



wwPDB EM Validation Summary Report ⓘ

Apr 15, 2026 – 03:03 AM UTC

PDB ID : 9QQP / pdb_00009qqp
EMDB ID : EMD-53310
Title : Mouse Ribosome rotated-2 PRE state
Authors : Santo, P.E.; Astier, A.; Plisson-Chastang, C.
Deposited on : 2025-04-01
Resolution : 2.80 Å(reported)
Based on initial model : 7LS1

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

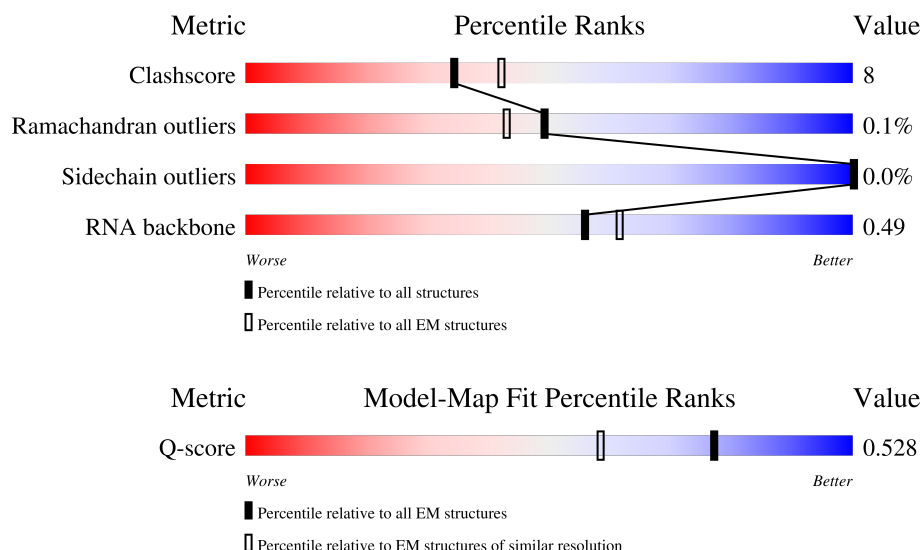
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 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	11806 (2.30 - 3.30)

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	<div> <div>8%</div> <div>62%</div> <div>20%</div> <div>18%</div> </div>
2	A2	3615	<div> <div>22%</div> <div>56%</div> <div>36%</div> <div>5%</div> <div>9%</div> </div>
3	A3	152	<div> <div>22%</div> <div>61%</div> <div>30%</div> <div>9%</div> </div>

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Mol	Chain	Length	Quality of chain
4	B1	266	
5	B2	121	
6	B3	145	
7	Bv	76	
8	Bx	10	
9	By	22	
10	C1	192	
11	C2	156	
12	C3	119	
13	D1	214	
14	D2	257	
15	D3	83	
16	E1	178	
17	E2	403	
18	E3	143	
19	F1	211	
20	F2	419	
21	F3	115	
22	G1	217	
23	G2	297	
24	G3	69	
25	H1	204	
26	H2	296	
27	H3	56	
28	I2	203	

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Mol	Chain	Length	Quality of chain
29	I3	317	
30	J2	184	
31	J3	293	
32	K2	188	
33	K3	249	
34	L2	196	
35	L3	194	
36	M2	176	
37	M3	132	
38	N2	160	
39	N3	151	
40	O2	128	
41	O3	151	
42	P2	140	
43	P3	130	
44	Q2	157	
45	Q3	133	
46	R2	156	
47	R3	125	
48	S2	145	
49	S3	84	
50	T2	136	
51	T3	133	
52	U2	148	
53	V2	160	

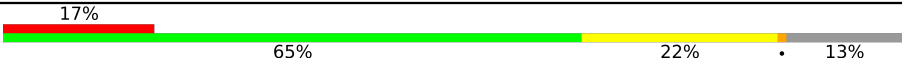
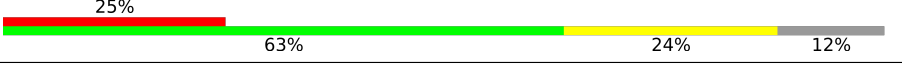
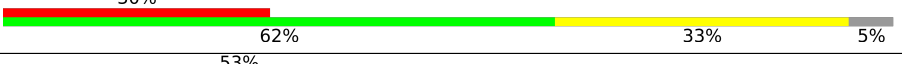
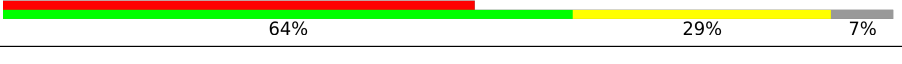
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Mol	Chain	Length	Quality of chain
54	W2	115	
55	X2	125	
56	Y2	135	
57	Z2	110	
58	a2	117	
59	b2	123	
60	c2	105	
61	d2	97	
62	e2	70	
63	f2	51	
64	g2	128	
65	h2	25	
66	i2	106	
67	j2	92	
68	k2	137	
69	m2	1635	
70	n2	73	
71	o2	295	
72	p2	264	
73	q2	243	
74	r2	257	
75	s2	204	
76	t2	194	
77	u2	208	
78	v2	165	

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Mol	Chain	Length	Quality of chain
79	w2	158	
80	x2	145	
81	y2	146	
82	z2	135	

2 Entry composition

There are 85 unique types of molecules in this entry. The entry contains 206901 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 Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A1	222	Total	C	N	O	S	0	0
			1843	1185	353	297	8		

- Molecule 2 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A2	3512	Total	C	N	O	P	0	0
			75341	33588	13744	24498	3511		

- Molecule 3 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A3	139	Total	C	N	O	S	0	0
			1154	725	233	195	1		

- Molecule 4 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B1	217	Total	C	N	O	S	1	0
			1764	1127	340	293	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B2	119	Total	C	N	O	P	0	0
			2538	1132	454	834	118		

- Molecule 6 is a protein called 40S ribosomal protein S19 (eS19).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B3	140	Total	C	N	O	S	0	0
			1091	686	210	192	3		

- Molecule 7 is a RNA chain called transfer RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Bv	66	Total	C	N	O	P	0	0
			1412	629	255	462	66		

- Molecule 8 is a RNA chain called messenger RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Bx	10	Total	C	N	O	P	0	0
			200	90	20	80	10		

- Molecule 9 is a protein called Nascent protein chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	By	22	Total	C	N	O	0	0
			110	66	22	22		

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

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

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

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

- Molecule 12 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	C3	97	Total	C	N	O	S	0	0
			769	483	144	138	4		

- Molecule 13 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	D1	204	Total	C	N	O	S	0	0
			1656	1052	319	272	13		

- Molecule 14 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	D2	245	Total	C	N	O	S	0	0
			1876	1177	383	310	6		

- Molecule 15 is a protein called 40S ribosomal protein S21 (eS21).

Mol	Chain	Residues	Atoms					AltConf	Trace
15	D3	83	Total	C	N	O	S	0	0
			589	369	111	104	5		

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

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

- Molecule 17 is a protein called Large ribosomal subunit protein uL3.

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

- Molecule 18 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	E3	139	Total	C	N	O	S	0	0
			1080	682	214	181	3		

- Molecule 19 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	F1	203	Total	C	N	O	S	0	0
			1643	1029	339	271	4		

- Molecule 20 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	F2	352	Total	C	N	O	S	0	0
			2823	1776	566	466	15		

- Molecule 21 is a protein called Small ribosomal subunit protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	F3	97	Total	C	N	O	S	0	0
			774	481	160	128	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F3	102	PRO	ARG	conflict	UNP P62855

- Molecule 22 is a protein called Large ribosomal subunit protein eL14.

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

- Molecule 23 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	G2	293	Total	C	N	O	S	0	0
			2389	1509	441	425	14		

- Molecule 24 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	G3	56	Total	C	N	O	S	0	0
			435	267	85	81	2		

- Molecule 25 is a protein called Large ribosomal subunit protein eL15.

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

- Molecule 26 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	H2	218	Total	C	N	O	S	0	0
			1766	1130	337	295	4		

- Molecule 27 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	H3	51	Total	C	N	O	S	0	0
			427	269	87	66	5		

- Molecule 28 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	I2	198	Total	C	N	O	S	0	0
			1618	1043	316	253	6		

- Molecule 29 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	I3	234	Total	C	N	O	S	0	0
			1800	1135	318	337	10		

- Molecule 30 is a protein called Large ribosomal subunit protein uL22.

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

- Molecule 31 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	J3	217	Total	C	N	O	S	0	0
			1590	1039	276	266	9		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J3	61	MET	ILE	conflict	UNP P25444

- Molecule 32 is a protein called Large ribosomal subunit protein eL18.

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

- Molecule 33 is a protein called Small ribosomal subunit protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	K3	211	Total	C	N	O	S	0	0
			1708	1073	342	286	7		

- Molecule 34 is a protein called Large ribosomal subunit protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	L2	169	Total	C	N	O	S	0	0
			1408	873	304	222	9		

- Molecule 35 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	L3	179	Total	C	N	O	S	0	0
			1495	953	299	241	2		

- Molecule 36 is a protein called Large ribosomal subunit protein eL20.

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

- Molecule 37 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	M3	84	Total	C	N	O	S	0	0
			525	332	97	91	5		

- Molecule 38 is a protein called Large ribosomal subunit protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	N2	159	Total	C	N	O	S	0	0
			1299	824	252	217	6		

- Molecule 39 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	N3	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 40 is a protein called Large ribosomal subunit protein eL22.

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

- Molecule 41 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	O3	135	Total	C	N	O	S	0	0
			1003	615	198	184	6		

- Molecule 42 is a protein called Large ribosomal subunit protein uL14.

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

- Molecule 43 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	P3	129	Total	C	N	O	S	0	0
			1027	655	192	174	6		

- Molecule 44 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Q2	62	Total	C	N	O	S	0	0
			519	332	101	83	3		

- Molecule 45 is a protein called Small ribosomal subunit protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Q3	121	Total	C	N	O	S	0	0
			981	620	192	164	5		

- Molecule 46 is a protein called Large ribosomal subunit protein uL23.

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

- Molecule 47 is a protein called Small ribosomal subunit protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	R3	73	Total	C	N	O	S	0	0
			585	374	108	102	1		

- Molecule 48 is a protein called Large ribosomal subunit protein uL24.

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

- Molecule 49 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S3	79	Total	C	N	O	S	0	0
			618	386	115	110	7		

- Molecule 50 is a protein called Large ribosomal subunit protein eL27.

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

- Molecule 51 is a protein called Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	T3	44	Total	C	N	O	S	0	0
			355	218	81	55	1		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
T3	55	PRO	ASN	conflict	UNP P62862
T3	56	ASN	VAL	conflict	UNP P62862
T3	57	ALA	VAL	conflict	UNP P62862

- Molecule 52 is a protein called Large ribosomal subunit protein uL15.

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

- Molecule 53 is a protein called Large ribosomal subunit protein eL29.

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

- Molecule 54 is a protein called Large ribosomal subunit protein eL30.

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

- Molecule 55 is a protein called Large ribosomal subunit protein eL31.

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

- Molecule 56 is a protein called Large ribosomal subunit protein eL32.

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

- Molecule 57 is a protein called Large ribosomal subunit protein eL33.

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

- Molecule 58 is a protein called Large ribosomal subunit protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	a2	107	Total	C	N	O	S	0	0
			854	535	176	137	6		

- Molecule 59 is a protein called Large ribosomal subunit protein uL29.

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

- Molecule 60 is a protein called Large ribosomal subunit protein eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	c2	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 61 is a protein called Large ribosomal subunit protein eL37.

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

- Molecule 62 is a protein called Large ribosomal subunit protein eL38.

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

- Molecule 63 is a protein called Large ribosomal subunit protein eL39.

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

- Molecule 64 is a protein called Ubiquitin-ribosomal protein eL40 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	g2	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 65 is a protein called 60S ribosomal protein L41.

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

- Molecule 66 is a protein called Large ribosomal subunit protein eL42.

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

- Molecule 67 is a protein called Large ribosomal subunit protein eL43.

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

- Molecule 68 is a protein called Large ribosomal subunit protein eL28.

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

- Molecule 69 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	m2	1625	Total	C	N	O	P	0	0
			34736	15523	6240	11348	1625		

- Molecule 70 is a RNA chain called transfer RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	n2	73	Total	C	N	O	P	0	0
			1562	698	291	501	72		

- Molecule 71 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	o2	215	Total	C	N	O	S	0	0
			1704	1083	298	315	8		

- Molecule 72 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	p2	212	Total	C	N	O	S	0	0
			1722	1093	308	307	14		

- Molecule 73 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	q2	213	Total	C	N	O	S	0	0
			1655	1056	301	291	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
q2	195	THR	SER	conflict	UNP P62908

- Molecule 74 is a protein called 40S ribosomal protein S4, X isoform (eS4).

Mol	Chain	Residues	Atoms					AltConf	Trace
74	r2	257	Total	C	N	O	S	0	0
			2031	1298	381	344	8		

- Molecule 75 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	s2	185	Total	C	N	O	S	0	0
			1468	919	277	265	7		

- Molecule 76 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	t2	174	Total	C	N	O	S	0	0
			1322	857	246	218	1		

- Molecule 77 is a protein called Small ribosomal subunit protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	u2	179	Total	C	N	O	S	0	0
			1397	879	274	239	5		

- Molecule 78 is a protein called Small ribosomal subunit protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	v2	83	Total	C	N	O	S	0	0
			705	462	122	115	6		

- Molecule 79 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	w2	138	Total	C	N	O	S	0	0
			1134	722	214	192	6		

- Molecule 80 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	x2	127	Total	C	N	O	S	0	0
			1045	663	198	177	7		

- Molecule 81 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	y2	139	Total	C	N	O	S	0	0
			1109	704	210	192	3		

- Molecule 82 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	z2	125	Total	C	N	O	S	0	0
			1011	634	187	186	4		

- Molecule 83 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
83	A2	83	Total	Mg	0
			83	83	
83	E3	1	Total	Mg	0
			1	1	
83	H1	1	Total	Mg	0
			1	1	
83	J2	1	Total	Mg	0
			1	1	
83	O3	1	Total	Mg	0
			1	1	
83	P2	1	Total	Mg	0
			1	1	
83	d2	1	Total	Mg	0
			1	1	
83	m2	34	Total	Mg	0
			34	34	

- Molecule 84 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
84	F3	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
84	H3	1	Total 1	Zn 1	0
84	d2	1	Total 1	Zn 1	0
84	g2	1	Total 1	Zn 1	0
84	i2	1	Total 1	Zn 1	0
84	j2	1	Total 1	Zn 1	0

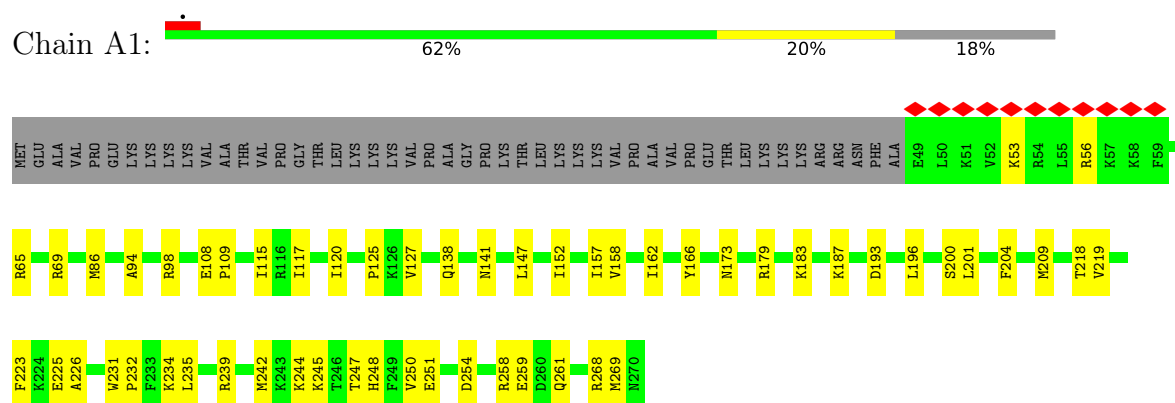
- Molecule 85 is water.

Mol	Chain	Residues	Atoms		AltConf
85	B1	1	Total 1	O 1	0

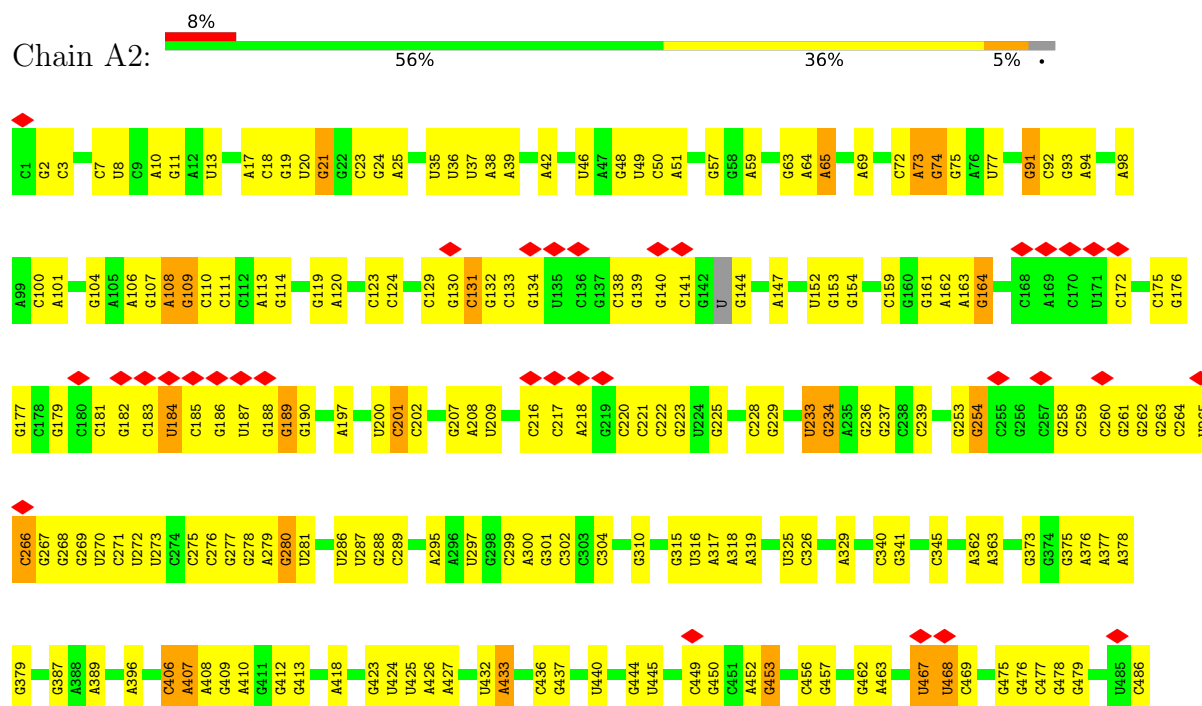
3 Residue-property plots

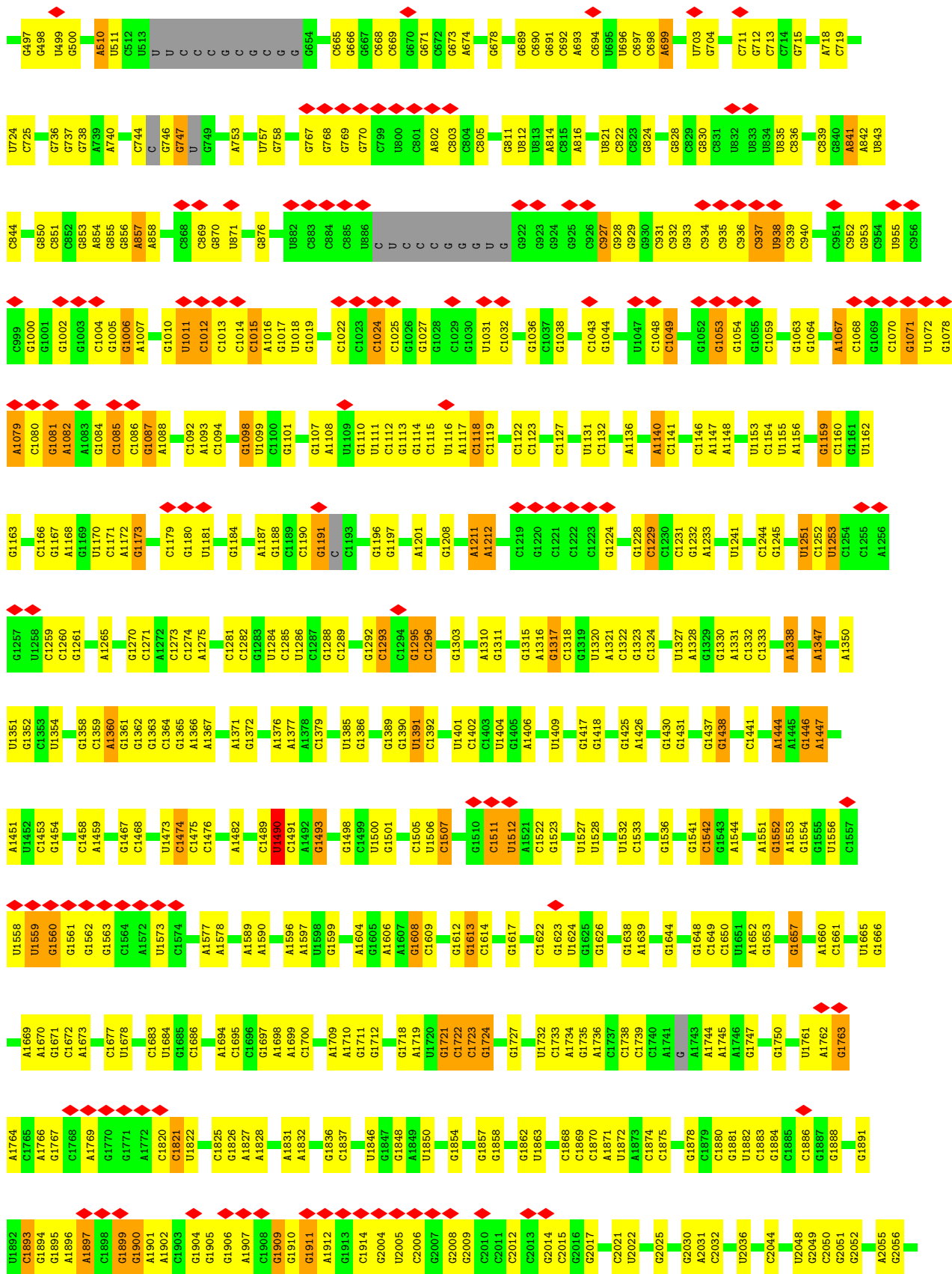
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: Large ribosomal subunit protein uL30

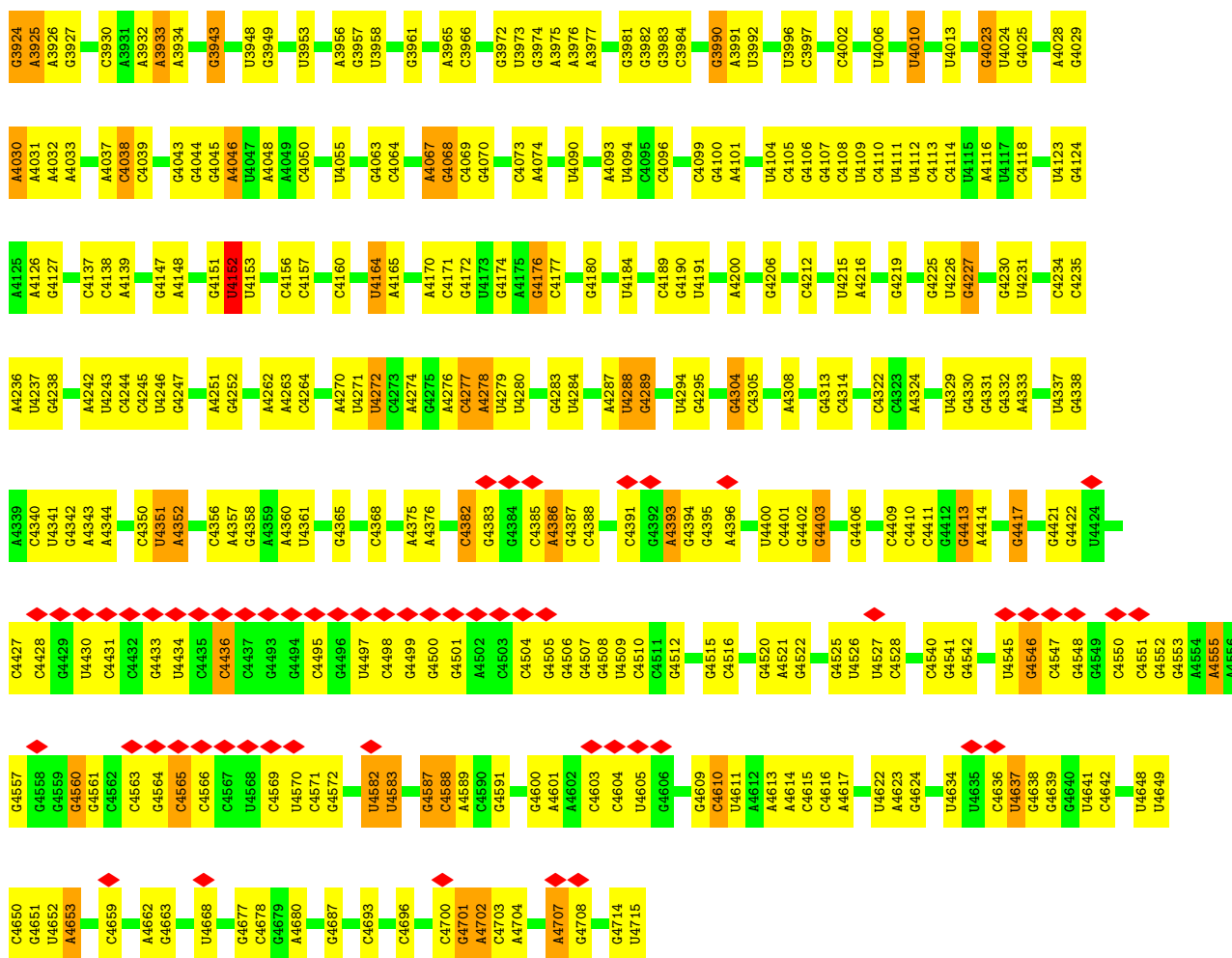


- Molecule 2: 28S ribosomal RNA

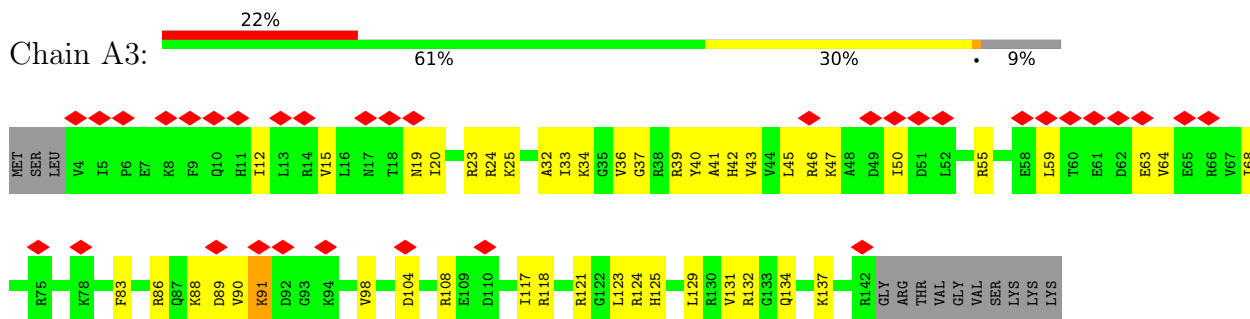




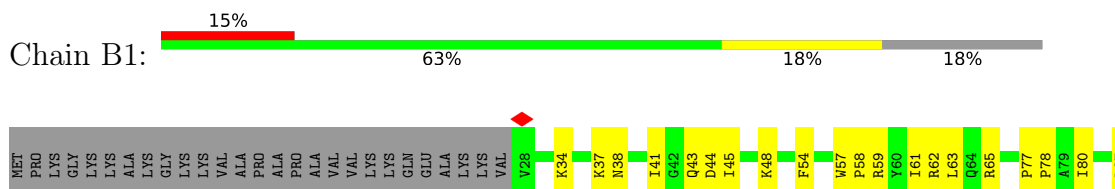


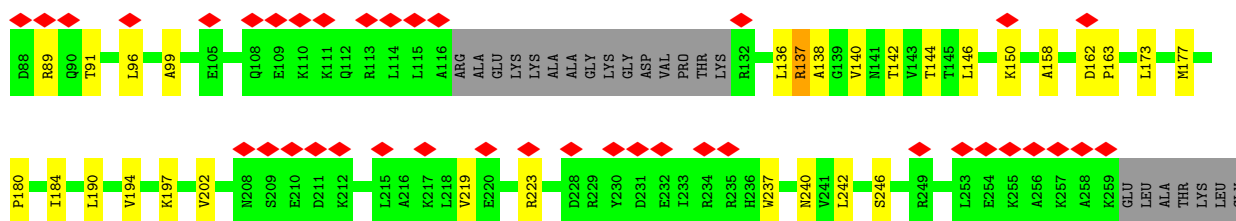


• Molecule 3: Small ribosomal subunit protein uS13



• Molecule 4: Large ribosomal subunit protein eL8





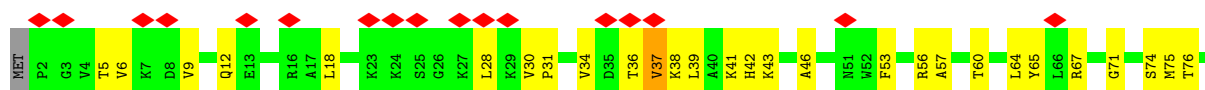
- Molecule 5: 5S ribosomal RNA

Chain B2: 69% 26% ..



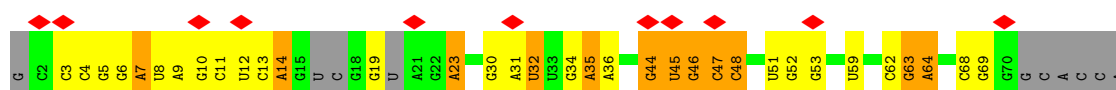
- Molecule 6: 40S ribosomal protein S19 (eS19)

Chain B3: 28% 64% 32% ..



- Molecule 7: transfer RNA

Chain Bv: 14% 42% 29% 16% 13%



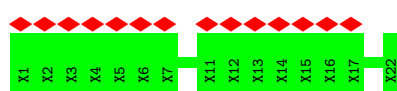
- Molecule 8: messenger RNA

Chain Bx: 50% 40% 10%

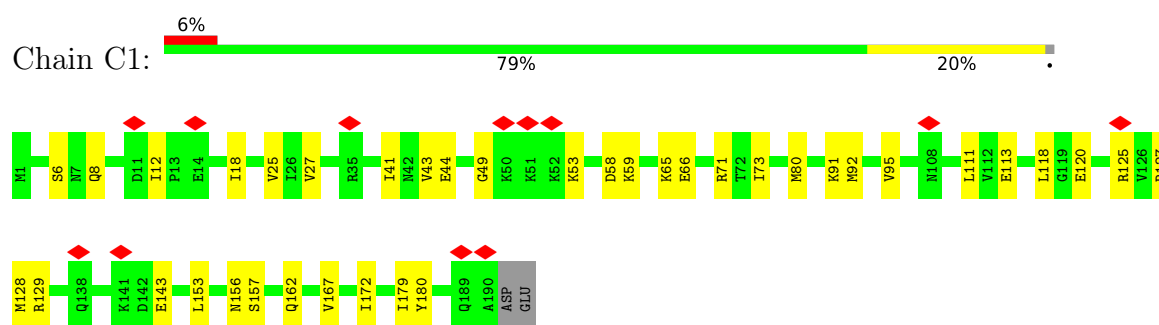


- Molecule 9: Nascent protein chain

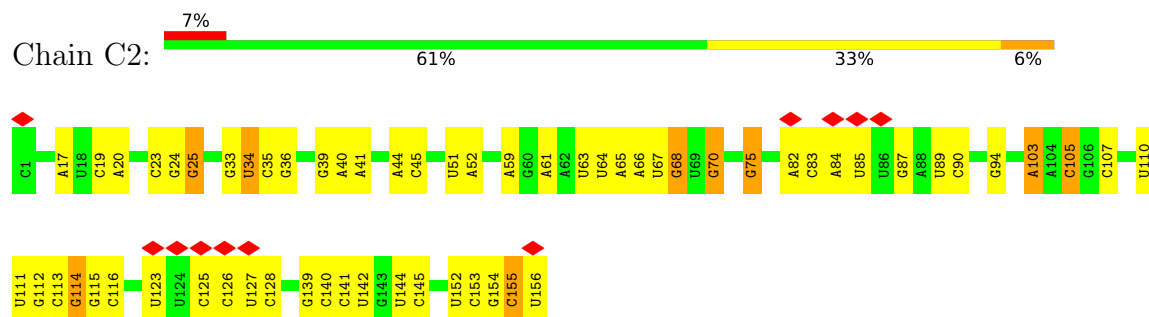
Chain By: 64% 100%



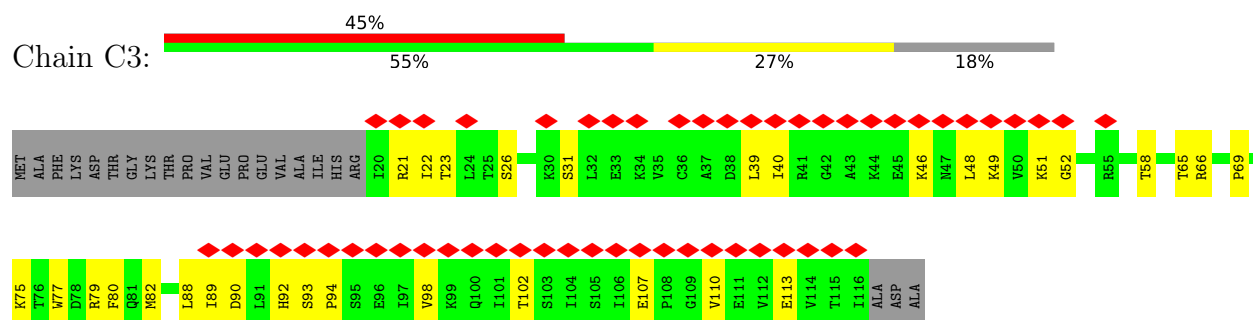
- Molecule 10: Large ribosomal subunit protein uL6



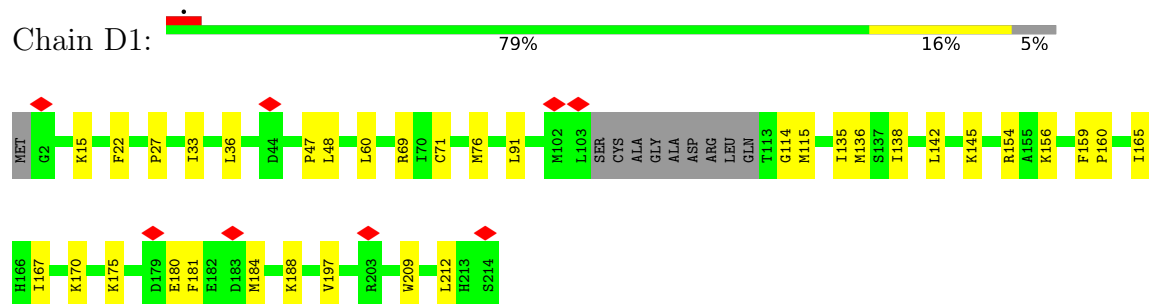
- Molecule 11: 5.8S ribosomal RNA



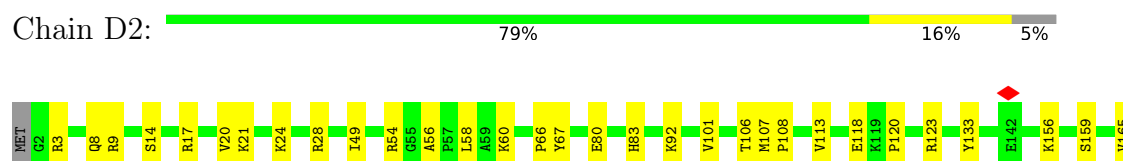
- Molecule 12: Small ribosomal subunit protein uS10

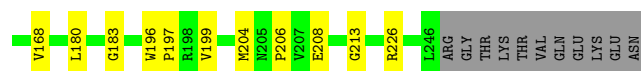


- Molecule 13: Large ribosomal subunit protein uL16

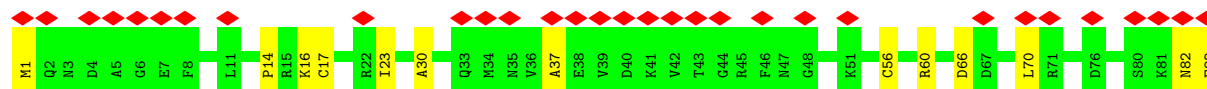
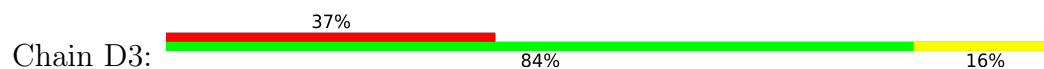


- Molecule 14: Large ribosomal subunit protein uL2

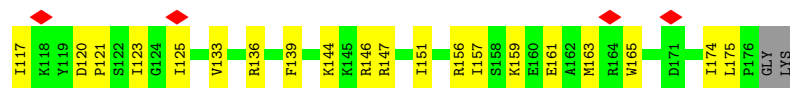
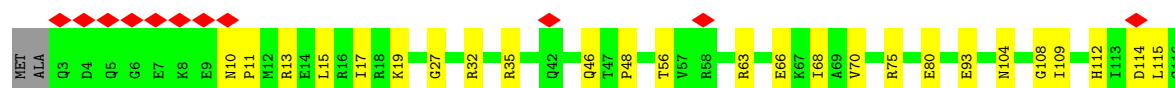
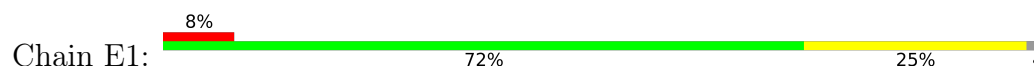




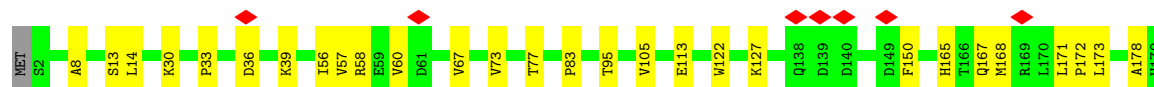
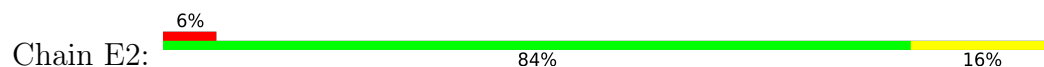
- Molecule 15: 40S ribosomal protein S21 (eS21)



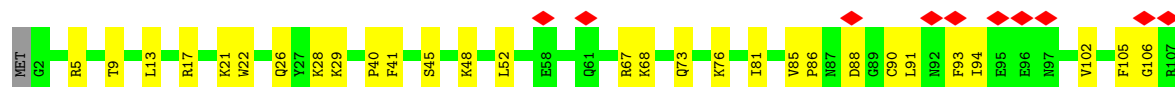
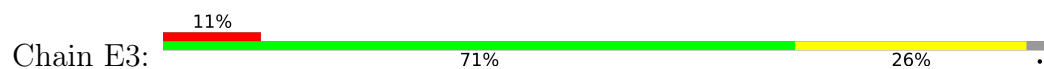
- Molecule 16: Large ribosomal subunit protein uL5



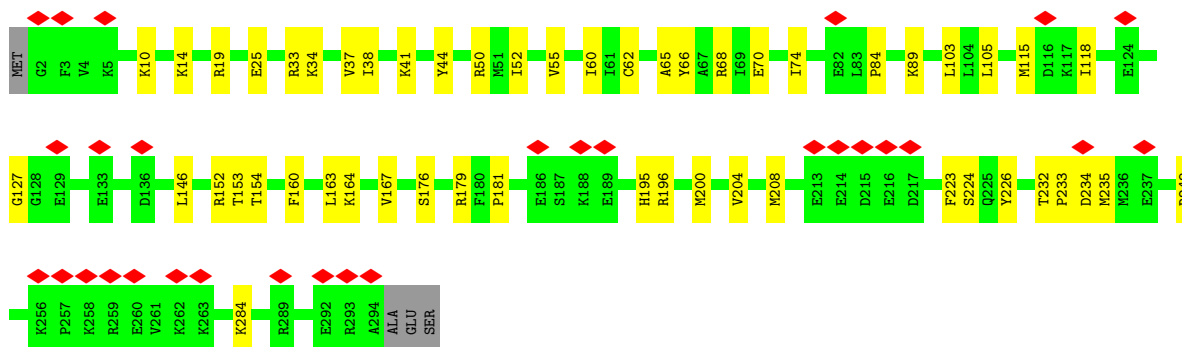
- Molecule 17: Large ribosomal subunit protein uL3



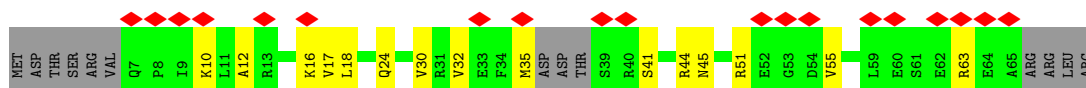
- Molecule 18: Small ribosomal subunit protein uS12



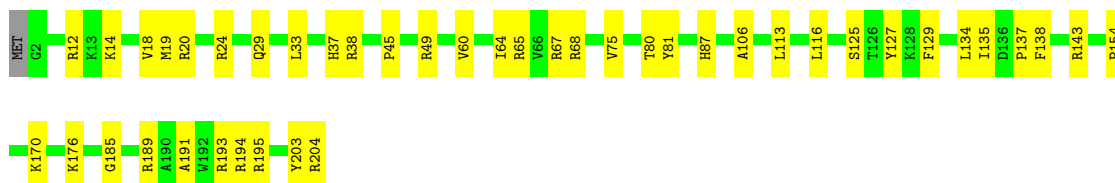
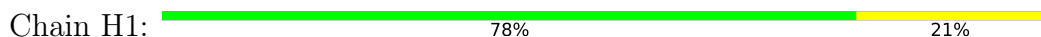
- Molecule 19: Large ribosomal subunit protein eL13



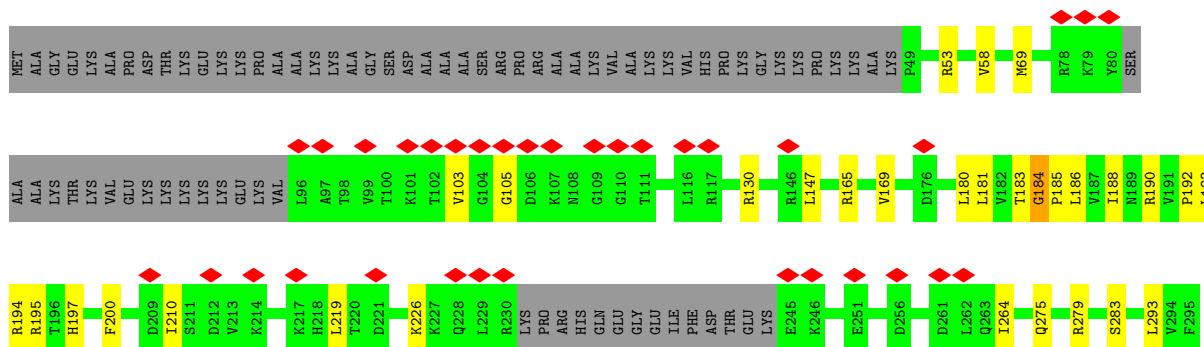
- Molecule 24: Small ribosomal subunit protein eS28



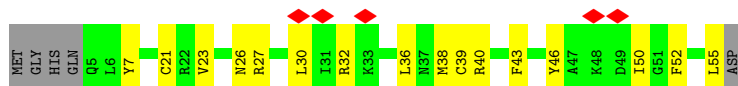
- Molecule 25: Large ribosomal subunit protein eL15




- Molecule 26: Large ribosomal subunit protein eL6

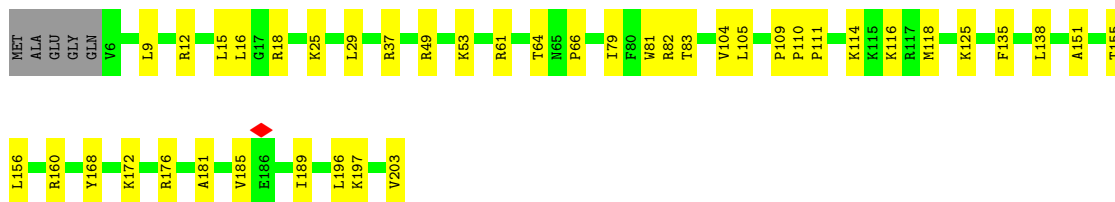


- Molecule 27: Small ribosomal subunit protein uS14



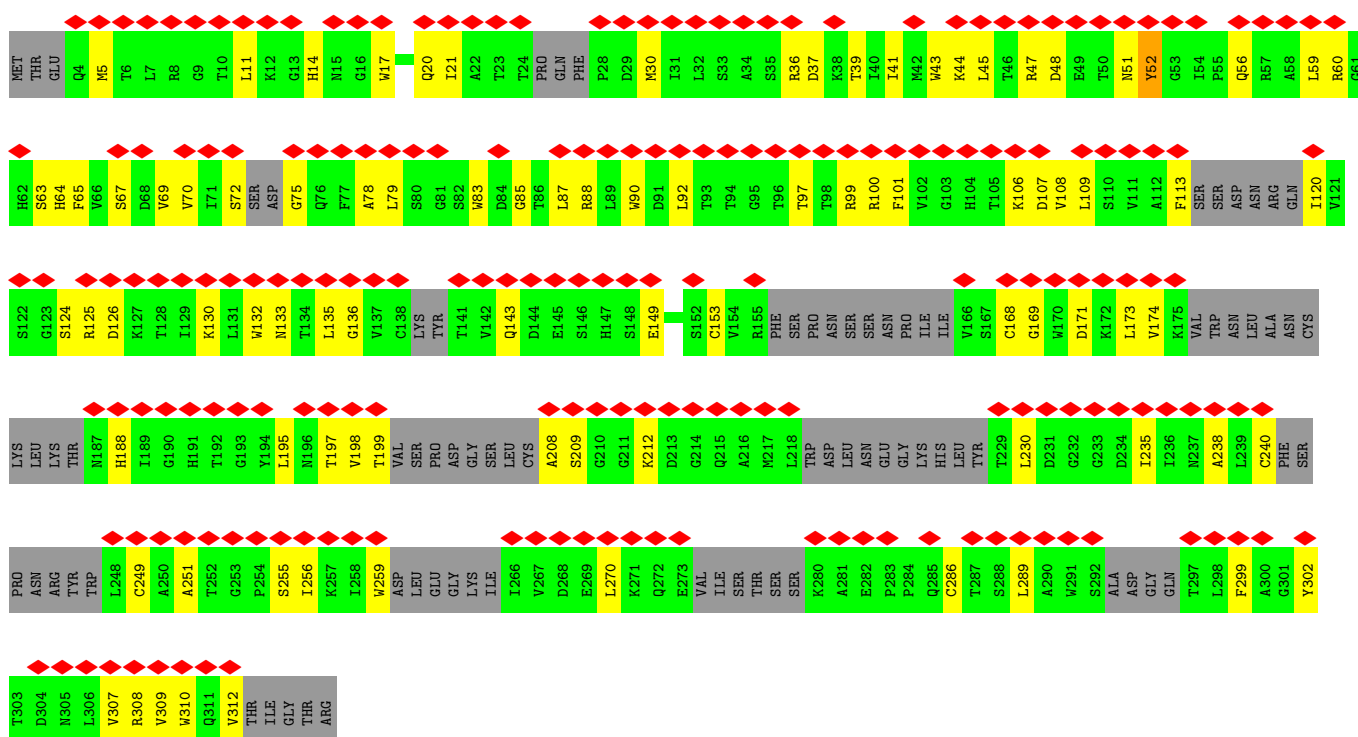
- Molecule 28: Large ribosomal subunit protein uL13

Chain I2: 



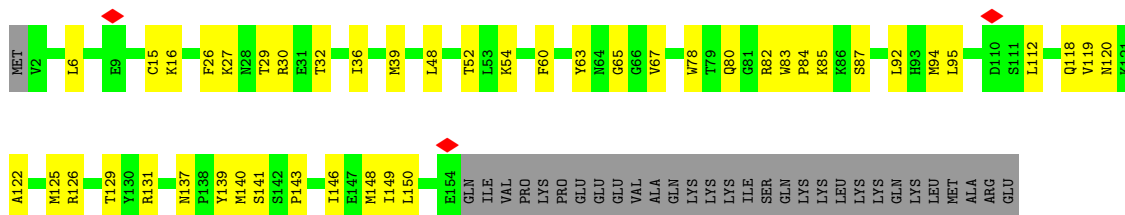
- Molecule 29: Small ribosomal subunit protein RACK1

Chain I3: 

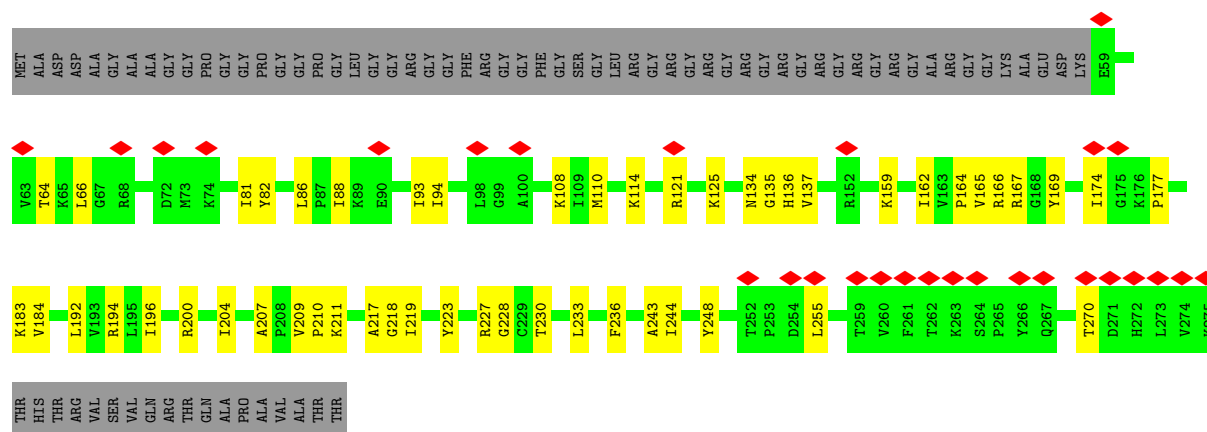


- Molecule 30: Large ribosomal subunit protein uL22

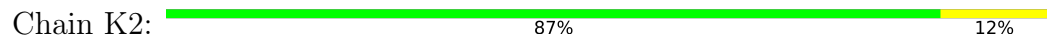
Chain J2: 



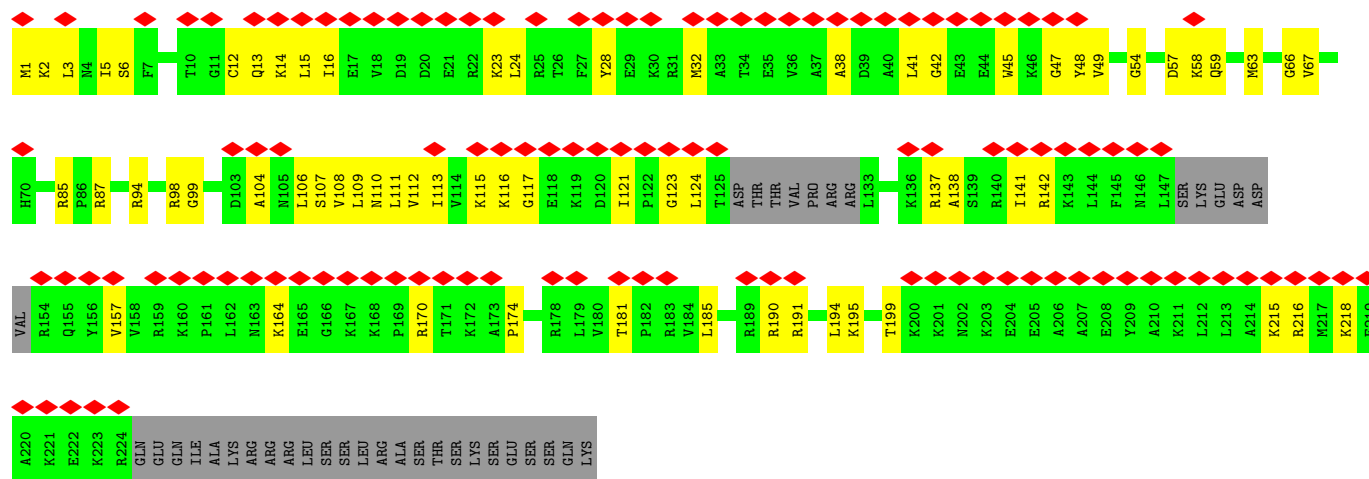
- Molecule 31: Small ribosomal subunit protein uS5



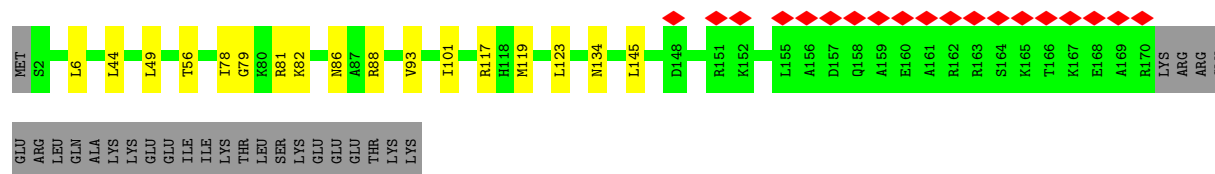
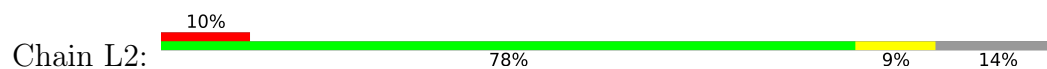
- Molecule 32: Large ribosomal subunit protein eL18



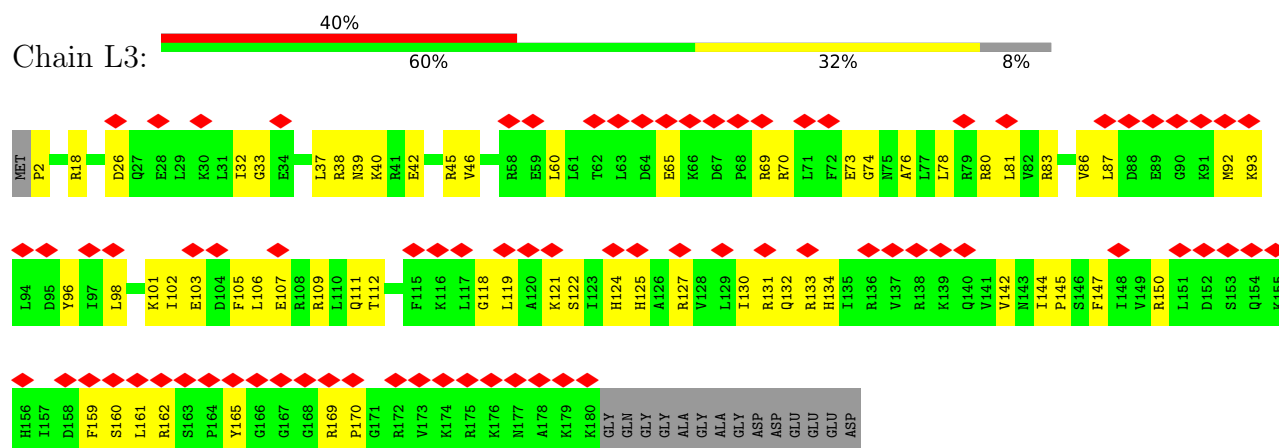
- Molecule 33: Small ribosomal subunit protein eS6



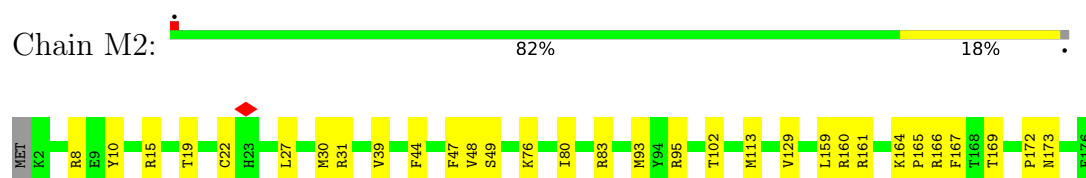
- Molecule 34: Large ribosomal subunit protein eL19



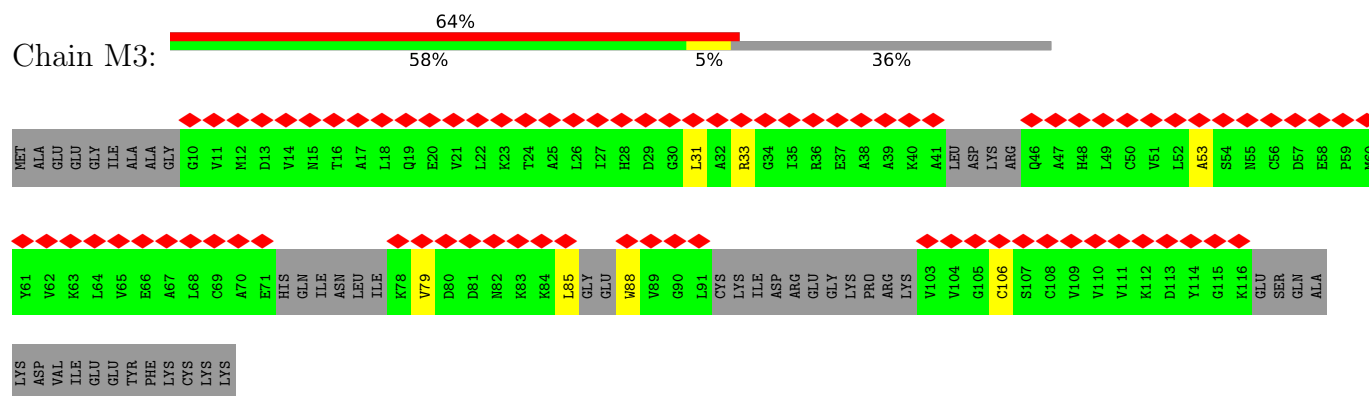
- Molecule 35: Small ribosomal subunit protein uS4



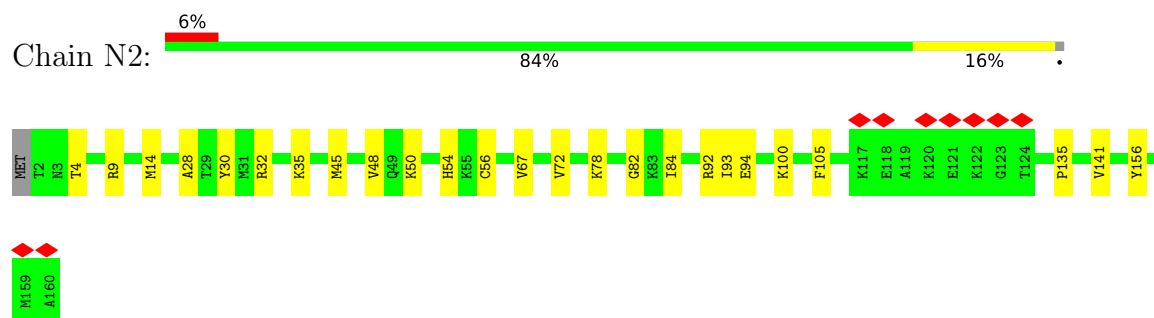
- Molecule 36: Large ribosomal subunit protein eL20



- Molecule 37: Small ribosomal subunit protein eS12

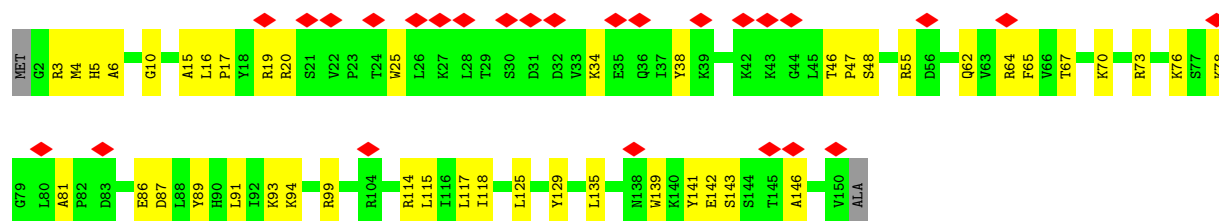


- Molecule 38: Large ribosomal subunit protein eL21

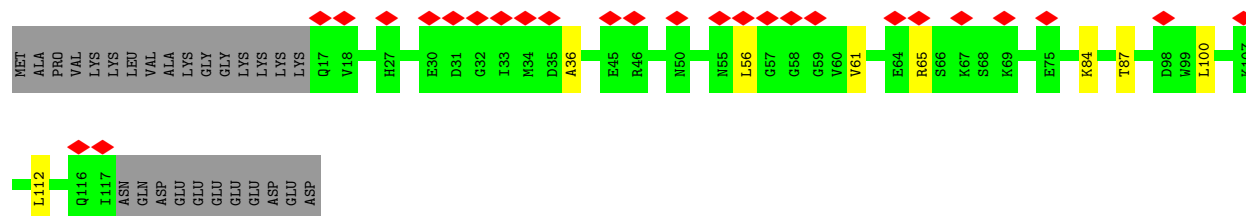
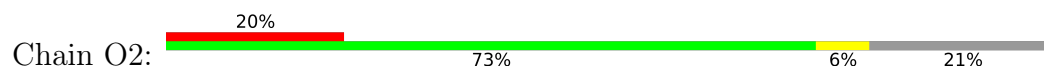


- Molecule 39: Small ribosomal subunit protein uS15

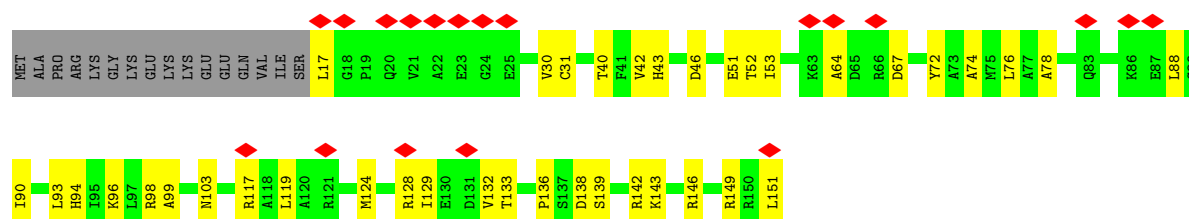




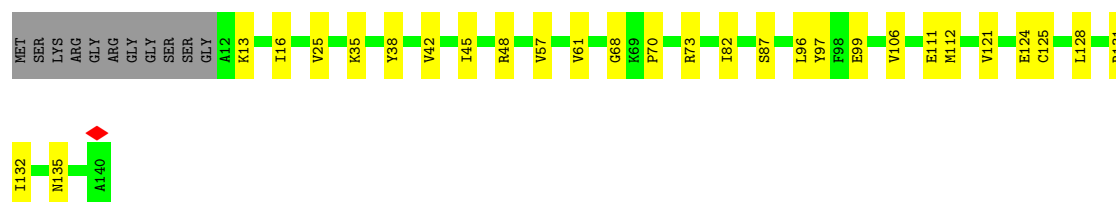
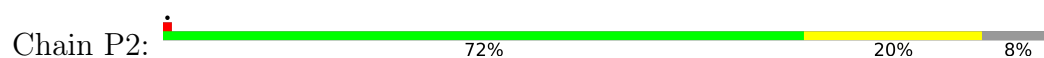
- Molecule 40: Large ribosomal subunit protein eL22



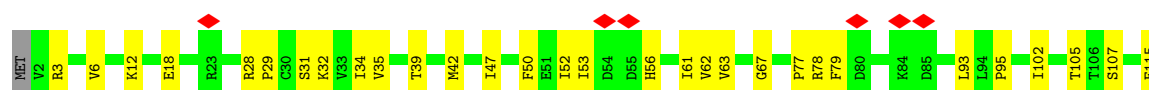
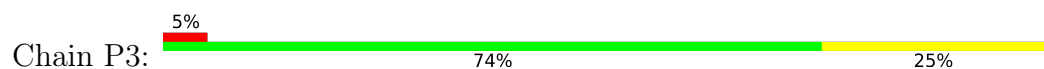
- Molecule 41: Small ribosomal subunit protein uS11

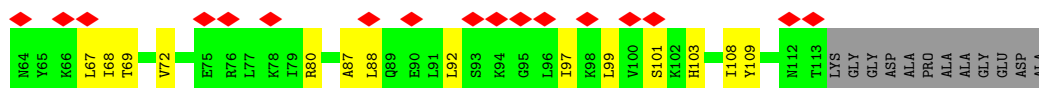


- Molecule 42: Large ribosomal subunit protein uL14

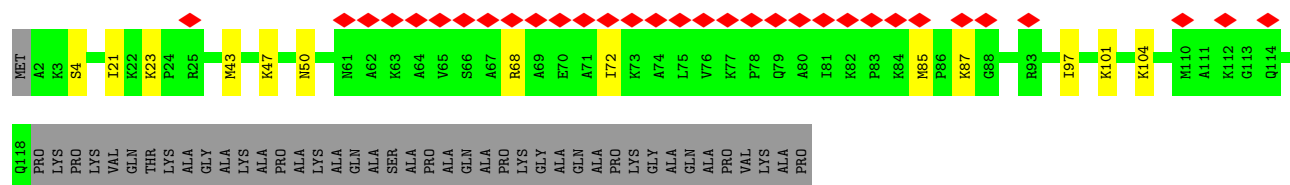


- Molecule 43: Small ribosomal subunit protein uS8





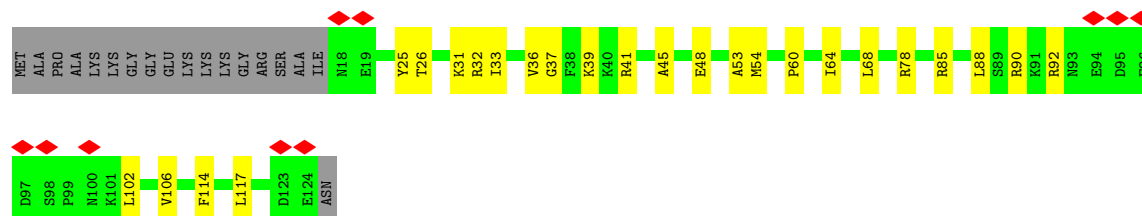
- Chain V2: 



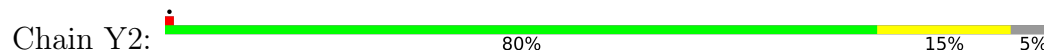
- Molecule 54: Large ribosomal subunit protein eL30



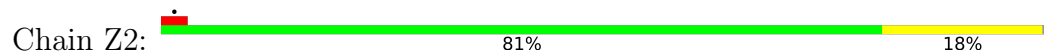
- Molecule 55: Large ribosomal subunit protein eL31



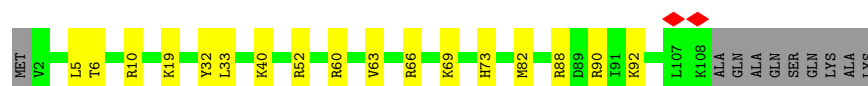
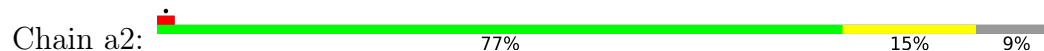
- Molecule 56: Large ribosomal subunit protein eL32




- Molecule 57: Large ribosomal subunit protein eL33

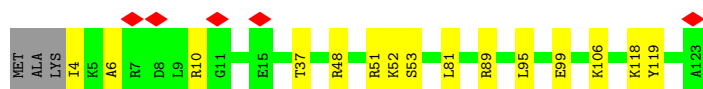


- Molecule 58: Large ribosomal subunit protein eL34




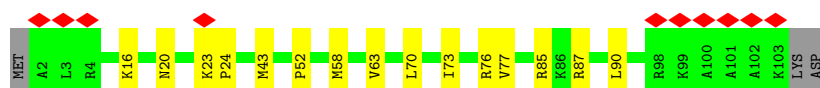
- Molecule 59: Large ribosomal subunit protein uL29

Chain b2: 



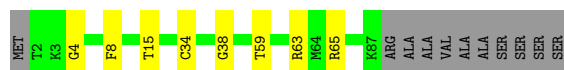
- Molecule 60: Large ribosomal subunit protein eL36

Chain c2: 




- Molecule 61: Large ribosomal subunit protein eL37

Chain d2: 




- Molecule 62: Large ribosomal subunit protein eL38

Chain e2: 




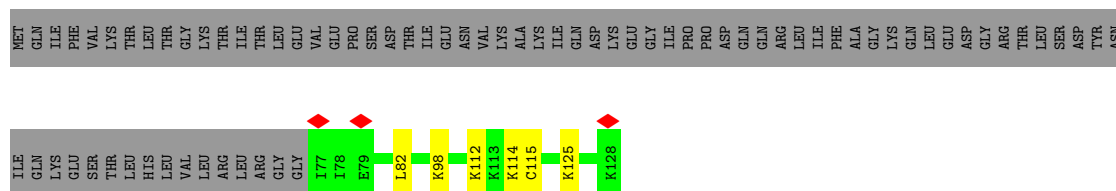
- Molecule 63: Large ribosomal subunit protein eL39

Chain f2: 



- Molecule 64: Ubiquitin-ribosomal protein eL40 fusion protein

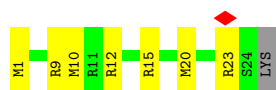
Chain g2: 



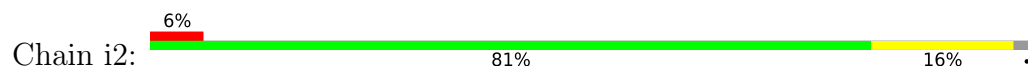
- Molecule 65: 60S ribosomal protein L41

Chain h2: 

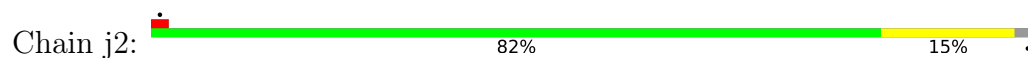




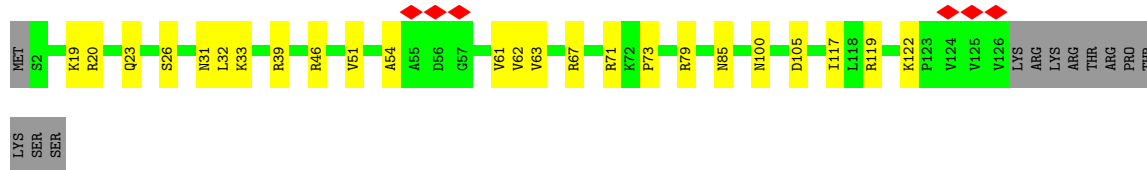
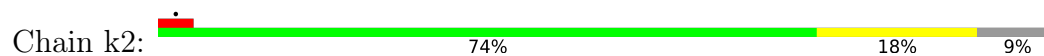
- Molecule 66: Large ribosomal subunit protein eL42



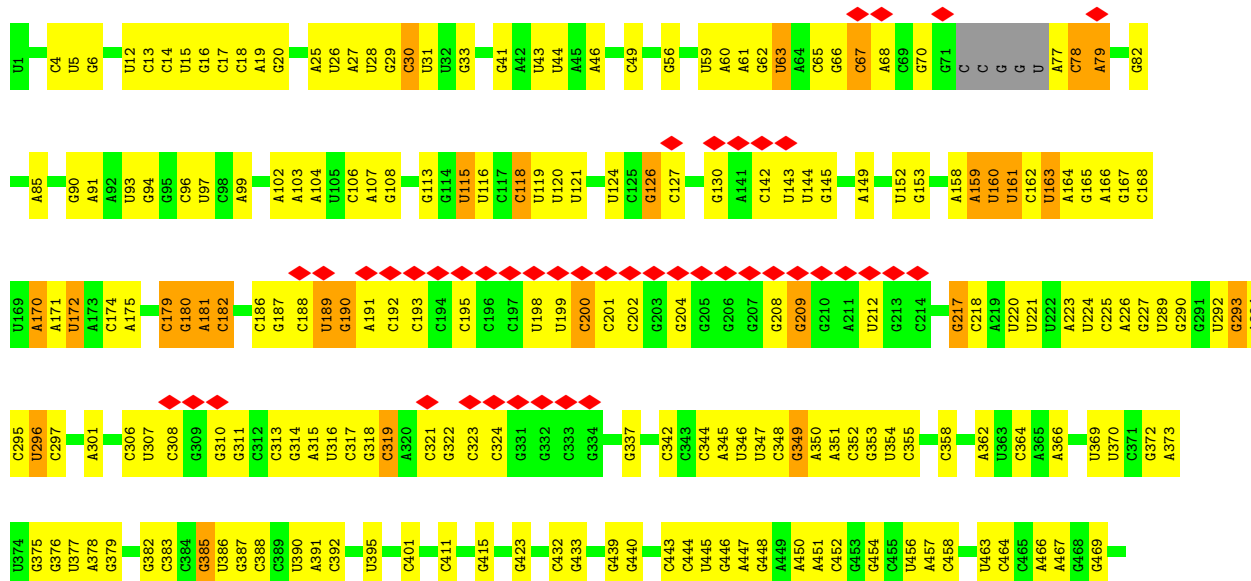
- Molecule 67: Large ribosomal subunit protein eL43



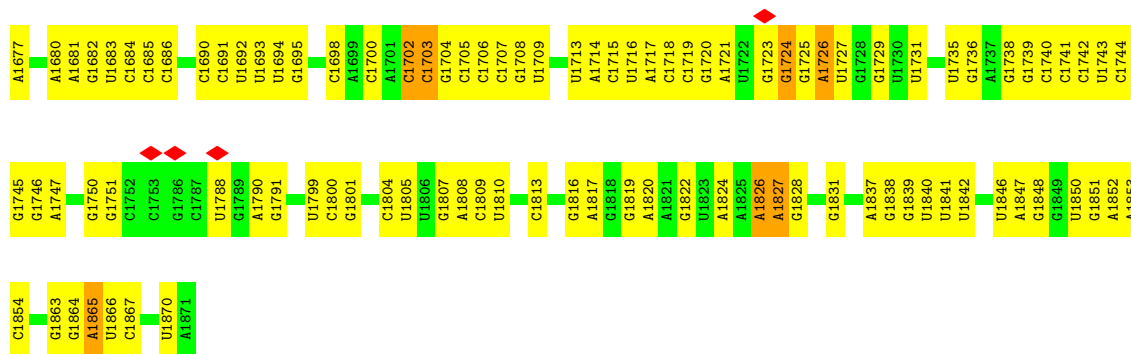
- Molecule 68: Large ribosomal subunit protein eL28



- Molecule 69: 18S ribosomal RNA



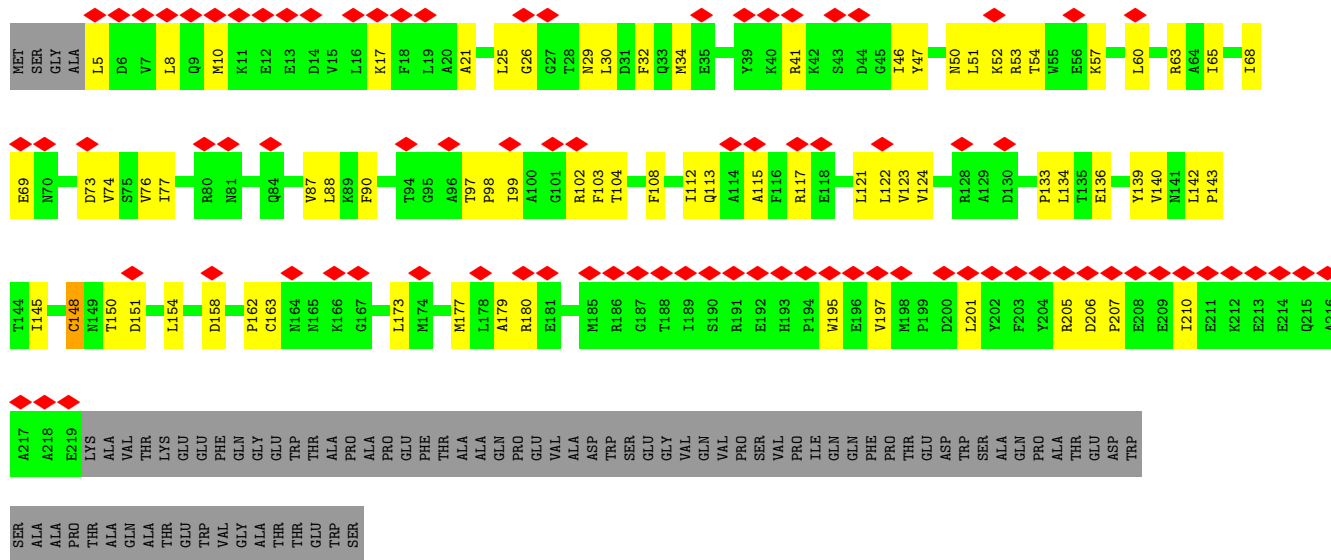




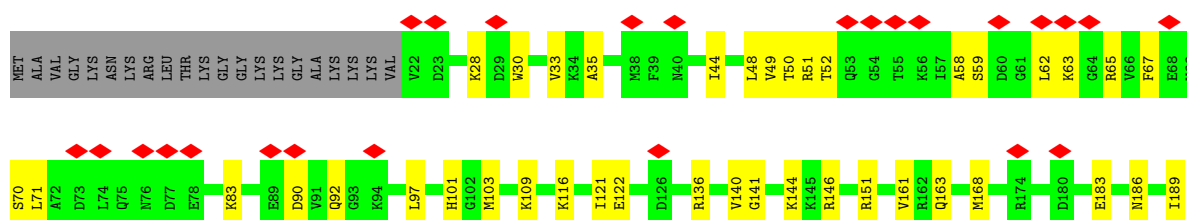
- Molecule 70: transfer RNA

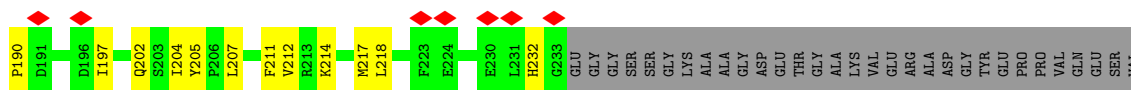


- Molecule 71: Small ribosomal subunit protein uS2

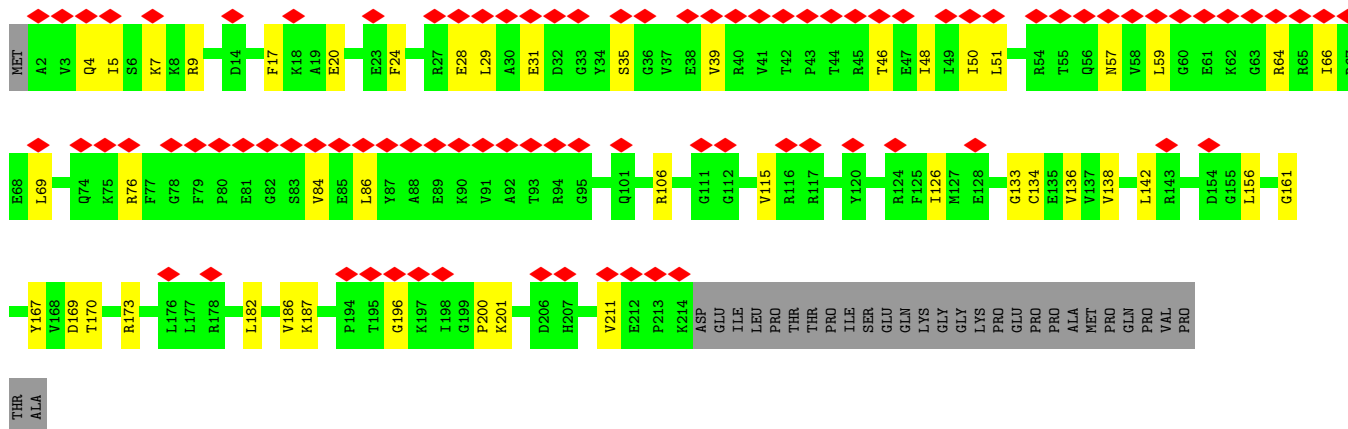


- Molecule 72: 40S ribosomal protein S3a

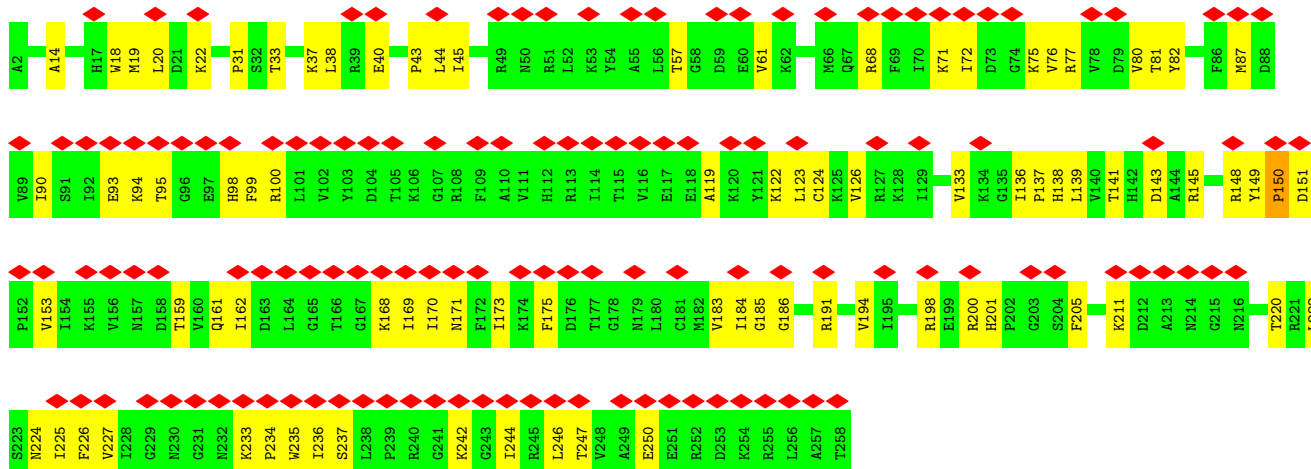




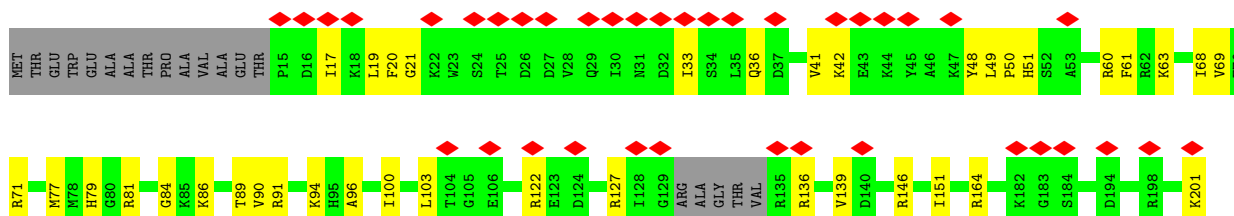
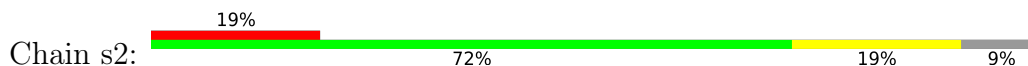
- Molecule 73: Small ribosomal subunit protein uS3

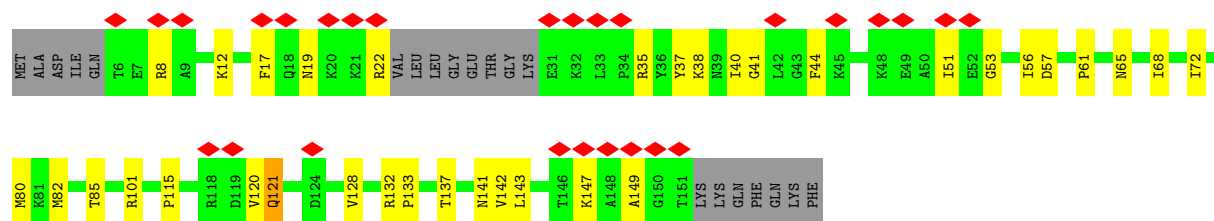


- Molecule 74: 40S ribosomal protein S4, X isoform (eS4)

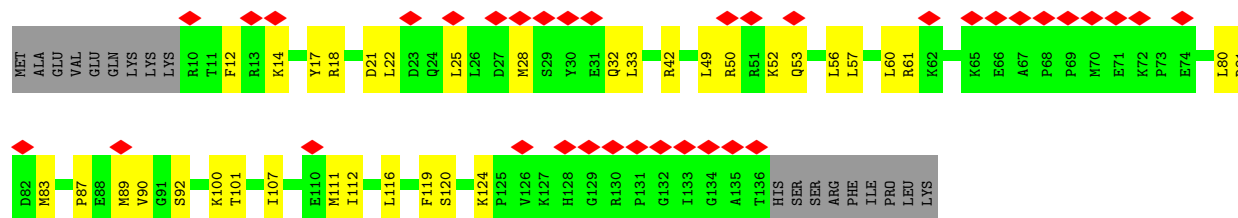


- Molecule 75: Small ribosomal subunit protein uS7

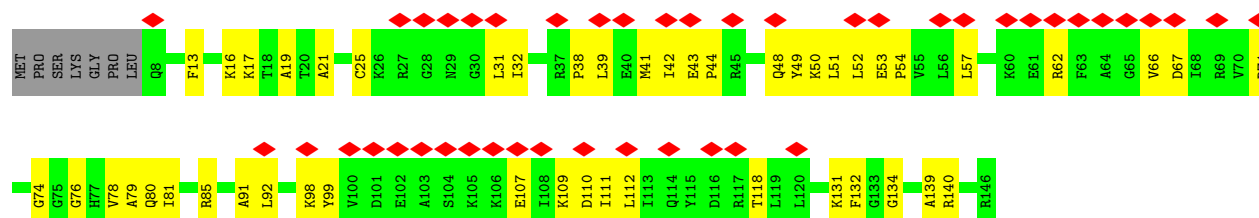




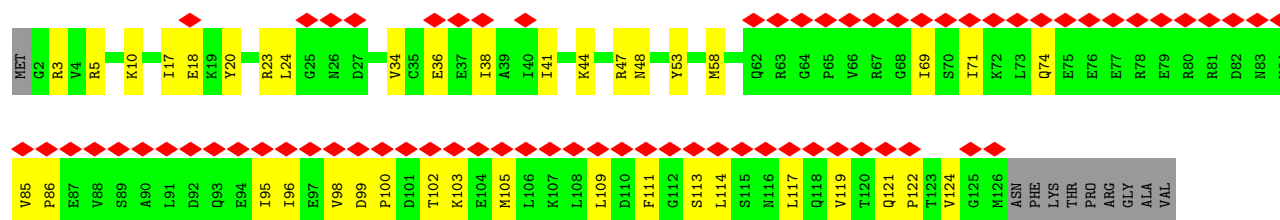
- Molecule 80: Small ribosomal subunit protein uS19



- Molecule 81: Small ribosomal subunit protein uS9



- Molecule 82: Small ribosomal subunit protein eS17



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	226576	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2900	Depositor
Magnification	100000	Depositor
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.102	Depositor
Minimum map value	-0.017	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.0198	Depositor
Map size (Å)	315.12, 315.12, 315.12	wwPDB
Map dimensions	312, 312, 312	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.01, 1.01, 1.01	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 5MC, UR3, OMU, OMC, B8T, ZN, B8N, OMG, MG, 1MA, 2MG, A2M, PSU, 4AC

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	0.18	0/1877	0.32	0/2502
2	A2	0.20	0/82439	0.29	0/128559
3	A3	0.18	0/1172	0.45	0/1570
4	B1	0.16	0/1799	0.31	0/2424
5	B2	0.18	0/2836	0.25	0/4421
6	B3	0.16	0/1109	0.40	0/1484
7	Bv	0.13	0/1576	0.30	0/2451
8	Bx	0.18	0/219	0.35	0/336
10	C1	0.17	0/1537	0.34	0/2065
11	C2	0.18	0/3675	0.26	0/5725
12	C3	0.14	0/778	0.33	0/1045
13	D1	0.17	0/1694	0.34	0/2261
14	D2	0.20	0/1914	0.36	0/2567
15	D3	0.16	0/596	0.36	0/800
16	E1	0.17	0/1420	0.40	0/1899
17	E2	0.20	0/3305	0.41	0/4422
18	E3	0.16	0/1097	0.39	0/1464
19	F1	0.17	0/1674	0.36	0/2241
20	F2	0.19	0/2877	0.37	0/3860
21	F3	0.19	0/786	0.42	0/1053
22	G1	0.16	0/1165	0.31	0/1558
23	G2	0.16	0/2435	0.35	0/3260
24	G3	0.15	0/436	0.29	0/582
25	H1	0.20	0/1746	0.36	0/2338
26	H2	0.15	0/1799	0.33	0/2413
27	H3	0.19	0/437	0.46	0/580
28	I2	0.19	0/1648	0.37	0/2203
29	I3	0.17	0/1827	0.44	0/2467
30	J2	0.20	0/1268	0.39	0/1700
31	J3	0.19	0/1626	0.43	0/2211
32	K2	0.18	0/1535	0.38	0/2048
33	K3	0.14	0/1728	0.37	0/2295

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
34	L2	0.15	0/1424	0.31	0/1884
35	L3	0.17	0/1520	0.47	0/2030
36	M2	0.20	0/1490	0.38	0/2000
37	M3	0.14	0/527	0.39	0/718
38	N2	0.16	0/1327	0.31	0/1771
39	N3	0.17	0/1226	0.44	0/1649
40	O2	0.12	0/839	0.29	0/1126
41	O3	0.18	0/1016	0.42	0/1363
42	P2	0.19	0/983	0.39	0/1319
43	P3	0.21	0/1044	0.41	0/1398
44	Q2	0.18	0/532	0.36	0/708
45	Q3	0.15	0/997	0.43	0/1325
46	R2	0.16	0/984	0.33	0/1323
47	R3	0.15	0/591	0.43	0/794
48	S2	0.17	0/1132	0.34	0/1504
49	S3	0.16	0/629	0.37	0/841
50	T2	0.16	0/1130	0.31	0/1507
51	T3	0.10	0/358	0.31	0/467
52	U2	0.19	0/1193	0.35	0/1593
53	V2	0.15	0/963	0.32	0/1275
54	W2	0.14	0/742	0.34	0/996
55	X2	0.18	0/903	0.33	0/1216
56	Y2	0.18	0/1071	0.31	0/1429
57	Z2	0.20	0/895	0.33	0/1198
58	a2	0.19	0/864	0.36	0/1152
59	b2	0.14	0/1009	0.37	0/1332
60	c2	0.14	0/843	0.37	0/1115
61	d2	0.18	0/720	0.37	0/952
62	e2	0.16	0/574	0.34	0/760
63	f2	0.19	0/454	0.32	0/599
64	g2	0.14	0/435	0.31	0/575
65	h2	0.19	0/231	0.53	0/294
66	i2	0.18	0/855	0.37	0/1128
67	j2	0.19	0/704	0.35	0/935
68	k2	0.19	0/1016	0.35	0/1363
69	m2	0.19	0/38048	0.29	0/59291
70	n2	0.12	0/1746	0.20	0/2717
71	o2	0.19	0/1741	0.45	0/2366
72	p2	0.17	0/1749	0.40	0/2340
73	q2	0.16	0/1681	0.38	0/2261
74	r2	0.16	0/2072	0.39	0/2793
75	s2	0.15	0/1489	0.41	0/1999
76	t2	0.15	0/1341	0.41	0/1803

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
77	u2	0.17	0/1424	0.37	0/1918
78	v2	0.23	0/725	0.56	0/974
79	w2	0.19	0/1154	0.46	0/1543
80	x2	0.19	0/1065	0.46	0/1423
81	y2	0.18	0/1126	0.47	0/1506
82	z2	0.15	0/1023	0.41	1/1373 (0.1%)
All	All	0.19	0/219635	0.32	1/322750 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
17	E2	0	1
26	H2	0	1
60	c2	0	1
71	o2	0	1
All	All	0	4

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
82	z2	95	ILE	N-CA-C	-5.18	107.30	111.91

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
17	E2	258	HIS	Peptide
26	H2	184	GLY	Peptide
60	c2	63	VAL	Peptide
71	o2	148	CYS	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within

the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A1	1843	0	1975	43	0
2	A2	75341	0	38149	861	0
3	A3	1154	0	1210	44	0
4	B1	1764	0	1892	34	0
5	B2	2538	0	1286	24	0
6	B3	1091	0	1130	43	0
7	Bv	1412	0	716	17	0
8	Bx	200	0	101	2	0
9	By	110	0	31	0	0
10	C1	1519	0	1603	25	0
11	C2	3315	0	1685	32	0
12	C3	769	0	837	23	0
13	D1	1656	0	1706	24	0
14	D2	1876	0	1970	34	0
15	D3	589	0	566	12	0
16	E1	1397	0	1425	33	0
17	E2	3238	0	3380	51	0
18	E3	1080	0	1147	29	0
19	F1	1643	0	1750	31	0
20	F2	2823	0	2996	48	0
21	F3	774	0	821	13	0
22	G1	1143	0	1219	13	0
23	G2	2389	0	2420	40	0
24	G3	435	0	461	11	0
25	H1	1701	0	1749	36	0
26	H2	1766	0	1902	21	0
27	H3	427	0	426	21	0
28	I2	1618	0	1775	33	0
29	I3	1800	0	1770	67	0
30	J2	1242	0	1274	35	0
31	J3	1590	0	1606	44	0
32	K2	1511	0	1636	17	0
33	K3	1708	0	1864	54	0
34	L2	1408	0	1550	17	0
35	L3	1495	0	1615	54	0
36	M2	1450	0	1488	24	0
37	M3	525	0	439	5	0
38	N2	1299	0	1368	25	0
39	N3	1202	0	1289	35	0
40	O2	825	0	850	4	0
41	O3	1003	0	1028	27	0
42	P2	969	0	1031	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	P3	1027	0	1067	29	0
44	Q2	519	0	533	9	0
45	Q3	981	0	1039	42	0
46	R2	967	0	1040	18	0
47	R3	585	0	640	16	0
48	S2	1115	0	1205	21	0
49	S3	618	0	634	13	0
50	T2	1107	0	1182	11	0
51	T3	355	0	391	9	0
52	U2	1164	0	1213	20	0
53	V2	945	0	1037	9	0
54	W2	732	0	769	9	0
55	X2	888	0	930	20	0
56	Y2	1053	0	1147	14	0
57	Z2	876	0	912	14	0
58	a2	854	0	945	16	0
59	b2	1001	0	1138	11	0
60	c2	832	0	917	10	0
61	d2	705	0	737	6	0
62	e2	568	0	635	11	0
63	f2	444	0	483	7	0
64	g2	429	0	465	5	0
65	h2	230	0	276	8	0
66	i2	842	0	912	12	0
67	j2	694	0	738	13	0
68	k2	1001	0	1066	17	0
69	m2	34736	0	17544	516	0
70	n2	1562	0	797	17	0
71	o2	1704	0	1702	58	0
72	p2	1722	0	1794	35	0
73	q2	1655	0	1750	31	0
74	r2	2031	0	2138	65	0
75	s2	1468	0	1519	29	0
76	t2	1322	0	1365	45	0
77	u2	1397	0	1378	31	0
78	v2	705	0	722	28	0
79	w2	1134	0	1197	29	0
80	x2	1045	0	1095	25	0
81	y2	1109	0	1174	43	0
82	z2	1011	0	1063	32	0
83	A2	83	0	0	0	0
83	E3	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
83	H1	1	0	0	0	0
83	J2	1	0	0	0	0
83	O3	1	0	0	0	0
83	P2	1	0	0	0	0
83	d2	1	0	0	0	0
83	m2	34	0	0	0	0
84	F3	1	0	0	0	0
84	H3	1	0	0	0	0
84	d2	1	0	0	0	0
84	g2	1	0	0	0	0
84	i2	1	0	0	0	0
84	j2	1	0	0	0	0
85	B1	1	0	0	0	0
All	All	206901	0	152425	2900	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 2900 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)
2:A2:3348:A:H62	2:A2:3479:G:N2	1.39	1.18
2:A2:3348:A:N6	2:A2:3479:G:H21	1.43	1.16
81:y2:43:GLU:HG3	81:y2:44:PRO:HD3	1.40	1.01
2:A2:740:A:H62	2:A2:828:G:H21	1.05	0.98
69:m2:153:G:H1	69:m2:165:G:H22	1.14	0.93

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	220/270 (82%)	214 (97%)	6 (3%)	0	100	100
3	A3	137/152 (90%)	124 (90%)	12 (9%)	1 (1%)	18	47
4	B1	214/266 (80%)	207 (97%)	7 (3%)	0	100	100
6	B3	136/145 (94%)	125 (92%)	10 (7%)	1 (1%)	18	47
10	C1	188/192 (98%)	185 (98%)	3 (2%)	0	100	100
12	C3	95/119 (80%)	93 (98%)	2 (2%)	0	100	100
13	D1	200/214 (94%)	194 (97%)	6 (3%)	0	100	100
14	D2	243/257 (95%)	228 (94%)	15 (6%)	0	100	100
15	D3	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
16	E1	172/178 (97%)	164 (95%)	8 (5%)	0	100	100
17	E2	400/403 (99%)	379 (95%)	21 (5%)	0	100	100
18	E3	137/143 (96%)	123 (90%)	14 (10%)	0	100	100
19	F1	201/211 (95%)	190 (94%)	11 (6%)	0	100	100
20	F2	350/419 (84%)	344 (98%)	6 (2%)	0	100	100
21	F3	95/115 (83%)	90 (95%)	5 (5%)	0	100	100
22	G1	137/217 (63%)	136 (99%)	1 (1%)	0	100	100
23	G2	291/297 (98%)	286 (98%)	5 (2%)	0	100	100
24	G3	52/69 (75%)	52 (100%)	0	0	100	100
25	H1	201/204 (98%)	196 (98%)	5 (2%)	0	100	100
26	H2	212/296 (72%)	204 (96%)	8 (4%)	0	100	100
27	H3	49/56 (88%)	45 (92%)	4 (8%)	0	100	100
28	I2	196/203 (97%)	193 (98%)	3 (2%)	0	100	100
29	I3	208/317 (66%)	185 (89%)	22 (11%)	1 (0%)	24	55
30	J2	151/184 (82%)	145 (96%)	6 (4%)	0	100	100
31	J3	215/293 (73%)	200 (93%)	15 (7%)	0	100	100
32	K2	184/188 (98%)	180 (98%)	4 (2%)	0	100	100
33	K3	205/249 (82%)	195 (95%)	10 (5%)	0	100	100
34	L2	167/196 (85%)	167 (100%)	0	0	100	100
35	L3	177/194 (91%)	161 (91%)	16 (9%)	0	100	100
36	M2	173/176 (98%)	164 (95%)	9 (5%)	0	100	100
37	M3	74/132 (56%)	65 (88%)	9 (12%)	0	100	100
38	N2	157/160 (98%)	153 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	N3	147/151 (97%)	133 (90%)	14 (10%)	0	100	100
40	O2	99/128 (77%)	97 (98%)	2 (2%)	0	100	100
41	O3	133/151 (88%)	125 (94%)	8 (6%)	0	100	100
42	P2	127/140 (91%)	126 (99%)	1 (1%)	0	100	100
43	P3	127/130 (98%)	120 (94%)	7 (6%)	0	100	100
44	Q2	60/157 (38%)	60 (100%)	0	0	100	100
45	Q3	117/133 (88%)	108 (92%)	9 (8%)	0	100	100
46	R2	116/156 (74%)	115 (99%)	1 (1%)	0	100	100
47	R3	71/125 (57%)	67 (94%)	4 (6%)	0	100	100
48	S2	132/145 (91%)	131 (99%)	1 (1%)	0	100	100
49	S3	75/84 (89%)	72 (96%)	3 (4%)	0	100	100
50	T2	133/136 (98%)	131 (98%)	2 (2%)	0	100	100
51	T3	40/133 (30%)	39 (98%)	0	1 (2%)	4	16
52	U2	145/148 (98%)	141 (97%)	4 (3%)	0	100	100
53	V2	115/160 (72%)	110 (96%)	5 (4%)	0	100	100
54	W2	92/115 (80%)	90 (98%)	2 (2%)	0	100	100
55	X2	105/125 (84%)	104 (99%)	1 (1%)	0	100	100
56	Y2	126/135 (93%)	125 (99%)	1 (1%)	0	100	100
57	Z2	107/110 (97%)	105 (98%)	2 (2%)	0	100	100
58	a2	105/117 (90%)	104 (99%)	1 (1%)	0	100	100
59	b2	118/123 (96%)	117 (99%)	1 (1%)	0	100	100
60	c2	100/105 (95%)	96 (96%)	4 (4%)	0	100	100
61	d2	84/97 (87%)	80 (95%)	4 (5%)	0	100	100
62	e2	67/70 (96%)	67 (100%)	0	0	100	100
63	f2	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
64	g2	50/128 (39%)	50 (100%)	0	0	100	100
65	h2	22/25 (88%)	22 (100%)	0	0	100	100
66	i2	101/106 (95%)	97 (96%)	4 (4%)	0	100	100
67	j2	87/92 (95%)	84 (97%)	3 (3%)	0	100	100
68	k2	123/137 (90%)	121 (98%)	2 (2%)	0	100	100
71	o2	213/295 (72%)	196 (92%)	17 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
72	p2	210/264 (80%)	195 (93%)	15 (7%)	0	100	100
73	q2	211/243 (87%)	208 (99%)	3 (1%)	0	100	100
74	r2	255/257 (99%)	239 (94%)	14 (6%)	2 (1%)	16	44
75	s2	181/204 (89%)	168 (93%)	13 (7%)	0	100	100
76	t2	166/194 (86%)	155 (93%)	11 (7%)	0	100	100
77	u2	175/208 (84%)	168 (96%)	7 (4%)	0	100	100
78	v2	81/165 (49%)	66 (82%)	14 (17%)	1 (1%)	10	34
79	w2	134/158 (85%)	127 (95%)	6 (4%)	1 (1%)	18	47
80	x2	125/145 (86%)	117 (94%)	8 (6%)	0	100	100
81	y2	137/146 (94%)	125 (91%)	12 (9%)	0	100	100
82	z2	123/135 (91%)	113 (92%)	10 (8%)	0	100	100
All	All	10701/12625 (85%)	10228 (96%)	465 (4%)	8 (0%)	49	77

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A3	91	LYS
79	w2	121	GLN
29	I3	52	TYR
78	v2	53	LYS
51	T3	22	GLN

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A1	193/234 (82%)	193 (100%)	0	100	100
3	A3	121/132 (92%)	121 (100%)	0	100	100
4	B1	189/223 (85%)	187 (99%)	2 (1%)	65	87
6	B3	111/115 (96%)	111 (100%)	0	100	100
10	C1	169/171 (99%)	169 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	C3	90/107 (84%)	90 (100%)	0	100	100
13	D1	174/181 (96%)	174 (100%)	0	100	100
14	D2	188/199 (94%)	188 (100%)	0	100	100
15	D3	53/67 (79%)	53 (100%)	0	100	100
16	E1	147/149 (99%)	147 (100%)	0	100	100
17	E2	347/348 (100%)	347 (100%)	0	100	100
18	E3	111/115 (96%)	111 (100%)	0	100	100
19	F1	170/178 (96%)	170 (100%)	0	100	100
20	F2	298/348 (86%)	298 (100%)	0	100	100
21	F3	84/98 (86%)	84 (100%)	0	100	100
22	G1	118/157 (75%)	118 (100%)	0	100	100
23	G2	246/249 (99%)	246 (100%)	0	100	100
24	G3	49/62 (79%)	49 (100%)	0	100	100
25	H1	171/172 (99%)	171 (100%)	0	100	100
26	H2	196/256 (77%)	196 (100%)	0	100	100
27	H3	45/49 (92%)	45 (100%)	0	100	100
28	I2	170/173 (98%)	170 (100%)	0	100	100
29	I3	197/275 (72%)	197 (100%)	0	100	100
30	J2	134/163 (82%)	134 (100%)	0	100	100
31	J3	155/224 (69%)	155 (100%)	0	100	100
32	K2	164/165 (99%)	164 (100%)	0	100	100
33	K3	182/218 (84%)	182 (100%)	0	100	100
34	L2	149/175 (85%)	149 (100%)	0	100	100
35	L3	160/168 (95%)	160 (100%)	0	100	100
36	M2	155/156 (99%)	155 (100%)	0	100	100
37	M3	35/108 (32%)	35 (100%)	0	100	100
38	N2	139/140 (99%)	139 (100%)	0	100	100
39	N3	130/131 (99%)	130 (100%)	0	100	100
40	O2	91/114 (80%)	91 (100%)	0	100	100
41	O3	103/119 (87%)	103 (100%)	0	100	100
42	P2	100/107 (94%)	100 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	P3	110/113 (97%)	110 (100%)	0	100	100
44	Q2	54/126 (43%)	54 (100%)	0	100	100
45	Q3	103/115 (90%)	103 (100%)	0	100	100
46	R2	106/133 (80%)	106 (100%)	0	100	100
47	R3	65/103 (63%)	65 (100%)	0	100	100
48	S2	124/135 (92%)	124 (100%)	0	100	100
49	S3	71/76 (93%)	71 (100%)	0	100	100
50	T2	117/118 (99%)	117 (100%)	0	100	100
51	T3	35/105 (33%)	35 (100%)	0	100	100
52	U2	120/121 (99%)	120 (100%)	0	100	100
53	V2	98/124 (79%)	98 (100%)	0	100	100
54	W2	79/97 (81%)	79 (100%)	0	100	100
55	X2	98/110 (89%)	98 (100%)	0	100	100
56	Y2	114/121 (94%)	114 (100%)	0	100	100
57	Z2	88/89 (99%)	88 (100%)	0	100	100
58	a2	93/100 (93%)	93 (100%)	0	100	100
59	b2	108/110 (98%)	108 (100%)	0	100	100
60	c2	86/89 (97%)	86 (100%)	0	100	100
61	d2	73/80 (91%)	73 (100%)	0	100	100
62	e2	64/65 (98%)	64 (100%)	0	100	100
63	f2	47/48 (98%)	47 (100%)	0	100	100
64	g2	48/116 (41%)	48 (100%)	0	100	100
65	h2	23/24 (96%)	23 (100%)	0	100	100
66	i2	91/94 (97%)	91 (100%)	0	100	100
67	j2	73/75 (97%)	73 (100%)	0	100	100
68	k2	109/121 (90%)	109 (100%)	0	100	100
71	o2	180/242 (74%)	180 (100%)	0	100	100
72	p2	193/229 (84%)	193 (100%)	0	100	100
73	q2	176/202 (87%)	175 (99%)	1 (1%)	78	92
74	r2	220/220 (100%)	220 (100%)	0	100	100
75	s2	157/170 (92%)	157 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
76	t2	132/174 (76%)	132 (100%)	0	100	100
77	u2	137/180 (76%)	137 (100%)	0	100	100
78	v2	75/136 (55%)	75 (100%)	0	100	100
79	w2	125/142 (88%)	125 (100%)	0	100	100
80	x2	113/130 (87%)	113 (100%)	0	100	100
81	y2	115/121 (95%)	115 (100%)	0	100	100
82	z2	113/121 (93%)	113 (100%)	0	100	100
All	All	9267/10721 (86%)	9264 (100%)	3 (0%)	100	100

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	B1	137[A]	ARG
4	B1	137[B]	ARG
73	q2	4	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 96 such sidechains are listed below:

Mol	Chain	Res	Type
44	Q2	17	HIS
64	g2	117	HIS
45	Q3	124	ASN
52	U2	60	HIS
71	o2	50	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	C2	155/156 (99%)	31 (20%)	0
2	A2	3484/3615 (96%)	648 (18%)	12 (0%)
5	B2	118/121 (97%)	11 (9%)	0
69	m2	1616/1635 (98%)	390 (24%)	0
7	Bv	63/76 (82%)	24 (38%)	0
70	n2	70/73 (95%)	9 (12%)	0
8	Bx	9/10 (90%)	4 (44%)	0
All	All	5515/5686 (96%)	1117 (20%)	12 (0%)

5 of 1117 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	A2	13	U
2	A2	17	A
2	A2	21	G
2	A2	25	A
2	A2	39	A

5 of 12 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	A2	3253	G
2	A2	3614	G
2	A2	4582	U
2	A2	4277	C
2	A2	2259	C

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

107 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	$\# Z > 2$
2	OMU	A2	3474	2	19,22,23	0.31	0	25,31,34	0.40	0
69	PSU	m2	1245	69	18,21,22	0.48	0	21,30,33	0.62	0
69	OMC	m2	519	69	19,22,23	0.22	0	25,31,34	0.43	0
2	A2M	A2	1673	2	22,25,26	0.10	0	30,36,39	0.47	0
2	OMU	A2	2592	2	19,22,23	0.27	0	25,31,34	0.67	0
2	A2M	A2	3486	2	22,25,26	0.09	0	30,36,39	0.36	0
2	A2M	A2	4175	2,83	22,25,26	0.09	0	30,36,39	0.38	0
2	OMC	A2	1154	2	19,22,23	0.23	0	25,31,34	0.42	0
69	A2M	m2	1680	69	22,25,26	0.11	0	30,36,39	0.25	0
2	A2M	A2	3374	2	22,25,26	0.10	0	30,36,39	0.25	0
2	OMG	A2	1438	2	23,26,27	0.24	0	32,38,41	0.40	0
2	OMG	A2	4289	2	23,26,27	0.29	0	32,38,41	0.42	0
2	PSU	A2	4288	2	18,21,22	0.49	0	21,30,33	0.62	0
69	OMC	m2	355	69	19,22,23	0.26	0	25,31,34	0.37	0
2	OMG	A2	3555	2,83	23,26,27	0.27	0	32,38,41	0.44	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PSU	A2	1496	2	18,21,22	0.50	0	21,30,33	0.61	0
69	OMG	m2	1330	69	23,26,27	0.29	0	32,38,41	0.43	0
69	OMC	m2	1705	69	19,22,23	0.20	0	25,31,34	0.37	0
2	A2M	A2	2570	2	22,25,26	0.09	0	30,36,39	0.18	0
2	OMU	A2	3958	2	19,22,23	0.23	0	25,31,34	0.44	0
2	OMG	A2	4151	2	23,26,27	0.29	0	32,38,41	0.44	0
2	OMG	A2	1335	2	23,26,27	0.27	0	32,38,41	0.44	0
2	A2M	A2	1337	2	22,25,26	0.14	0	30,36,39	0.40	0
69	OMU	m2	116	69	19,22,23	0.20	0	25,31,34	0.39	0
2	A2M	A2	3380	2	22,25,26	0.12	0	30,36,39	0.36	0
2	PSU	A2	2263	2	18,21,22	0.43	0	21,30,33	0.62	0
2	1MA	A2	4067	2	21,25,26	0.25	0	30,37,40	0.43	0
69	A2M	m2	1033	69	22,25,26	0.10	0	30,36,39	0.24	0
69	B8T	m2	1339	69	19,22,23	0.35	0	25,31,34	0.44	0
69	OMU	m2	172	69	19,22,23	0.20	0	25,31,34	0.61	1 (4%)
69	PSU	m2	1083	69	18,21,22	0.57	1 (5%)	21,30,33	0.64	0
69	PSU	m2	824	69	18,21,22	0.51	0	21,30,33	0.66	1 (4%)
69	PSU	m2	825	69	18,21,22	0.47	0	21,30,33	0.60	1 (4%)
69	4AC	m2	1844	69	21,24,25	0.28	0	28,34,37	0.30	0
69	OMG	m2	646	69	23,26,27	0.27	0	32,38,41	0.35	0
69	A2M	m2	99	83,69	22,25,26	0.10	0	30,36,39	0.34	0
2	PSU	A2	3945	2	18,21,22	0.48	0	21,30,33	0.58	0
2	PSU	A2	3385	2	18,21,22	0.53	0	21,30,33	0.56	0
2	OMG	A2	3400	2	23,26,27	0.24	0	32,38,41	0.38	0
2	2MG	A2	1330	2	23,26,27	0.28	0	33,38,41	0.39	0
2	OMC	A2	1683	2,83	19,22,23	0.25	0	25,31,34	0.53	0
2	OMC	A2	2120	2	19,22,23	0.23	0	25,31,34	0.48	0
2	OMU	A2	4150	2	19,22,23	0.22	0	25,31,34	0.46	0
69	OMG	m2	603	69	23,26,27	0.25	0	32,38,41	0.31	0
2	A2M	A2	1347	2,83	22,25,26	0.12	0	30,36,39	0.49	0
2	OMG	A2	4146	2	23,26,27	0.27	0	32,38,41	0.41	0
69	OMU	m2	430	69	19,22,23	0.22	0	25,31,34	0.46	0
2	OMG	A2	4022	2	23,26,27	0.27	0	32,38,41	0.39	0
2	PSU	A2	1490	2	18,21,22	0.58	1 (5%)	21,30,33	0.36	0
2	A2M	A2	3441	2	22,25,26	0.11	0	30,36,39	0.30	0
69	A2M	m2	578	69	22,25,26	0.09	0	30,36,39	0.24	0
2	A2M	A2	4223	2	22,25,26	0.10	0	30,36,39	0.22	0
2	OMG	A2	3848	2	23,26,27	0.26	0	32,38,41	0.37	0
69	OMG	m2	511	83,69	23,26,27	0.26	0	32,38,41	0.49	0
2	OMC	A2	2177	2,83	19,22,23	0.23	0	25,31,34	0.36	0
2	OMC	A2	3497	2	19,22,23	0.25	0	25,31,34	0.40	0
2	OMC	A2	2579	2	19,22,23	0.24	0	25,31,34	0.38	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	OMG	A2	3283	2	23,26,27	0.24	0	32,38,41	0.54	0
2	OMU	A2	3581	2	19,22,23	0.26	0	25,31,34	0.52	0
69	OMG	m2	869	69	23,26,27	0.23	0	32,38,41	0.31	0
2	A2M	A2	2118	2,83	22,25,26	0.08	0	30,36,39	0.21	0
69	A2M	m2	27	69	22,25,26	0.10	0	30,36,39	0.23	0
2	5MC	A2	3438	2,83	19,22,23	0.30	0	26,32,35	0.39	0
69	A2M	m2	514	69	22,25,26	0.10	0	30,36,39	0.37	0
2	OMC	A2	4188	2	19,22,23	0.27	0	25,31,34	0.50	0
2	PSU	A2	3371	2	18,21,22	0.50	0	21,30,33	0.56	0
69	OMC	m2	174	69	19,22,23	0.29	0	25,31,34	0.55	0
2	PSU	A2	4280	2	18,21,22	0.51	0	21,30,33	0.58	0
69	PSU	m2	614	69	18,21,22	0.49	0	21,30,33	0.62	1 (4%)
2	OMU	A2	4272	2	19,22,23	0.33	0	25,31,34	0.60	0
2	OMC	A2	2559	2	19,22,23	0.25	0	25,31,34	0.36	0
2	OMC	A2	3357	2	19,22,23	0.22	0	25,31,34	0.53	0
2	OMG	A2	4275	2	23,26,27	0.27	0	32,38,41	0.51	0
2	A2M	A2	1140	2	22,25,26	0.09	0	30,36,39	0.16	0
2	A2M	A2	3481	2	22,25,26	0.09	0	30,36,39	0.27	0
2	PSU	A2	1395	2	18,21,22	0.56	0	21,30,33	0.56	0
2	OMG	A2	4044	2	23,26,27	0.24	0	32,38,41	0.34	0
2	OMG	A2	3880	2	23,26,27	0.26	0	32,38,41	0.55	0
2	A2M	A2	2156	2	22,25,26	0.10	0	30,36,39	0.25	0
2	OMG	A2	3448	2	23,26,27	0.26	0	32,38,41	0.34	0
2	OMC	A2	4108	2	19,22,23	0.24	0	25,31,34	0.36	0
2	A2M	A2	2542	2	22,25,26	0.09	0	30,36,39	0.34	0
2	PSU	A2	4055	2	18,21,22	0.50	0	21,30,33	0.62	1 (4%)
2	OMC	A2	2106	2	19,22,23	0.24	0	25,31,34	0.32	0
2	A2M	A2	1137	2	22,25,26	0.10	0	30,36,39	0.17	0
2	OMC	A2	2616	2	19,22,23	0.22	0	25,31,34	0.35	0
2	OMG	A2	2119	2	23,26,27	0.24	0	32,38,41	0.38	0
2	OMG	A2	2179	2	23,26,27	0.24	0	32,38,41	0.32	0
69	A2M	m2	486	69	22,25,26	0.09	0	30,36,39	0.22	0
11	OMG	C2	75	11	23,26,27	0.25	0	32,38,41	0.36	0
69	OMG	m2	438	69	23,26,27	0.27	0	32,38,41	0.39	0
2	PSU	A2	4102	2,83	18,21,22	0.48	0	21,30,33	0.40	0
2	OMC	A2	3543	2	19,22,23	0.25	0	25,31,34	0.46	0
69	UR3	m2	1832	69	19,22,23	0.26	0	26,32,35	0.35	0
2	5MC	A2	4099	2	19,22,23	0.36	0	26,32,35	0.61	0
2	OMG	A2	1130	2	23,26,27	0.28	0	32,38,41	0.46	0
2	A2M	A2	398	2	22,25,26	0.10	0	30,36,39	0.27	0
69	OMU	m2	121	69	19,22,23	0.24	0	25,31,34	0.47	0
69	B8N	m2	1250	69	25,29,30	0.54	0	28,42,45	0.58	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	OMC	A2	3525	2	19,22,23	0.25	0	25,31,34	0.41	0
2	PSU	A2	4152	2	18,21,22	0.53	0	21,30,33	0.64	1 (4%)
69	OMG	m2	685	69	23,26,27	0.29	0	32,38,41	0.45	0
69	A2M	m2	670	83,69	22,25,26	0.13	0	30,36,39	0.27	0
2	PSU	A2	4183	2	18,21,22	0.50	0	21,30,33	0.39	0
2	OMC	A2	3464	2	19,22,23	0.25	0	25,31,34	0.35	0
2	PSU	A2	4094	2	18,21,22	0.49	0	21,30,33	0.63	1 (4%)
2	A2M	A2	4270	2	22,25,26	0.09	0	30,36,39	0.40	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.

'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	OMU	A2	3474	2	-	1/9/27/28	0/2/2/2
69	PSU	m2	1245	69	-	2/7/25/26	0/2/2/2
69	OMC	m2	519	69	-	2/9/27/28	0/2/2/2
2	A2M	A2	1673	2	-	0/9/27/28	0/3/3/3
2	OMU	A2	2592	2	-	0/9/27/28	0/2/2/2
2	A2M	A2	3486	2	-	0/9/27/28	0/3/3/3
2	A2M	A2	4175	2,83	-	1/9/27/28	0/3/3/3
2	OMC	A2	1154	2	-	0/9/27/28	0/2/2/2
69	A2M	m2	1680	69	-	0/9/27/28	0/3/3/3
2	A2M	A2	3374	2	-	0/9/27/28	0/3/3/3
2	OMG	A2	1438	2	-	1/9/27/28	0/3/3/3
2	OMG	A2	4289	2	-	3/9/27/28	0/3/3/3
2	PSU	A2	4288	2	-	3/7/25/26	0/2/2/2
69	OMC	m2	355	69	-	1/9/27/28	0/2/2/2
2	OMG	A2	3555	2,83	-	0/9/27/28	0/3/3/3
2	PSU	A2	1496	2	-	0/7/25/26	0/2/2/2
69	OMG	m2	1330	69	-	2/9/27/28	0/3/3/3
69	OMC	m2	1705	69	-	0/9/27/28	0/2/2/2
2	A2M	A2	2570	2	-	0/9/27/28	0/3/3/3
2	OMU	A2	3958	2	-	0/9/27/28	0/2/2/2
2	OMG	A2	4151	2	-	2/9/27/28	0/3/3/3
2	OMG	A2	1335	2	-	0/9/27/28	0/3/3/3
2	A2M	A2	1337	2	-	1/9/27/28	0/3/3/3
69	OMU	m2	116	69	-	0/9/27/28	0/2/2/2
2	A2M	A2	3380	2	-	2/9/27/28	0/3/3/3
2	PSU	A2	2263	2	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	1MA	A2	4067	2	-	2/7/25/26	0/3/3/3
69	A2M	m2	1033	69	-	0/9/27/28	0/3/3/3
69	B8T	m2	1339	69	-	0/7/27/28	0/2/2/2
69	OMU	m2	172	69	-	2/9/27/28	0/2/2/2
69	PSU	m2	1083	69	-	1/7/25/26	0/2/2/2
69	PSU	m2	824	69	-	0/7/25/26	0/2/2/2
69	PSU	m2	825	69	-	0/7/25/26	0/2/2/2
69	4AC	m2	1844	69	-	0/11/29/30	0/2/2/2
69	OMG	m2	646	69	-	3/9/27/28	0/3/3/3
69	A2M	m2	99	83,69	-	0/9/27/28	0/3/3/3
2	PSU	A2	3945	2	-	0/7/25/26	0/2/2/2
2	PSU	A2	3385	2	-	0/7/25/26	0/2/2/2
2	OMG	A2	3400	2	-	0/9/27/28	0/3/3/3
2	2MG	A2	1330	2	-	0/9/27/28	0/3/3/3
2	OMC	A2	1683	2,83	-	0/9/27/28	0/2/2/2
2	OMC	A2	2120	2	-	0/9/27/28	0/2/2/2
2	OMU	A2	4150	2	-	0/9/27/28	0/2/2/2
69	OMG	m2	603	69	-	1/9/27/28	0/3/3/3
2	A2M	A2	1347	2,83	-	3/9/27/28	0/3/3/3
2	OMG	A2	4146	2	-	0/9/27/28	0/3/3/3
69	OMU	m2	430	69	-	4/9/27/28	0/2/2/2
2	OMG	A2	4022	2	-	0/9/27/28	0/3/3/3
2	PSU	A2	1490	2	-	2/7/25/26	0/2/2/2
2	A2M	A2	3441	2	-	4/9/27/28	0/3/3/3
69	A2M	m2	578	69	-	3/9/27/28	0/3/3/3
2	A2M	A2	4223	2	-	0/9/27/28	0/3/3/3
2	OMG	A2	3848	2	-	1/9/27/28	0/3/3/3
69	OMG	m2	511	83,69	-	0/9/27/28	0/3/3/3
2	OMC	A2	2177	2,83	-	0/9/27/28	0/2/2/2
2	OMC	A2	3497	2	-	0/9/27/28	0/2/2/2
2	OMC	A2	2579	2	-	1/9/27/28	0/2/2/2
2	OMG	A2	3283	2	-	1/9/27/28	0/3/3/3
2	OMU	A2	3581	2	-	0/9/27/28	0/2/2/2
69	OMG	m2	869	69	-	1/9/27/28	0/3/3/3
2	A2M	A2	2118	2,83	-	0/9/27/28	0/3/3/3
69	A2M	m2	27	69	-	1/9/27/28	0/3/3/3
2	5MC	A2	3438	2,83	-	0/7/25/26	0/2/2/2
69	A2M	m2	514	69	-	0/9/27/28	0/3/3/3
2	OMC	A2	4188	2	-	0/9/27/28	0/2/2/2
2	PSU	A2	3371	2	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
69	OMC	m2	174	69	-	2/9/27/28	0/2/2/2
2	PSU	A2	4280	2	-	0/7/25/26	0/2/2/2
69	PSU	m2	614	69	-	0/7/25/26	0/2/2/2
2	OMU	A2	4272	2	-	2/9/27/28	0/2/2/2
2	OMC	A2	2559	2	-	0/9/27/28	0/2/2/2
2	OMC	A2	3357	2	-	4/9/27/28	0/2/2/2
2	OMG	A2	4275	2	-	0/9/27/28	0/3/3/3
2	A2M	A2	1140	2	-	4/9/27/28	0/3/3/3
2	A2M	A2	3481	2	-	0/9/27/28	0/3/3/3
2	PSU	A2	1395	2	-	0/7/25/26	0/2/2/2
2	OMG	A2	4044	2	-	0/9/27/28	0/3/3/3
2	OMG	A2	3880	2	-	0/9/27/28	0/3/3/3
2	A2M	A2	2156	2	-	0/9/27/28	0/3/3/3
2	OMG	A2	3448	2	-	0/9/27/28	0/3/3/3
2	OMC	A2	4108	2	-	0/9/27/28	0/2/2/2
2	A2M	A2	2542	2	-	3/9/27/28	0/3/3/3
2	PSU	A2	4055	2	-	0/7/25/26	0/2/2/2
2	OMC	A2	2106	2	-	2/9/27/28	0/2/2/2
2	A2M	A2	1137	2	-	1/9/27/28	0/3/3/3
2	OMC	A2	2616	2	-	0/9/27/28	0/2/2/2
2	OMG	A2	2119	2	-	2/9/27/28	0/3/3/3
2	OMG	A2	2179	2	-	1/9/27/28	0/3/3/3
69	A2M	m2	486	69	-	0/9/27/28	0/3/3/3
11	OMG	C2	75	11	-	2/9/27/28	0/3/3/3
69	OMG	m2	438	69	-	0/9/27/28	0/3/3/3
2	PSU	A2	4102	2,83	-	2/7/25/26	0/2/2/2
2	OMC	A2	3543	2	-	0/9/27/28	0/2/2/2
69	UR3	m2	1832	69	-	0/7/25/26	0/2/2/2
2	5MC	A2	4099	2	-	3/7/25/26	0/2/2/2
2	OMG	A2	1130	2	-	0/9/27/28	0/3/3/3
2	A2M	A2	398	2	-	0/9/27/28	0/3/3/3
69	OMU	m2	121	69	-	0/9/27/28	0/2/2/2
69	B8N	m2	1250	69	-	4/16/34/35	0/2/2/2
2	OMC	A2	3525	2	-	0/9/27/28	0/2/2/2
2	PSU	A2	4152	2	-	1/7/25/26	0/2/2/2
69	OMG	m2	685	69	-	0/9/27/28	0/3/3/3
69	A2M	m2	670	83,69	-	2/9/27/28	0/3/3/3
2	PSU	A2	4183	2	-	2/7/25/26	0/2/2/2
2	OMC	A2	3464	2	-	0/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PSU	A2	4094	2	-	0/7/25/26	0/2/2/2
2	A2M	A2	4270	2	-	0/9/27/28	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
69	m2	1083	PSU	O4'-C1'	-2.14	1.40	1.43
2	A2	1490	PSU	O4'-C1'	-2.07	1.41	1.43

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
69	m2	172	OMU	O2'-C2'-C1'	2.43	113.60	108.99
69	m2	824	PSU	O4'-C1'-C2'	2.23	108.24	105.15
69	m2	614	PSU	O4'-C1'-C2'	2.16	108.14	105.15
2	A2	4094	PSU	O4'-C1'-C2'	2.13	108.10	105.15
69	m2	825	PSU	O4'-C1'-C2'	2.08	108.03	105.15

There are no chirality outliers.

5 of 88 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	C2	75	OMG	O4'-C4'-C5'-O5'
11	C2	75	OMG	C3'-C4'-C5'-O5'
2	A2	1140	A2M	O4'-C4'-C5'-O5'
2	A2	1347	A2M	C4'-C5'-O5'-P
2	A2	1347	A2M	C3'-C4'-C5'-O5'

There are no ring outliers.

49 monomers are involved in 67 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A2	3474	OMU	1	0
2	A2	1673	A2M	1	0
2	A2	2592	OMU	1	0
2	A2	1154	OMC	1	0
69	m2	1680	A2M	1	0
2	A2	3374	A2M	3	0
2	A2	1438	OMG	1	0
2	A2	4289	OMG	1	0
2	A2	4288	PSU	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
69	m2	355	OMC	2	0
69	m2	1705	OMC	2	0
2	A2	3958	OMU	1	0
69	m2	116	OMU	2	0
2	A2	3380	A2M	1	0
2	A2	4067	1MA	1	0
69	m2	824	PSU	1	0
69	m2	825	PSU	1	0
69	m2	646	OMG	1	0
69	m2	99	A2M	1	0
2	A2	1330	2MG	1	0
2	A2	1683	OMC	1	0
69	m2	603	OMG	2	0
2	A2	1347	A2M	1	0
2	A2	1490	PSU	1	0
2	A2	3441	A2M	1	0
69	m2	578	A2M	1	0
2	A2	3848	OMG	1	0
69	m2	511	OMG	8	0
2	A2	2177	OMC	1	0
2	A2	3283	OMG	1	0
69	m2	869	OMG	1	0
2	A2	2118	A2M	1	0
69	m2	27	A2M	1	0
69	m2	514	A2M	2	0
69	m2	174	OMC	1	0
2	A2	4280	PSU	1	0
2	A2	4272	OMU	1	0
2	A2	1140	A2M	2	0
2	A2	4044	OMG	2	0
2	A2	4108	OMC	1	0
2	A2	2106	OMC	2	0
2	A2	2119	OMG	1	0
2	A2	2179	OMG	3	0
69	m2	486	A2M	1	0
11	C2	75	OMG	1	0
2	A2	4099	5MC	2	0
69	m2	121	OMU	2	0
2	A2	4152	PSU	1	0
2	A2	4270	A2M	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 129 ligands modelled in this entry, 129 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	A2	15
69	m2	6
70	n2	2
51	T3	1

The worst 5 of 24 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	m2	130:G	O3'	141:A	P	25.34
1	A2	1512:U	O3'	1521:A	P	24.97
1	m2	690:U	O3'	801:U	P	18.19
1	A2	4437:C	O3'	4493:G	P	17.28
1	A2	770:G	O3'	799:C	P	16.50

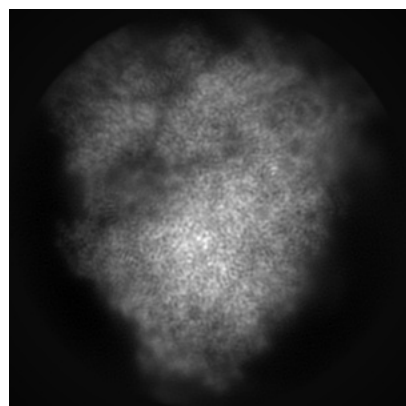
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53310. These allow visual inspection of the internal detail of the map and identification of artifacts.

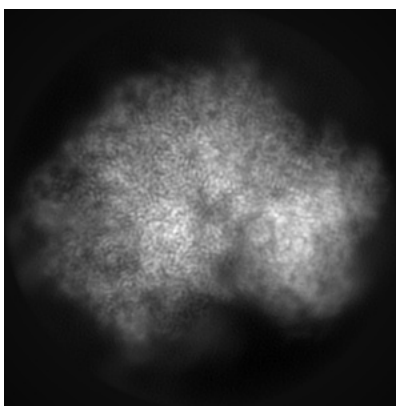
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

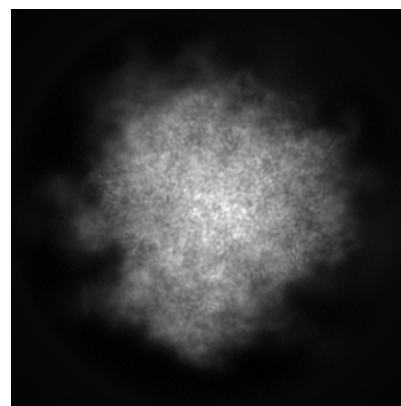
6.1.1 Primary map



X

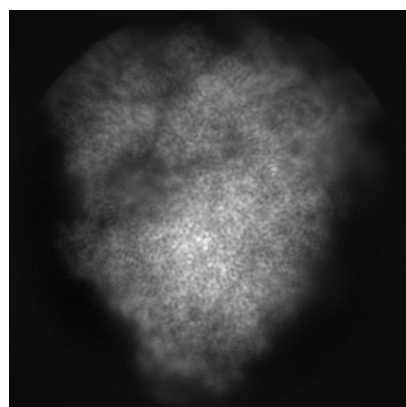


Y

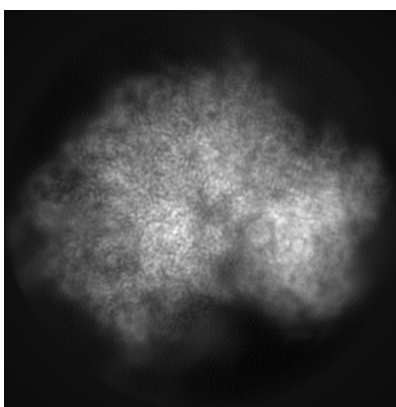


Z

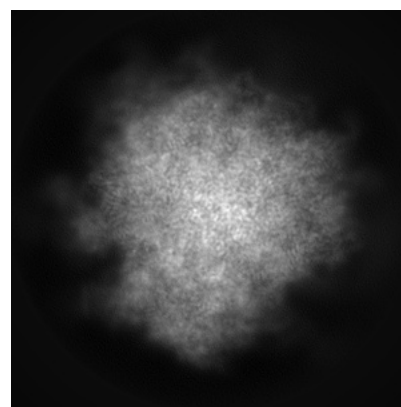
6.1.2 Raw map



X



Y

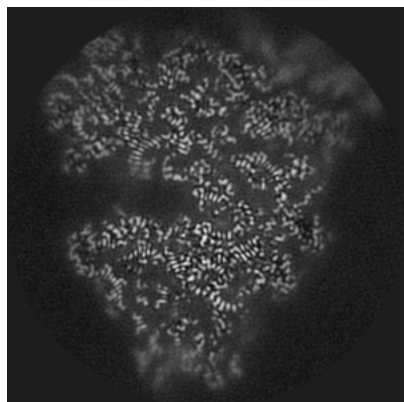


Z

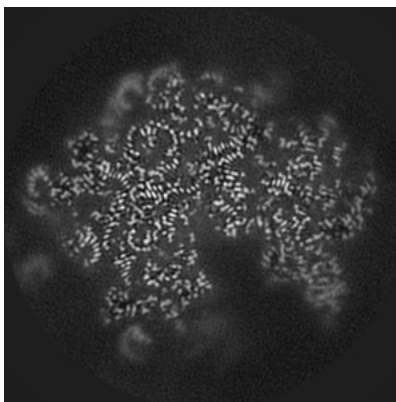
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

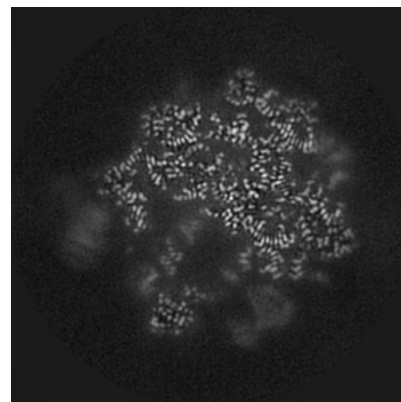
6.2.1 Primary map



X Index: 156

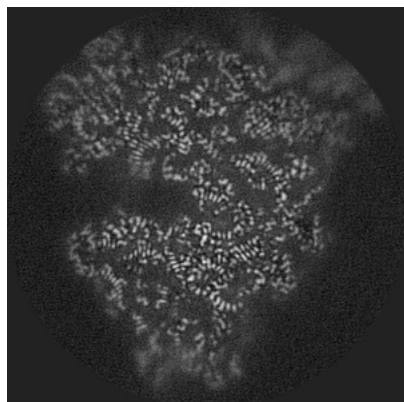


Y Index: 156

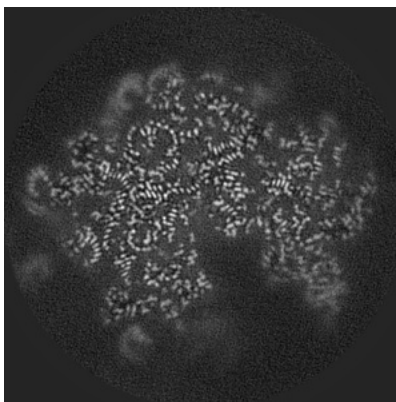


Z Index: 156

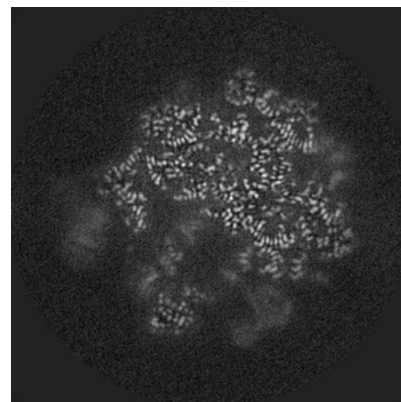
6.2.2 Raw map



X Index: 156



Y Index: 156

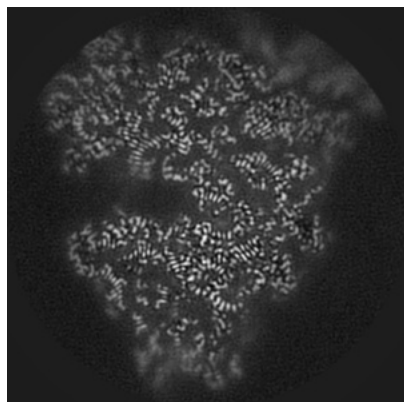


Z Index: 156

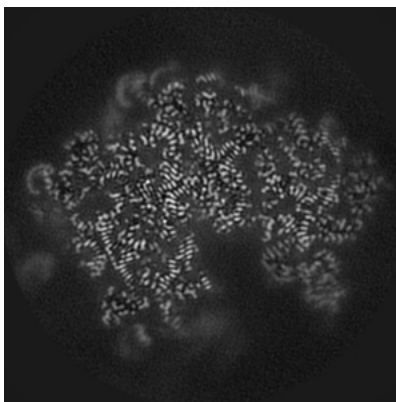
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

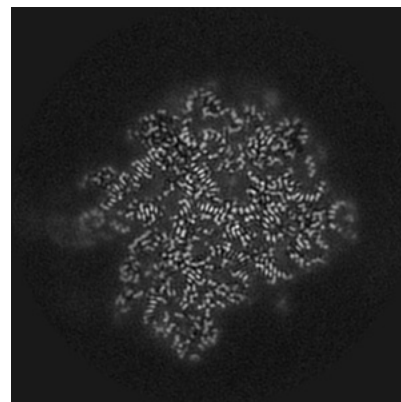
6.3.1 Primary map



X Index: 156

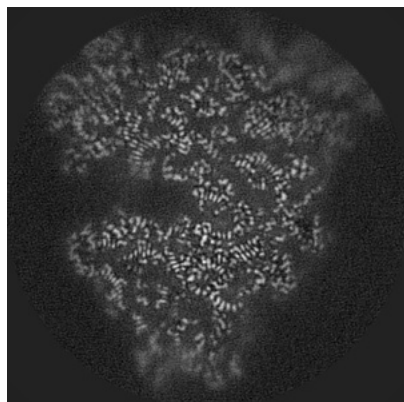


Y Index: 153

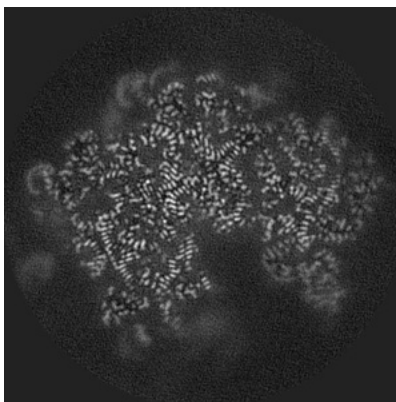


Z Index: 132

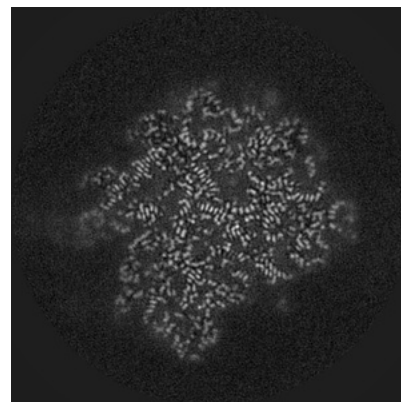
6.3.2 Raw map



X Index: 156



Y Index: 153

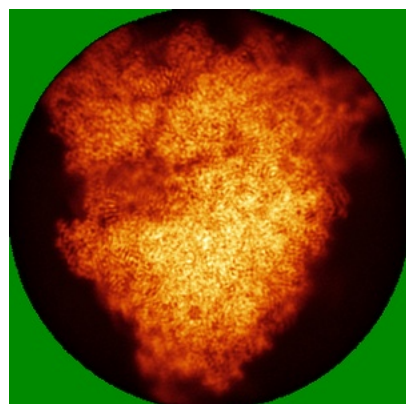


Z Index: 132

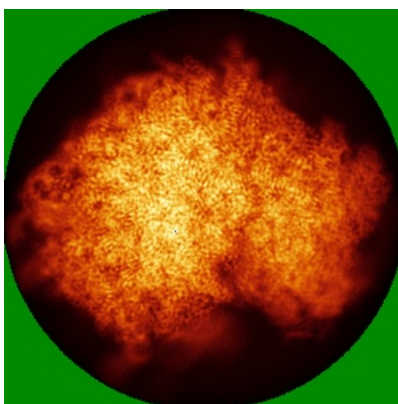
The images above show the largest variance slices of the map in three orthogonal directions.

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

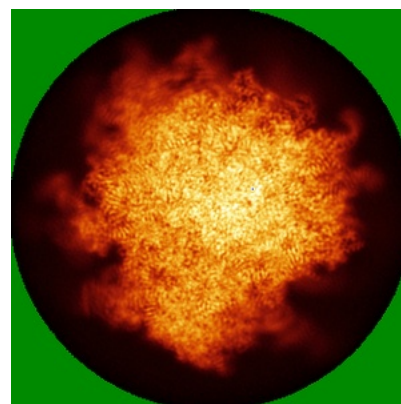
6.4.1 Primary map



X

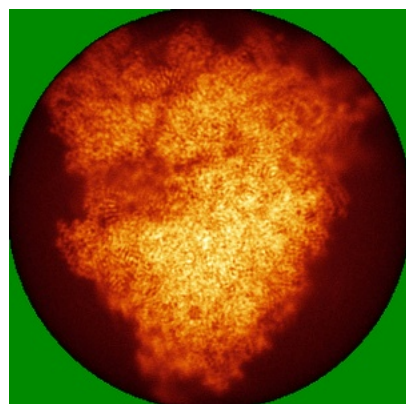


Y

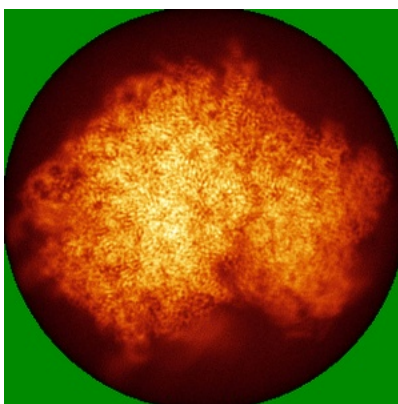


Z

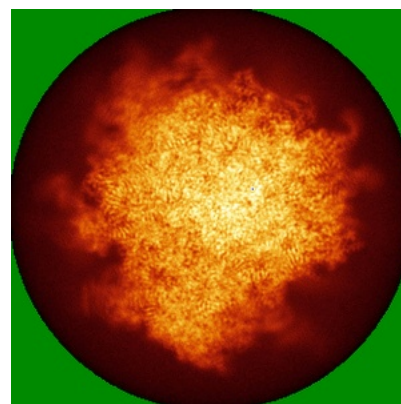
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0198. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

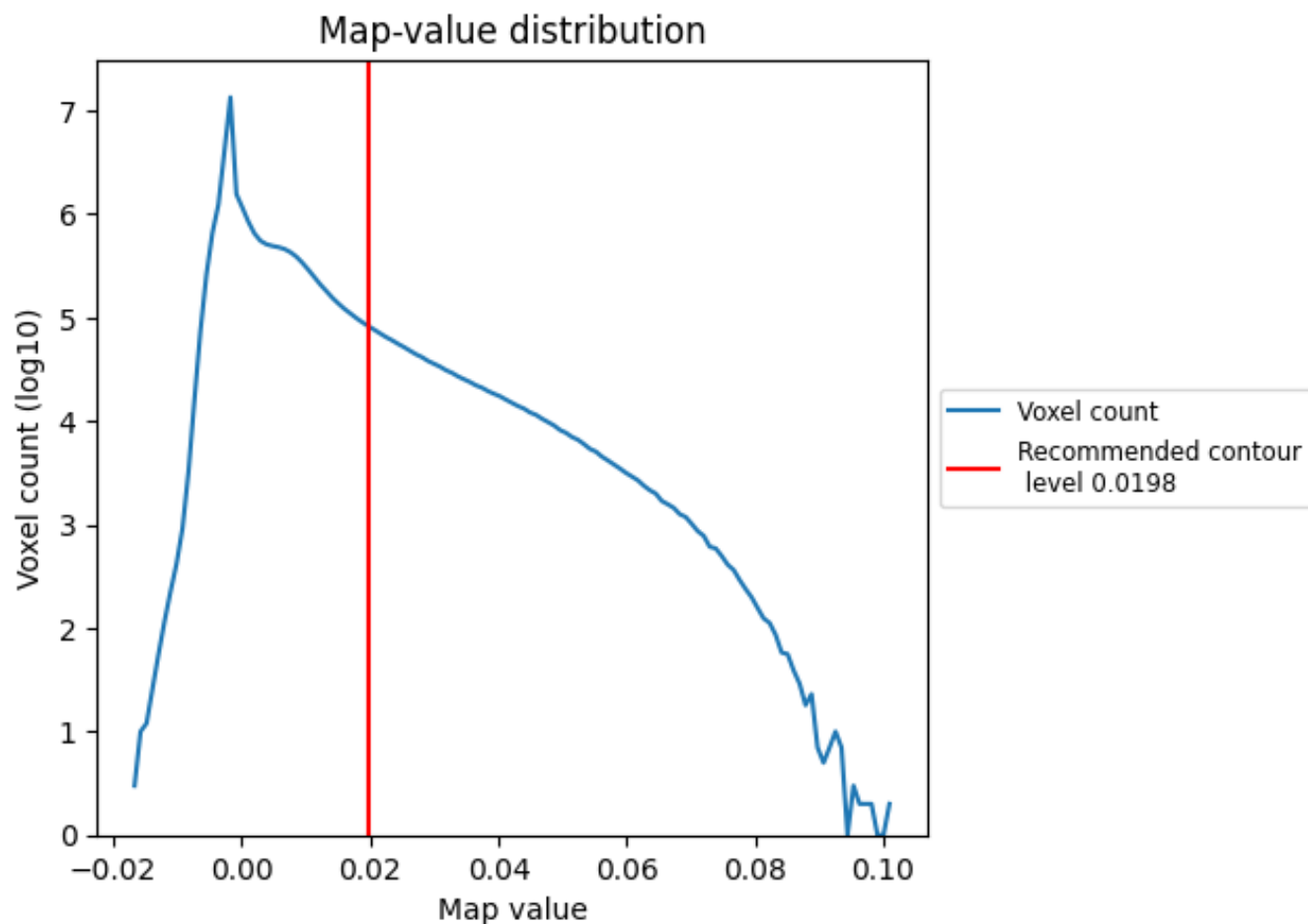
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

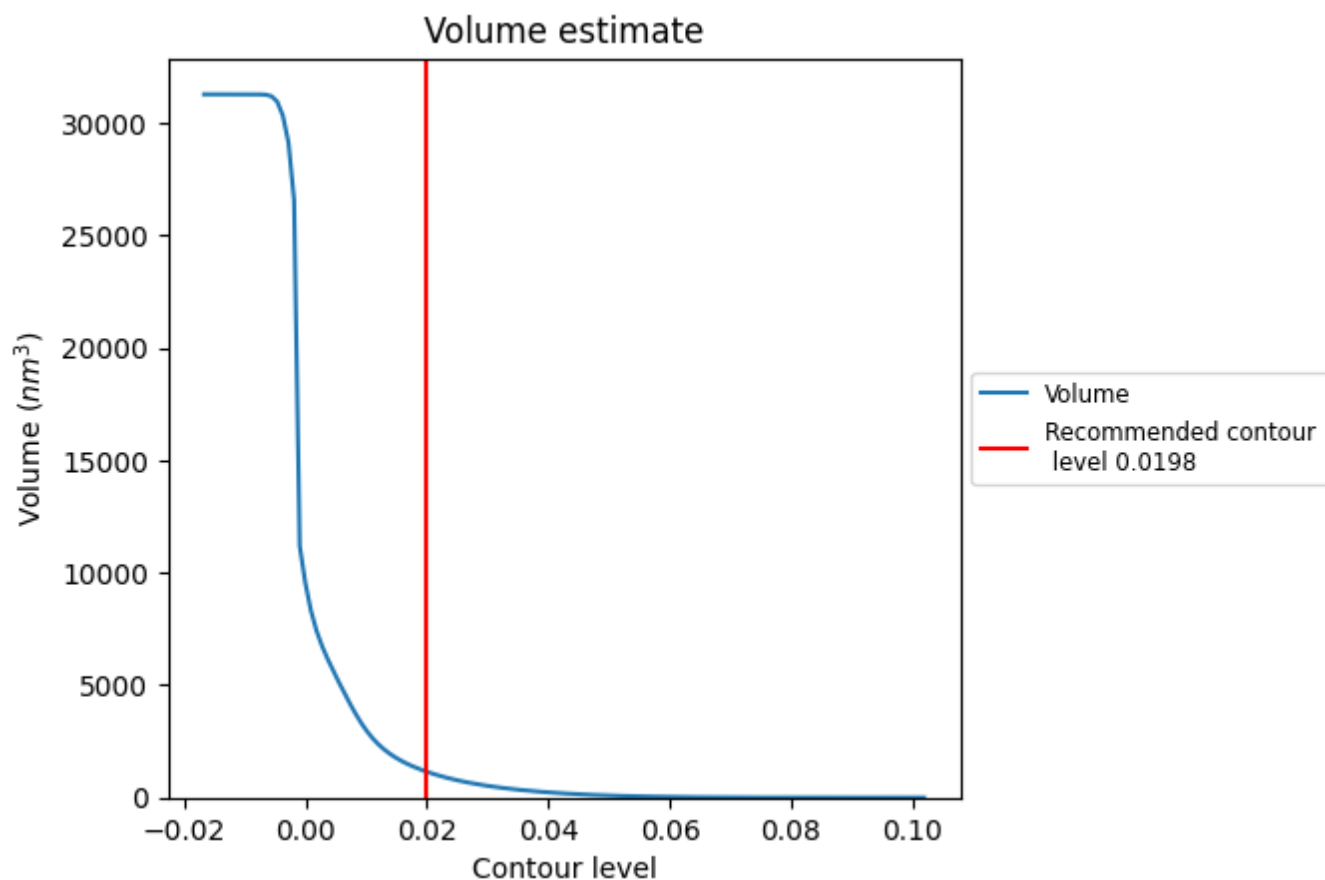
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

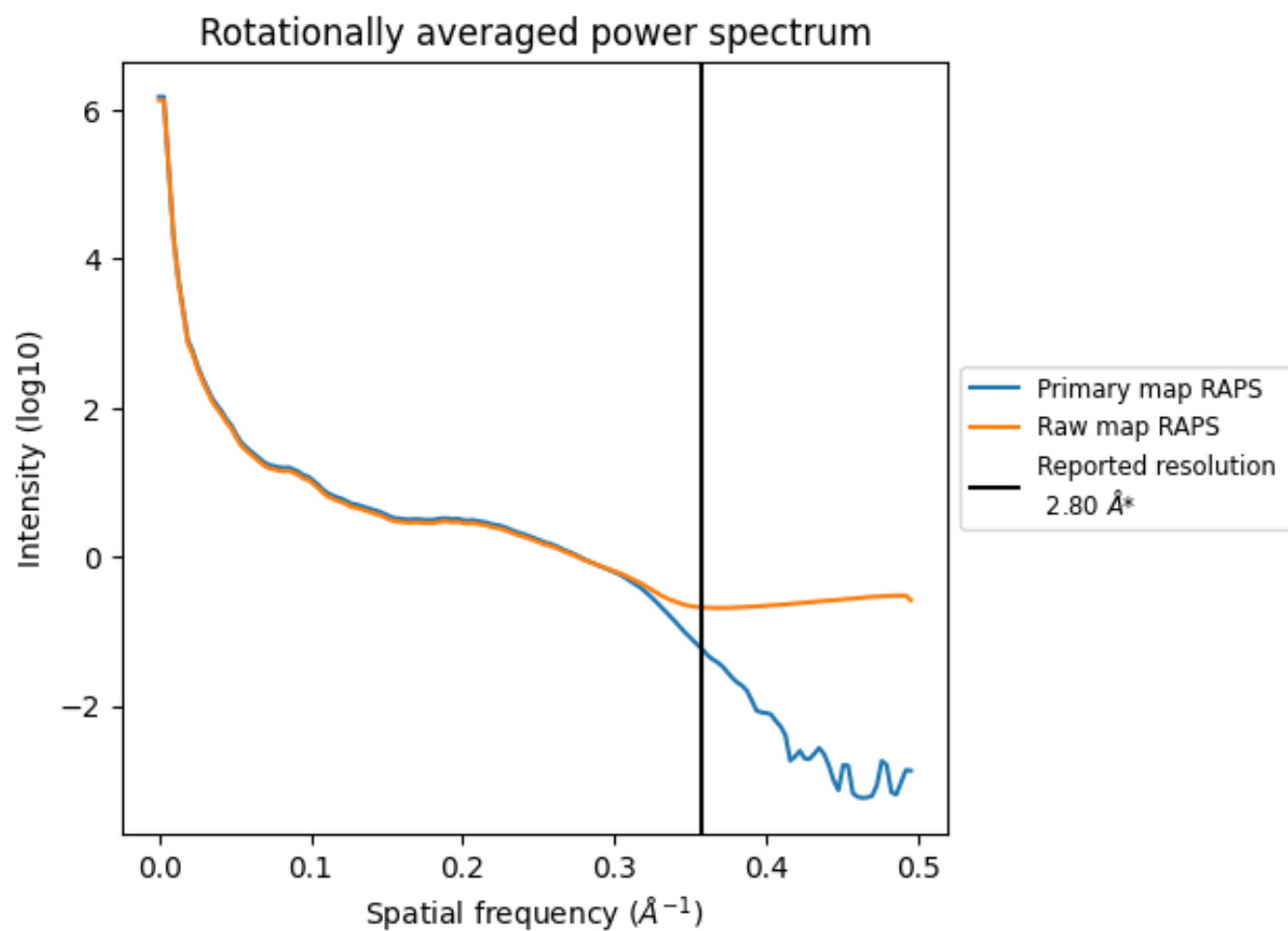
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1165 nm³; this corresponds to an approximate mass of 1052 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

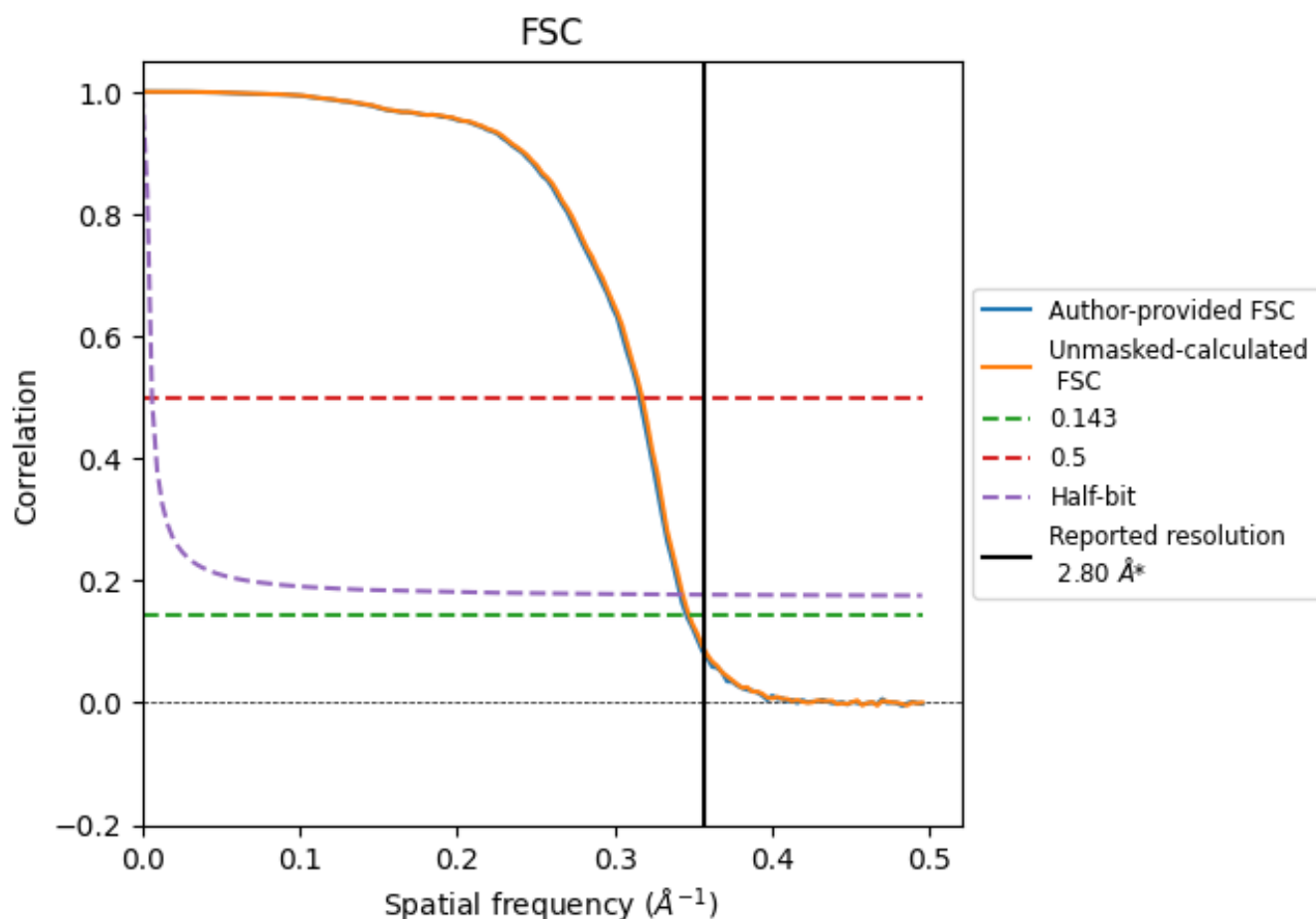


*Reported resolution corresponds to spatial frequency of 0.357 \AA^{-1}

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

8.2 Resolution estimates [i](#)

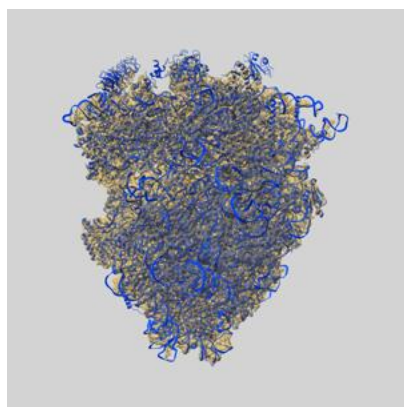
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.89	3.17	2.93
Unmasked-calculated*	2.88	3.15	2.91

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

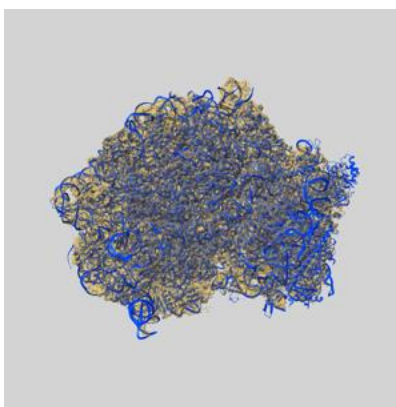
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-53310 and PDB model 9QQP. Per-residue inclusion information can be found in section [3](#) on page [21](#).

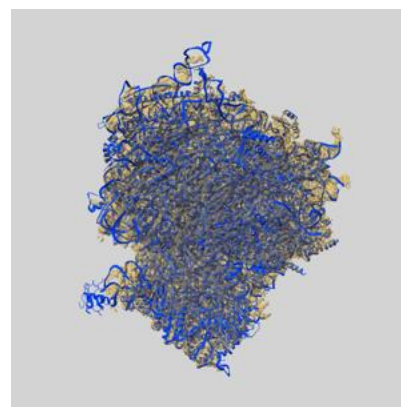
9.1 Map-model overlay [i](#)



X



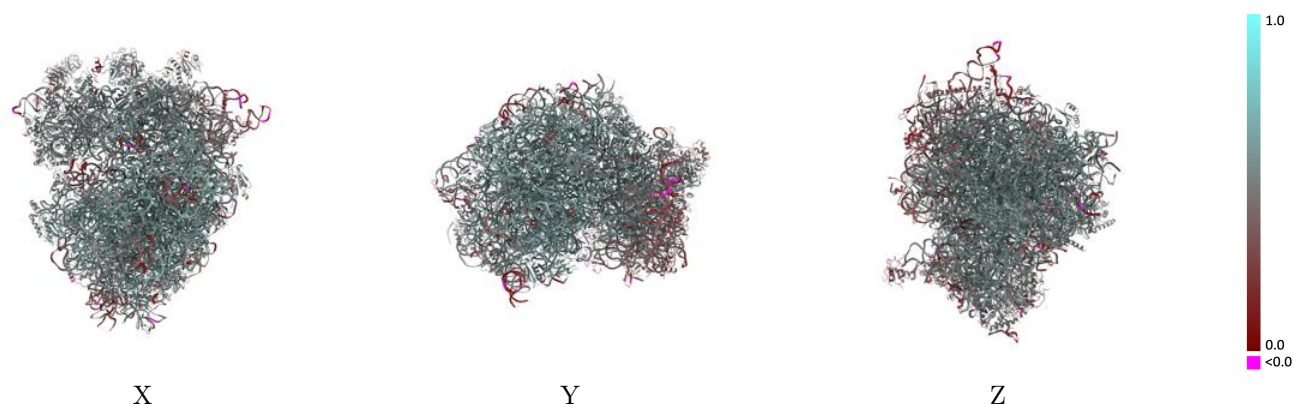
Y



Z

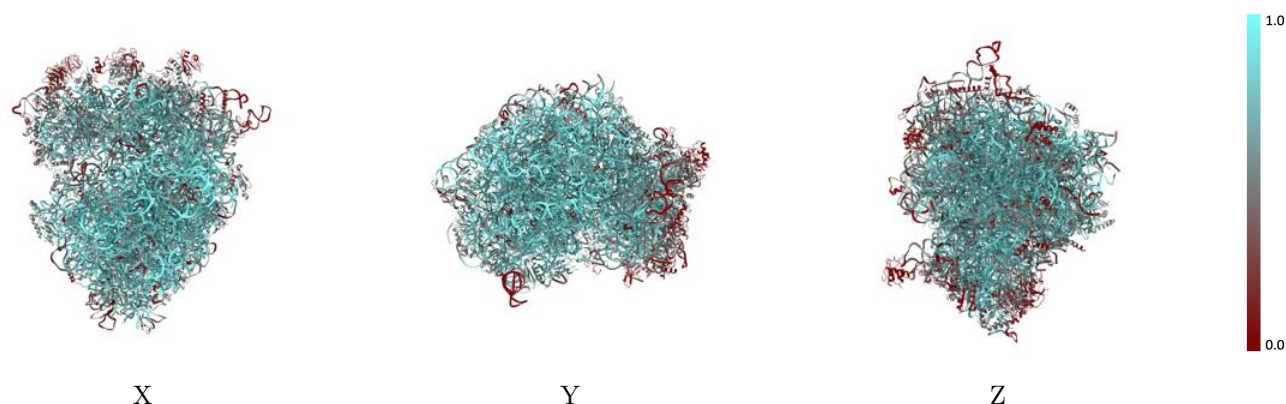
The images above show the 3D surface view of the map at the recommended contour level 0.0198 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



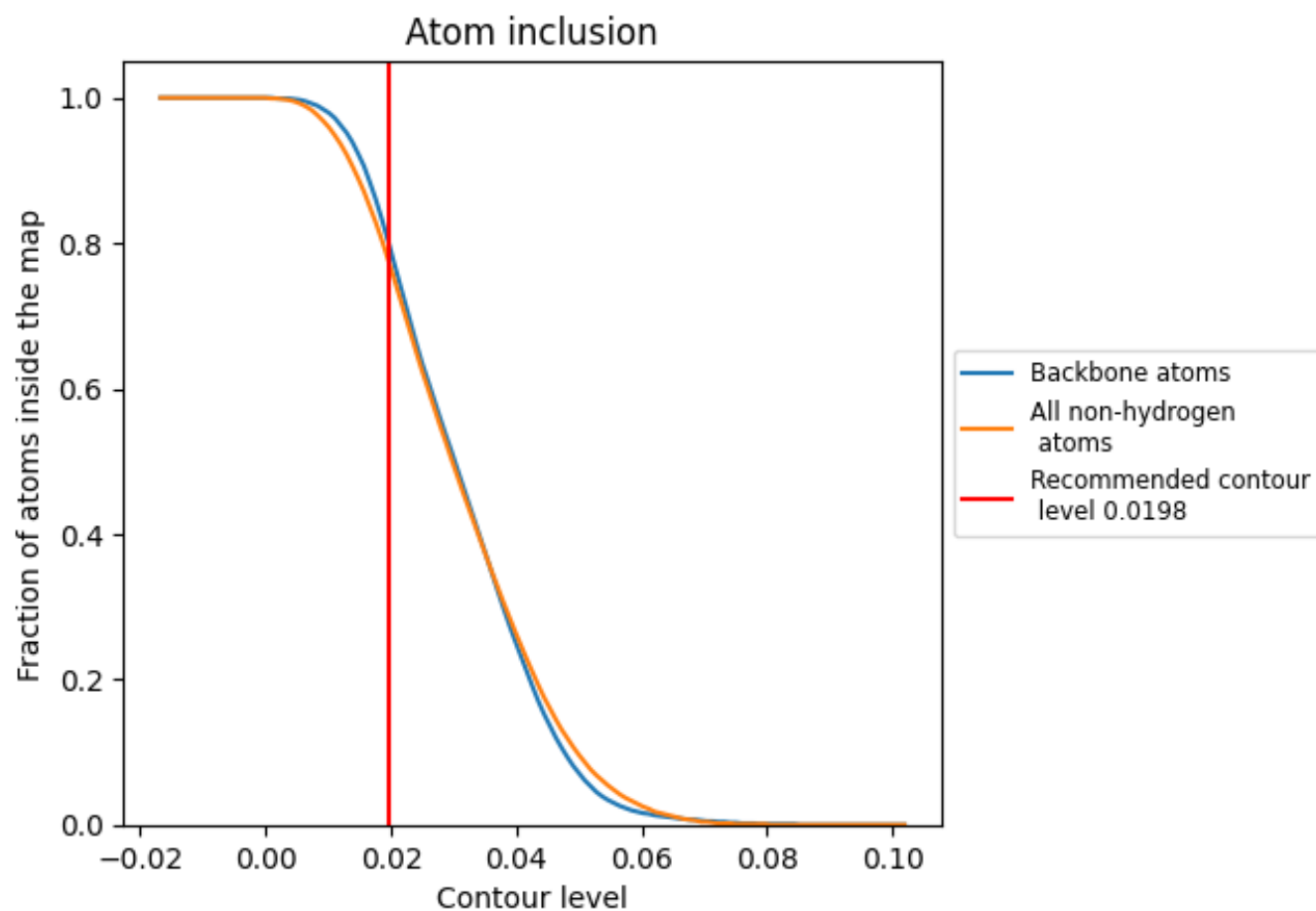
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0198).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 80% of all backbone atoms, 77% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (0.0198) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7710	 0.5280
A1	 0.8210	 0.5550
A2	 0.8760	 0.5480
A3	 0.5920	 0.4810
B1	 0.6540	 0.5270
B2	 0.9590	 0.5930
B3	 0.5480	 0.4640
Bv	 0.6090	 0.4090
Bx	 0.9050	 0.5370
By	 0.3640	 0.2960
C1	 0.7000	 0.5520
C2	 0.9000	 0.5570
C3	 0.3600	 0.4380
D1	 0.7970	 0.5620
D2	 0.8970	 0.5980
D3	 0.4520	 0.5310
E1	 0.6530	 0.4970
E2	 0.7960	 0.5660
E3	 0.6850	 0.4880
F1	 0.7430	 0.5420
F2	 0.8420	 0.5750
F3	 0.7390	 0.5420
G1	 0.7420	 0.5560
G2	 0.6840	 0.5360
G3	 0.5060	 0.5080
H1	 0.9200	 0.5980
H2	 0.6560	 0.5300
H3	 0.7070	 0.4840
I2	 0.8450	 0.5780
I3	 0.1770	 0.4210
J2	 0.8570	 0.5810
J3	 0.6440	 0.5330
K2	 0.8590	 0.5840
K3	 0.3530	 0.3680
L2	 0.7670	 0.5340















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Chain	Atom inclusion	Q-score
L3	 0.4390	 0.3900
M2	 0.8440	 0.5810
M3	 0.0000	 0.3110
N2	 0.7950	 0.5520
N3	 0.6400	 0.5110
O2	 0.5540	 0.4720
O3	 0.6400	 0.5210
P2	 0.8520	 0.5780
P3	 0.7060	 0.5420
Q2	 0.8280	 0.5590
Q3	 0.2240	 0.3220
R2	 0.7680	 0.5550
R3	 0.4390	 0.4590
S2	 0.7490	 0.5470
S3	 0.4690	 0.4840
T2	 0.6980	 0.5450
T3	 0.4230	 0.3990
U2	 0.8610	 0.5940
V2	 0.6070	 0.4730
W2	 0.7020	 0.5410
X2	 0.7490	 0.5470
Y2	 0.8600	 0.5820
Z2	 0.8820	 0.5960
a2	 0.8430	 0.5760
b2	 0.7350	 0.5440
c2	 0.6910	 0.5260
d2	 0.9290	 0.5950
e2	 0.5410	 0.4880
f2	 0.8840	 0.5760
g2	 0.7880	 0.5600
h2	 0.8420	 0.5170
i2	 0.8000	 0.5640
j2	 0.8240	 0.5760
k2	 0.8050	 0.5710
m2	 0.8250	 0.5150
n2	 0.8290	 0.4750
o2	 0.4200	 0.4770
p2	 0.5990	 0.5160
q2	 0.4440	 0.4580
r2	 0.4190	 0.4120
s2	 0.5550	 0.4900
t2	 0.2640	 0.4340

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Chain	Atom inclusion	Q-score
u2	 0.6150	 0.4770
v2	 0.3440	 0.3750
w2	 0.6380	 0.4860
x2	 0.5480	 0.4670
y2	 0.5210	 0.4650
z2	 0.3130	 0.4140