



wwPDB EM Validation Summary Report ⓘ

Jun 24, 2026 – 02:00 AM EDT

PDB ID : 7LS2 / pdb_00007ls2
EMDB ID : EMD-23501
Title : 80S ribosome from mouse bound to eEF2 (Class I)
Authors : Loerch, S.; Smith, P.R.; Kunder, N.; Stanowick, A.D.; Lou, T.-F.; Campbell, Z.T.
Deposited on : 2021-02-17
Resolution : 3.10 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

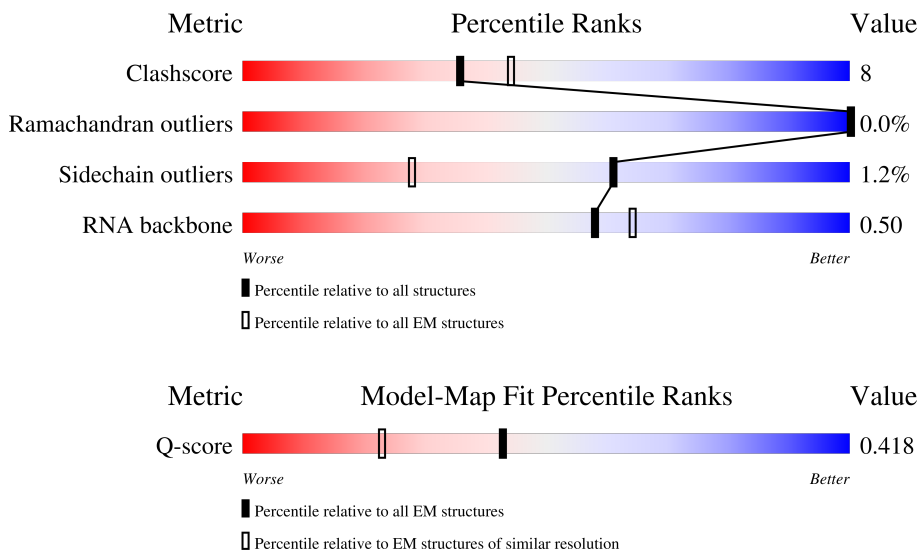
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.10 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.






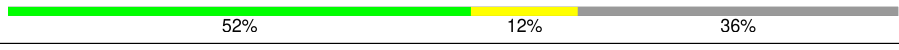

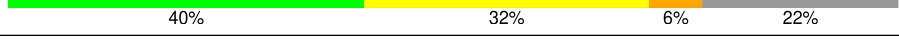
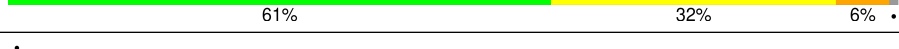
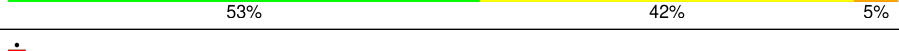
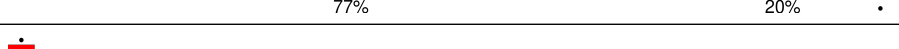
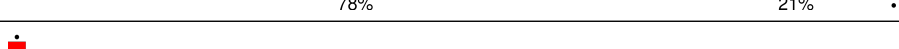
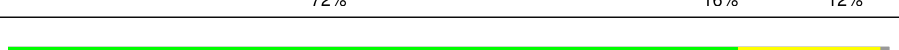

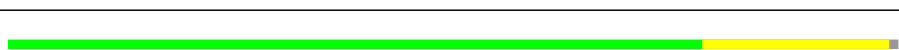

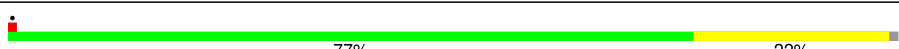





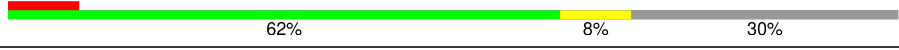
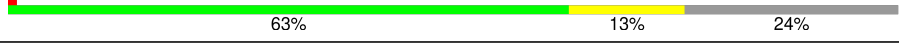



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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	A1	270	
2	B1	266	
3	C1	192	












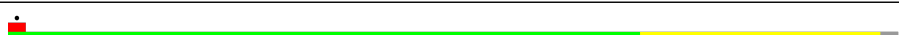

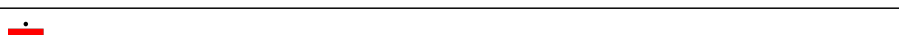
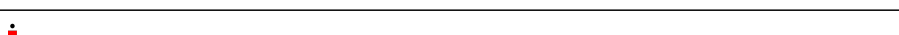
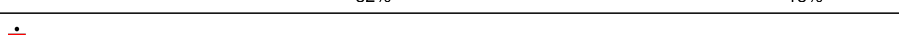

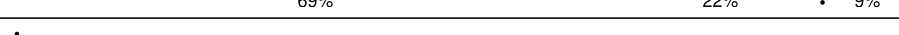







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Mol	Chain	Length	Quality of chain
4	D1	214	 80% 17%
5	E1	178	 79% 19%
6	F1	211	 80% 18%
7	G1	217	 52% 12% 36%
8	H1	204	 81% 19%
9	A2	4731	 40% 32% 6% 22%
10	B2	121	 61% 32% 6%
11	C2	156	 53% 42% 5%
12	D2	257	 77% 20%
13	E2	403	 78% 21%
14	F2	419	 72% 16% 12%
15	G2	297	 82% 16%
16	H2	296	 60% 14% 25%
17	I2	203	 78% 21%
18	J2	184	 66% 16% 17%
19	K2	188	 77% 22%
20	L2	196	 81% 12% 6%
21	M2	176	 88% 11%
22	N2	160	 79% 20%
23	O2	128	 71% 8% 21%
24	P2	140	 79% 14% 8%
25	Q2	157	 8% 62% 8% 30%
26	R2	156	 63% 13% 24%
27	S2	145	 71% 21% 8%
28	T2	136	 76% 23%

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Mol	Chain	Length	Quality of chain
29	U2	148	 80% 19%
30	V2	160	 8% 61% 12% 27%
31	W2	115	 63% 18% 18%
32	X2	125	 66% 20% 14%
33	Y2	135	 75% 20% 5%
34	Z2	110	 83% 15%
35	a2	117	 87% 10%
36	b2	123	 80% 18%
37	c2	105	 84% 13%
38	d2	97	 70% 19% 11%
39	e2	70	 79% 20%
40	f2	51	 71% 27%
41	g2	128	 34% 6% 59%
42	h2	25	 88% 8%
43	i2	106	 82% 15%
44	j2	92	 74% 22%
45	k2	137	 69% 22% 9%
46	m2	1871	 43% 42% 7% 8%
47	n2	75	 5% 47% 41% 12%
48	p2	264	 67% 14% 19%
49	q2	243	 76% 16% 7%
50	r2	263	 82% 17%
51	w2	158	 9% 82% 13%
52	z2	135	 86% 13%
53	o2	295	 59% 13% 27%



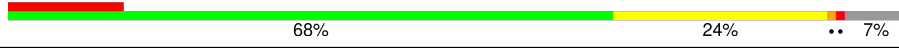



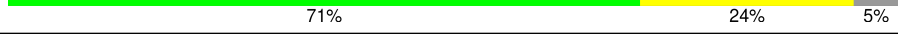
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Mol	Chain	Length	Quality of chain
54	s2	204	
55	v2	165	
56	x2	145	
57	y2	146	
58	A3	152	
59	B3	145	
60	C3	119	
61	D3	83	
62	E3	143	
63	F3	115	
64	G3	69	
65	H3	56	
66	I3	317	
67	J3	293	
68	K3	249	
69	L3	194	
70	M3	132	
71	N3	151	
72	O3	151	
73	P3	130	
74	Q3	133	
75	R3	125	
76	S3	84	
77	T3	133	
78	U3	156	

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Mol	Chain	Length	Quality of chain
79	m	858	 77% 22%
80	j	317	 49% 13% 38%
81	k	165	 13% 68% 24% 7%
82	A	386	 7% 13% 84%
83	t	194	 75% 19% 6%
84	u	208	 7% 72% 27%
85	L1	217	 29% 71% 24% 5%

2 Entry composition [i](#)

There are 89 unique types of molecules in this entry. The entry contains 227130 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A1	222	1851	1190	356	297	8	1	0

- Molecule 2 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B1	230	1863	1188	359	312	4	1	0

- Molecule 3 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C1	190	1519	956	284	273	6	0	0

- Molecule 4 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D1	208	1690	1073	327	278	12	0	0

- Molecule 5 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E1	174	1397	880	260	251	6	0	0

- Molecule 6 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F1	207	1676	1048	344	280	4	0	0

- Molecule 7 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G1	139	1143	732	221	183	7	0	0

- Molecule 8 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	H1	203	1701	1072	359	266	4	0	0

- Molecule 9 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
9	A2	3706	79519	35463	14497	25854	3705	0	0

- Molecule 10 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
10	B2	120	2558	1141	456	842	119	0	0

- Molecule 11 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
11	C2	156	3315	1481	585	1094	155	0	0

- Molecule 12 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	D2	251	1921	1204	393	318	6	0	0

- Molecule 13 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	E2	402	3238	2060	609	555	14	0	0

- Molecule 14 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	F2	367	2928	1842	583	488	15	0	0

- Molecule 15 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	G2	293	2385	1506	440	425	14	0	0

- Molecule 16 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	H2	221	1789	1145	342	298	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	I2	201	1640	1055	320	259	6	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	J2	153	1242	777	241	215	9	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	K2	186	1511	946	313	248	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	L2	184	1542	955	332	246	9	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	M2	175	1450	924	283	233	10	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	N2	159	1298	823	253	216	6	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	O2	101	825	529	144	150	2	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	P2	129	969	613	182	169	5	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	Q2	110	895	563	180	148	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	R2	118	967	618	181	167	1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	S2	134	1115	700	226	186	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	T2	135	1107	714	208	182	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	U2	147	1164	736	239	185	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	V2	117	945	596	198	146	5	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	W2	94	732	465	130	131	6	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	X2	107	888	560	171	155	2	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	Y2	128	1053	667	216	165	5	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	Z2	109	876	555	174	143	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
35	a2	114	Total	C	N	O	S	0	0
			906	565	187	148	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
36	b2	120	Total	C	N	O	S	0	0
			1001	634	201	165	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
37	c2	102	Total	C	N	O	S	0	0
			827	516	173	133	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
38	d2	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	e2	69	Total	C	N	O	S	0	0
			568	365	103	99	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	f2	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
41	g2	52	Total	C	N	O	S	0	0
			430	267	90	67	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
42	h2	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
43	i2	103	Total	C	N	O	S	0	0
			842	528	172	136	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
44	j2	89	Total	C	N	O	S	0	0
			694	436	133	118	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
45	k2	125	Total	C	N	O	S	0	0
			1001	621	207	168	5		

- Molecule 46 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	m2	1724	Total	C	N	O	P	0	0
			36817	16440	6606	12048	1723		

- Molecule 47 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	n2	75	Total	C	N	O	P	0	0
			1604	717	298	515	74		

- Molecule 48 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	p2	214	Total	C	N	O	S	0	0
			1738	1103	310	311	14		

- Molecule 49 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	q2	226	Total	C	N	O	S	0	0
			1756	1119	316	314	7		

- Molecule 50 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	r2	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 51 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	w2	153	Total	C	N	O	S	0	0
			1247	793	234	214	6		

- Molecule 52 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	z2	134	Total	C	N	O	S	0	0
			1080	678	201	197	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
53	o2	214	Total	C	N	O	S	0	0
			1694	1077	297	312	8		

- Molecule 54 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	s2	189	Total	C	N	O	S	0	0
			1496	934	285	270	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
55	v2	97	Total	C	N	O	S	0	0
			819	534	147	133	5		

- Molecule 56 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	x2	130	Total	C	N	O	S	0	0
			1073	681	205	180	7		

- Molecule 57 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	y2	144	Total	C	N	O	S	0	0
			1143	726	216	198	3		

- Molecule 58 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	A3	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 59 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	B3	141	Total	C	N	O	S	0	0
			1104	691	215	196	2		

- Molecule 60 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	C3	102	Total	C	N	O	S	0	0
			807	507	153	143	4		

- Molecule 61 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	D3	83	Total	C	N	O	S	0	0
			638	392	119	122	5		

- Molecule 62 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	E3	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 63 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	F3	100	811	506	169	131	5	1	0

- Molecule 64 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
64	G3	64	506	308	102	94	2	0	0

- Molecule 65 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
65	H3	54	455	284	93	73	5	0	0

- Molecule 66 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	I3	313	2436	1535	424	465	12	0	0

- Molecule 67 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
67	J3	222	1725	1116	298	302	9	0	0

- Molecule 68 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
68	K3	227	1840	1149	367	317	7	0	0

- Molecule 69 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
69	L3	185	1525	969	306	248	2	0	0

- Molecule 70 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	M3	122	Total	C	N	O	S	0	0
			942	593	164	177	8		

- Molecule 71 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	N3	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 72 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	O3	134	Total	C	N	O	S	0	0
			1002	612	197	187	6		

- Molecule 73 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	P3	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 74 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Q3	129	Total	C	N	O	S	0	0
			1049	662	206	176	5		

- Molecule 75 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	R3	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 76 is a protein called 40S ribosomal protein S27-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	S3	83	Total	C	N	O	S	0	0
			652	409	121	115	7		

- Molecule 77 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	T3	55	Total	C	N	O	S	0	0
			438	271	95	71	1		

- Molecule 78 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	U3	62	Total	C	N	O	S	0	0
			505	317	96	85	7		

- Molecule 79 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	m	851	Total	C	N	O	S	0	0
			6649	4217	1146	1242	44		

- Molecule 80 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	j	196	Total	C	N	O	S	0	0
			1507	959	263	276	9		

- Molecule 81 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	k	153	Total	C	N	O	S	0	0
			1159	721	218	217	3		

- Molecule 82 is a protein called Isoform 3 of Plasminogen activator inhibitor 1 RNA-binding protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
82	A	61	Total	C	N	O	0	0
			486	289	94	103		

- Molecule 83 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	t	183	Total	C	N	O	S	0	0
			1477	944	270	262	1		

- Molecule 84 is a protein called 40S ribosomal protein S8.

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

- Molecule 85 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
85	L1	206	1660	1061	300	291	8	0	0

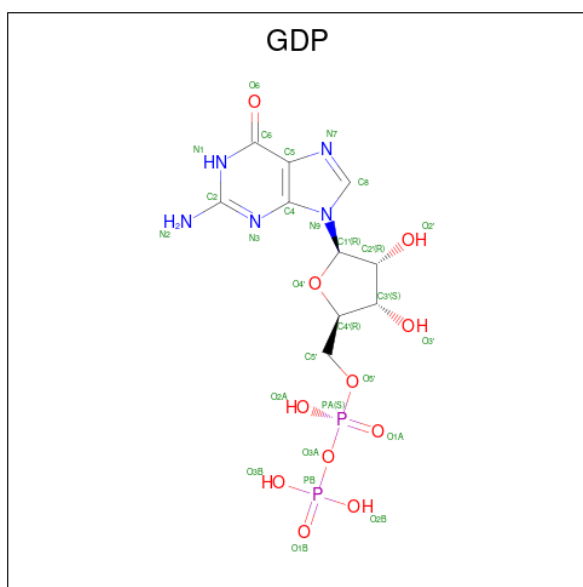
- Molecule 86 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
86	d2	1	Total 1	Zn 1	0
86	g2	1	Total 1	Zn 1	0
86	i2	1	Total 1	Zn 1	0
86	j2	1	Total 1	Zn 1	0
86	F3	1	Total 1	Zn 1	0
86	H3	1	Total 1	Zn 1	0
86	U3	1	Total 1	Zn 1	0

- Molecule 87 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
87	H3	1	Total 1	Mg 1	0

- Molecule 88 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
88	m	1	28	10	5	11	2	0

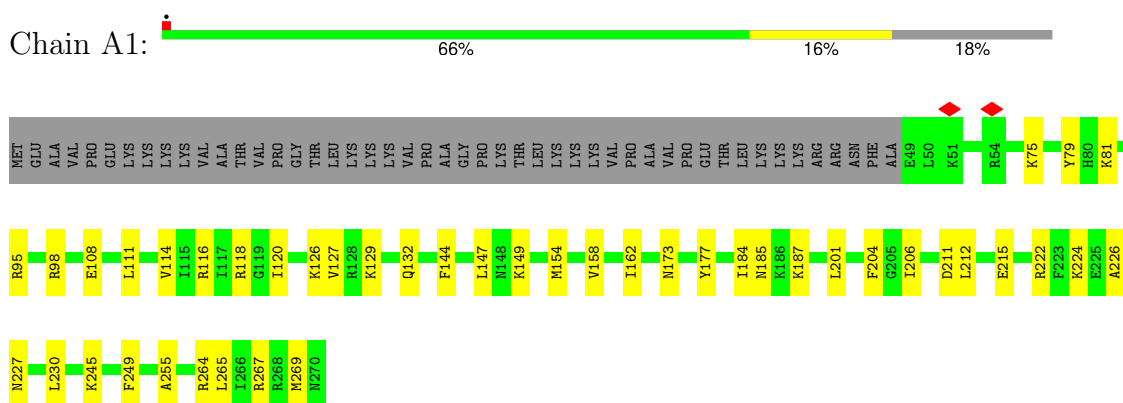
- Molecule 89 is water.

Mol	Chain	Residues	Atoms		AltConf
89	B1	1	Total	O	0
			1	1	
89	A2	1	Total	O	0
			1	1	
89	m2	2	Total	O	0
			2	2	

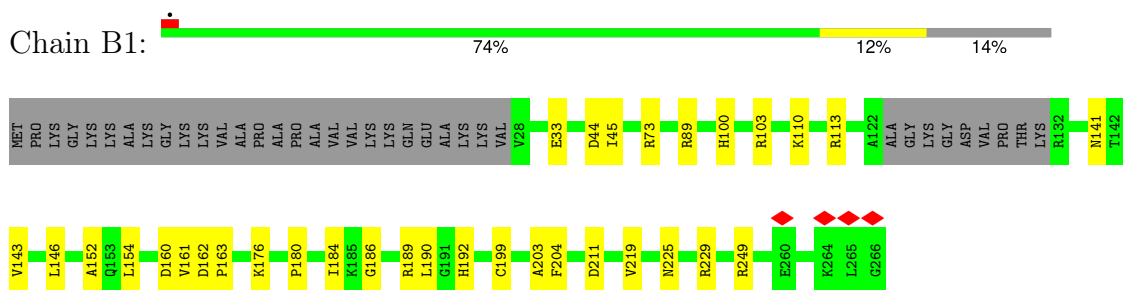
3 Residue-property plots [i](#)

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.

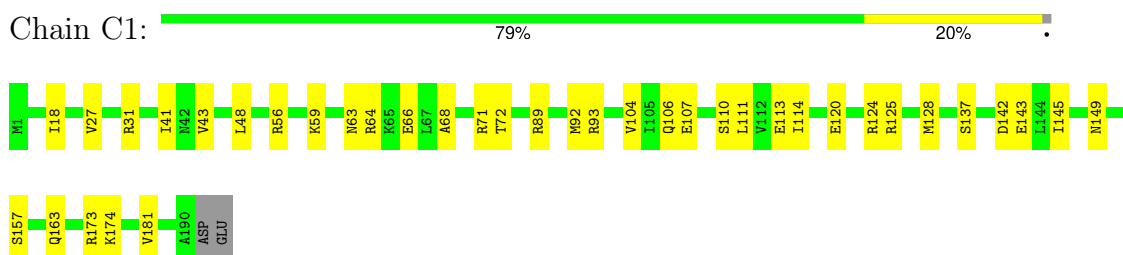
- Molecule 1: 60S ribosomal protein L7



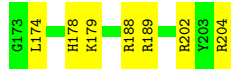
- Molecule 2: 60S ribosomal protein L7a



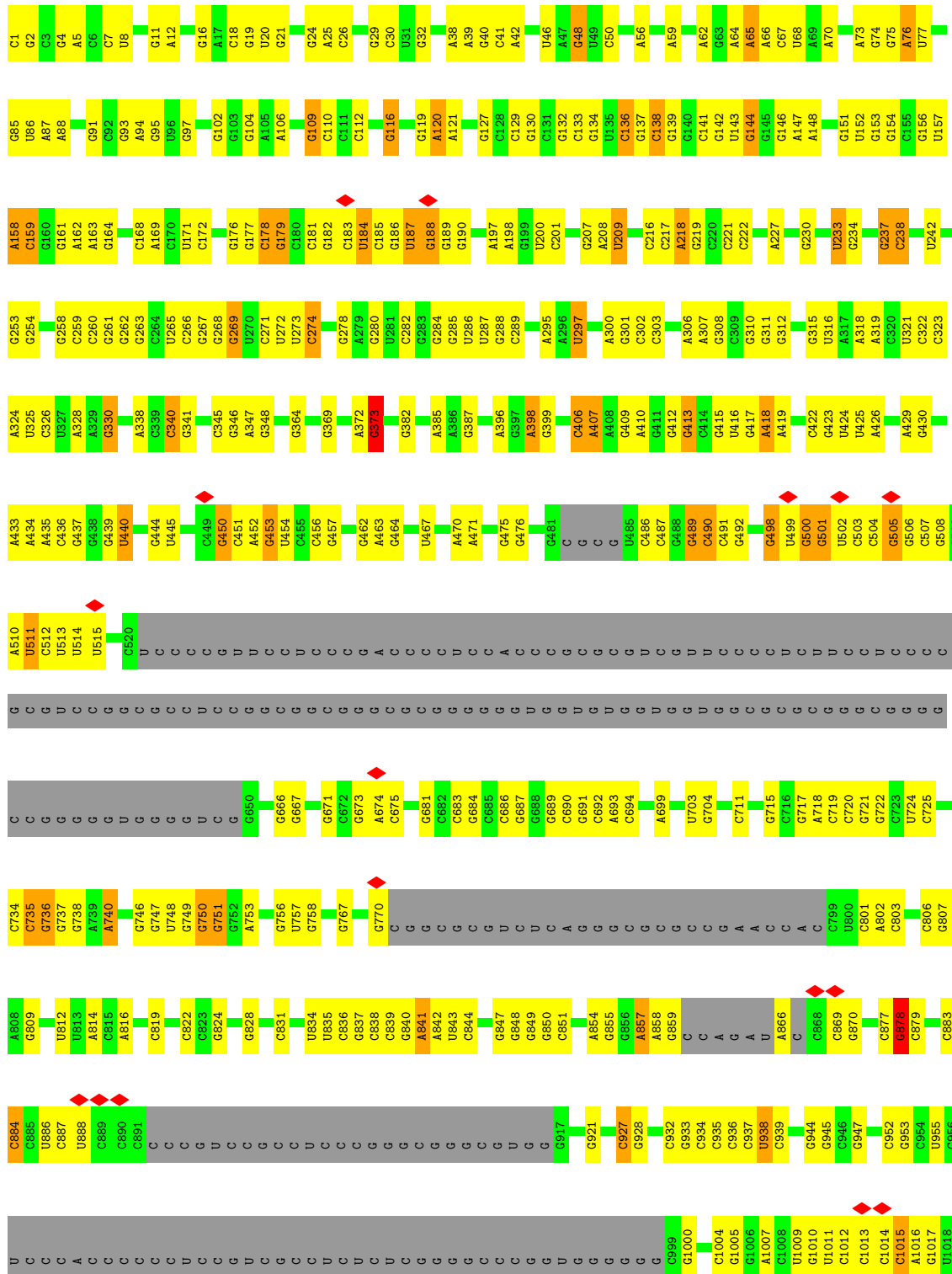
- Molecule 3: 60S ribosomal protein L9



- Molecule 4: 60S ribosomal protein L10-like

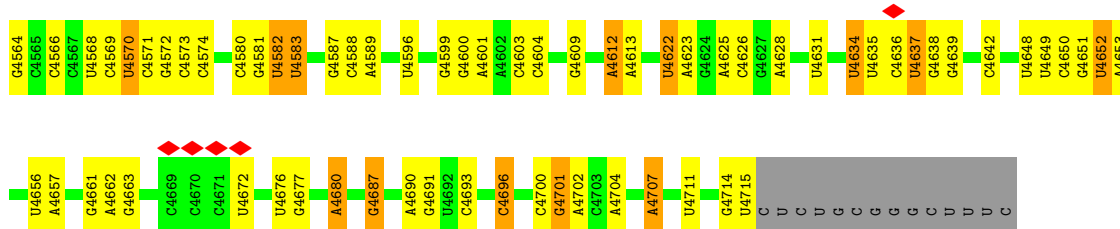


● Molecule 9: 28S rRNA

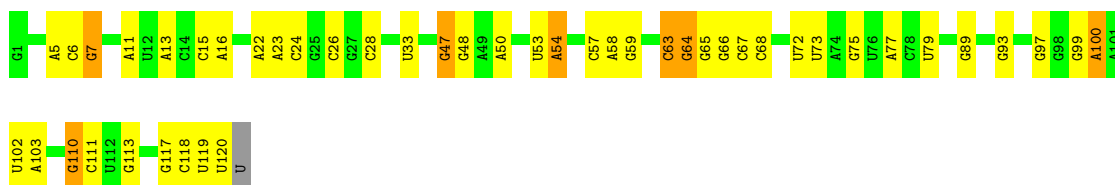


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A2068	C1022	C1094	C1166	A1360	G1442	U1528	G1621	G1692	G1774	G1852	C	G2069
G2071	C1023	G1097	G1167	A1361	G1443	U1529	G1622	C1695	G1775	U1856	G	G2070
C2072	C1024	G1098	G1168	A1362	A1444	U1530	G1623	C1696	U1776	G1857	U	C2071
C2073	G1099	U1099	A1172	G1362	A1445	A1531	G1624	G1697	U1777	G1858	U	G2072
C2074	C1025	C1100	G1173	G1365	G1446	A1532	U1624	A1698	G1778	C1864	C	C2073
G2075	G1027	G1101	G1174	A1366	A1447	C1534	G1625	A1699	G1779	G1870	C	G2074
C2076	G1028	G1104	G1175	A1367	A1448	U1535	G1626	C1700	C1780	A1870	C	G2075
G2077	U1031	G1105	G1176	G1368	A1451	A1538	A1628	G1701	C1781	A1871	C	C2076
C2078	C1032	G1107	G1177	A1371	G1454	A1539	G1632	U1708	U1782	G1872	C	G2077
C2079	C1037	G1108	U1178	G1372	A1455	G1541	G1633	A1709	G1783	A1873	C	C2078
C2080	C1038	A1108	G1179	A1377	C1458	C1542	C1634	A1710	G1784	G1874	C	G2079
G2081	C1039	U1109	G1180	G1378	A1459	C1543	G1635	G1711	A1785	A1875	C	C2080
U2084	C1040	G1110	G1184	A1379	C1463	A1544	U1636	G1716	A1786	G1876	C	U2084
C2085	C1041	U1111	U1184	C1379	A1463	G1552	G1637	C1717	G1787	G1877	C	G2085
G2086	G1044	G1112	C1184	U1380	A1463	A1553	G1638	G1718	U1788	G1878	C	C2086
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G2088	U1042	U1116	C1190	C1382	C1468	G1558	G1642	G1721	G1791	G1883	G	G2088
C2089	C1043	C1117	C1192	U1383	U1472	U1559	C1643	C1722	A1792	G1884	G	C2089
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G2103	U1048	C1119	C1195	A1388	C1475	G1562	G1646	A1725	C1795	C1887	C	G2103
C2106	C1049	C1120	C1197	G1389	C1476	G1563	U1647	C1726	C1796	G1888	C	C2106
G2110	G1054	A1121	G1201	U1390	U1477	G1564	G1648	G1727	G1797	G1889	C	G2110
C2115	G1055	C1124	A1201	G1391	U1478	G1565	C1649	C1728	U1799	G1890	C	C2115
G2116	G	C1129	G1204	C1392	U1479	C1566	G1650	U1729	A1800	G1891	C	G2116
U2117	A	G1130	G1205	C1393	U1496	C1567	G1651	U1730	A1801	G1892	C	U2117
C2119	C	U1131	G1208	C1394	U1497	G1568	U1652	C1733	G1802	G1893	C	C2119
G2120	G1060	C1132	U1207	U1395	C1489	A1567	G1653	A1734	G1803	G1894	C	G2120
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A2129	C1070	C1141	A1212	G1405	U1500	G1572	U1660	C1740	A1811	G1901	C	A2129
C2130	G1071	G1142	G1217	A1406	G1501	U1573	U1661	A1741	A1812	G1902	C	C2130
A2131	U1072	C1143	C1221	U1411	G1504	U1574	U1662	A1742	C1813	G1903	C	A2131
G2136	C	A1144	G1224	C1412	G1505	U1575	U1663	A1745	A1814	G1904	C	G2136
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C2138	C	C1146	A1328	C1416	C1507	A1581	A1670	G1750	A1819	G1906	C	C2138
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A2143	C	A1148	U1330	G1418	C1511	A1583	C1672	U1752	C1821	G1910	C	A2143
G2149	C	G1149	G1231	G1418	U1512	A1589	A1673	G1753	U1822	G1911	C	G2149
C2155	C	U1153	A1233	G1425	C	U1592	A1676	U1756	G1826	G1915	C	C2155
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A2151	C	U1155	C1244	A1426	C	A1598	U1678	G1757	A1828	C	C	A2151
G2152	C	U1156	G1245	A1430	C	G1599	G1679	U1761	U1829	C	C	G2152
G2155	C	U1157	A1340	G1430	A	G1605	G1680	A1762	C1830	C	C	G2155
		C1158	A1347	A1434	C	A1606	C1682	G1763	A1831	C	C	
		U1253	A1347	U1435	C	A1607	G1685	A1766	U1834	C	C	
		G1160	U1351	A1436	C	A1608	G1685	G1767	A1848	C	C	
		G1161	G1352	G1437	C	G1613	G1685	C1768	A1849	C	C	
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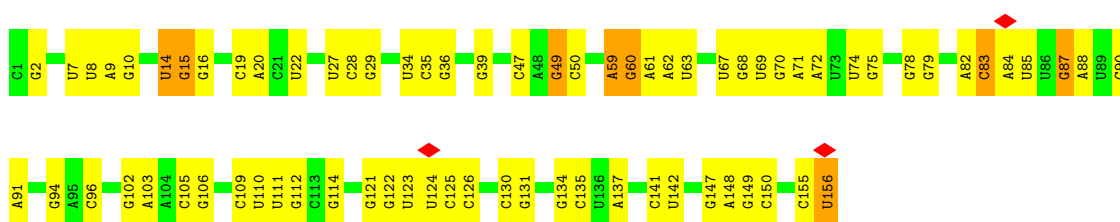
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C	C4437	A4357	C4278	U4115	A4021	G3927	U3844	U3763	C	G3564	U3494
C	U4438	A4358	U4279	C4116	G4022	G3927	G3845	G3764	C	A3565	G3495
C	U4439	U4359	U4280	U4117	G4023	A3931	G3846	G3765	C	C3566	U3496
C	G4440	C4360	U4281	U4118	A4024	A3932	G3847	C3766	C	C3567	C3499
C	U4441	C4361	U4282	C4119	U4025	A3933	G3848	C3767	C	U3568	U3500
C	U4442	G4362	A4283	A4120	G4026	A3934	U3849	U3768	C	A3569	A3501
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C	U4452	C4372	U4293	C4130	C4036	U3947	A3859	A3778	C	C3511	C3511
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C	G4463	C4383	G4304	U4141	A4050	C3962	A3887	A3726	C	C3526	C3526
C	U4464	G4384	U4305	A4142	U4051	C3963	G3888	A3727	C	C3527	C3527
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C	U4466	C4386	U4307	A4144	A4053	A3965	C3890	C3729	C	G3529	G3529
C	G4467	G4387	G4308	U4145	C4054	C3966	A3891	G3796	C	G3530	G3530
C	U4468	A4388	U4309	A4146	A4055	A3967	A3892	G3797	C	A3533	A3533
C	G4469	C4389	G4310	U4147	U4056	A3968	A3893	C3798	C	C3534	C3534
C	U4470	G4390	U4311	A4148	A4057	C3969	A3894	C3799	C	G3535	G3535
C	G4471	A4391	G4312	U4149	A4067	A3970	A3895	C3800	C	G3536	G3536
C	U4472	C4392	C4313	U4150	U4072	C3971	A3896	G3799	C	U3540	U3540
C	G4473	G4393	U4314	A4165	C4073	U3972	A3897	C3801	C	G3541	G3541
C	U4474	A4394	G4315	U4166	A4074	U3973	A3898	C3802	C	A3542	A3542
C	G4475	C4395	U4316	C4167	U4075	C3974	U3899	C3803	C	A3543	A3543
C	U4476	A4396	G4317	A4168	A4076	C3975	C3899	G3804	C	A3544	A3544
C	G4477	C4397	C4318	U4169	U4077	A3976	A3899	G3805	C	A3545	A3545
C	U4478	G4398	U4319	A4170	U4078	U3977	A3900	C3806	C	G3546	G3546
C	G4479	A4399	G4320	A4171	A4079	C3978	A3901	G3807	C	U3547	U3547
C	U4480	C4399	U4321	C4172	U4080	U3979	A3902	C3808	C	A3548	A3548
C	G4481	G4400	G4322	U4173	U4081	C3980	A3903	G3809	C	G3549	G3549
C	U4482	A4401	A4323	C4174	C4082	C3981	A3904	C3810	C	A3550	A3550
C	G4483	C4402	U4324	U4175	U4083	C3982	A3905	C3811	C	U3551	U3551
C	U4484	G4403	G4325	C4176	U4084	C3983	A3906	G3742	C	A3552	A3552
C	G4485	A4404	U4326	U4177	U4085	C3984	A3907	G3743	C	G3553	G3553
C	U4486	C4405	C4327	C4178	U4086	C3985	A3908	C3744	C	C3554	C3554
C	G4487	G4406	U4328	U4179	U4087	C3986	A3909	G3745	C	G3555	G3555
C	U4488	A4407	G4329	C4180	U4088	C3987	A3910	C3822	C	A3556	A3556
C	G4489	C4408	U4330	U4181	U4089	C3988	A3911	C3823	C	G4557	G4557
C	U4490	G4409	G4331	C4182	C4089	C3989	A3912	A3824	C	G4558	G4558
C	G4491	A4410	U4332	U4183	U4090	C3990	A3913		C	G4559	G4559
C	U4492	C4411	G4333	C4184	U4091	C3991	A3914		C	G4560	G4560
C	G4493	G4412	U4334	U4185	U4092	C3992	A3915		C	C4561	C4561
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C	G4495	C4414	U4336	U4187	U4094	C3994	A3917		C	G4563	G4563
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C	U4498	C4417	G4339	C4189	U4097	C3997	A3920		C		
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C	G4501	C4420	U4342	U4192	U4100	C4000	A3923		C		
C	U4502	G4421	G4343	C4193	U4101	C4001	A3924		C		
C	G4503	A4422	U4344	U4194	U4102	C4002	A3925		C		
C	U4504	C4423	G4345	C4195	U4103	C4003	A3926		C		
C	G4505	G4424	U4346	U4196	U4104	C4004	A3927		C		
C	U4506	A4425	C4347	C4197	U4105	C4005	A3928		C		
C	G4507	C4426	U4348	U4198	U4106	C4006	A3929		C		
C	U4508	G4427	G4349	C4199	U4107	C4007	A3930		C		
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C	G4511	G4430	U4352	A4202	U4110	C4010	A3933		C		
C	U4512	A4431	G4353	G4203	U4111	C4011	A3934		C		
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C	G4519	C4438	C4360	U4210	U4118	C4018	A3941		C		
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C	G4525	C4443	G4366	U4216	U4124	A4024	A3947		C		
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C	G4527	A4445	C4368	C4218	A4126	A4026	A3949		C		
C	U4528	C4446	A4369	U4219	A4127	A4027	A3950		C		
C	G4529	G4447	G4370	A4220	A4128	A4028	A3951		C		
C	U4530	A4448	C4371	G4221	U4129	A4029	A3952		C		
C	G4531	C4449	U4372	U4222	A4130	A4030	A3953		C		
C	U4532	G4450	G4373	A4223	U4131	A4031	A3954		C		
C	G4533	A4451	C4374	U4224	U4132	A4032	A3955		C		
C	U4534	C4452	U4375	G4225	U4133	A4033	A3956		C		
C	G4535	G4453	G4376	U4226	U4134	A4034	A3957		C		
C	U4536	A4454	C4377	G4227	U4135	A4035	A3958		C		
C	G4537	C4455	U4378	U4228	U4136	A4036	A3959		C		
C	U4538	G4456	G4379	A4229	A4137	A4037	A3960		C		
C	G4539	A4456	C4380	U4230	U4138	A4038	A3961		C		
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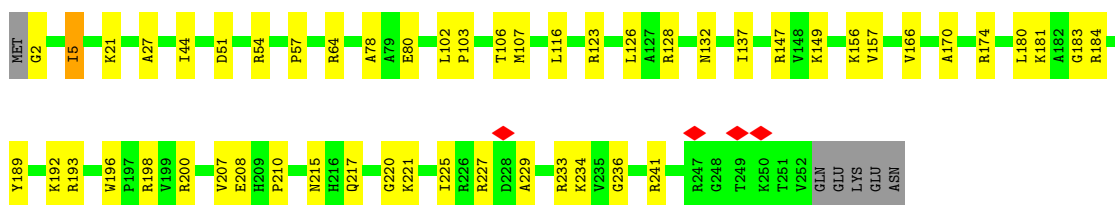
• Molecule 10: 5S rRNA



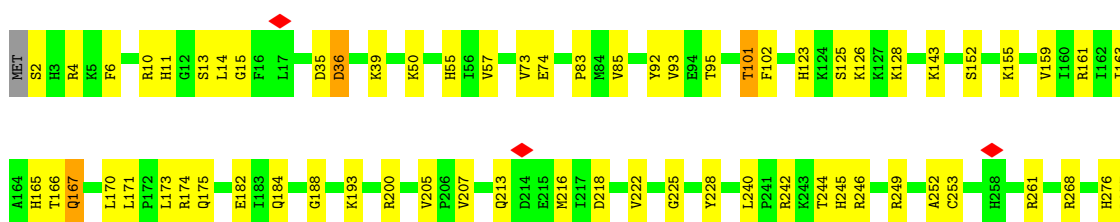
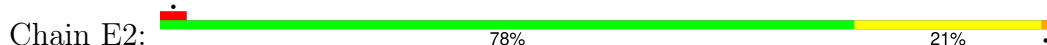
• Molecule 11: 5.8S rRNA



• Molecule 12: 60S ribosomal protein L8



• Molecule 13: 60S ribosomal protein L3

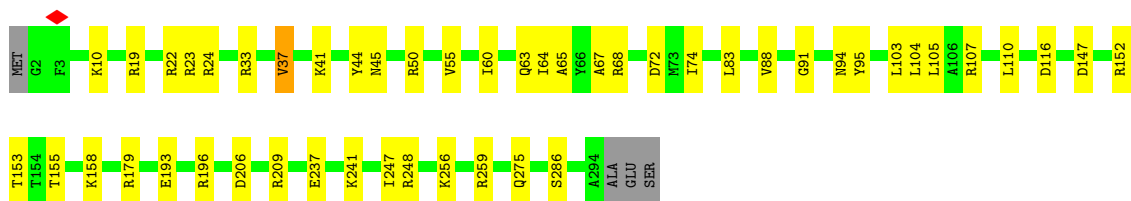
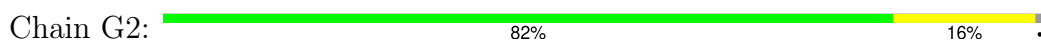




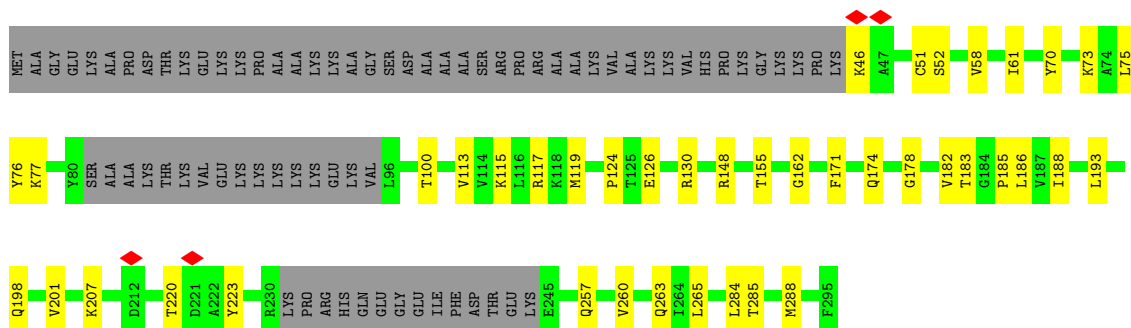
• Molecule 14: 60S ribosomal protein L4



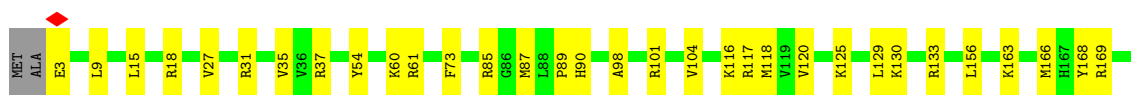
• Molecule 15: 60S ribosomal protein L5



• Molecule 16: 60S ribosomal protein L6

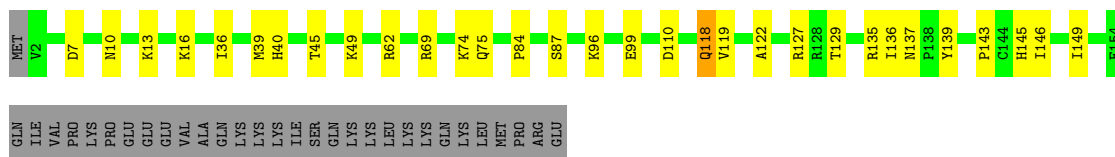


• Molecule 17: 60S ribosomal protein L13a

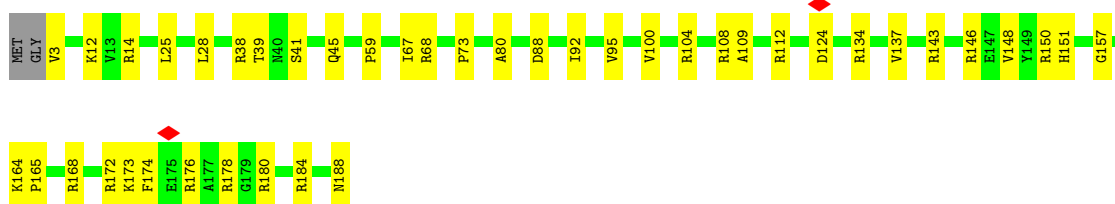
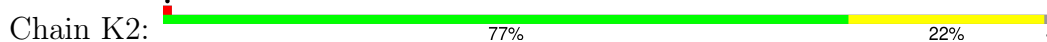




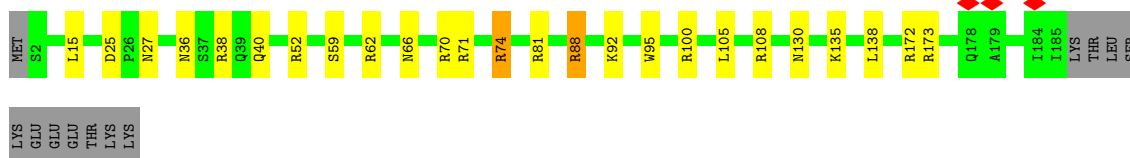
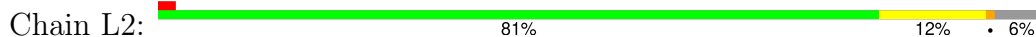
- Molecule 18: 60S ribosomal protein L17



- Molecule 19: 60S ribosomal protein L18



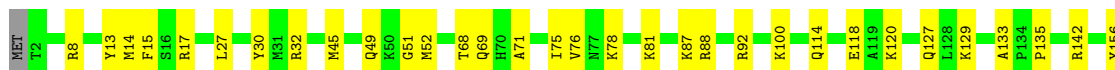
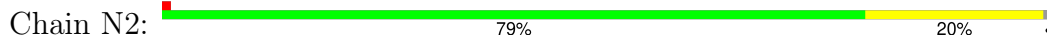
- Molecule 20: 60S ribosomal protein L19



- Molecule 21: 60S ribosomal protein L18a



- Molecule 22: 60S ribosomal protein L21

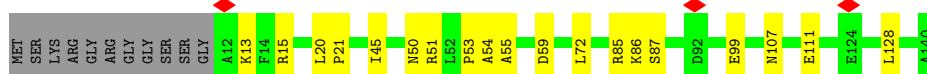
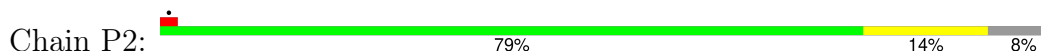




- Molecule 23: 60S ribosomal protein L22



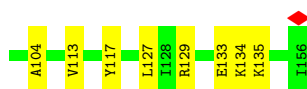
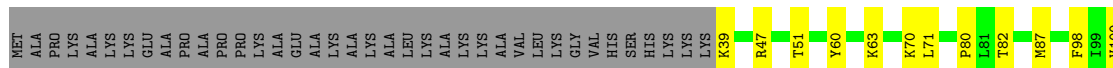
- Molecule 24: 60S ribosomal protein L23



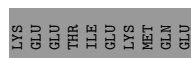
- Molecule 25: 60S ribosomal protein L24



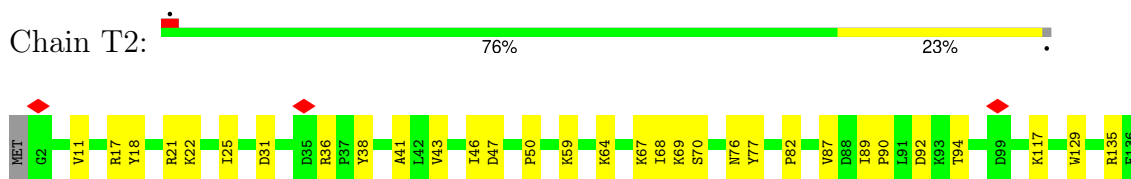
- Molecule 26: 60S ribosomal protein L23a



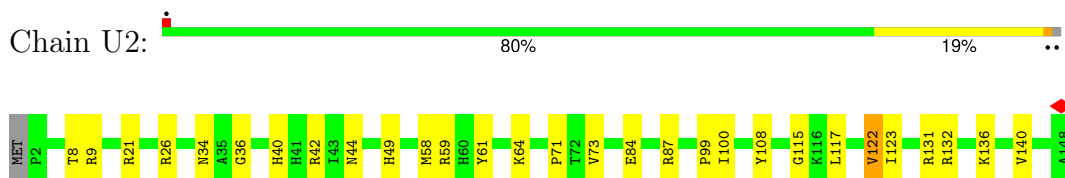
- Molecule 27: 60S ribosomal protein L26



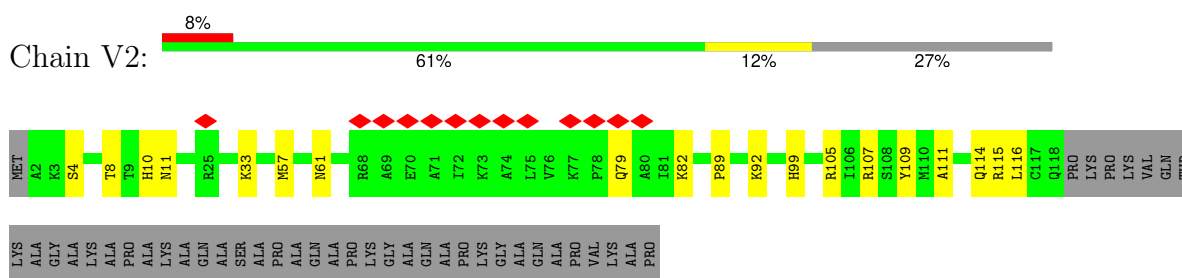
- Molecule 28: 60S ribosomal protein L27



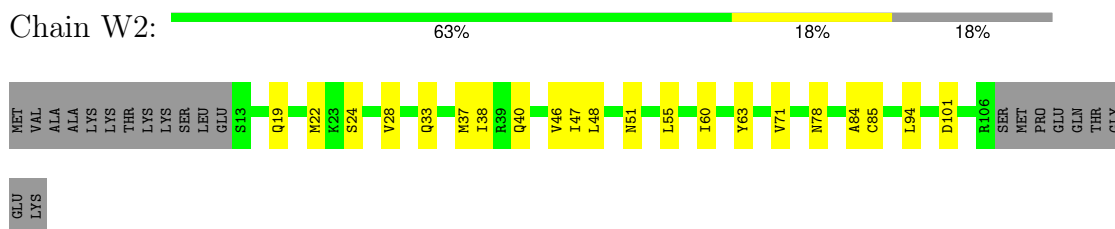
- Molecule 29: 60S ribosomal protein L27a



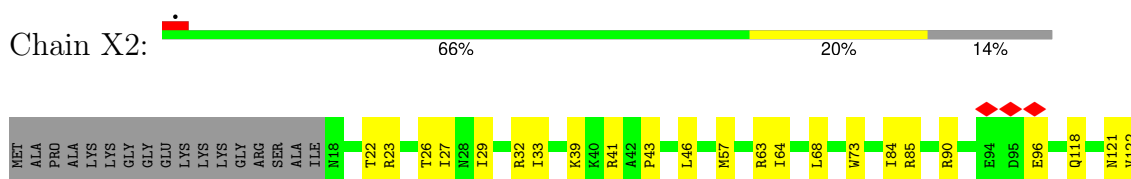
- Molecule 30: 60S ribosomal protein L29



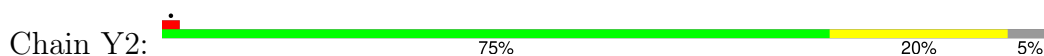
- Molecule 31: 60S ribosomal protein L30

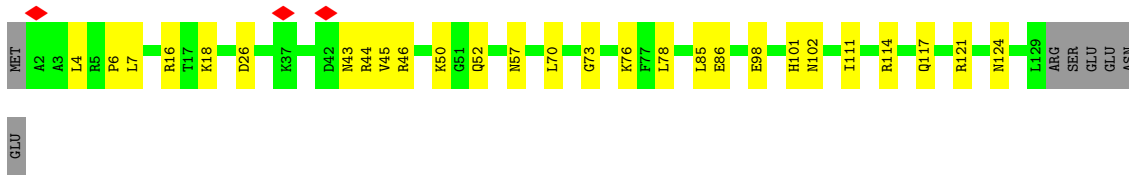


- Molecule 32: 60S ribosomal protein L31

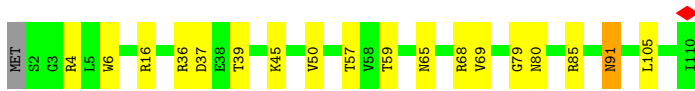
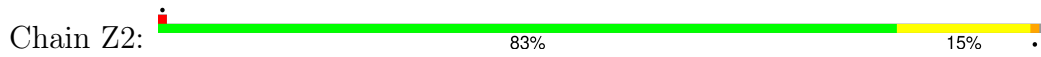


- Molecule 33: 60S ribosomal protein L32

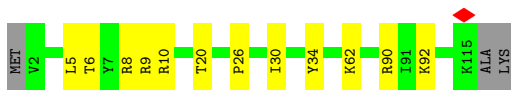
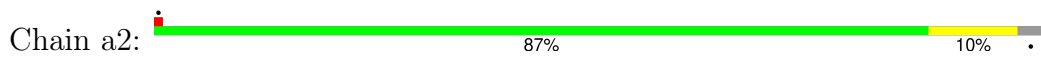




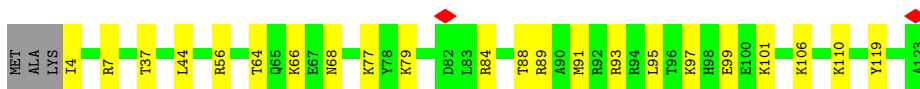
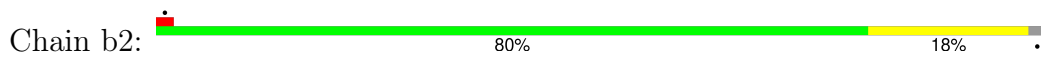
- Molecule 34: 60S ribosomal protein L35a



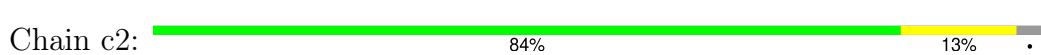
- Molecule 35: 60S ribosomal protein L34



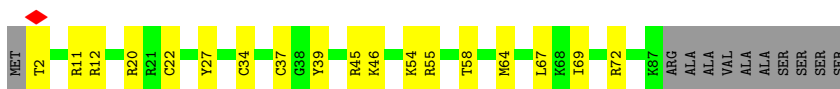
- Molecule 36: 60S ribosomal protein L35



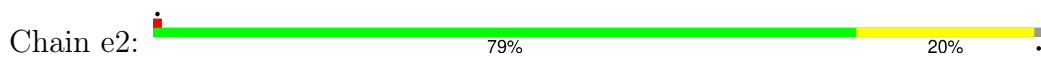
- Molecule 37: 60S ribosomal protein L36



- Molecule 38: 60S ribosomal protein L37



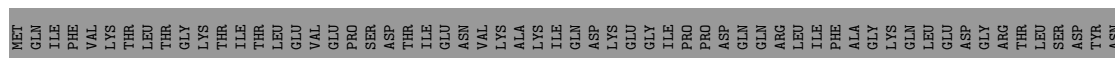
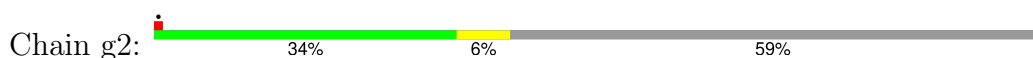
- Molecule 39: 60S ribosomal protein L38



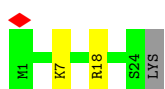
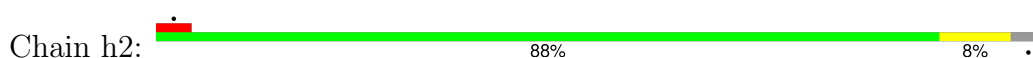
• Molecule 40: 60S ribosomal protein L39



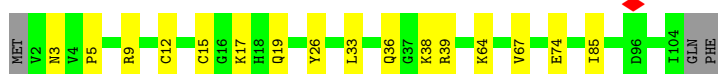
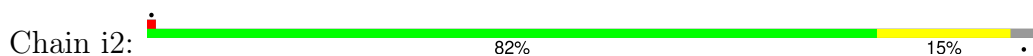
• Molecule 41: Ubiquitin-60S ribosomal protein L40



• Molecule 42: 60S ribosomal protein L41



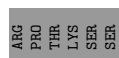
• Molecule 43: 60S ribosomal protein L36a



• Molecule 44: 60S ribosomal protein L37a

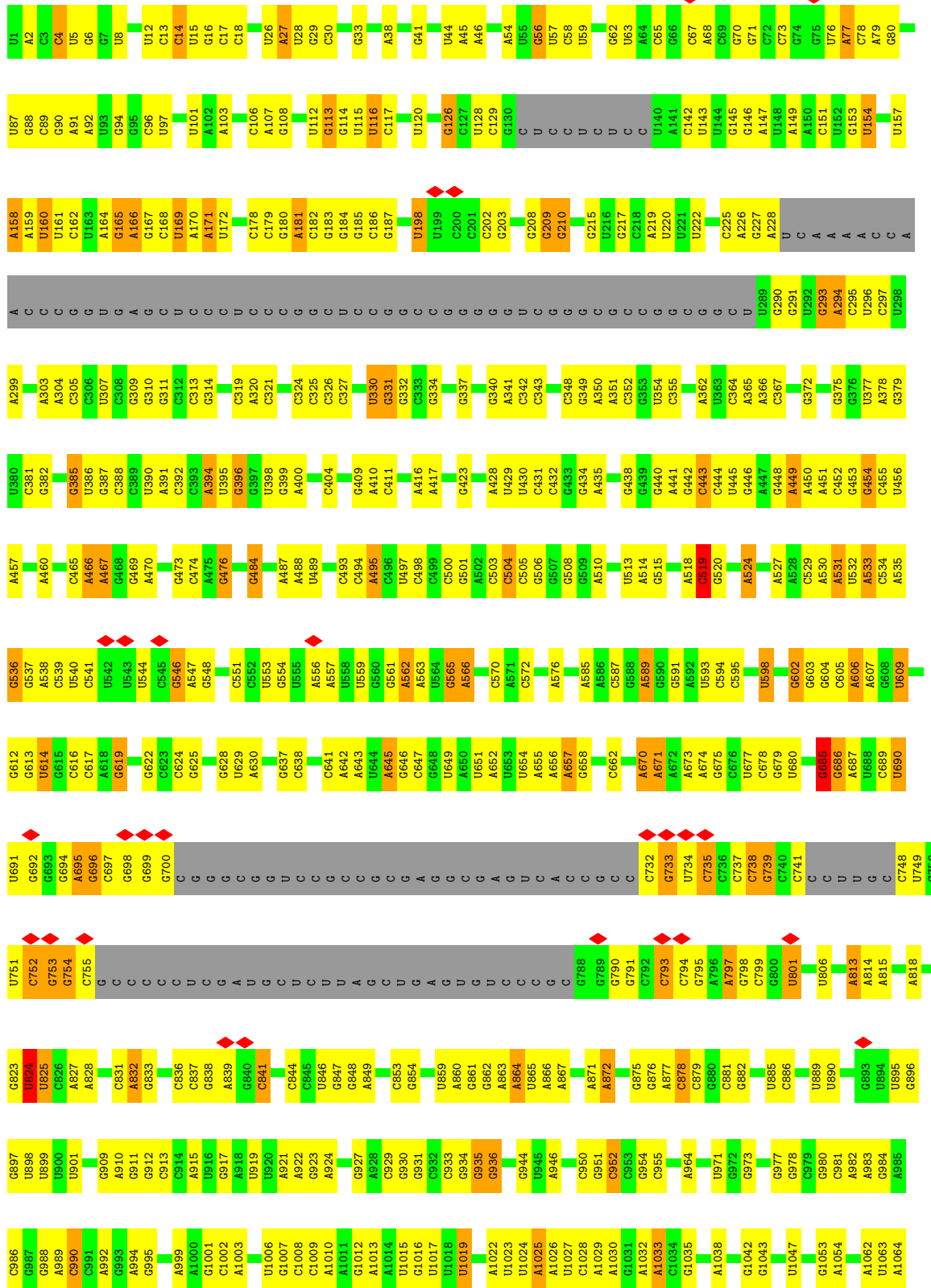


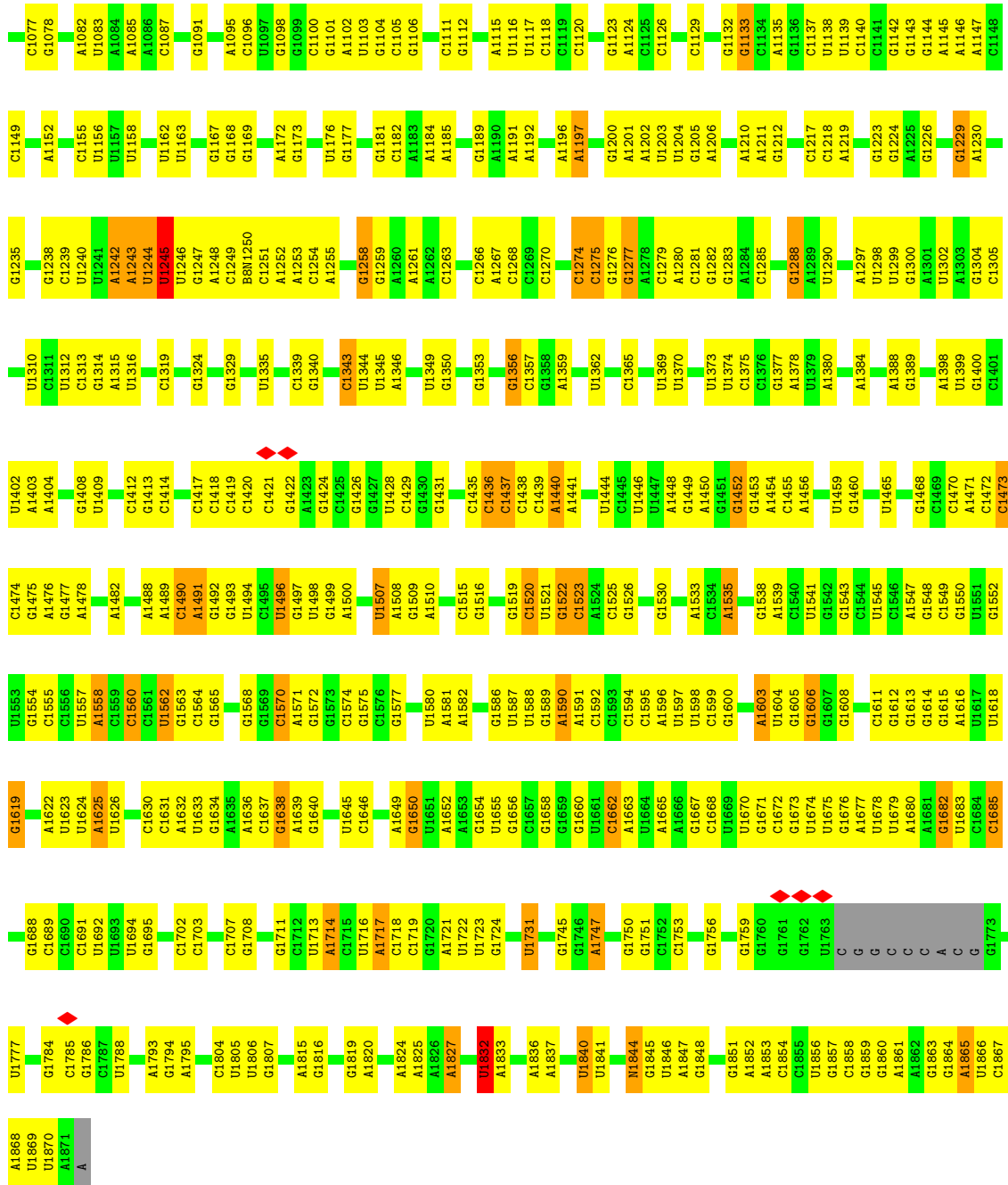
• Molecule 45: 60S ribosomal protein L28



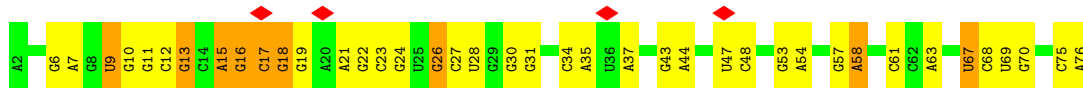
● Molecule 46: 18S rRNA

Chain m2:



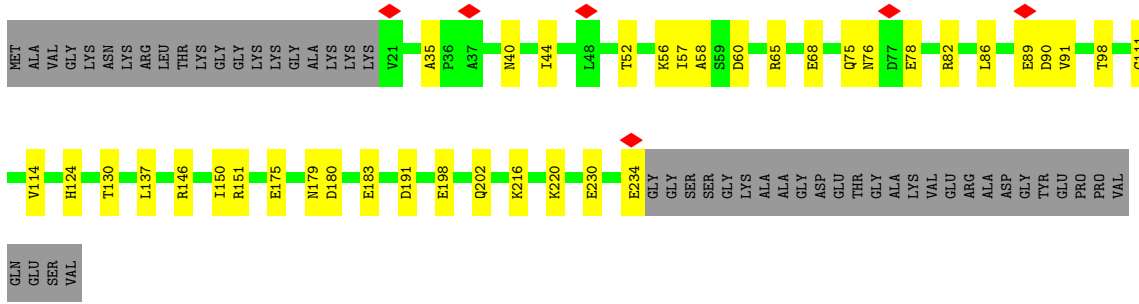


- Molecule 47: tRNA

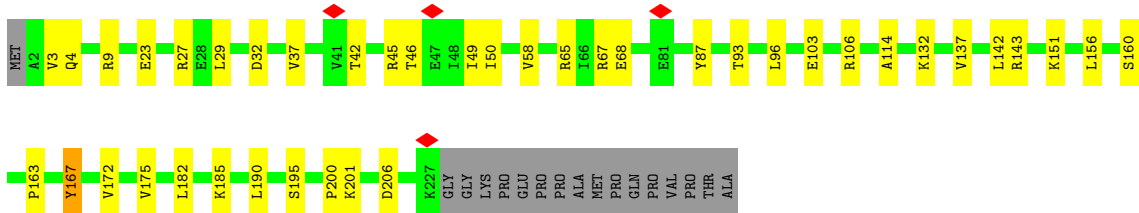
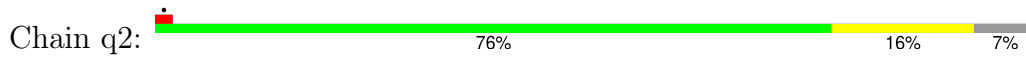


- Molecule 48: 40S ribosomal protein S3a

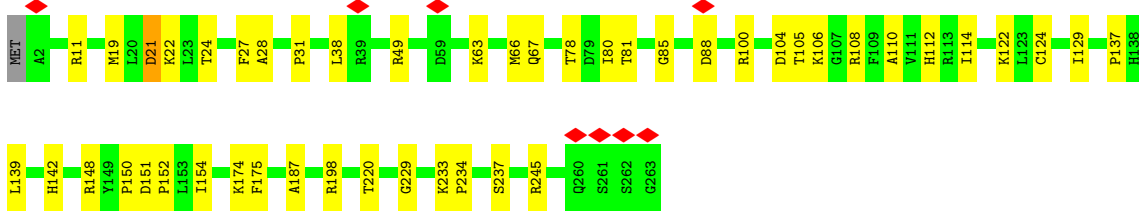
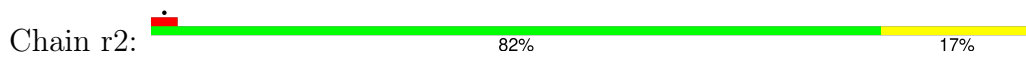




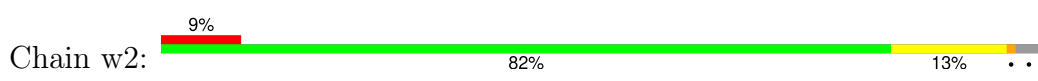
• Molecule 49: 40S ribosomal protein S3



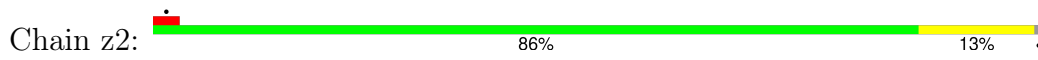
• Molecule 50: 40S ribosomal protein S4, X isoform



• Molecule 51: 40S ribosomal protein S11

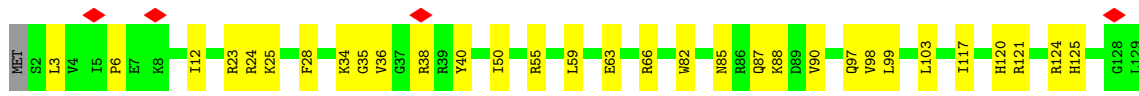


• Molecule 52: 40S ribosomal protein S17

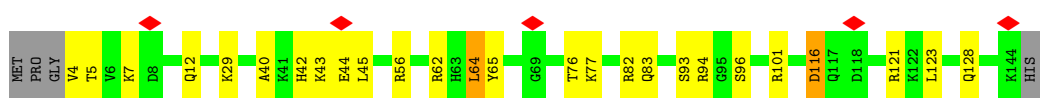
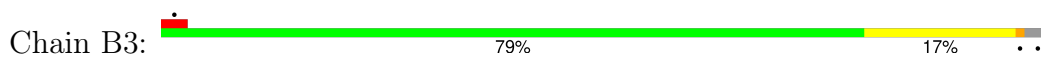




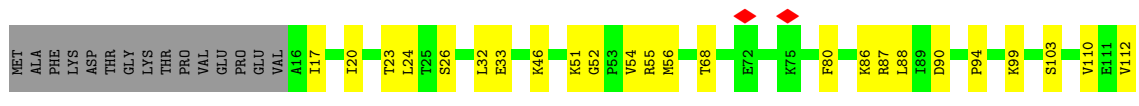
• Molecule 58: 40S ribosomal protein S18



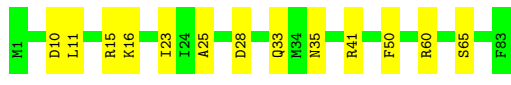
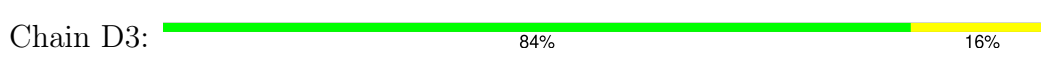
• Molecule 59: 40S ribosomal protein S19



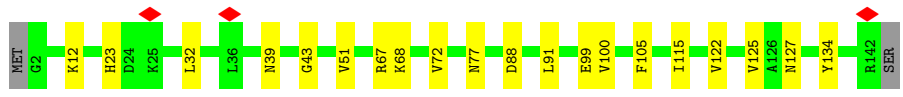
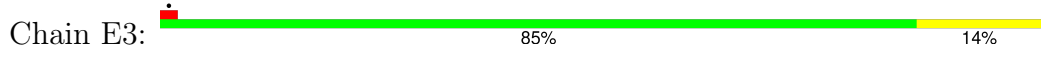
• Molecule 60: 40S ribosomal protein S20



• Molecule 61: 40S ribosomal protein S21

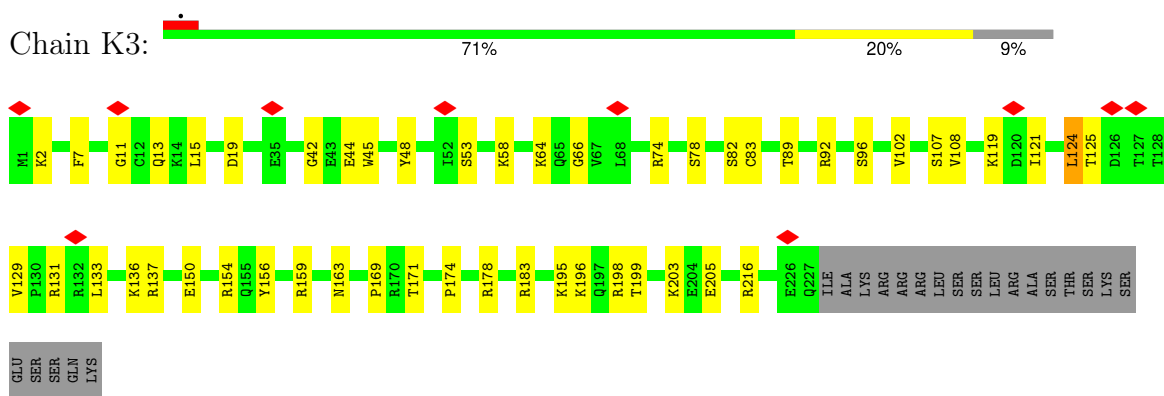


• Molecule 62: 40S ribosomal protein S23

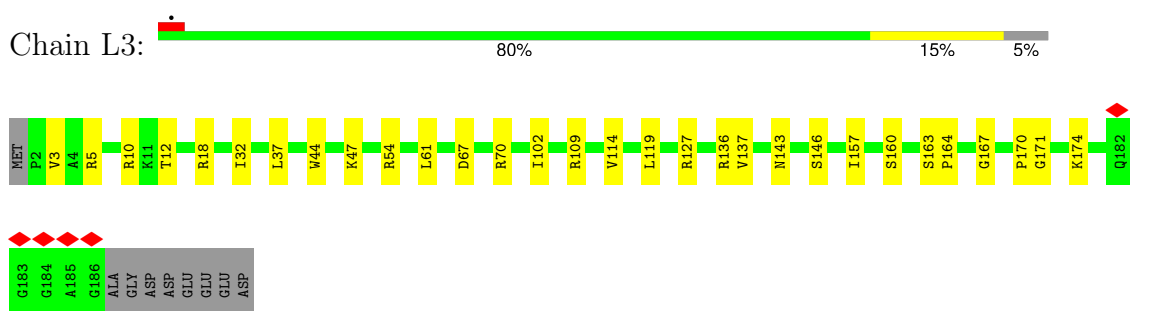


• Molecule 63: 40S ribosomal protein S26

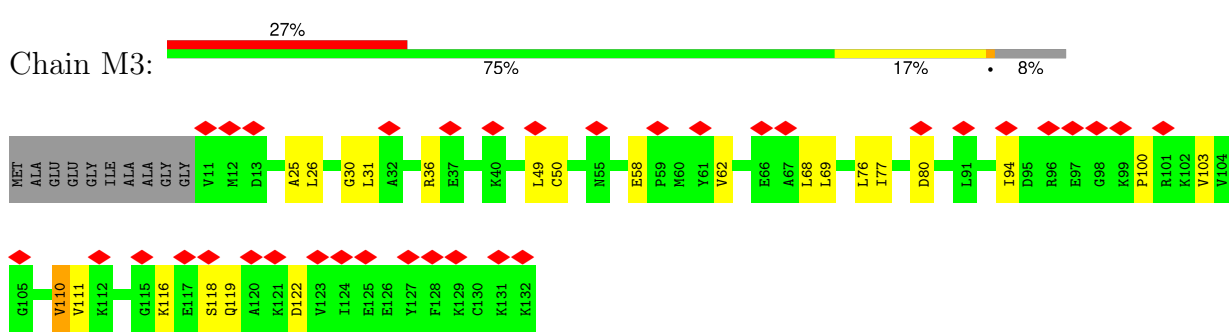
• Molecule 68: 40S ribosomal protein S6



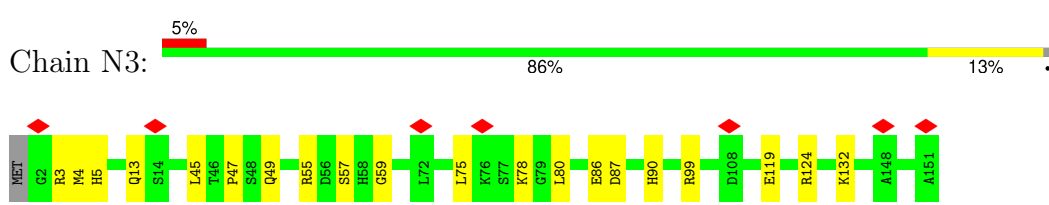
• Molecule 69: 40S ribosomal protein S9



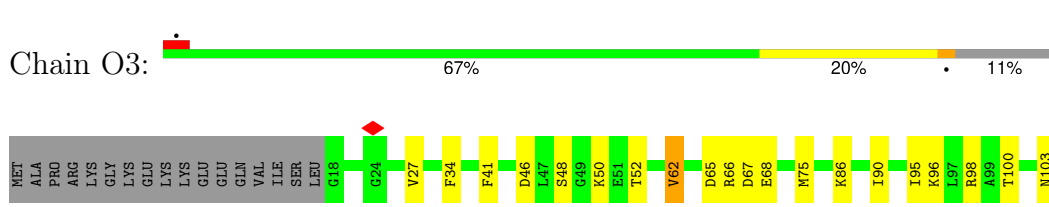
• Molecule 70: 40S ribosomal protein S12

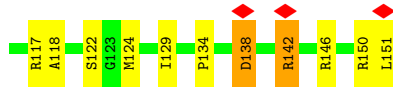


• Molecule 71: 40S ribosomal protein S13

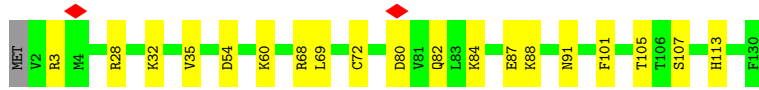
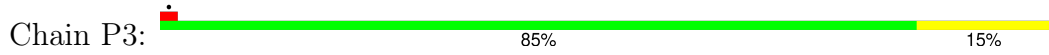


• Molecule 72: 40S ribosomal protein S14

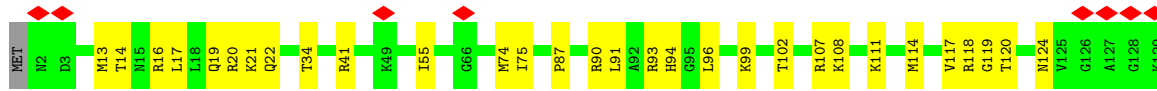
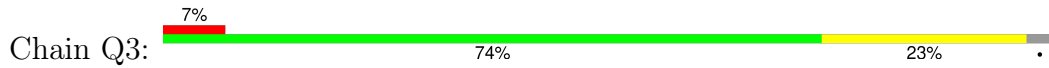




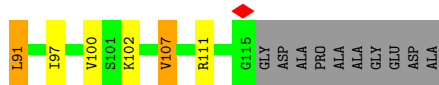
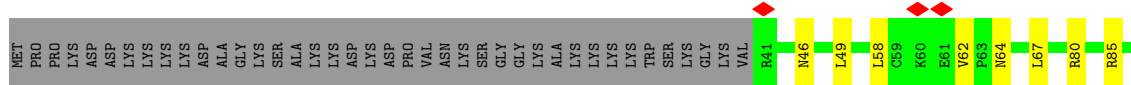
• Molecule 73: 40S ribosomal protein S15a



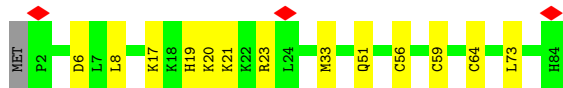
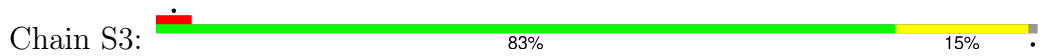
• Molecule 74: 40S ribosomal protein S24



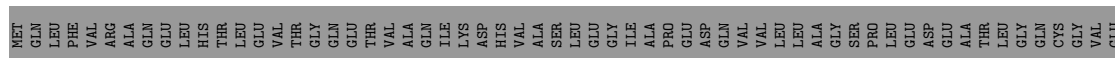
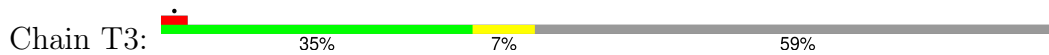
• Molecule 75: 40S ribosomal protein S25

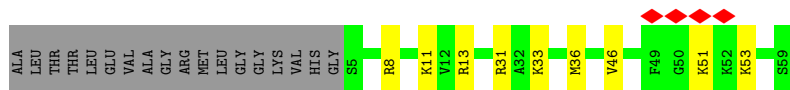


• Molecule 76: 40S ribosomal protein S27-like

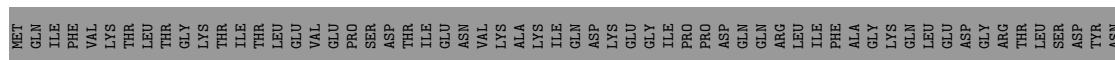


• Molecule 77: 40S ribosomal protein S30

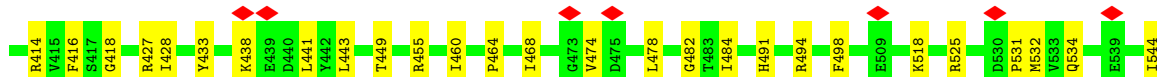
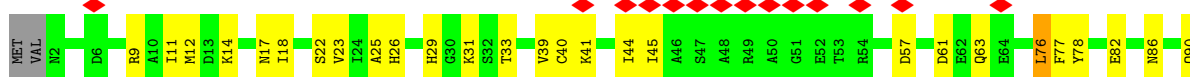
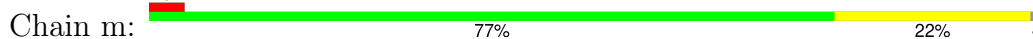




• Molecule 78: Ubiquitin-40S ribosomal protein S27a

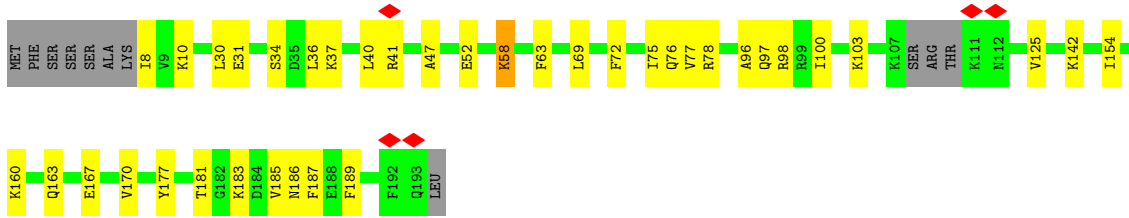


• Molecule 79: Elongation factor 2

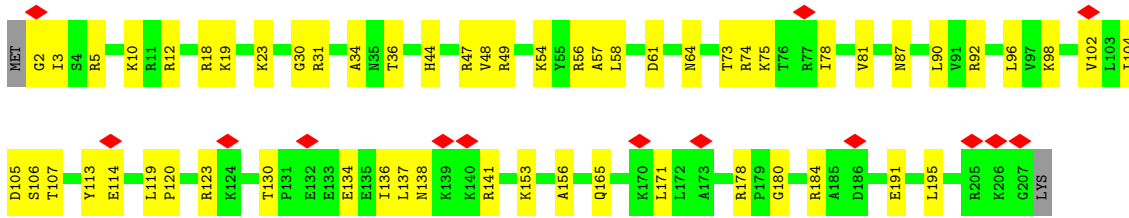


• Molecule 80: 60S acidic ribosomal protein P0

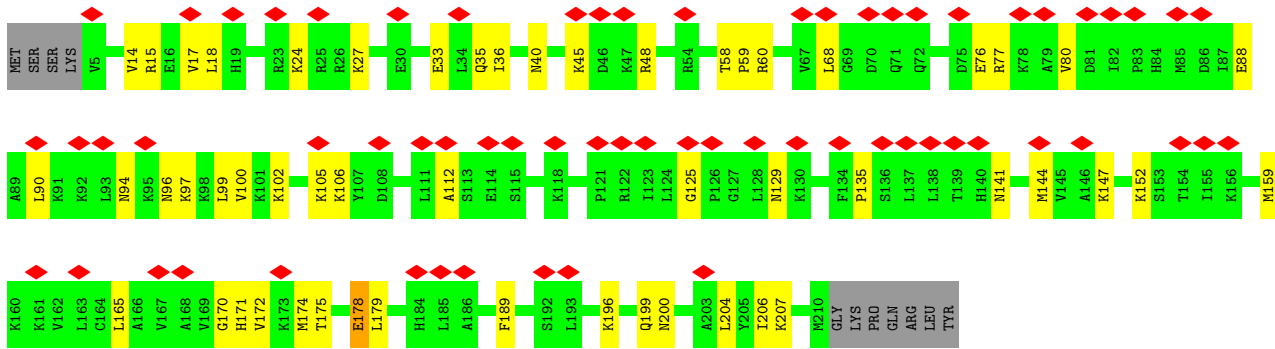




• Molecule 84: 40S ribosomal protein S8



• Molecule 85: 60S ribosomal protein L10a



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	23297	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.0	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	30.264	Depositor
Minimum map value	-17.005	Depositor
Average map value	-0.003	Depositor
Map value standard deviation	1.034	Depositor
Recommended contour level	4	Depositor
Map size (Å)	814.07996, 814.07996, 814.07996	wwPDB
Map dimensions	768, 768, 768	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: E6G, 1MA, GDP, B9B, B8Q, P7G, OMU, B8N, MLZ, DDE, 5MC, I4U, 6MZ, B9H, 2MG, UR3, E7G, MG, A2M, 4AC, B8W, B8T, OMG, G7M, ZN, PSU, MHG, OMC

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	A1	0.11	0/1888	0.27	0/2516
2	B1	0.10	0/1898	0.24	0/2553
3	C1	0.10	0/1537	0.25	0/2065
4	D1	0.09	0/1728	0.22	0/2306
5	E1	0.10	0/1420	0.27	0/1899
6	F1	0.11	0/1707	0.26	0/2286
7	G1	0.12	0/1165	0.24	0/1558
8	H1	0.11	0/1746	0.24	0/2338
9	A2	0.13	0/86883	0.24	0/135484
10	B2	0.11	0/2858	0.23	0/4455
11	C2	0.14	0/3679	0.25	0/5732
12	D2	0.11	0/1959	0.26	0/2627
13	E2	0.11	0/3305	0.27	0/4422
14	F2	0.10	0/2971	0.24	0/3987
15	G2	0.09	0/2431	0.22	0/3256
16	H2	0.09	0/1822	0.23	0/2443
17	I2	0.11	0/1670	0.26	0/2232
18	J2	0.10	0/1268	0.26	0/1700
19	K2	0.10	0/1535	0.25	0/2048
20	L2	0.09	0/1558	0.21	0/2059
21	M2	0.11	0/1490	0.27	0/2000
22	N2	0.09	0/1326	0.21	0/1769
23	O2	0.09	0/839	0.25	0/1126
24	P2	0.09	0/983	0.23	0/1319
25	Q2	0.10	0/909	0.26	0/1203
26	R2	0.09	0/984	0.24	0/1323
27	S2	0.09	0/1132	0.22	0/1504
28	T2	0.09	0/1130	0.21	0/1507
29	U2	0.10	0/1193	0.23	0/1593
30	V2	0.10	0/963	0.24	0/1275
31	W2	0.09	0/742	0.20	0/996

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	X2	0.10	0/903	0.25	0/1216
33	Y2	0.10	0/1071	0.25	0/1429
34	Z2	0.11	0/895	0.25	0/1198
35	a2	0.09	0/916	0.23	0/1221
36	b2	0.09	0/1009	0.22	0/1332
37	c2	0.10	0/838	0.25	0/1111
38	d2	0.10	0/720	0.25	0/952
39	e2	0.08	0/574	0.22	0/760
40	f2	0.10	0/454	0.22	0/599
41	g2	0.09	0/425	0.25	0/561
42	h2	0.09	0/231	0.18	0/294
43	i2	0.10	0/855	0.24	0/1128
44	j2	0.10	0/704	0.22	0/935
45	k2	0.11	0/1016	0.27	0/1363
46	m2	0.12	1/40772 (0.0%)	0.23	0/63546
47	n2	0.11	0/1795	0.26	0/2798
48	p2	0.08	0/1765	0.23	0/2362
49	q2	0.10	0/1784	0.24	0/2402
50	r2	0.08	0/2118	0.24	0/2849
51	w2	0.09	0/1268	0.24	0/1696
52	z2	0.09	0/1094	0.24	0/1469
53	o2	0.09	0/1731	0.23	0/2352
54	s2	0.08	0/1517	0.23	0/2038
55	v2	0.08	0/843	0.22	0/1137
56	x2	0.08	0/1094	0.23	0/1460
57	y2	0.10	0/1161	0.27	0/1553
58	A3	0.08	0/1208	0.24	0/1618
59	B3	0.08	0/1122	0.20	0/1503
60	C3	0.08	0/817	0.22	0/1097
61	D3	0.08	0/645	0.19	0/863
62	E3	0.10	0/1116	0.27	0/1490
63	F3	0.10	0/828	0.25	0/1109
64	G3	0.08	0/508	0.24	0/680
65	H3	0.10	0/466	0.29	0/618
66	I3	0.09	0/2493	0.29	0/3394
67	J3	0.10	0/1762	0.25	0/2382
68	K3	0.08	0/1863	0.24	0/2481
69	L3	0.08	0/1550	0.23	0/2069
70	M3	0.07	0/952	0.22	0/1278
71	N3	0.09	0/1232	0.21	0/1656
72	O3	0.09	0/1015	0.23	0/1361
73	P3	0.10	0/1051	0.27	0/1406
74	Q3	0.08	0/1066	0.23	0/1415

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	R3	0.09	0/604	0.26	0/810
76	S3	0.08	0/665	0.27	0/890
77	T3	0.08	0/443	0.25	0/582
78	U3	0.08	0/515	0.28	0/682
79	m	0.10	0/6756	0.26	0/9122
80	j	0.09	0/1530	0.24	0/2064
81	k	0.10	0/1173	0.29	0/1581
82	A	0.10	0/493	0.23	0/655
83	t	0.09	0/1499	0.23	0/2007
84	u	0.09	0/1715	0.25	0/2287
85	L1	0.11	0/1686	0.31	0/2262
All	All	0.12	1/241045 (0.0%)	0.24	0/352704

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	m2	670	A2M	O3'-P	5.03	1.61	1.56

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	A1	1851	0	1988	35	0
2	B1	1863	0	2003	23	0
3	C1	1519	0	1603	30	0
4	D1	1690	0	1745	22	0
5	E1	1397	0	1425	20	0
6	F1	1676	0	1777	34	0
7	G1	1143	0	1217	21	0
8	H1	1701	0	1749	30	0
9	A2	79519	0	40066	1127	0
10	B2	2558	0	1296	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	C2	3315	0	1685	52	0
12	D2	1921	0	2022	45	0
13	E2	3238	0	3380	63	0
14	F2	2928	0	3110	46	0
15	G2	2385	0	2409	34	0
16	H2	1789	0	1932	23	0
17	I2	1640	0	1790	34	0
18	J2	1242	0	1274	18	0
19	K2	1511	0	1636	32	0
20	L2	1542	0	1698	22	0
21	M2	1450	0	1488	17	0
22	N2	1298	0	1365	25	0
23	O2	825	0	850	8	0
24	P2	969	0	1031	15	0
25	Q2	895	0	948	11	0
26	R2	967	0	1040	17	0
27	S2	1115	0	1205	22	0
28	T2	1107	0	1182	18	0
29	U2	1164	0	1213	20	0
30	V2	945	0	1037	13	0
31	W2	732	0	769	13	0
32	X2	888	0	929	16	0
33	Y2	1053	0	1145	21	0
34	Z2	876	0	912	14	0
35	a2	906	0	997	11	0
36	b2	1001	0	1138	17	0
37	c2	827	0	895	11	0
38	d2	705	0	737	15	0
39	e2	568	0	635	9	0
40	f2	444	0	483	10	0
41	g2	430	0	465	9	0
42	h2	230	0	276	2	0
43	i2	842	0	912	11	0
44	j2	694	0	738	17	0
45	k2	1001	0	1066	23	0
46	m2	36817	0	18599	578	0
47	n2	1604	0	816	21	0
48	p2	1738	0	1809	25	0
49	q2	1756	0	1851	26	0
50	r2	2076	0	2177	32	0
51	w2	1247	0	1323	17	0
52	z2	1080	0	1135	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	o2	1694	0	1696	27	0
54	s2	1496	0	1548	24	0
55	v2	819	0	842	15	0
56	x2	1073	0	1128	31	0
57	y2	1143	0	1213	18	0
58	A3	1190	0	1249	28	0
59	B3	1104	0	1139	21	0
60	C3	807	0	874	14	0
61	D3	638	0	635	11	0
62	E3	1098	0	1167	15	0
63	F3	811	0	866	16	0
64	G3	506	0	536	14	0
65	H3	455	0	446	10	0
66	I3	2436	0	2393	57	0
67	J3	1725	0	1815	42	0
68	K3	1840	0	1989	41	0
69	L3	1525	0	1640	22	0
70	M3	942	0	971	14	0
71	N3	1208	0	1294	17	0
72	O3	1002	0	1023	25	0
73	P3	1034	0	1080	16	0
74	Q3	1049	0	1122	24	0
75	R3	598	0	656	9	0
76	S3	652	0	676	11	0
77	T3	438	0	484	8	0
78	U3	505	0	506	6	0
79	m	6649	0	6723	116	0
80	j	1507	0	1564	25	0
81	k	1159	0	1216	24	0
82	A	486	0	441	10	0
83	t	1477	0	1567	23	0
84	u	1686	0	1772	42	0
85	L1	1660	0	1768	33	0
86	F3	1	0	0	0	0
86	H3	1	0	0	0	0
86	U3	1	0	0	0	0
86	d2	1	0	0	0	0
86	g2	1	0	0	0	0
86	i2	1	0	0	0	0
86	j2	1	0	0	0	0
87	H3	1	0	0	0	0
88	m	28	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
89	A2	1	0	0	0	0
89	B1	1	0	0	0	0
89	m2	2	0	0	0	0
All	All	227130	0	171022	3010	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 8.

The worst 5 of 3010 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)
9:A2:3837:B8W:C1 ⁷	9:A2:3837:B8W:O4 ⁷	1.67	1.26
9:A2:2600:A:H61	9:A2:3499:C:N4	1.59	1.01
46:m2:1745:G:N2	46:m2:1793:A:H62	1.60	0.99
9:A2:2600:A:N6	9:A2:3499:C:H42	1.61	0.98
83:t:72:PHE:O	83:t:76:GLN:HB2	1.64	0.96

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A1	221/270 (82%)	214 (97%)	7 (3%)	0	100	100
2	B1	227/266 (85%)	220 (97%)	7 (3%)	0	100	100
3	C1	188/192 (98%)	185 (98%)	3 (2%)	0	100	100
4	D1	204/214 (95%)	201 (98%)	3 (2%)	0	100	100
5	E1	172/178 (97%)	167 (97%)	5 (3%)	0	100	100
6	F1	205/211 (97%)	194 (95%)	11 (5%)	0	100	100
7	G1	137/217 (63%)	133 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	H1	201/204 (98%)	198 (98%)	3 (2%)	0	100	100
12	D2	249/257 (97%)	234 (94%)	15 (6%)	0	100	100
13	E2	400/403 (99%)	397 (99%)	3 (1%)	0	100	100
14	F2	364/419 (87%)	359 (99%)	5 (1%)	0	100	100
15	G2	291/297 (98%)	284 (98%)	7 (2%)	0	100	100
16	H2	215/296 (73%)	208 (97%)	7 (3%)	0	100	100
17	I2	199/203 (98%)	195 (98%)	4 (2%)	0	100	100
18	J2	151/184 (82%)	146 (97%)	5 (3%)	0	100	100
19	K2	184/188 (98%)	181 (98%)	3 (2%)	0	100	100
20	L2	182/196 (93%)	181 (100%)	1 (0%)	0	100	100
21	M2	173/176 (98%)	166 (96%)	7 (4%)	0	100	100
22	N2	157/160 (98%)	155 (99%)	2 (1%)	0	100	100
23	O2	99/128 (77%)	97 (98%)	2 (2%)	0	100	100
24	P2	127/140 (91%)	125 (98%)	2 (2%)	0	100	100
25	Q2	106/157 (68%)	104 (98%)	2 (2%)	0	100	100
26	R2	116/156 (74%)	114 (98%)	2 (2%)	0	100	100
27	S2	132/145 (91%)	131 (99%)	1 (1%)	0	100	100
28	T2	133/136 (98%)	131 (98%)	2 (2%)	0	100	100
29	U2	145/148 (98%)	139 (96%)	6 (4%)	0	100	100
30	V2	115/160 (72%)	110 (96%)	5 (4%)	0	100	100
31	W2	92/115 (80%)	86 (94%)	6 (6%)	0	100	100
32	X2	105/125 (84%)	104 (99%)	1 (1%)	0	100	100
33	Y2	126/135 (93%)	125 (99%)	1 (1%)	0	100	100
34	Z2	107/110 (97%)	106 (99%)	1 (1%)	0	100	100
35	a2	112/117 (96%)	110 (98%)	2 (2%)	0	100	100
36	b2	118/123 (96%)	115 (98%)	3 (2%)	0	100	100
37	c2	100/105 (95%)	97 (97%)	3 (3%)	0	100	100
38	d2	84/97 (87%)	82 (98%)	2 (2%)	0	100	100
39	e2	67/70 (96%)	67 (100%)	0	0	100	100
40	f2	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
41	g2	49/128 (38%)	48 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	h2	22/25 (88%)	22 (100%)	0	0	100	100
43	i2	101/106 (95%)	95 (94%)	6 (6%)	0	100	100
44	j2	87/92 (95%)	83 (95%)	4 (5%)	0	100	100
45	k2	123/137 (90%)	119 (97%)	4 (3%)	0	100	100
48	p2	212/264 (80%)	210 (99%)	2 (1%)	0	100	100
49	q2	224/243 (92%)	217 (97%)	7 (3%)	0	100	100
50	r2	260/263 (99%)	252 (97%)	8 (3%)	0	100	100
51	w2	151/158 (96%)	144 (95%)	7 (5%)	0	100	100
52	z2	132/135 (98%)	128 (97%)	4 (3%)	0	100	100
53	o2	212/295 (72%)	211 (100%)	1 (0%)	0	100	100
54	s2	187/204 (92%)	182 (97%)	5 (3%)	0	100	100
55	v2	95/165 (58%)	93 (98%)	2 (2%)	0	100	100
56	x2	128/145 (88%)	124 (97%)	3 (2%)	1 (1%)	16	47
57	y2	142/146 (97%)	139 (98%)	3 (2%)	0	100	100
58	A3	142/152 (93%)	138 (97%)	4 (3%)	0	100	100
59	B3	139/145 (96%)	139 (100%)	0	0	100	100
60	C3	100/119 (84%)	97 (97%)	3 (3%)	0	100	100
61	D3	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
62	E3	139/143 (97%)	135 (97%)	4 (3%)	0	100	100
63	F3	99/115 (86%)	98 (99%)	1 (1%)	0	100	100
64	G3	62/69 (90%)	61 (98%)	1 (2%)	0	100	100
65	H3	52/56 (93%)	50 (96%)	2 (4%)	0	100	100
66	I3	311/317 (98%)	295 (95%)	16 (5%)	0	100	100
67	J3	220/293 (75%)	217 (99%)	3 (1%)	0	100	100
68	K3	225/249 (90%)	223 (99%)	2 (1%)	0	100	100
69	L3	183/194 (94%)	181 (99%)	2 (1%)	0	100	100
70	M3	120/132 (91%)	114 (95%)	6 (5%)	0	100	100
71	N3	148/151 (98%)	144 (97%)	4 (3%)	0	100	100
72	O3	132/151 (87%)	126 (96%)	6 (4%)	0	100	100
73	P3	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
74	Q3	127/133 (96%)	122 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
75	R3	73/125 (58%)	73 (100%)	0	0	100	100
76	S3	81/84 (96%)	80 (99%)	1 (1%)	0	100	100
77	T3	53/133 (40%)	50 (94%)	3 (6%)	0	100	100
78	U3	60/156 (38%)	59 (98%)	1 (2%)	0	100	100
79	m	846/858 (99%)	823 (97%)	23 (3%)	0	100	100
80	j	194/317 (61%)	191 (98%)	3 (2%)	0	100	100
81	k	151/165 (92%)	144 (95%)	6 (4%)	1 (1%)	18	49
82	A	57/386 (15%)	57 (100%)	0	0	100	100
83	t	179/194 (92%)	174 (97%)	5 (3%)	0	100	100
84	u	204/208 (98%)	195 (96%)	9 (4%)	0	100	100
85	L1	204/217 (94%)	187 (92%)	16 (8%)	1 (0%)	24	57
All	All	12686/14730 (86%)	12350 (97%)	333 (3%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
81	k	147	HIS
56	x2	108	LYS
85	L1	207	LYS

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A1	194/234 (83%)	194 (100%)	0	100	100
2	B1	198/223 (89%)	198 (100%)	0	100	100
3	C1	169/171 (99%)	169 (100%)	0	100	100
4	D1	177/180 (98%)	176 (99%)	1 (1%)	78	83
5	E1	147/149 (99%)	145 (99%)	2 (1%)	59	76
6	F1	174/178 (98%)	171 (98%)	3 (2%)	53	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	G1	118/157 (75%)	118 (100%)	0	100	100
8	H1	171/172 (99%)	170 (99%)	1 (1%)	78	83
12	D2	193/199 (97%)	191 (99%)	2 (1%)	68	79
13	E2	347/348 (100%)	340 (98%)	7 (2%)	48	72
14	F2	307/347 (88%)	305 (99%)	2 (1%)	76	82
15	G2	245/249 (98%)	244 (100%)	1 (0%)	84	86
16	H2	198/256 (77%)	195 (98%)	3 (2%)	57	75
17	I2	172/173 (99%)	171 (99%)	1 (1%)	78	83
18	J2	134/164 (82%)	131 (98%)	3 (2%)	45	71
19	K2	164/165 (99%)	163 (99%)	1 (1%)	78	83
20	L2	163/175 (93%)	161 (99%)	2 (1%)	63	78
21	M2	155/156 (99%)	154 (99%)	1 (1%)	78	83
22	N2	138/139 (99%)	137 (99%)	1 (1%)	76	82
23	O2	91/114 (80%)	91 (100%)	0	100	100
24	P2	100/107 (94%)	99 (99%)	1 (1%)	68	79
25	Q2	90/126 (71%)	90 (100%)	0	100	100
26	R2	106/133 (80%)	106 (100%)	0	100	100
27	S2	124/135 (92%)	124 (100%)	0	100	100
28	T2	117/118 (99%)	117 (100%)	0	100	100
29	U2	120/121 (99%)	118 (98%)	2 (2%)	53	74
30	V2	98/124 (79%)	95 (97%)	3 (3%)	35	64
31	W2	79/97 (81%)	78 (99%)	1 (1%)	61	77
32	X2	98/110 (89%)	98 (100%)	0	100	100
33	Y2	114/121 (94%)	114 (100%)	0	100	100
34	Z2	88/89 (99%)	87 (99%)	1 (1%)	65	78
35	a2	98/100 (98%)	98 (100%)	0	100	100
36	b2	108/110 (98%)	108 (100%)	0	100	100
37	c2	86/90 (96%)	86 (100%)	0	100	100
38	d2	73/80 (91%)	73 (100%)	0	100	100
39	e2	64/65 (98%)	64 (100%)	0	100	100
40	f2	47/48 (98%)	47 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	g2	47/115 (41%)	47 (100%)	0	100	100
42	h2	23/24 (96%)	23 (100%)	0	100	100
43	i2	91/94 (97%)	90 (99%)	1 (1%)	65	78
44	j2	73/75 (97%)	69 (94%)	4 (6%)	19	50
45	k2	109/121 (90%)	108 (99%)	1 (1%)	70	80
48	p2	195/229 (85%)	195 (100%)	0	100	100
49	q2	189/202 (94%)	188 (100%)	1 (0%)	81	85
50	r2	224/225 (100%)	222 (99%)	2 (1%)	70	80
51	w2	137/142 (96%)	135 (98%)	2 (2%)	57	75
52	z2	120/121 (99%)	118 (98%)	2 (2%)	53	74
53	o2	179/242 (74%)	178 (99%)	1 (1%)	78	83
54	s2	159/170 (94%)	158 (99%)	1 (1%)	78	83
55	v2	88/136 (65%)	87 (99%)	1 (1%)	65	78
56	x2	116/130 (89%)	112 (97%)	4 (3%)	32	63
57	y2	119/121 (98%)	118 (99%)	1 (1%)	73	81
58	A3	125/132 (95%)	123 (98%)	2 (2%)	55	75
59	B3	112/115 (97%)	109 (97%)	3 (3%)	39	67
60	C3	93/107 (87%)	91 (98%)	2 (2%)	45	71
61	D3	67/67 (100%)	67 (100%)	0	100	100
62	E3	113/115 (98%)	112 (99%)	1 (1%)	70	80
63	F3	88/98 (90%)	85 (97%)	3 (3%)	32	63
64	G3	57/62 (92%)	57 (100%)	0	100	100
65	H3	48/49 (98%)	47 (98%)	1 (2%)	47	71
66	I3	272/275 (99%)	265 (97%)	7 (3%)	40	68
67	J3	188/224 (84%)	186 (99%)	2 (1%)	65	78
68	K3	198/218 (91%)	195 (98%)	3 (2%)	57	75
69	L3	161/168 (96%)	158 (98%)	3 (2%)	50	73
70	M3	102/108 (94%)	99 (97%)	3 (3%)	37	66
71	N3	130/131 (99%)	130 (100%)	0	100	100
72	O3	104/119 (87%)	100 (96%)	4 (4%)	29	60
73	P3	112/113 (99%)	112 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
74	Q3	111/115 (96%)	111 (100%)	0	100	100
75	R3	66/103 (64%)	64 (97%)	2 (3%)	36	65
76	S3	75/76 (99%)	74 (99%)	1 (1%)	61	77
77	T3	45/106 (42%)	44 (98%)	1 (2%)	45	71
78	U3	55/140 (39%)	50 (91%)	5 (9%)	9	32
79	m	725/729 (100%)	719 (99%)	6 (1%)	73	81
80	j	164/255 (64%)	161 (98%)	3 (2%)	51	73
81	k	126/137 (92%)	122 (97%)	4 (3%)	34	64
82	A	52/304 (17%)	52 (100%)	0	100	100
83	t	164/174 (94%)	160 (98%)	4 (2%)	43	69
84	u	178/180 (99%)	175 (98%)	3 (2%)	53	74
85	L1	187/197 (95%)	182 (97%)	5 (3%)	39	67
All	All	11052/12487 (88%)	10924 (99%)	128 (1%)	61	78

5 of 128 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
81	k	156	ASN
83	t	77	VAL
51	w2	4	ILE
50	r2	220	THR
84	u	107	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 90 such sidechains are listed below:

Mol	Chain	Res	Type
61	D3	35	ASN
75	R3	46	ASN
62	E3	61	GLN
67	J3	113	GLN
79	m	201	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	B2	119/121 (98%)	16 (13%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	C2	155/156 (99%)	28 (18%)	2 (1%)
46	m2	1717/1871 (91%)	385 (22%)	0
47	n2	74/75 (98%)	24 (32%)	0
9	A2	3691/4731 (78%)	788 (21%)	13 (0%)
All	All	5756/6954 (82%)	1241 (21%)	15 (0%)

5 of 1241 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	A2	2	G
9	A2	25	A
9	A2	39	A
9	A2	42	A
9	A2	48	G

5 of 15 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
9	A2	2382	C
11	C2	59	A
9	A2	2430	G
11	C2	83	C
9	A2	4351	U

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

101 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
9	5MC	A2	3987	9	19,22,23	3.90	8 (42%)	26,32,35	1.02	2 (7%)
9	A2M	A2	3374	9	22,25,26	2.64	11 (50%)	30,36,39	2.36	8 (26%)
46	4AC	m2	1844	46	21,24,25	3.67	9 (42%)	28,34,37	1.15	4 (14%)
9	5MC	A2	3438	9	19,22,23	3.92	8 (42%)	26,32,35	0.97	1 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	OMC	A2	2616	9	19,22,23	3.08	8 (42%)	25,31,34	0.92	1 (4%)
9	PSU	A2	4055	9	18,21,22	4.53	6 (33%)	21,30,33	3.00	7 (33%)
9	PSU	A2	1496	9	18,21,22	4.51	6 (33%)	21,30,33	3.04	6 (28%)
9	P7G	A2	1711	10,9	24,28,29	3.61	10 (41%)	25,41,44	1.23	2 (8%)
9	UR3	A2	4249	9	19,22,23	3.20	8 (42%)	26,32,35	1.57	4 (15%)
11	OMU	C2	14	11	19,22,23	3.09	8 (42%)	25,31,34	1.81	5 (20%)
9	PSU	A2	3420	9	18,21,22	4.52	6 (33%)	21,30,33	2.87	5 (23%)
9	A2M	A2	1337	9	22,25,26	2.64	11 (50%)	30,36,39	2.35	9 (30%)
9	B8T	A2	4135	9	19,22,23	3.29	8 (42%)	25,31,34	0.86	1 (4%)
9	OMG	A2	1852	9	23,26,27	2.46	9 (39%)	32,38,41	2.07	10 (31%)
9	OMG	A2	2528	9	23,26,27	2.49	8 (34%)	32,38,41	2.14	10 (31%)
9	OMC	A2	3543	9	19,22,23	3.04	8 (42%)	25,31,34	0.85	0
9	2MG	A2	1330	9	23,26,27	2.62	8 (34%)	33,38,41	2.30	12 (36%)
9	OMU	A2	3958	9	19,22,23	3.02	8 (42%)	25,31,34	1.81	5 (20%)
9	A2M	A2	1673	9	22,25,26	2.63	11 (50%)	30,36,39	2.45	10 (33%)
46	A2M	m2	166	46	22,25,26	2.66	11 (50%)	30,36,39	2.34	9 (30%)
9	E7G	A2	1599	9	24,27,28	3.35	11 (45%)	28,40,43	2.35	9 (32%)
9	OMG	A2	1685	9	23,26,27	2.47	9 (39%)	32,38,41	2.11	11 (34%)
9	A2M	A2	1140	9	22,25,26	2.66	11 (50%)	30,36,39	2.33	9 (30%)
9	UR3	A2	1668	9	19,22,23	3.25	8 (42%)	26,32,35	1.64	4 (15%)
9	OMC	A2	2120	9	19,22,23	3.04	7 (36%)	25,31,34	1.05	3 (12%)
9	G7M	A2	2277	9	23,26,27	3.52	11 (47%)	34,39,42	1.74	6 (17%)
9	OMU	A2	4272	9	19,22,23	3.05	8 (42%)	25,31,34	1.76	5 (20%)
46	PSU	m2	614	46	18,21,22	4.50	6 (33%)	21,30,33	2.94	6 (28%)
46	PSU	m2	1083	46	18,21,22	4.52	6 (33%)	21,30,33	3.00	7 (33%)
9	A2M	A2	3481	9	22,25,26	2.63	11 (50%)	30,36,39	2.33	10 (33%)
9	I4U	A2	1472	9	20,24,25	4.77	15 (75%)	27,34,37	1.84	3 (11%)
9	I4U	A2	3846	9	20,24,25	4.77	15 (75%)	27,34,37	1.63	2 (7%)
9	OMG	A2	4022	9	23,26,27	2.46	9 (39%)	32,38,41	2.09	11 (34%)
9	OMG	A2	3848	9	23,26,27	2.46	9 (39%)	32,38,41	2.08	11 (34%)
9	G7M	A2	1418	9	23,26,27	3.53	11 (47%)	34,39,42	1.74	6 (17%)
46	OMC	m2	519	46	19,22,23	3.07	8 (42%)	25,31,34	0.91	1 (4%)
9	A2M	A2	3379	9	22,25,26	2.65	11 (50%)	30,36,39	2.31	10 (33%)
9	PSU	A2	1395	9	18,21,22	4.54	7 (38%)	21,30,33	2.92	5 (23%)
9	2MG	A2	878	9	23,26,27	2.64	7 (30%)	33,38,41	2.29	11 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	B8W	A2	3837	9	23,26,27	3.94	13 (56%)	33,38,41	3.43	17 (51%)
9	OMC	A2	4188	9	19,22,23	3.03	8 (42%)	25,31,34	0.79	0
46	UR3	m2	1832	46	19,22,23	3.21	8 (42%)	26,32,35	1.62	3 (11%)
9	A2M	A2	2156	9	22,25,26	2.65	11 (50%)	30,36,39	2.33	9 (30%)
9	OMG	A2	3448	9	23,26,27	2.47	9 (39%)	32,38,41	2.16	11 (34%)
9	A2M	A2	2118	9	22,25,26	2.64	11 (50%)	30,36,39	2.32	9 (30%)
9	OMG	A2	1438	9	23,26,27	2.47	8 (34%)	32,38,41	2.15	10 (31%)
9	OMC	A2	3565	9	19,22,23	3.06	8 (42%)	25,31,34	0.82	0
9	G7M	A2	4202	9	23,26,27	3.52	11 (47%)	34,39,42	1.71	7 (20%)
9	OMG	A2	4275	9	23,26,27	2.47	9 (39%)	32,38,41	2.08	11 (34%)
9	PSU	A2	2263	9	18,21,22	4.56	6 (33%)	21,30,33	2.90	6 (28%)
9	OMC	A2	3525	9	19,22,23	3.03	8 (42%)	25,31,34	0.76	0
9	PSU	A2	4152	9	18,21,22	4.56	7 (38%)	21,30,33	3.06	6 (28%)
46	PSU	m2	1245	46	18,21,22	4.55	6 (33%)	21,30,33	2.95	6 (28%)
9	PSU	A2	3371	9	18,21,22	4.51	6 (33%)	21,30,33	2.93	6 (28%)
9	1MA	A2	4067	9	21,25,26	2.47	5 (23%)	30,37,40	1.93	7 (23%)
46	A2M	m2	1033	46	22,25,26	2.64	11 (50%)	30,36,39	2.29	9 (30%)
9	OMC	A2	2559	9	19,22,23	3.03	8 (42%)	25,31,34	0.73	0
9	PSU	A2	3945	9	18,21,22	4.49	6 (33%)	21,30,33	3.01	5 (23%)
9	A2M	A2	1347	9	22,25,26	2.67	11 (50%)	30,36,39	2.32	8 (26%)
9	B9B	A2	237	9	25,28,29	3.46	11 (44%)	35,40,43	2.47	13 (37%)
46	OMU	m2	116	46	19,22,23	3.05	8 (42%)	25,31,34	1.71	4 (16%)
9	OMG	A2	4146	9	23,26,27	2.47	9 (39%)	32,38,41	2.09	11 (34%)
9	A2M	A2	4223	9	22,25,26	2.65	11 (50%)	30,36,39	2.34	10 (33%)
9	6MZ	A2	3872	9	22,25,26	2.46	4 (18%)	29,36,39	2.21	10 (34%)
9	P7G	A2	3536	9	24,28,29	3.56	10 (41%)	25,41,44	1.29	2 (8%)
46	OMG	m2	646	46	23,26,27	2.48	8 (34%)	32,38,41	2.12	11 (34%)
9	OMC	A2	2177	9	19,22,23	3.05	8 (42%)	25,31,34	0.98	1 (4%)
46	A2M	m2	27	46	22,25,26	2.64	11 (50%)	30,36,39	2.29	8 (26%)
46	PSU	m2	825	46	18,21,22	4.54	6 (33%)	21,30,33	3.02	6 (28%)
9	PSU	A2	4183	9	18,21,22	4.54	6 (33%)	21,30,33	3.09	6 (28%)
79	DDE	m	714	79	18,20,21	2.13	6 (33%)	17,28,30	1.07	1 (5%)
9	B8Q	A2	1269	9	18,22,23	3.02	4 (22%)	21,32,35	1.85	6 (28%)
9	B9B	A2	1387	9	25,28,29	3.47	10 (40%)	35,40,43	2.39	14 (40%)
9	OMG	A2	373	9	23,26,27	2.46	9 (39%)	32,38,41	2.04	11 (34%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	A2M	A2	398	9	22,25,26	2.65	11 (50%)	30,36,39	2.36	10 (33%)
9	OMC	A2	3357	9	19,22,23	3.04	8 (42%)	25,31,34	0.72	0
46	OMG	m2	685	46	23,26,27	2.46	9 (39%)	32,38,41	2.08	11 (34%)
9	OMG	A2	2119	9	23,26,27	2.45	9 (39%)	32,38,41	2.06	11 (34%)
9	OMG	A2	4289	9	23,26,27	2.44	8 (34%)	32,38,41	2.11	11 (34%)
9	E7G	A2	2052	9	24,27,28	3.34	11 (45%)	28,40,43	2.33	8 (28%)
9	B9H	A2	2541	9	21,25,26	2.95	4 (19%)	22,35,38	1.82	5 (22%)
41	MLZ	g2	98	41	8,9,10	0.72	0	4,9,11	0.90	0
46	A2M	m2	670	46	22,25,26	2.68	11 (50%)	30,36,39	2.30	10 (33%)
9	A2M	A2	3523	9	22,25,26	2.65	11 (50%)	30,36,39	2.27	9 (30%)
9	PSU	A2	4280	9	18,21,22	4.54	6 (33%)	21,30,33	2.99	6 (28%)
9	MHG	A2	4023	9	29,32,33	3.64	10 (34%)	34,46,49	2.55	12 (35%)
9	5MC	A2	4099	9	19,22,23	3.83	8 (42%)	26,32,35	1.01	1 (3%)
9	PSU	A2	4102	9	18,21,22	4.51	6 (33%)	21,30,33	2.97	5 (23%)
9	PSU	A2	4288	9	18,21,22	4.53	7 (38%)	21,30,33	2.98	5 (23%)
46	PSU	m2	824	46	18,21,22	4.54	6 (33%)	21,30,33	2.96	5 (23%)
46	B8N	m2	1250	46	25,29,30	2.49	6 (24%)	28,42,45	2.13	7 (25%)
9	E6G	A2	4007	9	24,27,28	3.54	10 (41%)	34,39,42	2.46	13 (38%)
9	OMG	A2	1335	9	23,26,27	2.46	9 (39%)	32,38,41	2.09	11 (34%)
14	MLZ	F2	333	14	8,9,10	0.73	0	4,9,11	0.91	0
9	PSU	A2	1490	9	18,21,22	4.53	6 (33%)	21,30,33	3.02	7 (33%)
9	2MG	A2	4517	9	23,26,27	2.62	8 (34%)	33,38,41	2.27	12 (36%)
9	OMG	A2	4515	9	23,26,27	2.46	8 (34%)	32,38,41	2.14	10 (31%)
9	PSU	A2	3385	9	18,21,22	4.52	6 (33%)	21,30,33	3.00	5 (23%)
9	A2M	A2	3441	9	22,25,26	2.70	11 (50%)	30,36,39	2.47	11 (36%)
9	OMG	A2	2179	9	23,26,27	2.48	8 (34%)	32,38,41	2.04	10 (31%)
9	PSU	A2	4094	9	18,21,22	4.58	7 (38%)	21,30,33	2.99	6 (28%)

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
9	5MC	A2	3987	9	-	1/7/25/26	0/2/2/2
9	A2M	A2	3374	9	-	1/9/27/28	0/3/3/3
46	4AC	m2	1844	46	-	0/11/29/30	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	5MC	A2	3438	9	-	2/7/25/26	0/2/2/2
9	OMC	A2	2616	9	-	0/9/27/28	0/2/2/2
9	PSU	A2	4055	9	-	0/7/25/26	0/2/2/2
9	PSU	A2	1496	9	-	0/7/25/26	0/2/2/2
9	P7G	A2	1711	10,9	-	2/10/40/41	0/3/3/3
9	UR3	A2	4249	9	-	0/7/25/26	0/2/2/2
11	OMU	C2	14	11	-	1/9/27/28	0/2/2/2
9	PSU	A2	3420	9	-	2/7/25/26	0/2/2/2
9	A2M	A2	1337	9	-	1/9/27/28	0/3/3/3
9	B8T	A2	4135	9	-	0/7/27/28	0/2/2/2
9	OMG	A2	1852	9	-	0/9/27/28	0/3/3/3
9	OMG	A2	2528	9	-	2/9/27/28	0/3/3/3
9	OMC	A2	3543	9	-	3/9/27/28	0/2/2/2
9	2MG	A2	1330	9	-	0/9/27/28	0/3/3/3
9	OMU	A2	3958	9	-	3/9/27/28	0/2/2/2
9	A2M	A2	1673	9	-	0/9/27/28	0/3/3/3
46	A2M	m2	166	46	-	3/9/27/28	0/3/3/3
9	E7G	A2	1599	9	-	1/9/39/40	0/3/3/3
9	OMG	A2	1685	9	-	2/9/27/28	0/3/3/3
9	A2M	A2	1140	9	-	1/9/27/28	0/3/3/3
9	UR3	A2	1668	9	-	2/7/25/26	0/2/2/2
9	OMC	A2	2120	9	-	0/9/27/28	0/2/2/2
9	G7M	A2	2277	9	-	0/7/25/26	0/3/3/3
9	OMU	A2	4272	9	-	1/9/27/28	0/2/2/2
46	PSU	m2	614	46	-	0/7/25/26	0/2/2/2
46	PSU	m2	1083	46	-	1/7/25/26	0/2/2/2
9	A2M	A2	3481	9	-	1/9/27/28	0/3/3/3
9	I4U	A2	1472	9	-	0/9/29/30	0/2/2/2
9	I4U	A2	3846	9	-	2/9/29/30	0/2/2/2
9	OMG	A2	4022	9	-	0/9/27/28	0/3/3/3
9	OMG	A2	3848	9	-	0/9/27/28	0/3/3/3
9	G7M	A2	1418	9	-	0/7/25/26	0/3/3/3
46	OMC	m2	519	46	-	4/9/27/28	0/2/2/2
9	A2M	A2	3379	9	-	1/9/27/28	0/3/3/3
9	PSU	A2	1395	9	-	2/7/25/26	0/2/2/2
9	2MG	A2	878	9	-	2/9/27/28	0/3/3/3
9	B8W	A2	3837	9	-	2/9/27/28	0/3/3/3
9	OMC	A2	4188	9	-	0/9/27/28	0/2/2/2
46	UR3	m2	1832	46	-	4/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	A2M	A2	2156	9	-	2/9/27/28	0/3/3/3
9	OMG	A2	3448	9	-	0/9/27/28	0/3/3/3
9	A2M	A2	2118	9	-	0/9/27/28	0/3/3/3
9	OMG	A2	1438	9	-	5/9/27/28	0/3/3/3
9	OMC	A2	3565	9	-	0/9/27/28	0/2/2/2
9	G7M	A2	4202	9	-	0/7/25/26	0/3/3/3
9	OMG	A2	4275	9	-	0/9/27/28	0/3/3/3
9	PSU	A2	2263	9	-	0/7/25/26	0/2/2/2
9	OMC	A2	3525	9	-	0/9/27/28	0/2/2/2
9	PSU	A2	4152	9	-	4/7/25/26	0/2/2/2
46	PSU	m2	1245	46	-	3/7/25/26	0/2/2/2
9	PSU	A2	3371	9	-	0/7/25/26	0/2/2/2
9	1MA	A2	4067	9	-	2/7/25/26	0/3/3/3
46	A2M	m2	1033	46	-	1/9/27/28	0/3/3/3
9	OMC	A2	2559	9	-	0/9/27/28	0/2/2/2
9	PSU	A2	3945	9	-	2/7/25/26	0/2/2/2
9	A2M	A2	1347	9	-	2/9/27/28	0/3/3/3
9	B9B	A2	237	9	-	6/11/29/30	0/3/3/3
46	OMU	m2	116	46	-	1/9/27/28	0/2/2/2
9	OMG	A2	4146	9	-	0/9/27/28	0/3/3/3
9	A2M	A2	4223	9	-	1/9/27/28	0/3/3/3
9	6MZ	A2	3872	9	-	5/9/27/28	0/3/3/3
9	P7G	A2	3536	9	-	3/10/40/41	0/3/3/3
46	OMG	m2	646	46	-	2/9/27/28	0/3/3/3
9	OMC	A2	2177	9	-	3/9/27/28	0/2/2/2
46	A2M	m2	27	46	-	1/9/27/28	0/3/3/3
46	PSU	m2	825	46	-	0/7/25/26	0/2/2/2
9	PSU	A2	4183	9	-	2/7/25/26	0/2/2/2
79	DDE	m	714	79	-	6/20/21/23	0/1/1/1
9	B8Q	A2	1269	9	-	0/7/42/43	0/2/2/2
9	B9B	A2	1387	9	-	3/11/29/30	0/3/3/3
9	OMG	A2	373	9	-	1/9/27/28	0/3/3/3
9	A2M	A2	398	9	-	3/9/27/28	0/3/3/3
9	OMC	A2	3357	9	-	5/9/27/28	0/2/2/2
46	OMG	m2	685	46	-	2/9/27/28	0/3/3/3
9	OMG	A2	2119	9	-	2/9/27/28	0/3/3/3
9	OMG	A2	4289	9	-	2/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	E7G	A2	2052	9	-	4/9/39/40	0/3/3/3
9	B9H	A2	2541	9	-	0/12/47/48	0/2/2/2
41	MLZ	g2	98	41	-	1/7/8/10	-
46	A2M	m2	670	46	-	1/9/27/28	0/3/3/3
9	A2M	A2	3523	9	-	3/9/27/28	0/3/3/3
9	PSU	A2	4280	9	-	0/7/25/26	0/2/2/2
9	MHG	A2	4023	9	-	4/16/46/47	0/3/3/3
9	5MC	A2	4099	9	-	4/7/25/26	0/2/2/2
9	PSU	A2	4102	9	-	3/7/25/26	0/2/2/2
9	PSU	A2	4288	9	-	5/7/25/26	0/2/2/2
46	PSU	m2	824	46	-	3/7/25/26	0/2/2/2
46	B8N	m2	1250	46	-	3/16/34/35	0/2/2/2
9	E6G	A2	4007	9	-	3/10/28/29	0/3/3/3
9	OMG	A2	1335	9	-	0/9/27/28	0/3/3/3
14	MLZ	F2	333	14	-	1/7/8/10	-
9	PSU	A2	1490	9	-	2/7/25/26	0/2/2/2
9	2MG	A2	4517	9	-	0/9/27/28	0/3/3/3
9	OMG	A2	4515	9	-	1/9/27/28	0/3/3/3
9	PSU	A2	3385	9	-	2/7/25/26	0/2/2/2
9	A2M	A2	3441	9	-	3/9/27/28	0/3/3/3
9	OMG	A2	2179	9	-	3/9/27/28	0/3/3/3
9	PSU	A2	4094	9	-	0/7/25/26	0/2/2/2

The worst 5 of 845 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	m2	1245	PSU	C6-C5	12.72	1.49	1.35
9	A2	4094	PSU	C6-C5	12.65	1.49	1.35
9	A2	2263	PSU	C6-C5	12.63	1.49	1.35
9	A2	4183	PSU	C6-C5	12.60	1.49	1.35
9	A2	4152	PSU	C6-C5	12.59	1.49	1.35

The worst 5 of 686 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A2	3837	B8W	N2-C2-N3	8.58	130.08	117.22
9	A2	3837	B8W	O6-C6-N1	8.28	129.96	118.96
9	A2	4183	PSU	N1-C2-N3	8.07	123.68	115.17
9	A2	4152	PSU	N1-C2-N3	7.93	123.53	115.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A2	4023	MHG	C2-N3-C4	7.92	121.90	112.00

There are no chirality outliers.

5 of 162 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
14	F2	333	MLZ	CD-CE-NZ-CM
41	g2	98	MLZ	C-CA-CB-CG
79	m	714	DDE	O-C-CA-CB
79	m	714	DDE	NAD-CBI-CBW-NCB
79	m	714	DDE	CAT-CAU-CBW-CBI

There are no ring outliers.

48 monomers are involved in 81 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A2	1496	PSU	2	0
9	A2	3420	PSU	1	0
9	A2	1852	OMG	3	0
9	A2	3543	OMC	1	0
9	A2	1673	A2M	1	0
9	A2	1599	E7G	1	0
9	A2	1140	A2M	5	0
9	A2	1668	UR3	1	0
9	A2	2277	G7M	1	0
9	A2	4272	OMU	2	0
46	m2	614	PSU	2	0
9	A2	3481	A2M	2	0
9	A2	3846	I4U	1	0
46	m2	519	OMC	1	0
9	A2	3379	A2M	5	0
9	A2	878	2MG	1	0
9	A2	3837	B8W	1	0
9	A2	4188	OMC	2	0
46	m2	1832	UR3	1	0
9	A2	2118	A2M	1	0
9	A2	3565	OMC	2	0
9	A2	4275	OMG	2	0
9	A2	4152	PSU	1	0
46	m2	1245	PSU	2	0
46	m2	1033	A2M	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A2	2559	OMC	1	0
9	A2	3945	PSU	1	0
9	A2	1347	A2M	1	0
46	m2	116	OMU	3	0
9	A2	4223	A2M	2	0
9	A2	3872	6MZ	2	0
9	A2	2177	OMC	3	0
46	m2	27	A2M	3	0
46	m2	825	PSU	1	0
9	A2	4183	PSU	1	0
79	m	714	DDE	2	0
9	A2	1269	B8Q	1	0
9	A2	1387	B9B	2	0
9	A2	373	OMG	1	0
46	m2	685	OMG	1	0
9	A2	2052	E7G	1	0
9	A2	3523	A2M	2	0
9	A2	4099	5MC	1	0
9	A2	4288	PSU	1	0
46	m2	824	PSU	1	0
9	A2	4517	2MG	1	0
9	A2	4515	OMG	5	0
9	A2	3385	PSU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 8 are monoatomic - leaving 1 for Mogul analysis.

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
88	GDP	m	900	-	29,30,30	3.23	17 (58%)	45,47,47	2.11	12 (26%)

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
88	GDP	m	900	-	-	4/16/32/32	0/3/3/3

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
88	m	900	GDP	C4-N3	6.54	1.49	1.34
88	m	900	GDP	O4'-C4'	-6.03	1.31	1.45
88	m	900	GDP	C2-N3	5.58	1.46	1.33
88	m	900	GDP	C3'-C4'	5.48	1.66	1.53
88	m	900	GDP	PA-O3A	5.28	1.65	1.59

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
88	m	900	GDP	C1'-N9-C8	-6.41	108.53	126.73
88	m	900	GDP	N9-C8-N7	-4.82	104.46	113.40
88	m	900	GDP	C5-C4-N3	-4.49	121.25	128.39
88	m	900	GDP	C2-N3-C4	4.12	119.39	112.30
88	m	900	GDP	C1'-N9-C4	4.11	138.62	126.49

There are no chirality outliers.

All (4) torsion outliers are listed below:

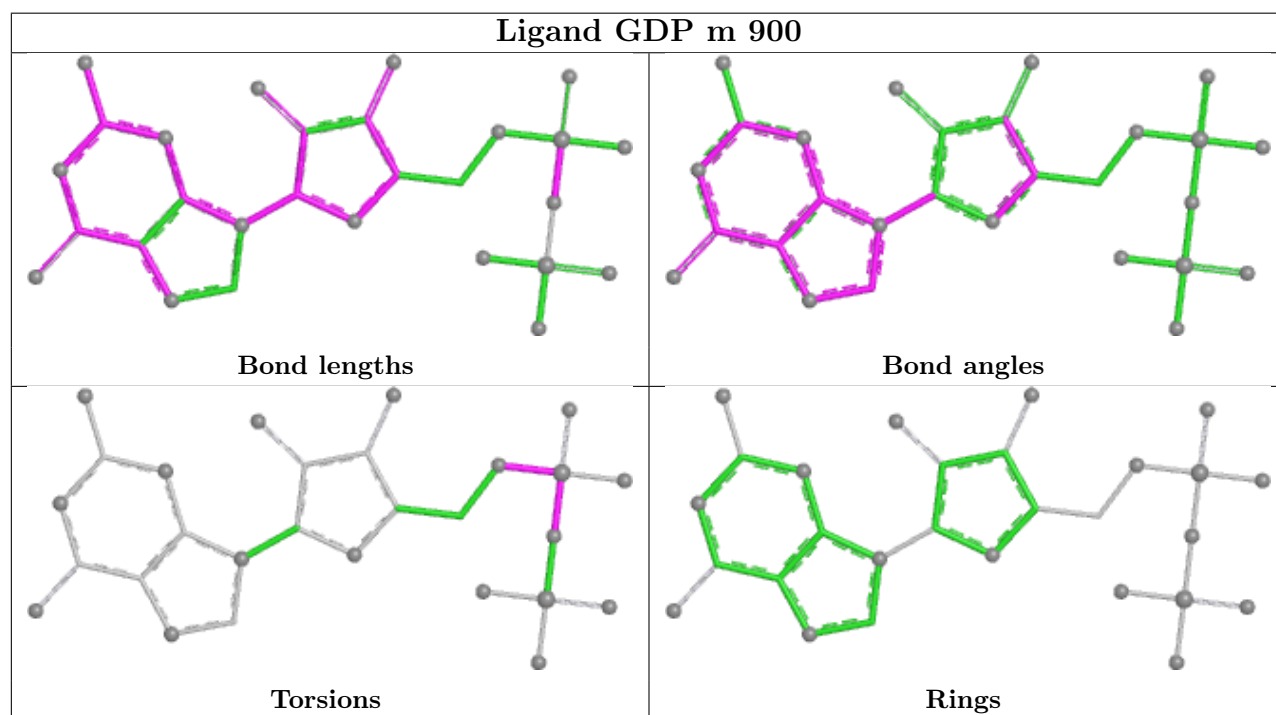
Mol	Chain	Res	Type	Atoms
88	m	900	GDP	C5'-O5'-PA-O3A
88	m	900	GDP	C5'-O5'-PA-O1A
88	m	900	GDP	C5'-O5'-PA-O2A
88	m	900	GDP	PB-O3A-PA-O2A

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
88	m	900	GDP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [\(i\)](#)

There are no chain breaks in this entry.

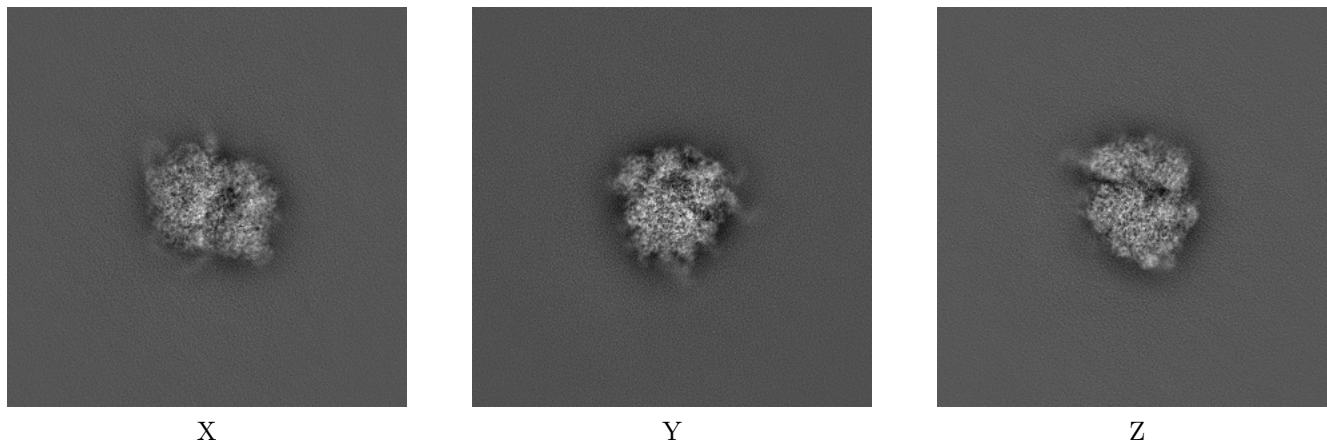
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23501. These allow visual inspection of the internal detail of the map and identification of artifacts.

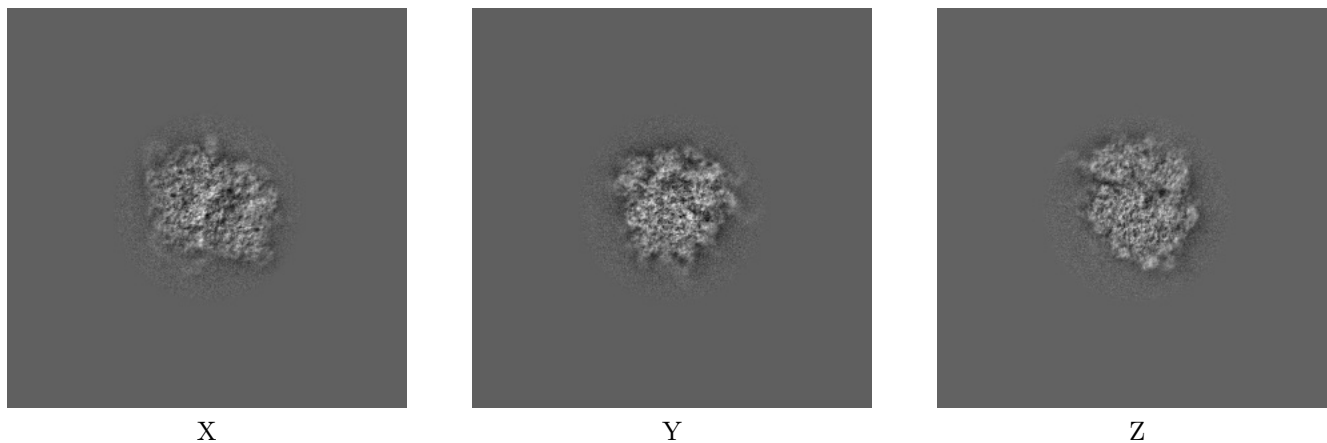
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



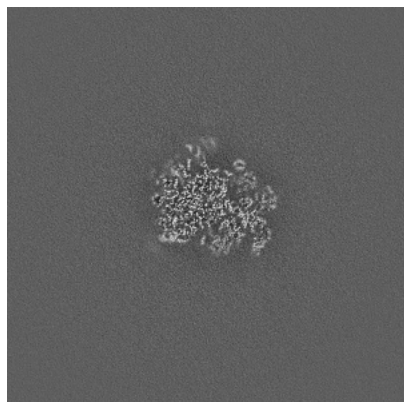
6.1.2 Raw map



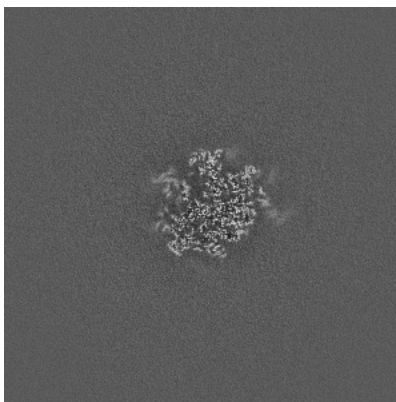
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

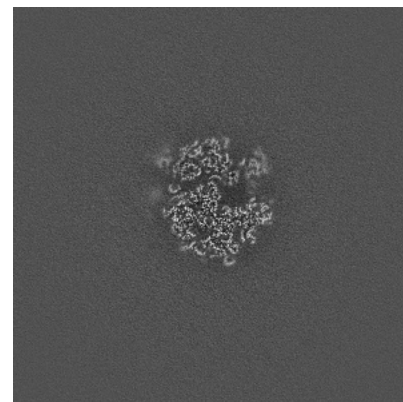
6.2.1 Primary map



X Index: 384

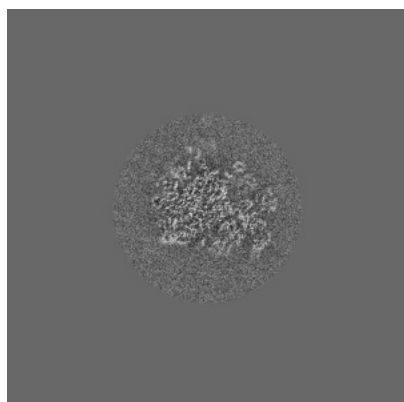


Y Index: 384

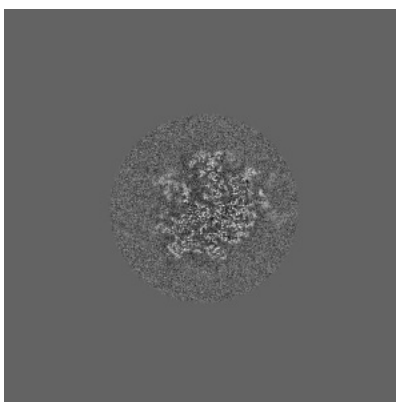


Z Index: 384

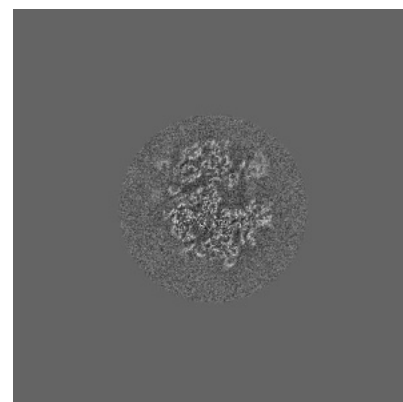
6.2.2 Raw map



X Index: 384



Y Index: 384

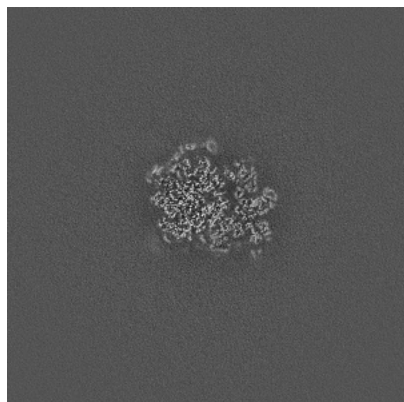


Z Index: 384

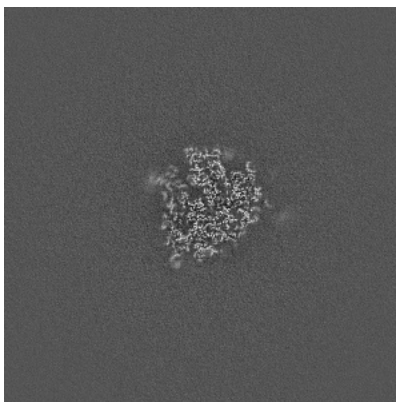
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

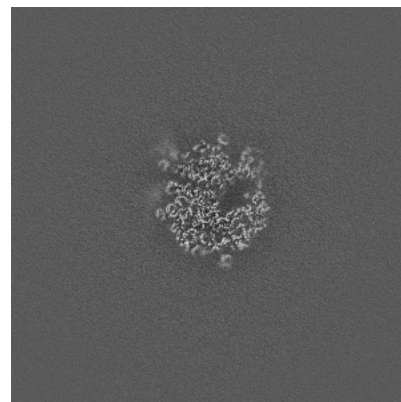
6.3.1 Primary map



X Index: 390

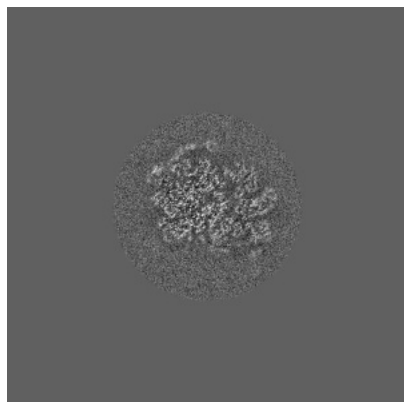


Y Index: 376

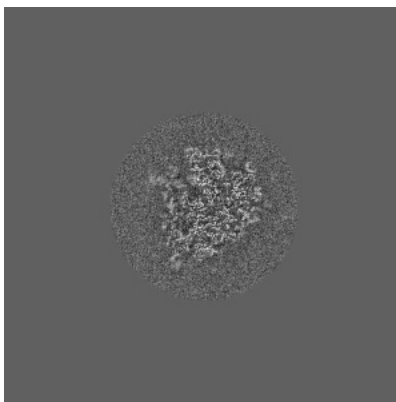


Z Index: 375

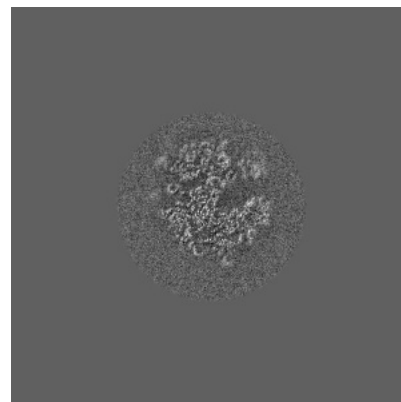
6.3.2 Raw map



X Index: 390



Y Index: 376

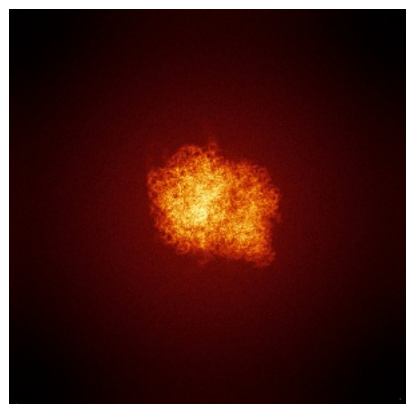


Z Index: 381

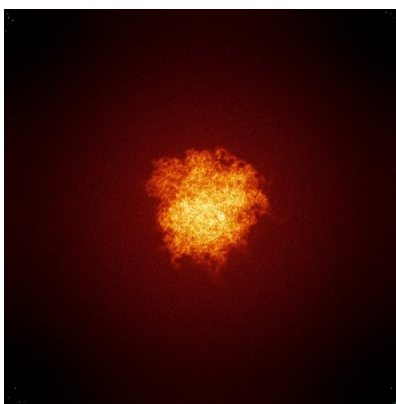
The images above show the largest variance slices of the map in three orthogonal directions.

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

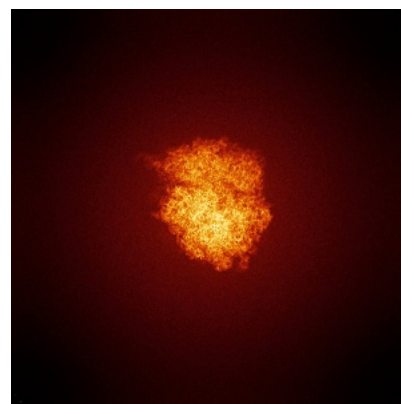
6.4.1 Primary map



X

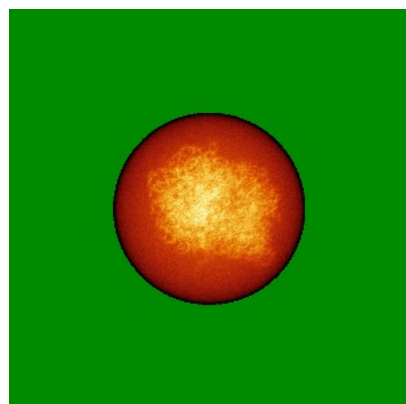


Y

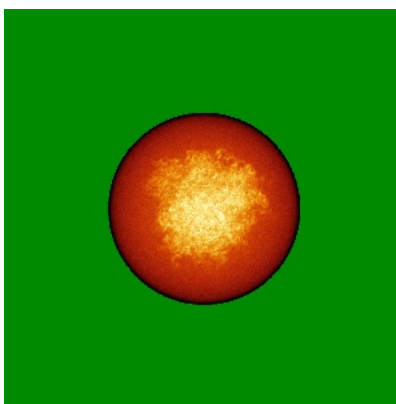


Z

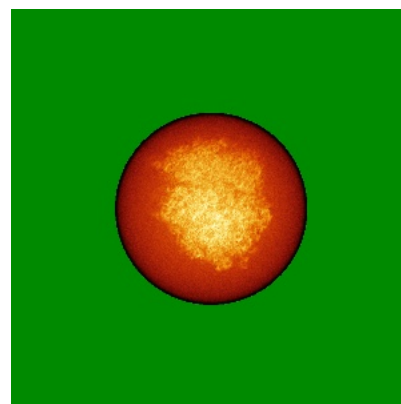
6.4.2 Raw map



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](#)

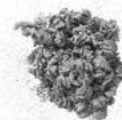
6.5.1 Primary map



X



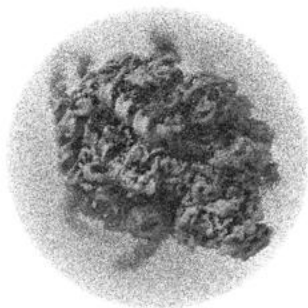
Y



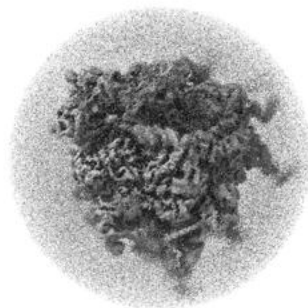
Z

The images above show the 3D surface view of the map at the recommended contour level 4.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

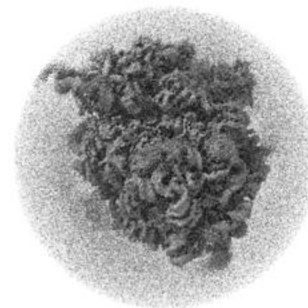
6.5.2 Raw map



X



Y



Z

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.

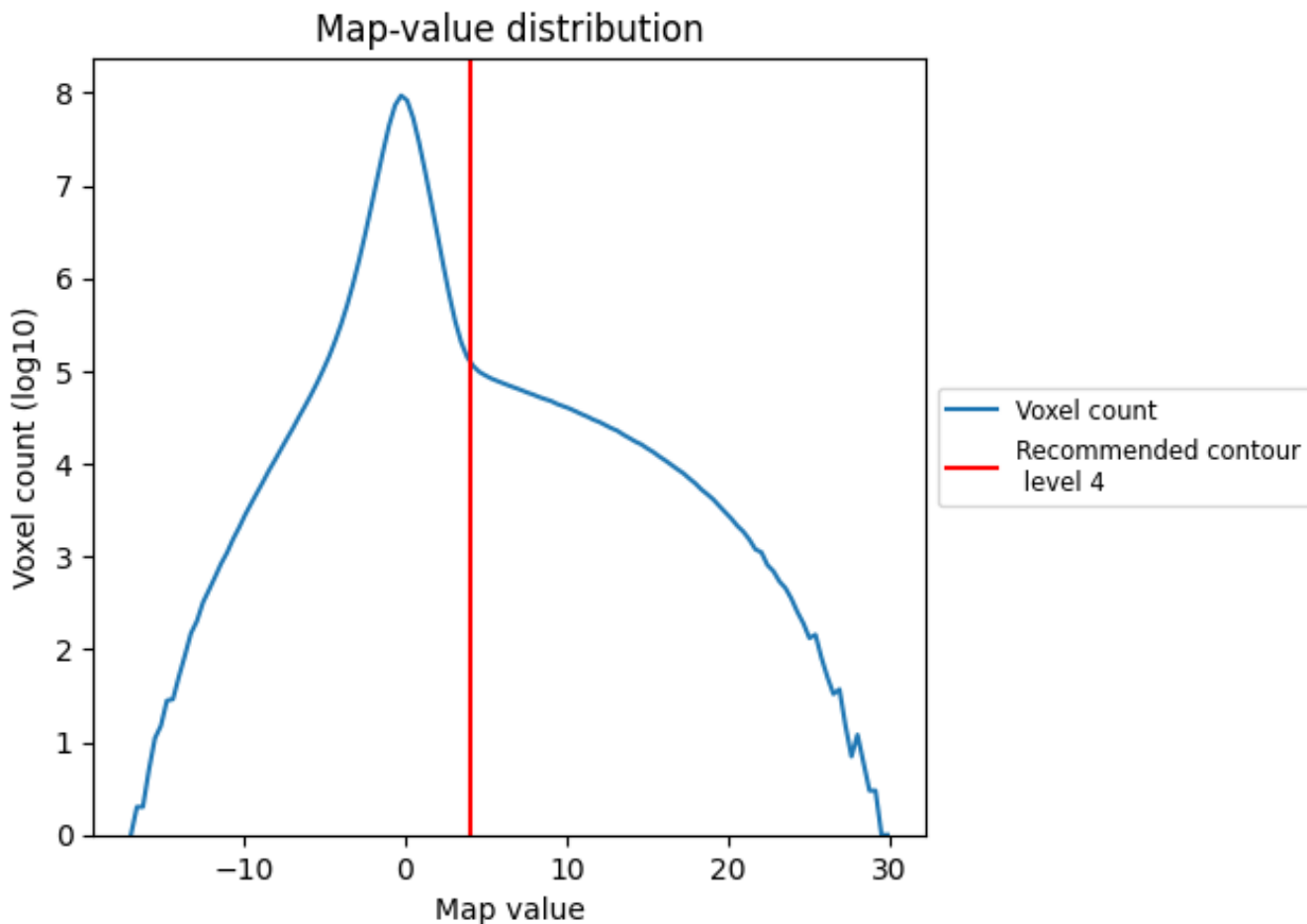
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

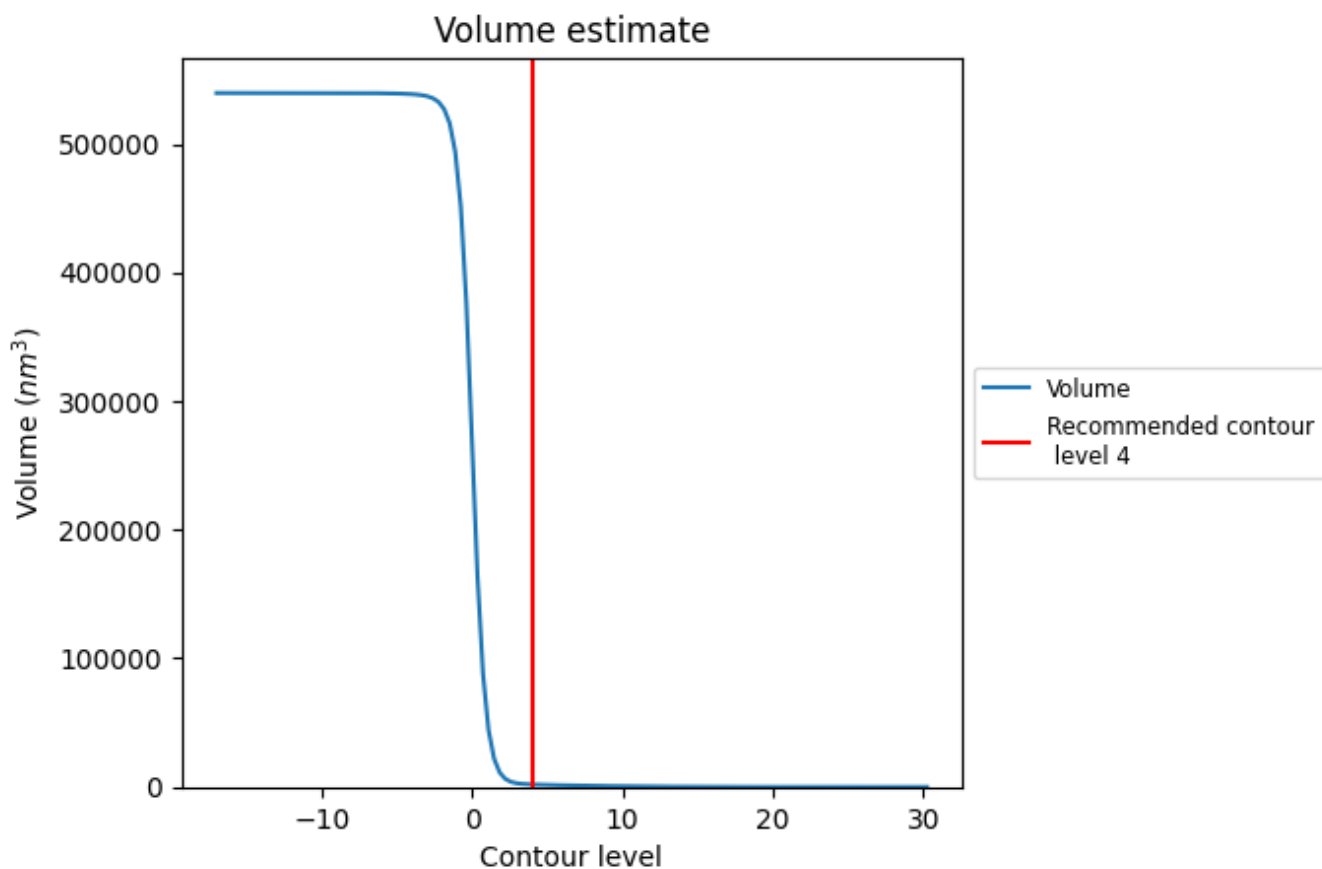
This section contains the results of statistical analysis of the map.

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.

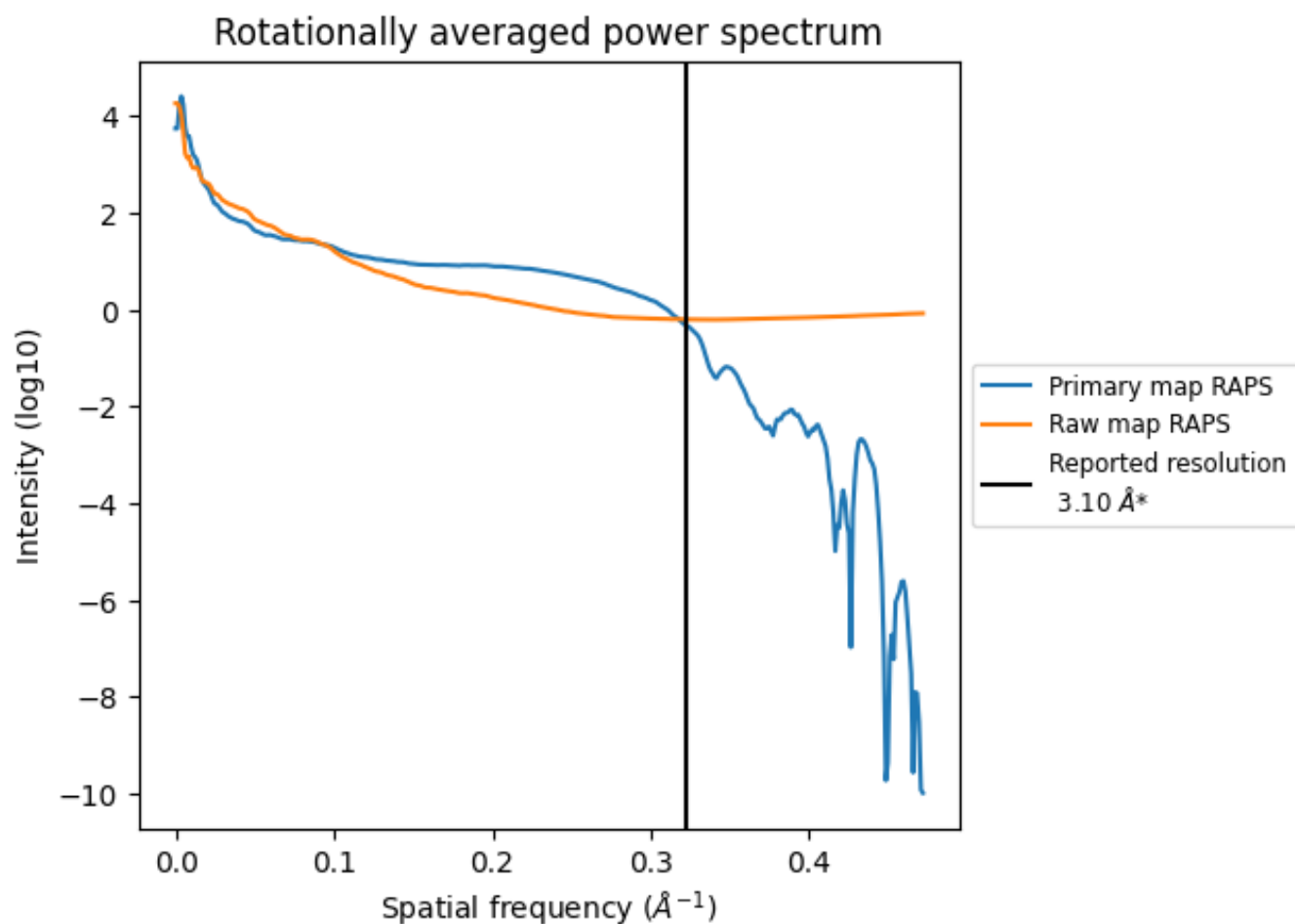
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 1947 nm^3 ; this corresponds to an approximate mass of 1759 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 [i](#)

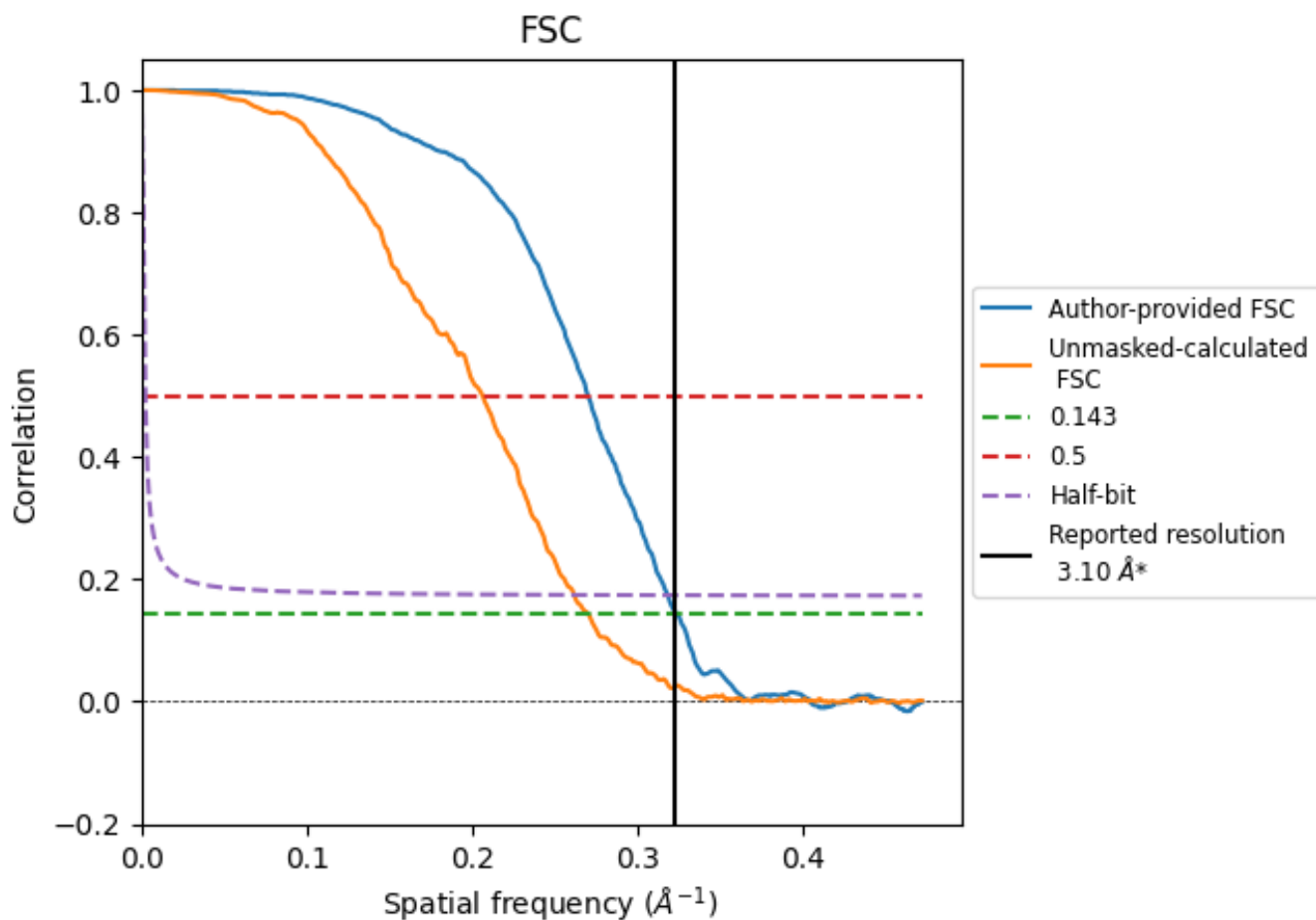


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.323\AA^{-1}

8.2 Resolution estimates [i](#)

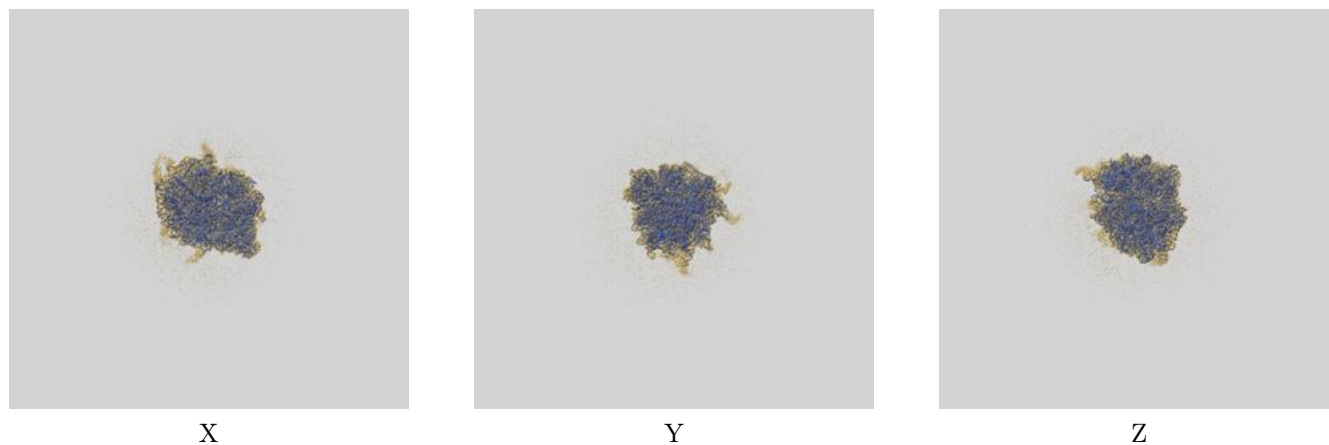
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.08	3.71	3.14
Unmasked-calculated*	3.70	4.85	3.82

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.70 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

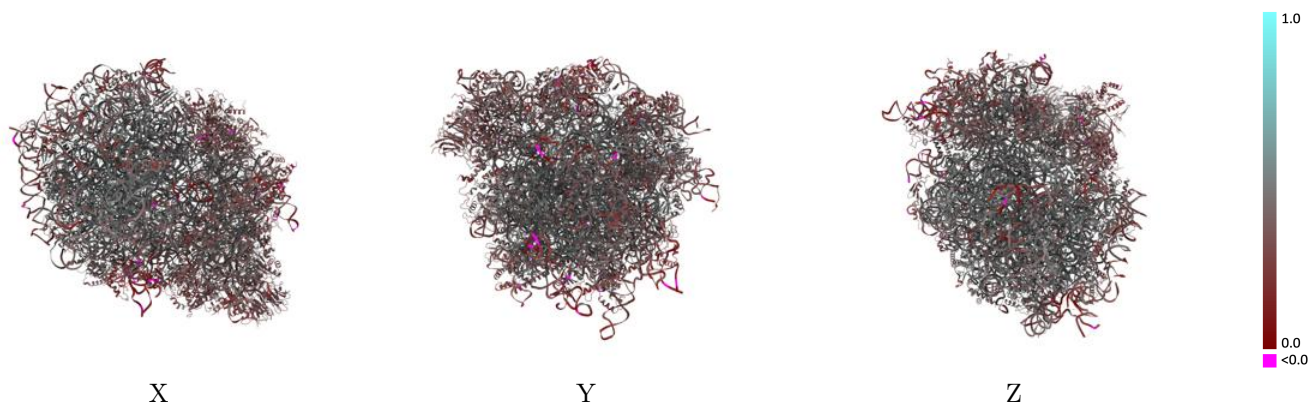
This section contains information regarding the fit between EMDB map EMD-23501 and PDB model 7LS2. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)



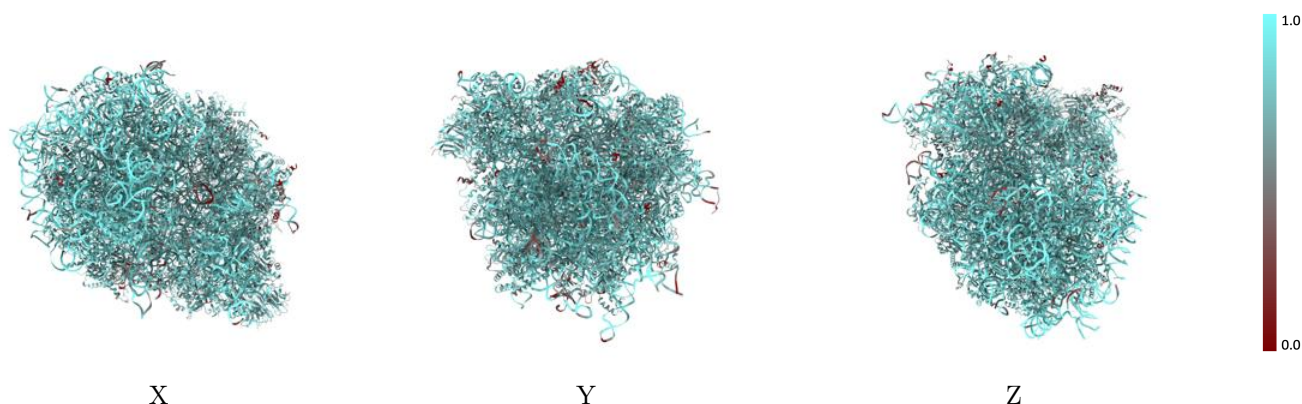
The images above show the 3D surface view of the map at the recommended contour level 4.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



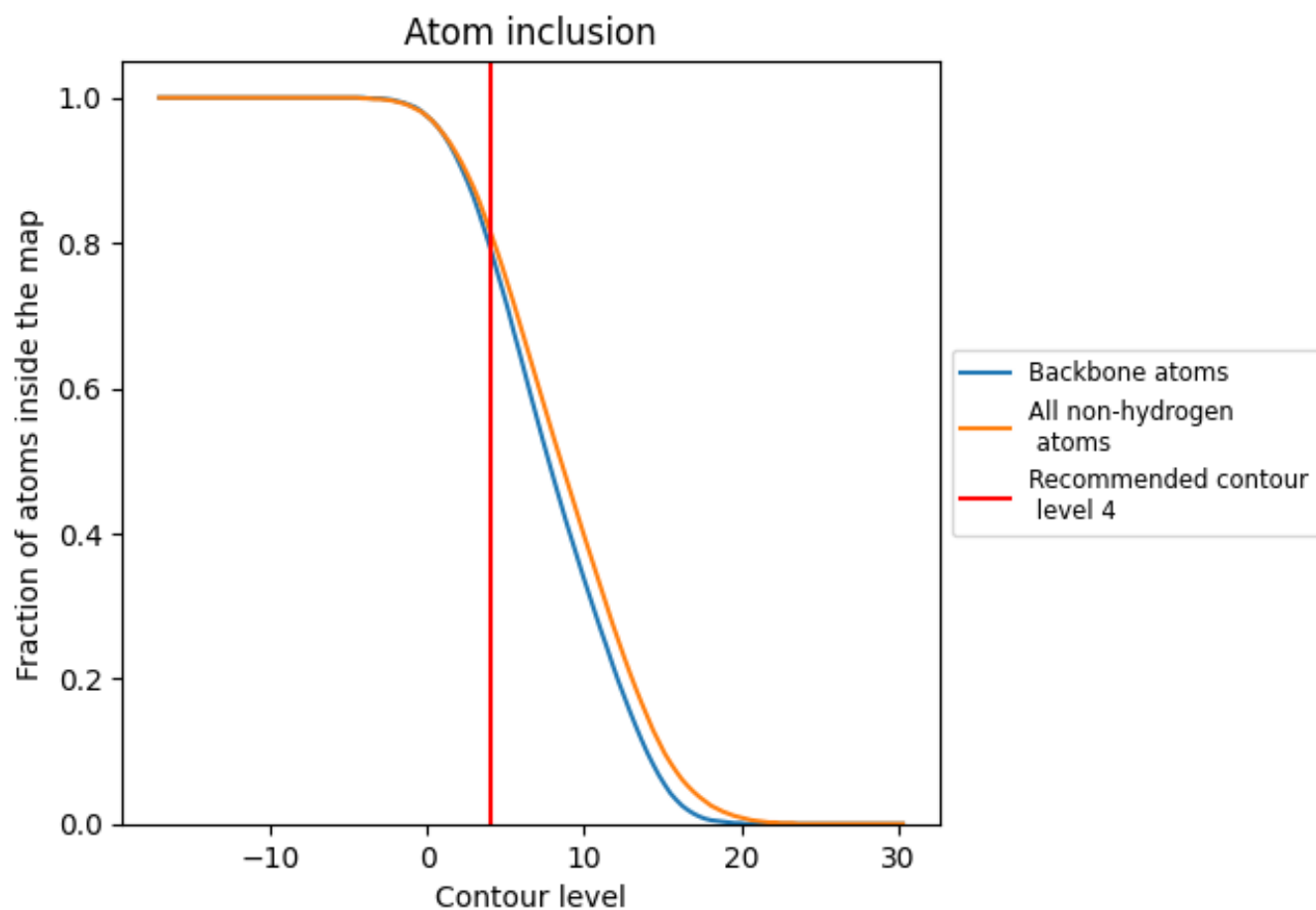
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (4).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 82% 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 (4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8180	 0.4180
A	 0.4700	 0.3630
A1	 0.7780	 0.4580
A2	 0.8970	 0.4300
A3	 0.7120	 0.3420
B1	 0.7880	 0.4240
B2	 0.9540	 0.4720
B3	 0.7440	 0.3570
C1	 0.7800	 0.4590
C2	 0.9040	 0.4380
C3	 0.7140	 0.3830
D1	 0.7730	 0.4580
D2	 0.7590	 0.4860
D3	 0.7780	 0.4410
E1	 0.7680	 0.4040
E2	 0.7830	 0.4710
E3	 0.6950	 0.4540
F1	 0.8060	 0.4500
F2	 0.7790	 0.4700
F3	 0.7430	 0.4340
G1	 0.8210	 0.4530
G2	 0.8280	 0.4350
G3	 0.5950	 0.3320
H1	 0.8020	 0.4830
H2	 0.8040	 0.4460
H3	 0.7470	 0.4140
I2	 0.7930	 0.4640
I3	 0.7380	 0.3410
J2	 0.8090	 0.4840
J3	 0.7490	 0.4370
K2	 0.7850	 0.4790
K3	 0.6940	 0.3330
L1	 0.5420	 0.2240
L2	 0.7780	 0.4350
L3	 0.7300	 0.3840





















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Chain	Atom inclusion	Q-score
M2	 0.8200	 0.4820
M3	 0.5300	 0.2310
N2	 0.7910	 0.4700
N3	 0.7250	 0.4080
O2	 0.7560	 0.3970
O3	 0.7060	 0.3950
P2	 0.7270	 0.4840
P3	 0.7230	 0.4420
Q2	 0.7210	 0.3850
Q3	 0.6740	 0.3340
R2	 0.7830	 0.4460
R3	 0.6790	 0.3080
S2	 0.8010	 0.4570
S3	 0.7300	 0.4000
T2	 0.8160	 0.4530
T3	 0.6970	 0.4040
U2	 0.8140	 0.4920
U3	 0.6830	 0.2920
V2	 0.7270	 0.4210
W2	 0.7940	 0.4470
X2	 0.7890	 0.4580
Y2	 0.7800	 0.4850
Z2	 0.8150	 0.4950
a2	 0.7790	 0.4630
b2	 0.7760	 0.4260
c2	 0.8060	 0.4400
d2	 0.7870	 0.4870
e2	 0.7230	 0.4070
f2	 0.7610	 0.4530
g2	 0.7890	 0.4750
h2	 0.7030	 0.4520
i2	 0.7770	 0.4710
j	 0.7270	 0.3390
j2	 0.7560	 0.4500
k	 0.6280	 0.2890
k2	 0.8350	 0.4750
m	 0.7040	 0.3900
m2	 0.8860	 0.3980
n2	 0.8430	 0.3610
o2	 0.7720	 0.4090
p2	 0.7020	 0.3900
q2	 0.7120	 0.3860

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Chain	Atom inclusion	Q-score
r2	 0.7160	 0.4040
s2	 0.6480	 0.3140
t	 0.7170	 0.3620
u	 0.6780	 0.3720
v2	 0.7150	 0.3530
w2	 0.6800	 0.4210
x2	 0.7060	 0.3510
y2	 0.7120	 0.3540
z2	 0.7150	 0.3830