



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 04:38 PM UTC

PDB ID : 9Y4G / pdb_00009y4g
EMDB ID : EMD-72482
Title : Structure of tuco-tuco ribosome (rotated, tRNAs, and mRNA)
Authors : Gutierrez-Vargas, C.; De, S.; Maji, S.; Liu, Z.; Nieb, M.; Seluanov, A.; Gorbunova, V.; Frank, J.
Deposited on : 2025-09-03
Resolution : 3.30 Å(reported)
Based on initial model : 4v6x

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

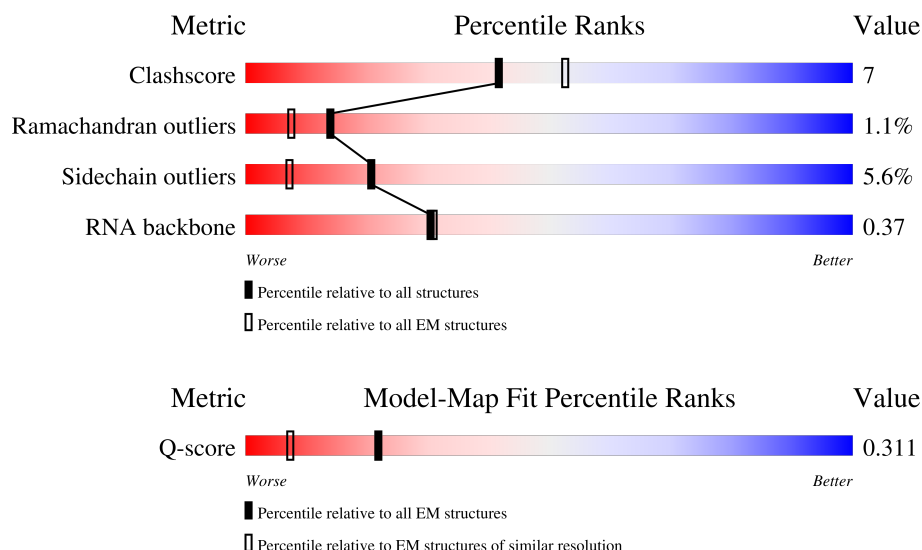
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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.











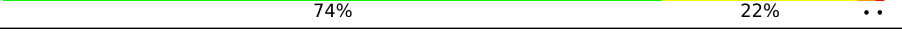

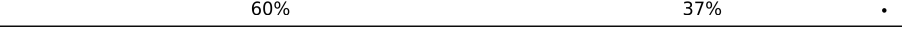
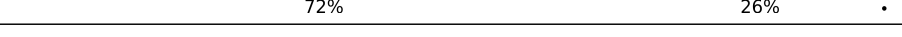

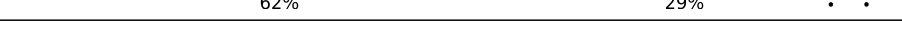


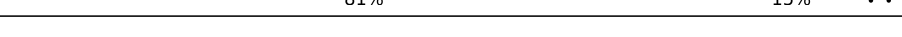

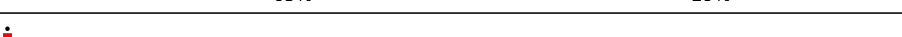






Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15087 (2.80 - 3.80)

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	Ag	313	 68% 28%
2	AU	104	 62% 38%
3	AK	98	 65% 31%









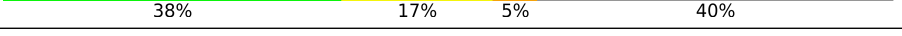

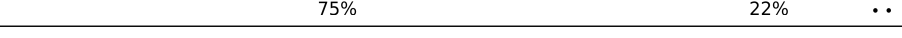
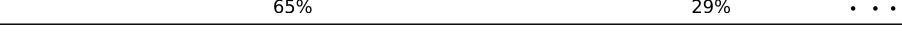

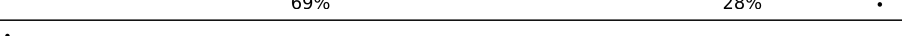


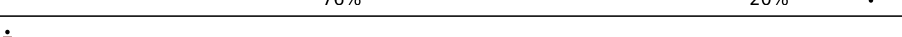

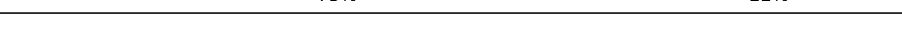






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Mol	Chain	Length	Quality of chain
4	AM	124	
5	AS	137	
6	Ad	53	
7	AR	126	
8	AP	127	
9	AT	141	
10	AZ	75	
11	Ac	64	
12	AD	227	
13	Af	71	
14	AF	191	
15	AQ	141	
16	B2	1796	
17	AO	136	
18	AX	142	
19	AN	150	
20	AL	158	
21	AB	215	
22	AA	208	
23	AV	82	
24	AY	126	
25	Aa	107	
26	Ab	84	
27	Ae	59	
28	AJ	182	







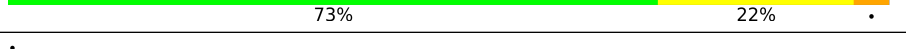
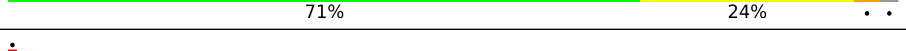
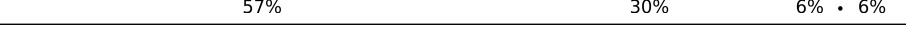
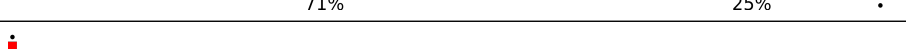
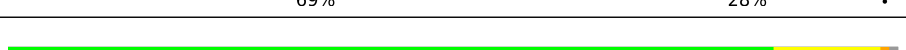

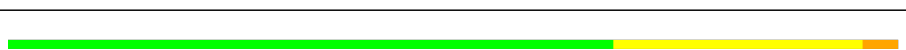

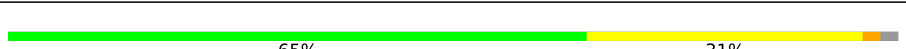
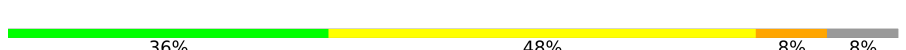




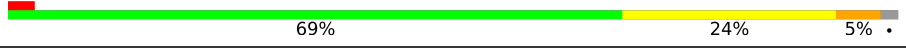
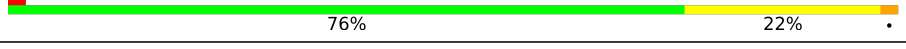



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Mol	Chain	Length	Quality of chain
29	AE	263	 70%28%..
30	AC	226	 62%34%..
31	AG	237	 76%23%.
32	AH	190	 73%24%..
33	AW	129	 67%29%.
34	AI	206	 72%27%.
35	CR	189	 63%33%..
36	CW	124	 65%33%.
37	Cz	217	 38%17%5%40%
38	CO	202	 58%36%..
39	CL	210	 75%22%..
40	CV	133	 65%29%...
41	CM	139	 63%35%..
42	Ca	147	 69%28%.
43	CN	203	 64%32%..
44	CI	213	 74%23%.
45	CD	289	 76%20%.
46	CQ	188	 65%26%5%.
47	CA	255	 75%22%.
48	CS	175	 68%29%.
49	CT	159	 74%24%.
50	CP	152	 70%28%.
51	CU	112	 6%79%14%6%
52	CX	121	 69%27%.
53	CY	133	 65%32%.

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Mol	Chain	Length	Quality of chain
54	CZ	135	
55	Cr	137	
56	Ch	123	
57	Cb	78	
58	CB	397	
59	CF	229	
60	Cd	113	
61	Ce	133	
62	Cf	109	
63	Cg	114	
64	Ci	103	
65	Cj	90	
66	Ck	69	
67	Cl	50	
68	CC	368	
69	Cm	52	
70	Cn	25	
71	Cp	90	
72	Co	105	
73	CJ	168	
74	CH	191	
75	CE	262	
76	CG	246	
77	A5	1778	
78	A7	121	

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Mol	Chain	Length	Quality of chain
79	A8	157	<div><div></div><div>57%38%</div><div></div></div>
80	Cc	77	<div><div></div><div>62%35%</div><div></div></div>
81	Bb	76	<div><div></div><div>47%34%14%</div><div></div></div>
82	Dd	13	<div><div></div><div>77%23%</div><div></div></div>
83	A6	2108	<div><div></div><div>57%36%6%</div><div></div></div>

2 Entry composition [i](#)

There are 85 unique types of molecules in this entry. The entry contains 219326 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Guanine nucleotide-binding protein subunit beta-2-like 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Ag	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 2 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AU	104	Total	C	N	O	S	0	0
			822	514	156	148	4		

- Molecule 3 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AK	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 4 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AM	106	Total	C	N	O	S	0	0
			818	512	145	155	6		

- Molecule 5 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AS	137	Total	C	N	O	S	0	0
			1139	714	231	193	1		

- Molecule 6 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Ad	53	Total	C	N	O	S	0	0
			445	278	90	72	5		

- Molecule 7 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AR	126	Total	C	N	O	S	0	0
			1019	639	188	187	5		

- Molecule 8 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AP	117	Total	C	N	O	S	0	0
			970	616	182	165	7		

- Molecule 9 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AT	141	Total	C	N	O	S	0	0
			1101	690	212	196	3		

- Molecule 10 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AZ	74	Total	C	N	O	S	0	0
			594	380	110	103	1		

- Molecule 11 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	Ac	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 12 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AD	226	Total	C	N	O	S	0	0
			1757	1120	316	314	7		

- Molecule 13 is a protein called 40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Af	71	Total	C	N	O	S	0	0
			581	367	109	98	7		

- Molecule 14 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AF	191	Total	C	N	O	S	0	0
			1509	943	286	273	7		

- Molecule 15 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AQ	141	Total	C	N	O	S	0	0
			1124	715	212	194	3		

- Molecule 16 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	B2	1778	Total	C	N	O	P	0	0
			37608	16773	6715	12343	1777		

- Molecule 17 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AO	130	Total	C	N	O	S	0	0
			975	595	192	182	6		

- Molecule 18 is a protein called 40S ribosomal protein S23.

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

- Molecule 19 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AN	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 20 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AL	157	Total	C	N	O	S	0	0
			1288	822	240	220	6		

- Molecule 21 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AB	215	Total	C	N	O	S	0	0
			1747	1110	313	310	14		

- Molecule 22 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AA	203	Total	C	N	O	S	0	0
			1611	1027	284	292	8		

- Molecule 23 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AV	82	Total	C	N	O	S	0	0
			625	384	116	120	5		

- Molecule 24 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AY	126	Total	C	N	O	S	0	0
			1023	646	200	172	5		

- Molecule 25 is a protein called 40S ribosomal protein S26.

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

- Molecule 26 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Ab	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 27 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Ae	52	Total	C	N	O	S	0	0
			419	259	92	67	1		

- Molecule 28 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AJ	175	Total	C	N	O	S	0	0
			1463	933	292	236	2		

- Molecule 29 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AE	261	Total	C	N	O	S	0	0
			2073	1324	385	355	9		

- Molecule 30 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AC	223	Total	C	N	O	S	0	0
			1727	1116	296	305	10		

- Molecule 31 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 32 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	AH	189	Total	C	N	O	S	0	0
			1521	969	280	271	1		

- Molecule 33 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	AW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 34 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	AI	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 35 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	CR	188	Total	C	N	O	S	0	0
			1574	976	337	251	10		

- Molecule 36 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	CW	124	Total	C	N	O	S	0	0
			1015	634	207	170	4		

- Molecule 37 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Cz	131	Total	C	N	O	S	0	0
			1043	668	182	187	6		

- Molecule 38 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	CO	199	Total	C	N	O	S	0	0
			1634	1053	319	257	5		

- Molecule 39 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	CL	208	Total	C	N	O	S	0	0
			1682	1052	348	278	4		

- Molecule 40 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	CV	130	Total	C	N	O	S	0	0
			973	615	183	170	5		

- Molecule 41 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	CM	139	Total	C	N	O	S	0	0
			1139	730	218	183	8		

- Molecule 42 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Ca	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 43 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	CN	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 44 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	CI	213	Total	C	N	O	S	0	0
			1711	1082	329	285	15		

- Molecule 45 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	CD	289	Total	C	N	O	S	0	0
			2353	1483	429	427	14		

- Molecule 46 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	CQ	181	Total	C	N	O	S	0	0
			1465	915	303	242	5		

- Molecule 47 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	CA	254	Total	C	N	O	S	0	0
			1948	1220	398	324	6		

- Molecule 48 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	CS	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

- Molecule 49 is a protein called 60S ribosomal protein L21.

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

- Molecule 50 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	CP	152	Total	C	N	O	S	0	0
			1233	771	240	213	9		

- Molecule 51 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	CU	105	Total	C	N	O	S	0	0
			884	562	151	169	2		

- Molecule 52 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	CX	121	Total	C	N	O	S	0	0
			994	636	187	170	1		

- Molecule 53 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	CY	133	Total	C	N	O	S	0	0
			1107	695	225	185	2		

- Molecule 54 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	CZ	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 55 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Cr	137	Total	C	N	O	S	0	0
			1104	682	231	185	6		

- Molecule 56 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Ch	123	Total	C	N	O	S	0	0
			1023	646	206	169	2		

- Molecule 57 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Cb	74	Total	C	N	O	S	0	0
			603	373	129	98	3		

- Molecule 58 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	CB	394	Total	C	N	O	S	0	0
			3178	2024	596	544	14		

- Molecule 59 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	CF	229	Total	C	N	O	S	0	0
			1910	1226	370	305	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Cd	113	Total	C	N	O	S	0	0
			931	586	181	162	2		

- Molecule 61 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Ce	131	Total	C	N	O	S	0	0
			1078	681	222	169	6		

- Molecule 62 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Cf	103	Total	C	N	O	S	0	0
			838	531	167	137	3		

- Molecule 63 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Cg	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 64 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Ci	103	Total	C	N	O	S	0	0
			840	526	178	130	6		

- Molecule 65 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Cj	89	Total	C	N	O	S	0	0
			726	446	161	114	5		

- Molecule 66 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Ck	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 67 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Cl	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 68 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	CC	362	Total	C	N	O	S	0	0
			2882	1814	576	479	13		

- Molecule 69 is a protein called 60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Cm	51	Total	C	N	O	S	0	0
			421	260	89	66	6		

- Molecule 70 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Cn	23	Total	C	N	O	S	0	0
			222	134	61	25	2		

- Molecule 71 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Cp	89	Total	C	N	O	S	0	0
			693	437	133	116	7		

- Molecule 72 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Co	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 73 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	CJ	158	Total	C	N	O	S	0	0
			1271	802	240	223	6		

- Molecule 74 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	CH	191	Total	C	N	O	S	0	0
			1526	960	285	275	6		

- Molecule 75 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	CE	257	Total	C	N	O	S	0	0
			2076	1334	395	343	4		

- Molecule 76 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	CG	246	Total	C	N	O	S	0	0
			1973	1256	379	334	4		

- Molecule 77 is a RNA chain called LSU-alpha rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	A5	1733	Total	C	N	O	P	0	0
			36611	16271	6688	11920	1732		

- Molecule 78 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	A7	121	Total	C	N	O	P	0	0
			2578	1150	458	850	120		

- Molecule 79 is a RNA chain called 5.8S rRNA (157-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
79	A8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 80 is a RNA chain called tRNA (78-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Cc	77	Total	C	N	O	P	0	0
			1644	732	298	537	77		

- Molecule 81 is a RNA chain called tRNA (77-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Bb	65	Total	C	N	O	P	0	0
			1407	633	258	452	64		

- Molecule 82 is a RNA chain called RNA (5'-R(P*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*U*P*UP*UP*U*(MG))-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Dd	13	Total	C	N	O	P	0	0
			260	117	26	104	13		

- Molecule 83 is a RNA chain called LSU-beta rRNA (2108-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
83	A6	2103	Total	C	N	O	P	0	0
			43784	19452	7821	14408	2103		

- Molecule 84 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
84	Cc	1	Total 1	Mg 1	0
84	Bb	1	Total 1	Mg 1	0
84	Dd	1	Total 1	Mg 1	0

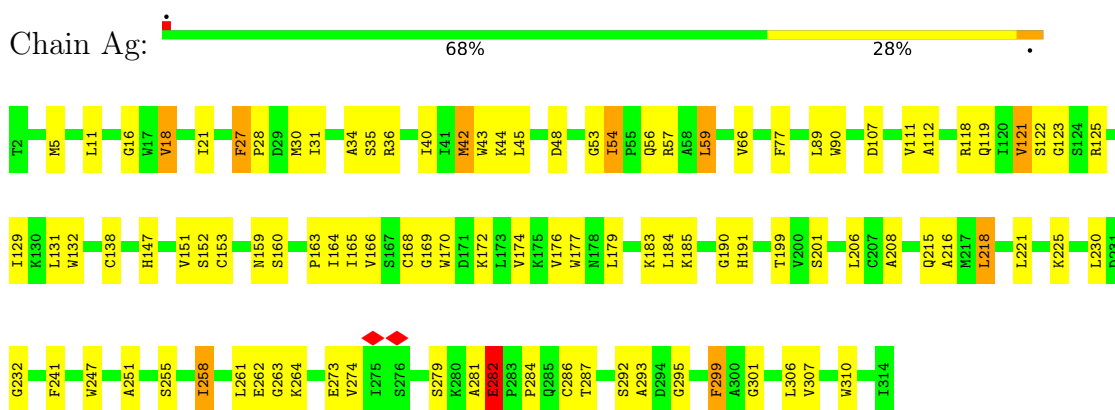
- Molecule 85 is water.

Mol	Chain	Residues	Atoms		AltConf
85	B2	3	Total 3	O 3	0
85	Cc	5	Total 5	O 5	0
85	Bb	5	Total 5	O 5	0
85	Dd	1	Total 1	O 1	0
85	A6	1	Total 1	O 1	0

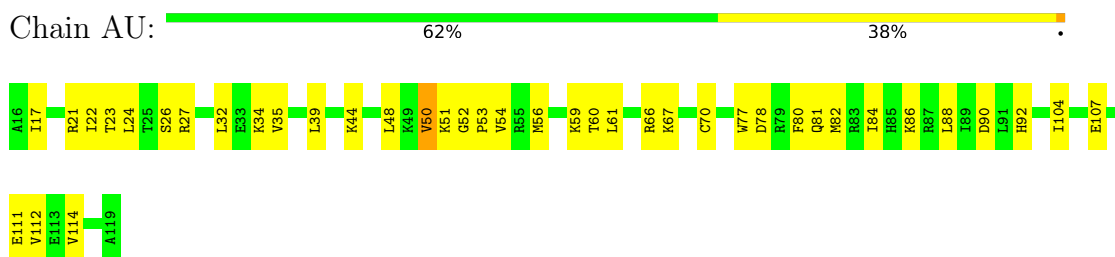
3 Residue-property plots [i](#)

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

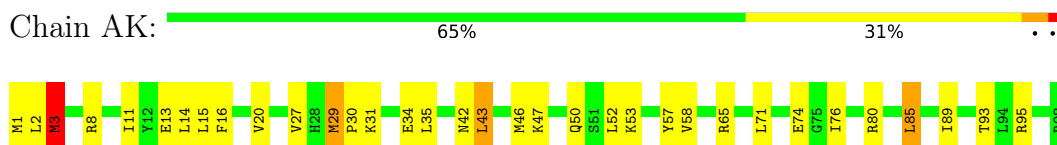
- Molecule 1: Guanine nucleotide-binding protein subunit beta-2-like 1



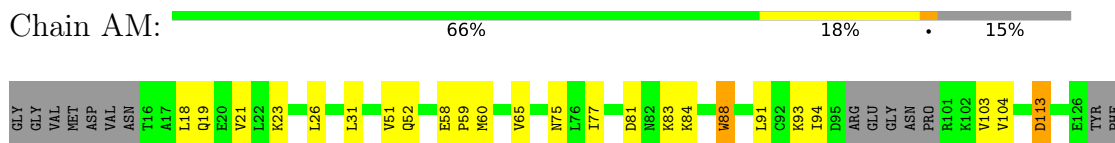
- Molecule 2: 40S ribosomal protein S20



- Molecule 3: 40S ribosomal protein S10



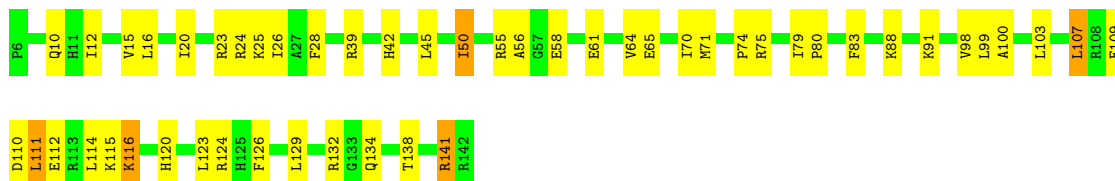
- Molecule 4: 40S ribosomal protein S12



LYS
CYS
LYS
LYS

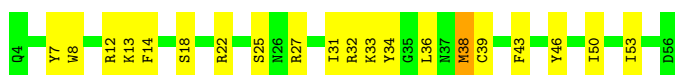
• Molecule 5: 40S ribosomal protein S18

Chain AS:  64% 33%




• Molecule 6: 40S ribosomal protein S29

Chain Ad:  62% 36%



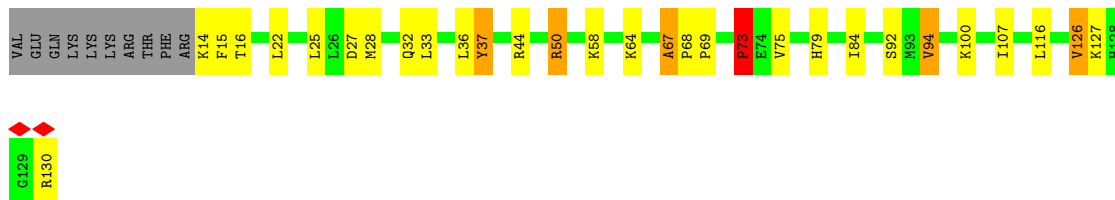
• Molecule 7: 40S ribosomal protein S17

Chain AR:  76% 18% 6%




• Molecule 8: 40S ribosomal protein S15

Chain AP:  69% 19% 8%



• Molecule 9: 40S ribosomal protein S19

Chain AT:  74% 23%



• Molecule 10: 40S ribosomal protein S25

Chain AZ:  65% 31%



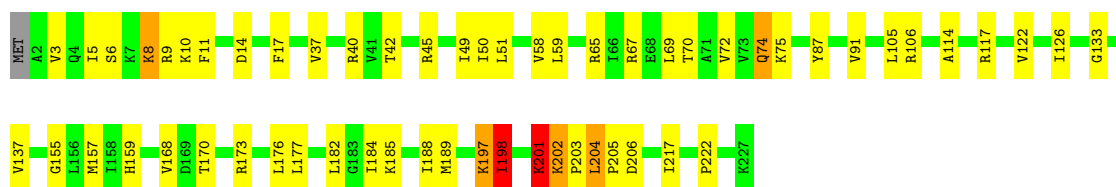
- Molecule 11: 40S ribosomal protein S28

Chain Ac: 78% 22%



- Molecule 12: 40S ribosomal protein S3

Chain AD: 74% 22% ..



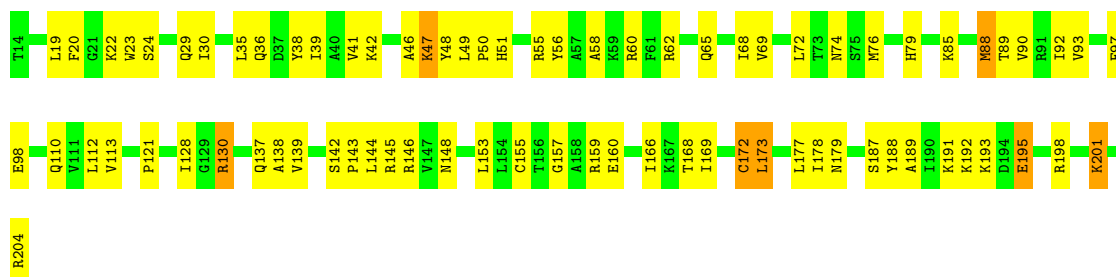
- Molecule 13: 40S ribosomal protein S27a

Chain Af: 75% 24% .



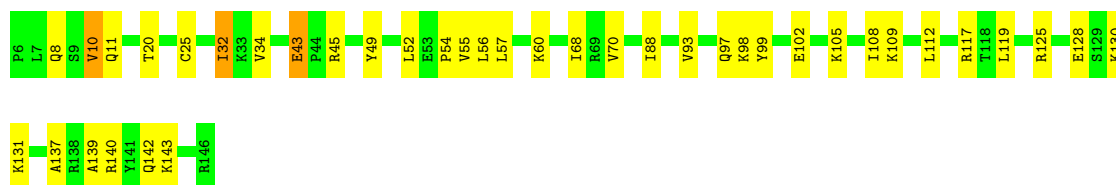
- Molecule 14: 40S ribosomal protein S5

Chain AF: 60% 37% .

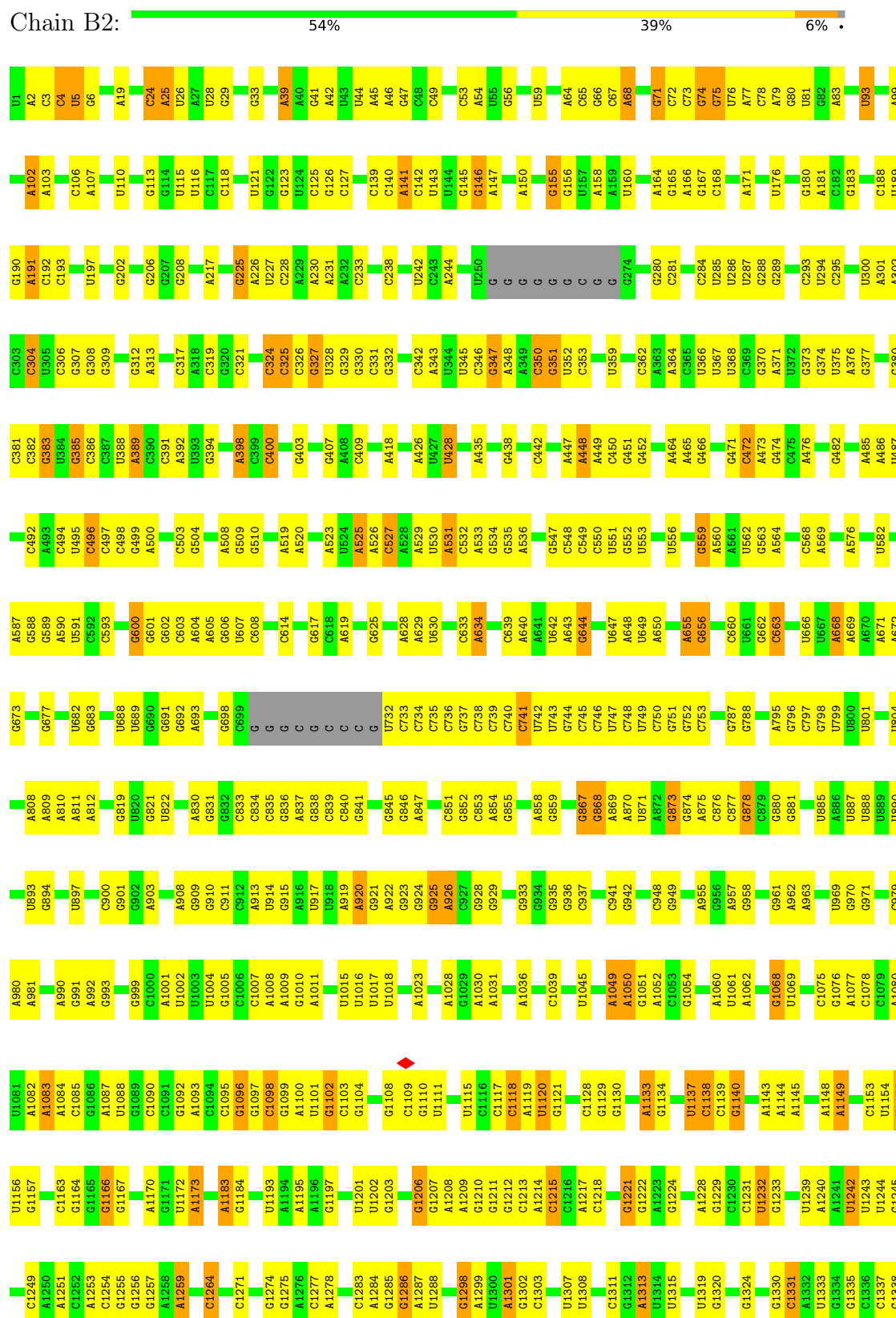


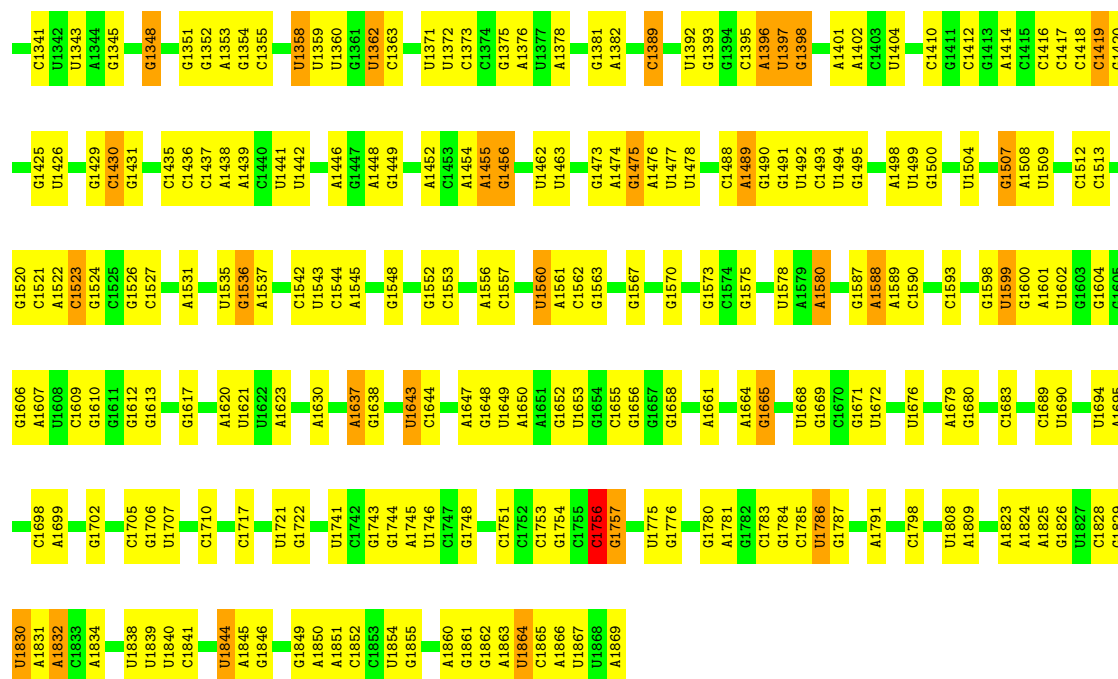
- Molecule 15: 40S ribosomal protein S16

Chain AQ: 72% 26% .

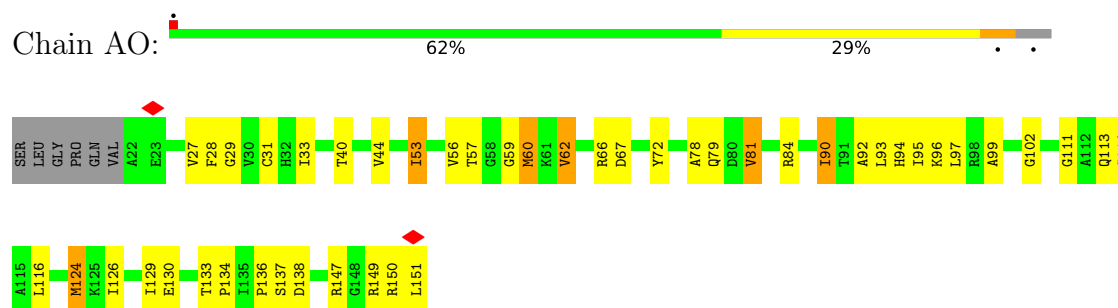


● Molecule 16: 18S ribosomal RNA

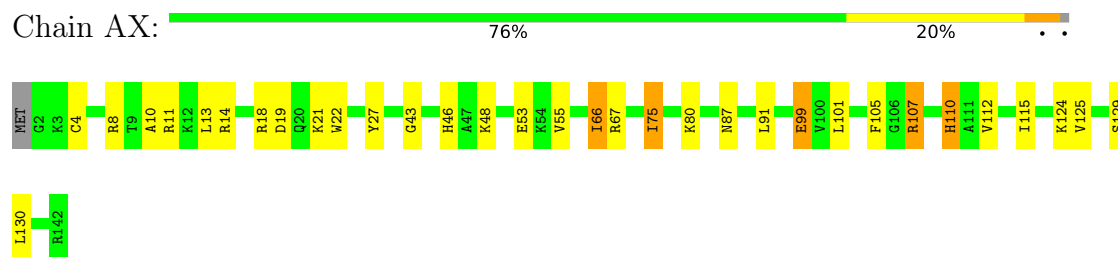




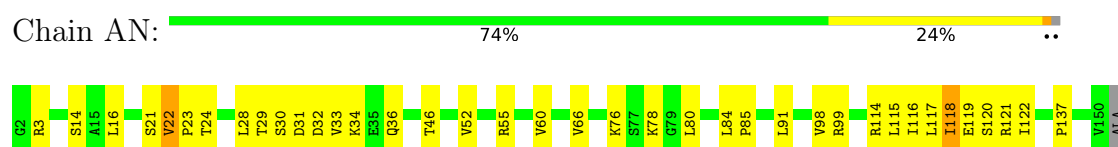
- Molecule 17: 40S ribosomal protein S14




- Molecule 18: 40S ribosomal protein S23



- Molecule 19: 40S ribosomal protein S13



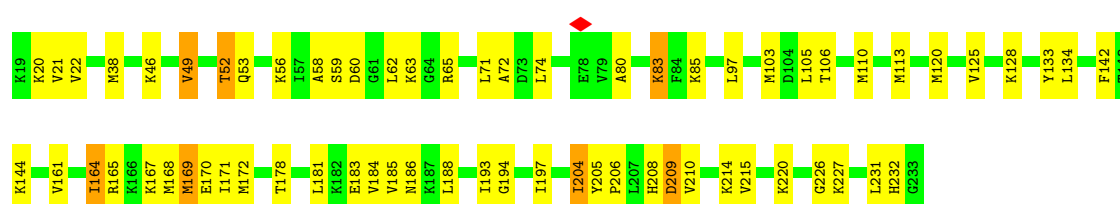
- Molecule 20: 40S ribosomal protein S11

Chain AL:  81% 15% ..



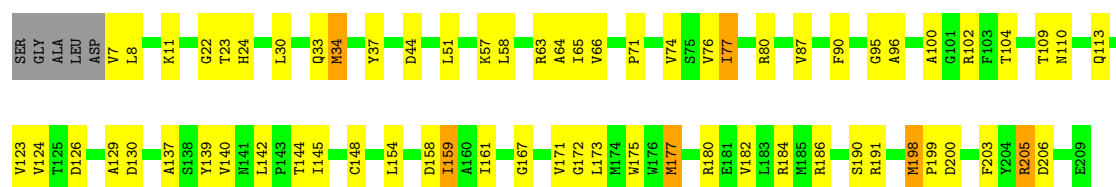
- Molecule 21: 40S ribosomal protein S3a

Chain AB:  69% 27% .



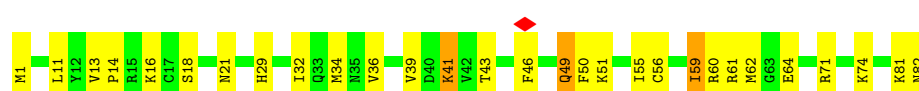
- Molecule 22: 40S ribosomal protein SA

Chain AA:  65% 29% ..



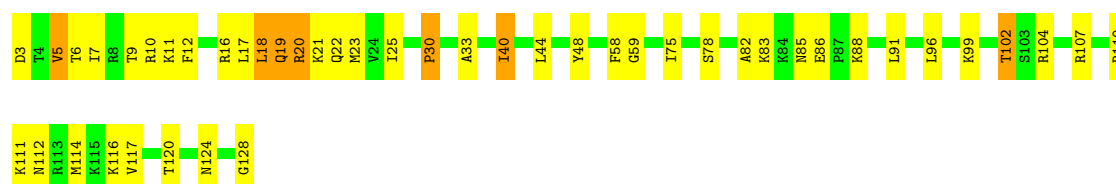
- Molecule 23: 40S ribosomal protein S21

Chain AV:  65% 32% .



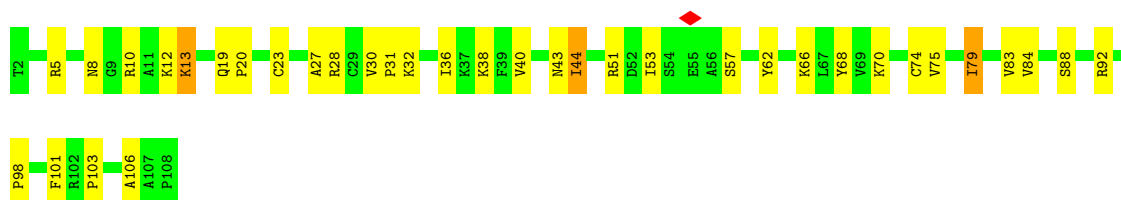
- Molecule 24: 40S ribosomal protein S24

Chain AY:  63% 31% 6%

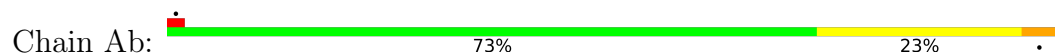


- Molecule 25: 40S ribosomal protein S26

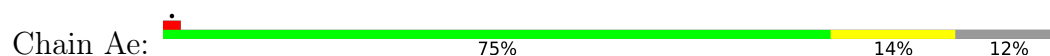
Chain Aa:  66% 31% .



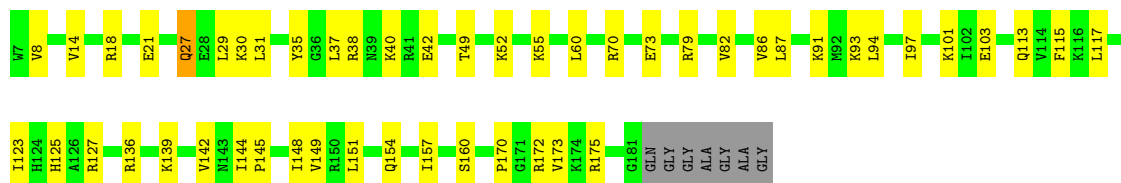
- Molecule 26: 40S ribosomal protein S27



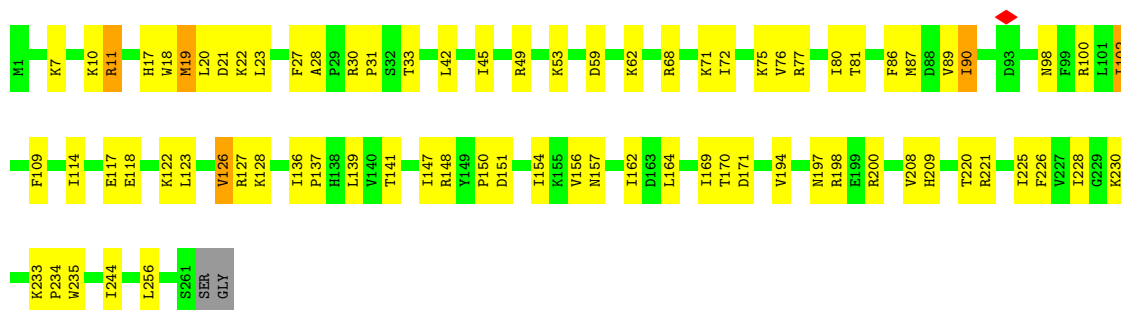
- Molecule 27: 40S ribosomal protein S30



- Molecule 28: 40S ribosomal protein S9

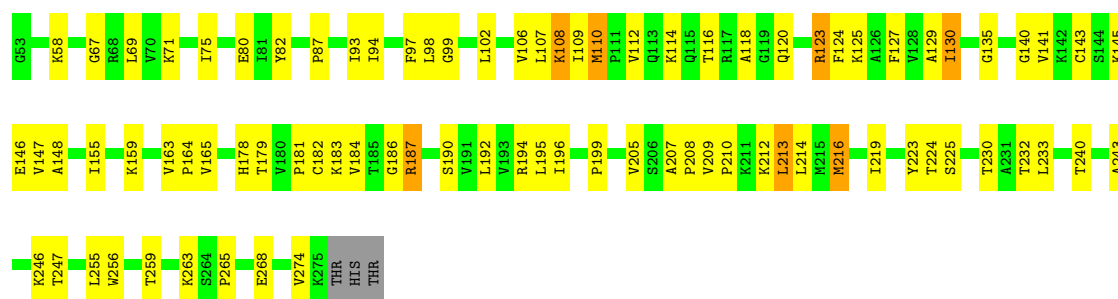


- Molecule 29: 40S ribosomal protein S4, X isoform



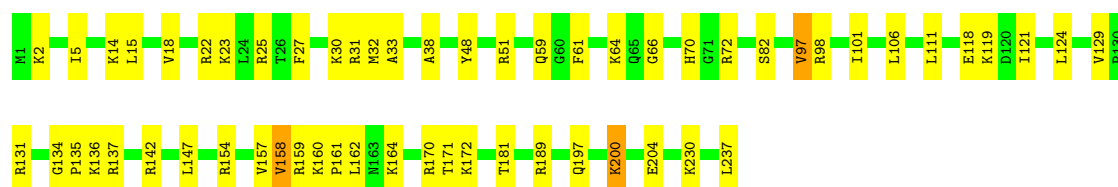
- Molecule 30: 40S ribosomal protein S2





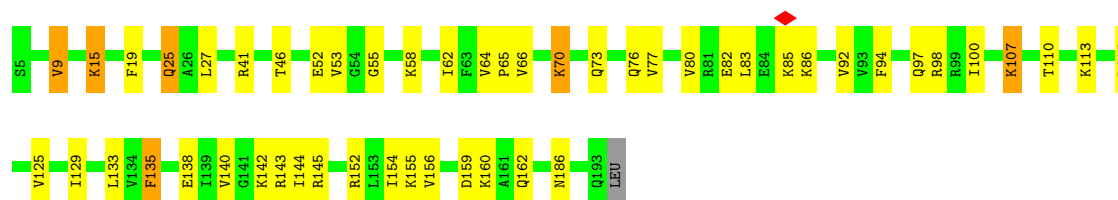
- Molecule 31: 40S ribosomal protein S6

Chain AG: 76% 23%



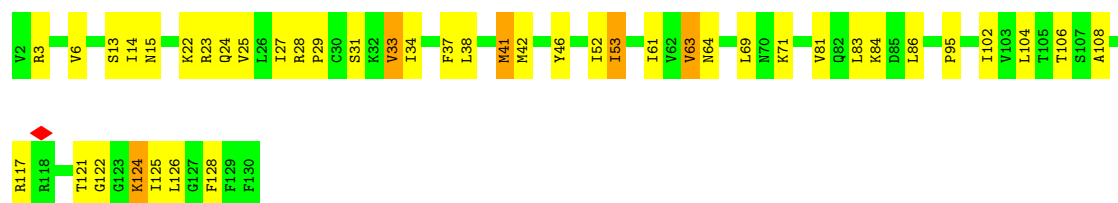
- Molecule 32: 40S ribosomal protein S7

Chain AH: 73% 24%



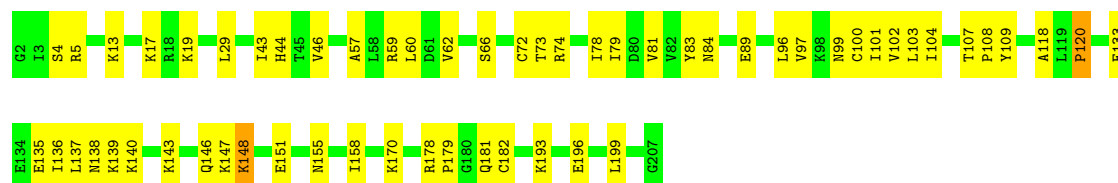
- Molecule 33: 40S ribosomal protein S15a

Chain AW: 67% 29%

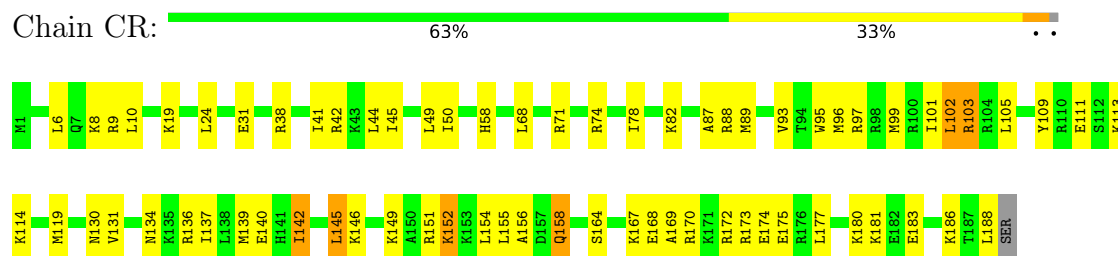


- Molecule 34: 40S ribosomal protein S8

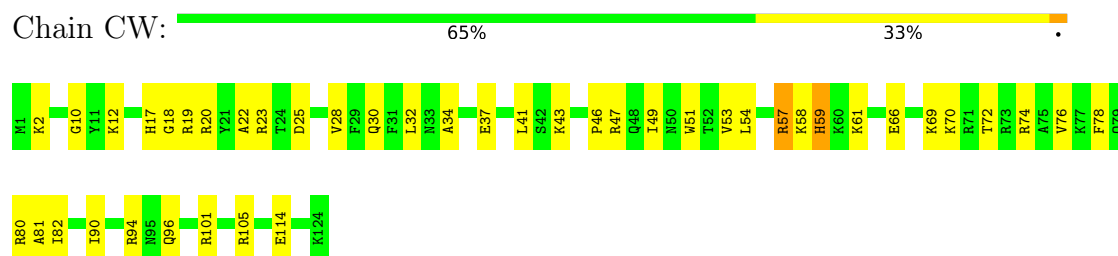
Chain AI: 72% 27%



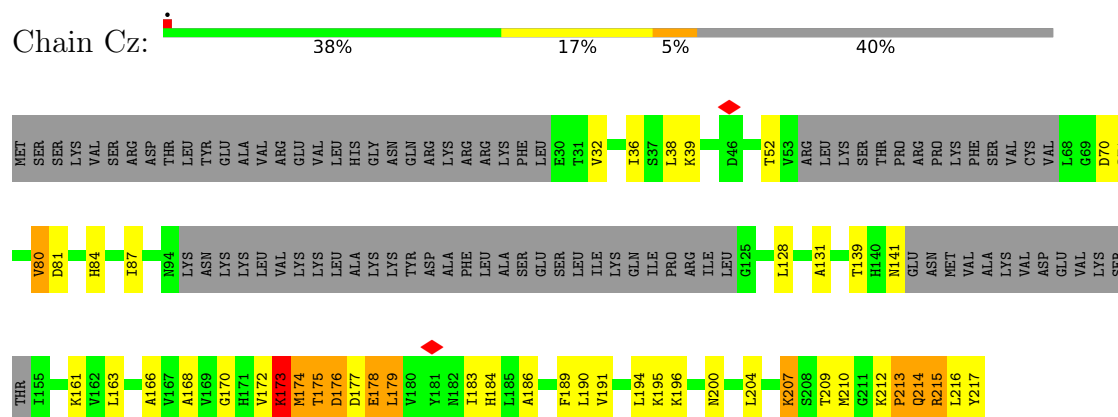
- Molecule 35: 60S ribosomal protein L19



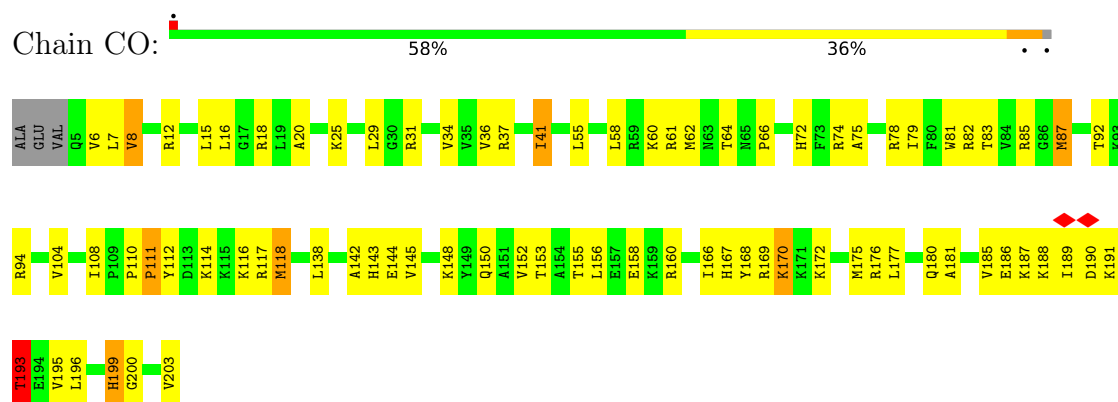
- Molecule 36: 60S ribosomal protein L24



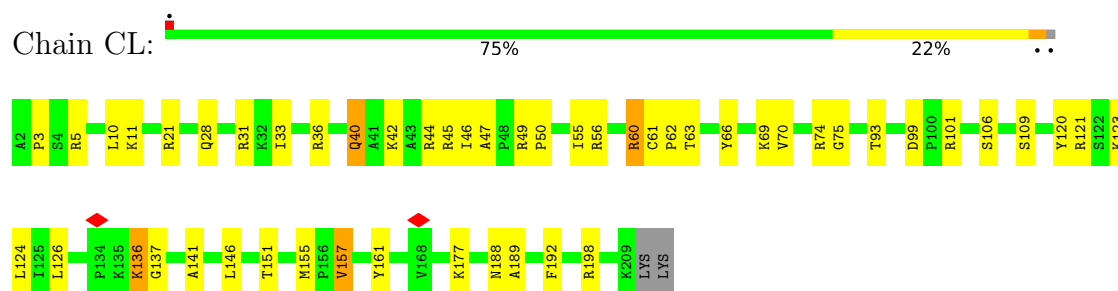
- Molecule 37: 60S ribosomal protein L10a



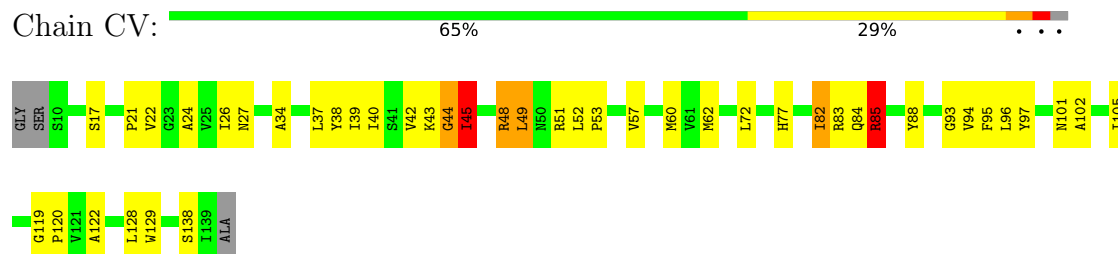
- Molecule 38: 60S ribosomal protein L13a



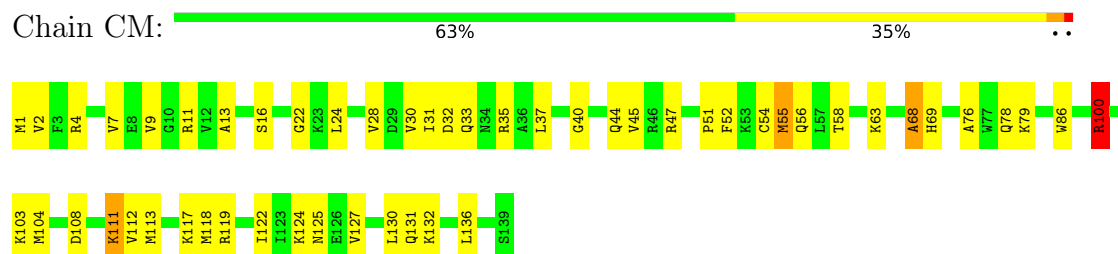
- Molecule 39: 60S ribosomal protein L13



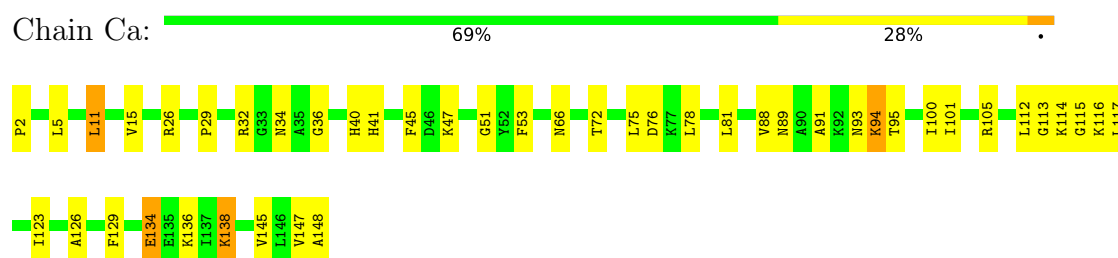
- Molecule 40: 60S ribosomal protein L23



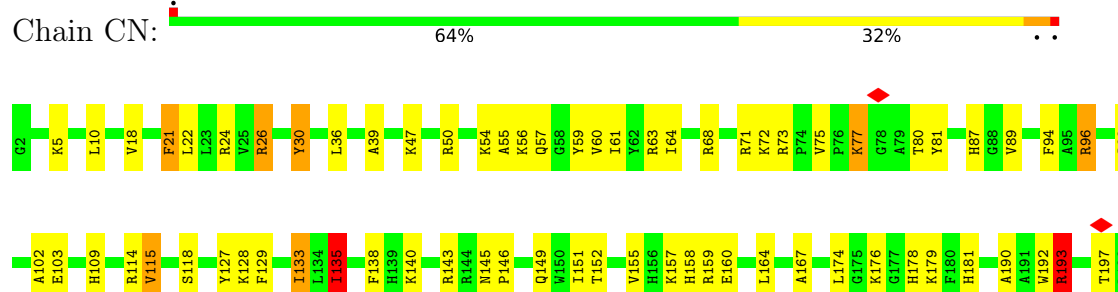
- Molecule 41: 60S ribosomal protein L14



- Molecule 42: 60S ribosomal protein L27a

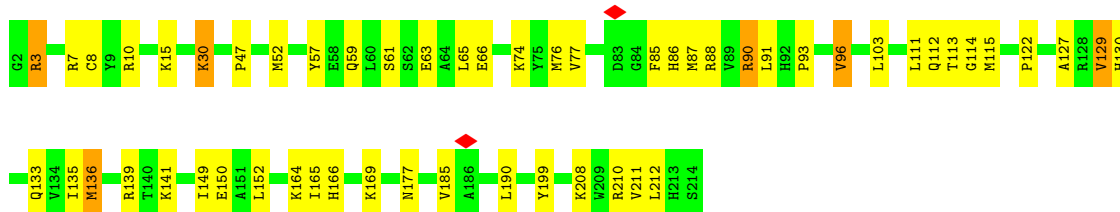
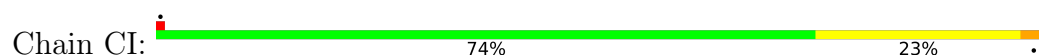


- Molecule 43: 60S ribosomal protein L15

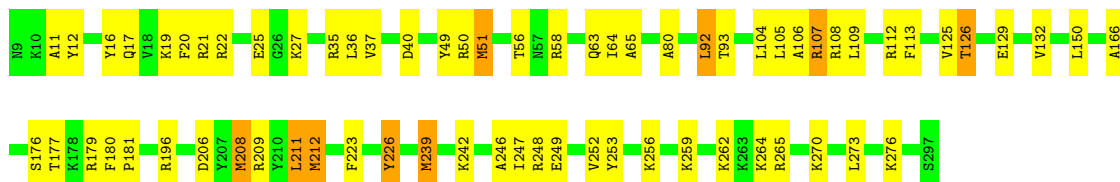
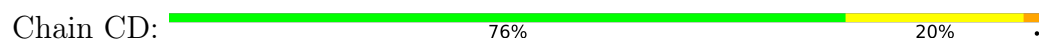




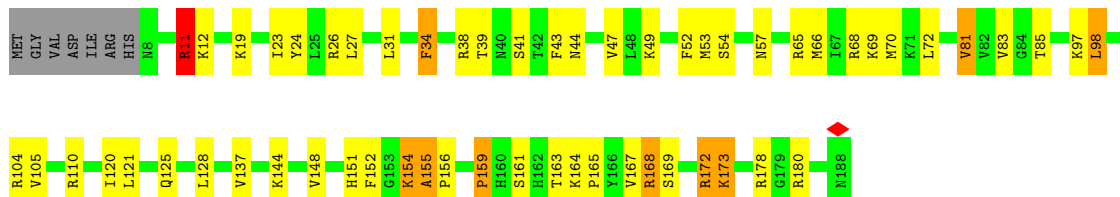
- Molecule 44: 60S ribosomal protein L10-like



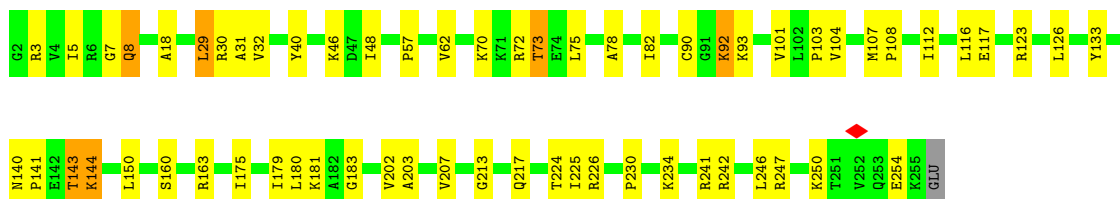
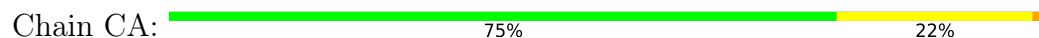
- Molecule 45: 60S ribosomal protein L5



- Molecule 46: 60S ribosomal protein L18

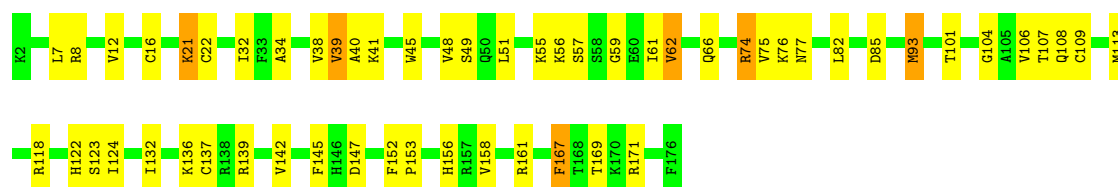


- Molecule 47: 60S ribosomal protein L8



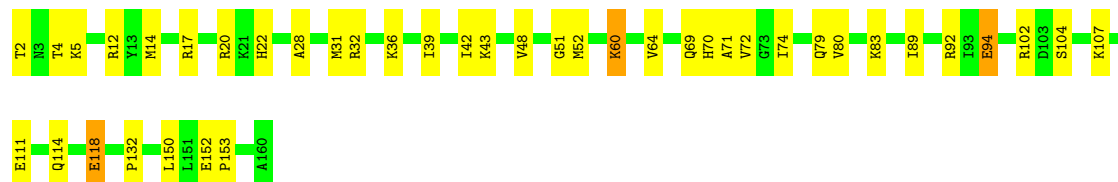
- Molecule 48: 60S ribosomal protein L18a





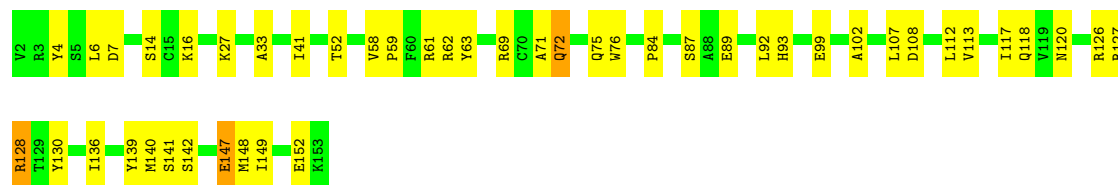
- Molecule 49: 60S ribosomal protein L21

Chain CT: 74% 24% .



- Molecule 50: 60S ribosomal protein L17

Chain CP: 70% 28% .



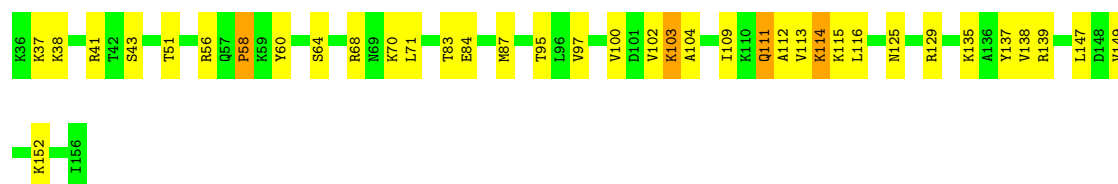
- Molecule 51: 60S ribosomal protein L22

Chain CU: 6% 79% 14% 6% .



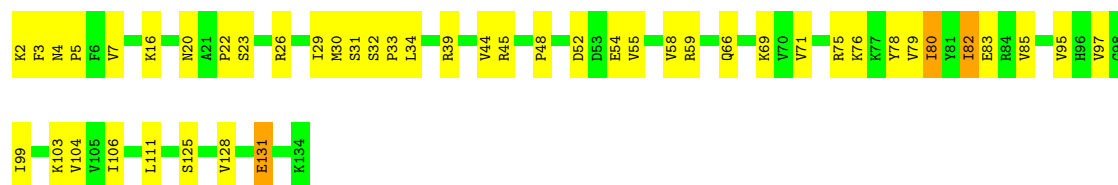
- Molecule 52: 60S ribosomal protein L23a

Chain CX: 69% 27% .

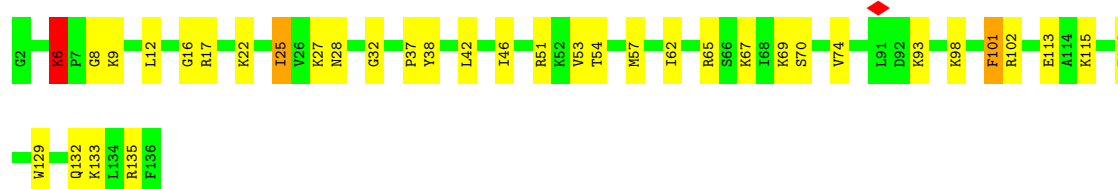
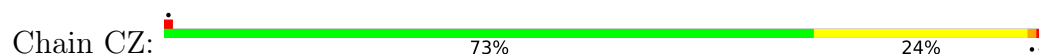


- Molecule 53: 60S ribosomal protein L26

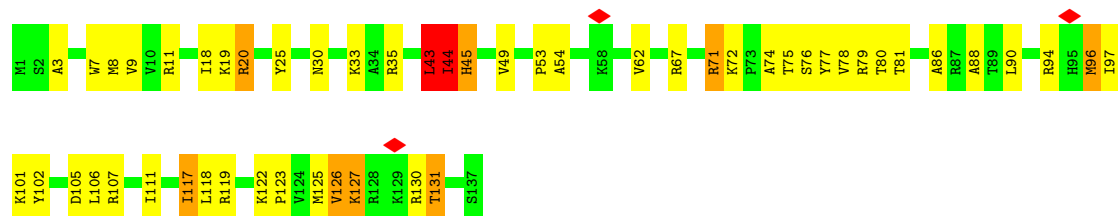
Chain CY: 65% 32% .



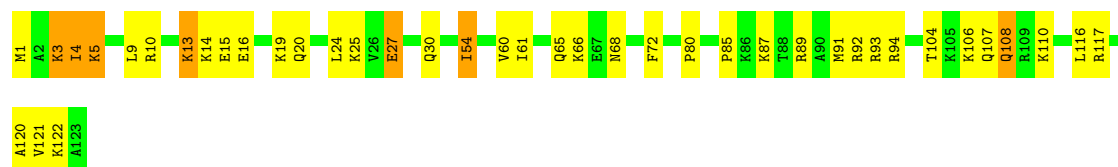
- Molecule 54: 60S ribosomal protein L27



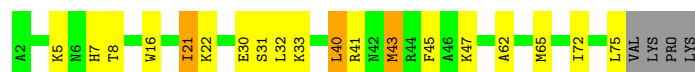
- Molecule 55: 60S ribosomal protein L28



- Molecule 56: 60S ribosomal protein L35

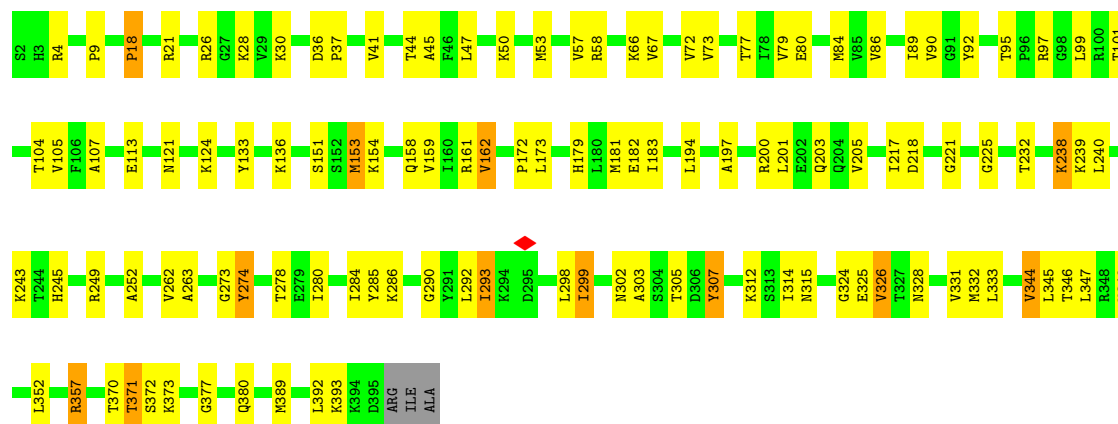


- Molecule 57: 60S ribosomal protein L29



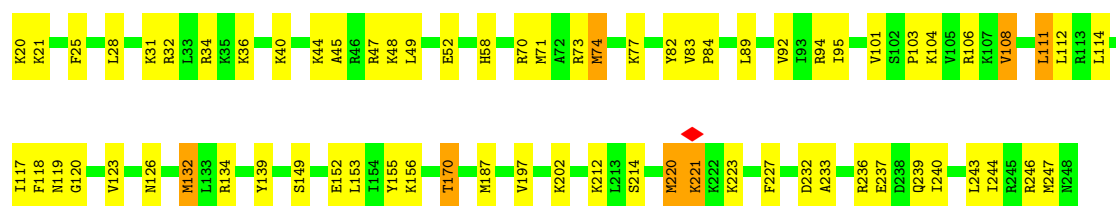
- Molecule 58: 60S ribosomal protein L3





• Molecule 59: 60S ribosomal protein L7

Chain CF: 69% 28% .



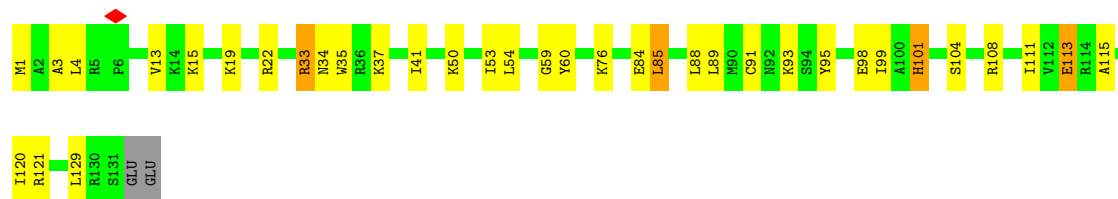
• Molecule 60: 60S ribosomal protein L31

Chain Cd: 73% 22% .



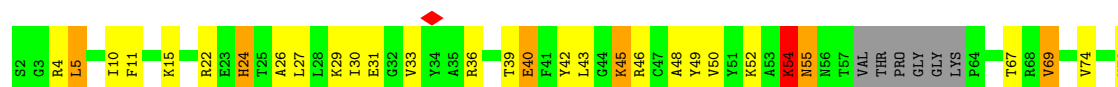
• Molecule 61: 60S ribosomal protein L32

Chain Ce: 71% 24% . .



• Molecule 62: 60S ribosomal protein L35a

Chain Cf: 57% 30% 6% . 6%





- Molecule 63: 60S ribosomal protein L34

Chain Cg: 71% 25% .



- Molecule 64: 60S ribosomal protein L36

Chain Ci: 69% 28% .



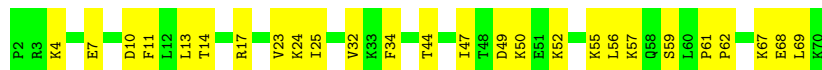
- Molecule 65: 60S ribosomal protein L37

Chain Cj: 86% 12% ..



- Molecule 66: 60S ribosomal protein L38

Chain Ck: 62% 38%



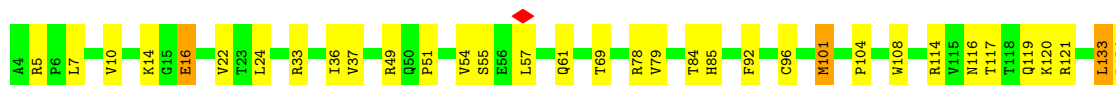
- Molecule 67: 60S ribosomal protein L39

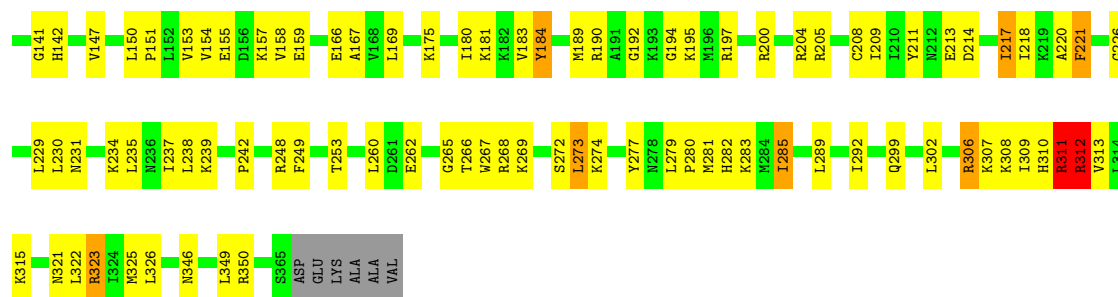
Chain Cl: 68% 28% .



- Molecule 68: 60S ribosomal protein L4

Chain CC: 65% 30% . . .





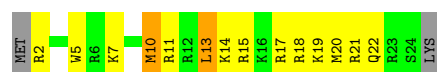
- Molecule 69: 60S ribosomal protein L40

Chain Cm: 65% 31% ..



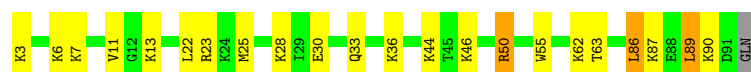
- Molecule 70: 60S ribosomal protein L41

Chain Cn: 36% 48% 8% 8%



- Molecule 71: 60S ribosomal protein L37a

Chain Cp: 74% 21% ..



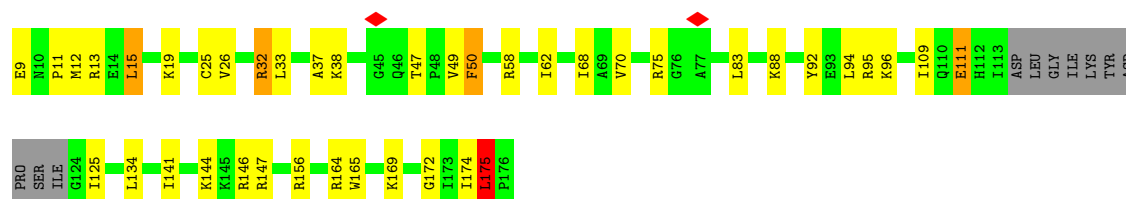
- Molecule 72: 60S ribosomal protein L36a

Chain Co: 70% 21% 9%




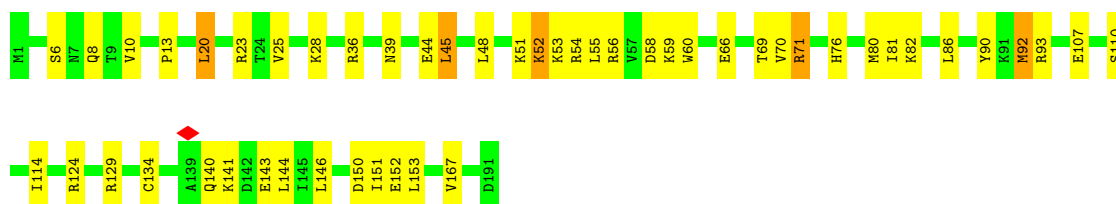
- Molecule 73: 60S ribosomal protein L11

Chain CJ: 70% 21% .. 6%



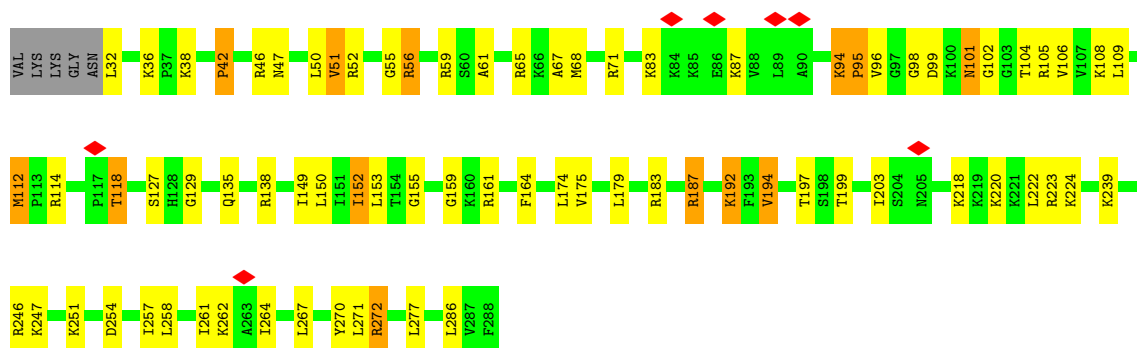
- Molecule 74: 60S ribosomal protein L9

Chain CH:  74% 24% .




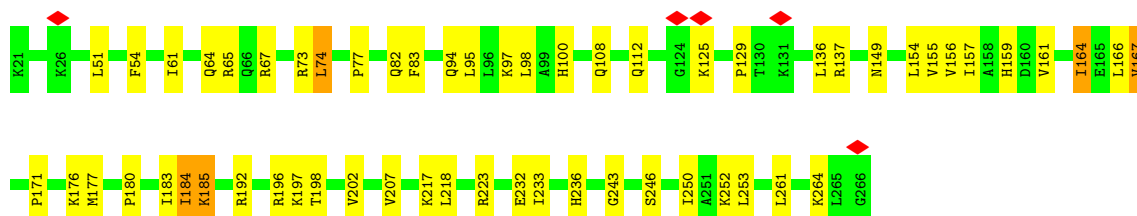
- Molecule 75: 60S ribosomal protein L6

Chain CE:  69% 24% 5% .



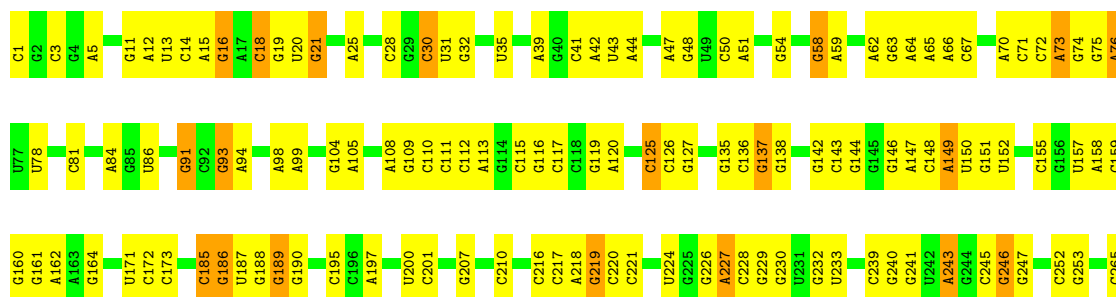
- Molecule 76: 60S ribosomal protein L7a

Chain CG:  76% 22% .

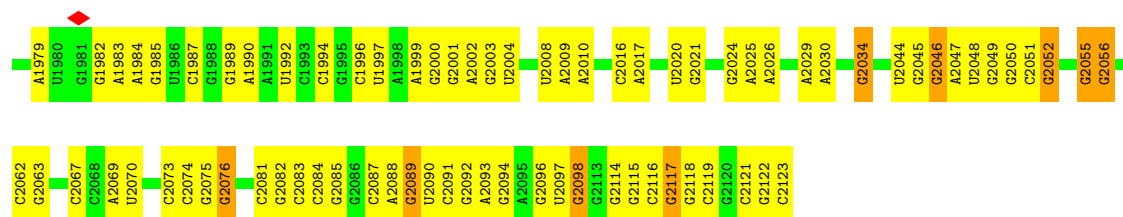


- Molecule 77: LSU-alpha rRNA

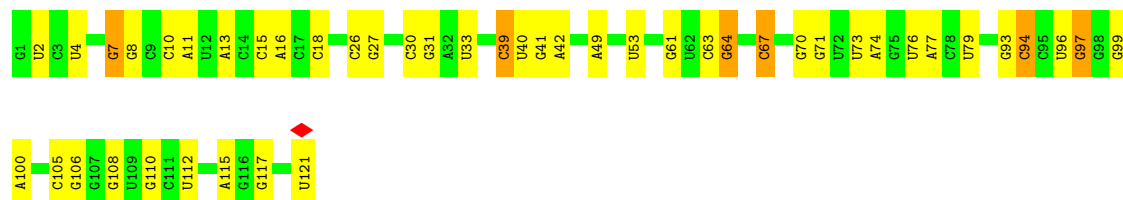
Chain A5:  52% 39% 6% .



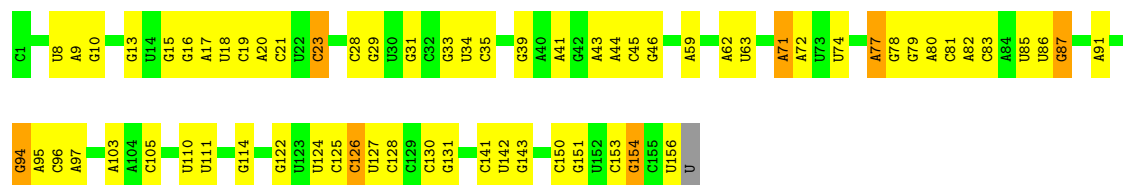




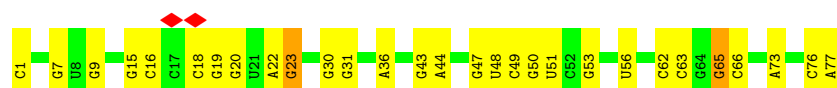
• Molecule 78: 5S ribosomal RNA



• Molecule 79: 5.8S rRNA (157-MER)



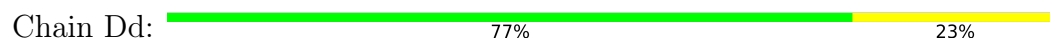
• Molecule 80: tRNA (78-MER)



• Molecule 81: tRNA (77-MER)



• Molecule 82: RNA (5'-R(P*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*U*(MG))-3')





G5023	C4935	A4762	G4680	A4590	U4500	G4392	A4304	U4208	G4099
G5024	G4936	U4763	G4691	C4593	U4500	G4393	G4305	G4209	G4104
G5025	C4937	A4764	G4692	U4594	C4504	A4394	U4306	G4210	A4105
U5026	A4938	G4765	G4693	G4595	U4505	U4395	U4307	G4211	G4106
G5027	C4939	G4766	G4694	G4596	U4512	A4396	U4312	A4212	G4107
G5028	C4940	G4767	G4695	G4597	A4513	A4397	C4314	A4213	G4108
G5031	G4941	G4768	G4696	A4599	A4517	G4405	G4317	A4214	G4109
C4942	C4942	G4771	U4697	G4600	G4516	C4413	A4317	U4218	C4114
A4943	A4943	G4772	C4698	U4601	A4517	A4414	C4318	G4225	G4115
C4944	C4944	G4773	U4699	A4602	A4518	A4415	C4319	G4226	G4116
G4945	G4945	G4774	A4700	G4617	A4519	U4419	G4320	U4227	U4117
U4946	U4946	G4775	C4704	G4618	A4523	U4420	G4321	G4228	U4118
U4947	U4947	G4776	A4705	U4620	G4524	U4421	G4322	U4229	U4119
C4948	C4948	G4777	G4706	C4621	C4525	C4421	A4323	U4230	C4120
G4949	G4949	G4778	A4707	A4622	C4526	A4422	G4324	U4231	G4121
U4950	U4950	G4779	U4708	G4623	G4527	U4423	G4325	U4232	U4122
G4951	G4951	G4780	U4709	G4624	G4528	U4424	G4326	A4233	
G4952	G4952	G4781	C4710	U4625	G4529	U4425	G4327	A4234	
		G4782	G4713	U4626	U4530	G4426	G4328	G4235	
A4955	A4955	G4783	C4714	G4630	U4531	C4427	G4329	G4236	
		G4784	G4715	G4631	G4534	U4432	G4330	U4237	
A4966	A4966	G4785	C4716	U4632	A4535	C4433	G4331	A4238	
A4967	A4967	G4786	G4717	U4633	A4536	U4434	C4332	G4239	
C4968	C4968	G4787	G4718	G4634	C4537	U4435	C4333	G4240	
G4969	G4969	G4788	G4719	U4635	C4538	U4436	U4334	G4142	
C4970	C4970	G4789	G4720	A4636	C4539	U4437	C4335	G4143	
U4971	U4971	G4790	G4721	U4637	G4540	U4438	A4336	G4144	
U4972	U4972	G4791	G4722	U4638	A4544	U4439	A4337	G4151	
C4973	C4973	G4792	A4723	U4639	C4547	U4440	U4338	G4152	
U4974	U4974	G4793	G4724	G4640	A4548	U4441	U4339	G4153	
C4975	C4975	G4794	G4725	U4641	G4549	U4442	U4340	G4154	
U4976	U4976	G4795	G4726	G4642	U4552	U4443	U4341	C4160	
		G4796	G4730	C4643	A4553	U4444	U4342	U4163	
G4981	G4981	G4797	G4731	G4644	U4554	U4445	G4343	G4267	
U4985	U4985	G4798	G4732	C4645	U4555	U4446	C4344	C4164	
		G4799	G4733	G4646	U4556	U4447	U4345	C4165	
U4988	U4988	G4800	G4734	U4647	U4557	G4454	U4346	A4170	
U4989	U4989	G4801	G4735	U4648	C4560	G4455	G4347	C4171	
C4990	C4990	G4802	G4736	A4649	U4561	U4456	A4348	A4172	
U4991	U4991	G4803	G4737	C4650	G4562	U4457	U4349	G4173	
G4992	G4992	G4804	G4738	G4651	G4563	U4458	C4350	U4174	
G4993	G4993	G4805	G4739	C4652	U4564	U4459	U4351	G4175	
		G4806	G4740	G4653	U4565	U4460	U4352	G4180	
G4997	G4997	G4807	G4741	A4654	U4566	U4461	U4353	A4183	
G4998	G4998	G4808	G4742	U4655	U4567	U4462	U4354	G4184	
U5002	U5002	G4809	G4743	U4656	U4568	U4463	G4355	G4185	
U5003	U5003	G4810	G4744	U4657	U4569	U4464	U4356	G4186	
C5004	C5004	G4811	G4745	U4658	U4570	U4465	U4357	U4187	
G5005	G5005	G4812	G4746	A4659	U4571	U4466	U4358	U4188	
U5006	U5006	G4813	G4747	C4660	U4572	U4467	U4359	G4191	
A5007	A5007	G4814	G4748	G4661	U4573	U4468	U4360	G4195	
		G4815	G4749	C4662	U4574	U4469	U4361	G4196	
C5013	C5013	G4816	G4750	G4663	U4575	G4470	U4362	U4295	
A5014	A5014	G4817	G4751	A4664	U4576	U4471	U4363	U4296	
		G4818	G4752	U4665	U4577	U4472	U4364	G4297	
G5017	G5017	G4819	G4753	U4666	U4578	U4473	U4365		
		G4820	G4754	U4667	U4579	U4474	U4366		
		G4821	G4755	U4668	C4582	U4475	U4367		
		G4822	G4756	G4669	U4583	U4476	U4368		
		G4823	G4757	C4670	U4584	U4477	U4369		
		G4824	G4758	G4671	U4585	U4478	U4370		
		G4825	G4759	U4672	U4586	U4479	U4371		
		G4826	G4760	G4673	U4587	U4480	U4372		
		G4827	G4761	U4674	U4588	U4481	U4373		
		G4828	G4762	G4675	U4589	U4482	U4374		
		G4829	G4763	U4676	U4590	U4483	U4375		
		G4830	G4764	U4677	U4591	U4484	U4376		
		G4831	G4765	G4678	C4583	U4485	U4377		
		G4832	G4766	G4679	U4584	U4486	U4378		
		G4833	G4767	U4680	U4585	U4487	U4379		
		G4834	G4768	G4681	U4586	U4488	U4380		
		G4835	G4769	U4682	U4587	U4489	U4381		
		G4836	G4770	U4683	U4588	U4490	U4382		
		G4837	G4771	U4684	U4589	U4491	U4383		
		G4838	G4772	U4685	U4590	U4492	U4384		
		G4839	G4773	U4686	U4591	U4493	U4385		
		G4840	G4774	U4687	U4592	U4494	U4386		
		G4841	G4775	U4688	U4593	U4495	U4387		
		G4842	G4776	U4689	U4594	U4496	U4388		
		G4843	G4777	U4690	U4595		U4389		
		G4844	G4778	U4691	U4596		U4390		
		G4845	G4779	U4692	U4597		U4391		
		G4846	G4780	U4693	U4598		U4392		
		G4847	G4781	U4694	U4599		U4393		
		G4848	G4782	U4695	U4600		U4394		
		G4849	G4783	U4696	U4601		U4395		
		G4850	G4784	U4697	U4602		U4396		
		G4851	G4785	U4698	U4603		U4397		
		G4852	G4786	U4699	U4604		U4398		
		G4853	G4787	U4700	U4605		U4399		
		G4854	G4788	U4701	U4606		U4400		
		G4855	G4789	U4702	U4607		U4401		
		G4856	G4790	U4703	U4608		U4402		
		G4857	G4791	U4704	U4609		U4403		
		G4858	G4792	U4705	U4610		U4404		
		G4859	G4793	U4706	U4611		U4405		
		G4860	G4794	U4707	U4612		U4406		
		G4861	G4795	U4708	U4613		U4407		
		G4862	G4796	U4709	U4614		U4408		
		G4863	G4797	U4710	U4615		U4409		
		G4864	G4798	U4711	U4616		U4410		
		G4865	G4799	U4712	U4617		U4411		
		G4866	G4800	U4713	U4618		U4412		
		G4867	G4801	U4714	U4619		U4413		
		G4868	G4802	U4715	U4620		U4414		
		G4869	G4803	U4716	U4621		U4415		
		G4870	G4804	U4717	U4622		U4416		
		G4871	G4805	U4718	U4623		U4417		
		G4872	G4806	U4719	U4624		U4418		
		G4873	G4807	U4720	U4625		U4419		
		G4874	G4808	U4721	U4626		U4420		
		G4875	G4809	U4722	U4627		U4421		
		G4876	G4810	U4723	U4628		U4422		
		G4877	G4811	U4724	U4629		U4423		
		G4878	G4812	U4725	U4630		U4424		
		G4879	G4813	U4726	U4631		U4425		
		G4880	G4814	U4727	U4632		U4426		
		G4881	G4815	U4728	U4633		U4427		
		G4882	G4816	U4729	U4634		U4428		
		G4883	G4817	U4730	U4635		U4429		
		G4884	G4818	U4731	U4636		U4430		
		G4885	G4819	U4732	U4637		U4431		
		G4886	G4820	U4733	U4638		U4432		
		G4887	G4821	U4734	U4639		U4433		
		G4888	G4822	U4735	U4640		U4434		
		G4889	G4823	U4736	U4641		U4435		
		G4890	G4824	U4737	U4642		U4436		
		G4891	G4825	U4738	U4643		U4437		
		G4892	G4826	U4739	U4644		U4438		
		G4893	G4827	U4740	U4645		U4439		
		G4894	G4828	U4741	U4646		U4440		
		G4895	G4829	U4742	U4647		U4441		
		G4896	G4830	U4743	U4648		U4442		
		G4897	G4831	U4744	U4649		U4443		
		G4898	G4832	U4745	U4650		U4444		
		G4899	G4833	U4746	U4651		U4445		
		G4900	G4834	U4747	U4652		U4446		
		G4901	G4835	U4748	U4653		U4447		
		G4902	G4836	U4749	U4654		U4448		
		G4903	G4837	U4750	U4655		U4449		
		G4904	G4838	U4751	U4656		U4450		
		G4905	G4839	U4752	U4657		U4451		
		G4906	G4840	U4753	U4658		U4452		
		G4907	G4841	U4754	U4659		U4453		
		G4908	G4842	U4755	U4660		U4454		
		G4909	G4843	U4756	U4661		U4455		
		G4910	G4844	U4757	U4662		U4456		
		G4911	G4845	U4758	U4663		U4457		
		G4912	G4846	U4759	U4664		U4458		
		G4913	G4847	U4760	U4665		U4459		
		G4914	G4848	U4761	U4666		U4460		
		G4915	G4849	U4762	U4667		U4461		
		G4916	G4850	U4763	U4668				

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	232230	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 ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.043	Depositor
Minimum map value	-0.014	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.002	Depositor
Map size (Å)	417.99997, 417.99997, 417.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, YYG

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	Ag	0.26	0/2493	0.75	4/3394 (0.1%)
2	AU	0.39	0/832	1.06	2/1117 (0.2%)
3	AK	0.44	0/851	1.22	9/1147 (0.8%)
4	AM	0.33	0/824	0.94	6/1106 (0.5%)
5	AS	0.37	0/1157	1.15	16/1548 (1.0%)
6	Ad	0.30	0/455	0.81	1/603 (0.2%)
7	AR	0.38	0/1031	1.16	9/1383 (0.7%)
8	AP	0.37	0/988	1.05	2/1319 (0.2%)
9	AT	0.30	0/1119	0.85	5/1499 (0.3%)
10	AZ	0.30	0/600	0.78	2/805 (0.2%)
11	Ac	0.28	0/508	0.78	0/680
12	AD	0.35	0/1785	0.98	7/2404 (0.3%)
13	Af	0.33	0/593	0.87	2/786 (0.3%)
14	AF	0.36	0/1531	0.98	11/2059 (0.5%)
15	AQ	0.30	0/1142	0.82	2/1528 (0.1%)
16	B2	0.19	0/42028	0.44	6/65468 (0.0%)
17	AO	0.38	0/987	1.04	6/1322 (0.5%)
18	AX	0.33	0/1116	0.87	4/1490 (0.3%)
19	AN	0.37	0/1226	1.04	8/1649 (0.5%)
20	AL	0.36	0/1311	0.92	3/1751 (0.2%)
21	AB	0.36	0/1774	1.02	17/2372 (0.7%)
22	AA	0.37	0/1648	1.01	8/2241 (0.4%)
23	AV	0.38	0/631	1.05	5/844 (0.6%)
24	AY	0.34	0/1040	1.02	7/1382 (0.5%)
25	Aa	0.33	0/863	0.86	1/1159 (0.1%)
26	Ab	0.30	0/665	0.99	6/891 (0.7%)
27	Ae	0.28	0/424	0.89	0/556
28	AJ	0.32	0/1487	0.92	3/1985 (0.2%)
29	AE	0.29	0/2115	0.84	7/2846 (0.2%)
30	AC	0.35	0/1763	0.89	5/2379 (0.2%)
31	AG	0.28	0/1946	0.75	4/2590 (0.2%)
32	AH	0.32	0/1544	0.92	4/2068 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	AW	0.38	0/1051	1.02	2/1406 (0.1%)
34	AI	0.32	0/1715	0.91	5/2287 (0.2%)
35	CR	0.38	0/1590	1.12	12/2101 (0.6%)
36	CW	0.37	0/1030	0.95	6/1364 (0.4%)
37	Cz	0.60	1/1059 (0.1%)	1.50	25/1420 (1.8%)
38	CO	0.41	0/1666	1.10	12/2228 (0.5%)
39	CL	0.34	0/1713	0.93	7/2293 (0.3%)
40	CV	0.35	0/987	0.97	7/1325 (0.5%)
41	CM	0.43	0/1161	1.14	14/1552 (0.9%)
42	Ca	0.33	0/1191	0.94	3/1591 (0.2%)
43	CN	0.35	0/1746	0.95	3/2338 (0.1%)
44	CI	0.36	0/1751	1.06	6/2340 (0.3%)
45	CD	0.29	0/2398	0.84	5/3210 (0.2%)
46	CQ	0.35	0/1488	1.04	14/1986 (0.7%)
47	CA	0.35	0/1986	0.95	13/2662 (0.5%)
48	CS	0.35	0/1493	0.96	9/2003 (0.4%)
49	CT	0.35	0/1326	0.99	9/1770 (0.5%)
50	CP	0.33	0/1259	0.91	5/1689 (0.3%)
51	CU	0.28	0/897	0.85	6/1201 (0.5%)
52	CX	0.38	0/1011	1.00	5/1356 (0.4%)
53	CY	0.36	0/1124	0.98	4/1494 (0.3%)
54	CZ	0.29	0/1130	0.77	3/1507 (0.2%)
55	Cr	0.44	0/1120	1.24	15/1497 (1.0%)
56	Ch	0.38	0/1031	1.14	9/1361 (0.7%)
57	Cb	0.36	0/613	1.06	4/809 (0.5%)
58	CB	0.32	0/3246	0.86	7/4345 (0.2%)
59	CF	0.35	0/1945	0.91	4/2589 (0.2%)
60	Cd	0.34	0/946	0.93	5/1272 (0.4%)
61	Ce	0.33	0/1096	0.92	2/1461 (0.1%)
62	Cf	0.38	0/855	1.07	7/1141 (0.6%)
63	Cg	0.31	0/916	0.92	4/1220 (0.3%)
64	Ci	0.35	0/851	0.98	3/1125 (0.3%)
65	Cj	0.28	0/741	0.85	1/980 (0.1%)
66	Ck	0.33	0/575	0.88	1/761 (0.1%)
67	Cl	0.43	0/454	1.08	4/599 (0.7%)
68	CC	0.36	0/2936	1.01	17/3943 (0.4%)
69	Cm	0.39	0/427	0.99	2/564 (0.4%)
70	Cn	0.52	0/223	1.28	1/284 (0.4%)
71	Cp	0.39	0/703	0.90	0/934
72	Co	0.36	0/864	1.01	0/1140
73	CJ	0.31	0/1291	0.93	10/1724 (0.6%)
74	CH	0.33	0/1545	0.94	7/2077 (0.3%)
75	CE	0.38	0/2116	1.10	21/2830 (0.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	CG	0.37	0/2006	1.01	6/2697 (0.2%)
77	A5	0.21	0/40908	0.47	13/63750 (0.0%)
78	A7	0.19	0/2880	0.39	0/4489
79	A8	0.21	0/3701	0.47	2/5766 (0.0%)
80	Cc	0.15	0/1836	0.29	0/2859
81	Bb	0.18	0/1530	0.42	0/2382
82	Dd	0.21	0/285	0.57	0/438
83	A6	0.20	0/48889	0.45	13/76116 (0.0%)
All	All	0.27	1/235778 (0.0%)	0.69	505/346647 (0.1%)

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
1	Ag	0	1
2	AU	0	1
4	AM	0	1
7	AR	0	1
8	AP	0	5
13	Af	0	2
14	AF	0	3
15	AQ	0	1
17	AO	0	1
18	AX	0	1
20	AL	0	2
23	AV	0	1
24	AY	0	2
25	Aa	0	1
26	Ab	0	1
27	Ae	0	1
28	AJ	0	1
29	AE	0	4
30	AC	0	3
32	AH	0	2
33	AW	0	1
37	Cz	0	1
38	CO	0	2
39	CL	0	1
40	CV	0	1
41	CM	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
42	Ca	0	2
43	CN	0	3
44	CI	0	2
45	CD	0	3
46	CQ	0	3
47	CA	0	2
51	CU	0	1
53	CY	0	1
55	Cr	0	4
58	CB	0	3
59	CF	0	1
61	Ce	0	1
62	Cf	0	1
65	Cj	0	1
67	Cl	0	1
68	CC	0	11
71	Cp	0	1
72	Co	0	3
73	CJ	0	1
74	CH	0	2
75	CE	0	2
76	CG	0	2
All	All	0	95

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
37	Cz	215	ARG	N-CA	5.21	1.52	1.45

The worst 5 of 505 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	AD	197	LYS	CA-C-N	9.60	138.99	121.70
12	AD	197	LYS	C-N-CA	9.60	138.99	121.70
39	CL	60	ARG	CA-C-N	9.09	134.50	120.68
39	CL	60	ARG	C-N-CA	9.09	134.50	120.68
9	AT	107	LEU	CA-CB-CG	9.02	147.87	116.30

There are no chirality outliers.

5 of 95 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	AM	59	PRO	Peptide
8	AP	27	ASP	Peptide
7	AR	91	LEU	Peptide
2	AU	81	GLN	Peptide
1	Ag	282	GLU	Peptide

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	Ag	2436	0	2393	55	0
2	AU	822	0	887	23	0
3	AK	827	0	854	17	0
4	AM	818	0	848	9	0
5	AS	1139	0	1191	32	0
6	Ad	445	0	442	10	0
7	AR	1019	0	1075	15	0
8	AP	970	0	1017	14	0
9	AT	1101	0	1135	18	0
10	AZ	594	0	653	15	0
11	Ac	506	0	536	8	0
12	AD	1757	0	1853	31	0
13	Af	581	0	599	6	0
14	AF	1509	0	1563	42	0
15	AQ	1124	0	1193	24	0
16	B2	37608	0	18955	321	0
17	AO	975	0	996	26	0
18	AX	1098	0	1167	16	0
19	AN	1202	0	1289	20	0
20	AL	1288	0	1362	15	0
21	AB	1747	0	1829	31	0
22	AA	1611	0	1618	38	0
23	AV	625	0	628	15	0
24	AY	1023	0	1090	23	0
25	Aa	847	0	897	21	0
26	Ab	651	0	672	13	0
27	Ae	419	0	463	6	0
28	AJ	1463	0	1578	27	0
29	AE	2073	0	2181	40	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	AC	1727	0	1814	46	0
31	AG	1923	0	2089	38	0
32	AH	1521	0	1616	26	0
33	AW	1034	0	1080	24	0
34	AI	1686	0	1772	30	0
35	CR	1574	0	1741	42	0
36	CW	1015	0	1079	26	0
37	Cz	1043	0	1080	31	0
38	CO	1634	0	1779	50	0
39	CL	1682	0	1792	33	0
40	CV	973	0	1034	28	0
41	CM	1139	0	1209	27	0
42	Ca	1162	0	1213	26	0
43	CN	1701	0	1749	47	0
44	CI	1711	0	1749	30	0
45	CD	2353	0	2372	40	0
46	CQ	1465	0	1581	30	0
47	CA	1948	0	2049	34	0
48	CS	1453	0	1490	36	0
49	CT	1298	0	1366	21	0
50	CP	1233	0	1263	24	0
51	CU	884	0	893	5	0
52	CX	994	0	1079	17	0
53	CY	1107	0	1193	22	0
54	CZ	1107	0	1182	17	0
55	Cr	1104	0	1189	29	0
56	Ch	1023	0	1160	24	0
57	Cb	603	0	641	10	0
58	CB	3178	0	3314	63	0
59	CF	1910	0	2048	43	0
60	Cd	931	0	980	15	0
61	Ce	1078	0	1177	15	0
62	Cf	838	0	870	27	0
63	Cg	906	0	999	21	0
64	Ci	840	0	929	21	0
65	Cj	726	0	764	7	0
66	Ck	569	0	637	15	0
67	Cl	444	0	483	9	0
68	CC	2882	0	3059	74	0
69	Cm	421	0	458	9	0
70	Cn	222	0	264	10	0
71	Cp	693	0	747	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
72	Co	851	0	922	18	0
73	CJ	1271	0	1304	22	0
74	CH	1526	0	1605	24	0
75	CE	2076	0	2276	44	0
76	CG	1973	0	2128	35	0
77	A5	36611	0	18460	298	0
78	A7	2578	0	1306	25	0
79	A8	3314	0	1683	27	0
80	Cc	1644	0	837	8	0
81	Bb	1407	0	721	5	0
82	Dd	260	0	131	2	0
83	A6	43784	0	21891	352	0
84	Bb	1	0	0	0	0
84	Cc	1	0	0	0	0
84	Dd	1	0	0	0	0
85	A6	1	0	0	0	0
85	B2	3	0	0	0	0
85	Bb	5	0	0	0	0
85	Cc	5	0	0	0	0
85	Dd	1	0	0	0	0
All	All	219326	0	161211	2571	0

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

The worst 5 of 2571 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)
16:B2:1288:U:H3	16:B2:1311:C:N4	1.49	1.07
16:B2:677:G:N2	16:B2:1028:A:H62	1.58	1.00
16:B2:677:G:H21	16:B2:1028:A:N6	1.60	1.00
16:B2:562:U:H3	16:B2:587:A:H62	1.06	0.98
83:A6:4344:U:H3	83:A6:4368:G:H1	1.10	0.98

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Ag	311/313 (99%)	268 (86%)	41 (13%)	2 (1%)	21	52
2	AU	102/104 (98%)	90 (88%)	9 (9%)	3 (3%)	3	21
3	AK	96/98 (98%)	68 (71%)	24 (25%)	4 (4%)	2	14
4	AM	102/124 (82%)	83 (81%)	16 (16%)	3 (3%)	3	21
5	AS	135/137 (98%)	120 (89%)	14 (10%)	1 (1%)	18	49
6	Ad	51/53 (96%)	41 (80%)	10 (20%)	0	100	100
7	AR	124/126 (98%)	107 (86%)	15 (12%)	2 (2%)	7	31
8	AP	115/127 (91%)	90 (78%)	21 (18%)	4 (4%)	3	18
9	AT	139/141 (99%)	130 (94%)	8 (6%)	1 (1%)	18	49
10	AZ	72/75 (96%)	63 (88%)	9 (12%)	0	100	100
11	Ac	62/64 (97%)	54 (87%)	8 (13%)	0	100	100
12	AD	224/227 (99%)	194 (87%)	27 (12%)	3 (1%)	9	35
13	Af	69/71 (97%)	52 (75%)	14 (20%)	3 (4%)	2	14
14	AF	189/191 (99%)	165 (87%)	23 (12%)	1 (0%)	24	55
15	AQ	139/141 (99%)	122 (88%)	16 (12%)	1 (1%)	18	49
17	AO	128/136 (94%)	104 (81%)	23 (18%)	1 (1%)	16	45
18	AX	139/142 (98%)	132 (95%)	6 (4%)	1 (1%)	18	49
19	AN	147/150 (98%)	134 (91%)	12 (8%)	1 (1%)	18	49
20	AL	155/158 (98%)	133 (86%)	21 (14%)	1 (1%)	21	52
21	AB	213/215 (99%)	189 (89%)	21 (10%)	3 (1%)	9	33
22	AA	201/208 (97%)	160 (80%)	38 (19%)	3 (2%)	8	32
23	AV	80/82 (98%)	65 (81%)	14 (18%)	1 (1%)	9	35
24	AY	124/126 (98%)	105 (85%)	15 (12%)	4 (3%)	3	19
25	Aa	105/107 (98%)	88 (84%)	15 (14%)	2 (2%)	6	28
26	Ab	81/84 (96%)	70 (86%)	11 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	Ae	50/59 (85%)	41 (82%)	8 (16%)	1 (2%)	6	27
28	AJ	173/182 (95%)	156 (90%)	16 (9%)	1 (1%)	21	52
29	AE	259/263 (98%)	228 (88%)	29 (11%)	2 (1%)	16	45
30	AC	221/226 (98%)	204 (92%)	17 (8%)	0	100	100
31	AG	235/237 (99%)	217 (92%)	18 (8%)	0	100	100
32	AH	187/190 (98%)	159 (85%)	24 (13%)	4 (2%)	5	26
33	AW	127/129 (98%)	110 (87%)	17 (13%)	0	100	100
34	AI	204/206 (99%)	172 (84%)	27 (13%)	5 (2%)	4	23
35	CR	186/189 (98%)	173 (93%)	13 (7%)	0	100	100
36	CW	122/124 (98%)	108 (88%)	13 (11%)	1 (1%)	16	45
37	Cz	123/217 (57%)	85 (69%)	32 (26%)	6 (5%)	1	12
38	CO	197/202 (98%)	174 (88%)	20 (10%)	3 (2%)	8	32
39	CL	206/210 (98%)	177 (86%)	27 (13%)	2 (1%)	12	40
40	CV	128/133 (96%)	122 (95%)	5 (4%)	1 (1%)	16	45
41	CM	137/139 (99%)	123 (90%)	14 (10%)	0	100	100
42	Ca	145/147 (99%)	120 (83%)	22 (15%)	3 (2%)	5	26
43	CN	201/203 (99%)	180 (90%)	21 (10%)	0	100	100
44	CI	211/213 (99%)	190 (90%)	20 (10%)	1 (0%)	24	55
45	CD	287/289 (99%)	257 (90%)	29 (10%)	1 (0%)	36	65
46	CQ	179/188 (95%)	157 (88%)	18 (10%)	4 (2%)	5	26
47	CA	252/255 (99%)	234 (93%)	18 (7%)	0	100	100
48	CS	173/175 (99%)	153 (88%)	19 (11%)	1 (1%)	21	52
49	CT	157/159 (99%)	143 (91%)	14 (9%)	0	100	100
50	CP	150/152 (99%)	141 (94%)	8 (5%)	1 (1%)	18	49
51	CU	101/112 (90%)	90 (89%)	11 (11%)	0	100	100
52	CX	119/121 (98%)	104 (87%)	13 (11%)	2 (2%)	7	30
53	CY	131/133 (98%)	123 (94%)	8 (6%)	0	100	100
54	CZ	133/135 (98%)	124 (93%)	9 (7%)	0	100	100
55	Cr	135/137 (98%)	103 (76%)	28 (21%)	4 (3%)	3	20
56	Ch	121/123 (98%)	104 (86%)	15 (12%)	2 (2%)	7	30
57	Cb	72/78 (92%)	64 (89%)	7 (10%)	1 (1%)	9	33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
58	CB	392/397 (99%)	357 (91%)	30 (8%)	5 (1%)	9	35
59	CF	227/229 (99%)	209 (92%)	16 (7%)	2 (1%)	14	43
60	Cd	111/113 (98%)	99 (89%)	10 (9%)	2 (2%)	6	29
61	Ce	129/133 (97%)	117 (91%)	12 (9%)	0	100	100
62	Cf	99/109 (91%)	88 (89%)	10 (10%)	1 (1%)	12	40
63	Cg	112/114 (98%)	101 (90%)	11 (10%)	0	100	100
64	Ci	101/103 (98%)	88 (87%)	12 (12%)	1 (1%)	12	40
65	Cj	87/90 (97%)	75 (86%)	11 (13%)	1 (1%)	11	39
66	Ck	67/69 (97%)	60 (90%)	6 (9%)	1 (2%)	8	32
67	Cl	48/50 (96%)	42 (88%)	6 (12%)	0	100	100
68	CC	360/368 (98%)	300 (83%)	53 (15%)	7 (2%)	6	28
69	Cm	49/52 (94%)	48 (98%)	1 (2%)	0	100	100
70	Cn	21/25 (84%)	21 (100%)	0	0	100	100
71	Cp	87/90 (97%)	80 (92%)	7 (8%)	0	100	100
72	Co	102/105 (97%)	80 (78%)	17 (17%)	5 (5%)	1	12
73	CJ	154/168 (92%)	143 (93%)	11 (7%)	0	100	100
74	CH	189/191 (99%)	175 (93%)	13 (7%)	1 (0%)	24	55
75	CE	255/262 (97%)	206 (81%)	40 (16%)	9 (4%)	3	18
76	CG	244/246 (99%)	217 (89%)	25 (10%)	2 (1%)	16	45
All	All	11259/11640 (97%)	9869 (88%)	1262 (11%)	128 (1%)	14	39

5 of 128 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	Ag	282	GLU
2	AU	107	GLU
3	AK	2	LEU
3	AK	30	PRO
3	AK	43	LEU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Ag	272/272 (100%)	253 (93%)	19 (7%)	14	41
2	AU	94/94 (100%)	92 (98%)	2 (2%)	47	67
3	AK	89/89 (100%)	85 (96%)	4 (4%)	24	53
4	AM	89/104 (86%)	87 (98%)	2 (2%)	45	66
5	AS	119/119 (100%)	115 (97%)	4 (3%)	32	59
6	Ad	47/47 (100%)	39 (83%)	8 (17%)	2	10
7	AR	114/114 (100%)	108 (95%)	6 (5%)	20	49
8	AP	106/116 (91%)	102 (96%)	4 (4%)	29	57
9	AT	112/112 (100%)	104 (93%)	8 (7%)	13	40
10	AZ	66/66 (100%)	62 (94%)	4 (6%)	17	45
11	Ac	57/57 (100%)	54 (95%)	3 (5%)	20	49
12	AD	189/190 (100%)	178 (94%)	11 (6%)	18	47
13	Af	64/64 (100%)	61 (95%)	3 (5%)	23	52
14	AF	161/161 (100%)	152 (94%)	9 (6%)	19	47
15	AQ	117/117 (100%)	112 (96%)	5 (4%)	26	54
17	AO	101/106 (95%)	92 (91%)	9 (9%)	9	32
18	AX	113/114 (99%)	104 (92%)	9 (8%)	11	36
19	AN	130/130 (100%)	125 (96%)	5 (4%)	29	57
20	AL	141/142 (99%)	132 (94%)	9 (6%)	16	44
21	AB	196/196 (100%)	189 (96%)	7 (4%)	31	58
22	AA	171/174 (98%)	165 (96%)	6 (4%)	32	58
23	AV	66/66 (100%)	60 (91%)	6 (9%)	9	31
24	AY	108/108 (100%)	102 (94%)	6 (6%)	19	47
25	Aa	90/90 (100%)	83 (92%)	7 (8%)	11	36
26	Ab	75/76 (99%)	73 (97%)	2 (3%)	39	63
27	Ae	43/48 (90%)	42 (98%)	1 (2%)	44	66
28	AJ	156/157 (99%)	149 (96%)	7 (4%)	24	53
29	AE	224/225 (100%)	211 (94%)	13 (6%)	18	47
30	AC	187/190 (98%)	173 (92%)	14 (8%)	12	38
31	AG	207/207 (100%)	198 (96%)	9 (4%)	26	54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	AH	169/170 (99%)	161 (95%)	8 (5%)	23	52
33	AW	112/112 (100%)	103 (92%)	9 (8%)	11	36
34	AI	178/178 (100%)	168 (94%)	10 (6%)	19	47
35	CR	167/168 (99%)	162 (97%)	5 (3%)	36	61
36	CW	103/103 (100%)	98 (95%)	5 (5%)	22	51
37	Cz	116/196 (59%)	111 (96%)	5 (4%)	26	54
38	CO	171/173 (99%)	161 (94%)	10 (6%)	18	47
39	CL	174/176 (99%)	165 (95%)	9 (5%)	21	49
40	CV	101/102 (99%)	94 (93%)	7 (7%)	14	41
41	CM	118/118 (100%)	111 (94%)	7 (6%)	18	46
42	Ca	120/120 (100%)	112 (93%)	8 (7%)	15	42
43	CN	171/171 (100%)	153 (90%)	18 (10%)	6	25
44	CI	180/180 (100%)	171 (95%)	9 (5%)	22	50
45	CD	243/243 (100%)	233 (96%)	10 (4%)	27	55
46	CQ	159/165 (96%)	148 (93%)	11 (7%)	14	41
47	CA	196/197 (100%)	189 (96%)	7 (4%)	31	58
48	CS	156/156 (100%)	148 (95%)	8 (5%)	21	50
49	CT	139/139 (100%)	131 (94%)	8 (6%)	18	47
50	CP	133/133 (100%)	120 (90%)	13 (10%)	7	28
51	CU	100/102 (98%)	96 (96%)	4 (4%)	28	56
52	CX	109/109 (100%)	103 (94%)	6 (6%)	19	48
53	CY	123/123 (100%)	108 (88%)	15 (12%)	5	19
54	CZ	117/117 (100%)	108 (92%)	9 (8%)	12	37
55	Cr	121/121 (100%)	111 (92%)	10 (8%)	10	34
56	Ch	110/110 (100%)	106 (96%)	4 (4%)	31	58
57	Cb	62/66 (94%)	60 (97%)	2 (3%)	34	60
58	CB	343/345 (99%)	329 (96%)	14 (4%)	27	55
59	CF	198/198 (100%)	186 (94%)	12 (6%)	17	45
60	Cd	102/102 (100%)	95 (93%)	7 (7%)	14	41
61	Ce	117/119 (98%)	102 (87%)	15 (13%)	4	18
62	Cf	84/88 (96%)	78 (93%)	6 (7%)	13	40

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
63	Cg	98/98 (100%)	92 (94%)	6 (6%)	17	45
64	Ci	87/87 (100%)	83 (95%)	4 (5%)	24	53
65	Cj	74/75 (99%)	72 (97%)	2 (3%)	39	63
66	Ck	64/64 (100%)	61 (95%)	3 (5%)	23	52
67	Cl	47/47 (100%)	44 (94%)	3 (6%)	16	44
68	CC	301/305 (99%)	289 (96%)	12 (4%)	28	56
69	Cm	47/48 (98%)	45 (96%)	2 (4%)	26	54
70	Cn	22/24 (92%)	19 (86%)	3 (14%)	3	16
71	Cp	73/74 (99%)	68 (93%)	5 (7%)	14	42
72	Co	92/93 (99%)	87 (95%)	5 (5%)	20	49
73	CJ	133/142 (94%)	125 (94%)	8 (6%)	17	46
74	CH	170/170 (100%)	163 (96%)	7 (4%)	27	55
75	CE	228/232 (98%)	216 (95%)	12 (5%)	20	49
76	CG	209/209 (100%)	201 (96%)	8 (4%)	29	57
All	All	9841/10019 (98%)	9288 (94%)	553 (6%)	21	47

5 of 553 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
61	Ce	85	LEU
63	Cg	38	VAL
61	Ce	54	LEU
73	CJ	50	PHE
31	AG	97	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 120 such sidechains are listed below:

Mol	Chain	Res	Type
35	CR	40	GLN
69	Cm	87	GLN
45	CD	63	GLN
68	CC	343	GLN
76	CG	153	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
16	B2	1747/1796 (97%)	503 (28%)	40 (2%)
77	A5	1681/1778 (94%)	521 (30%)	62 (3%)
78	A7	120/121 (99%)	26 (21%)	0
79	A8	155/157 (98%)	38 (24%)	3 (1%)
80	Cc	76/77 (98%)	18 (23%)	0
81	Bb	63/76 (82%)	24 (38%)	0
82	Dd	12/13 (92%)	2 (16%)	0
83	A6	2004/2108 (95%)	570 (28%)	56 (2%)
All	All	5858/6126 (95%)	1702 (29%)	161 (2%)

5 of 1702 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
16	B2	2	A
16	B2	3	C
16	B2	4	C
16	B2	5	U
16	B2	25	A

5 of 161 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
83	A6	2661	U
83	A6	4713	G
83	A6	3672	G
83	A6	4036	G
83	A6	4889	G

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

1 non-standard protein/DNA/RNA residue is 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	$\# Z > 2$
81	YYG	Bb	37	81,84	38,42,43	0.58	0	45,62,65	1.30	8 (17%)

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
81	YYG	Bb	37	81,84	-	10/24/42/43	0/4/4/4

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(°)
81	Bb	37	YYG	O6-C6-N1	3.28	124.56	119.87
81	Bb	37	YYG	C5-C4-N3	-3.21	121.38	123.99
81	Bb	37	YYG	N9-C4-N3	2.90	134.14	129.45
81	Bb	37	YYG	C2-N1-C12	-2.63	105.20	109.94
81	Bb	37	YYG	C3-N3-C4	2.61	128.17	123.11

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
81	Bb	37	YYG	C14-C15-N20-C21
81	Bb	37	YYG	O23-C21-N20-C15
81	Bb	37	YYG	N20-C21-O23-C24
81	Bb	37	YYG	O22-C21-O23-C24
81	Bb	37	YYG	C15-C16-O18-C19

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
81	Bb	37	YYG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
77	A5	5
16	B2	4
83	A6	4

The worst 5 of 13 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A5	2098:G	O3'	2113:G	P	29.39
1	B2	755:C	O3'	785:C	P	18.43
1	A6	3988:C	O3'	4012:G	P	18.21
1	A5	763:C	O3'	888:G	P	18.02
1	B2	1761:U	O3'	1769:C	P	17.36

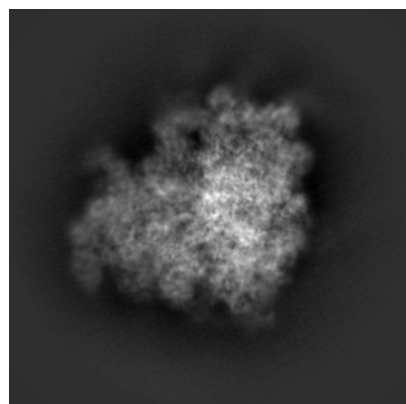
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72482. These allow visual inspection of the internal detail of the map and identification of artifacts.

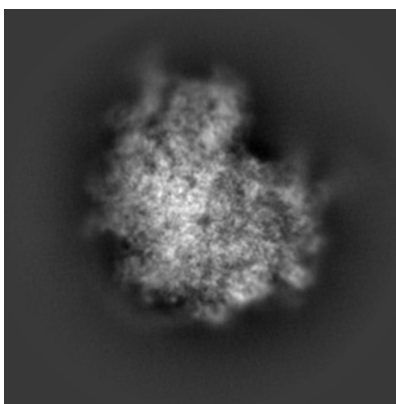
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

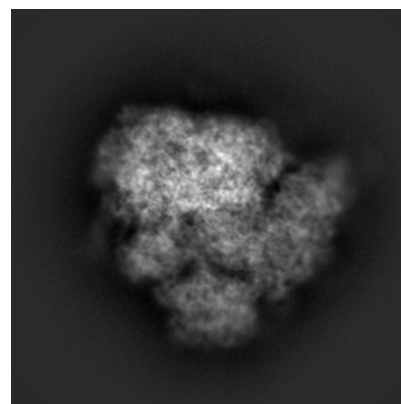
6.1.1 Primary map



X

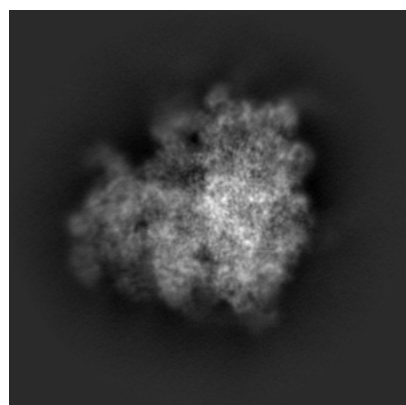


Y

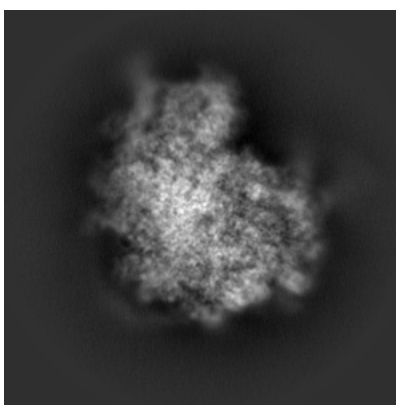


Z

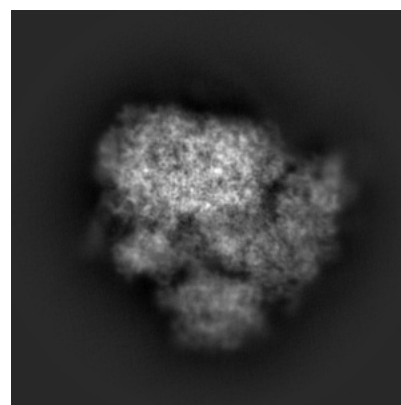
6.1.2 Raw map



X



Y

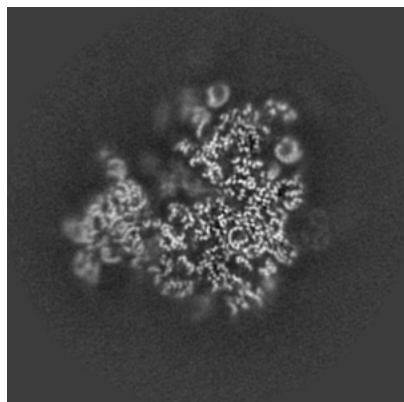


Z

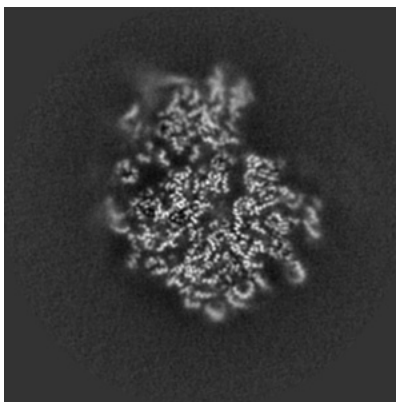
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

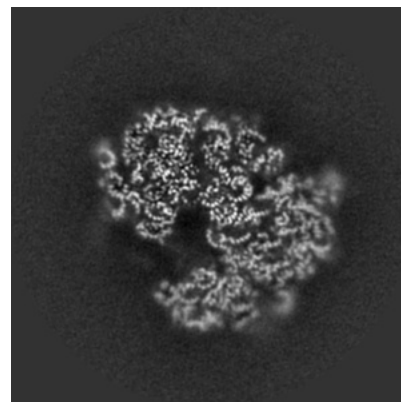
6.2.1 Primary map



X Index: 200

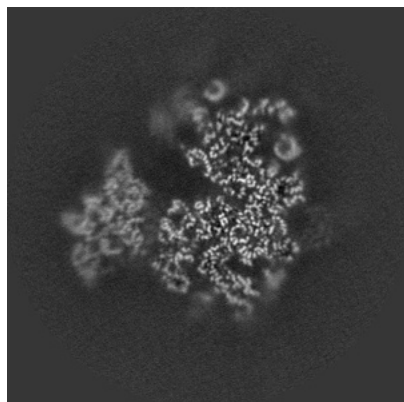


Y Index: 200

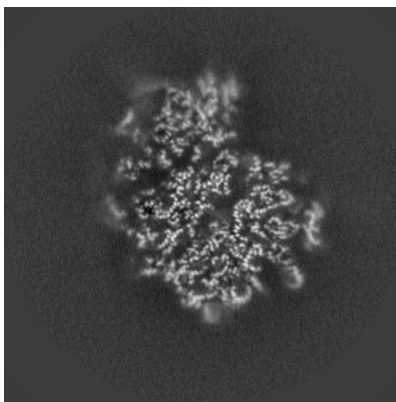


Z Index: 200

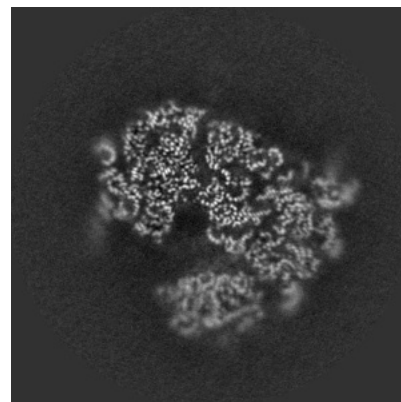
6.2.2 Raw map



X Index: 200



Y Index: 200

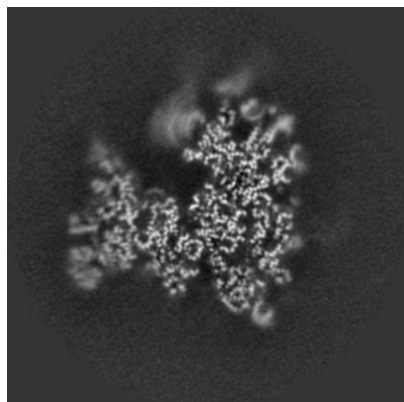


Z Index: 200

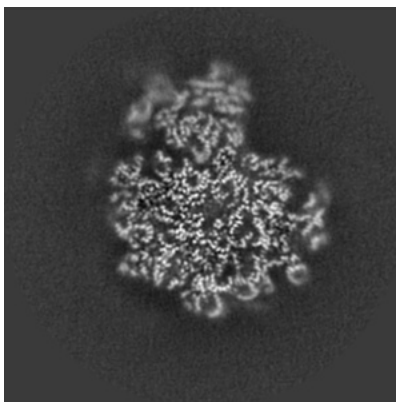
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

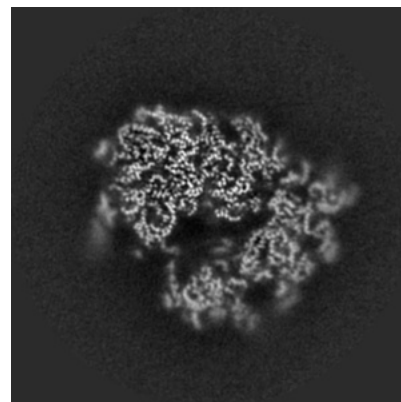
6.3.1 Primary map



X Index: 219

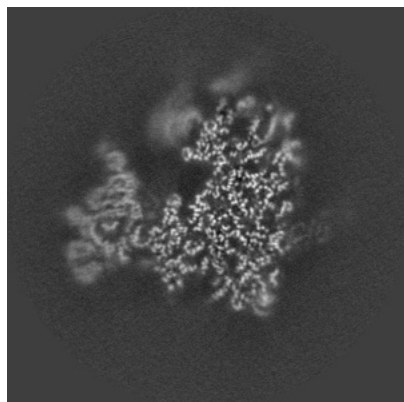


Y Index: 208

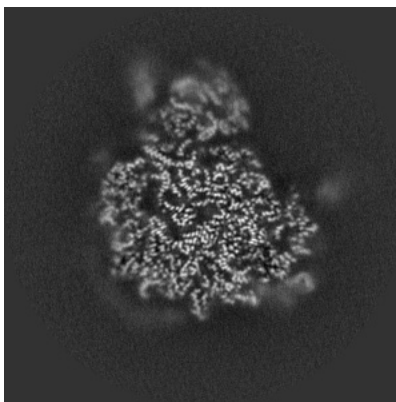


Z Index: 209

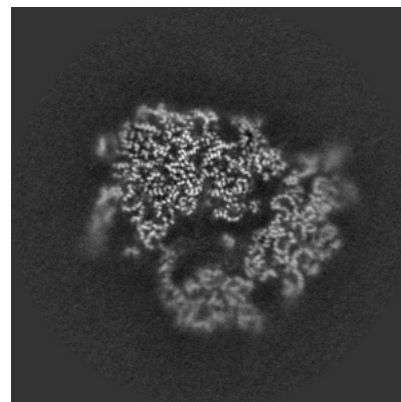
6.3.2 Raw map



X Index: 213



Y Index: 227

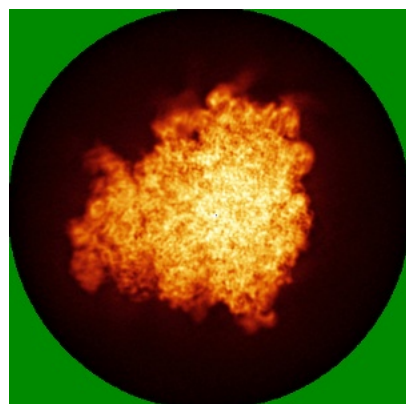


Z Index: 210

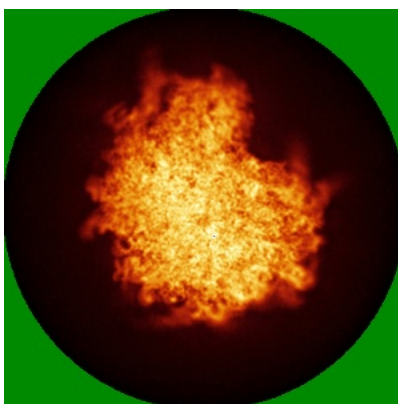
The images above show the largest variance slices of the map in three orthogonal directions.

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

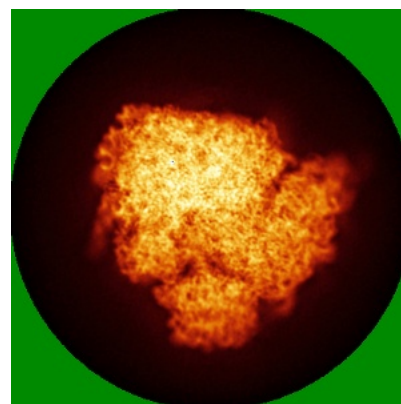
6.4.1 Primary map



X

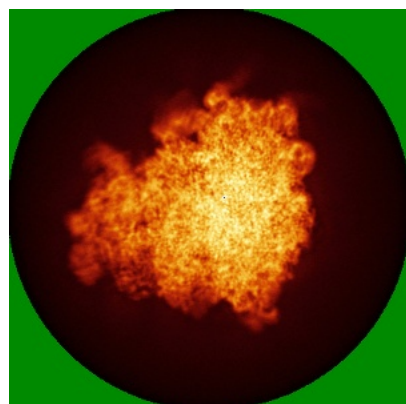


Y

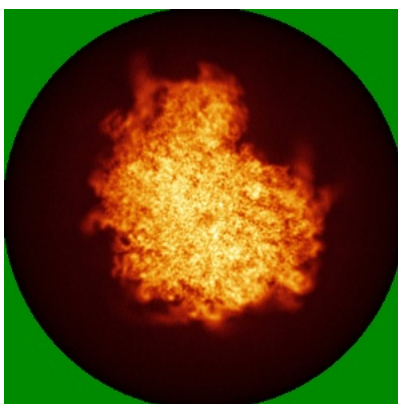


Z

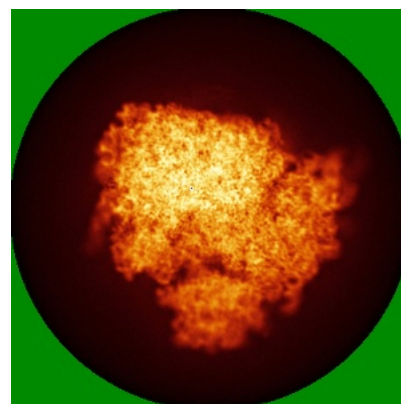
6.4.2 Raw map



X



Y

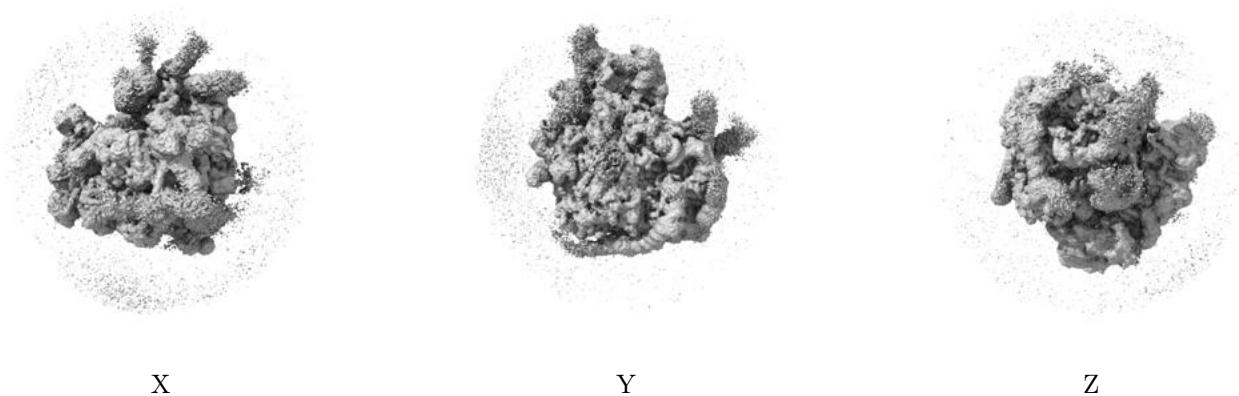


Z

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

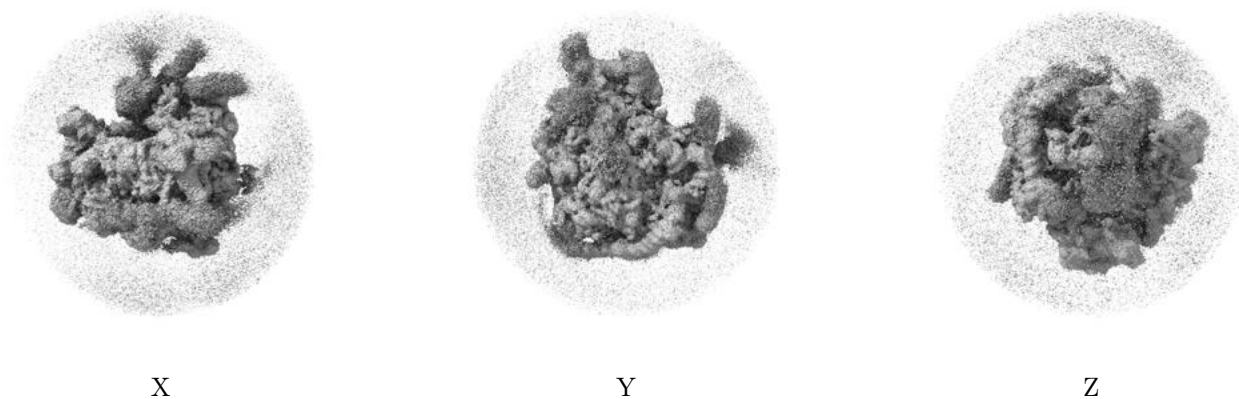
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.002. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

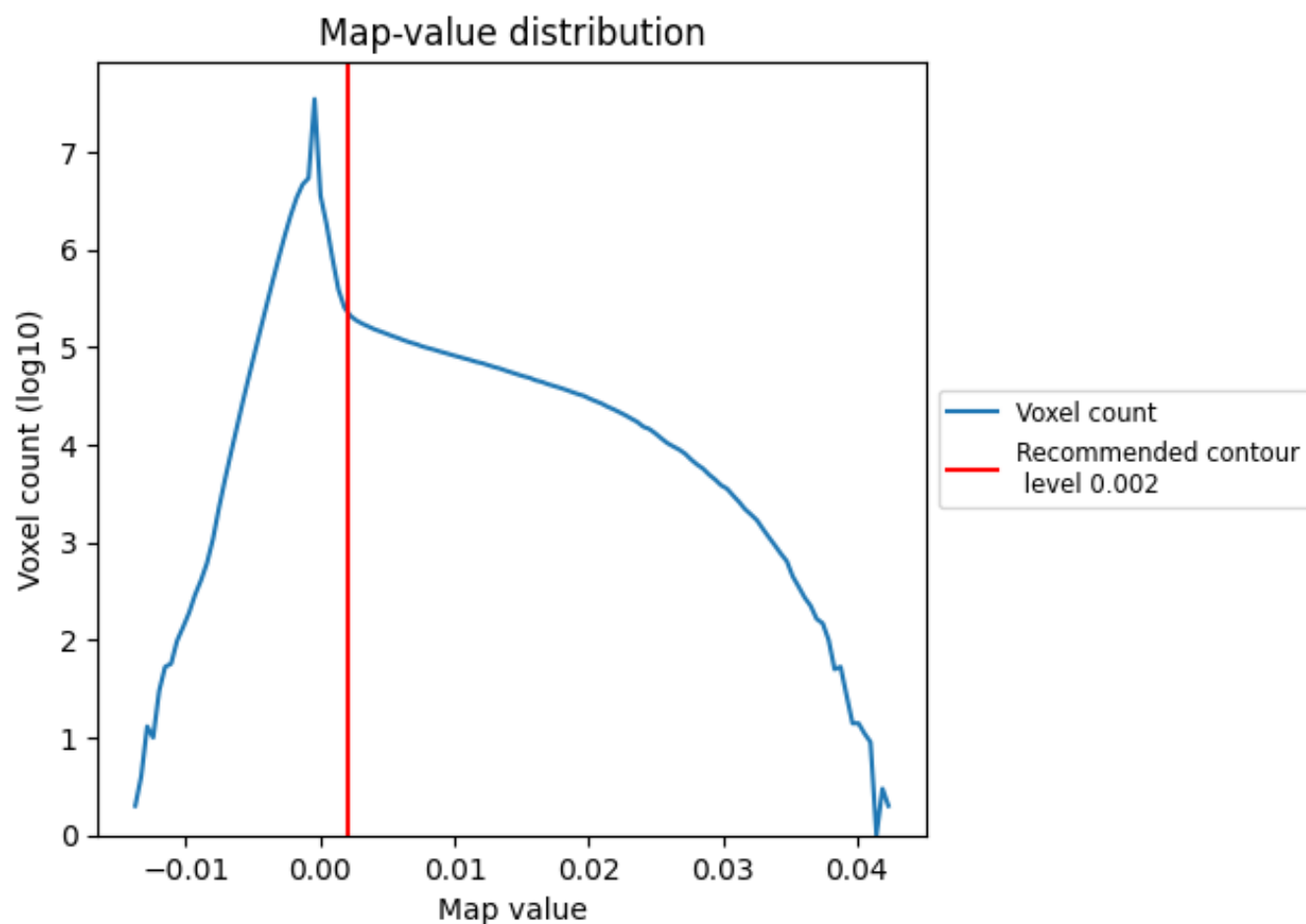
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

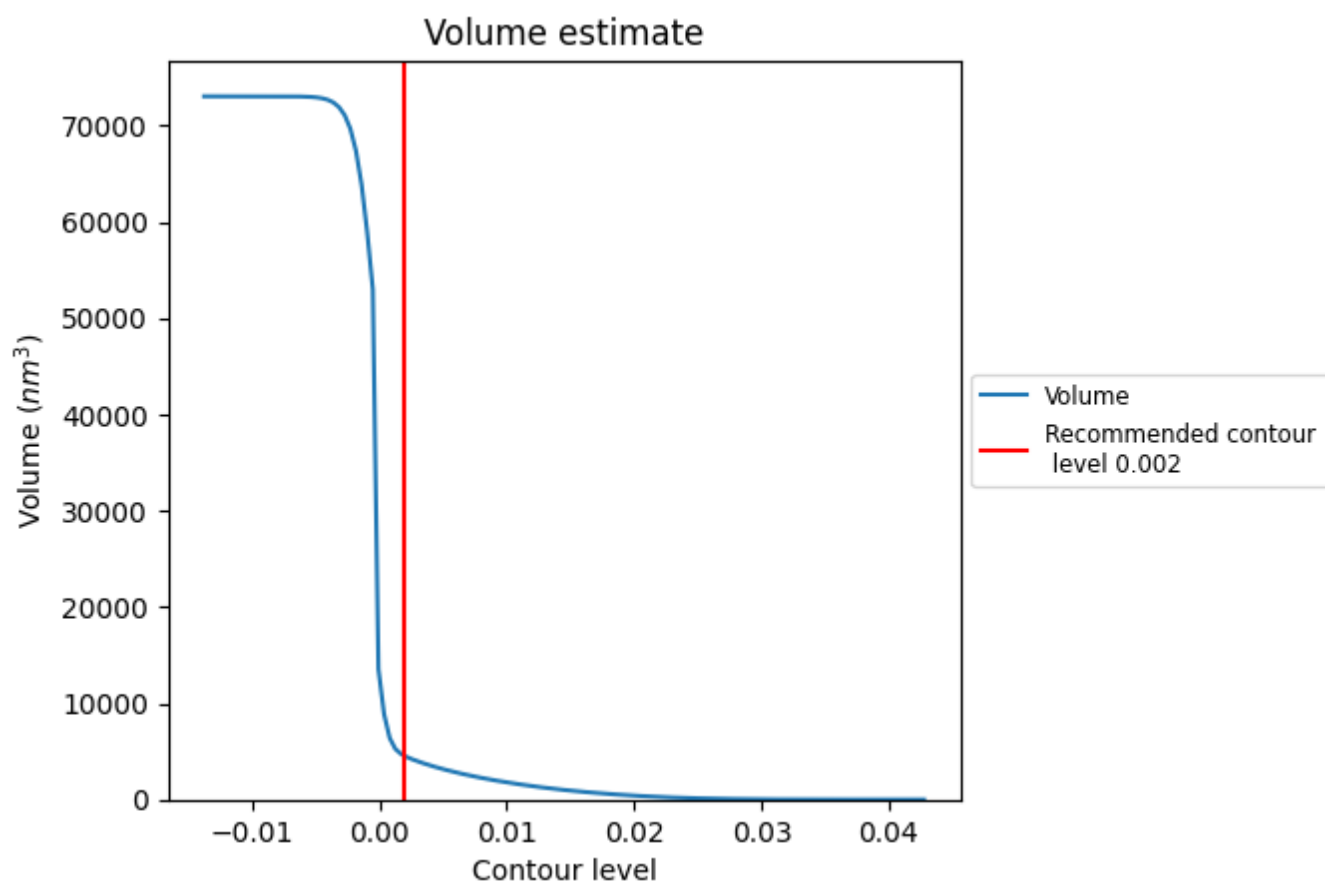
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

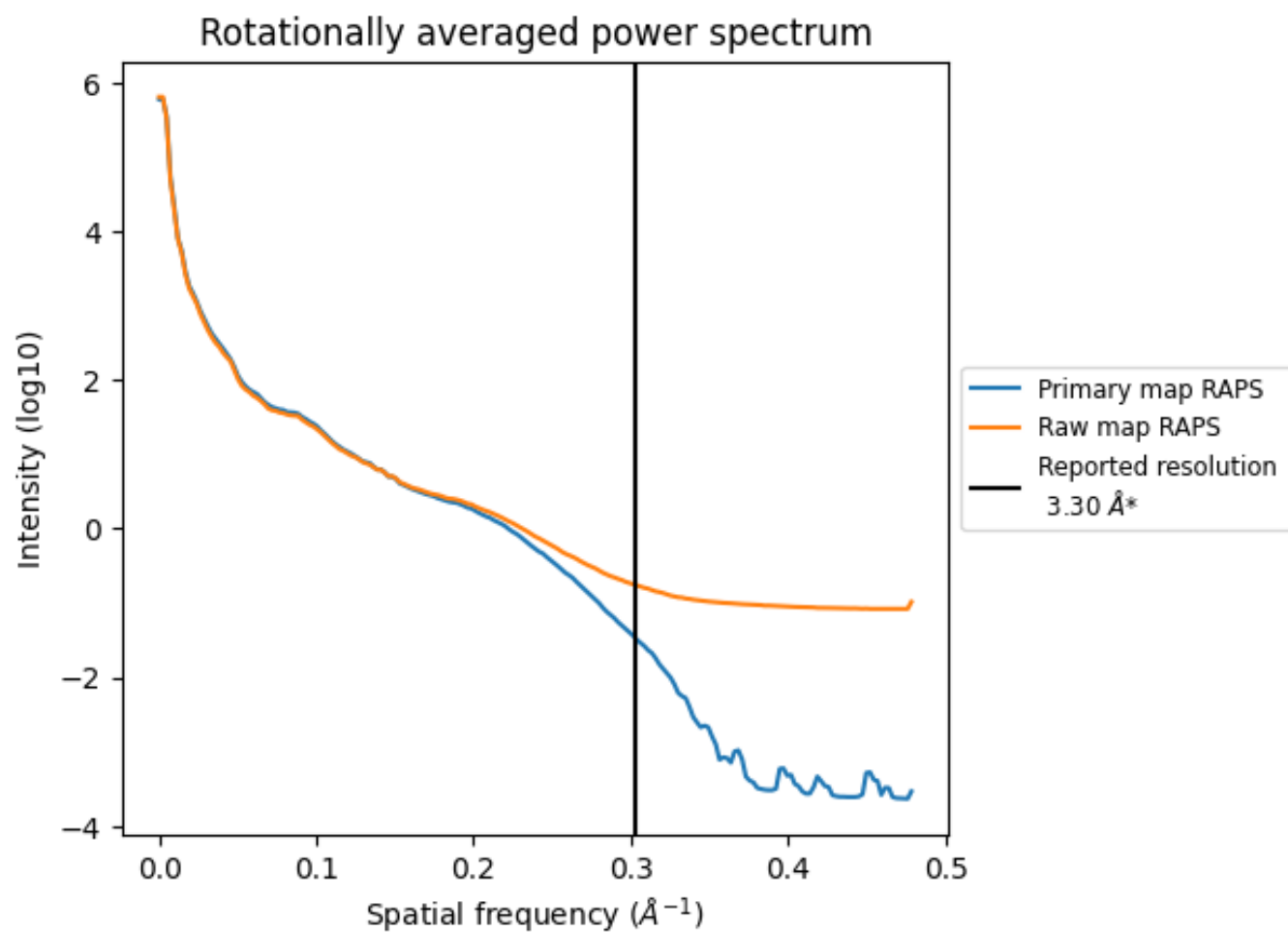
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4520 nm³; this corresponds to an approximate mass of 4083 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 ⓘ

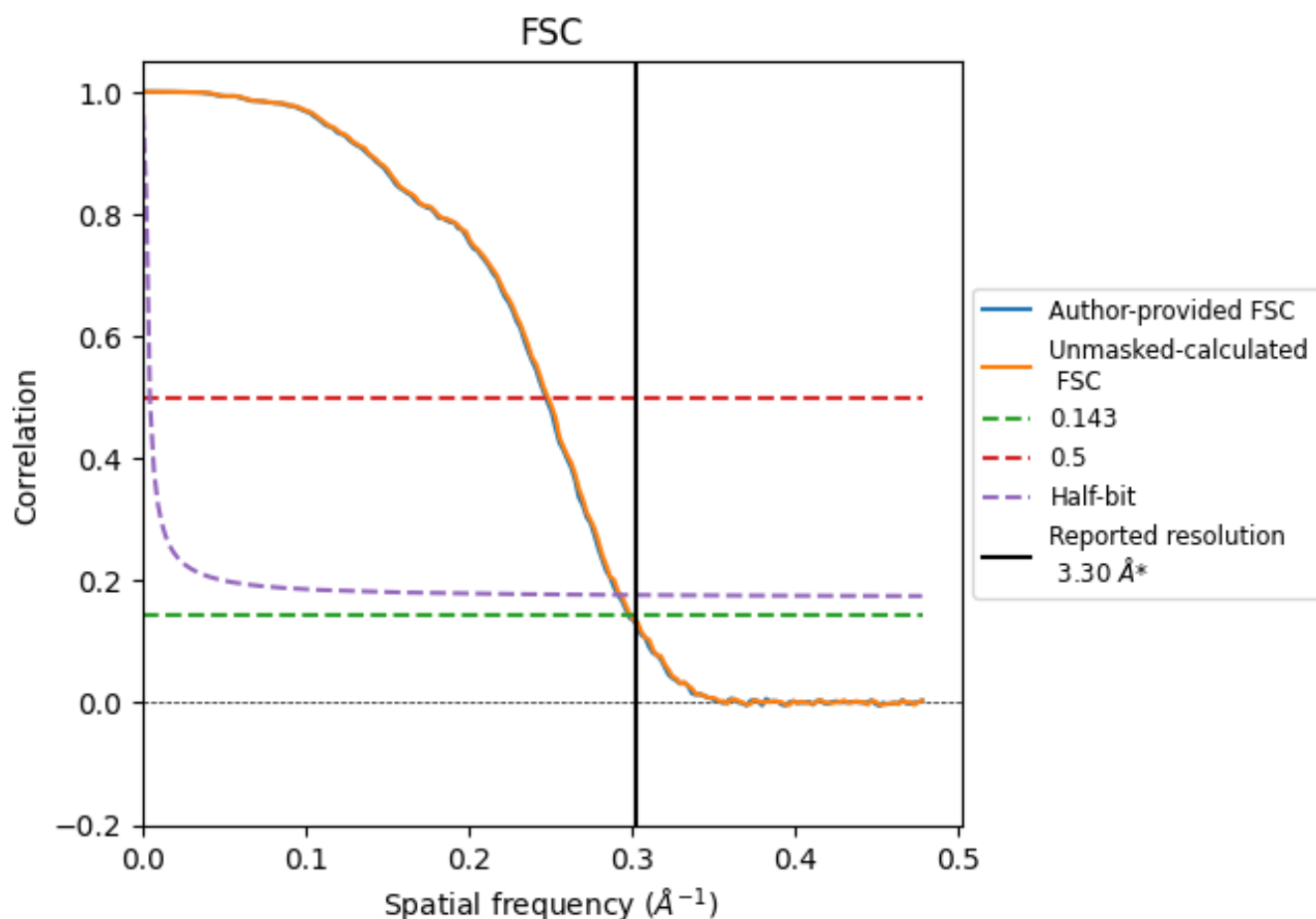


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

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 0.303 Å⁻¹

8.2 Resolution estimates [i](#)

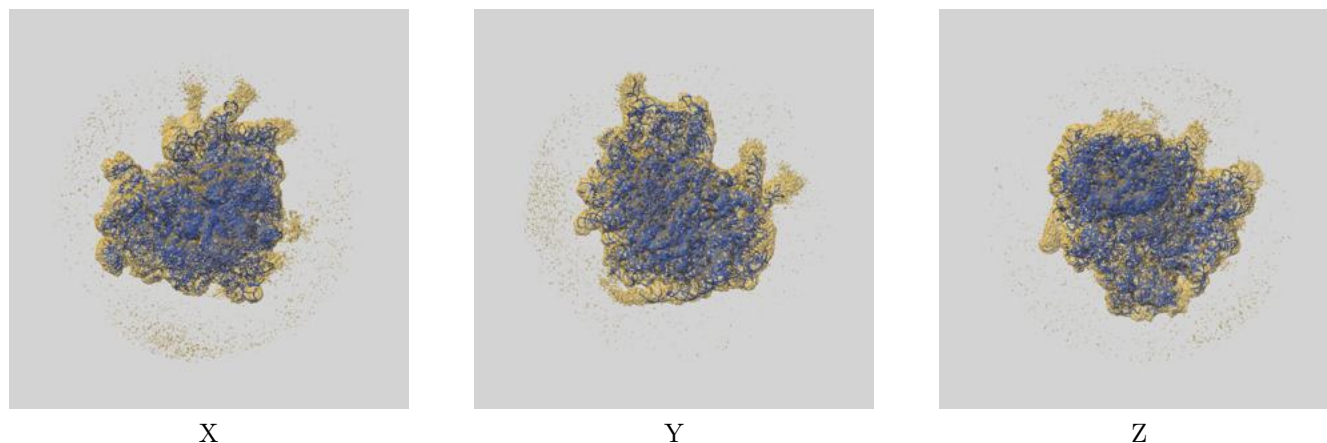
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.35	4.04	3.43
Unmasked-calculated*	3.34	4.02	3.41

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

9 Map-model fit [i](#)

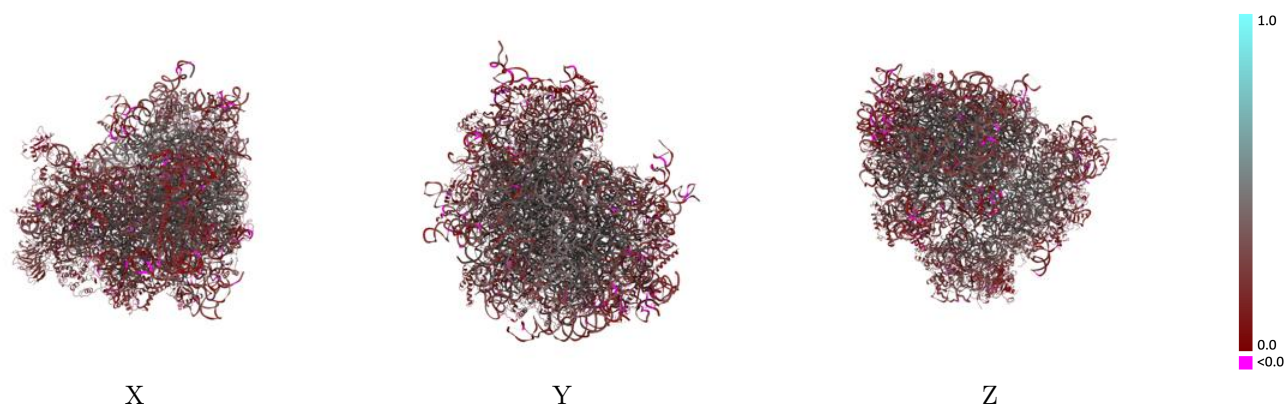
This section contains information regarding the fit between EMDB map EMD-72482 and PDB model 9Y4G. Per-residue inclusion information can be found in section [3](#) on page [20](#).

9.1 Map-model overlay [i](#)



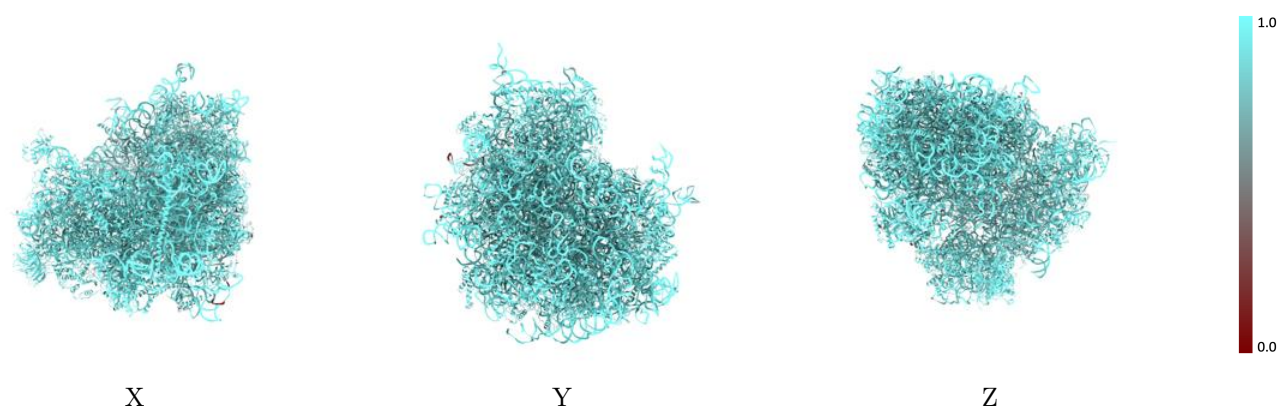
The images above show the 3D surface view of the map at the recommended contour level 0.002 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



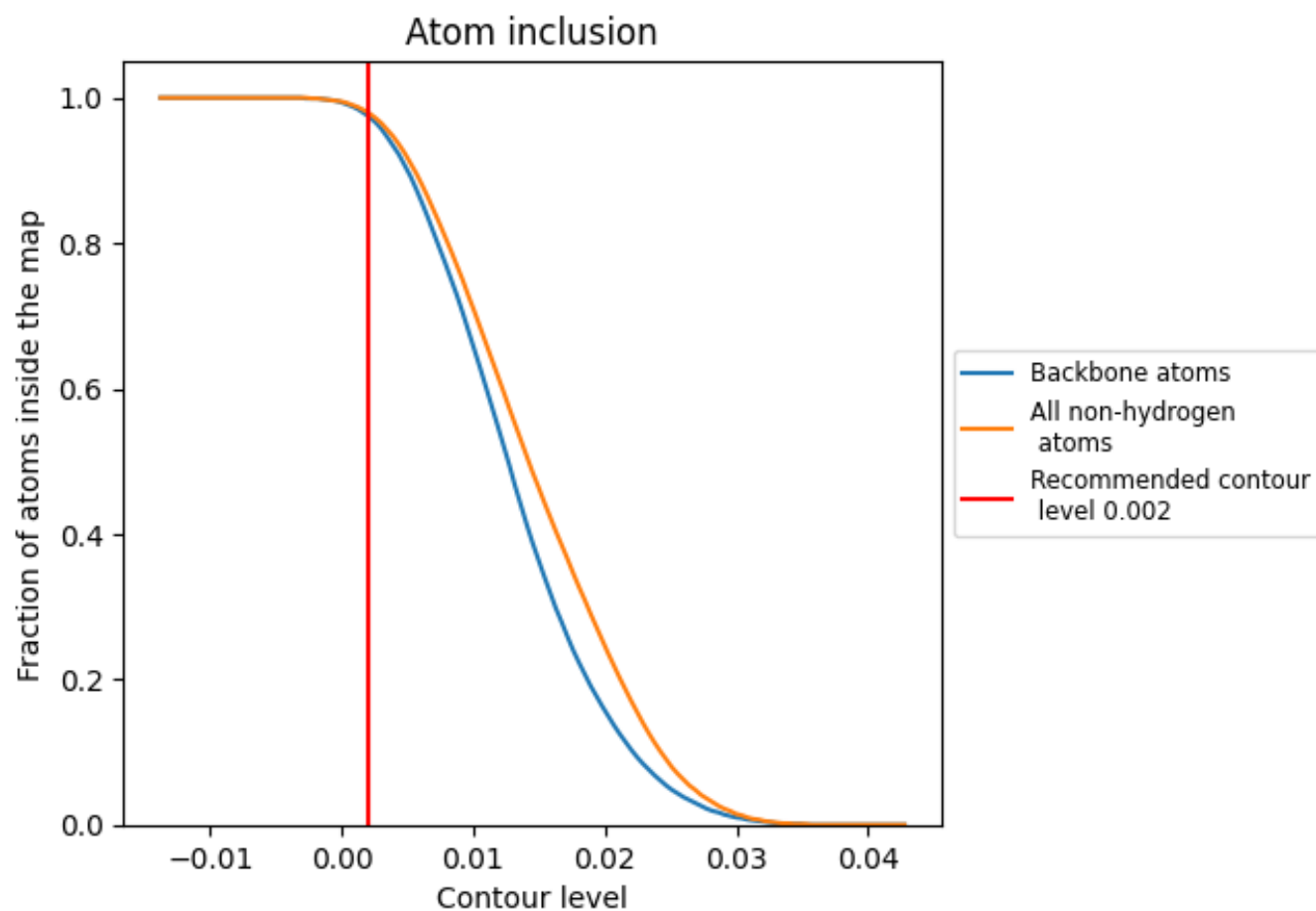
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.002).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 98% 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 (0.002) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9800	 0.3110
A5	 0.9920	 0.3290
A6	 0.9940	 0.3680
A7	 0.9920	 0.3220
A8	 0.9930	 0.3570
AA	 0.9730	 0.2710
AB	 0.9630	 0.2590
AC	 0.9520	 0.2840
AD	 0.9730	 0.2530
AE	 0.9790	 0.2230
AF	 0.9730	 0.2280
AG	 0.9900	 0.2010
AH	 0.9730	 0.2200
AI	 0.9770	 0.2300
AJ	 0.9690	 0.1940
AK	 0.9930	 0.2050
AL	 0.9480	 0.2810
AM	 0.9670	 0.1390
AN	 0.9580	 0.2920
AO	 0.9470	 0.2740
AP	 0.9560	 0.2060
AQ	 0.9790	 0.2250
AR	 0.9670	 0.2310
AS	 0.9850	 0.2330
AT	 0.9910	 0.2210
AU	 0.9810	 0.2400
AV	 0.9360	 0.2320
AW	 0.9610	 0.3070
AX	 0.9860	 0.3340
AY	 0.9800	 0.1660
AZ	 0.9670	 0.1930
Aa	 0.9570	 0.2990
Ab	 0.9410	 0.2390
Ac	 0.9630	 0.2050
Ad	 0.9700	 0.2470

















Continued on next page...

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Chain	Atom inclusion	Q-score
Ae	 0.9630	 0.2330
Af	 0.9650	 0.1430
Ag	 0.9900	 0.2280
B2	 0.9940	 0.3190
Bb	 0.8880	 0.2280
CA	 0.9450	 0.3850
CB	 0.9690	 0.3220
CC	 0.9650	 0.3300
CD	 0.9940	 0.2670
CE	 0.9240	 0.1570
CF	 0.9700	 0.3360
CG	 0.9340	 0.2440
CH	 0.9650	 0.2910
CI	 0.9450	 0.3200
CJ	 0.9460	 0.1860
CL	 0.9570	 0.2650
CM	 0.9690	 0.2750
CN	 0.9610	 0.3600
CO	 0.9580	 0.3290
CP	 0.9770	 0.3830
CQ	 0.9480	 0.3360
CR	 0.9750	 0.3210
CS	 0.9700	 0.3010
CT	 0.9450	 0.3130
CU	 0.8800	 0.1730
CV	 0.9620	 0.3530
CW	 0.9630	 0.2390
CX	 0.9700	 0.3020
CY	 0.9860	 0.3250
CZ	 0.9240	 0.1980
Ca	 0.9790	 0.3710
Cb	 0.9510	 0.2990
Cc	 0.9780	 0.2870
Cd	 0.9760	 0.3120
Ce	 0.9690	 0.4000
Cf	 0.9630	 0.3780
Cg	 0.9710	 0.3090
Ch	 0.9780	 0.2890
Ci	 0.9370	 0.2460
Cj	 0.9770	 0.3830
Ck	 0.9170	 0.2320
Cl	 0.9760	 0.3630

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Chain	Atom inclusion	Q-score
Cm	 0.9560	 0.3310
Cn	 0.9600	 0.3630
Co	 0.9640	 0.3390
Cp	 0.9330	 0.3600
Cr	 0.9180	 0.2270
Cz	 0.9740	 0.1350
Dd	 0.9850	 0.3430