	146 (99%)	2 (1%)	62	75
14	2F	176/177 (99%)	176 (100%)	0	100	100
15	2G	118/161 (73%)	117 (99%)	1 (1%)	79	84
16	2H	171/172 (99%)	171 (100%)	0	100	100
17	2I	173/174 (99%)	173 (100%)	0	100	100
18	2J	134/163 (82%)	132 (98%)	2 (2%)	60	74
19	2K	164/165 (99%)	164 (100%)	0	100	100
20	2L	166/175 (95%)	166 (100%)	0	100	100
21	2M	156/157 (99%)	155 (99%)	1 (1%)	84	88
22	2N	139/140 (99%)	139 (100%)	0	100	100
23	2O	91/115 (79%)	91 (100%)	0	100	100
24	2P	101/107 (94%)	100 (99%)	1 (1%)	73	81
25	2Q	103/126 (82%)	103 (100%)	0	100	100
26	2R	107/133 (80%)	107 (100%)	0	100	100
27	2S	124/135 (92%)	124 (100%)	0	100	100
28	2T	117/118 (99%)	117 (100%)	0	100	100
29	2U	120/121 (99%)	118 (98%)	2 (2%)	56	72
30	2V	88/126 (70%)	88 (100%)	0	100	100
31	2W	83/97 (86%)	83 (100%)	0	100	100
32	2X	98/110 (89%)	97 (99%)	1 (1%)	73	81
33	2Y	114/121 (94%)	114 (100%)	0	100	100
34	2Z	88/89 (99%)	88 (100%)	0	100	100
35	2a	97/100 (97%)	97 (100%)	0	100	100
36	2b	109/110 (99%)	109 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	2c	86/89 (97%)	86 (100%)	0	100	100
38	2d	73/80 (91%)	73 (100%)	0	100	100
39	2e	64/65 (98%)	64 (100%)	0	100	100
40	2f	47/48 (98%)	47 (100%)	0	100	100
41	2g	48/116 (41%)	47 (98%)	1 (2%)	48	67
42	2h	23/24 (96%)	23 (100%)	0	100	100
43	2i	93/94 (99%)	92 (99%)	1 (1%)	70	79
44	2j	74/75 (99%)	74 (100%)	0	100	100
45	2k	109/121 (90%)	109 (100%)	0	100	100
46	2l	195/196 (100%)	195 (100%)	0	100	100
48	2n	183/243 (75%)	183 (100%)	0	100	100
49	2o	195/231 (84%)	195 (100%)	0	100	100
50	2p	190/202 (94%)	190 (100%)	0	100	100
51	2q	224/225 (100%)	224 (100%)	0	100	100
52	2r	157/170 (92%)	156 (99%)	1 (1%)	84	88
53	2s	169/174 (97%)	168 (99%)	1 (1%)	84	88
54	2t	178/180 (99%)	177 (99%)	1 (1%)	84	88
55	2u	89/136 (65%)	89 (100%)	0	100	100
56	2v	137/142 (96%)	137 (100%)	0	100	100
57	2w	87/130 (67%)	87 (100%)	0	100	100
58	2x	121/121 (100%)	121 (100%)	0	100	100
59	2y	120/122 (98%)	120 (100%)	0	100	100
60	2z	130/132 (98%)	130 (100%)	0	100	100
61	20	113/115 (98%)	113 (100%)	0	100	100
62	21	94/107 (88%)	94 (100%)	0	100	100
63	3A	67/67 (100%)	67 (100%)	0	100	100
64	3B	113/115 (98%)	113 (100%)	0	100	100
65	3C	90/98 (92%)	89 (99%)	1 (1%)	70	79
66	3D	57/62 (92%)	57 (100%)	0	100	100
67	3E	47/49 (96%)	47 (100%)	0	100	100
68	3F	272/275 (99%)	272 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	3G	188/225 (84%)	188 (100%)	0	100	100
70	3H	207/218 (95%)	207 (100%)	0	100	100
71	3I	161/168 (96%)	161 (100%)	0	100	100
72	3J	104/108 (96%)	104 (100%)	0	100	100
73	3K	130/131 (99%)	130 (100%)	0	100	100
74	3L	110/119 (92%)	110 (100%)	0	100	100
75	3M	112/113 (99%)	112 (100%)	0	100	100
76	3N	113/115 (98%)	113 (100%)	0	100	100
77	3O	66/103 (64%)	66 (100%)	0	100	100
78	3P	75/76 (99%)	75 (100%)	0	100	100
79	3Q	47/48 (98%)	47 (100%)	0	100	100
80	3R	60/140 (43%)	60 (100%)	0	100	100
82	zx	16/16 (100%)	16 (100%)	0	100	100
All	All	10065/11013 (91%)	10045 (100%)	20 (0%)	91	94

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
41	2g	83	ARG
53	2s	121	THR
65	3C	15	ARG
54	2t	123	ARG
15	2G	122	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 69 such sidechains are listed below:

Mol	Chain	Res	Type
59	2y	48	ASN
64	3B	20	GLN
77	3O	64	ASN
26	2R	107	HIS
22	2N	79	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1A	3704/5070 (73%)	1237 (33%)	31 (0%)
2	1B	119/121 (98%)	25 (21%)	1 (0%)
3	1C	155/157 (98%)	40 (25%)	2 (1%)
47	2m	1716/1869 (91%)	660 (38%)	0
81	zv	5/6 (83%)	4 (80%)	0
83	zu	74/75 (98%)	25 (33%)	0
83	zy	74/75 (98%)	16 (21%)	0
All	All	5847/7373 (79%)	2007 (34%)	34 (0%)

5 of 2007 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1A	15	A
1	1A	17	A
1	1A	18	C
1	1A	22	G
1	1A	23	C

5 of 34 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1A	4896	G
1	1A	4913	G
3	1C	86	U
1	1A	2389	A
1	1A	2299	G

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

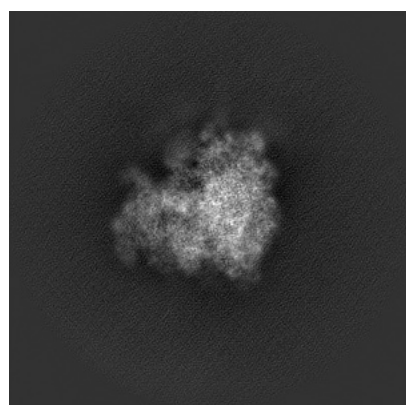
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9701. These allow visual inspection of the internal detail of the map and identification of artifacts.

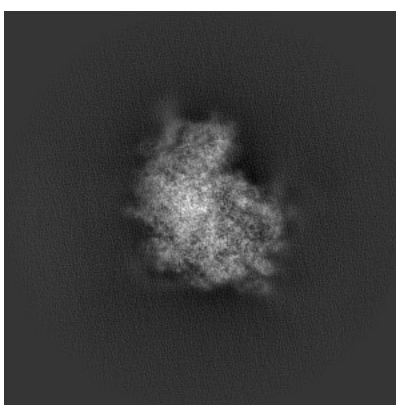
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

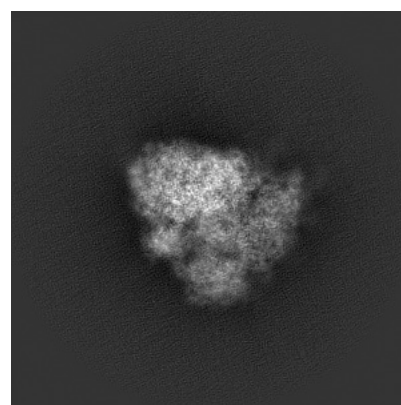
6.1.1 Primary map



X



Y

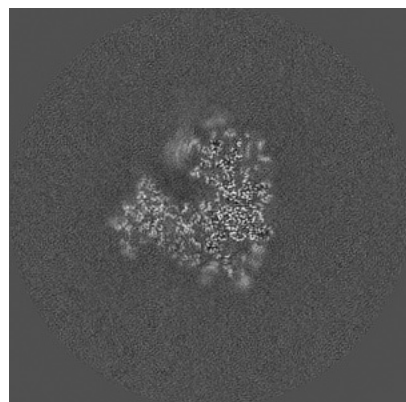


Z

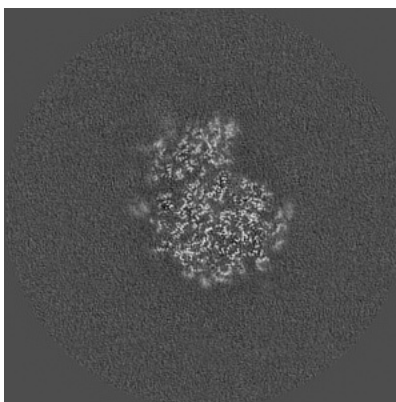
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

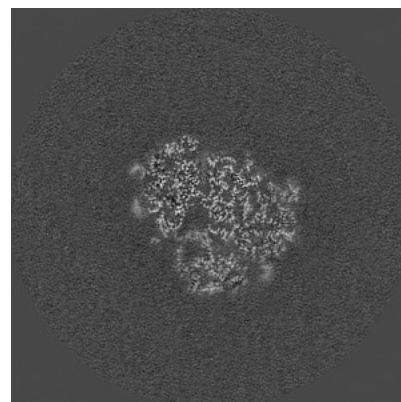
6.2.1 Primary map



X Index: 210



Y Index: 210

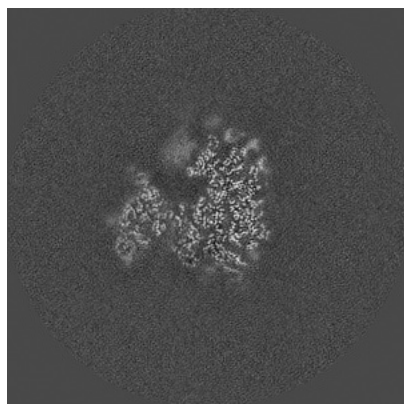


Z Index: 210

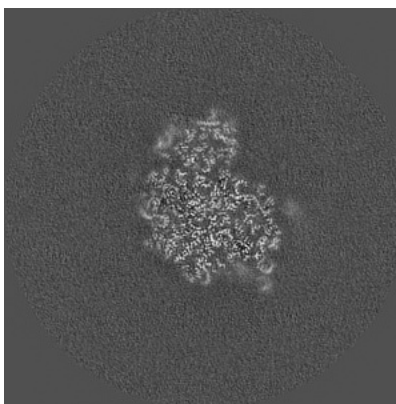
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

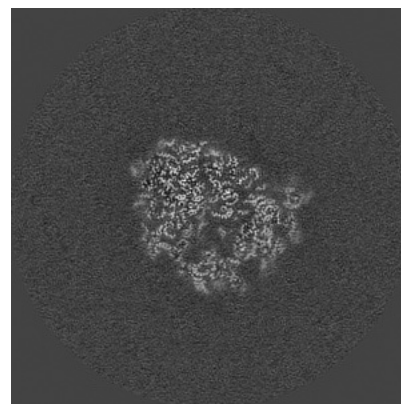
6.3.1 Primary map



X Index: 215



Y Index: 219

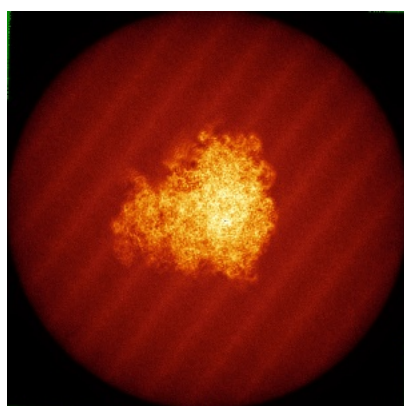


Z Index: 217

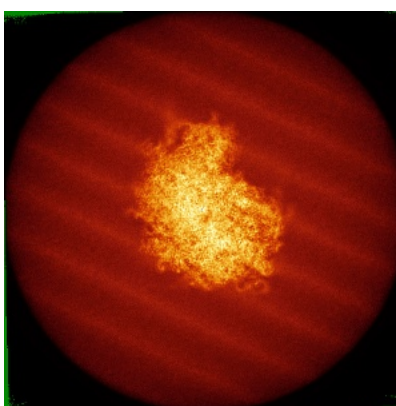
The images above show the largest variance slices of the map in three orthogonal directions.

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

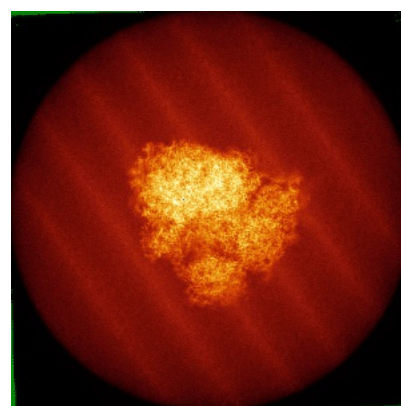
6.4.1 Primary map



X



Y

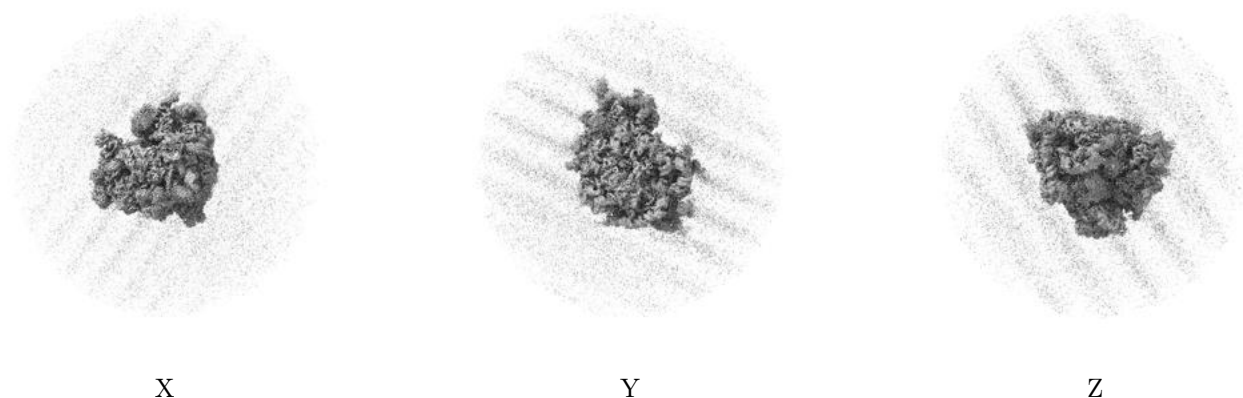


Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

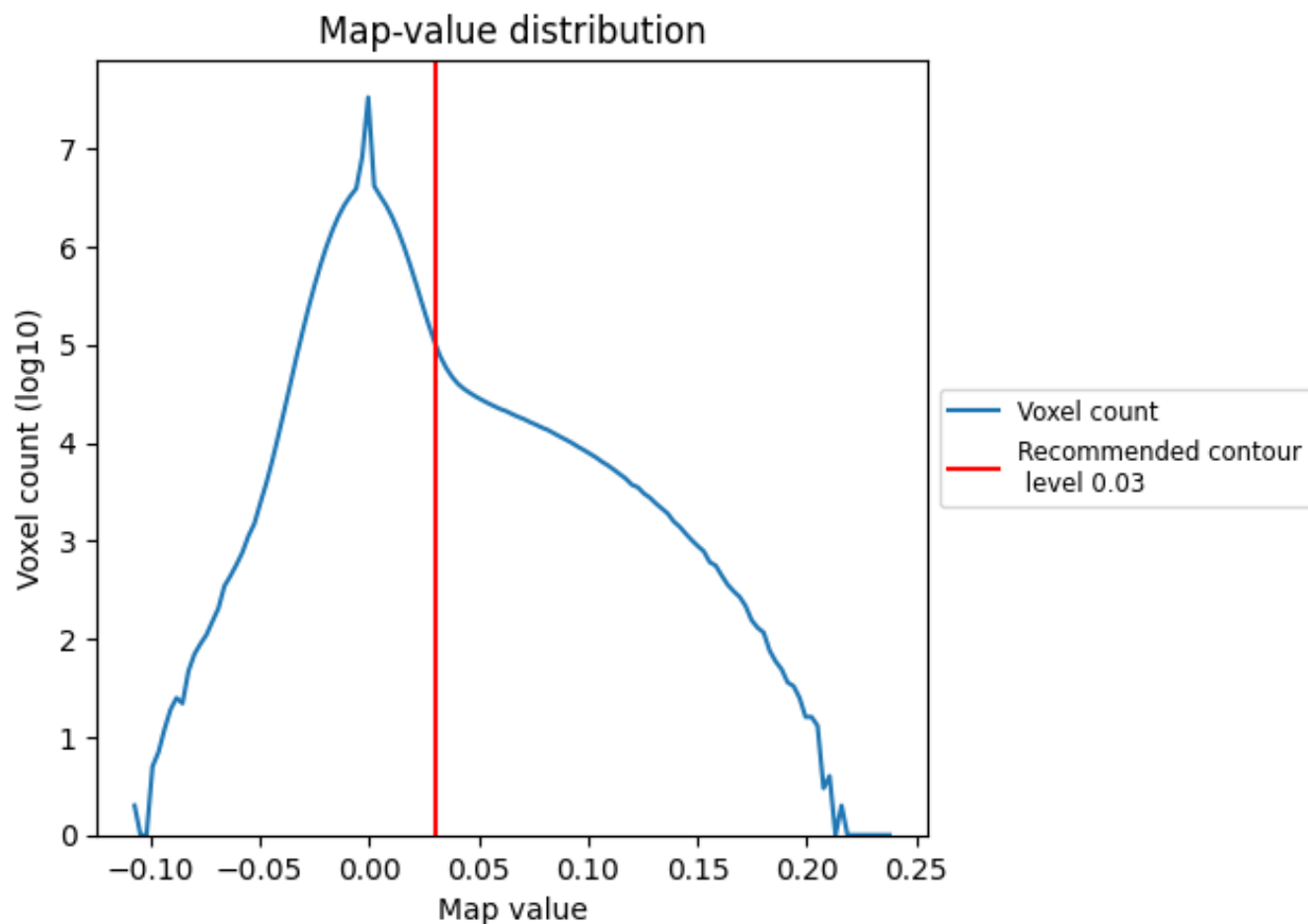
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

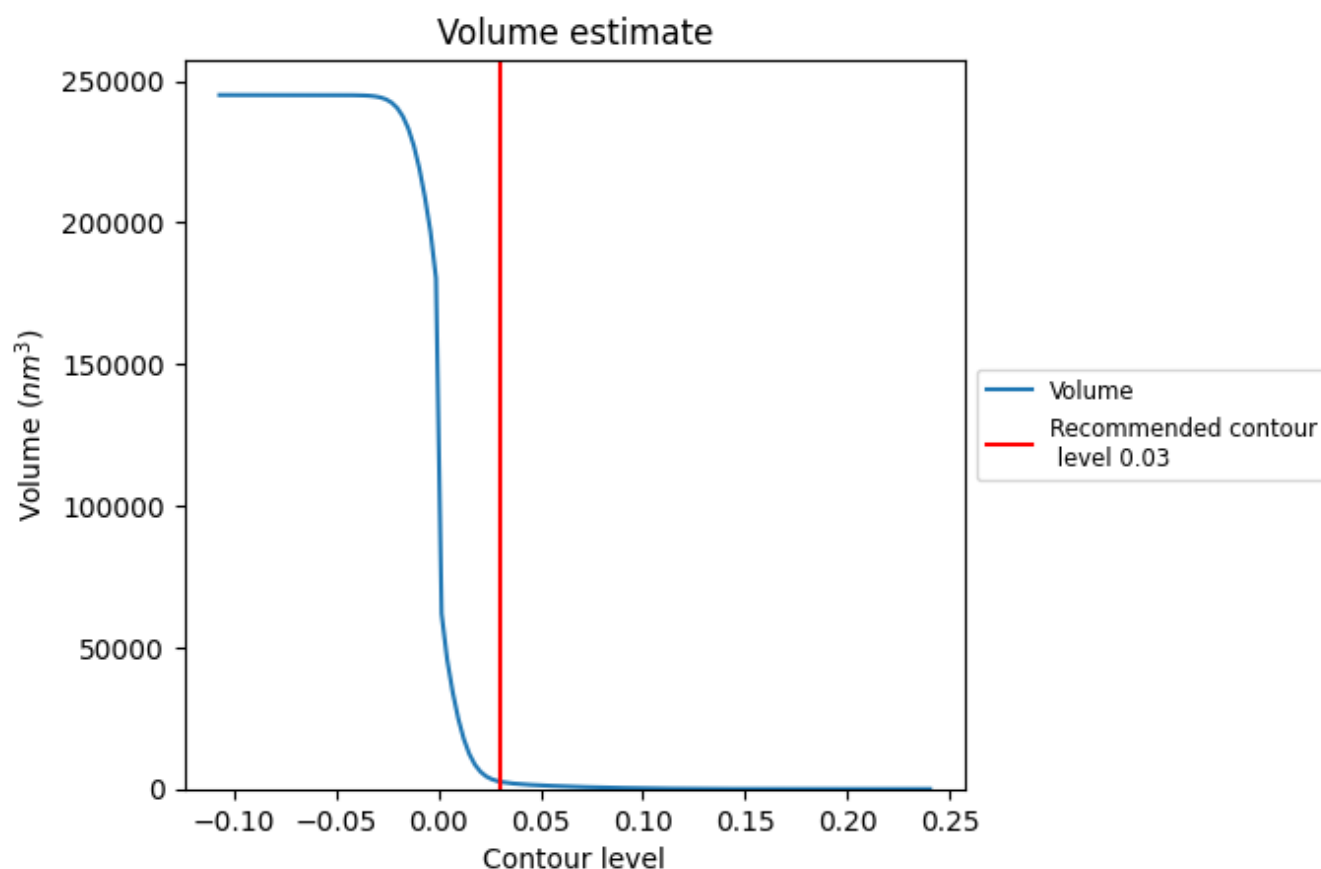
This section contains the results of statistical analysis of the map.

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.

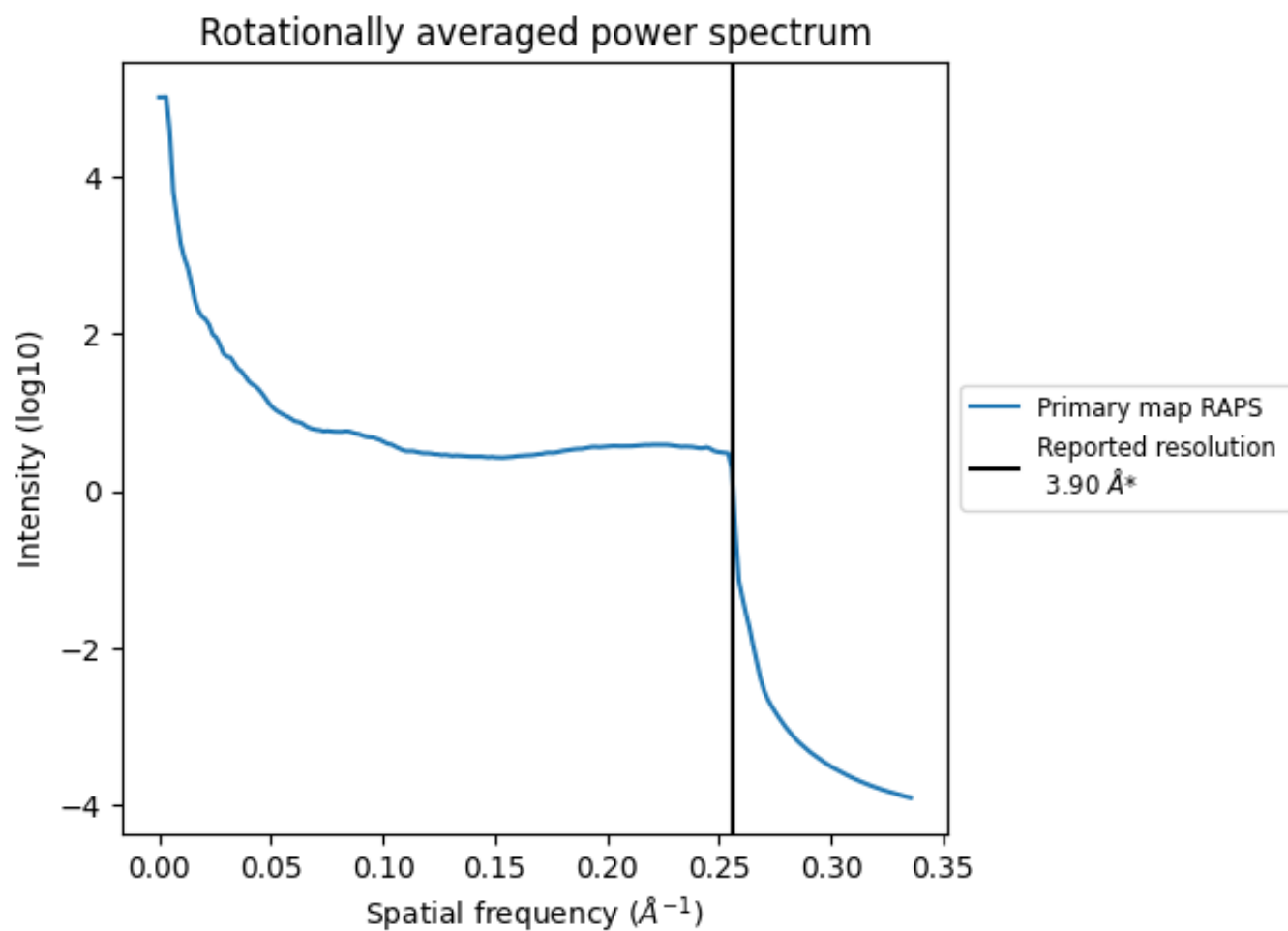
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2603 nm^3 ; this corresponds to an approximate mass of 2351 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 ⓘ

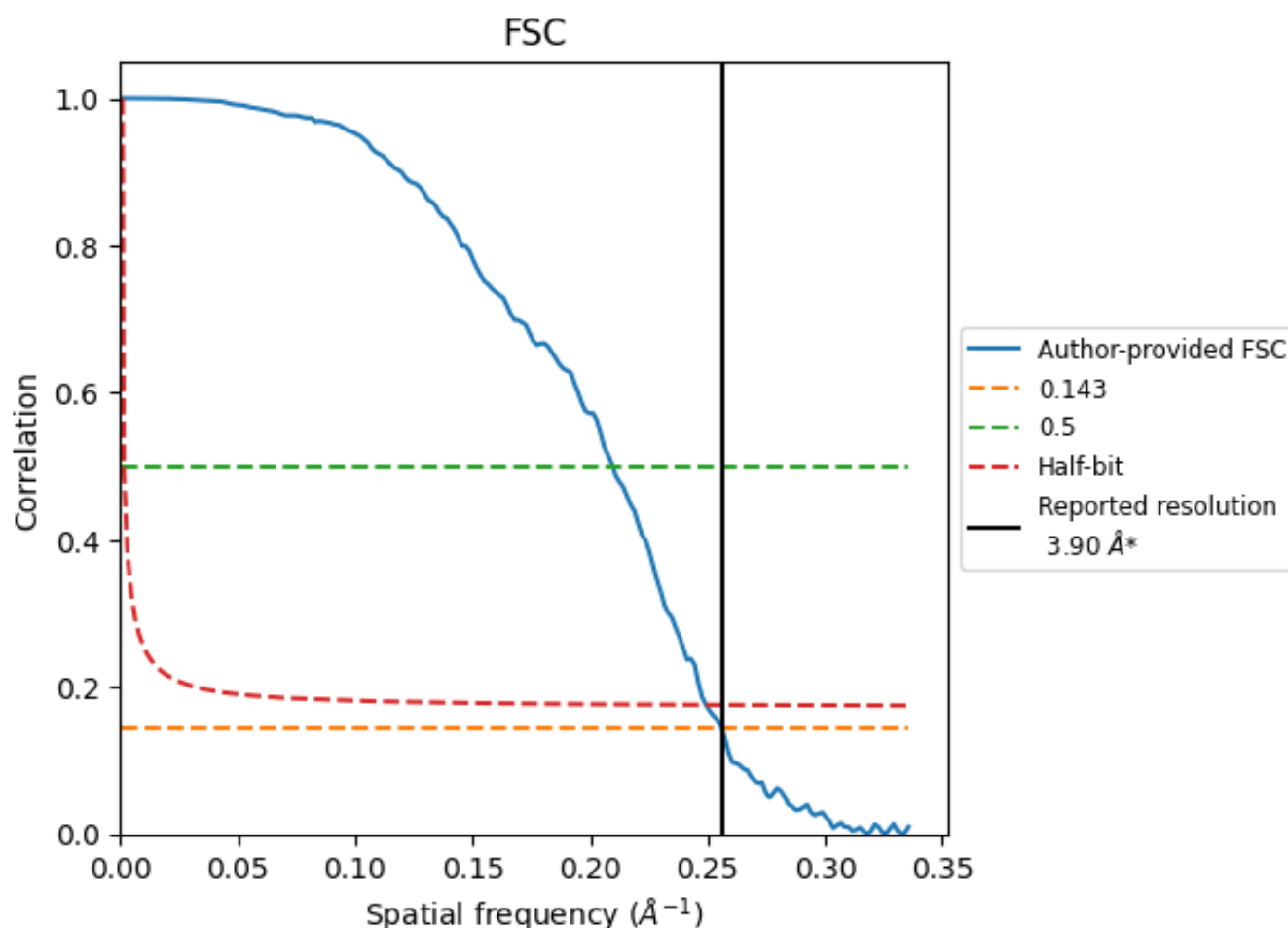


*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

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 0.256 Å⁻¹

8.2 Resolution estimates [i](#)

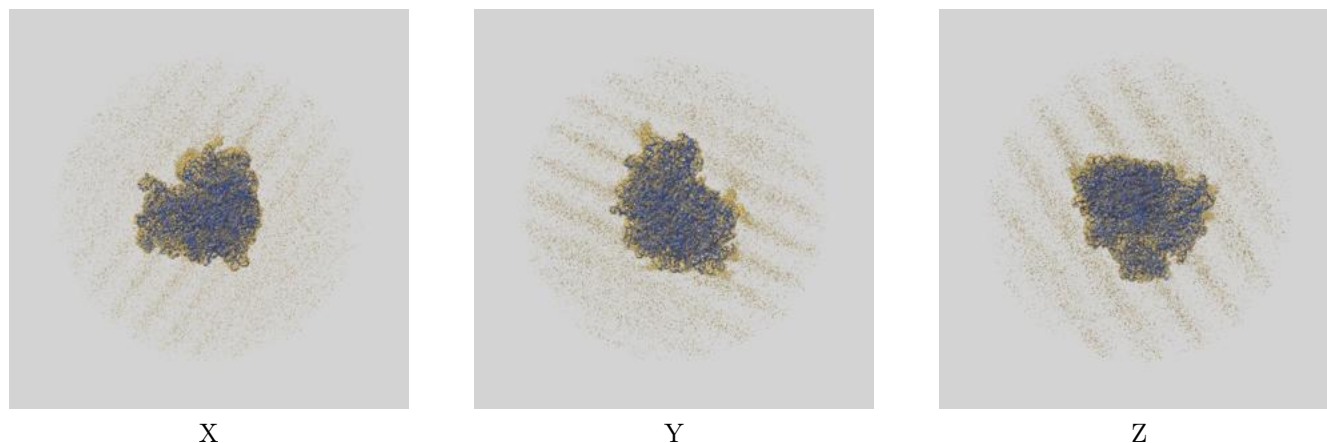
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	3.91	4.77	4.01
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

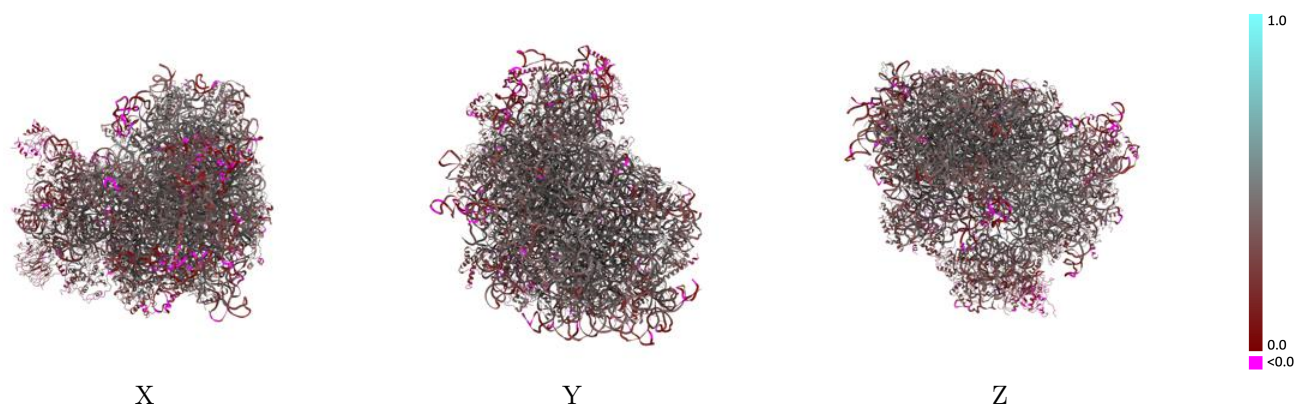
This section contains information regarding the fit between EMDB map EMD-9701 and PDB model 6IP5. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

9.1 Map-model overlay [i](#)



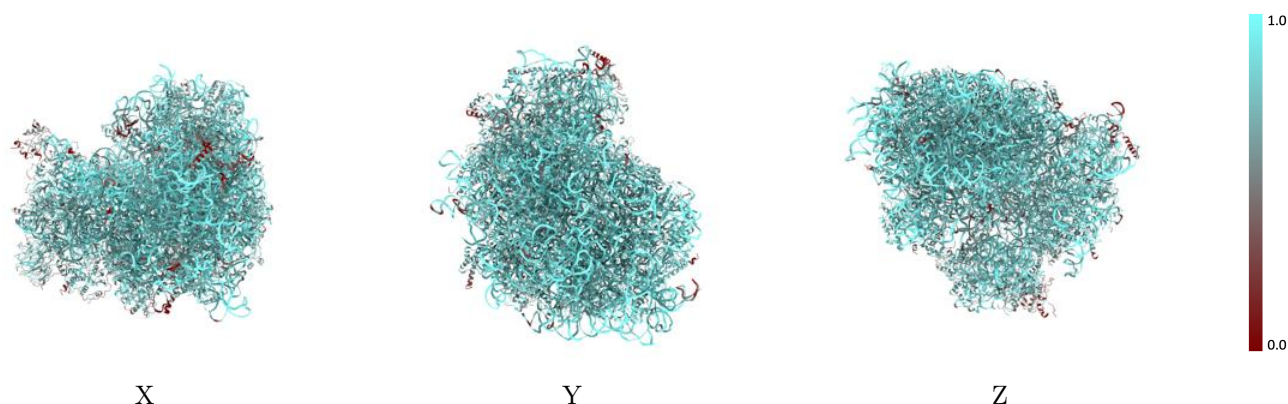
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



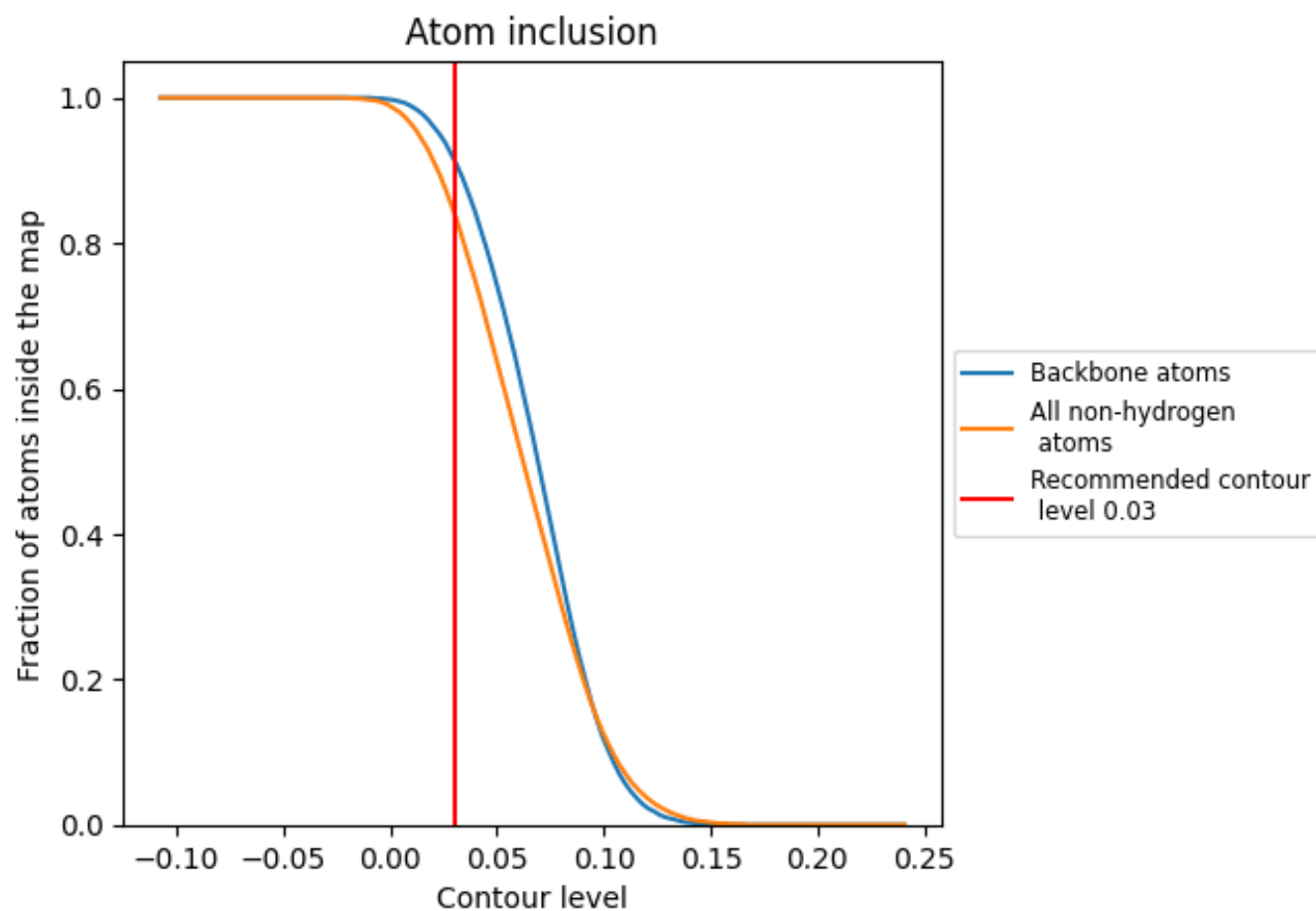
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 84% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8420	 0.3560
1A	 0.9250	 0.3700
1B	 0.9730	 0.4160
1C	 0.9500	 0.3860
1D	 0.7900	 0.4130
1E	 0.7950	 0.4030
1F	 0.7970	 0.4020
1G	 0.8130	 0.3590
1H	 0.7450	 0.3460
20	 0.7540	 0.3090
21	 0.6460	 0.2840
2A	 0.8080	 0.4040
2B	 0.6950	 0.3250
2C	 0.7730	 0.3980
2D	 0.7530	 0.3660
2E	 0.7340	 0.3250
2F	 0.7640	 0.3650
2G	 0.8110	 0.3880
2H	 0.8110	 0.4160
2I	 0.7940	 0.4090
2J	 0.8100	 0.4100
2K	 0.8050	 0.4050
2L	 0.7490	 0.3680
2M	 0.8330	 0.4180
2N	 0.7970	 0.4120
2O	 0.7370	 0.3280
2P	 0.7680	 0.4160
2Q	 0.4840	 0.2410
2R	 0.7770	 0.3870
2S	 0.8010	 0.3790
2T	 0.7870	 0.3700
2U	 0.8310	 0.4210
2V	 0.7430	 0.3480
2W	 0.7510	 0.3700
2X	 0.8090	 0.4090



















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Chain	Atom inclusion	Q-score
2Y	 0.8250	 0.4320
2Z	 0.8180	 0.4330
2a	 0.7530	 0.3820
2b	 0.7720	 0.3610
2c	 0.7660	 0.3470
2d	 0.8360	 0.4220
2e	 0.7090	 0.3240
2f	 0.7940	 0.4010
2g	 0.7880	 0.3950
2h	 0.7940	 0.4090
2i	 0.7670	 0.3760
2j	 0.7640	 0.4050
2k	 0.8280	 0.4080
2l	 0.0900	 0.0020
2m	 0.9310	 0.3540
2n	 0.7140	 0.3410
2o	 0.7040	 0.3460
2p	 0.6540	 0.2790
2q	 0.7590	 0.3730
2r	 0.7070	 0.2990
2s	 0.6470	 0.2860
2t	 0.7670	 0.3610
2u	 0.6740	 0.2550
2v	 0.7120	 0.3660
2w	 0.6860	 0.2450
2x	 0.7300	 0.2970
2y	 0.6150	 0.2680
2z	 0.7060	 0.2640
3A	 0.7360	 0.3480
3B	 0.7810	 0.3970
3C	 0.7240	 0.3380
3D	 0.6400	 0.2980
3E	 0.7840	 0.3390
3F	 0.6750	 0.2300
3G	 0.7400	 0.3630
3H	 0.7140	 0.2800
3I	 0.7520	 0.3340
3J	 0.3090	 0.0650
3K	 0.7660	 0.3950
3L	 0.6970	 0.3470
3M	 0.7780	 0.3900
3N	 0.7430	 0.3010

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Chain	Atom inclusion	Q-score
3O	 0.6480	 0.2540
3P	 0.7210	 0.3460
3Q	 0.6600	 0.3050
3R	 0.4950	 0.1450
zu	 0.5410	 0.1500
zv	 0.9020	 0.3800
zx	 0.2580	 0.1930
zy	 0.8780	 0.3500