



wwPDB EM Validation Summary Report ⓘ

Mar 30, 2026 – 03:47 AM UTC

PDB ID : 9Y44 / pdb_00009y44
EMDB ID : EMD-72470
Title : Structure of naked mole-rat 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 : 2025-09-02
Resolution : 4.90 Å (reported)
Based on initial models : 4v6x, 707y

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:

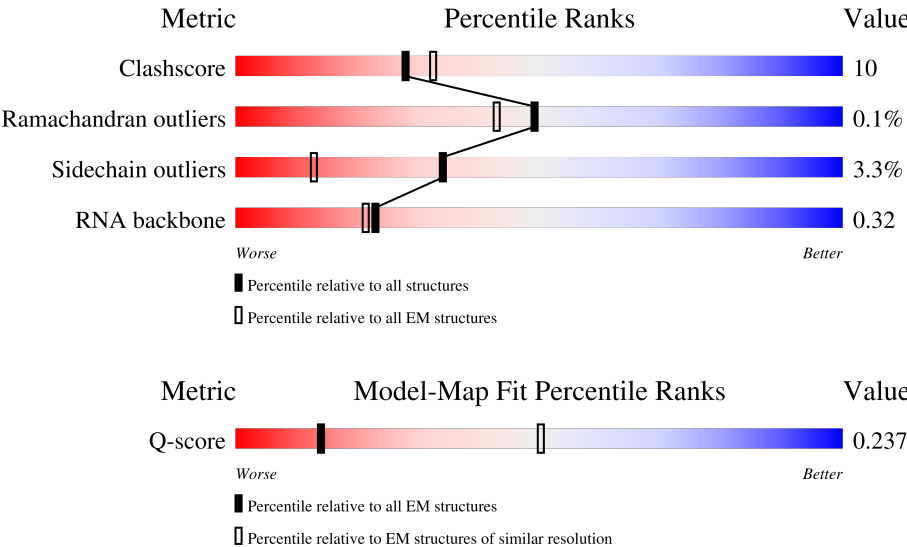
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
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 4.90 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.




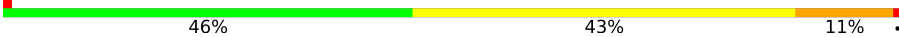








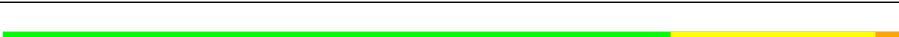


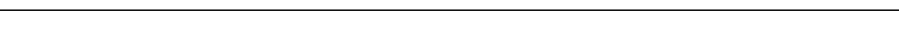
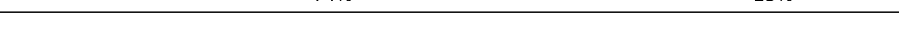
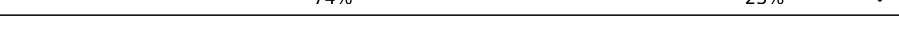



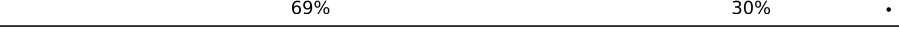





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	1274 (4.40 - 5.40)

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	A5	1717	<div> <div>40%</div> <div>46%</div> <div>14%</div> <div>.</div> </div>
2	A7	120	<div> <div>62%</div> <div>32%</div> <div>5%</div> </div>
3	A8	156	<div> <div>44%</div> <div>43%</div> <div>13%</div> </div>







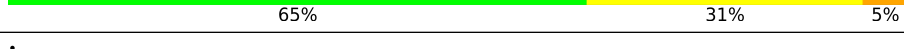
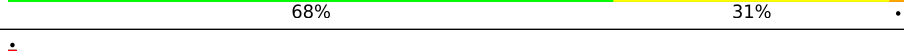
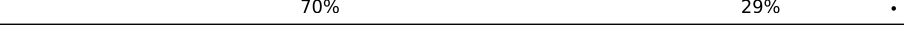
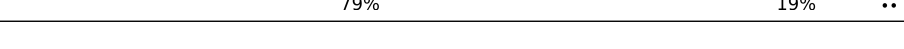
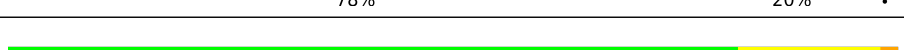

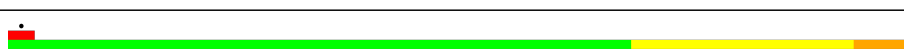

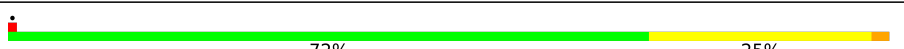





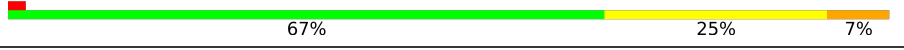
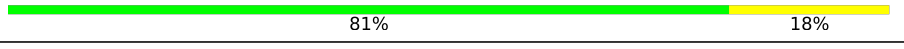



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Mol	Chain	Length	Quality of chain
4	B2	1804	
5	A6	2092	
6	A	248	
7	n	25	
8	B	398	
9	C	363	
10	D	293	
11	E	224	
12	F	225	
13	G	215	
14	H	190	
15	I	213	
16	J	170	
17	L	205	
18	M	136	
19	N	203	
20	O	199	
21	P	153	
22	Q	187	
23	S	176	
24	T	159	
25	U	99	
26	V	131	
27	X	118	
28	Y	134	


























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Mol	Chain	Length	Quality of chain
29	Z	135	
30	a	147	
31	b	100	
32	d	107	
33	e	128	
34	f	110	
35	g	110	
36	h	121	
37	i	102	
38	j	86	
39	k	69	
40	l	50	
41	m	51	
42	o	105	
43	p	91	
44	r	127	
45	s	103	
46	t	156	
47	cc	61	
48	ff	67	
49	gg	313	
50	dd	55	
51	AA	214	
52	BB	218	
53	DD	225	





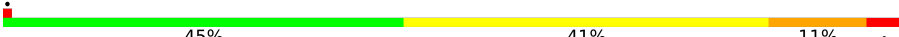
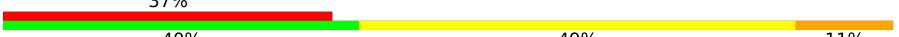

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Mol	Chain	Length	Quality of chain
54	FF	189	 79%16%...
55	KK	96	 73%24%.
56	MM	124	 13%78%21%.
57	OO	134	 69%28%.
58	PP	118	 70%28%..
59	QQ	141	 74%23%.
60	RR	132	 80%19%.
61	SS	145	 73%26%.
62	TT	141	 80%18%.
63	UU	99	 85%14%.
64	ZZ	75	 80%19%.
65	bb	82	 77%21%.
66	ee	49	 65%35%
67	aa	98	 78%22%
68	CC	218	 74%24%.
69	EE	262	 81%19%
70	GG	228	 78%21%.
71	HH	190	 77%19%..
72	II	206	 79%20%.
73	JJ	180	 68%30%..
74	LL	149	 73%21%5%
75	NN	149	 80%20%
76	VV	83	 83%17%
77	WW	129	 83%16%.
78	XX	122	 93%7%

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Mol	Chain	Length	Quality of chain
79	YY	125	
80	W	180	
81	c	121	
82	u	100	
83	Cc	76	
84	Bb	65	
85	Dd	13	

2 Entry composition [i](#)

There are 88 unique types of molecules in this entry. The entry contains 219186 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 LSU alpha rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A5	1717	Total	C	N	O	P	0	0
			36275	16121	6621	11816	1717		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A7	120	Total	C	N	O	P	0	0
			2558	1140	453	845	120		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A8	156	Total	C	N	O	P	0	0
			3317	1480	584	1097	156		

- Molecule 4 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B2	1804	Total	C	N	O	P	0	0
			37897	16889	6738	12466	1804		

- Molecule 5 is a RNA chain called LSU beta rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A6	2092	Total	C	N	O	P	0	0
			43564	19354	7784	14334	2092		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	248	Total	C	N	O	S	0	0
			1648	1036	305	301	6		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	72	LYS	ARG	conflict	UNP A0A0P6J3A4
A	123	LYS	ARG	conflict	UNP A0A0P6J3A4
A	128	LYS	ARG	conflict	UNP A0A0P6J3A4
A	147	LYS	ARG	conflict	UNP A0A0P6J3A4

- Molecule 7 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	n	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 8 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	398	Total	C	N	O	S	0	0
			3206	2042	605	546	13		

- Molecule 9 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	363	Total	C	N	O	S	0	0
			2884	1815	576	479	14		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	1	ACE	-	acetylation	UNP G5AN81
C	262	ASP	GLU	conflict	UNP G5AN81
C	362	GLY	-	expression tag	UNP G5AN81
C	363	GLY	-	expression tag	UNP G5AN81

- Molecule 10 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	293	Total	C	N	O	S	0	0
			2389	1511	437	427	14		

- Molecule 11 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	224	Total	C	N	O	S	0	0
			1789	1149	340	297	3		

- Molecule 12 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

- Molecule 13 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	215	Total	C	N	O	S	0	0
			1741	1111	333	293	4		

- Molecule 14 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	H	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 15 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	I	199	Total	C	N	O	S	0	0
			1620	1029	313	266	12		

- Molecule 16 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	J	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 17 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	205	Total	C	N	O	S	0	0
			1658	1037	346	271	4		

- Molecule 18 is a protein called Large ribosomal subunit protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	136	Total	C	N	O	S	0	0
			1125	720	220	178	7		

- Molecule 19 is a protein called Ribosomal protein L15.

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

- Molecule 20 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	O	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 21 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	P	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 22 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Q	187	Total	C	N	O	S	0	0
			1512	946	313	249	4		

- Molecule 23 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S	176	Total	C	N	O	S	0	0
			1461	930	284	236	11		

- Molecule 24 is a protein called Large ribosomal subunit protein eL21.

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

- Molecule 25 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	U	99	Total	C	N	O	S	0	0
			808	518	141	147	2		

- Molecule 26 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	V	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 27 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	X	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 28 is a protein called 60S ribosomal protein L26.

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

- Molecule 29 is a protein called 60S ribosomal protein L27.

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

- Molecule 30 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	a	147	Total	C	N	O	S	0	0
			1163	734	239	186	4		

- Molecule 31 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	b	65	Total	C	N	O	S	0	0
			545	338	122	84	1		

- Molecule 32 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	d	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	e	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 34 is a protein called Large ribosomal subunit protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	110	Total	C	N	O	S	0	0
			884	560	175	144	5		

- Molecule 35 is a protein called Large ribosomal subunit protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	110	Total	C	N	O	S	0	0
			873	547	180	140	6		

- Molecule 36 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	h	121	Total	C	N	O	S	0	0
			1011	640	204	166	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
h	119	TYR	PHE	conflict	UNP G5B6W3

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

Mol	Chain	Residues	Atoms					AltConf	Trace
37	i	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 38 is a protein called Ribosomal protein L37.

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

- Molecule 39 is a protein called Large ribosomal subunit protein eL38.

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

- Molecule 40 is a protein called Large ribosomal subunit protein eL39.

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

- Molecule 41 is a protein called Ubiquitin-ribosomal protein eL40 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	m	51	Total	C	N	O	S	0	0
			422	263	88	65	6		

- Molecule 42 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	o	105	Total	C	N	O	S	0	0
			863	543	175	139	6		

- Molecule 43 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	p	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 44 is a protein called Large ribosomal subunit protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	r	127	Total	C	N	O	S	0	0
			1015	630	209	170	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
r	1	ACE	-	acetylation	UNP G5BVZ2

- Molecule 45 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	s	103	Total	C	N	O	S	0	0
			825	525	150	143	7		

- Molecule 46 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	t	156	Total	C	N	O	S	0	0
			1178	733	221	220	4		

- Molecule 47 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	cc	61	Total	C	N	O	S	0	0
			479	292	95	90	2		

- Molecule 48 is a protein called Ubiquitin-ribosomal protein eS31 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	ff	67	Total	C	N	O	S	0	0
			548	346	102	93	7		

- Molecule 49 is a protein called Small ribosomal subunit protein RACK1.

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

- Molecule 50 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	dd	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 51 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	AA	214	Total	C	N	O	S	0	0
			1689	1074	295	312	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AA	1	ACE	-	acetylation	UNP A0A0P6K1L6

- Molecule 52 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BB	218	Total	C	N	O	S	0	0
			1768	1120	320	314	14		

- Molecule 53 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	DD	225	Total	C	N	O	S	0	0
			1751	1116	315	313	7		

- Molecule 54 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	FF	184	Total	C	N	O	S	0	0
			1461	914	276	264	7		

- Molecule 55 is a protein called Small ribosomal subunit protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	KK	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 56 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	MM	124	Total	C	N	O	S	0	0
			958	600	170	179	9		

- Molecule 57 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	OO	134	Total	C	N	O	S	0	0
			1002	612	197	187	6		

- Molecule 58 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	PP	118	Total	C	N	O	S	0	0
			979	621	185	166	7		

- Molecule 59 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 60 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	RR	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 61 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SS	145	Total	C	N	O	S	0	0
			1193	748	241	203	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SS	1	ACE	-	acetylation	UNP G5BAZ4

- Molecule 62 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	TT	141	Total	C	N	O	S	0	0
			1097	687	211	196	3		

- Molecule 63 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	UU	99	Total	C	N	O	S	0	0
			790	495	151	140	4		

- Molecule 64 is a protein called 40S ribosomal protein S25.

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

- Molecule 65 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	bb	82	Total	C	N	O	S	0	0
			640	402	118	113	7		

- Molecule 66 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	ee	49	Total	C	N	O	S	0	0
			398	243	90	64	1		

- Molecule 67 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	aa	98	Total	C	N	O	S	0	0
			781	486	161	129	5		

- Molecule 68 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	CC	218	Total	C	N	O	S	0	0
			1689	1095	289	296	9		

- Molecule 69 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	EE	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
70	GG	228	Total	C	N	O	S	0	0
			1848	1155	368	318	7		

- Molecule 71 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	HH	184	Total	C	N	O	S	0	0
			1490	953	271	265	1		

- Molecule 72 is a protein called 40S ribosomal protein S8.

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

- Molecule 73 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	JJ	180	Total	C	N	O	S	0	0
			1499	955	300	242	2		

- Molecule 74 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	LL	141	Total	C	N	O	S	0	0
			1157	737	218	196	6		

- Molecule 75 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 76 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	VV	83	Total	C	N	O	S	0	0
			637	392	117	123	5		

- Molecule 77 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 78 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	XX	122	Total	C	N	O	S	0	0
			810	510	150	147	3		

- Molecule 79 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	YY	125	Total	C	N	O	S	0	0
			1015	642	199	169	5		

- Molecule 80 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	W	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 81 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	c	113	Total	C	N	O	S	0	0
			921	575	190	153	3		

- Molecule 82 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	u	100	Total	C	N	O	S	0	0
			775	491	136	141	7		

- Molecule 83 is a RNA chain called P/E tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Cc	76	Total	C	N	O	P	0	0
			1623	723	295	529	76		

- Molecule 84 is a RNA chain called tRNA (65-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Bb	65	Total	C	N	O	P	0	0
			1409	633	258	453	65		

- Molecule 85 is a RNA chain called mRNA.

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

- Molecule 86 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
86	A5	9	Total	Mg	0
			9	9	
86	A7	4	Total	Mg	0
			4	4	
86	A8	4	Total	Mg	0
			4	4	
86	B2	7	Total	Mg	0
			7	7	
86	A6	7	Total	Mg	0
			7	7	
86	P	1	Total	Mg	0
			1	1	
86	l	1	Total	Mg	0
			1	1	
86	BB	1	Total	Mg	0
			1	1	
86	Cc	1	Total	Mg	0
			1	1	
86	Bb	1	Total	Mg	0
			1	1	

- Molecule 87 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
87	B2	1	Total	Zn	0
			1	1	
87	g	1	Total	Zn	0
			1	1	
87	j	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
87	m	1	Total 1	Zn 1	0
87	o	1	Total 1	Zn 1	0
87	p	1	Total 1	Zn 1	0
87	ff	1	Total 1	Zn 1	0
87	aa	1	Total 1	Zn 1	0

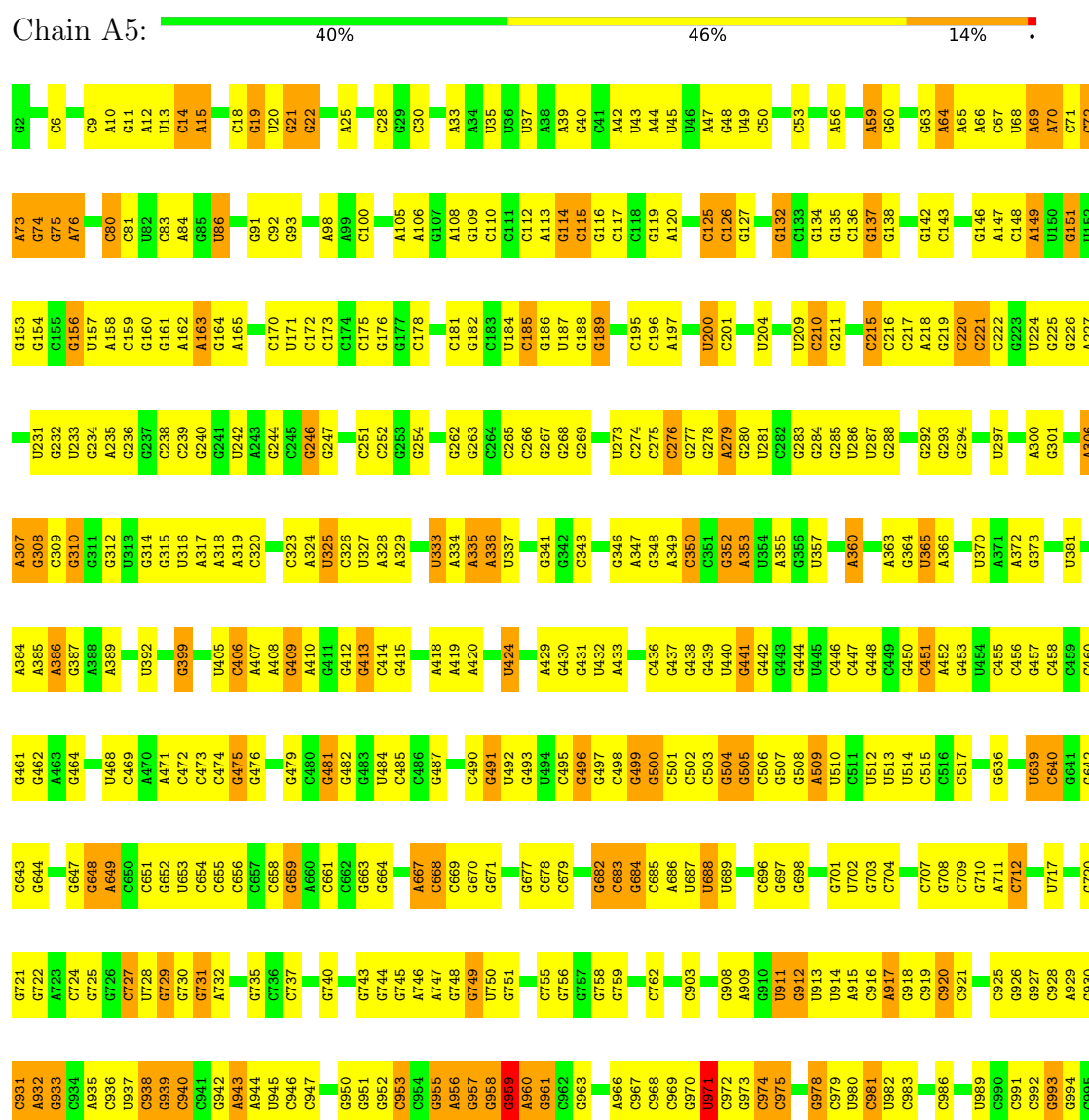
- Molecule 88 is water.

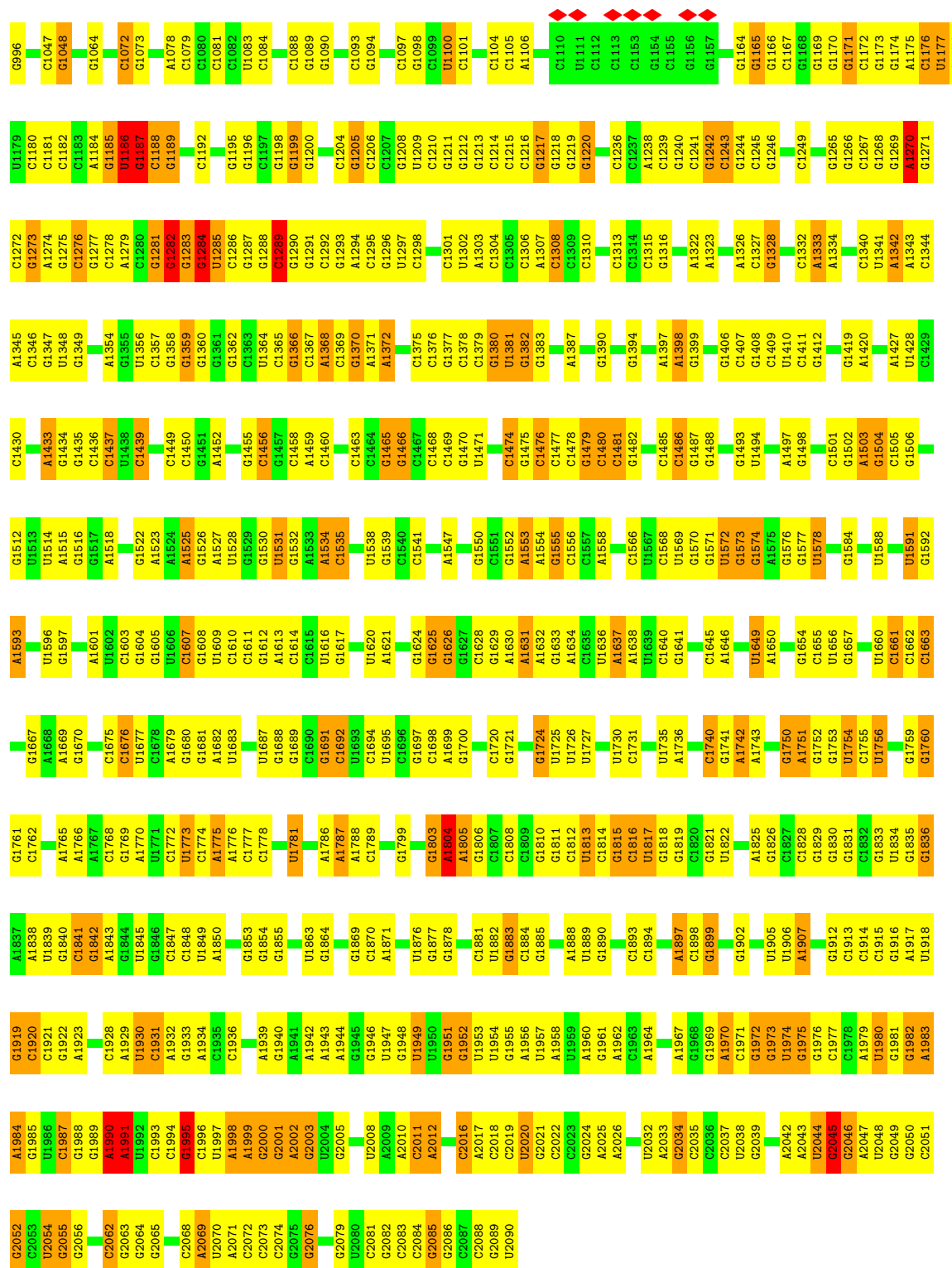
Mol	Chain	Residues	Atoms		AltConf
88	B2	4	Total 4	O 4	0
88	A6	1	Total 1	O 1	0
88	Cc	5	Total 5	O 5	0
88	Bb	5	Total 5	O 5	0

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: LSU alpha rRNA





• Molecule 2: 5S ribosomal RNA

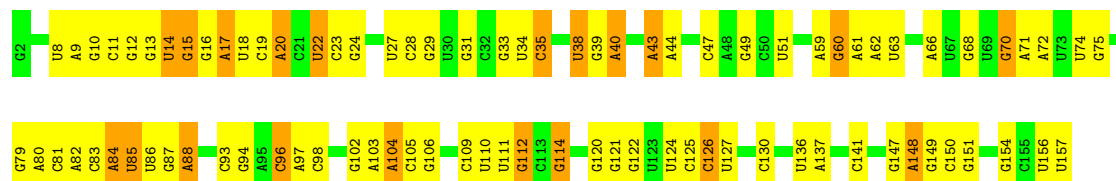
Chain A7:





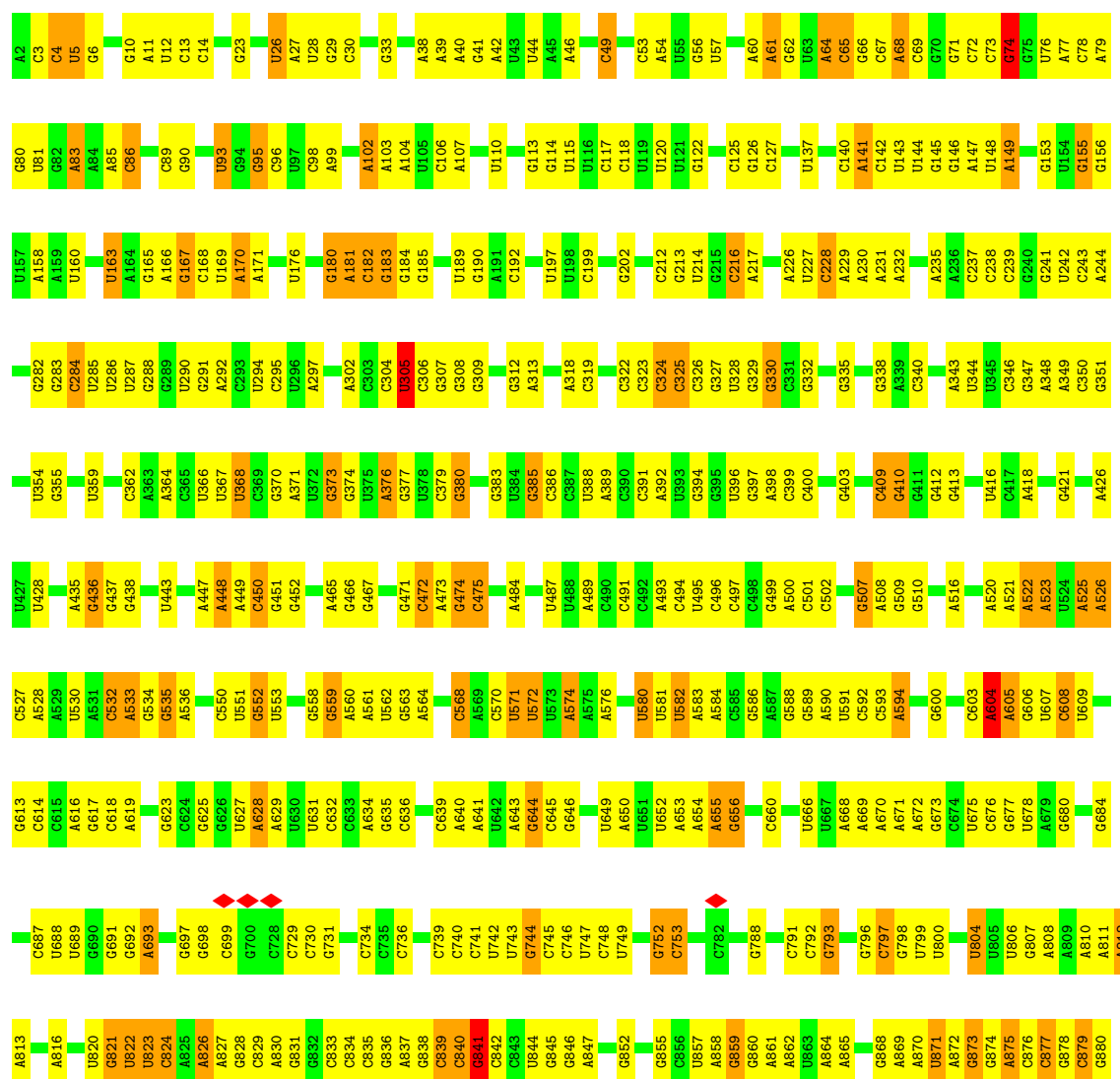
• Molecule 3: 5.8S ribosomal RNA

Chain A8: 44% 43% 13%



• Molecule 4: 18S ribosomal RNA

Chain B2: 42% 45% 12%

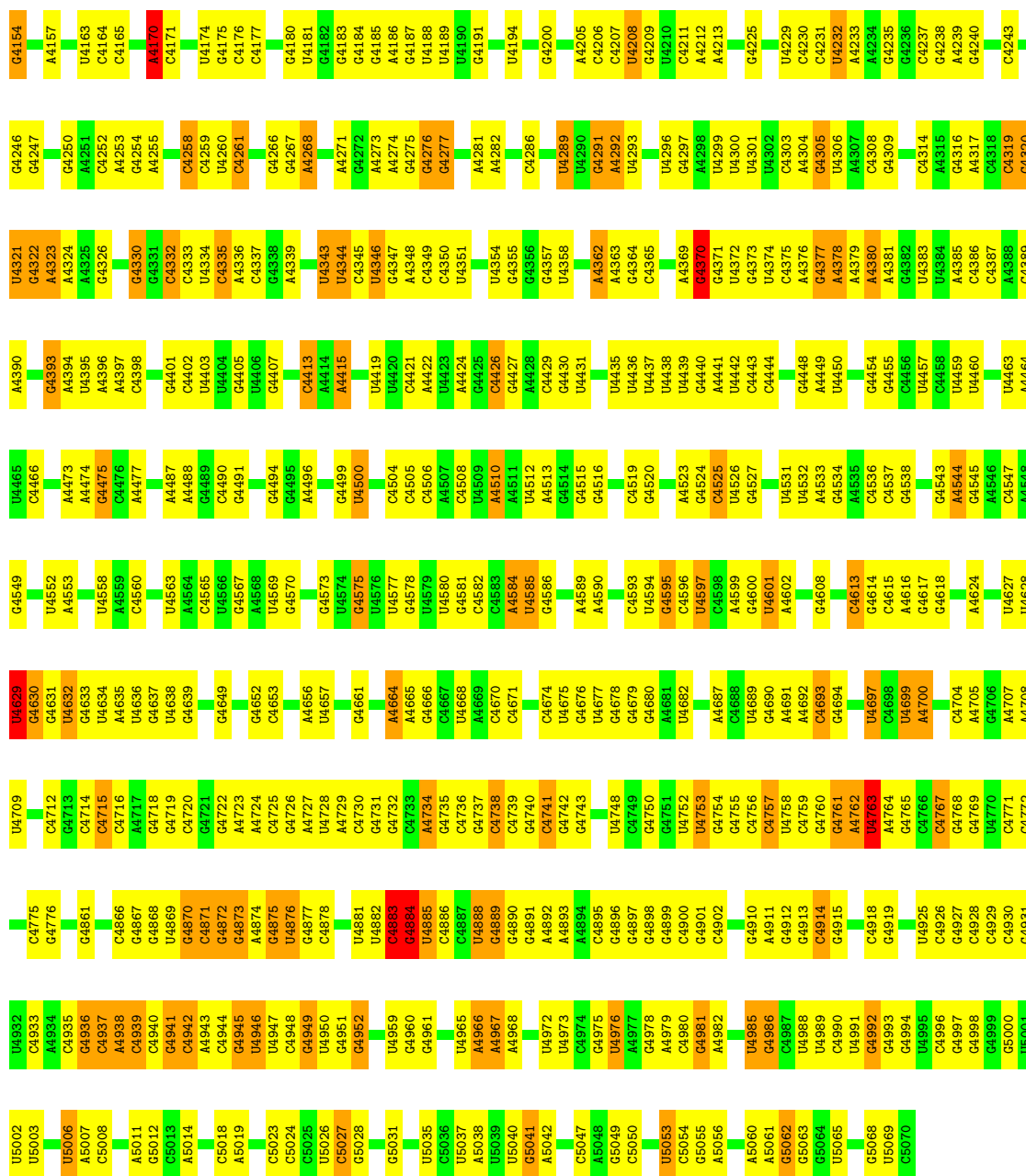


G1861	G1782	C1682	G1613	A1545	U1477	U1407	U1333	A1251	A1181	U1115	A1036	G956	G881
G1862	C1783	C1683	A1614	G1548	U1478	U1408	U1337	C1282	A1182	C1116	A1036	A957	G885
A1863	G1784	G1684	U1615	U1549	G1479	U1409	G1338	A1252	A1183	C1117	A1036	G958	U886
U1864	C1785	U1690	U1616	U1549	G1479	C1410	U1339	C1254	G1184	C1118	C1039	G959	A886
A1865	U1786	U1691	G1617	U1550	A1483	C1412	U1342	G1256	A1188	U1120	U1045	G961	U887
A1866	G1787	U1692	C1618	G1552	U1485	G1416	U1343	G1257	A1188	G1121	U1046	A962	U889
U1867	G1693	G1693	U1621	C1583	A1486	C1417	U1343	A1288	A1188	G1122	U1046	A963	U890
U1868	U1694	U1694	U1622	C1584	A1487	C1418	A1344	A1289	U1193	C1123	A1048	A963	U891
A1869	A1695	A1695	A1623	C1585	A1488	C1419	G1345	A1290	A1194	C1124	U1048	U969	U892
	U1624	U1624	U1624	A1556	A1489	C1420	G1345	C1261	A1195	C1125	U1048	G970	U893
				A1557	A1490	G1420	G1348	C1262	A1196	G1126	A1050	G971	G894
				C1557	G1491	G1420	G1348	C1263	A1197	G1127	A1050		G895
				C1558	U1492	C1423	G1351	C1264	G1198	C1128	C1053	G976	U898
				C1559	C1493	G1424	G1352	A1286	A1199	G1129	C1056	G977	U899
				U1560	U1494	G1425	A1353	C1266		G1130	U1056	G978	C900
				A1561	C1495	U1426	G1354	C1267	U1202	G1131	G1059	G979	G901
				C1562	U1496	C1430	G1355	C1268	G1203	G1132	A1060	A980	G902
				G1563	G1497	G1431	G1356	C1269	A1204	A1133	U1061	A981	A903
				C1564	A1498	G1432	A1357	G1270	G1205	G1134	U1062	G982	
				C1565	U1499	U1433	G1358	C1271	G1206	C1135	C1063	A983	
				U1566	G1500	C1434	U1359	C1272	G1207	U1136	G1068	A987	U906
				C1567	C1501	C1435	U1360	C1273	A1208	U1137	U1069	C988	A908
				A1569	U1504	C1436	U1364	G1275	A1209	C1138	G1068	C989	G909
				G1570	U1505	C1437	U1367	A1276	A1214	G1142	U1073	A990	G910
					A1506	A1438	U1367	C1277	C1216	G1143	U1073	G991	C911
					G1507		U1371	C1283	C1216	A1143	U1073	A992	C912
					A1508	U1441	U1372	A1284	C1218	A1144	C1078	G999	A913
					U1509	U1442	C1373	G1285	C1219	A1145	C1078	C1000	U914
					G1510	C1443	C1374	G1286	A1220	C1146	A1082	C1001	U917
					U1511	U1444	G1375	A1287	G1221	A1148	A1083	U1004	U918
					C1518	U1445	A1376	U1288	G1222	A1149	A1084	U1005	A919
					U1519	G1447	U1377	U1289	A1223	A1150	G1086	G1006	A920
					G1520	A1448	A1378	G1290	G1224		A1087	C1007	G921
					G1521	G1449	G1381	G1298	G1227	G1153	U1088	C1007	A922
					A1522	G1450	A1382	A1299	A1228	U1154	G1089	A1008	G923
					C1523	G1451	U1382	U1300	G1229	U1155	G1089	A1009	G924
					G1524	A1452	G1385	A1301	G1230	U1156	C1090	G1010	G925
					C1525	C1453	A1386	G1302	G1231	G1157	G1091	A1011	A926
					G1526	A1454	A1387	C1303	U1232	G1158	G1092	A1012	C927
					C1527	A1455	A1388	G1303	U1233	G1159	A1093	U1013	G928
					G1528	G1456	C1389	U1308	C1234	U1160	C1094	G1014	
					C1529	U1457	U1389	C1309	G1235	C1163	C1095	G932	G932
					U1530		U1389	U1310	G1236	U1164	G1096	U1017	G933
					A1531	G1461	U1392	C1311	G1236	G1165	G1097	U1018	G934
					C1532	U1462	G1393	G1312	C1237	G1166	C1098	C1019	G935
					A1533	U1463	C1394	G1312		G1167	G1099	G936	G936
					C1534	C1464	C1395	U1315	A1240	G1168	A1100	U1021	C937
					U1535	A1465	A1396	U1315	A1241	G1169	U1101	U1022	
					G1600	G1466	U1397	U1315	U1242	G1170	G1102	A1023	C941
					A1601	U1467	U1397	U1311	U1243	A1170	G1103	A1024	G942
					G1598	C1467	G1398	G1322	U1244	G1171	G1104	U1025	U943
					U1599	C1468	G1398	U1322	U1244	U1172	G1104	C1026	A944
					U1600	A1469	A1401	G1324	G1245	A1173	C1109	A1027	
					A1601	A1469	A1402	U1329	G1247	U1174	G1110	A1028	G949
					G1601	G1473	C1403	U1330	U1248	G1175	U1111	G1029	U954
					A1602	G1474	U1404	G1330	C1249	G1176	U1111	A1030	
					G1603	G1475	A1405	C1331	C1249	G1176	U1111	A1031	A955
					U1604	G1476	U1406	A1332	A1250	U1177	U1114		

• Molecule 5: LSU beta rRNA

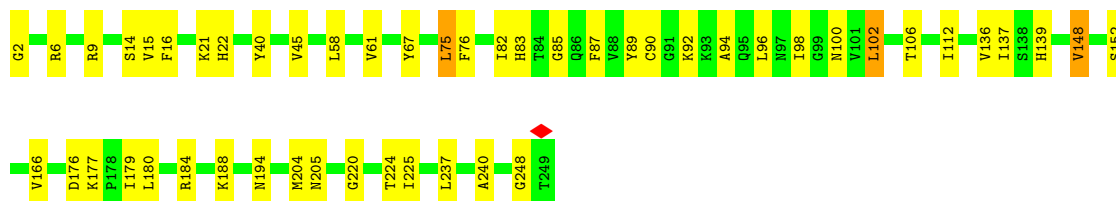


U4070	G3941	C3789	C3701	C3805	G2897	C2805	U2794	U2661	C2589	A2513	A2412	G2383	G2262
U4071	A3942	U3790	A3702	U3806	G2898	A2806	G2785	G2662	G2590	G2514	G2415	C2334	A2263
A4072	A3943	C3791	G3705	A3612	G2899	G2811	G2736	G2663	G2596	G2515	U2416	C2335	G2264
A4073	G3944	C3794	C3706	C3611	G2900	C2814	U2740	G2665	A2598	G2517	A2417	G2336	G2265
U4074	G3945	C3795	U3707	A3612	G2902	A2815	U2741	G2668	A2599	C2520	C2422	G2341	U2267
A4075	G3946	C3796	C3708	U3613	G2903	G2816	G2742	G2669	A2601	G2521	A2423	G2342	A2268
G4076	A3947	U3798	U3709	U3616	G2904	G2820	A2744	G2670	A2602	G2522	G2424	G2343	C2269
A4077	G3948	A3799	G3710	G3617	G2905	C2827	G2752	G2671	A2603	G2523	U2425	U2344	G2270
	A3949	U3800	G3711	C3618	U2908	G2828	C2748	G2672	C2604	U2524	A2428	A2347	C2274
G4080	U3884	A3801	A3712	G3619	G2909	C2829	C2749	G2673	G2605	G2525	A2429	G2348	G2275
A4082	G3888	U3802	G3713	G3620	G2910	U2826	G2750	A2674	G2607	U2526	A2431	A2349	A2276
U4083	G3889	A3803	G3714	G3621	C2913	G2827	G2751	G2675	G2608	G2527	G2432	G2351	C2277
G4084	A3890	G3804		G3622	U2914	U2829	A2755	G2676	G2609	U2528	C2437	G2355	A2278
A4085	A3891	C3810	G3720	G3623	U2915	U2832	A2756	G2677	A2610	U2529	A2437	A2356	G2279
G4086	U3892	G3811	A3721	G3624	A2923	A2832	C2756	G2682	A2611	U2530	U2440	G2358	G2283
A4087	A3893	C3812	G3722	G3625	A2924	C2833	A2757	C2683	G2612	C2531	C2441	U2359	G2284
G4088	G3894	A3813	A3723	G3626	G2925	C2834	G2758	C2684	C2613	C2532	G2442	A2360	G2288
A4089	A3895	U3814	A3724	A3630	G2926	A2835	G2759	G2685	C2614	C2533	G2443	A2361	G2289
G4090	G3896	G3815	A3725	A3631	C2927	A2836	G2760	G2686	C2615	U2534	A2449	U2362	C2290
U4091	A3897	A3816	A3726	C3632	G2928	U2837	U2761	G2687	G2616	G2541	G2450	A2363	
A4092	G3898	G3817	C3731	C3633	G2929	G2838	G2762	G2688	G2617	G2542			
A3966	G3899	G3818	A3732	C3634	G2930	C2839	G2763	G2689	G2618	A2543	G2455		C2295
G3967	G3900	G3819	A3733	A3635	G2931	U2839	U2764	G2690	G2619	G2544	G2456		G2296
	A3901	G3820		C3636	G2932	G2842	A2765	U2691	G2620	U2545	G2457		G2297
G3970	A3902	C3833	G3743	U3639	G2933	G2843	G2766	U2692	G2621	G2546	G2458		U2298
G3971	A3905	C3834	A3746	A3646	G2934	A2945	U2767	G2693	A2622	G2547	C2459		C2300
A4105	A3906	U3838	C3747	A3647	G2935	G2846	U2768	A2695	C2627		G2461		G2301
G4106	G3907	G3839	G3748	A3652	G2936	G2847	U2769	A2696	G2628	G2551	C2462		G2302
A4107	A3908	U3840	C3749	A3653	G2937	G2848	C2770	A2697	U2631	G2552	C2463		G2303
G4108	C3911	G3841	G3750	C3658	G2938	A2849	G2771	U2701	U2632	U2553	G2464		U2304
	U3912	C3842		G3659	G2939	A2850	C2772		U2633	G2554	U2465		U2305
G4114	G3915	U3844	G3755	C3660	G2940	G2855	G2773		U2634	G2555	C2466		A2306
G4115	G3916	A3845	A3756	G3661	G2941	G2863	C3774		C2634	G2556	C2467		A2307
U4044	A3917	U3846	A3757	A3662	G2942	A2864	G2775		U2635	G2557	C2470		A2308
G4045	G3918	A3847	A3758	A3663	G2943	U2865	G2776		U2636	G2558	G2471		
A4046	C3919	A3848	A3759	G3664	G2944	U2866	G2777		U2637	G2559			
U4047	G3920	C3849	C3761	G3665	G2945	U2867	G2778		U2638	G2560			
U4120	U3921	A3852		G3672	G2946	U2868	C2779		G2640	G2561			
G4121	G3922	U3853	U3770	C3673	G2947	A2870	C2780		A2641		G2474		C2311
A4049	A3923	C3854	C3771	G3674	G2948	G2876	G2781		G2642		G2475		U2312
A4050	C3924	C3855	U3772	G3675	G2949	G2877	G2782		A2643		G2476		A2313
G4051	U3925	A3856	U3773	G3676	G2950	U2878	G2783		G2644		G2477		G2314
A4052	C3926	G3857	A3774	U3679	G2951	A2879	C2784		A2645		C2478		
A4053	C3927	C3858	A3775	U3680	G2952	U2880	A2785		A2646		G2479		C2317
A4056	A3928	G3859	G3776	U3681	G2953	A2881	U2786		A2647				G2318
A4127	G3929	A3860	G3777	C3683	G2954	A2882	A2789		A2648		C2488		G2319
A4128	U3930	A3861	U3778	G3572	G2955	G2887	G2790		G2649		G2489		G2320
	C3931	U3865	A3779	G3573	G2956	G2888	U2791		G2650		U2490		G2322
G4134	U3932	A3866	G3780	G3574	G2957	U2889	C2792		G2651				C2323
G4135	G3933	A3867		A3692	G2958	G2890	G2793		G2652		G2503		C2324
C4142	C3934	A3868	A3783	U3695	G2959	G2891	G2794		G2653		G2504		C2325
G4143	G3935	A3869	A3784	C3696	G2960	U2892			G2654		C2505		G2326
C4144	A3936	C3870	A3785	G3697	G2961	G2893			G2655		G2506		G2327
C4145	U4067	A3871	U3786	G3698	G2962	U2894			G2656		A2507		G2328
	G3938	A3872	C3788		G2963	A2894			G2657		G2508		G2329
C4153					G2964				G2658		G2509		U2330
					G2965				G2659		A2510		G2331
					G2966				G2660		A2512		A2332




• Molecule 6: Large ribosomal subunit protein uL2

Chain A: 80% 19% .




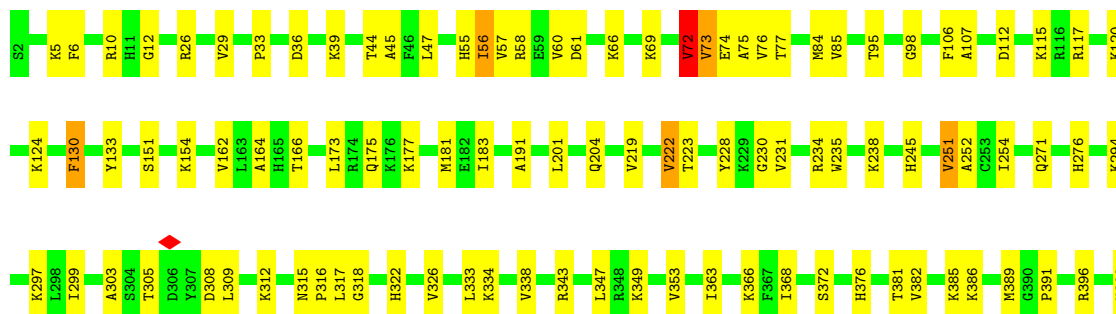
• Molecule 7: 60S ribosomal protein L41

Chain n:  52% 48%



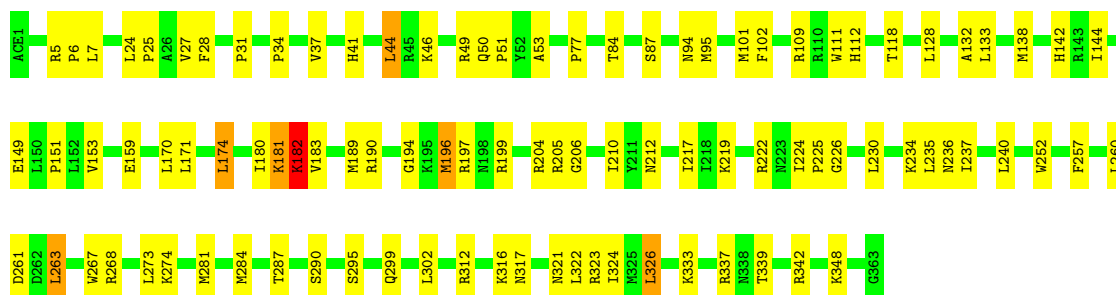
• Molecule 8: 60S ribosomal protein L3

Chain B:  75% 24%



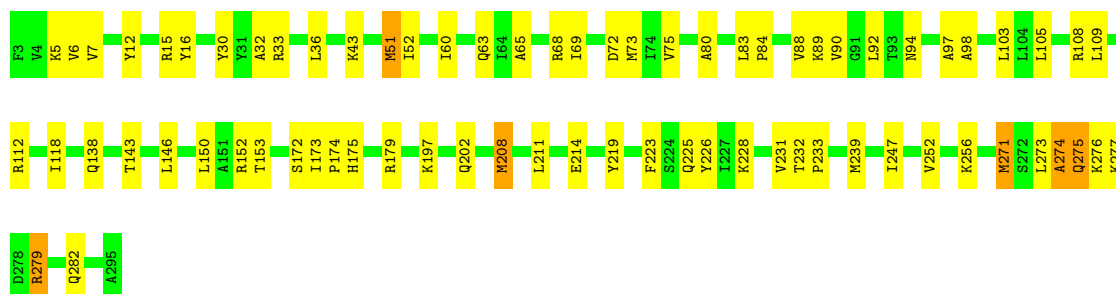
• Molecule 9: Large ribosomal subunit protein uL4

Chain C:  73% 25%



• Molecule 10: Large ribosomal subunit protein uL18

Chain D:  75% 23%



• Molecule 11: 60S ribosomal protein L6

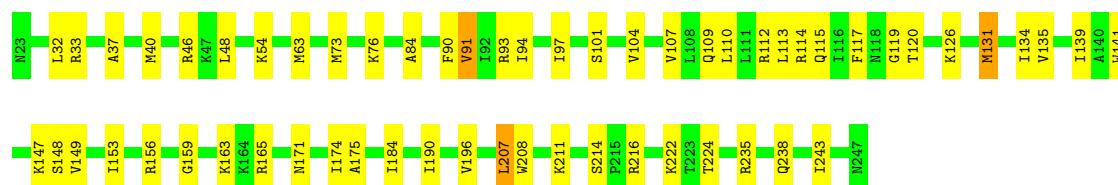
Chain E:  69% 28%





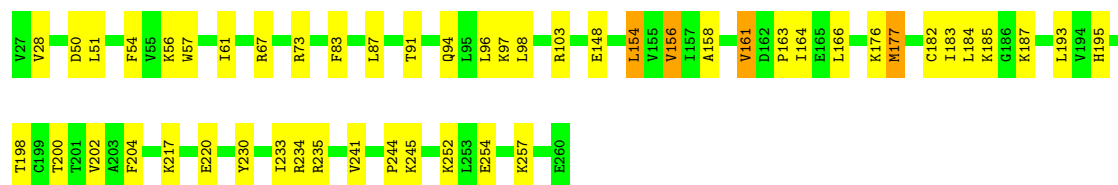
- Molecule 12: 60S ribosomal protein L7

Chain F: 74% 24%



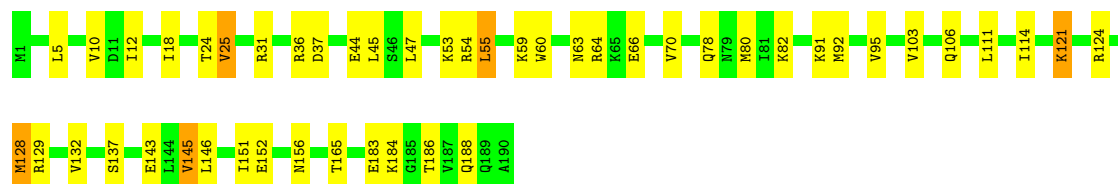
- Molecule 13: 60S ribosomal protein L7a

Chain G: 77% 21%



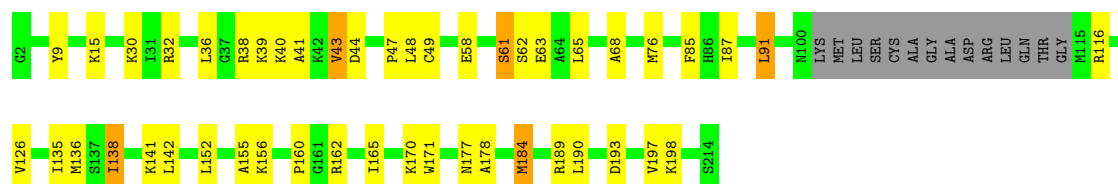
- Molecule 14: 60S ribosomal protein L9

Chain H: 75% 23%

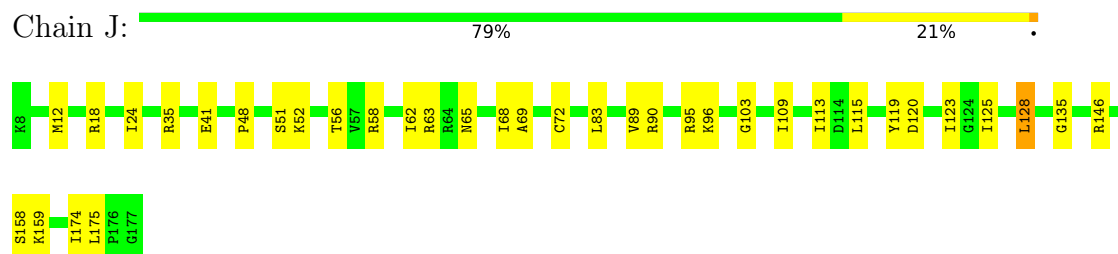


- Molecule 15: 60S ribosomal protein L10

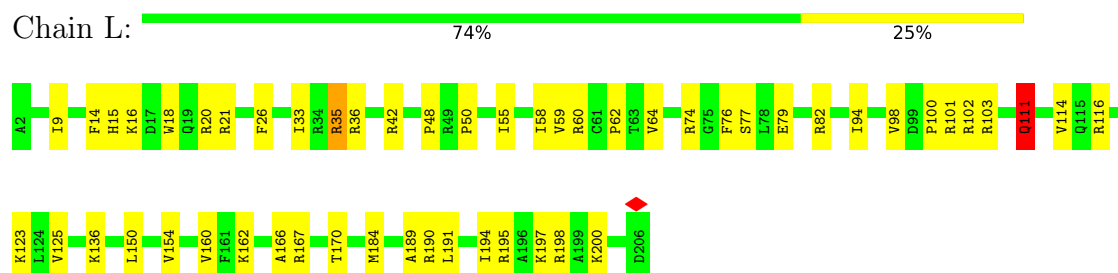
Chain I: 71% 20% 7%



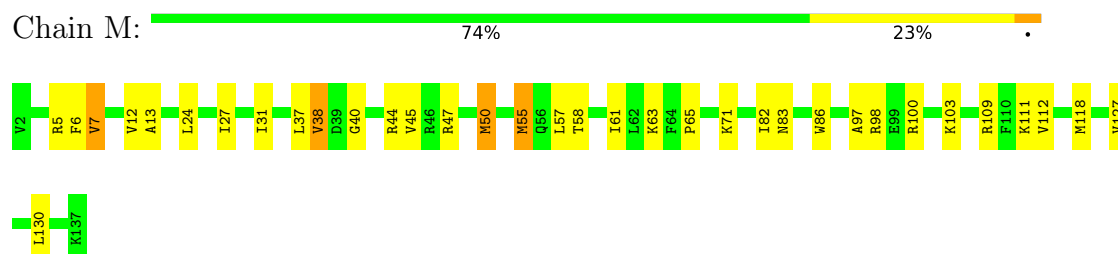
- Molecule 16: Large ribosomal subunit protein uL5



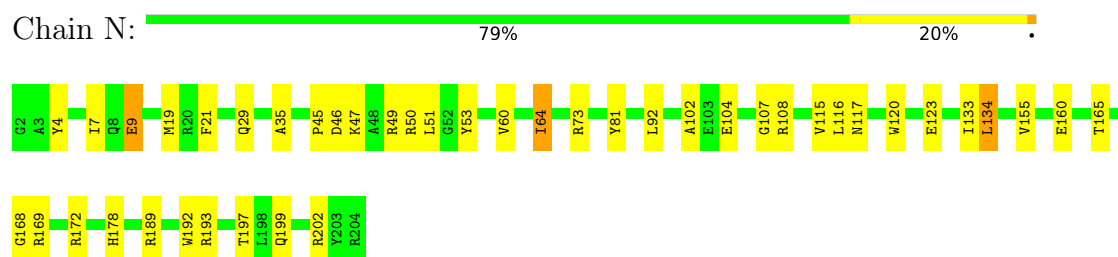
- Molecule 17: 60S ribosomal protein L13



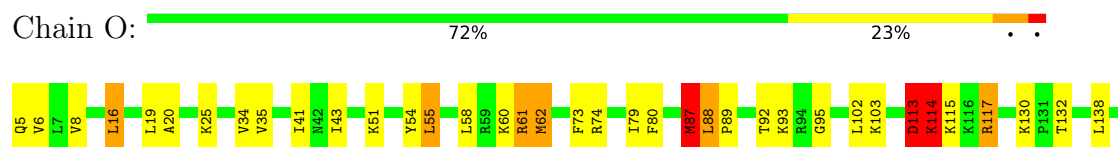
- Molecule 18: Large ribosomal subunit protein eL14



- Molecule 19: Ribosomal protein L15



- Molecule 20: 60S ribosomal protein L13a





- Molecule 21: 60S ribosomal protein L17

Chain P: 72% 24% .



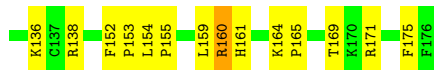
- Molecule 22: 60S ribosomal protein L18

Chain Q: 69% 30% .



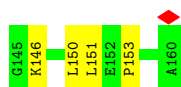
- Molecule 23: Large ribosomal subunit protein eL20

Chain S: 71% 27% .



- Molecule 24: Large ribosomal subunit protein eL21

Chain T: 76% 23% .

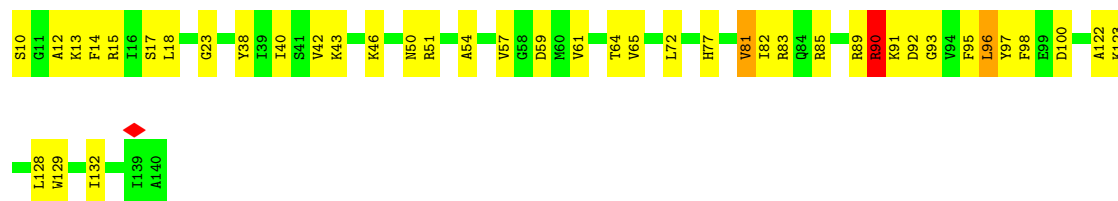


- Molecule 25: 60S ribosomal protein L22

Chain U: 74% 22% . .



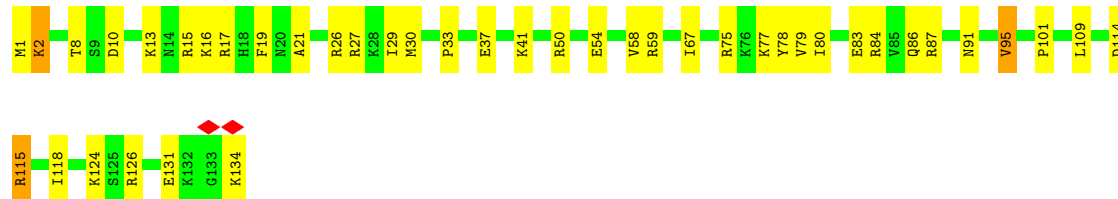
- Molecule 26: Large ribosomal subunit protein uL14



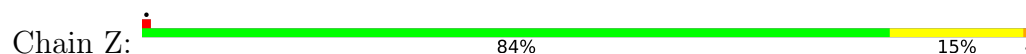
- Molecule 27: Large ribosomal subunit protein uL23



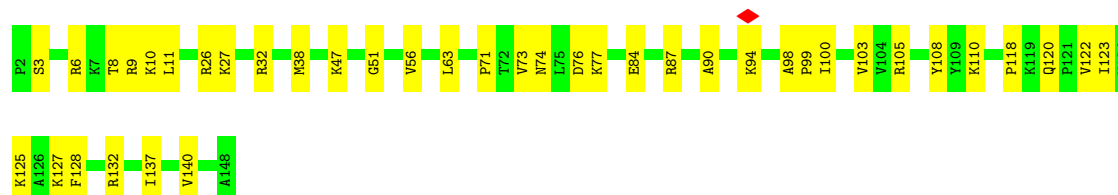
- Molecule 28: 60S ribosomal protein L26



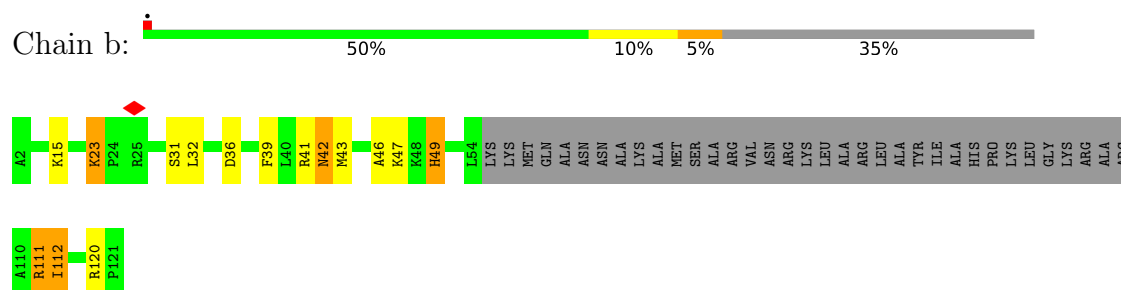
- Molecule 29: 60S ribosomal protein L27



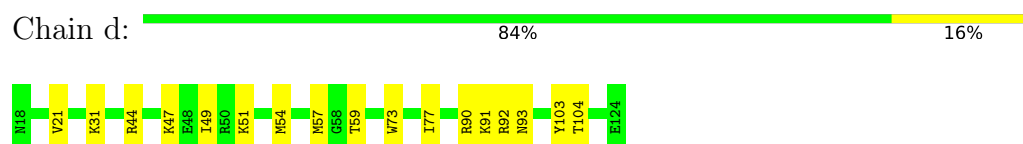
- Molecule 30: 60S ribosomal protein L27a



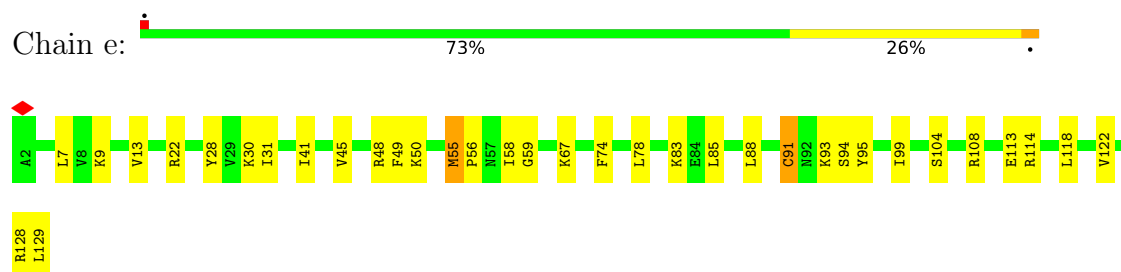
- Molecule 31: 60S ribosomal protein L29



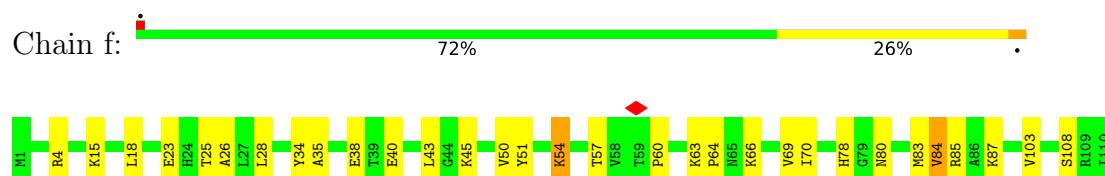
- Molecule 32: Large ribosomal subunit protein eL31



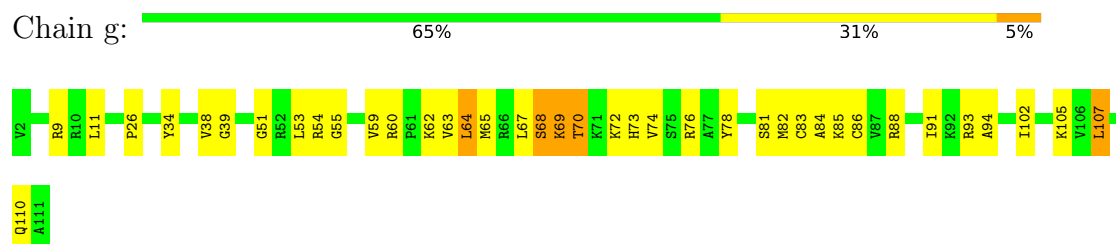
- Molecule 33: 60S ribosomal protein L32



- Molecule 34: Large ribosomal subunit protein eL33

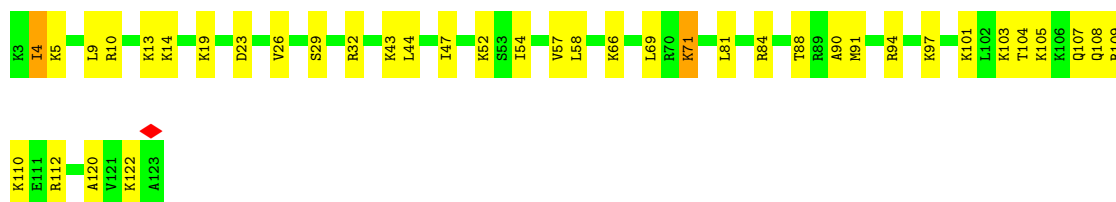


- Molecule 35: Large ribosomal subunit protein eL34



- Molecule 36: Large ribosomal subunit protein uL29

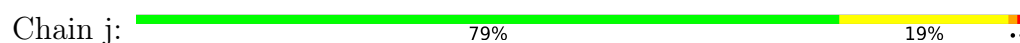




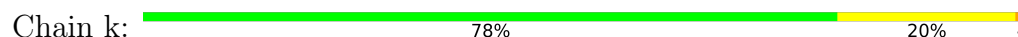
- Molecule 37: 60S ribosomal protein L36



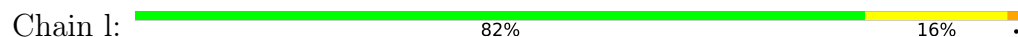
- Molecule 38: Ribosomal protein L37



- Molecule 39: Large ribosomal subunit protein eL38



- Molecule 40: Large ribosomal subunit protein eL39




- Molecule 41: Ubiquitin-ribosomal protein eL40 fusion protein



- Molecule 42: 60S ribosomal protein L36a



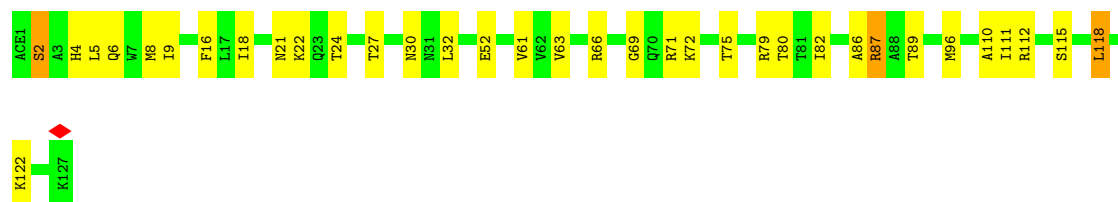
- Molecule 43: Large ribosomal subunit protein eL43

Chain p:  76% 23%



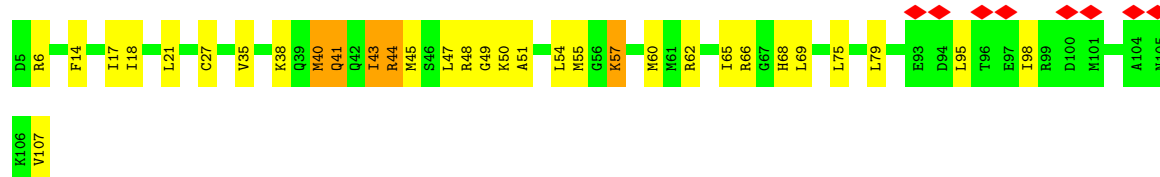
- Molecule 44: Large ribosomal subunit protein eL28

Chain r:  72% 25%




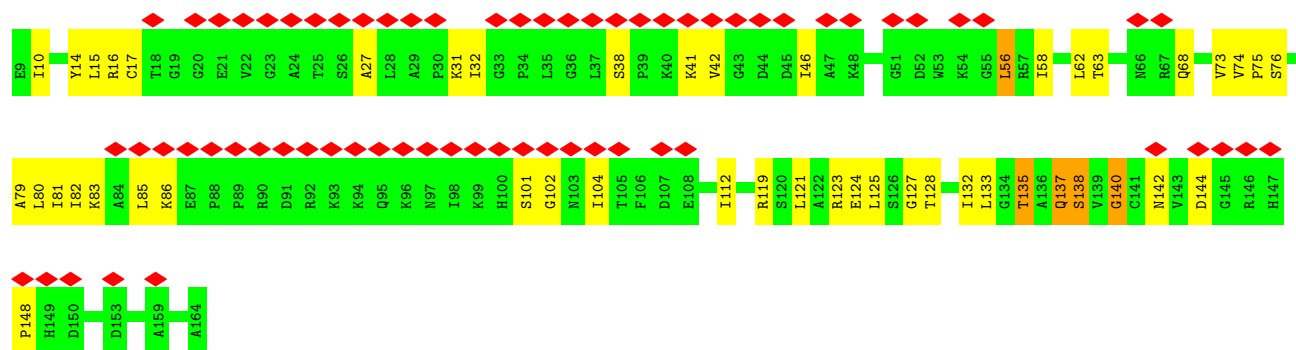
- Molecule 45: 60S acidic ribosomal protein P0

Chain s:  8% 69% 26% 5%



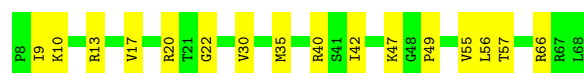
- Molecule 46: 60S ribosomal protein L12

Chain t:  43% 69% 28%

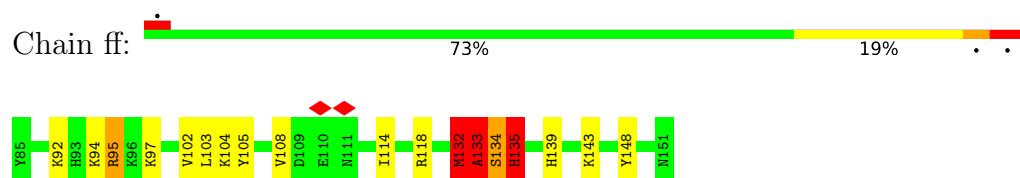


- Molecule 47: 40S ribosomal protein S28

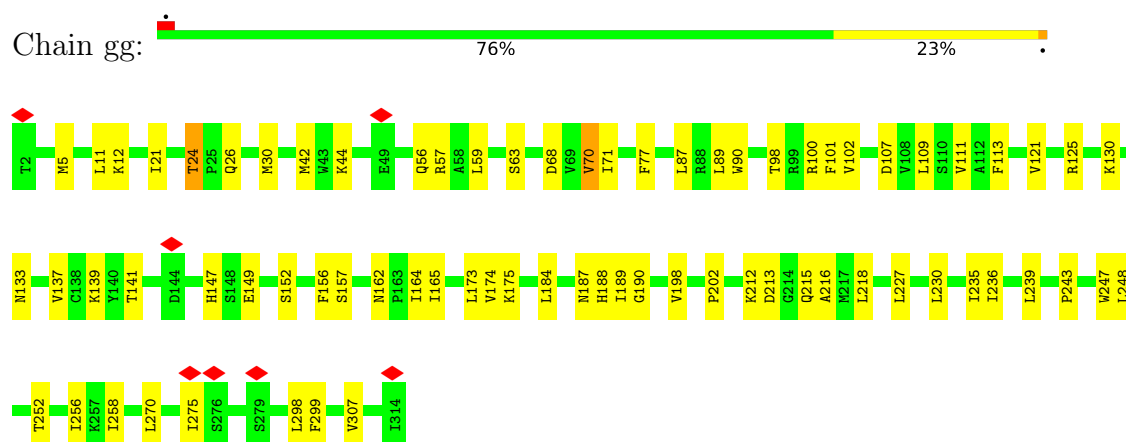
Chain cc:  74% 26%



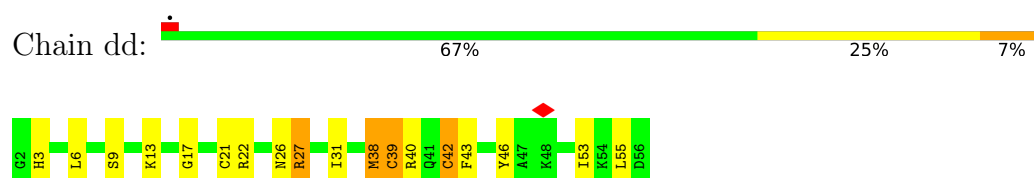
- Molecule 48: Ubiquitin-ribosomal protein eS31 fusion protein



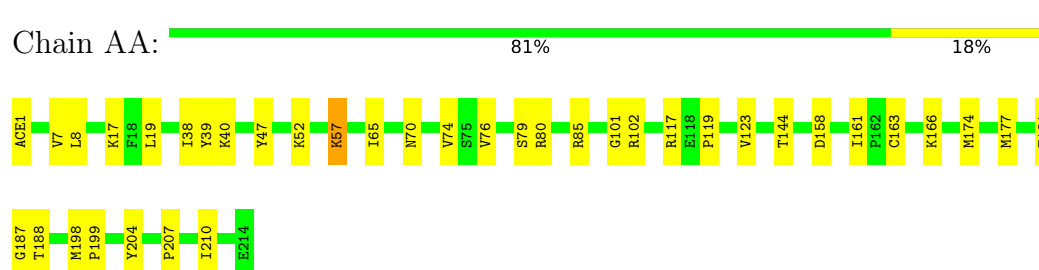
- Molecule 49: Small ribosomal subunit protein RACK1



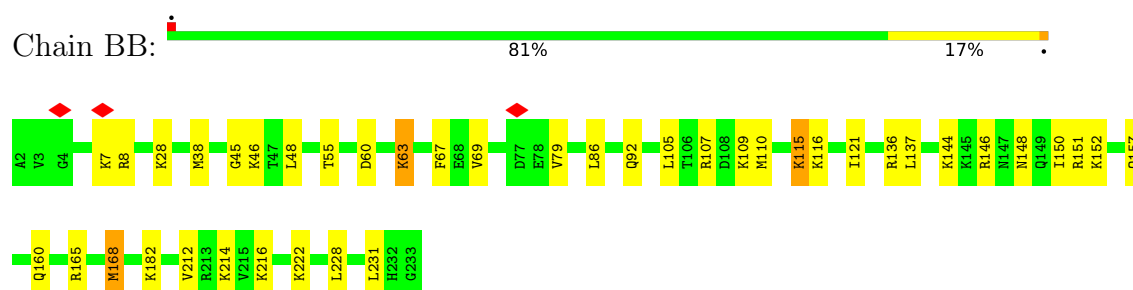
- Molecule 50: Small ribosomal subunit protein uS14



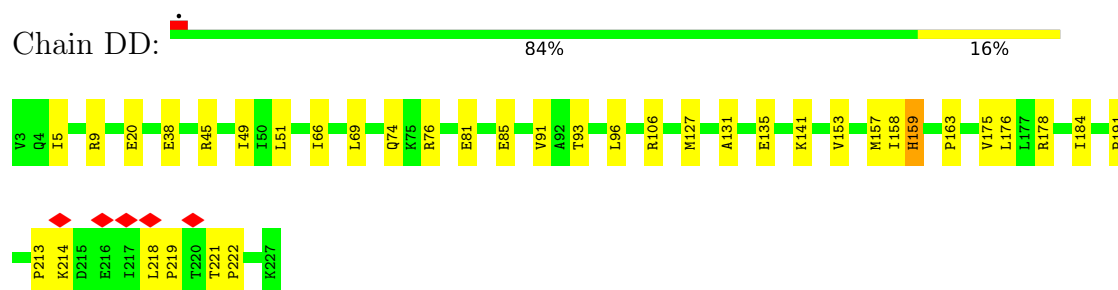
- Molecule 51: Small ribosomal subunit protein uS2



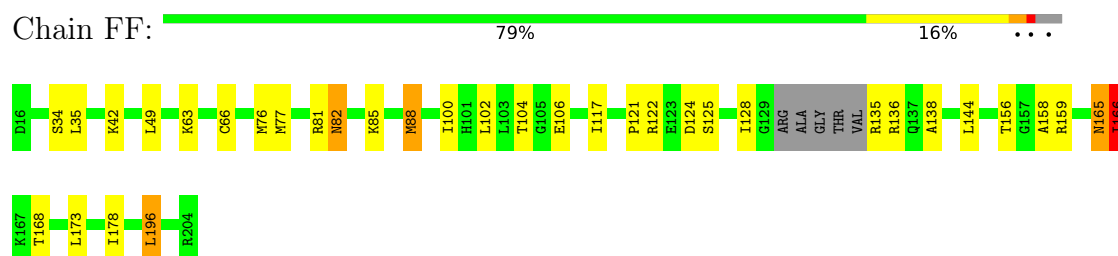
- Molecule 52: 40S ribosomal protein S3a



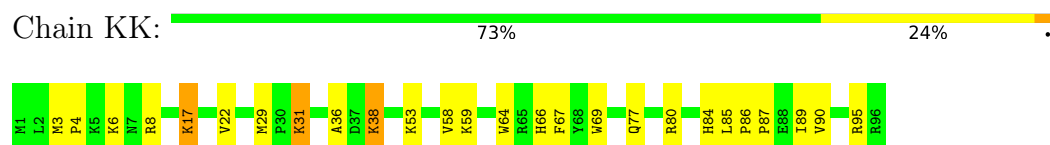
- Molecule 53: Small ribosomal subunit protein uS3



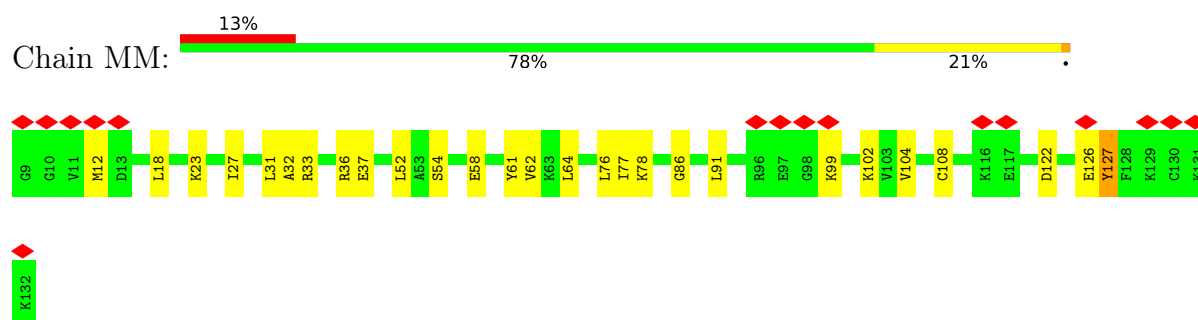
- Molecule 54: Small ribosomal subunit protein uS7



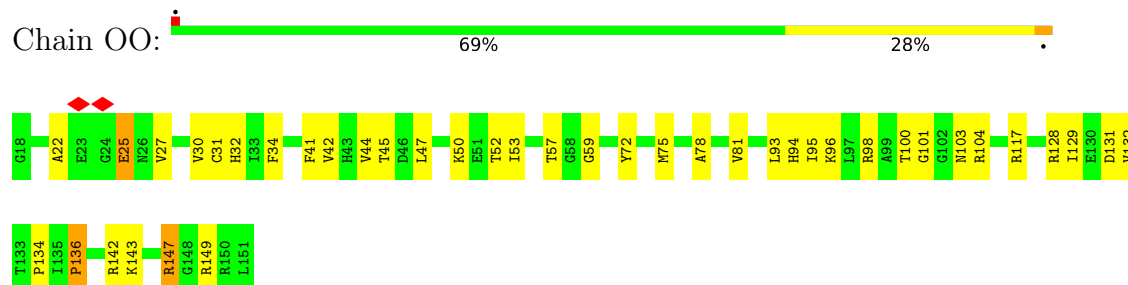
- Molecule 55: Small ribosomal subunit protein eS10



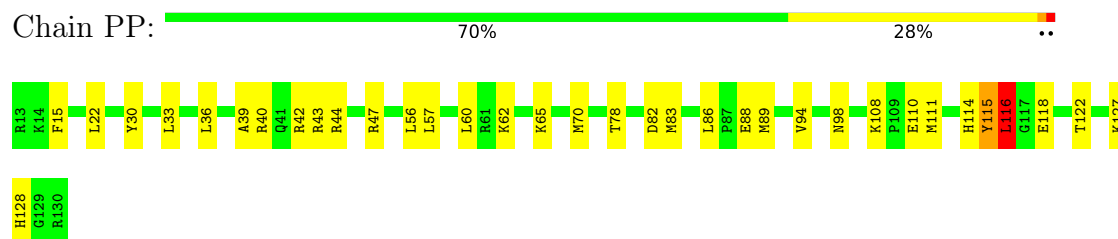
- Molecule 56: 40S ribosomal protein S12



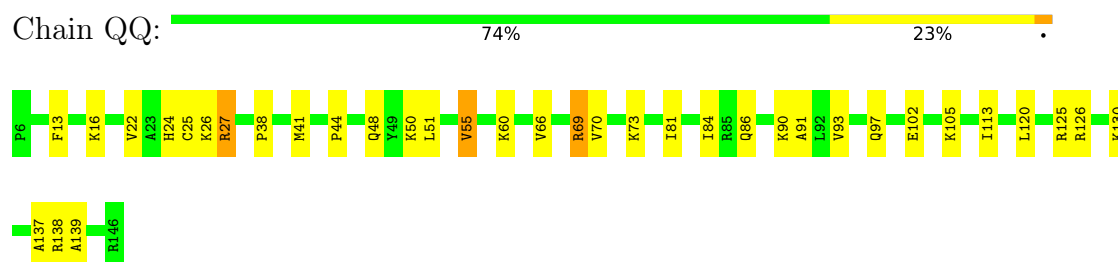
- Molecule 57: 40S ribosomal protein S14



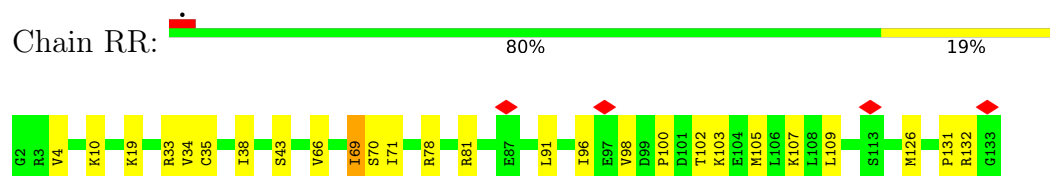
- Molecule 58: 40S ribosomal protein S15



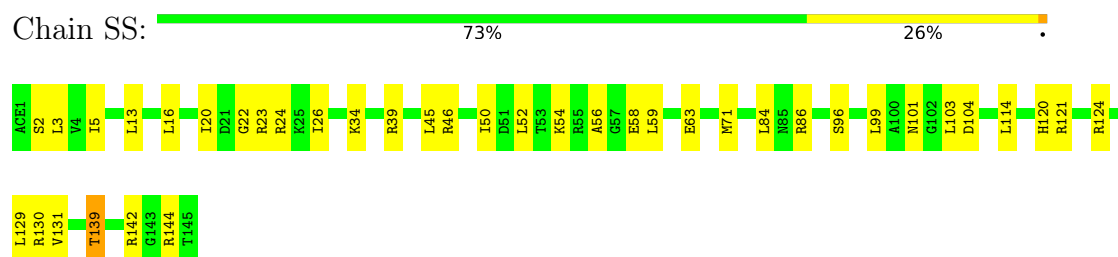
- Molecule 59: Small ribosomal subunit protein uS9



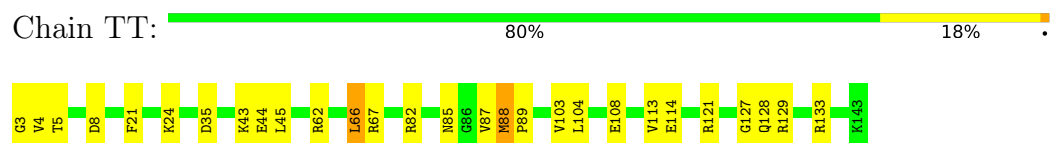
- Molecule 60: Small ribosomal subunit protein eS17



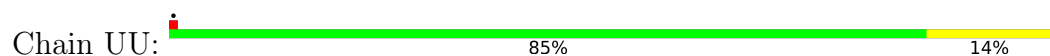
- Molecule 61: Small ribosomal subunit protein uS13



- Molecule 62: Small ribosomal subunit protein eS19

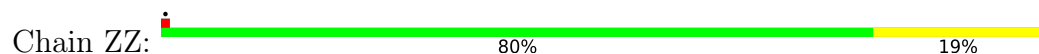


- Molecule 63: 40S ribosomal protein S20

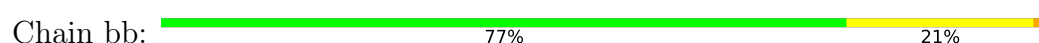




- Molecule 64: 40S ribosomal protein S25



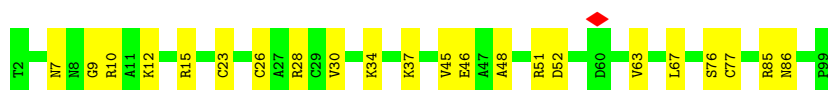
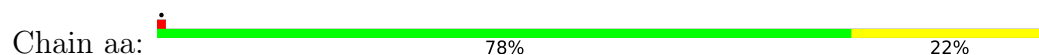
- Molecule 65: 40S ribosomal protein S27



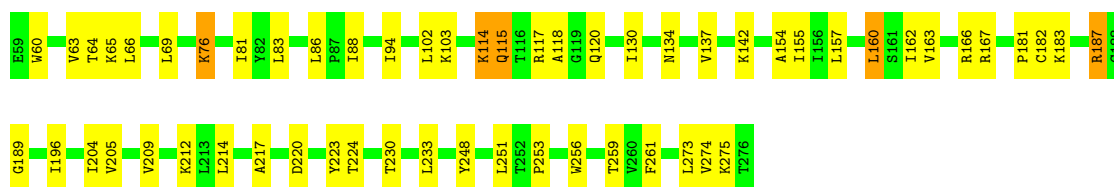
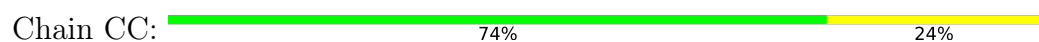
- Molecule 66: 40S ribosomal protein S30



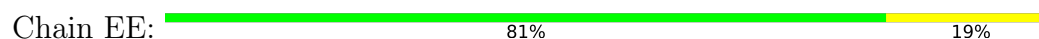
- Molecule 67: 40S ribosomal protein S26

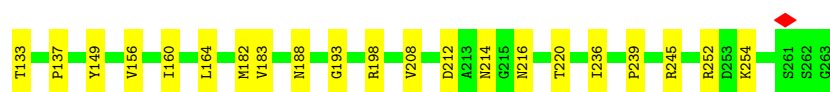


- Molecule 68: 40S ribosomal protein S2

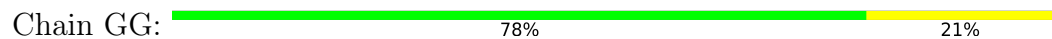


- Molecule 69: 40S ribosomal protein S4, X isoform

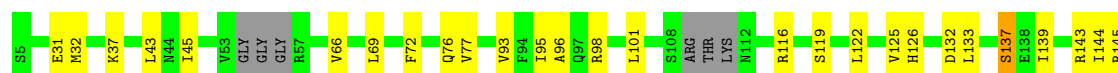
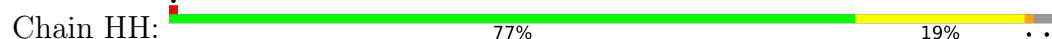




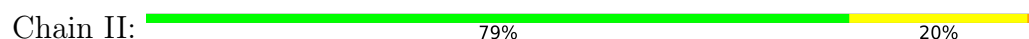
- Molecule 70: 40S ribosomal protein S6



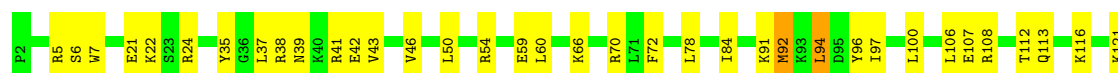
- Molecule 71: 40S ribosomal protein S7



- Molecule 72: 40S ribosomal protein S8

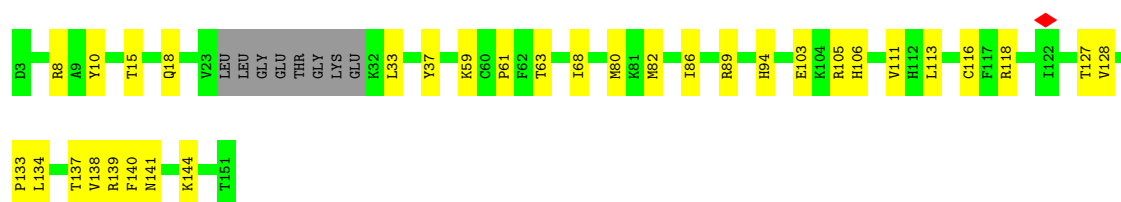


- Molecule 73: Small ribosomal subunit protein uS4



- Molecule 74: Small ribosomal subunit protein uS17





- Molecule 75: Small ribosomal subunit protein uS15

Chain NN: 80% 20%



- Molecule 76: 40S ribosomal protein S21

Chain VV: 83% 17%



- Molecule 77: Small ribosomal subunit protein uS8

Chain WW: 83% 16%



- Molecule 78: 40S ribosomal protein S23

Chain XX: 93% 7%



- Molecule 79: 40S ribosomal protein S24

Chain YY: 72% 26%



- Molecule 80: Ribosomal protein L19

Chain W: 72% 24%

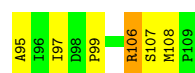




- Molecule 81: Large ribosomal subunit protein eL24



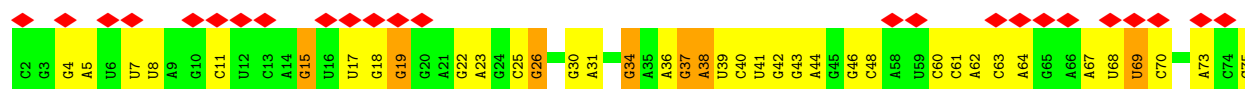
- Molecule 82: Large ribosomal subunit protein eL30



- Molecule 83: P/E tRNA



- Molecule 84: tRNA (65-MER)



- Molecule 85: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	48893	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.060	Depositor
Minimum map value	-0.019	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.009	Depositor
Map size (Å)	459.8, 459.8, 459.8	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: NMM, V5N, ACE, M3L, ZN, MG, HIC, YYG, MLZ

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	A5	1.44	46/40529 (0.1%)	0.59	60/63155 (0.1%)
2	A7	0.23	0/2857	0.41	0/4452
3	A8	0.26	0/3704	0.51	1/5770 (0.0%)
4	B2	1.59	56/42333 (0.1%)	0.53	32/65918 (0.0%)
5	A6	1.39	49/48645 (0.1%)	0.53	39/75740 (0.1%)
6	A	0.28	0/1684	0.72	2/2307 (0.1%)
7	n	0.42	0/240	1.21	2/305 (0.7%)
8	B	0.26	0/3261	0.65	1/4364 (0.0%)
9	C	0.46	2/2936 (0.1%)	0.82	10/3941 (0.3%)
10	D	0.34	1/2435 (0.0%)	0.80	10/3261 (0.3%)
11	E	4.78	12/1823 (0.7%)	1.15	16/2445 (0.7%)
12	F	0.31	0/1911	0.85	5/2549 (0.2%)
13	G	0.25	0/1772	0.63	2/2387 (0.1%)
14	H	2.77	1/1535 (0.1%)	0.73	2/2063 (0.1%)
15	I	0.25	0/1658	0.68	2/2214 (0.1%)
16	J	0.27	0/1385	0.69	0/1852
17	L	0.31	0/1689	0.75	1/2261 (0.0%)
18	M	0.34	0/1146	0.90	8/1531 (0.5%)
19	N	0.32	0/1746	0.68	2/2338 (0.1%)
20	O	1.21	5/1661 (0.3%)	1.39	12/2219 (0.5%)
21	P	3.01	6/1268 (0.5%)	0.93	9/1700 (0.5%)
22	Q	0.31	0/1537	0.86	6/2052 (0.3%)
23	S	0.29	0/1501	0.73	2/2013 (0.1%)
24	T	0.29	0/1326	0.79	1/1770 (0.1%)
25	U	0.33	0/822	0.92	9/1103 (0.8%)
26	V	0.36	0/993	0.96	2/1332 (0.2%)
27	X	0.25	0/984	0.67	0/1323
28	Y	0.30	0/1132	0.78	1/1504 (0.1%)
29	Z	0.29	0/1130	0.78	4/1507 (0.3%)
30	a	0.30	0/1179	0.77	3/1572 (0.2%)
31	b	3.07	4/544 (0.7%)	1.73	11/717 (1.5%)
32	d	0.30	0/903	0.79	1/1216 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	e	0.30	0/1071	0.83	2/1429 (0.1%)
34	f	0.42	0/903	0.92	4/1208 (0.3%)
35	g	1.64	3/883 (0.3%)	1.46	6/1177 (0.5%)
36	h	0.23	0/1019	0.70	0/1344
37	i	0.39	0/841	1.05	7/1112 (0.6%)
38	j	0.36	0/720	0.82	2/952 (0.2%)
39	k	0.32	0/575	0.81	3/761 (0.4%)
40	l	0.29	0/454	0.82	0/599
41	m	0.40	0/416	1.06	1/553 (0.2%)
42	o	0.39	0/866	0.90	3/1141 (0.3%)
43	p	0.34	0/718	0.96	3/953 (0.3%)
44	r	0.30	0/1028	0.88	4/1377 (0.3%)
45	s	4.01	4/837 (0.5%)	1.46	9/1121 (0.8%)
46	t	0.42	1/1193 (0.1%)	0.83	5/1609 (0.3%)
47	cc	0.29	0/481	0.67	1/643 (0.2%)
48	ff	0.62	2/560 (0.4%)	1.16	10/745 (1.3%)
49	gg	0.24	0/2493	0.66	3/3394 (0.1%)
50	dd	0.71	2/470 (0.4%)	1.38	10/623 (1.6%)
51	AA	0.27	0/1724	0.69	3/2343 (0.1%)
52	BB	2.57	1/1794 (0.1%)	0.77	5/2396 (0.2%)
53	DD	0.25	0/1779	0.64	2/2395 (0.1%)
54	FF	3.00	3/1481 (0.2%)	1.16	10/1988 (0.5%)
55	KK	0.37	0/834	0.91	4/1125 (0.4%)
56	MM	0.34	0/968	0.80	3/1296 (0.2%)
57	OO	0.30	0/1015	0.79	2/1361 (0.1%)
58	PP	1.45	2/997 (0.2%)	1.30	6/1330 (0.5%)
59	QQ	0.21	0/1142	0.59	0/1528
60	RR	0.29	0/1082	0.80	1/1452 (0.1%)
61	SS	0.30	0/1209	0.71	2/1620 (0.1%)
62	TT	0.29	0/1102	0.73	4/1476 (0.3%)
63	UU	0.23	0/800	0.63	1/1074 (0.1%)
64	ZZ	0.41	0/604	0.71	1/810 (0.1%)
65	bb	0.25	0/653	0.68	4/876 (0.5%)
66	ee	0.29	0/399	0.82	0/520
67	aa	0.23	0/794	0.59	0/1065
68	CC	1.18	2/1725 (0.1%)	1.02	6/2332 (0.3%)
69	EE	0.24	0/2118	0.59	1/2849 (0.0%)
70	GG	0.33	1/1870 (0.1%)	0.62	1/2489 (0.0%)
71	HH	0.23	0/1509	0.59	3/2016 (0.1%)
72	II	1.01	2/1715 (0.1%)	1.01	5/2287 (0.2%)
73	JJ	0.30	0/1524	0.75	5/2035 (0.2%)
74	LL	0.29	0/1177	0.76	1/1575 (0.1%)
75	NN	0.20	0/1226	0.53	0/1649

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	VV	0.27	0/644	0.73	2/862 (0.2%)
77	WW	0.31	0/1051	0.76	2/1406 (0.1%)
78	XX	0.24	0/819	0.69	2/1115 (0.2%)
79	YY	1.50	3/1032 (0.3%)	1.00	8/1371 (0.6%)
80	W	1.14	3/1524 (0.2%)	1.38	9/2013 (0.4%)
81	c	0.36	0/935	0.99	4/1241 (0.3%)
82	u	3.42	1/786 (0.1%)	1.33	8/1055 (0.8%)
83	Cc	1.75	6/1812 (0.3%)	1.13	12/2821 (0.4%)
84	Bb	2.65	1/1531 (0.1%)	0.50	2/2380 (0.1%)
85	Dd	0.19	0/285	0.35	0/438
All	All	1.37	219/235457 (0.1%)	0.68	448/346211 (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
6	A	0	2
7	n	0	1
8	B	0	2
9	C	0	2
10	D	0	1
11	E	0	1
17	L	0	1
20	O	0	1
22	Q	0	1
23	S	0	1
26	V	0	1
28	Y	0	1
29	Z	0	1
32	d	0	1
36	h	0	1
41	m	0	1
42	o	0	2
44	r	0	1
45	s	0	2
46	t	0	1
48	ff	0	4
53	DD	0	1
54	FF	0	1
56	MM	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
57	OO	0	2
62	TT	0	1
68	CC	0	1
73	JJ	0	1
76	VV	0	1
80	W	0	1
81	c	0	1
82	u	0	2
All	All	0	42

The worst 5 of 219 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	E	104	ASN	CA-CB	113.02	3.18	1.53
52	BB	115	LYS	CB-CG	108.20	4.77	1.52
14	H	121	LYS	CG-CD	107.94	4.76	1.52
54	FF	82	ASN	CB-CG	107.34	4.20	1.52
11	E	127	LYS	CG-CD	106.23	4.71	1.52

The worst 5 of 448 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	Cc	77	A	N3-C4-C5	-36.20	18.21	126.80
83	Cc	77	A	C6-N1-C2	-34.66	14.62	118.60
20	O	113	ASP	CA-C-N	33.00	167.57	121.71
20	O	113	ASP	C-N-CA	33.00	167.57	121.71
80	W	74	ARG	CA-C-N	29.73	164.17	122.85

There are no chirality outliers.

5 of 42 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	A	176	ASP	Peptide
6	A	96	LEU	Peptide
8	B	130	PHE	Peptide
8	B	73	VAL	Peptide
7	n	1	MET	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	A5	36275	0	18295	660	0
2	A7	2558	0	1294	20	0
3	A8	3317	0	1681	37	0
4	B2	37897	0	19056	706	0
5	A6	43564	0	21782	714	0
6	A	1648	0	1474	31	0
7	n	239	0	289	6	0
8	B	3206	0	3353	68	0
9	C	2884	0	3055	80	0
10	D	2389	0	2423	46	0
11	E	1789	0	1942	123	0
12	F	1875	0	1995	37	0
13	G	1741	0	1861	31	0
14	H	1516	0	1597	35	0
15	I	1620	0	1663	32	0
16	J	1362	0	1399	24	0
17	L	1658	0	1766	44	0
18	M	1125	0	1198	22	0
19	N	1701	0	1749	32	0
20	O	1630	0	1776	71	0
21	P	1242	0	1274	47	0
22	Q	1512	0	1629	40	0
23	S	1461	0	1502	35	0
24	T	1298	0	1366	24	0
25	U	808	0	831	13	0
26	V	979	0	1039	36	0
27	X	967	0	1040	20	0
28	Y	1115	0	1205	34	0
29	Z	1107	0	1182	12	0
30	a	1163	0	1202	31	0
31	b	545	0	578	39	0
32	d	888	0	930	11	0
33	e	1053	0	1147	17	0
34	f	884	0	924	17	0
35	g	873	0	963	47	0
36	h	1011	0	1150	31	0
37	i	830	0	916	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	j	705	0	737	13	0
39	k	569	0	637	8	0
40	l	444	0	483	7	0
41	m	422	0	457	7	0
42	o	863	0	927	27	0
43	p	708	0	756	15	0
44	r	1015	0	1085	22	0
45	s	825	0	865	52	0
46	t	1178	0	1235	31	0
47	cc	479	0	507	13	0
48	ff	548	0	552	15	0
49	gg	2436	0	2393	40	0
50	dd	459	0	449	18	0
51	AA	1689	0	1691	25	0
52	BB	1768	0	1846	37	0
53	DD	1751	0	1846	24	0
54	FF	1461	0	1511	52	0
55	KK	810	0	836	18	0
56	MM	958	0	993	15	0
57	OO	1002	0	1023	25	0
58	PP	979	0	1028	42	0
59	QQ	1124	0	1193	26	0
60	RR	1068	0	1121	22	0
61	SS	1193	0	1253	27	0
62	TT	1097	0	1123	14	0
63	UU	790	0	857	8	0
64	ZZ	598	0	656	13	0
65	bb	640	0	665	13	0
66	ee	398	0	443	14	0
67	aa	781	0	828	14	0
68	CC	1689	0	1778	58	0
69	EE	2076	0	2177	28	0
70	GG	1848	0	1999	52	0
71	HH	1490	0	1582	20	0
72	II	1686	0	1771	39	0
73	JJ	1499	0	1618	42	0
74	LL	1157	0	1223	21	0
75	NN	1202	0	1289	20	0
76	VV	637	0	631	7	0
77	WW	1034	0	1080	14	0
78	XX	810	0	711	3	0
79	YY	1015	0	1086	44	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	W	1508	0	1663	50	0
81	c	921	0	965	39	0
82	u	775	0	810	41	0
83	Cc	1623	0	827	69	0
84	Bb	1409	0	721	31	0
85	Dd	260	0	131	3	0
86	A5	9	0	0	0	0
86	A6	7	0	0	0	0
86	A7	4	0	0	0	0
86	A8	4	0	0	0	0
86	B2	7	0	0	0	0
86	BB	1	0	0	0	0
86	Bb	1	0	0	0	0
86	Cc	1	0	0	0	0
86	P	1	0	0	0	0
86	l	1	0	0	0	0
87	B2	1	0	0	0	0
87	aa	1	0	0	0	0
87	ff	1	0	0	0	0
87	g	1	0	0	0	0
87	j	1	0	0	0	0
87	m	1	0	0	0	0
87	o	1	0	0	0	0
87	p	1	0	0	0	0
88	A6	1	0	0	0	0
88	B2	4	0	0	0	0
88	Bb	5	0	0	0	0
88	Cc	5	0	0	0	0
All	All	219186	0	160584	3551	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 10.

The worst 5 of 3551 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A5:1972:G:C5	1:A5:1972:G:C6	1.86	1.62
5:A6:4613:C:N1	5:A6:4613:C:C6	1.68	1.60
4:B2:1869:A:C2	4:B2:1869:A:N1	1.68	1.60
5:A6:4613:C:C4	5:A6:4613:C:N3	1.70	1.59
4:B2:1869:A:C4	4:B2:1869:A:N3	1.68	1.58

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	A	246/248 (99%)	229 (93%)	16 (6%)	1 (0%)	30	67
7	n	23/25 (92%)	23 (100%)	0	0	100	100
8	B	395/398 (99%)	369 (93%)	26 (7%)	0	100	100
9	C	359/363 (99%)	341 (95%)	18 (5%)	0	100	100
10	D	291/293 (99%)	271 (93%)	20 (7%)	0	100	100
11	E	218/224 (97%)	199 (91%)	19 (9%)	0	100	100
12	F	223/225 (99%)	210 (94%)	13 (6%)	0	100	100
13	G	211/215 (98%)	204 (97%)	7 (3%)	0	100	100
14	H	188/190 (99%)	182 (97%)	6 (3%)	0	100	100
15	I	195/213 (92%)	182 (93%)	13 (7%)	0	100	100
16	J	168/170 (99%)	161 (96%)	7 (4%)	0	100	100
17	L	203/205 (99%)	194 (96%)	9 (4%)	0	100	100
18	M	134/136 (98%)	128 (96%)	6 (4%)	0	100	100
19	N	201/203 (99%)	193 (96%)	8 (4%)	0	100	100
20	O	195/199 (98%)	188 (96%)	7 (4%)	0	100	100
21	P	151/153 (99%)	148 (98%)	3 (2%)	0	100	100
22	Q	185/187 (99%)	179 (97%)	6 (3%)	0	100	100
23	S	174/176 (99%)	161 (92%)	12 (7%)	1 (1%)	21	58
24	T	157/159 (99%)	148 (94%)	9 (6%)	0	100	100
25	U	97/99 (98%)	94 (97%)	3 (3%)	0	100	100
26	V	129/131 (98%)	114 (88%)	15 (12%)	0	100	100
27	X	116/118 (98%)	108 (93%)	8 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	Y	132/134 (98%)	127 (96%)	5 (4%)	0	100	100
29	Z	133/135 (98%)	124 (93%)	9 (7%)	0	100	100
30	a	144/147 (98%)	136 (94%)	8 (6%)	0	100	100
31	b	60/100 (60%)	56 (93%)	4 (7%)	0	100	100
32	d	105/107 (98%)	100 (95%)	5 (5%)	0	100	100
33	e	126/128 (98%)	120 (95%)	6 (5%)	0	100	100
34	f	108/110 (98%)	95 (88%)	13 (12%)	0	100	100
35	g	108/110 (98%)	103 (95%)	4 (4%)	1 (1%)	14	49
36	h	119/121 (98%)	116 (98%)	3 (2%)	0	100	100
37	i	100/102 (98%)	99 (99%)	1 (1%)	0	100	100
38	j	84/86 (98%)	73 (87%)	11 (13%)	0	100	100
39	k	67/69 (97%)	67 (100%)	0	0	100	100
40	l	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
41	m	48/51 (94%)	44 (92%)	4 (8%)	0	100	100
42	o	102/105 (97%)	90 (88%)	11 (11%)	1 (1%)	12	47
43	p	89/91 (98%)	85 (96%)	4 (4%)	0	100	100
44	r	125/127 (98%)	112 (90%)	13 (10%)	0	100	100
45	s	101/103 (98%)	89 (88%)	12 (12%)	0	100	100
46	t	154/156 (99%)	135 (88%)	19 (12%)	0	100	100
47	cc	59/61 (97%)	54 (92%)	5 (8%)	0	100	100
48	ff	65/67 (97%)	56 (86%)	8 (12%)	1 (2%)	8	38
49	gg	311/313 (99%)	292 (94%)	19 (6%)	0	100	100
50	dd	53/55 (96%)	46 (87%)	7 (13%)	0	100	100
51	AA	212/214 (99%)	201 (95%)	11 (5%)	0	100	100
52	BB	214/218 (98%)	202 (94%)	12 (6%)	0	100	100
53	DD	223/225 (99%)	213 (96%)	10 (4%)	0	100	100
54	FF	180/189 (95%)	174 (97%)	6 (3%)	0	100	100
55	KK	94/96 (98%)	88 (94%)	6 (6%)	0	100	100
56	MM	122/124 (98%)	110 (90%)	12 (10%)	0	100	100
57	OO	132/134 (98%)	123 (93%)	9 (7%)	0	100	100
58	PP	116/118 (98%)	111 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
59	QQ	139/141 (99%)	131 (94%)	8 (6%)	0	100	100
60	RR	130/132 (98%)	125 (96%)	5 (4%)	0	100	100
61	SS	143/145 (99%)	134 (94%)	8 (6%)	1 (1%)	18	55
62	TT	138/141 (98%)	134 (97%)	4 (3%)	0	100	100
63	UU	97/99 (98%)	93 (96%)	4 (4%)	0	100	100
64	ZZ	73/75 (97%)	71 (97%)	2 (3%)	0	100	100
65	bb	80/82 (98%)	77 (96%)	3 (4%)	0	100	100
66	ee	45/49 (92%)	45 (100%)	0	0	100	100
67	aa	96/98 (98%)	90 (94%)	6 (6%)	0	100	100
68	CC	216/218 (99%)	203 (94%)	13 (6%)	0	100	100
69	EE	260/262 (99%)	248 (95%)	12 (5%)	0	100	100
70	GG	224/228 (98%)	215 (96%)	9 (4%)	0	100	100
71	HH	174/190 (92%)	168 (97%)	6 (3%)	0	100	100
72	II	204/206 (99%)	194 (95%)	10 (5%)	0	100	100
73	JJ	178/180 (99%)	166 (93%)	11 (6%)	1 (1%)	21	58
74	LL	137/149 (92%)	126 (92%)	11 (8%)	0	100	100
75	NN	147/149 (99%)	144 (98%)	3 (2%)	0	100	100
76	VV	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
77	WW	127/129 (98%)	118 (93%)	9 (7%)	0	100	100
78	XX	114/122 (93%)	108 (95%)	6 (5%)	0	100	100
79	YY	123/125 (98%)	118 (96%)	5 (4%)	0	100	100
80	W	178/180 (99%)	165 (93%)	11 (6%)	2 (1%)	11	45
81	c	109/121 (90%)	93 (85%)	16 (15%)	0	100	100
82	u	98/100 (98%)	77 (79%)	21 (21%)	0	100	100
All	All	11304/11580 (98%)	10636 (94%)	659 (6%)	9 (0%)	49	83

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
23	S	169	THR
42	o	54	PRO
48	ff	133	ALA
35	g	68	SER
61	SS	2	SER

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	A	136/190 (72%)	126 (93%)	10 (7%)	13	34
7	n	24/24 (100%)	23 (96%)	1 (4%)	26	48
8	B	344/344 (100%)	327 (95%)	17 (5%)	22	44
9	C	301/301 (100%)	290 (96%)	11 (4%)	30	51
10	D	247/247 (100%)	241 (98%)	6 (2%)	43	63
11	E	197/197 (100%)	191 (97%)	6 (3%)	36	57
12	F	196/196 (100%)	188 (96%)	8 (4%)	27	49
13	G	187/187 (100%)	181 (97%)	6 (3%)	34	55
14	H	169/169 (100%)	160 (95%)	9 (5%)	20	42
15	I	170/180 (94%)	164 (96%)	6 (4%)	32	53
16	J	143/143 (100%)	138 (96%)	5 (4%)	32	53
17	L	170/170 (100%)	162 (95%)	8 (5%)	23	45
18	M	116/116 (100%)	113 (97%)	3 (3%)	40	61
19	N	171/171 (100%)	166 (97%)	5 (3%)	37	58
20	O	171/171 (100%)	162 (95%)	9 (5%)	20	42
21	P	134/134 (100%)	133 (99%)	1 (1%)	76	79
22	Q	164/164 (100%)	162 (99%)	2 (1%)	63	74
23	S	157/157 (100%)	152 (97%)	5 (3%)	34	55
24	T	139/139 (100%)	132 (95%)	7 (5%)	22	43
25	U	89/89 (100%)	84 (94%)	5 (6%)	19	41
26	V	101/101 (100%)	94 (93%)	7 (7%)	14	36
27	X	106/106 (100%)	106 (100%)	0	100	100
28	Y	124/124 (100%)	122 (98%)	2 (2%)	55	69
29	Z	117/117 (100%)	116 (99%)	1 (1%)	70	77
30	a	118/118 (100%)	118 (100%)	0	100	100
31	b	56/82 (68%)	53 (95%)	3 (5%)	20	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	d	98/98 (100%)	98 (100%)	0	100	100
33	e	114/114 (100%)	104 (91%)	10 (9%)	9	29
34	f	89/89 (100%)	84 (94%)	5 (6%)	19	41
35	g	94/94 (100%)	88 (94%)	6 (6%)	16	38
36	h	109/109 (100%)	106 (97%)	3 (3%)	38	59
37	i	86/86 (100%)	81 (94%)	5 (6%)	18	40
38	j	73/73 (100%)	70 (96%)	3 (4%)	27	49
39	k	64/64 (100%)	63 (98%)	1 (2%)	55	69
40	l	47/47 (100%)	46 (98%)	1 (2%)	47	65
41	m	46/46 (100%)	44 (96%)	2 (4%)	26	48
42	o	92/92 (100%)	89 (97%)	3 (3%)	33	55
43	p	74/74 (100%)	73 (99%)	1 (1%)	59	72
44	r	110/110 (100%)	105 (96%)	5 (4%)	24	46
45	s	90/90 (100%)	88 (98%)	2 (2%)	45	64
46	t	128/128 (100%)	124 (97%)	4 (3%)	35	56
47	cc	54/54 (100%)	54 (100%)	0	100	100
48	ff	60/60 (100%)	59 (98%)	1 (2%)	53	68
49	gg	272/272 (100%)	265 (97%)	7 (3%)	40	61
50	dd	48/48 (100%)	46 (96%)	2 (4%)	26	48
51	AA	179/179 (100%)	175 (98%)	4 (2%)	45	64
52	BB	197/197 (100%)	191 (97%)	6 (3%)	36	57
53	DD	189/189 (100%)	187 (99%)	2 (1%)	65	74
54	FF	156/159 (98%)	154 (99%)	2 (1%)	61	72
55	KK	87/87 (100%)	86 (99%)	1 (1%)	65	74
56	MM	104/104 (100%)	100 (96%)	4 (4%)	29	51
57	OO	104/104 (100%)	101 (97%)	3 (3%)	37	58
58	PP	107/107 (100%)	103 (96%)	4 (4%)	30	51
59	QQ	117/117 (100%)	113 (97%)	4 (3%)	32	54
60	RR	119/119 (100%)	117 (98%)	2 (2%)	53	68
61	SS	125/125 (100%)	122 (98%)	3 (2%)	43	63
62	TT	110/110 (100%)	105 (96%)	5 (4%)	24	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
63	UU	92/92 (100%)	89 (97%)	3 (3%)	33	55
64	ZZ	66/66 (100%)	65 (98%)	1 (2%)	57	71
65	bb	74/74 (100%)	74 (100%)	0	100	100
66	ee	41/41 (100%)	40 (98%)	1 (2%)	43	63
67	aa	85/85 (100%)	80 (94%)	5 (6%)	18	40
68	CC	183/183 (100%)	175 (96%)	8 (4%)	25	47
69	EE	224/224 (100%)	215 (96%)	9 (4%)	28	49
70	GG	199/199 (100%)	192 (96%)	7 (4%)	32	53
71	HH	167/170 (98%)	161 (96%)	6 (4%)	31	52
72	II	178/178 (100%)	176 (99%)	2 (1%)	65	74
73	JJ	160/160 (100%)	157 (98%)	3 (2%)	50	66
74	LL	128/134 (96%)	125 (98%)	3 (2%)	44	63
75	NN	130/130 (100%)	124 (95%)	6 (5%)	24	46
76	VV	68/68 (100%)	66 (97%)	2 (3%)	37	58
77	WW	112/112 (100%)	109 (97%)	3 (3%)	39	60
78	XX	65/98 (66%)	63 (97%)	2 (3%)	35	56
79	YY	107/107 (100%)	100 (94%)	7 (6%)	15	37
80	W	159/159 (100%)	153 (96%)	6 (4%)	29	51
81	c	92/100 (92%)	88 (96%)	4 (4%)	26	48
82	u	85/85 (100%)	81 (95%)	4 (5%)	23	45
All	All	9804/9947 (99%)	9478 (97%)	326 (3%)	34	55

5 of 326 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
59	QQ	55	VAL
73	JJ	94	LEU
61	SS	139	THR
68	CC	224	THR
77	WW	81	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 106 such sidechains are listed below:

Mol	Chain	Res	Type
49	gg	296	GLN
57	OO	79	GLN
78	XX	16	HIS
51	AA	141	ASN
54	FF	65	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A5	1665/1717 (96%)	698 (41%)	66 (3%)
2	A7	119/120 (99%)	30 (25%)	0
3	A8	155/156 (99%)	66 (42%)	4 (2%)
4	B2	1754/1804 (97%)	686 (39%)	43 (2%)
5	A6	1994/2092 (95%)	737 (36%)	44 (2%)
83	Cc	75/76 (98%)	31 (41%)	0
84	Bb	62/65 (95%)	28 (45%)	0
85	Dd	12/13 (92%)	3 (25%)	0
All	All	5836/6043 (96%)	2279 (39%)	157 (2%)

5 of 2279 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A5	6	C
1	A5	9	C
1	A5	12	A
1	A5	13	U
1	A5	14	C

5 of 157 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	A6	2266	C
5	A6	4629	U
5	A6	2395	A
5	A6	3799	A
5	A6	4946	U

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

7 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul

statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
42	MLZ	o	53	42	8,9,10	1.35	1 (12%)	4,9,11	0.88	0
31	MLZ	b	5	31	8,9,10	0.80	0	4,9,11	0.67	0
84	YYG	Bb	37	85,86,84	38,42,43	0.63	0	45,62,65	1.40	9 (20%)
8	HIC	B	245	8	10,11,12	0.55	0	9,14,16	0.71	0
62	NMM	TT	67	62	8,11,12	0.67	0	7,12,14	2.15	2 (28%)
30	V5N	a	39	30	8,11,12	0.57	0	8,14,16	0.90	0
41	M3L	m	98	41	10,11,12	0.41	0	9,14,16	0.28	0

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
42	MLZ	o	53	42	-	3/7/8/10	-
31	MLZ	b	5	31	-	1/7/8/10	-
84	YYG	Bb	37	85,86,84	-	8/24/42/43	0/4/4/4
8	HIC	B	245	8	-	2/5/6/8	0/1/1/1
62	NMM	TT	67	62	-	2/9/11/13	-
30	V5N	a	39	30	-	5/9/10/12	0/1/1/1
41	M3L	m	98	41	-	1/9/10/12	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	o	53	MLZ	O-C	3.70	1.34	1.20

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	TT	67	NMM	NE-CZ-NH2	-4.84	115.05	119.48
84	Bb	37	YYG	O6-C6-N1	3.86	125.39	119.87
84	Bb	37	YYG	C5-C4-N3	-3.39	121.24	123.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	Bb	37	YYG	N9-C4-N3	2.87	134.10	129.45
84	Bb	37	YYG	C1'-N9-C8	-2.69	119.09	126.73

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
42	o	53	MLZ	N-CA-CB-CG
42	o	53	MLZ	C-CA-CB-CG
42	o	53	MLZ	CD-CE-NZ-CM
62	TT	67	NMM	C-CA-CB-CG
62	TT	67	NMM	N-CA-CB-CG

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
84	Bb	37	YYG	2	0
8	B	245	HIC	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 44 ligands modelled in this entry, 44 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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A5	11
5	A6	5
4	B2	4
78	XX	3
11	E	2
84	Bb	2
71	HH	2
20	O	2
52	BB	1
66	ee	1
13	G	1
70	GG	1
83	Cc	1
9	C	1
80	W	1
45	s	1
68	CC	1
35	g	1
58	PP	1
72	II	1

The worst 5 of 43 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BB	8:ARG	C	23:ASP	N	19.98
1	E	78:ALA	C	90:LYS	N	19.53
1	A5	1249:C	O3'	1261:G	P	17.69
1	A6	3295:G	O3'	3571:C	P	16.69
1	A5	1703:C	O3'	1720:C	P	16.31

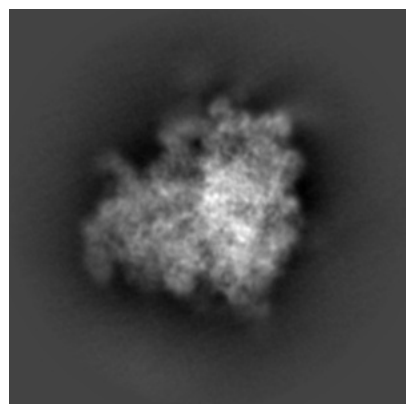
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72470. These allow visual inspection of the internal detail of the map and identification of artifacts.

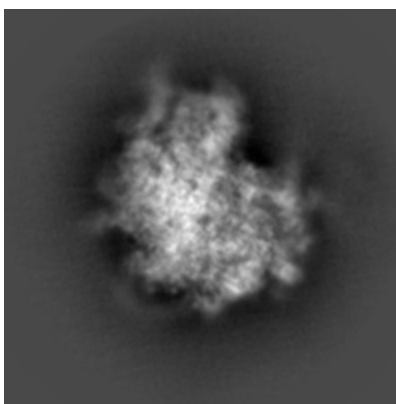
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

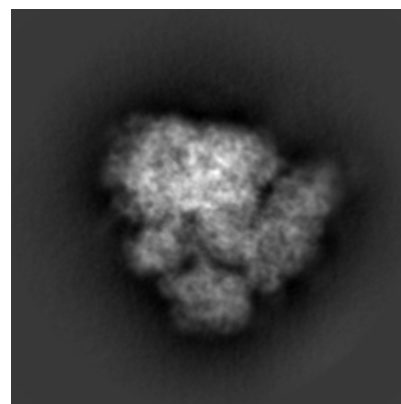
6.1.1 Primary map



X

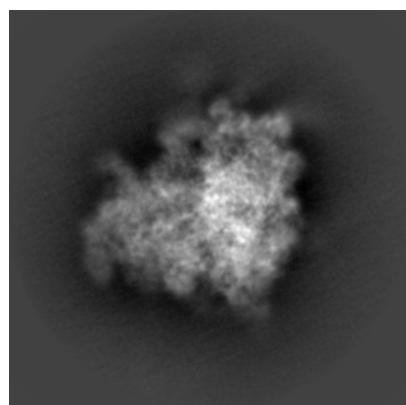


Y

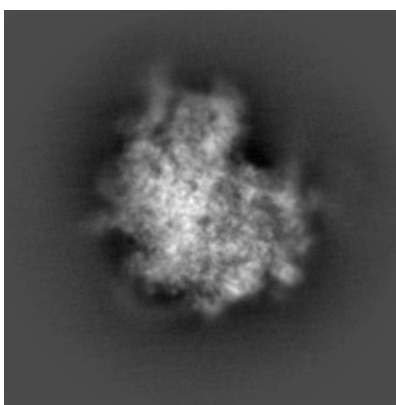


Z

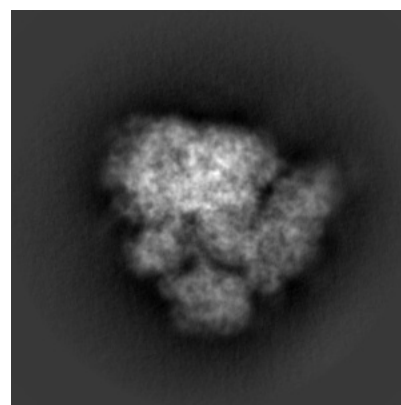
6.1.2 Raw map



X



Y

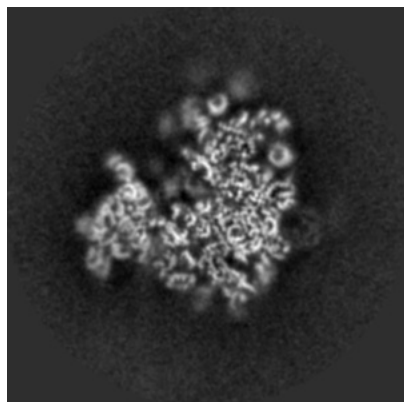


Z

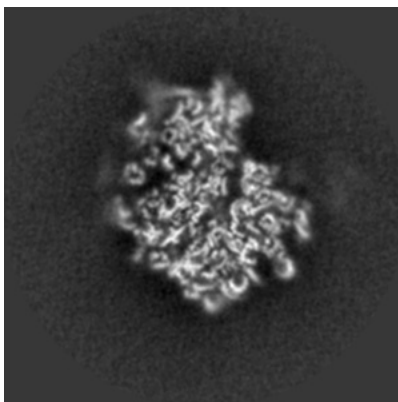
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

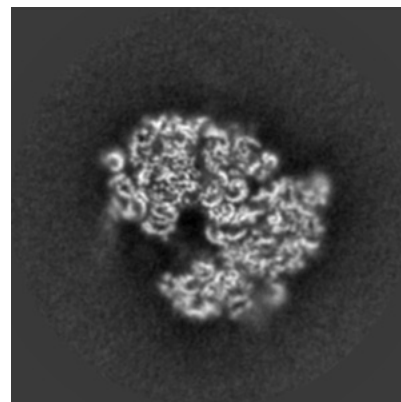
6.2.1 Primary map



X Index: 220

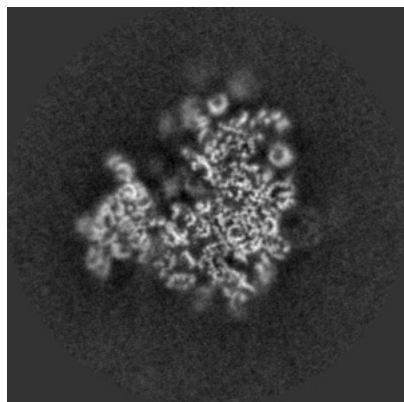


Y Index: 220

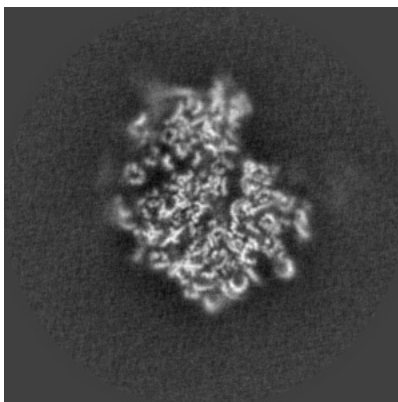


Z Index: 220

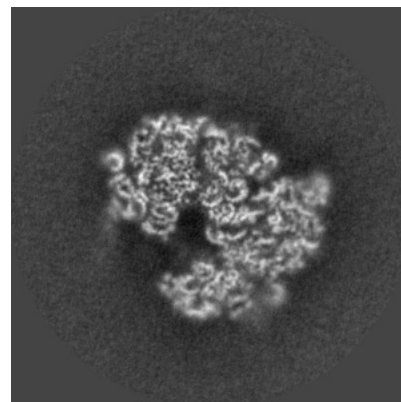
6.2.2 Raw map



X Index: 220



Y Index: 220

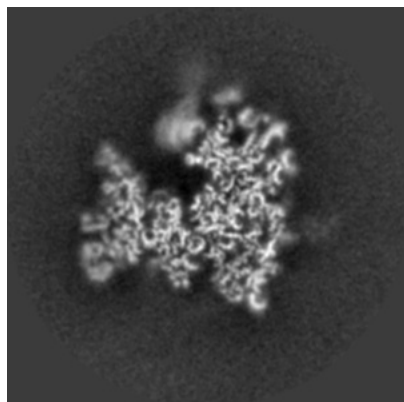


Z Index: 220

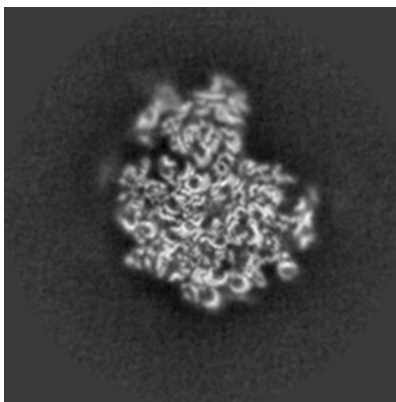
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

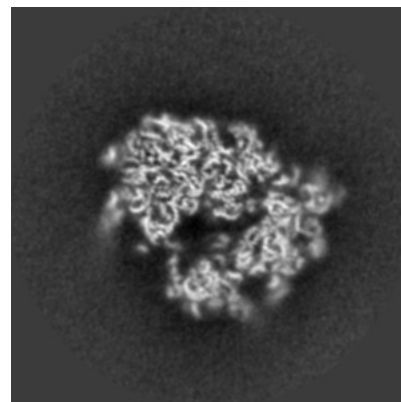
6.3.1 Primary map



X Index: 237

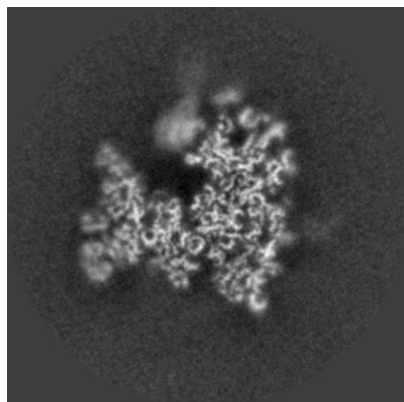


Y Index: 228

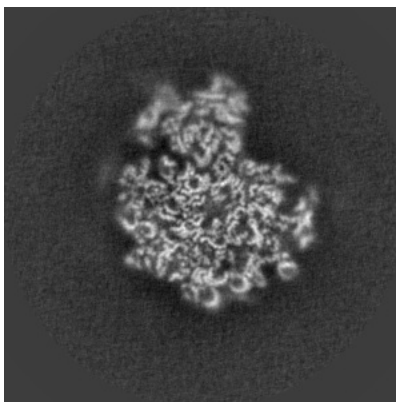


Z Index: 229

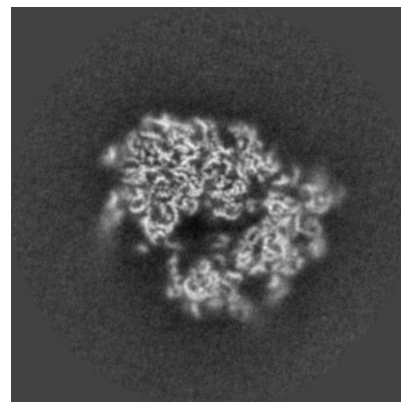
6.3.2 Raw map



X Index: 238



Y Index: 228

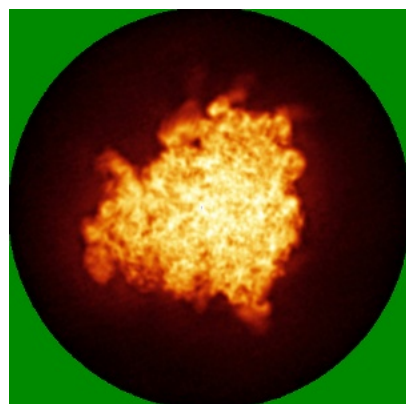


Z Index: 229

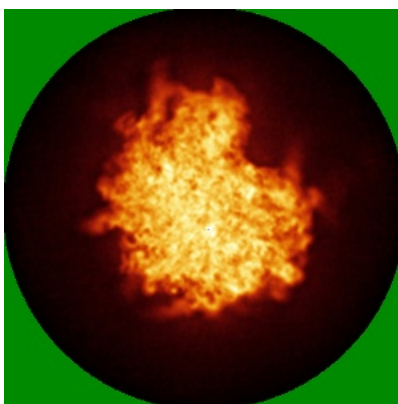
The images above show the largest variance slices of the map in three orthogonal directions.

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

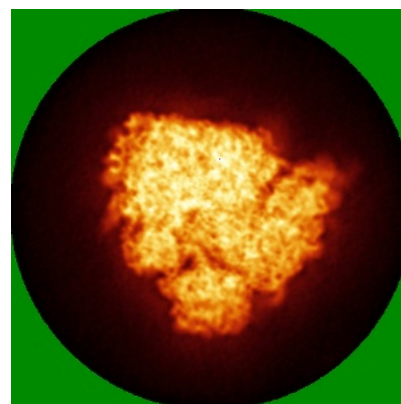
6.4.1 Primary map



X

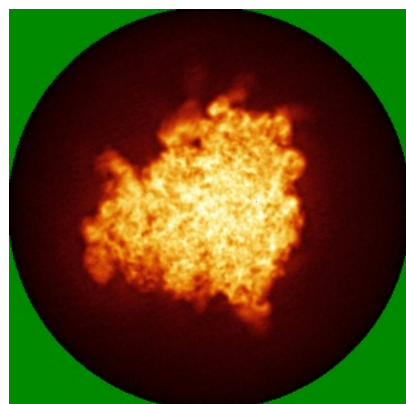


Y

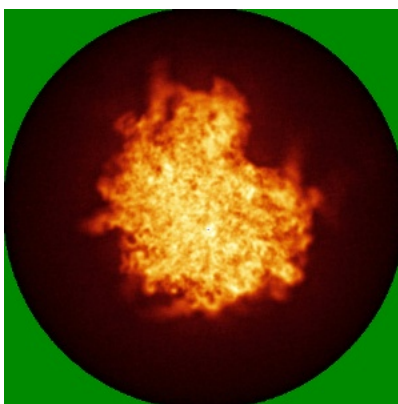


Z

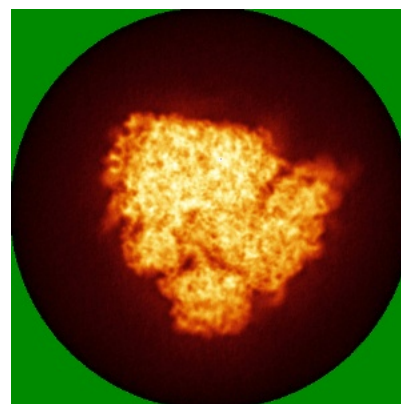
6.4.2 Raw map



X



Y

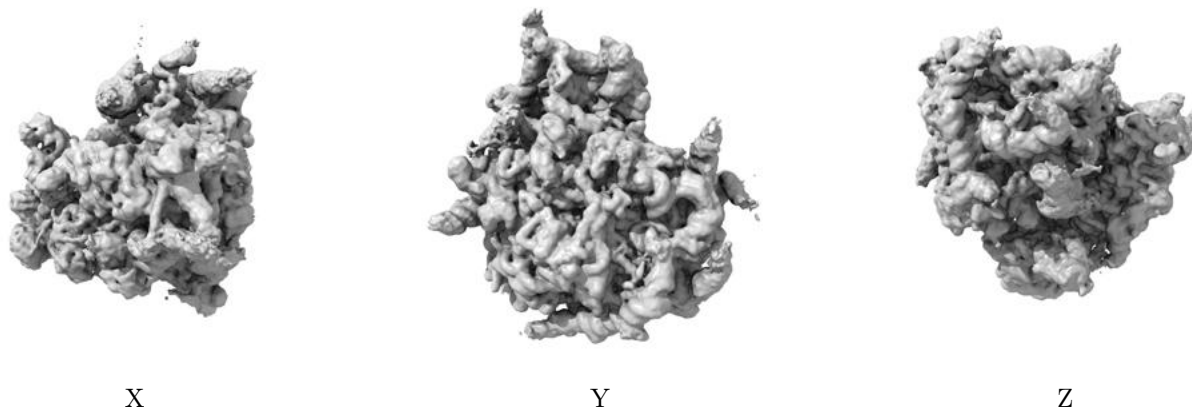


Z

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.

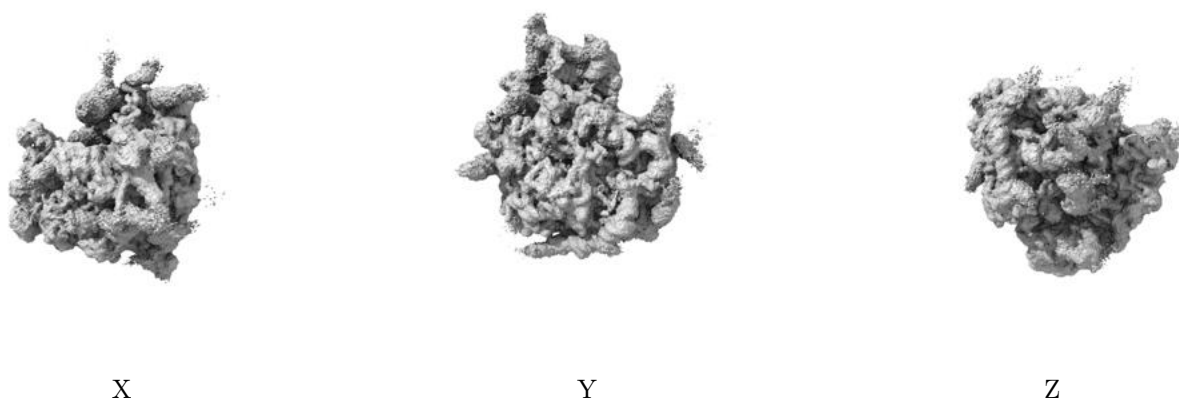
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.009. 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.

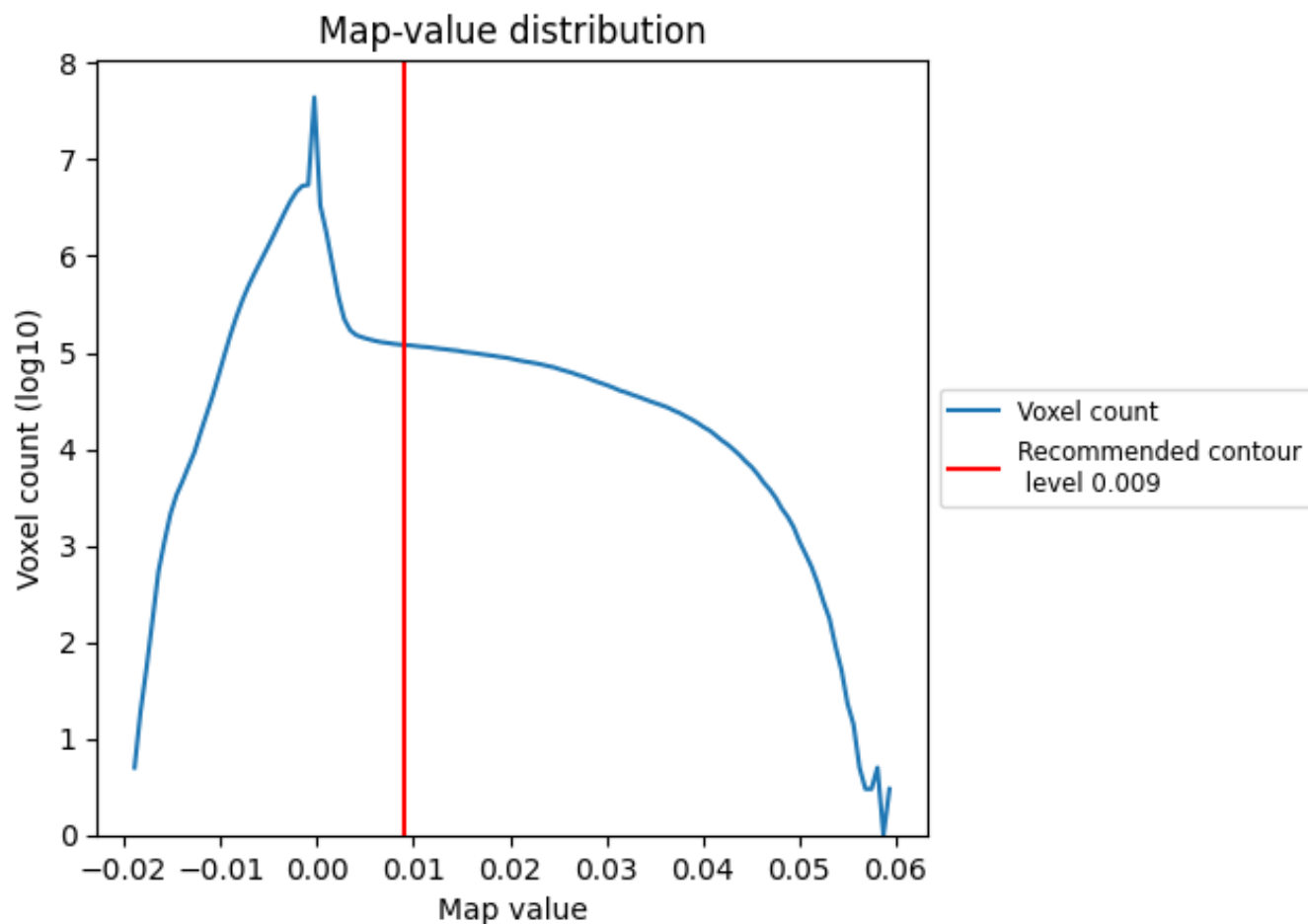
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

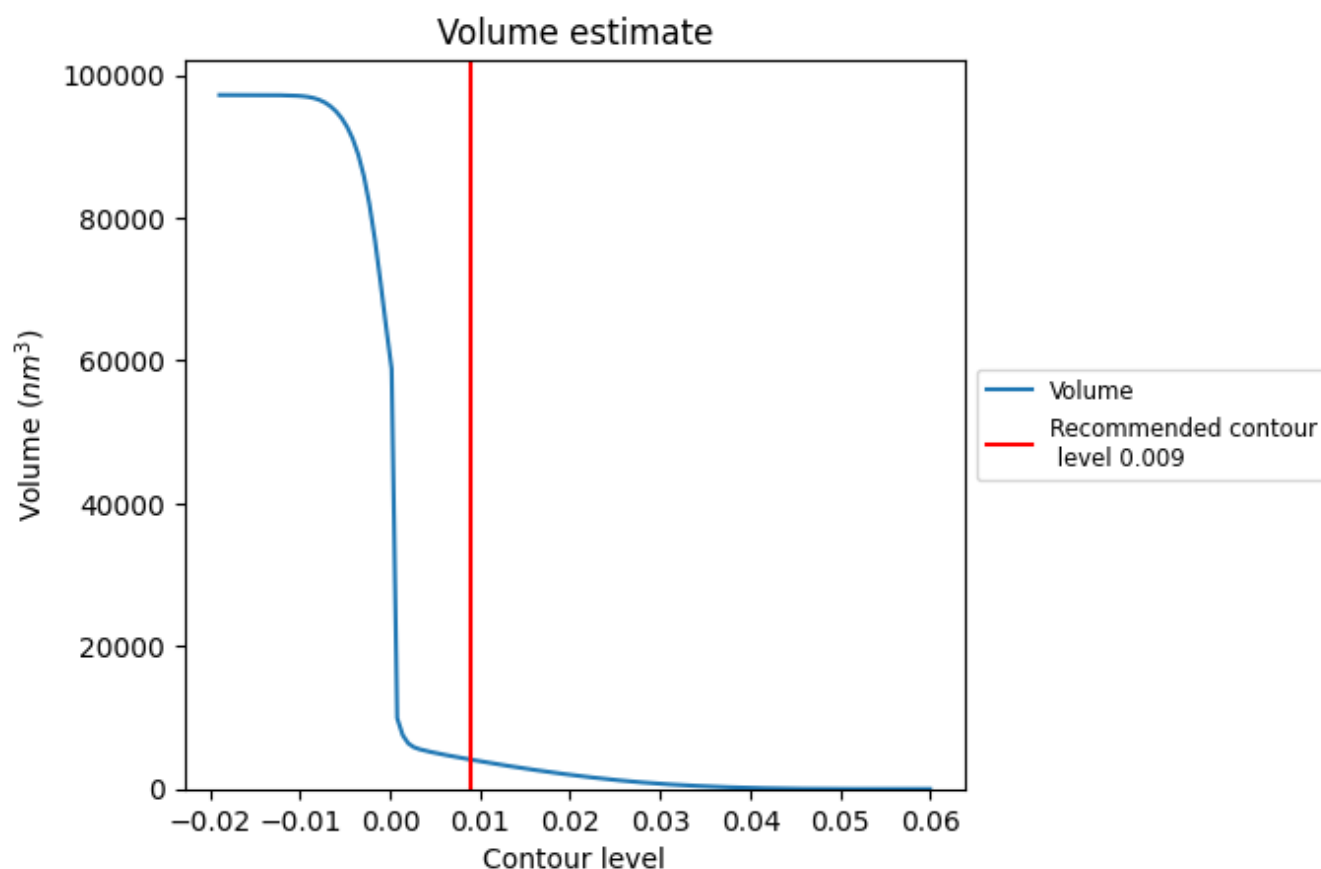
This section contains the results of statistical analysis of the map.

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.

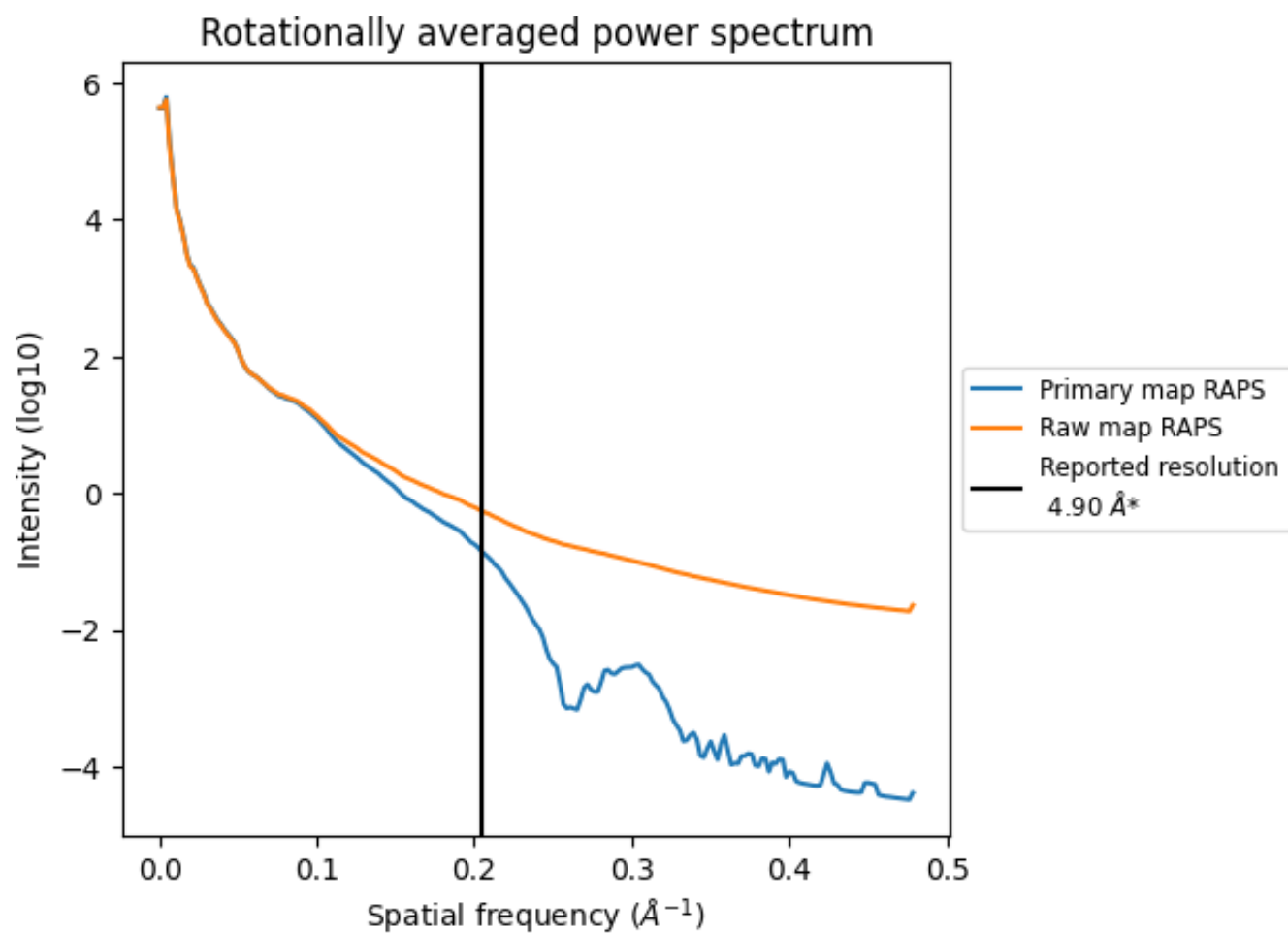
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4107 nm^3 ; this corresponds to an approximate mass of 3710 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 ⓘ

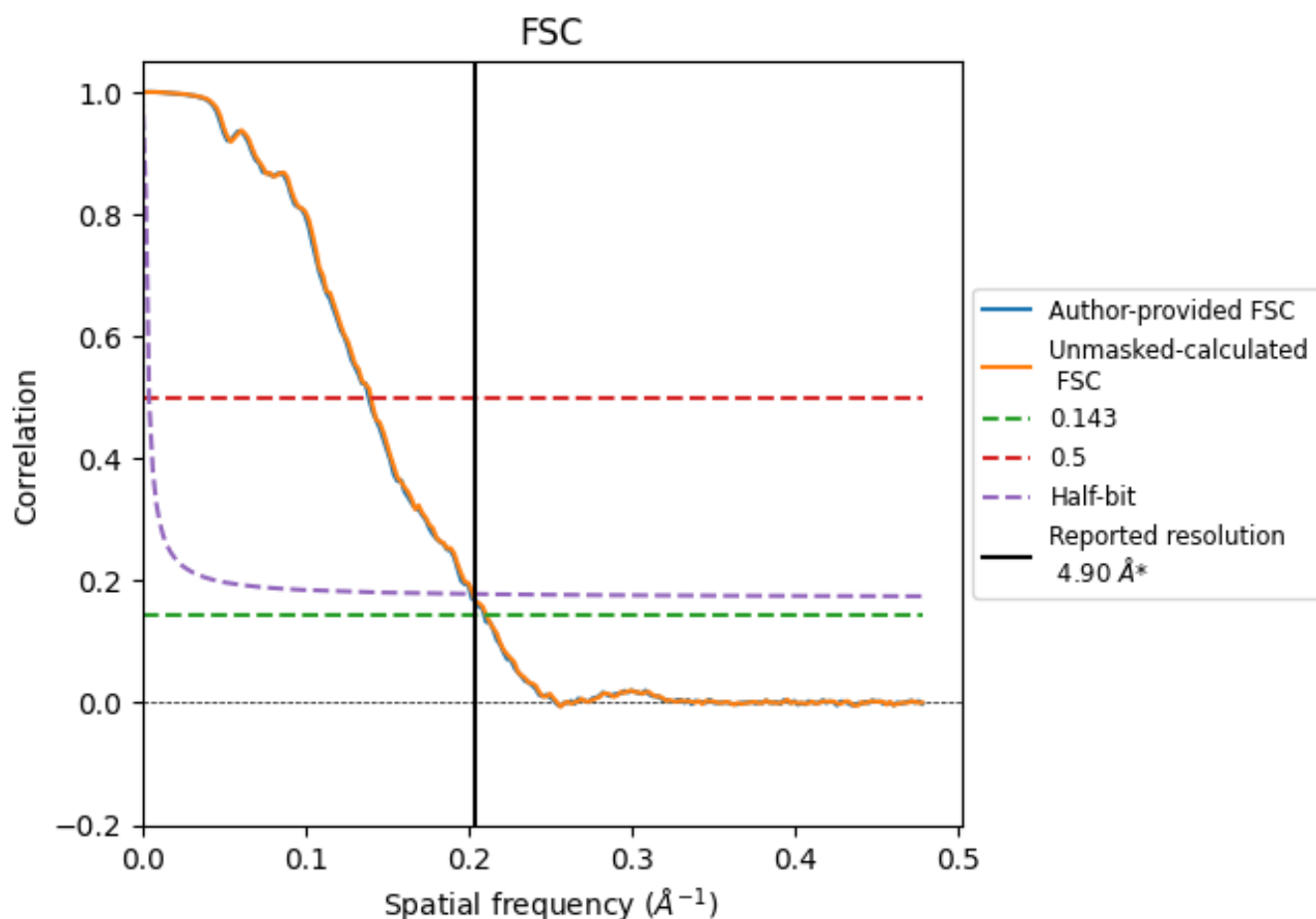


*Reported resolution corresponds to spatial frequency of 0.204 \AA^{-1}

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.204 Å⁻¹

8.2 Resolution estimates [i](#)

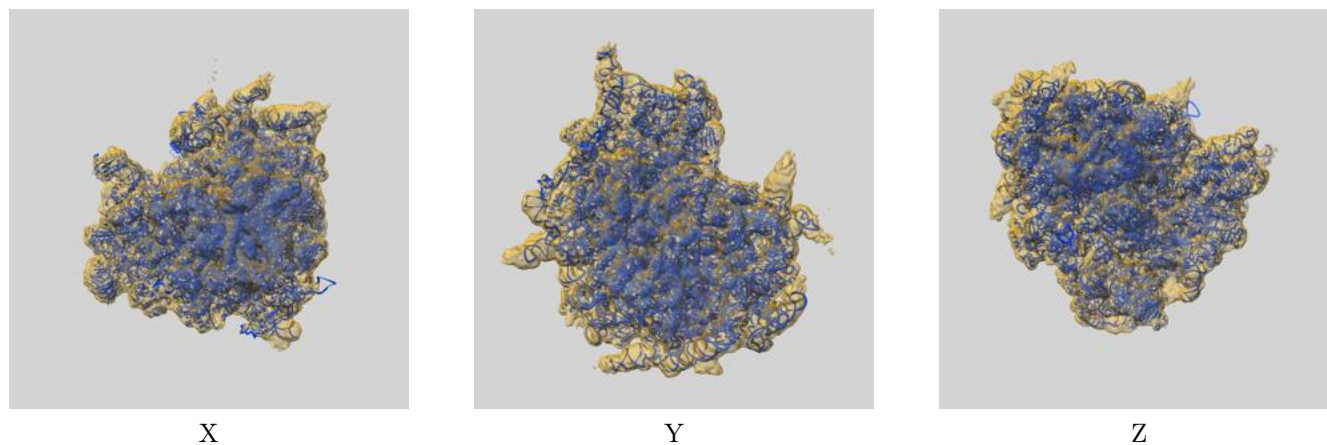
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.90	-	-
Author-provided FSC curve	4.76	7.20	4.96
Unmasked-calculated*	4.74	7.13	4.93

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

9 Map-model fit [i](#)

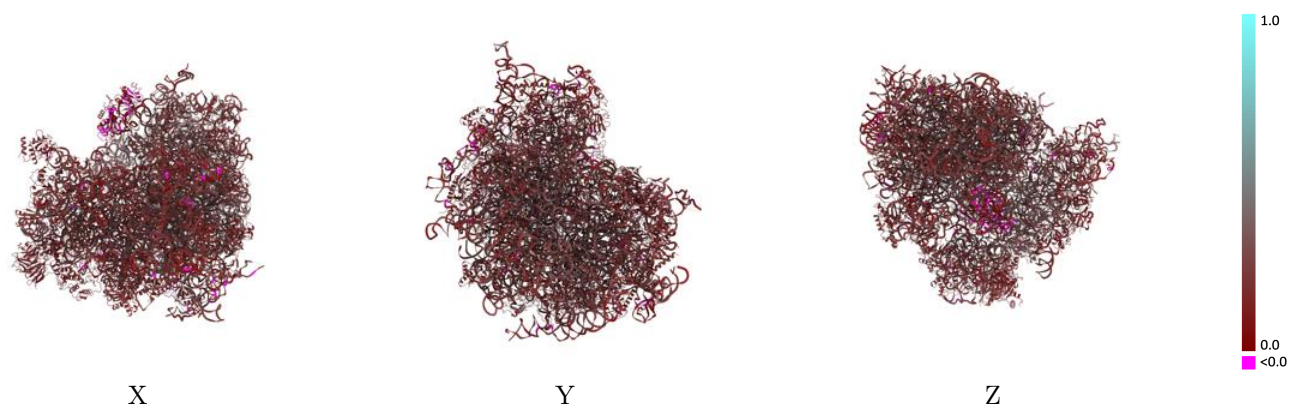
This section contains information regarding the fit between EMDB map EMD-72470 and PDB model 9Y44. Per-residue inclusion information can be found in [section 3](#) on [page 22](#).

9.1 Map-model overlay [i](#)



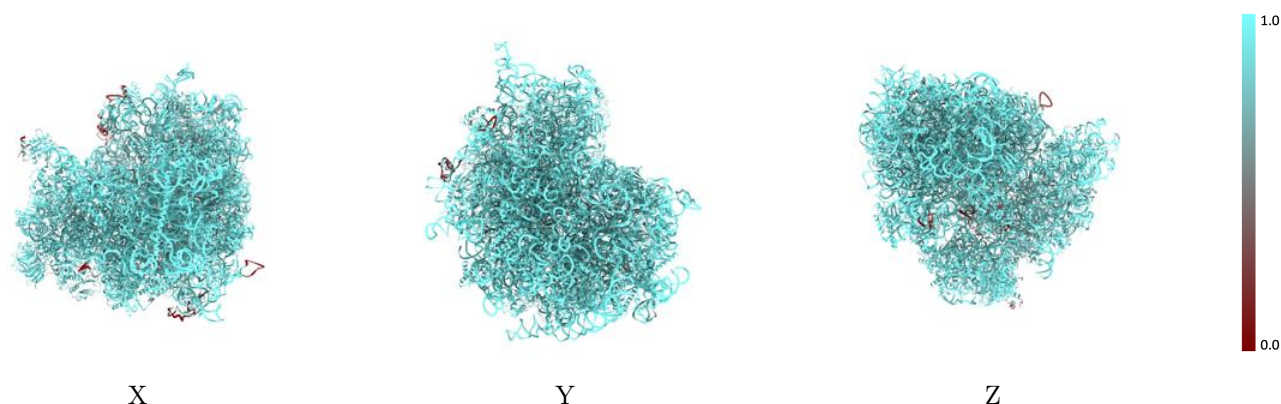
The images above show the 3D surface view of the map at the recommended contour level 0.009 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



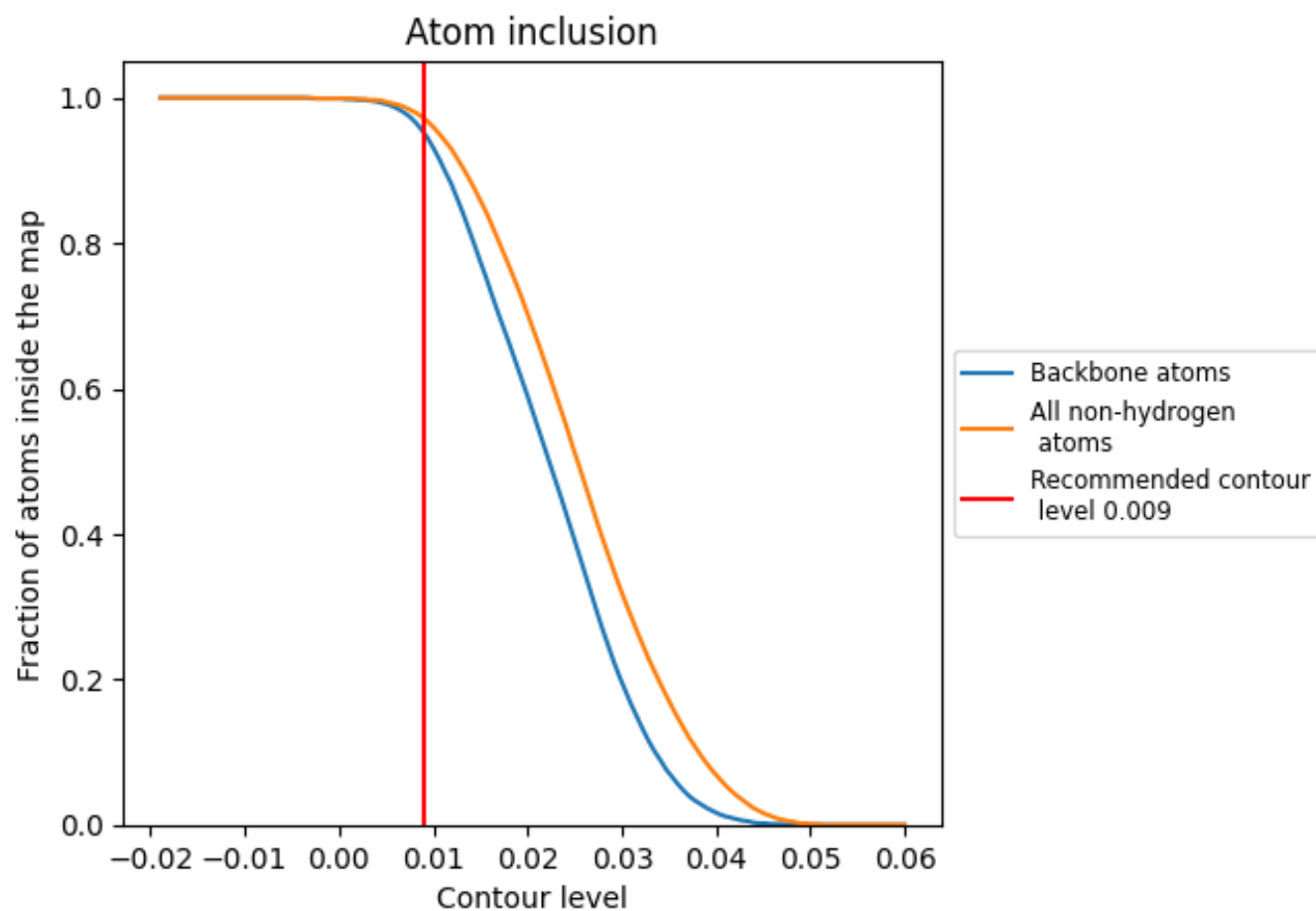
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.009).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 97% 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 (0.009) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9720	 0.2370
A	 0.9490	 0.2730
A5	 0.9930	 0.2540
A6	 0.9920	 0.2700
A7	 1.0000	 0.2790
A8	 0.9990	 0.2670
AA	 0.9320	 0.2090
B	 0.9660	 0.2300
B2	 0.9940	 0.2480
BB	 0.9510	 0.2150
Bb	 0.5620	 0.1610
C	 0.9600	 0.2360
CC	 0.9350	 0.2280
Cc	 0.9770	 0.2290
D	 0.9860	 0.2060
DD	 0.9020	 0.1990
Dd	 0.9580	 0.2620
E	 0.9770	 0.2270
EE	 0.9750	 0.1960
F	 0.9470	 0.2270
FF	 0.9590	 0.1900
G	 0.9660	 0.2180
GG	 0.9810	 0.1850
H	 0.9580	 0.2280
HH	 0.9100	 0.2060
I	 0.9540	 0.2460
II	 0.9690	 0.1920
J	 0.9750	 0.2090
JJ	 0.9700	 0.1750
KK	 0.9700	 0.1860
L	 0.9690	 0.2390
LL	 0.9490	 0.2350
M	 0.9860	 0.2330
MM	 0.7970	 0.1590
N	 0.9640	 0.2210





















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Chain	Atom inclusion	Q-score
NN	 0.9300	 0.2110
O	 0.9460	 0.2180
OO	 0.9530	 0.2140
P	 0.9710	 0.2310
PP	 0.9890	 0.1950
Q	 0.9400	 0.2400
QQ	 0.9840	 0.1700
RR	 0.8800	 0.1880
S	 0.9830	 0.2330
SS	 0.9740	 0.1880
T	 0.9570	 0.2500
TT	 0.9910	 0.1800
U	 0.9870	 0.2190
UU	 0.9550	 0.1890
V	 0.9230	 0.2160
VV	 0.9450	 0.2120
W	 0.9630	 0.1970
WW	 0.9220	 0.2210
X	 0.9770	 0.2330
XX	 0.9840	 0.2630
Y	 0.9810	 0.2200
YY	 0.9860	 0.1750
Z	 0.9740	 0.2160
ZZ	 0.9610	 0.1800
a	 0.9550	 0.2400
aa	 0.9720	 0.2340
b	 0.9730	 0.1950
bb	 0.9600	 0.2280
c	 0.9440	 0.1620
cc	 0.9390	 0.2200
d	 0.9770	 0.2350
dd	 0.9680	 0.1510
e	 0.9450	 0.2420
ee	 0.9970	 0.1770
f	 0.9570	 0.2220
ff	 0.9380	 0.1540
g	 0.9760	 0.2230
gg	 0.9610	 0.1820
h	 0.9790	 0.2110
i	 0.9560	 0.2200
j	 0.9690	 0.1990
k	 0.9430	 0.2130

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Chain	Atom inclusion	Q-score
l	 0.9740	 0.2180
m	 0.9760	 0.2310
n	 0.8900	 0.1680
o	 0.9180	 0.2120
p	 0.9060	 0.2200
r	 0.9620	 0.2560
s	 0.9010	 0.0860
t	 0.5540	 0.0650
u	 0.8550	 0.1450