



wwPDB EM Validation Summary Report ⓘ

Nov 3, 2024 – 08:48 pm GMT

PDB ID : 8BHF
EMDB ID : EMD-16052
Title : Cryo-EM structure of stalled rabbit 80S ribosomes in complex with human CCR4-NOT and CNOT4
Authors : Absmeier, E.; Chandrasekaran, V.; O'Reilly, F.J.; Stowell, J.A.W.; Rappsilber, J.; Passmore, L.A.
Deposited on : 2022-10-31
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.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

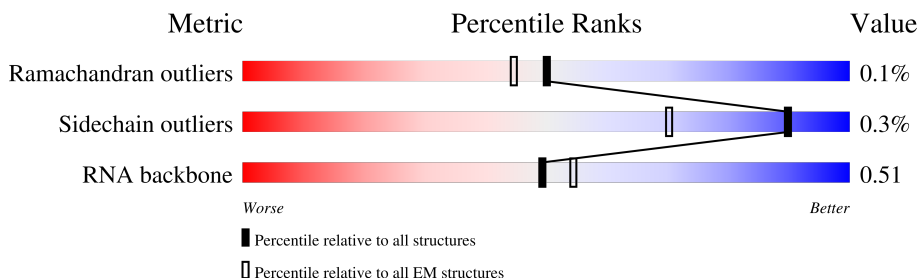
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A1	203	
2	B1	199	
3	C1	153	
4	D1	187	
5	E1	180	
6	F1	176	
7	G1	159	
8	H1	99	

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Mol	Chain	Length	Quality of chain
9	I1	139	9% 99%
10	J1	106	42% 99%
11	K1	118	100%
12	L1	134	98%
13	M1	135	8% 99%
14	N1	147	99%
15	O1	116	21% 86% 10%
16	P1	98	7% 99%
17	Q1	107	7% 98%
18	R1	128	98%
19	S1	109	97%
20	T1	114	10% 99%
21	U1	122	99%
22	V1	102	6% 100%
23	W1	86	100%
24	X1	69	20% 100%
25	Y1	50	6% 100%
26	Z1	52	98%
27	a1	25	100%
28	b1	104	99%
29	c1	91	7% 99%
30	d1	124	99%
31	e1	196	98%
32	f1	153	99%
33	l1	206	100% 97%

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Mol	Chain	Length	Quality of chain
34	m1	3	
35	n1	236	
36	21	76	
37	11	5	
38	A2	5051	
39	B2	119	
40	C2	156	
41	A3	1697	
42	B3	217	
43	C3	213	
44	D3	221	
45	E3	228	
46	F3	262	
47	G3	191	
48	H3	237	
49	I3	189	
50	J3	206	
51	K3	185	
52	L3	96	
53	M3	151	
54	N3	117	
55	O3	149	
56	P3	136	
57	Q3	129	
58	R3	142	

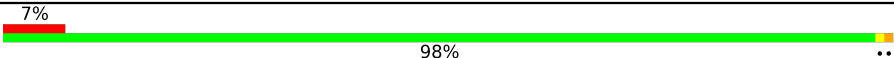
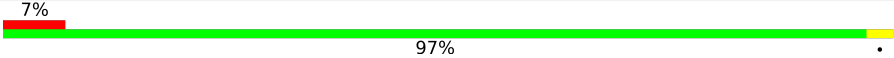
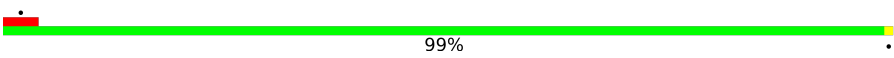
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Mol	Chain	Length	Quality of chain
59	S3	132	55% 100%
60	T3	144	46% 99%
61	U3	141	35% 98%
62	V3	100	53% 100%
63	W3	83	31% 99%
64	X3	129	12% 99%
65	Y3	141	23% 96%
66	Z3	124	56% 97%
67	a3	75	10% 100%
68	b3	101	34% 100%
69	c3	83	35% 100%
70	d3	62	31% 100%
71	e3	55	37% 100%
72	f3	57	94% 97%
73	g3	68	79% 97%
74	h3	313	98%
75	j3	248	99%
76	k3	394	98%
77	l3	362	100%
78	m3	293	9%
79	n3	251	86% 14%
80	o3	225	18% 97%
81	p3	240	5% 99%
82	q3	190	95%
83	r3	213	

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Mol	Chain	Length	Quality of chain
84	s3	170	 7% 98% ••
85	t3	210	 7% 97% •
86	u3	138	 • 99% •

2 Entry composition

There are 88 unique types of molecules in this entry. The entry contains 219017 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 Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A1	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 2 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B1	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 3 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C1	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 4 is a protein called Ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D1	187	Total	C	N	O	S	0	0
			1515	946	315	250	4		

- Molecule 5 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E1	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E1	38	ARG	HIS	conflict	UNP G1TYL6
E1	151	ARG	HIS	conflict	UNP G1TYL6

- Molecule 6 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F1	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

- Molecule 7 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G1	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 8 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H1	99	Total	C	N	O	S	0	0
			809	519	141	147	2		

- Molecule 9 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I1	139	Total	C	N	O	S	0	0
			1034	648	199	182	5		

- Molecule 10 is a protein called TRASH domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J1	106	Total	C	N	O	S	0	0
			860	538	174	144	4		

- Molecule 11 is a protein called Ribosomal protein L23/L25 N-terminal domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K1	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 12 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L1	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 13 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M1	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 14 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N1	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

- Molecule 15 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O1	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

- Molecule 16 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P1	98	Total	C	N	O	S	0	0
			761	481	134	140	6		

- Molecule 17 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q1	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 18 is a protein called Ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R1	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 19 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S1	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 20 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T1	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 21 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U1	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 22 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V1	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V1	31	GLY	ARG	conflict	UNP G1TBH2
V1	58	MET	ILE	conflict	UNP G1TBH2

- Molecule 23 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W1	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 24 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X1	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X1	24	LYS	ASN	conflict	UNP G1U001

- Molecule 25 is a protein called 60S ribosomal protein L39-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y1	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 26 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z1	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 27 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	a1	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 28 is a protein called Ribosomal protein L36a like.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b1	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 29 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c1	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 30 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d1	124	Total	C	N	O	S	0	0
			994	616	205	167	6		

- Molecule 31 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	e1	196	Total	C	N	O	S	0	0
			1507	959	263	276	9		

- Molecule 32 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f1	153	Total	C	N	O	S	0	0
			1160	722	218	217	3		

- Molecule 33 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	l1	206	Total	C	N	O	S	0	0
			1654	1058	297	291	8		

- Molecule 34 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	m1	3	Total	C	N	O	P	0	0
			62	28	9	22	3		

- Molecule 35 is a protein called CCR4-NOT transcription complex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	n1	236	Total	C	N	O	S	0	0
			1948	1209	346	387	6		

- Molecule 36 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	21	76	Total	C	N	O	P	0	0
			1620	723	287	534	76		

- Molecule 37 is a protein called nascent chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	11	5	Total	C	N	O	0	0
			34	23	5	6		

- Molecule 38 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	A2	3603	Total	C	N	O	P	0	0
			77264	34409	14151	25101	3603		

- Molecule 39 is a RNA chain called 5S ribosomal RNA.

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

- Molecule 40 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	C2	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 41 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	A3	1697	Total	C	N	O	P	0	0
			36229	16171	6507	11855	1696		

- Molecule 42 is a protein called 40S_SA_C domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	B3	217	Total	C	N	O	S	0	0
			1710	1086	300	316	8		

- Molecule 43 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	C3	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 44 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	D3	221	Total	C	N	O	S	0	0
			1716	1111	295	301	9		

- Molecule 45 is a protein called Ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	E3	228	Total	C	N	O	S	0	0
			1768	1126	318	316	8		

- Molecule 46 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	F3	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F3	25	GLY	SER	conflict	UNP G1TK17
F3	51	ARG	LYS	conflict	UNP G1TK17
F3	78	THR	ALA	conflict	UNP G1TK17
F3	156	VAL	MET	conflict	UNP G1TK17

- Molecule 47 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	G3	185	Total	C	N	O	S	0	0
			1471	921	277	266	7		

- Molecule 48 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	H3	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 49 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	I3	185	Total	C	N	O	S	0	0
			1488	952	271	264	1		

- Molecule 50 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	J3	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J3	47	ARG	GLY	variant	UNP G1TJW1

- Molecule 51 is a protein called Ribosomal protein S9 (Predicted).

Mol	Chain	Residues	Atoms					AltConf	Trace
51	K3	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 52 is a protein called Plectin/S10 N-terminal domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	L3	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 53 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	M3	143	Total	C	N	O	S	0	0
			1175	749	222	198	6		

- Molecule 54 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	N3	117	Total	C	N	O	S	0	0
			908	570	161	169	8		

- Molecule 55 is a protein called ribosomal protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	O3	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 56 is a protein called Ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	P3	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Q3	129	Total	C	N	O	S	0	0
			1058	670	201	180	7		

- Molecule 58 is a protein called Ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	R3	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
59	S3	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	T3	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
61	U3	141	Total	C	N	O	S	0	0
			1097	688	211	195	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U3	119	GLY	TRP	conflict	UNP G1TN62

- Molecule 62 is a protein called Ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	V3	100	Total	C	N	O	S	0	0
			795	498	152	141	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
63	W3	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 64 is a protein called Ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	X3	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 65 is a protein called Ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Y3	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 66 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Z3	124	Total	C	N	O	S	0	0
			1011	640	198	168	5		

- Molecule 67 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	a3	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 68 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	b3	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

- Molecule 69 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	c3	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 70 is a protein called Ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	d3	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 71 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	e3	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 72 is a protein called Ubiquitin-like domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	f3	57	Total	C	N	O	S	0	0
			457	282	101	73	1		

- Molecule 73 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	g3	68	Total	C	N	O	S	0	0
			555	351	103	94	7		

- Molecule 74 is a protein called Ribosomal protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	h3	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 75 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	j3	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 76 is a protein called Ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	k3	394	Total	C	N	O	S	0	0
			3172	2020	597	542	13		

- Molecule 77 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	l3	362	Total	C	N	O	S	0	0
			2883	1812	577	480	14		

- Molecule 78 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	m3	293	Total	C	N	O	S	0	0
			2391	1512	438	427	14		

- Molecule 79 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	n3	216	Total	C	N	O	S	0	0
			1729	1115	329	282	3		

- Molecule 80 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	o3	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

- Molecule 81 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	p3	233	Total	C	N	O	S	0	0
			1879	1199	361	315	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
p3	244	GLY	CYS	conflict	UNP G1STW0

- Molecule 82 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	q3	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 83 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	r3	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 84 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	s3	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 85 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	t3	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
t3	74	ARG	HIS	conflict	UNP G1TKB3
t3	190	ARG	HIS	conflict	UNP G1TKB3

- Molecule 86 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	u3	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 87 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
87	C1	1	Total	Mg	0
			1	1	
87	I1	1	Total	Mg	0
			1	1	
87	N1	1	Total	Mg	0
			1	1	
87	T1	1	Total	Mg	0
			1	1	
87	A2	189	Total	Mg	0
			189	189	
87	B2	6	Total	Mg	0
			6	6	
87	C2	4	Total	Mg	0
			4	4	
87	A3	69	Total	Mg	0
			69	69	
87	M3	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
87	j3	1	Total 1	Mg 1	0
87	r3	1	Total 1	Mg 1	0

- Molecule 88 is ZINC ION (three-letter code: ZN) (formula: Zn).

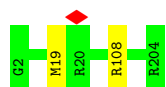
Mol	Chain	Residues	Atoms		AltConf
88	T1	1	Total 1	Zn 1	0
88	W1	1	Total 1	Zn 1	0
88	Z1	1	Total 1	Zn 1	0
88	b1	1	Total 1	Zn 1	0
88	c1	1	Total 1	Zn 1	0
88	b3	1	Total 1	Zn 1	0
88	e3	1	Total 1	Zn 1	0

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: Ribosomal protein L15

Chain A1:  99%



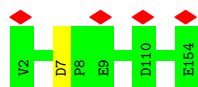
- Molecule 2: 60S ribosomal protein L13a

Chain B1:  100%



- Molecule 3: 60S ribosomal protein L17

Chain C1:  99%



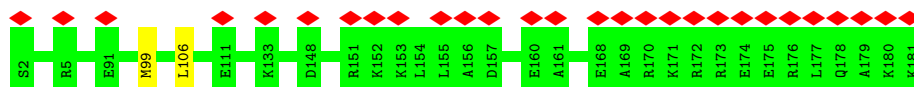
- Molecule 4: Ribosomal protein L18

Chain D1:  98%

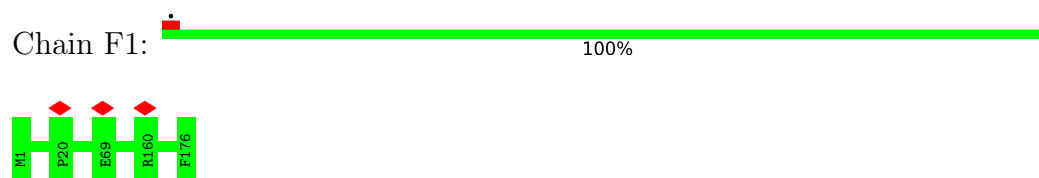


- Molecule 5: Ribosomal protein L19

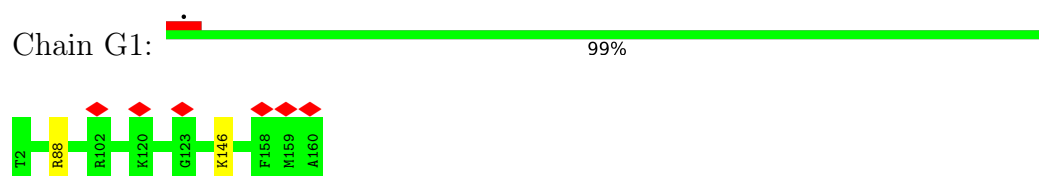
Chain E1:  16% 99%



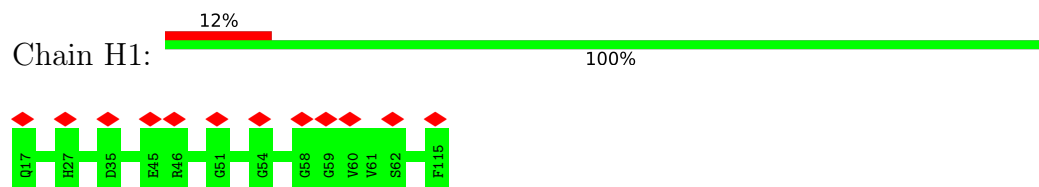
- Molecule 6: 60S ribosomal protein L18a



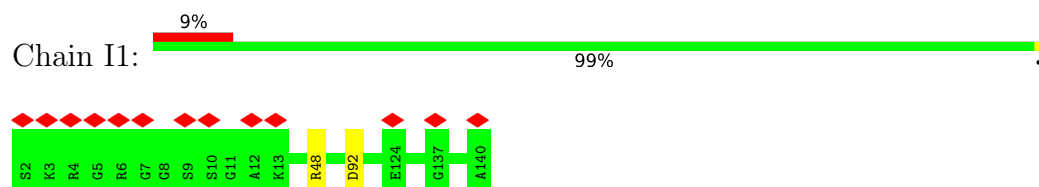
- Molecule 7: 60S ribosomal protein L21



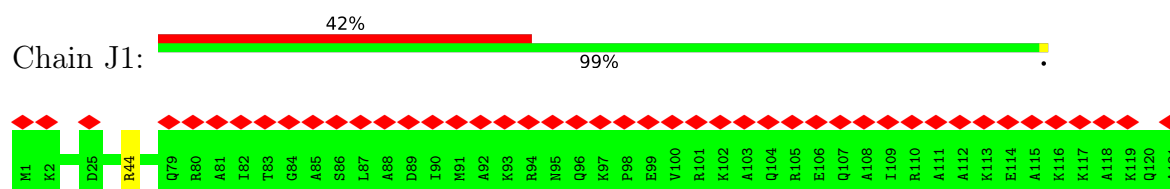
- Molecule 8: 60S ribosomal protein L22



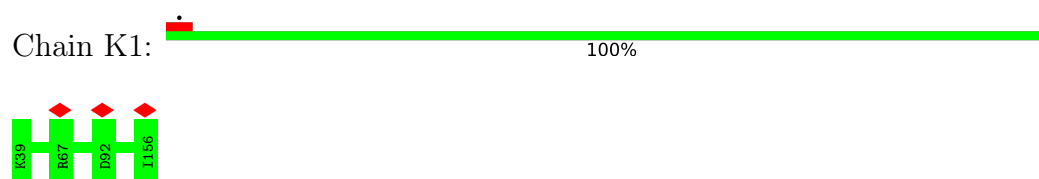
- Molecule 9: 60S ribosomal protein L23



- Molecule 10: TRASH domain-containing protein

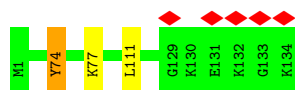


- Molecule 11: Ribosomal protein L23/L25 N-terminal domain-containing protein

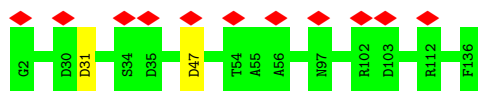


- Molecule 12: Ribosomal protein L26

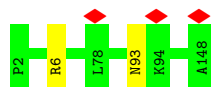




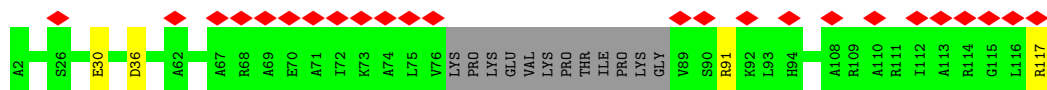
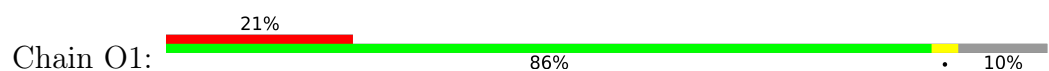
- Molecule 13: 60S ribosomal protein L27



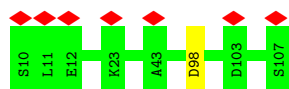
- Molecule 14: 60S ribosomal protein L27a



- Molecule 15: 60S ribosomal protein L29



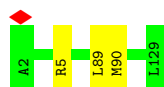
- Molecule 16: 60S ribosomal protein L30



- Molecule 17: 60S ribosomal protein L31

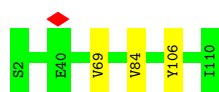


- Molecule 18: Ribosomal protein L32



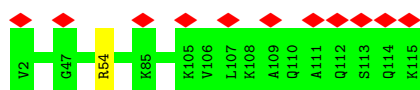
- Molecule 19: 60S ribosomal protein L35a

Chain S1:  97%



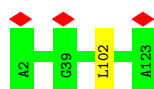
- Molecule 20: 60S ribosomal protein L34

Chain T1:  99%



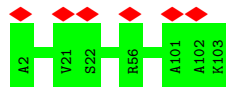
- Molecule 21: 60S ribosomal protein L35

Chain U1:  99%



- Molecule 22: 60S ribosomal protein L36

Chain V1:  100%



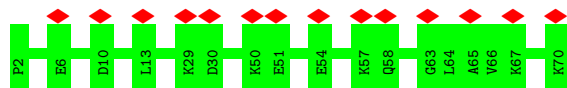
- Molecule 23: Ribosomal protein L37

Chain W1:  100%

There are no outlier residues recorded for this chain.

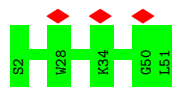
- Molecule 24: 60S ribosomal protein L38

Chain X1:  100%



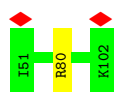
- Molecule 25: 60S ribosomal protein L39-like

Chain Y1:  100%



- Molecule 26: Ubiquitin-60S ribosomal protein L40

Chain Z1:  98%



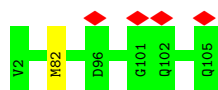
- Molecule 27: 60S ribosomal protein L41

Chain a1:  100%

There are no outlier residues recorded for this chain.

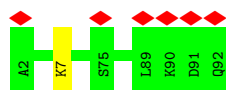
- Molecule 28: Ribosomal protein L36a like

Chain b1:  99%



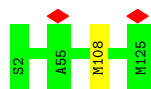
- Molecule 29: 60S ribosomal protein L37a

Chain c1:  99%



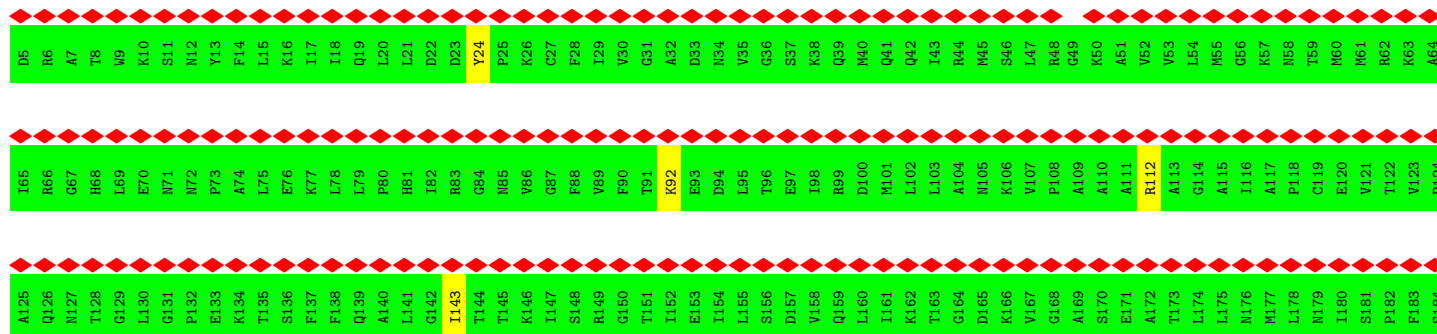
- Molecule 30: 60S ribosomal protein L28

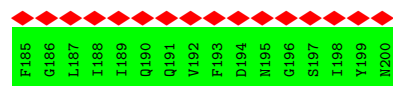
Chain d1:  99%



- Molecule 31: 60S acidic ribosomal protein P0

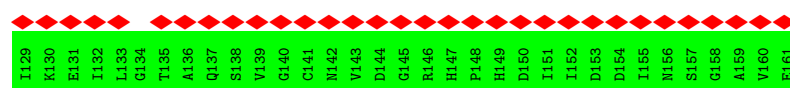
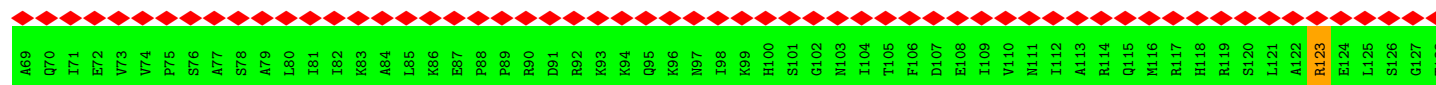
Chain e1:  99%
98%





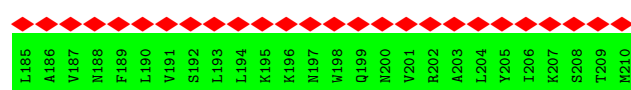
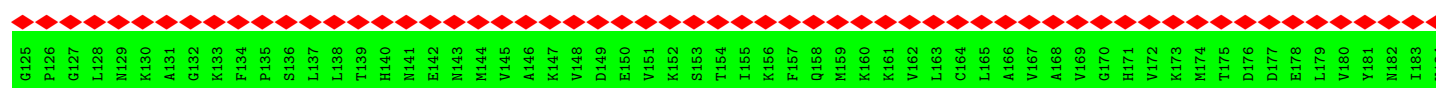
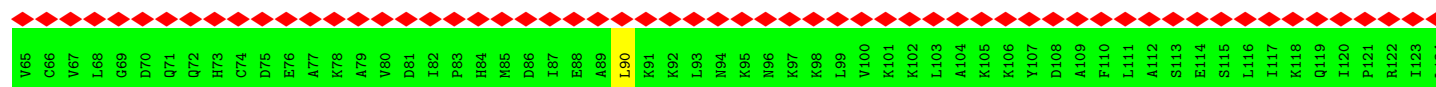
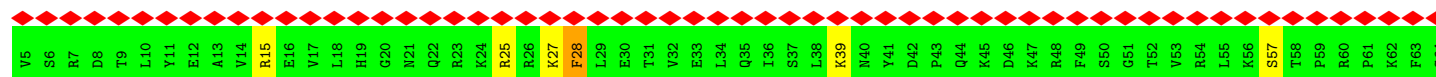
• Molecule 32: 60S ribosomal protein L12

Chain f1: 99%
99%



• Molecule 33: 60S ribosomal protein L10a

Chain l1: 100%
97%



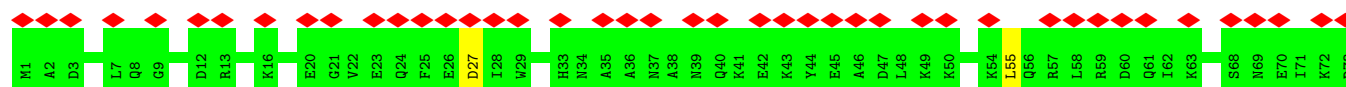
• Molecule 34: mRNA

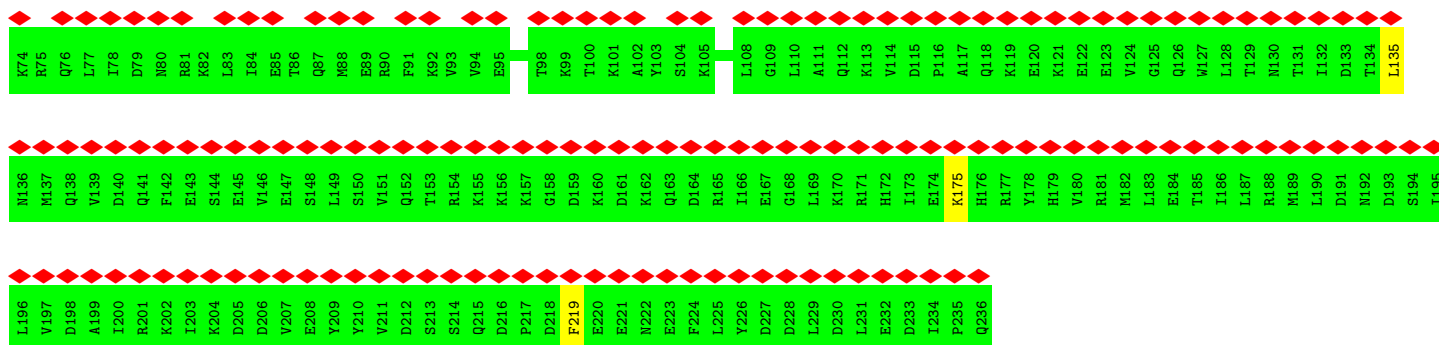
Chain m1: 67%
33%



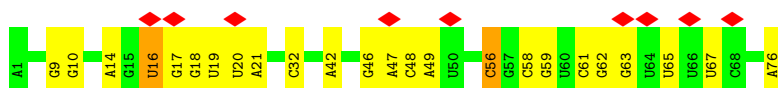
• Molecule 35: CCR4-NOT transcription complex subunit 3

Chain n1: 83%
98%

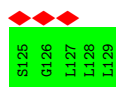




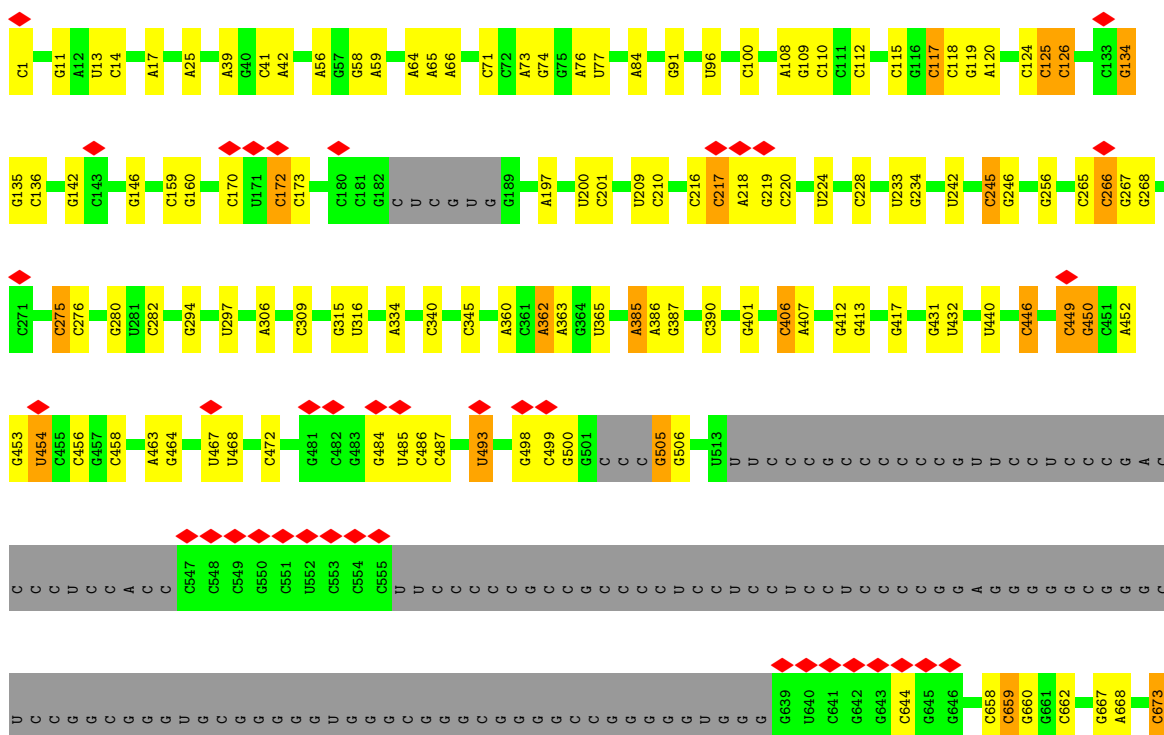
• Molecule 36: P-site tRNA

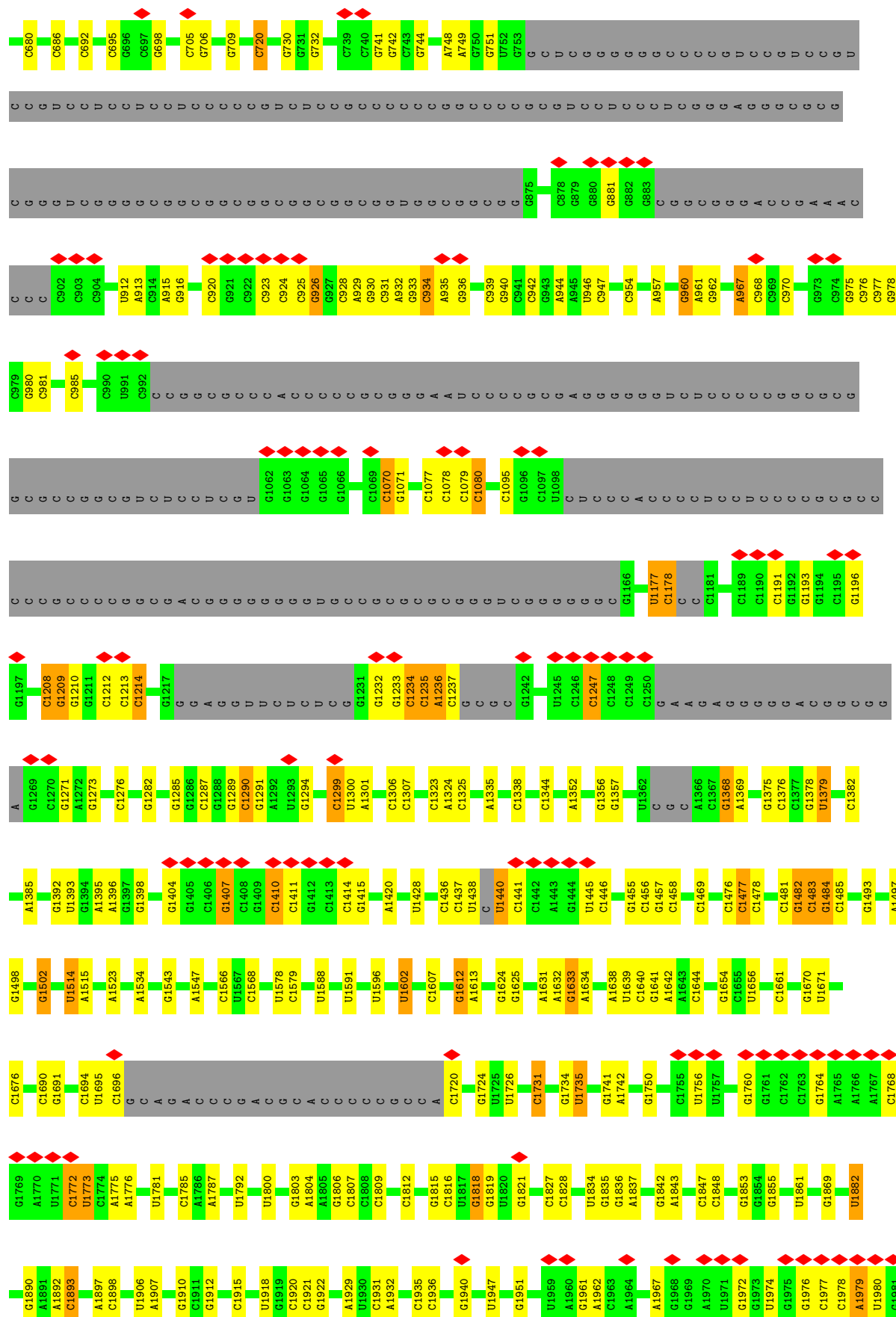


• Molecule 37: nascent chain



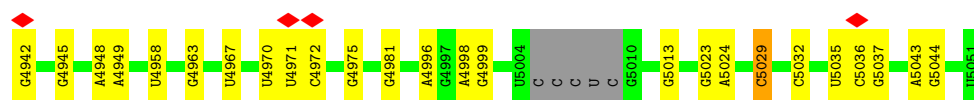
• Molecule 38: 28S ribosomal RNA











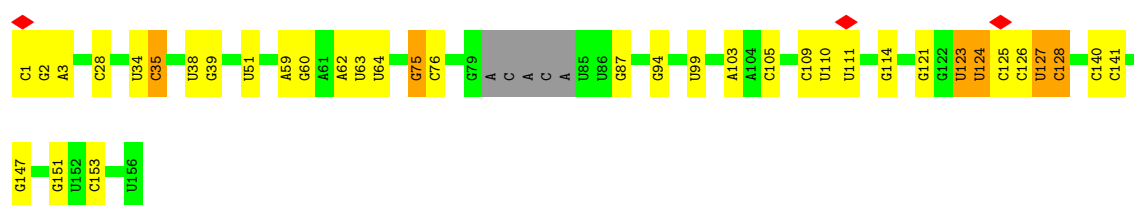
• Molecule 39: 5S ribosomal RNA

Chain B2: 86% 13%



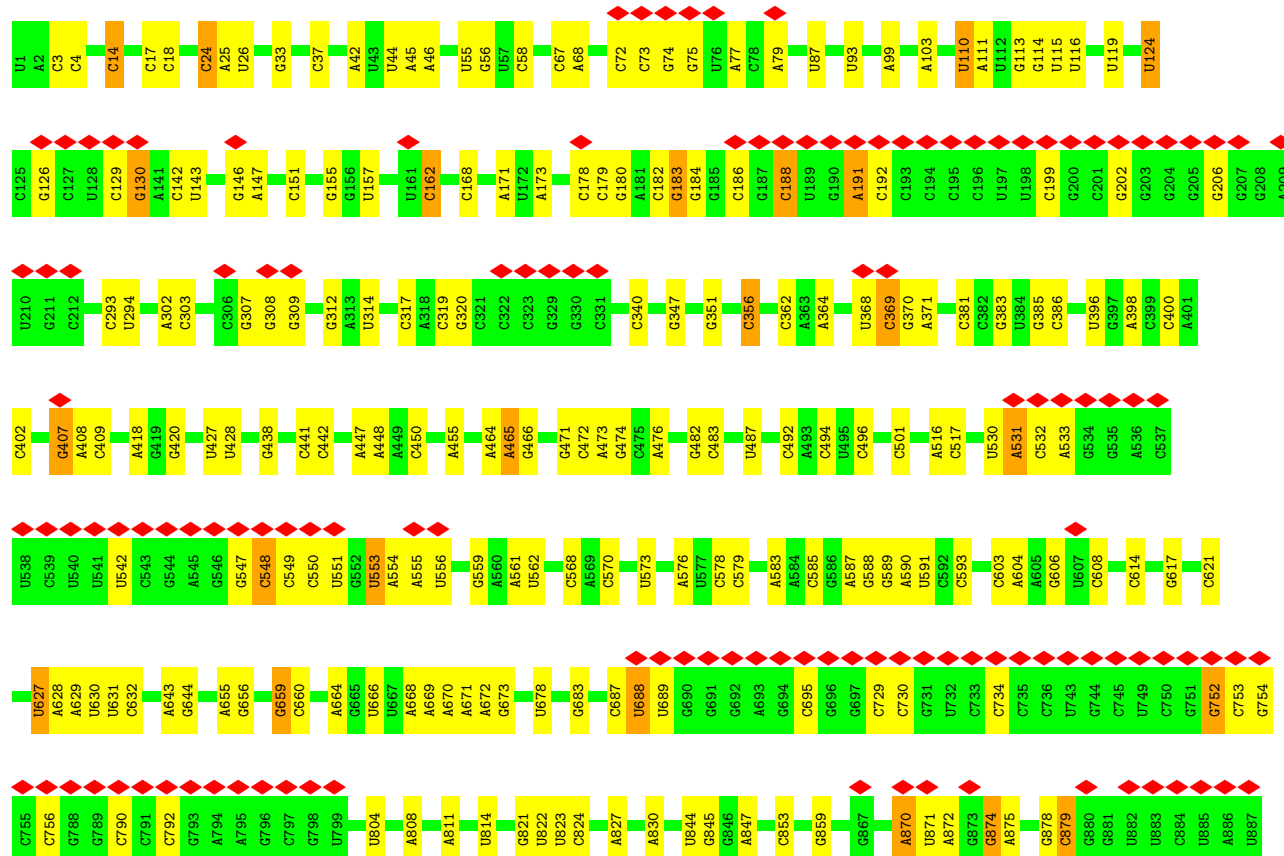
• Molecule 40: 5.8S ribosomal RNA

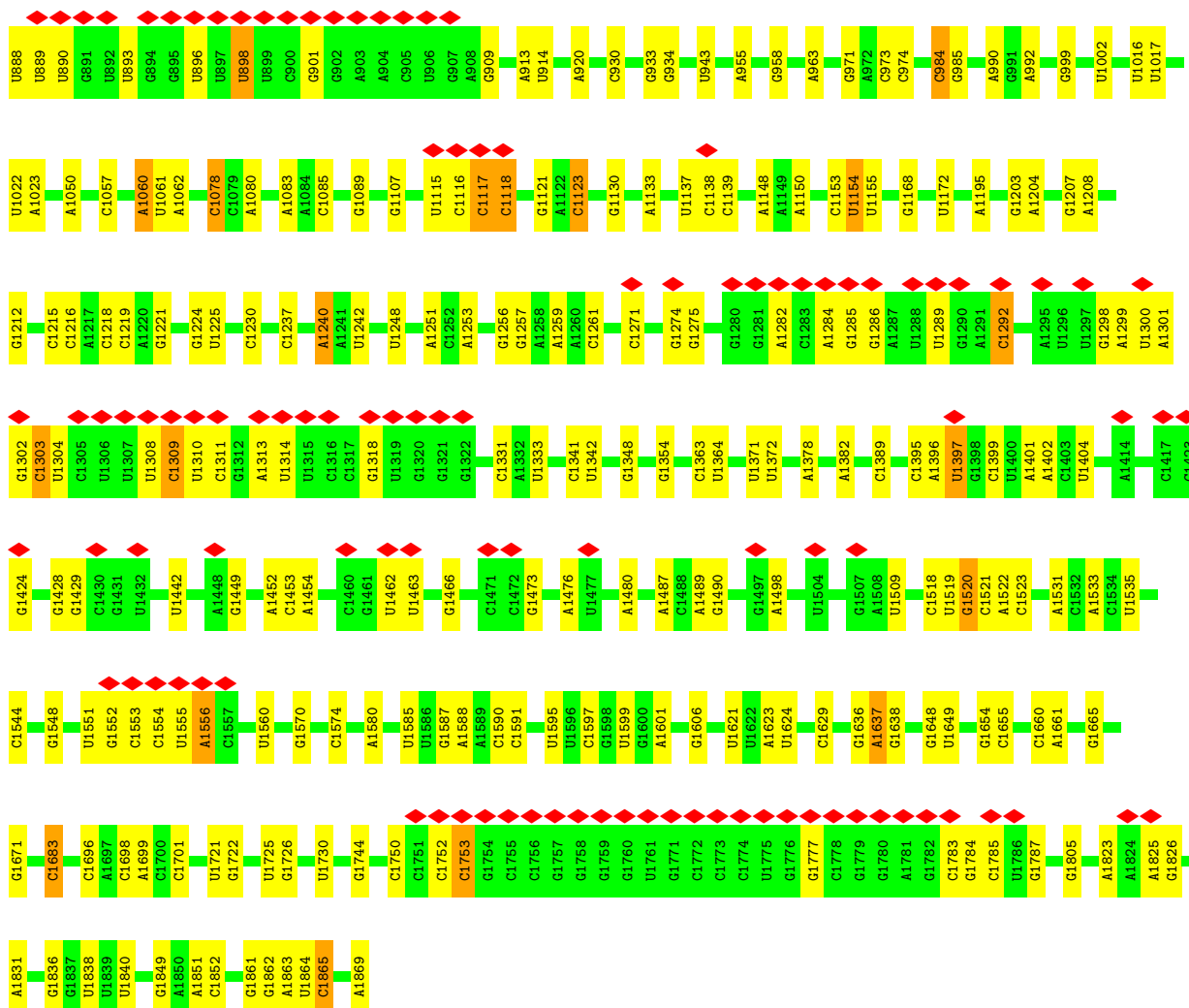
Chain C2: 73% 20%



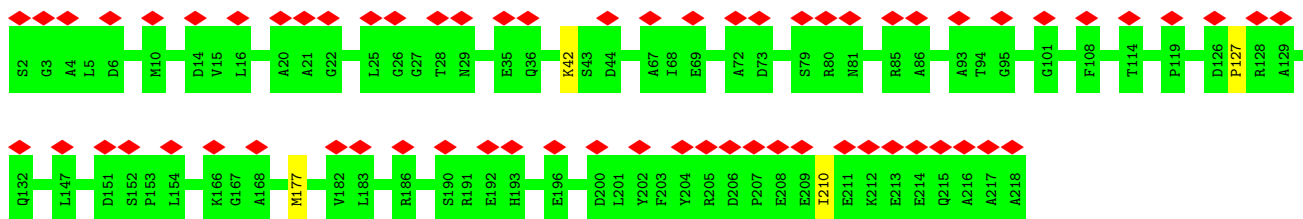
• Molecule 41: 18S ribosomal RNA

Chain A3: 14% 74% 24%

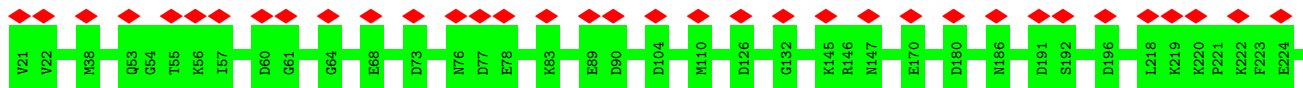


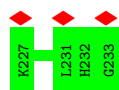


• Molecule 42: 40S_SA_C domain-containing protein

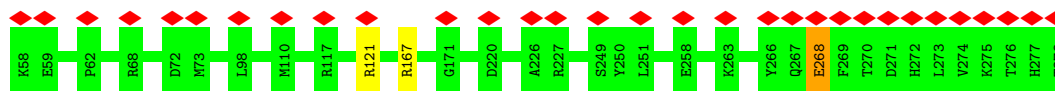


• Molecule 43: 40S ribosomal protein S3a

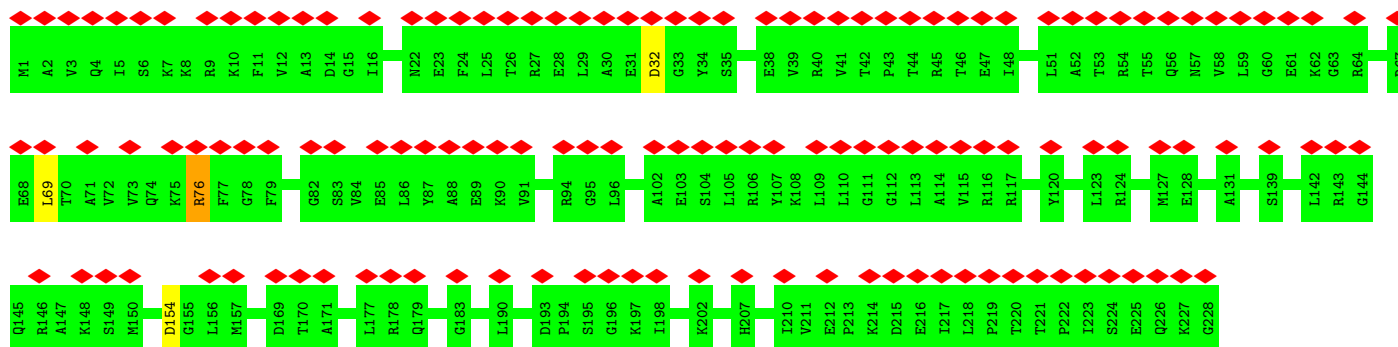




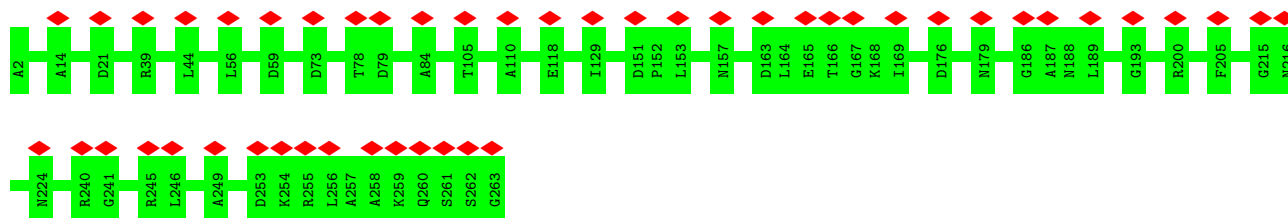
- Molecule 44: 40S ribosomal protein S2



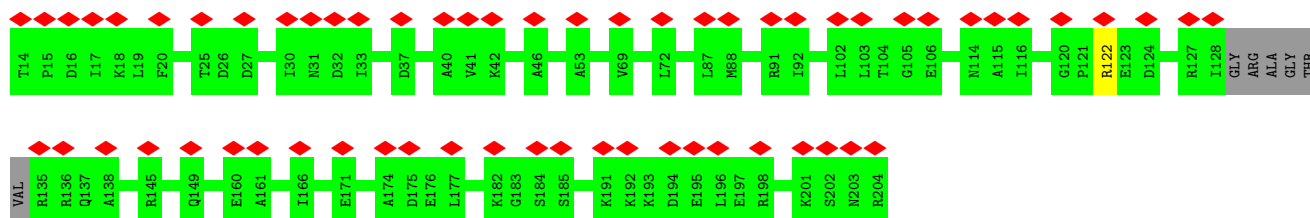
- Molecule 45: Ribosomal protein S3



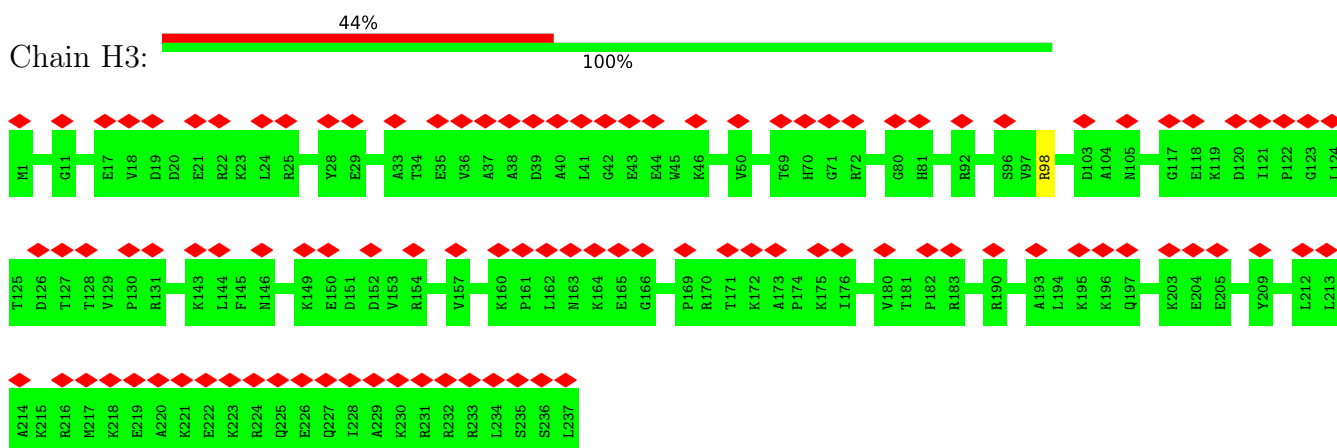
- Molecule 46: 40S ribosomal protein S4



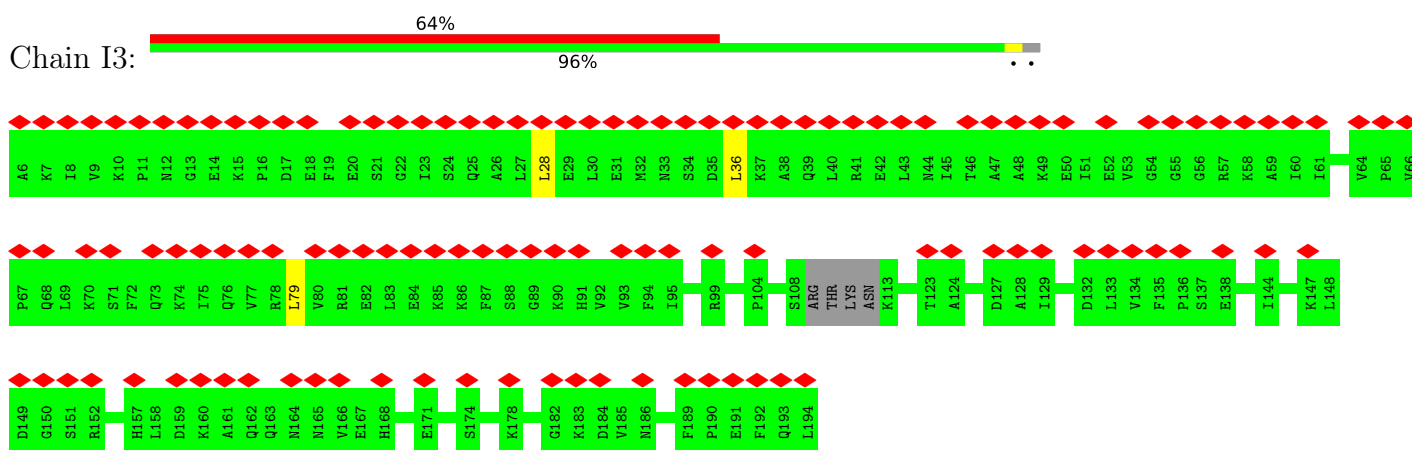
- Molecule 47: Ribosomal protein S5



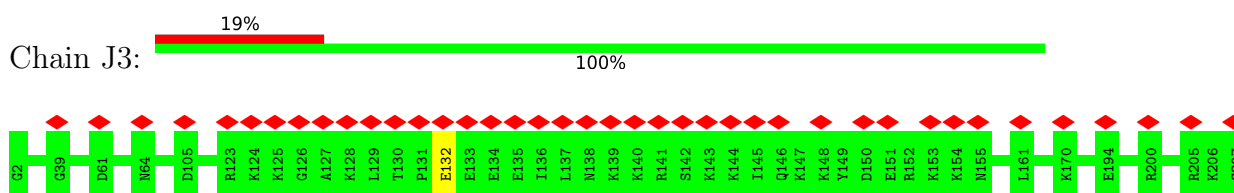
- Molecule 48: 40S ribosomal protein S6



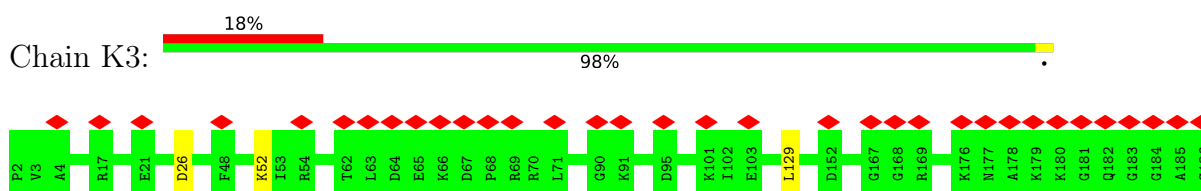
• Molecule 49: 40S ribosomal protein S7



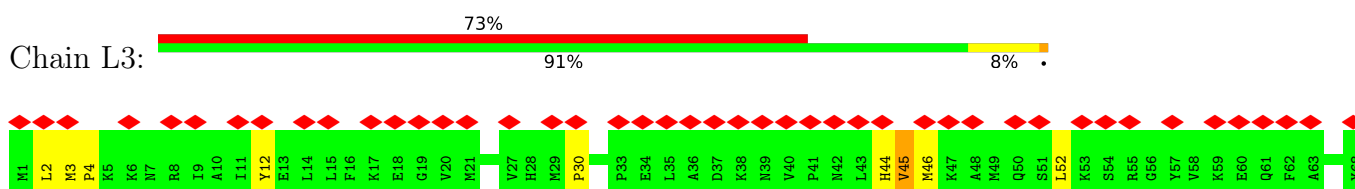
• Molecule 50: 40S ribosomal protein S8

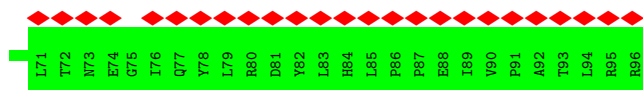


• Molecule 51: Ribosomal protein S9 (Predicted)

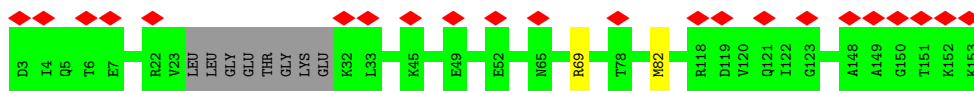


• Molecule 52: Plectin/S10 N-terminal domain-containing protein

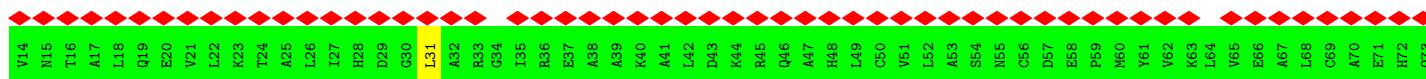




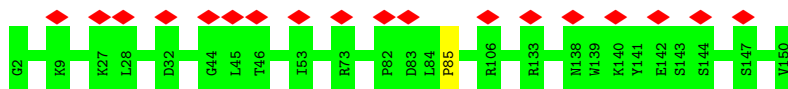
- Molecule 53: 40S ribosomal protein S11



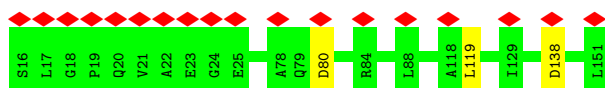
- Molecule 54: 40S ribosomal protein S12



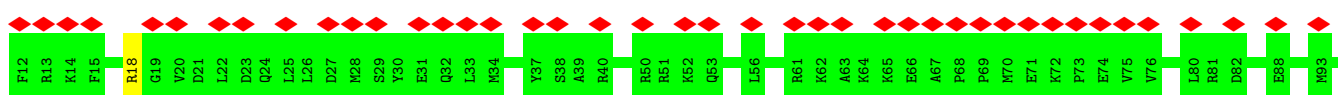
- Molecule 55: ribosomal protein uS15



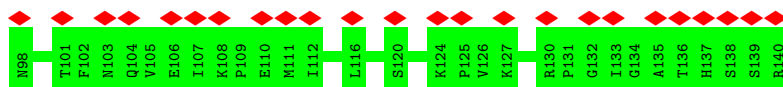
- Molecule 56: Ribosomal protein S14



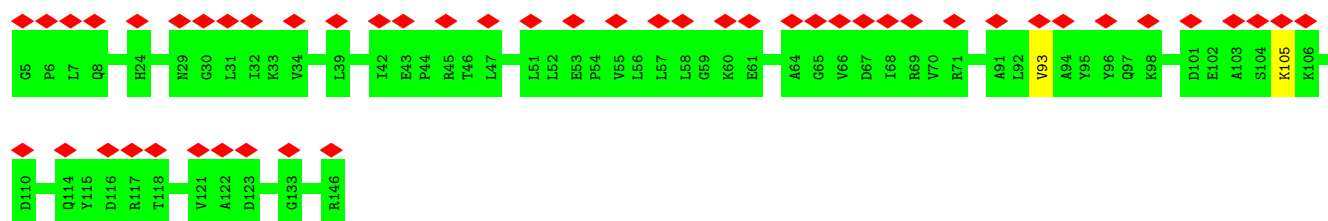
- Molecule 57: 40S ribosomal protein S15



- Molecule 58: Ribosomal protein S16

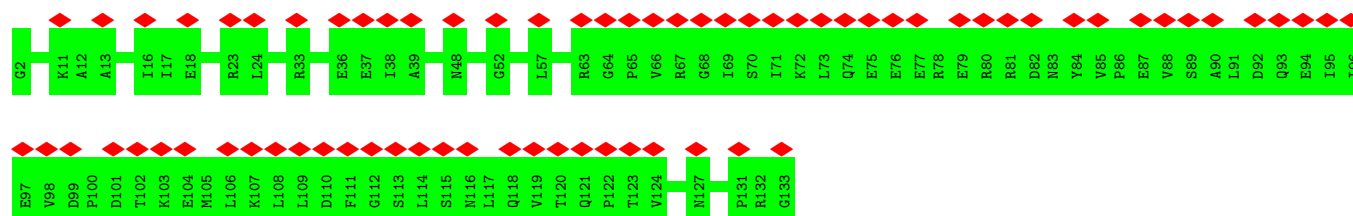


Chain R3: 



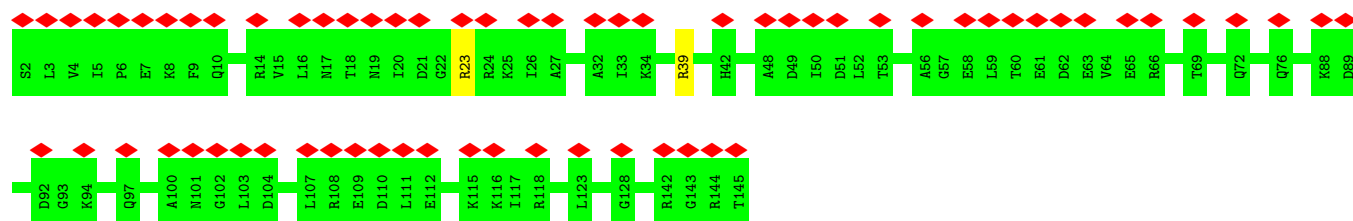
- Molecule 59: 40S ribosomal protein S17

Chain S3: 



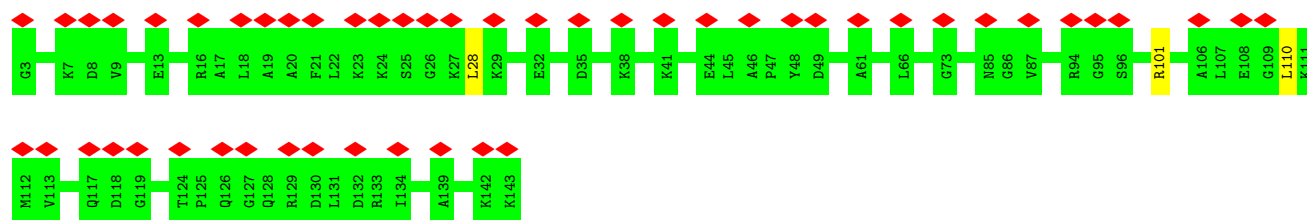
- Molecule 60: 40S ribosomal protein S18

Chain T3: 



- Molecule 61: 40S ribosomal protein S19

Chain U3: 



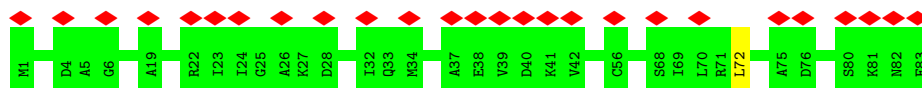
- Molecule 62: Ribosomal protein S20

Chain V3: 

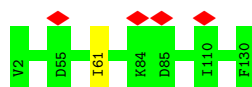




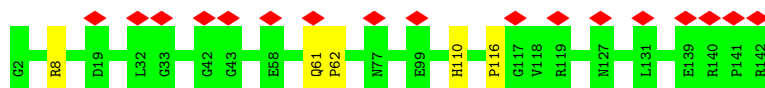
- Molecule 63: 40S ribosomal protein S21



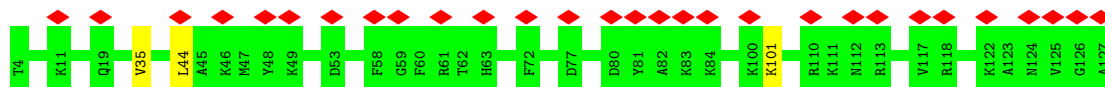
- Molecule 64: Ribosomal protein S15a



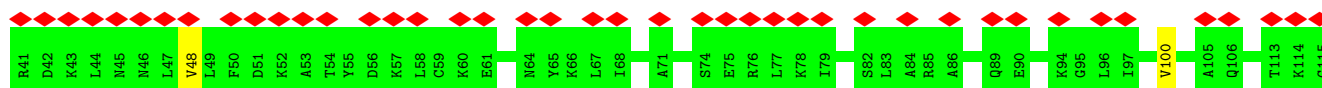
- Molecule 65: Ribosomal protein S23



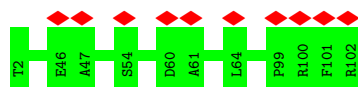
- Molecule 66: 40S ribosomal protein S24



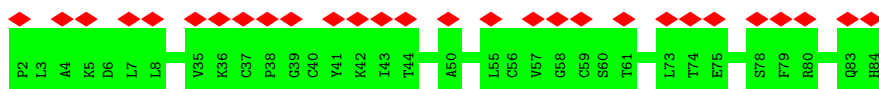
- Molecule 67: 40S ribosomal protein S25



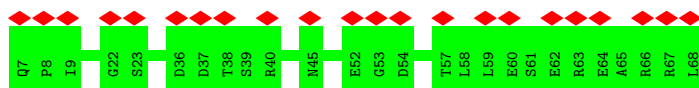
- Molecule 68: 40S ribosomal protein S26



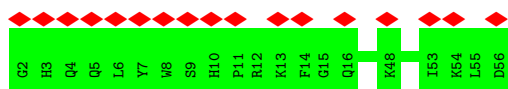
- Molecule 69: 40S ribosomal protein S27



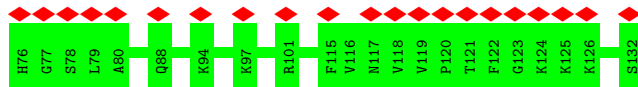
- Molecule 70: Ribosomal protein S28



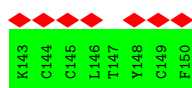
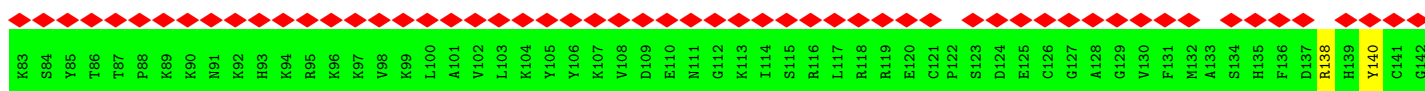
- Molecule 71: 40S ribosomal protein S29



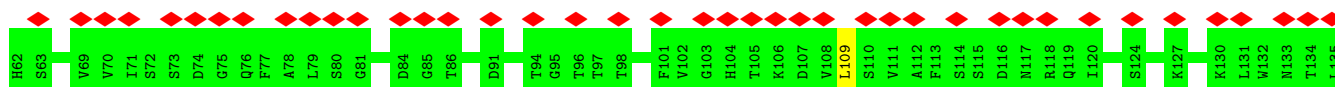
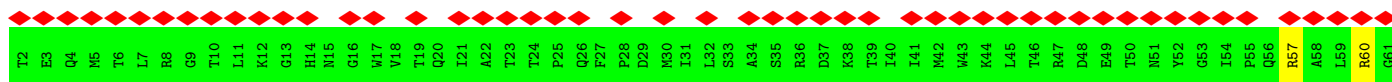
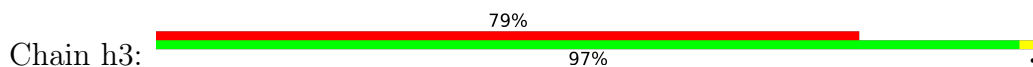
- Molecule 72: Ubiquitin-like domain-containing protein

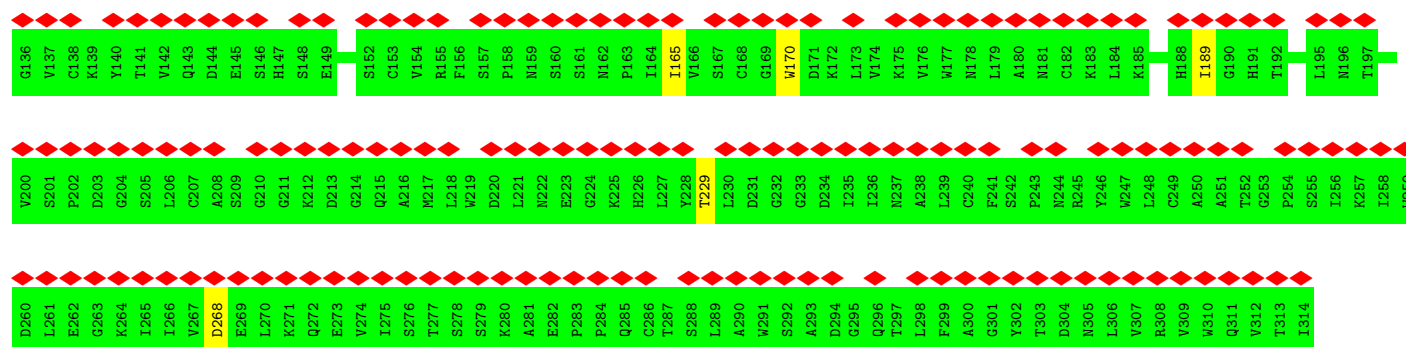


- Molecule 73: Ubiquitin-40S ribosomal protein S27a



- Molecule 74: Ribosomal protein RACK1





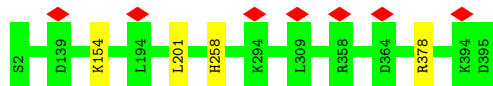
- Molecule 75: 60S ribosomal protein L8

Chain j3: 98%



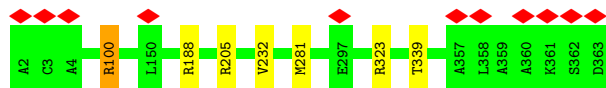
- Molecule 76: Ribosomal protein L3

Chain k3: 99%



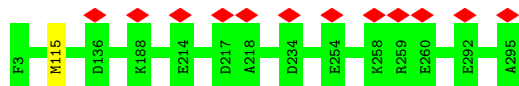
- Molecule 77: 60S ribosomal protein L4

Chain l3: 98%



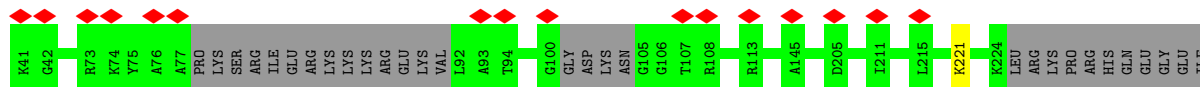
- Molecule 78: 60S ribosomal protein L5

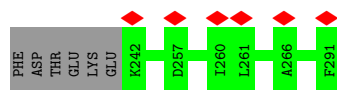
Chain m3: 100%



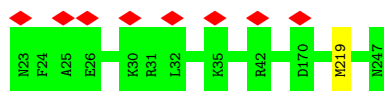
- Molecule 79: 60S ribosomal protein L6

Chain n3: 9% 86% 14%

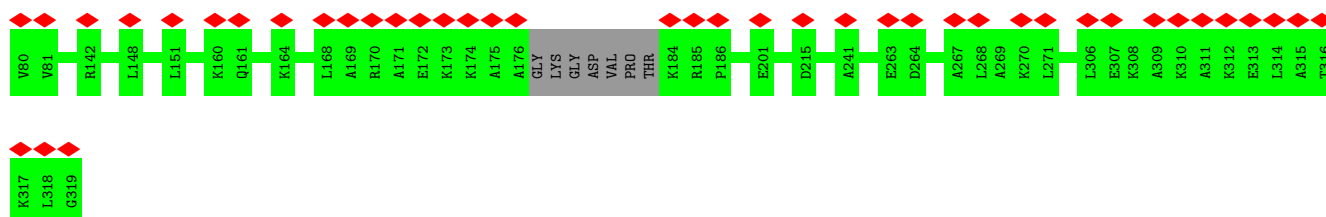




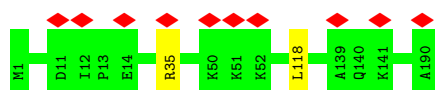
- Molecule 80: 60S ribosomal protein L7



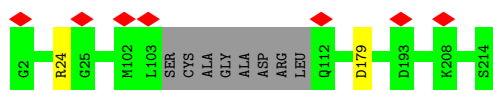
- Molecule 81: 60S ribosomal protein L7a



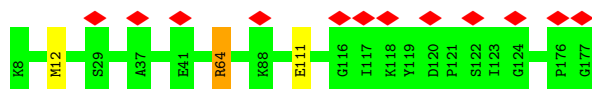
- Molecule 82: 60S ribosomal protein L9



- Molecule 83: Ribosomal protein L10

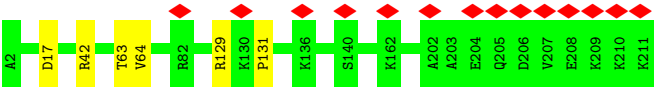


- Molecule 84: 60S ribosomal protein L11

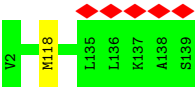


- Molecule 85: 60S ribosomal protein L13





• Molecule 86: 60S ribosomal protein L14



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	19437	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	47.5	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.087	Depositor
Minimum map value	-0.036	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	414.5, 414.5, 414.5	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.829, 0.829, 0.829	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.46	0/1746	0.72	1/2338 (0.0%)
2	B1	0.43	0/1662	0.71	0/2222
3	C1	0.45	0/1268	0.74	1/1700 (0.1%)
4	D1	0.48	1/1539 (0.1%)	0.79	2/2054 (0.1%)
5	E1	0.37	0/1524	0.73	2/2013 (0.1%)
6	F1	0.44	0/1501	0.71	0/2012
7	G1	0.46	0/1326	0.71	1/1770 (0.1%)
8	H1	0.39	0/823	0.72	0/1104
9	I1	0.42	0/1048	0.70	1/1402 (0.1%)
10	J1	0.42	0/873	0.71	1/1158 (0.1%)
11	K1	0.37	0/984	0.68	0/1323
12	L1	0.52	2/1132 (0.2%)	0.81	3/1504 (0.2%)
13	M1	0.40	0/1130	0.69	2/1507 (0.1%)
14	N1	0.44	0/1191	0.68	0/1590
15	O1	0.42	1/861 (0.1%)	0.76	1/1138 (0.1%)
16	P1	0.49	0/771	0.76	1/1034 (0.1%)
17	Q1	0.51	1/903 (0.1%)	0.72	0/1216
18	R1	0.44	0/1071	0.72	3/1429 (0.2%)
19	S1	0.51	1/895 (0.1%)	0.74	1/1198 (0.1%)
20	T1	0.46	0/916	0.69	0/1220
21	U1	0.35	0/1021	0.71	1/1348 (0.1%)
22	V1	0.33	0/841	0.69	0/1112
23	W1	0.42	0/720	0.71	0/952
24	X1	0.40	0/575	0.72	0/761
25	Y1	0.43	0/459	0.71	0/608
26	Z1	0.39	0/435	0.66	0/575
27	a1	0.44	0/240	0.86	0/305
28	b1	0.43	0/864	0.71	1/1140 (0.1%)
29	c1	0.42	0/718	0.72	0/953
30	d1	0.41	0/1010	0.74	1/1354 (0.1%)
31	e1	0.54	3/1530 (0.2%)	0.84	8/2064 (0.4%)
32	f1	0.34	0/1174	0.77	1/1582 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	l1	0.43	0/1680	0.81	2/2255 (0.1%)
34	m1	0.50	0/68	1.33	2/103 (1.9%)
35	n1	0.47	1/1971 (0.1%)	0.74	5/2639 (0.2%)
36	21	0.50	0/1810	1.16	13/2819 (0.5%)
37	11	0.28	0/33	0.89	0/43
38	A2	1.58	15/86400 (0.0%)	1.18	693/134684 (0.5%)
39	B2	0.65	0/2836	1.08	13/4421 (0.3%)
40	C2	0.71	0/3581	1.16	32/5577 (0.6%)
41	A3	0.52	1/40502 (0.0%)	1.16	345/63100 (0.5%)
42	B3	0.39	0/1747	0.73	3/2374 (0.1%)
43	C3	0.35	0/1756	0.66	0/2350
44	D3	0.45	2/1753 (0.1%)	0.69	1/2369 (0.0%)
45	E3	0.43	0/1796	0.82	5/2417 (0.2%)
46	F3	0.34	0/2118	0.67	0/2849
47	G3	0.34	0/1492	0.67	0/2005
48	H3	0.36	0/1946	0.72	0/2590
49	I3	0.34	0/1510	0.76	3/2022 (0.1%)
50	J3	0.36	0/1715	0.70	1/2287 (0.0%)
51	K3	0.35	0/1550	0.74	3/2069 (0.1%)
52	L3	1.07	3/834 (0.4%)	1.45	11/1125 (1.0%)
53	M3	0.39	0/1195	0.66	1/1597 (0.1%)
54	N3	0.36	0/918	0.76	2/1233 (0.2%)
55	O3	0.76	1/1226 (0.1%)	1.02	3/1649 (0.2%)
56	P3	0.39	0/1029	0.76	3/1380 (0.2%)
57	Q3	0.39	0/1079	0.74	0/1441
58	R3	0.42	1/1146 (0.1%)	0.77	3/1534 (0.2%)
59	S3	0.36	0/1082	0.74	0/1452
60	T3	0.40	0/1208	0.84	1/1618 (0.1%)
61	U3	0.36	0/1115	0.75	3/1493 (0.2%)
62	V3	0.33	0/805	0.78	0/1081
63	W3	0.36	0/643	0.68	1/860 (0.1%)
64	X3	0.42	0/1051	0.72	1/1406 (0.1%)
65	Y3	0.35	0/1116	0.67	1/1490 (0.1%)
66	Z3	0.44	1/1028 (0.1%)	0.72	1/1366 (0.1%)
67	a3	0.41	1/604 (0.2%)	0.82	1/810 (0.1%)
68	b3	0.35	0/828	0.71	0/1109
69	c3	0.31	0/665	0.65	0/891
70	d3	0.33	0/490	0.64	0/656
71	e3	0.35	0/470	0.69	0/623
72	f3	0.36	0/462	0.69	0/607
73	g3	0.62	2/567 (0.4%)	0.83	1/753 (0.1%)
74	h3	0.44	2/2493 (0.1%)	0.83	6/3394 (0.2%)
75	j3	0.44	0/1936	0.74	3/2596 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	k3	0.45	0/3240	0.71	1/4339 (0.0%)
77	l3	0.43	1/2937 (0.0%)	0.71	3/3946 (0.1%)
78	m3	0.39	0/2437	0.65	1/3264 (0.0%)
79	n3	0.35	0/1762	0.66	1/2362 (0.0%)
80	o3	0.42	0/1911	0.69	1/2549 (0.0%)
81	p3	0.38	0/1910	0.70	0/2569
82	q3	0.42	0/1535	0.76	1/2063 (0.0%)
83	r3	0.45	0/1702	0.73	1/2272 (0.0%)
84	s3	0.45	1/1385 (0.1%)	0.76	3/1852 (0.2%)
85	t3	0.54	2/1733 (0.1%)	1.00	5/2316 (0.2%)
86	u3	0.41	0/1158	0.73	1/1547 (0.1%)
All	All	1.03	43/234715 (0.0%)	1.03	1213/343902 (0.4%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A1	0	1
12	L1	0	1
14	N1	0	1
17	Q1	0	1
19	S1	0	1
33	l1	0	2
42	B3	0	1
44	D3	0	2
52	L3	0	2
61	U3	0	1
65	Y3	0	1
76	k3	0	1
77	l3	0	3
82	q3	0	1
84	s3	0	1
85	t3	0	3
All	All	0	23

The worst 5 of 43 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	A2	935	A	N7-C5	203.95	2.61	1.39
38	A2	935	A	N9-C4	197.60	2.56	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	A2	935	A	C8-N7	167.52	2.48	1.31
38	A2	935	A	N9-C8	160.18	2.65	1.37
38	A2	935	A	C5-C4	146.96	2.41	1.38

The worst 5 of 1213 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	L3	4	PRO	N-CD-CG	-29.06	59.62	103.20
38	A2	935	A	N1-C2-N3	24.68	141.64	129.30
38	A2	935	A	N7-C8-N9	-23.29	102.16	113.80
38	A2	935	A	C6-N1-C2	21.66	131.59	118.60
85	t3	131	PRO	N-CD-CG	-21.39	71.12	103.20

There are no chirality outliers.

5 of 23 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A1	108	ARG	Sidechain
12	L1	74	TYR	Sidechain
14	N1	6	ARG	Sidechain
17	Q1	95	ASP	Peptide
19	S1	106	TYR	Peptide

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A1	201/203 (99%)	193 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B1	197/199 (99%)	191 (97%)	6 (3%)	0	100	100
3	C1	151/153 (99%)	148 (98%)	3 (2%)	0	100	100
4	D1	185/187 (99%)	177 (96%)	8 (4%)	0	100	100
5	E1	178/180 (99%)	174 (98%)	4 (2%)	0	100	100
6	F1	174/176 (99%)	164 (94%)	10 (6%)	0	100	100
7	G1	157/159 (99%)	153 (98%)	4 (2%)	0	100	100
8	H1	97/99 (98%)	91 (94%)	6 (6%)	0	100	100
9	I1	137/139 (99%)	134 (98%)	3 (2%)	0	100	100
10	J1	102/106 (96%)	101 (99%)	1 (1%)	0	100	100
11	K1	116/118 (98%)	114 (98%)	2 (2%)	0	100	100
12	L1	132/134 (98%)	130 (98%)	2 (2%)	0	100	100
13	M1	133/135 (98%)	127 (96%)	6 (4%)	0	100	100
14	N1	145/147 (99%)	136 (94%)	9 (6%)	0	100	100
15	O1	100/116 (86%)	98 (98%)	2 (2%)	0	100	100
16	P1	96/98 (98%)	94 (98%)	2 (2%)	0	100	100
17	Q1	105/107 (98%)	100 (95%)	5 (5%)	0	100	100
18	R1	126/128 (98%)	121 (96%)	5 (4%)	0	100	100
19	S1	107/109 (98%)	104 (97%)	3 (3%)	0	100	100
20	T1	112/114 (98%)	111 (99%)	1 (1%)	0	100	100
21	U1	120/122 (98%)	118 (98%)	2 (2%)	0	100	100
22	V1	100/102 (98%)	99 (99%)	1 (1%)	0	100	100
23	W1	84/86 (98%)	83 (99%)	1 (1%)	0	100	100
24	X1	67/69 (97%)	63 (94%)	4 (6%)	0	100	100
25	Y1	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
26	Z1	50/52 (96%)	50 (100%)	0	0	100	100
27	a1	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
28	b1	102/104 (98%)	99 (97%)	3 (3%)	0	100	100
29	c1	89/91 (98%)	86 (97%)	3 (3%)	0	100	100
30	d1	122/124 (98%)	119 (98%)	3 (2%)	0	100	100
31	e1	194/196 (99%)	176 (91%)	18 (9%)	0	100	100
32	f1	151/153 (99%)	134 (89%)	17 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	l1	204/206 (99%)	173 (85%)	30 (15%)	1 (0%)	25	58
35	n1	234/236 (99%)	229 (98%)	5 (2%)	0	100	100
37	l1	3/5 (60%)	1 (33%)	2 (67%)	0	100	100
42	B3	215/217 (99%)	207 (96%)	8 (4%)	0	100	100
43	C3	211/213 (99%)	202 (96%)	9 (4%)	0	100	100
44	D3	219/221 (99%)	212 (97%)	7 (3%)	0	100	100
45	E3	226/228 (99%)	216 (96%)	10 (4%)	0	100	100
46	F3	260/262 (99%)	249 (96%)	11 (4%)	0	100	100
47	G3	181/191 (95%)	173 (96%)	8 (4%)	0	100	100
48	H3	235/237 (99%)	226 (96%)	9 (4%)	0	100	100
49	I3	181/189 (96%)	174 (96%)	7 (4%)	0	100	100
50	J3	204/206 (99%)	193 (95%)	11 (5%)	0	100	100
51	K3	183/185 (99%)	180 (98%)	3 (2%)	0	100	100
52	L3	94/96 (98%)	83 (88%)	9 (10%)	2 (2%)	5	25
53	M3	139/151 (92%)	129 (93%)	10 (7%)	0	100	100
54	N3	115/117 (98%)	102 (89%)	13 (11%)	0	100	100
55	O3	147/149 (99%)	144 (98%)	3 (2%)	0	100	100
56	P3	134/136 (98%)	130 (97%)	4 (3%)	0	100	100
57	Q3	127/129 (98%)	123 (97%)	3 (2%)	1 (1%)	16	48
58	R3	140/142 (99%)	135 (96%)	5 (4%)	0	100	100
59	S3	130/132 (98%)	124 (95%)	6 (5%)	0	100	100
60	T3	142/144 (99%)	136 (96%)	6 (4%)	0	100	100
61	U3	139/141 (99%)	129 (93%)	10 (7%)	0	100	100
62	V3	98/100 (98%)	93 (95%)	5 (5%)	0	100	100
63	W3	81/83 (98%)	81 (100%)	0	0	100	100
64	X3	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
65	Y3	139/141 (99%)	131 (94%)	7 (5%)	1 (1%)	19	51
66	Z3	122/124 (98%)	119 (98%)	3 (2%)	0	100	100
67	a3	73/75 (97%)	71 (97%)	2 (3%)	0	100	100
68	b3	99/101 (98%)	93 (94%)	6 (6%)	0	100	100
69	c3	81/83 (98%)	78 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
70	d3	60/62 (97%)	58 (97%)	2 (3%)	0	100	100
71	e3	53/55 (96%)	51 (96%)	2 (4%)	0	100	100
72	f3	55/57 (96%)	53 (96%)	2 (4%)	0	100	100
73	g3	66/68 (97%)	59 (89%)	7 (11%)	0	100	100
74	h3	311/313 (99%)	287 (92%)	24 (8%)	0	100	100
75	j3	246/248 (99%)	233 (95%)	13 (5%)	0	100	100
76	k3	392/394 (100%)	373 (95%)	19 (5%)	0	100	100
77	l3	360/362 (99%)	345 (96%)	15 (4%)	0	100	100
78	m3	291/293 (99%)	282 (97%)	9 (3%)	0	100	100
79	n3	208/251 (83%)	199 (96%)	9 (4%)	0	100	100
80	o3	223/225 (99%)	215 (96%)	8 (4%)	0	100	100
81	p3	229/240 (95%)	221 (96%)	8 (4%)	0	100	100
82	q3	188/190 (99%)	179 (95%)	9 (5%)	0	100	100
83	r3	201/213 (94%)	195 (97%)	6 (3%)	0	100	100
84	s3	168/170 (99%)	168 (100%)	0	0	100	100
85	t3	208/210 (99%)	197 (95%)	10 (5%)	1 (0%)	25	58
86	u3	136/138 (99%)	131 (96%)	5 (4%)	0	100	100
All	All	11979/12239 (98%)	11459 (96%)	514 (4%)	6 (0%)	50	79

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
33	l1	57	SER
52	L3	45	VAL
52	L3	46	MET
57	Q3	18	ARG
85	t3	64	VAL

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	171/171 (100%)	171 (100%)	0	100	100
2	B1	171/171 (100%)	171 (100%)	0	100	100
3	C1	134/134 (100%)	134 (100%)	0	100	100
4	D1	164/164 (100%)	164 (100%)	0	100	100
5	E1	159/159 (100%)	159 (100%)	0	100	100
6	F1	157/157 (100%)	157 (100%)	0	100	100
7	G1	139/139 (100%)	138 (99%)	1 (1%)	81	90
8	H1	89/89 (100%)	89 (100%)	0	100	100
9	I1	106/106 (100%)	105 (99%)	1 (1%)	75	88
10	J1	86/86 (100%)	86 (100%)	0	100	100
11	K1	106/106 (100%)	106 (100%)	0	100	100
12	L1	124/124 (100%)	124 (100%)	0	100	100
13	M1	117/117 (100%)	117 (100%)	0	100	100
14	N1	119/119 (100%)	118 (99%)	1 (1%)	79	89
15	O1	84/95 (88%)	82 (98%)	2 (2%)	44	70
16	P1	84/84 (100%)	84 (100%)	0	100	100
17	Q1	98/98 (100%)	98 (100%)	0	100	100
18	R1	114/114 (100%)	114 (100%)	0	100	100
19	S1	88/88 (100%)	88 (100%)	0	100	100
20	T1	98/98 (100%)	97 (99%)	1 (1%)	73	86
21	U1	109/109 (100%)	109 (100%)	0	100	100
22	V1	86/86 (100%)	86 (100%)	0	100	100
23	W1	73/73 (100%)	73 (100%)	0	100	100
24	X1	64/64 (100%)	64 (100%)	0	100	100
25	Y1	47/47 (100%)	47 (100%)	0	100	100
26	Z1	48/48 (100%)	47 (98%)	1 (2%)	48	72
27	a1	24/24 (100%)	24 (100%)	0	100	100
28	b1	92/92 (100%)	92 (100%)	0	100	100
29	c1	74/74 (100%)	73 (99%)	1 (1%)	62	81
30	d1	108/108 (100%)	108 (100%)	0	100	100
31	e1	164/164 (100%)	163 (99%)	1 (1%)	84	91
32	f1	126/126 (100%)	124 (98%)	2 (2%)	58	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	l1	186/186 (100%)	183 (98%)	3 (2%)	58	79
35	n1	213/219 (97%)	213 (100%)	0	100	100
37	11	4/4 (100%)	4 (100%)	0	100	100
42	B3	180/181 (99%)	180 (100%)	0	100	100
43	C3	194/194 (100%)	194 (100%)	0	100	100
44	D3	187/187 (100%)	186 (100%)	1 (0%)	86	92
45	E3	190/190 (100%)	189 (100%)	1 (0%)	86	92
46	F3	224/224 (100%)	224 (100%)	0	100	100
47	G3	158/161 (98%)	157 (99%)	1 (1%)	84	91
48	H3	207/207 (100%)	206 (100%)	1 (0%)	86	92
49	I3	165/169 (98%)	165 (100%)	0	100	100
50	J3	178/178 (100%)	178 (100%)	0	100	100
51	K3	161/161 (100%)	161 (100%)	0	100	100
52	L3	87/87 (100%)	87 (100%)	0	100	100
53	M3	130/136 (96%)	129 (99%)	1 (1%)	79	89
54	N3	99/99 (100%)	99 (100%)	0	100	100
55	O3	130/130 (100%)	130 (100%)	0	100	100
56	P3	106/106 (100%)	106 (100%)	0	100	100
57	Q3	115/115 (100%)	115 (100%)	0	100	100
58	R3	117/117 (100%)	117 (100%)	0	100	100
59	S3	119/119 (100%)	119 (100%)	0	100	100
60	T3	125/125 (100%)	124 (99%)	1 (1%)	79	89
61	U3	111/111 (100%)	111 (100%)	0	100	100
62	V3	92/92 (100%)	92 (100%)	0	100	100
63	W3	67/67 (100%)	67 (100%)	0	100	100
64	X3	112/112 (100%)	112 (100%)	0	100	100
65	Y3	113/113 (100%)	111 (98%)	2 (2%)	54	76
66	Z3	107/107 (100%)	106 (99%)	1 (1%)	75	88
67	a3	66/66 (100%)	66 (100%)	0	100	100
68	b3	88/88 (100%)	88 (100%)	0	100	100
69	c3	75/75 (100%)	75 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
70	d3	55/55 (100%)	55 (100%)	0	100	100
71	e3	48/48 (100%)	48 (100%)	0	100	100
72	f3	47/47 (100%)	47 (100%)	0	100	100
73	g3	61/61 (100%)	60 (98%)	1 (2%)	58	79
74	h3	272/272 (100%)	270 (99%)	2 (1%)	81	90
75	j3	190/190 (100%)	188 (99%)	2 (1%)	70	84
76	k3	342/342 (100%)	340 (99%)	2 (1%)	84	91
77	l3	302/302 (100%)	300 (99%)	2 (1%)	81	90
78	m3	247/247 (100%)	247 (100%)	0	100	100
79	n3	190/223 (85%)	190 (100%)	0	100	100
80	o3	196/196 (100%)	196 (100%)	0	100	100
81	p3	200/205 (98%)	200 (100%)	0	100	100
82	q3	169/169 (100%)	169 (100%)	0	100	100
83	r3	175/180 (97%)	174 (99%)	1 (1%)	84	91
84	s3	143/143 (100%)	143 (100%)	0	100	100
85	t3	175/175 (100%)	175 (100%)	0	100	100
86	u3	117/117 (100%)	117 (100%)	0	100	100
All	All	10458/10532 (99%)	10425 (100%)	33 (0%)	90	95

5 of 33 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
76	k3	154	LYS
76	k3	378	ARG
83	r3	24	ARG
33	l1	25	ARG
33	l1	15	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
51	K3	154	GLN
60	T3	73	ASN
74	h3	296	GLN
33	l1	171	HIS

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Mol	Chain	Res	Type
45	E3	101	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	m1	2/3 (66%)	0	0
36	21	75/76 (98%)	21 (28%)	0
38	A2	3554/5051 (70%)	731 (20%)	58 (1%)
39	B2	118/119 (99%)	11 (9%)	0
40	C2	149/156 (95%)	28 (18%)	1 (0%)
41	A3	1678/1697 (98%)	350 (20%)	15 (0%)
All	All	5576/7102 (78%)	1141 (20%)	74 (1%)

5 of 1141 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
36	21	9	G
36	21	10	G
36	21	14	A
36	21	16	U
36	21	17	G

5 of 74 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
38	A2	4929	U
41	A3	1137	U
41	A3	24	C
41	A3	627	U
38	A2	1633	G

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 282 ligands modelled in this entry, 282 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
38	A2	27
41	A3	18
10	J1	1

The worst 5 of 46 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	J1	63:GLN	C	79:GLN	N	38.60
1	A2	1403:C	O3'	1404:G	P	20.34
1	A2	1407:G	O3'	1408:C	P	19.15
1	A2	1408:C	O3'	1409:G	P	17.91
1	A2	1404:G	O3'	1405:G	P	17.70

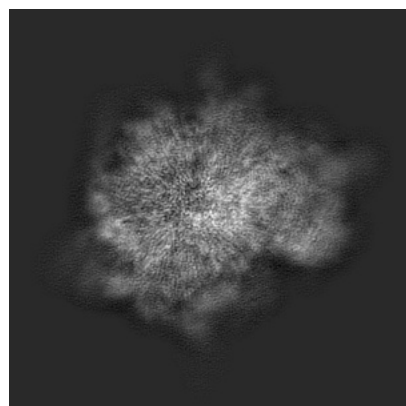
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16052. These allow visual inspection of the internal detail of the map and identification of artifacts.

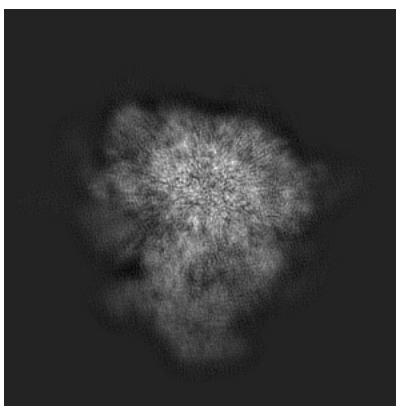
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

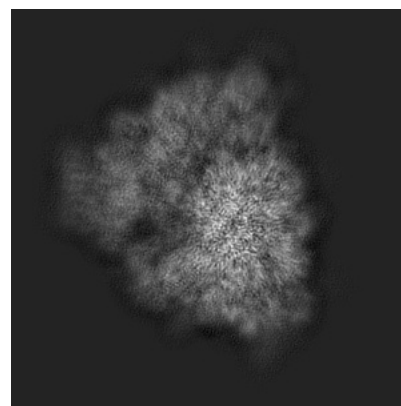
6.1.1 Primary map



X

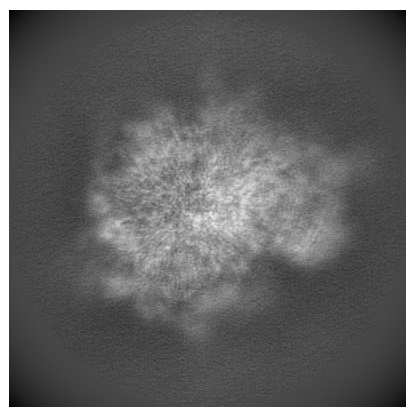


Y

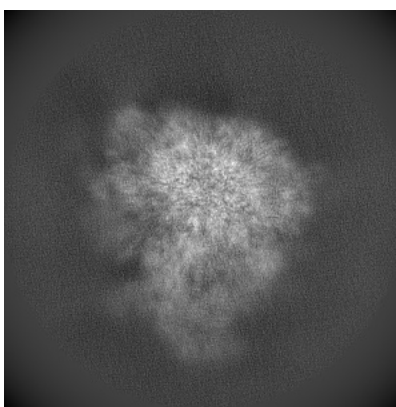


Z

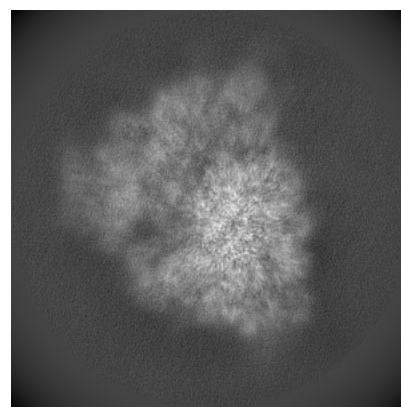
6.1.2 Raw map



X



Y

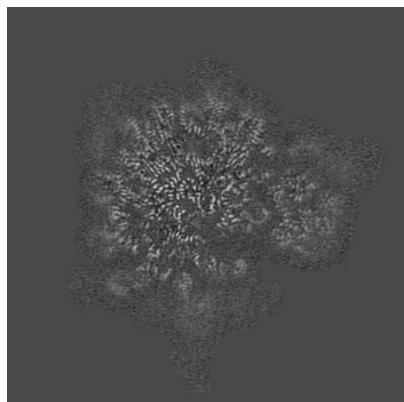


Z

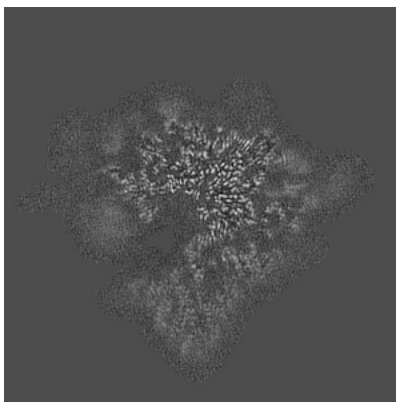
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

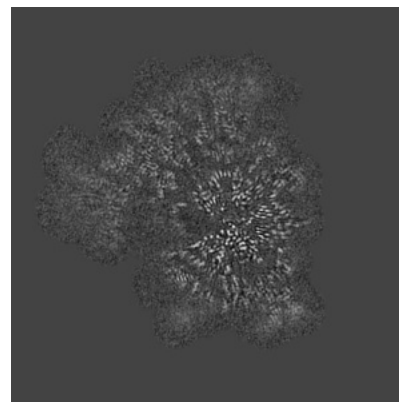
6.2.1 Primary map



X Index: 250

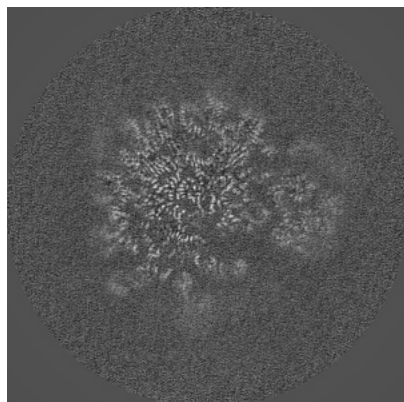


Y Index: 250

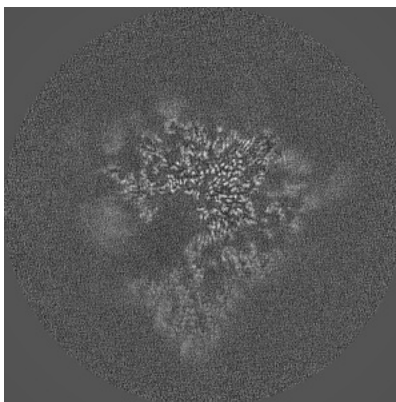


Z Index: 250

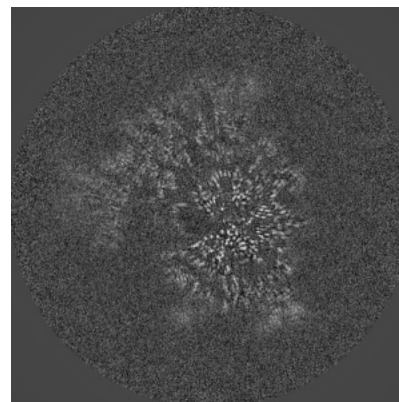
6.2.2 Raw map



X Index: 250



Y Index: 250

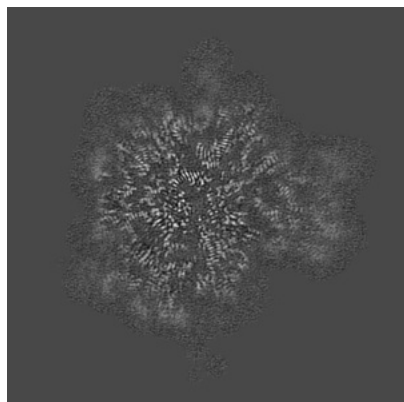


Z Index: 250

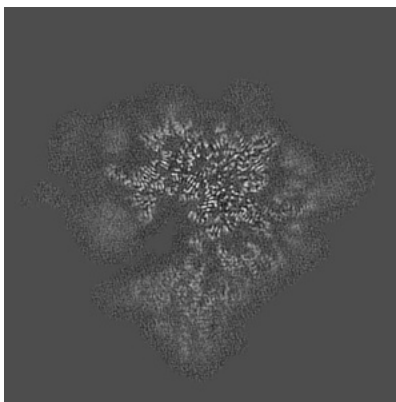
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

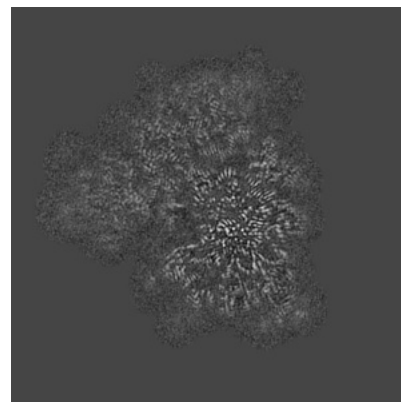
6.3.1 Primary map



X Index: 276

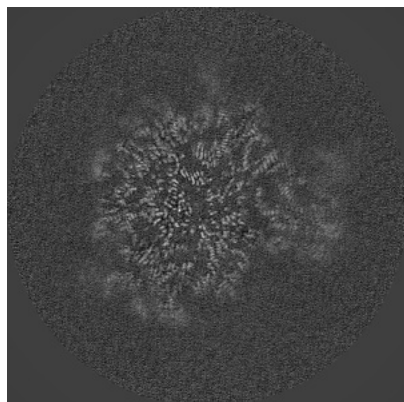


Y Index: 255

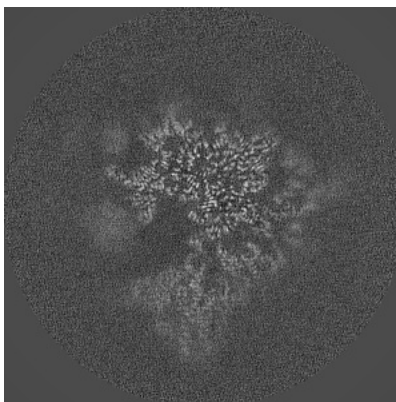


Z Index: 244

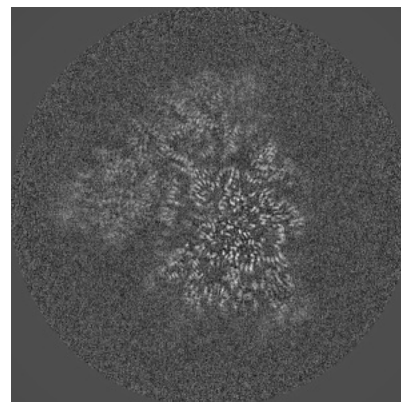
6.3.2 Raw map



X Index: 275



Y Index: 255

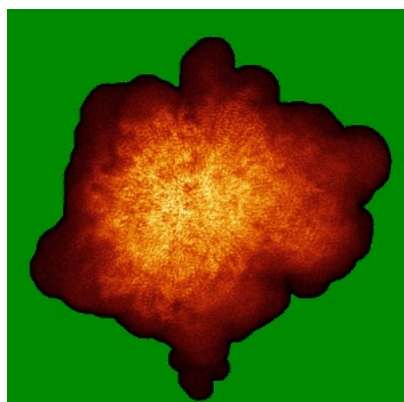


Z Index: 241

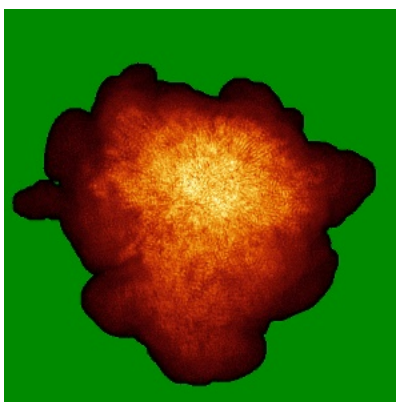
The images above show the largest variance slices of the map in three orthogonal directions.

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

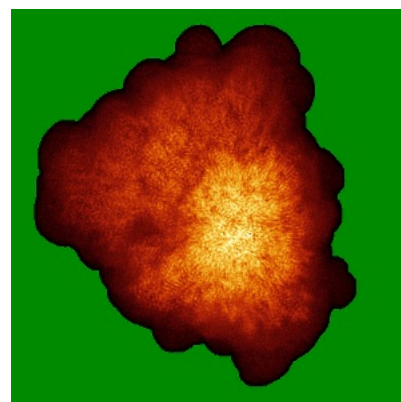
6.4.1 Primary map



X

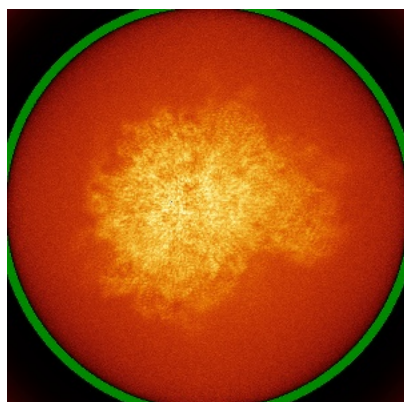


Y

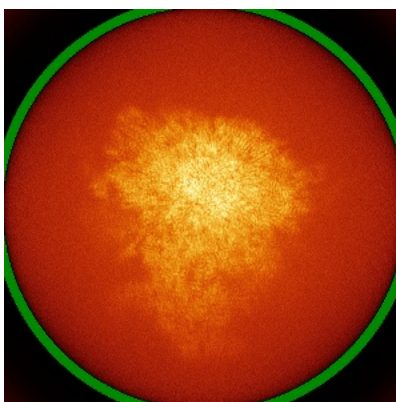


Z

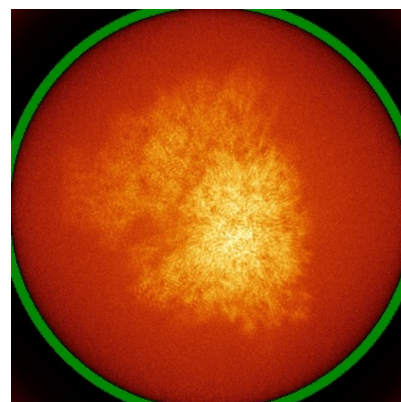
6.4.2 Raw map



X



Y

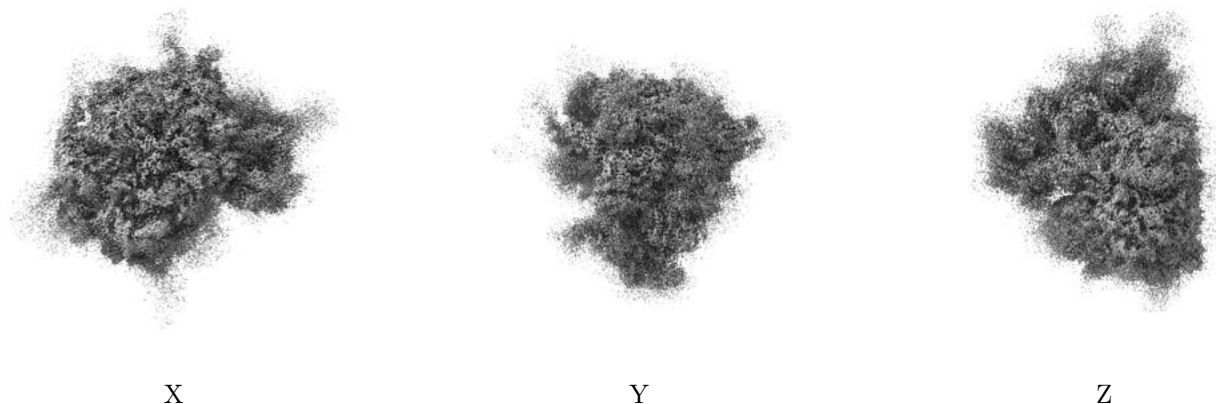


Z

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.

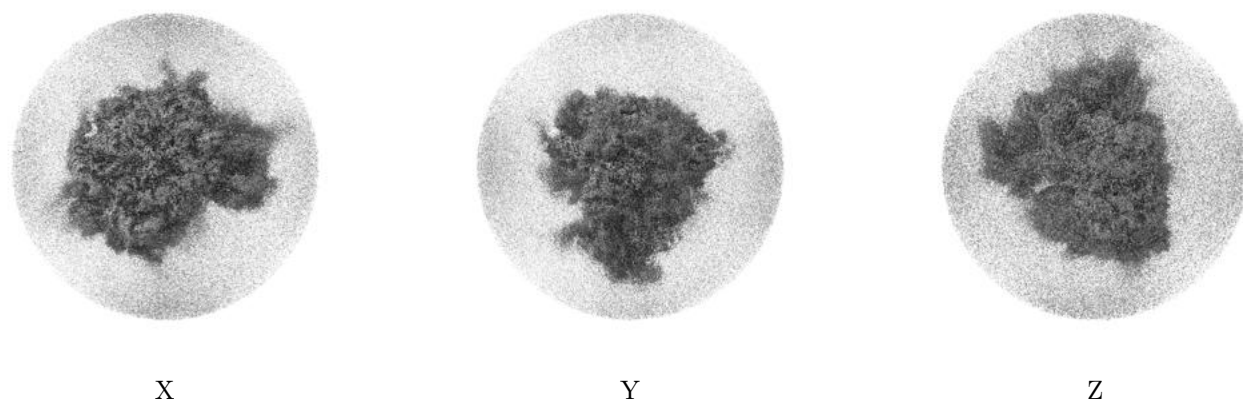
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. 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.

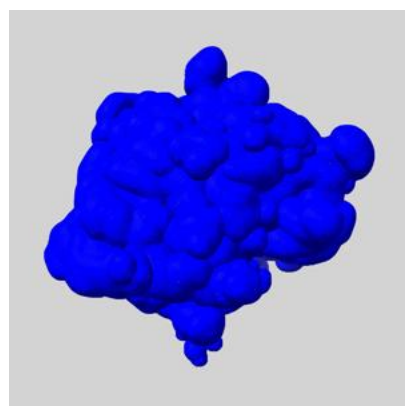
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

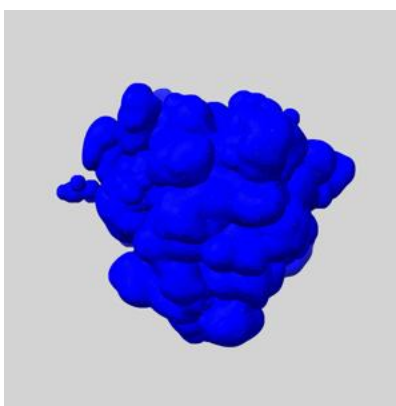
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

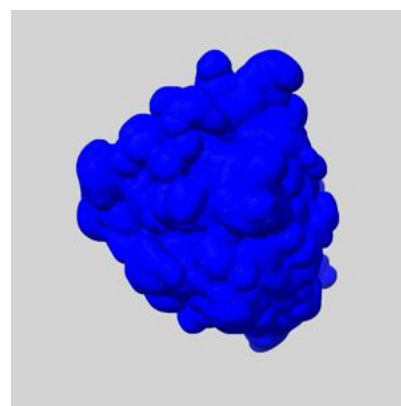
6.6.1 emd_16052_msk_1.map [i](#)



X



Y

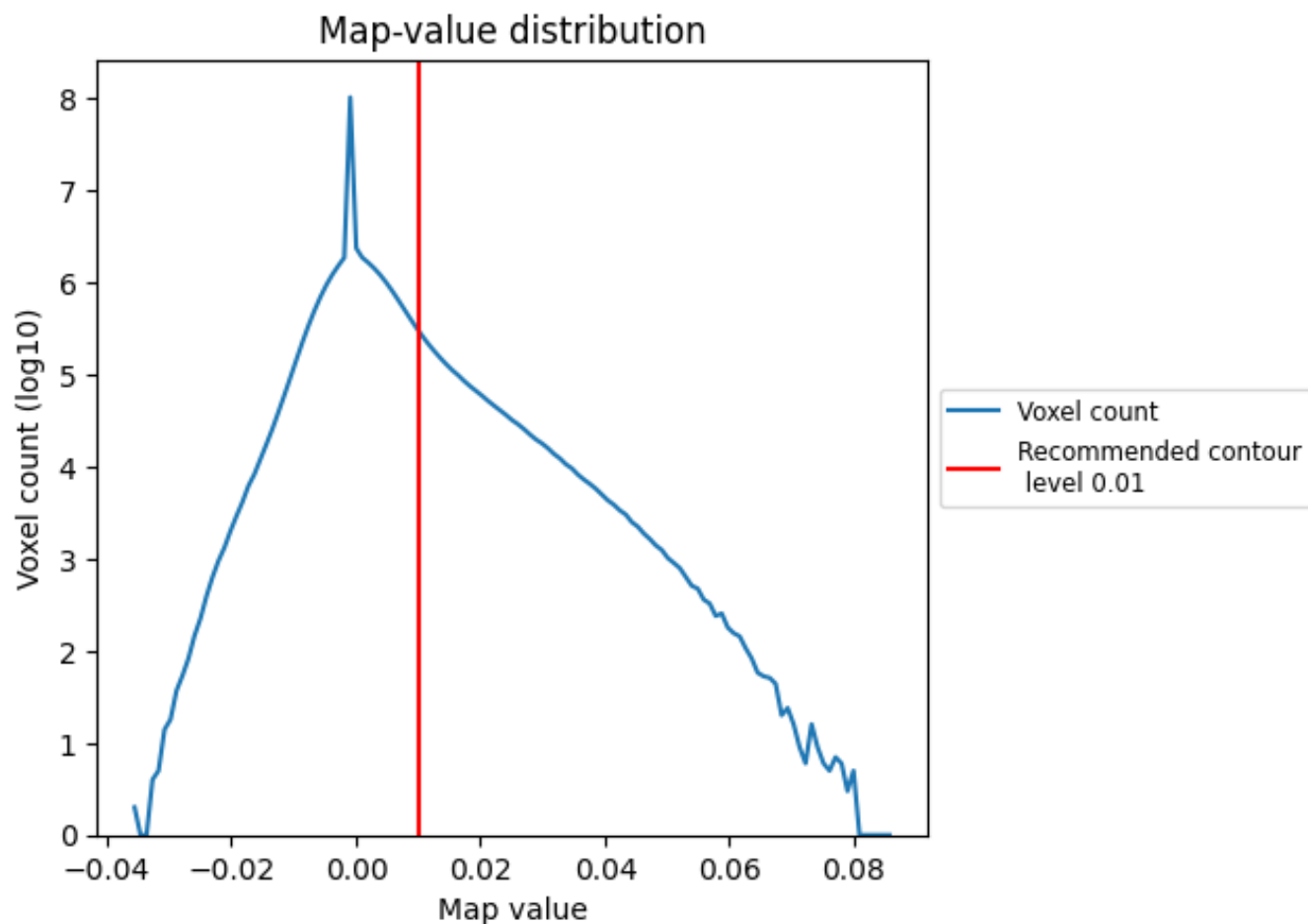


Z

7 Map analysis [i](#)

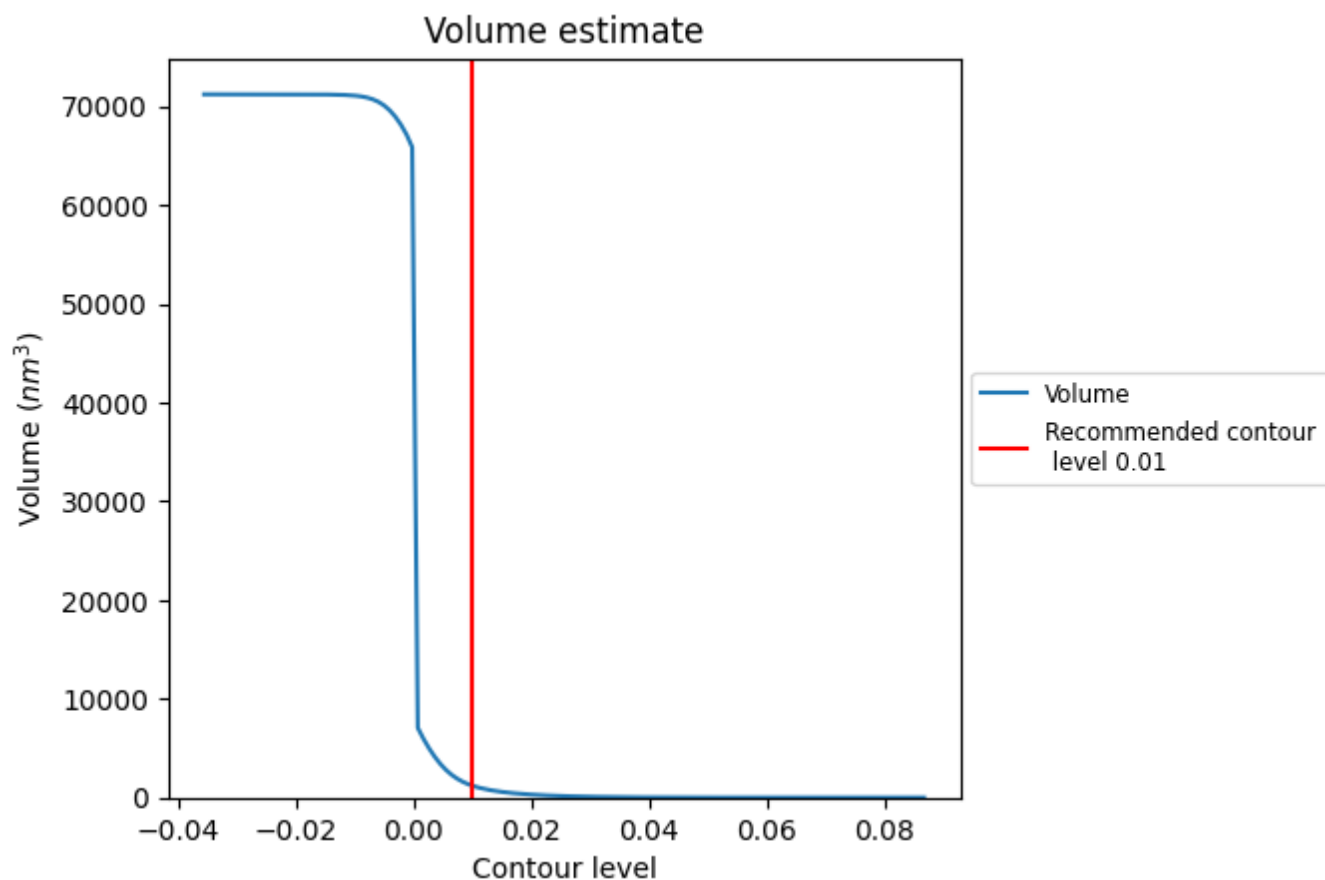
This section contains the results of statistical analysis of the map.

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.

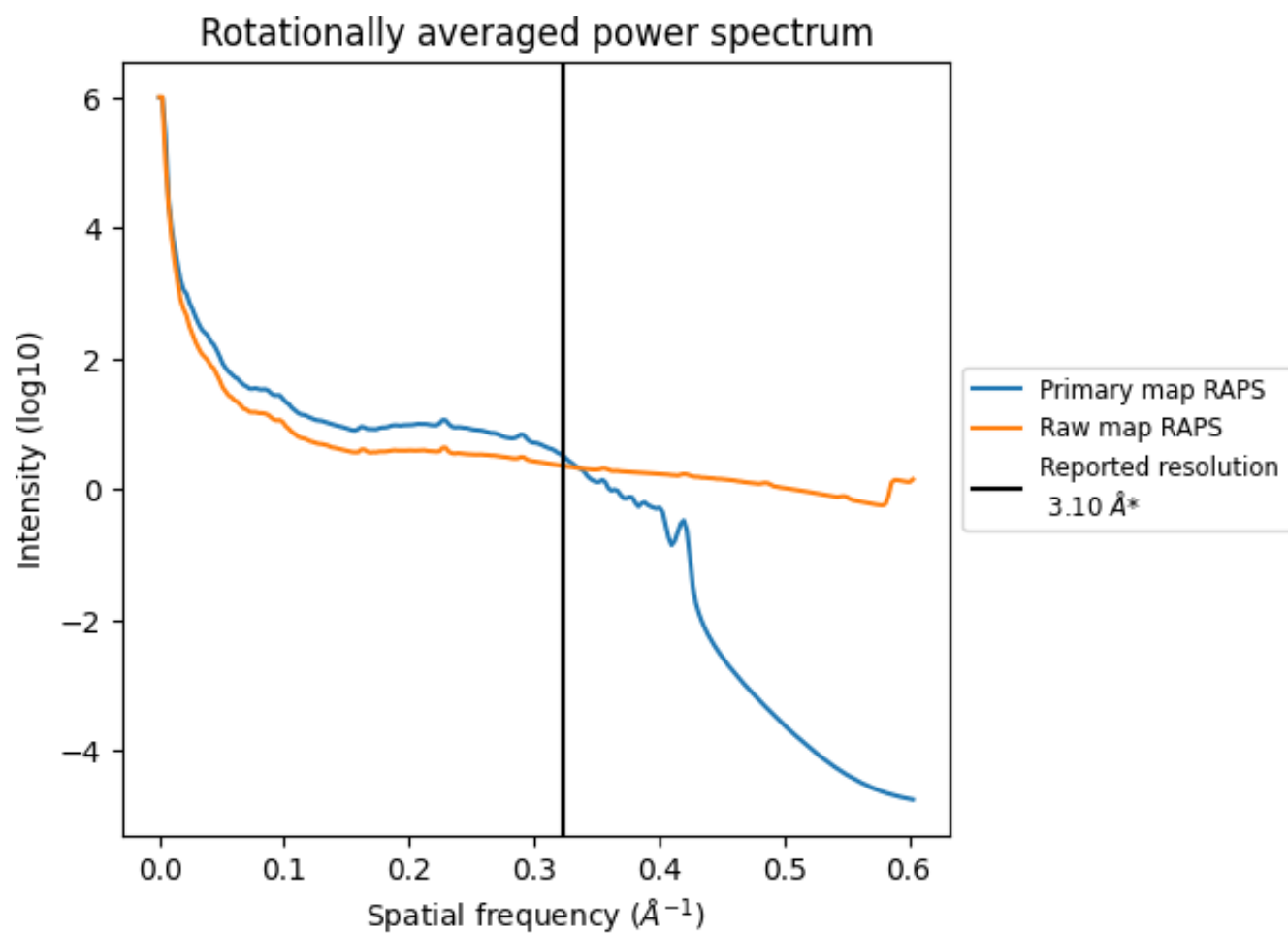
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1202 nm³; this corresponds to an approximate mass of 1086 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 ⓘ

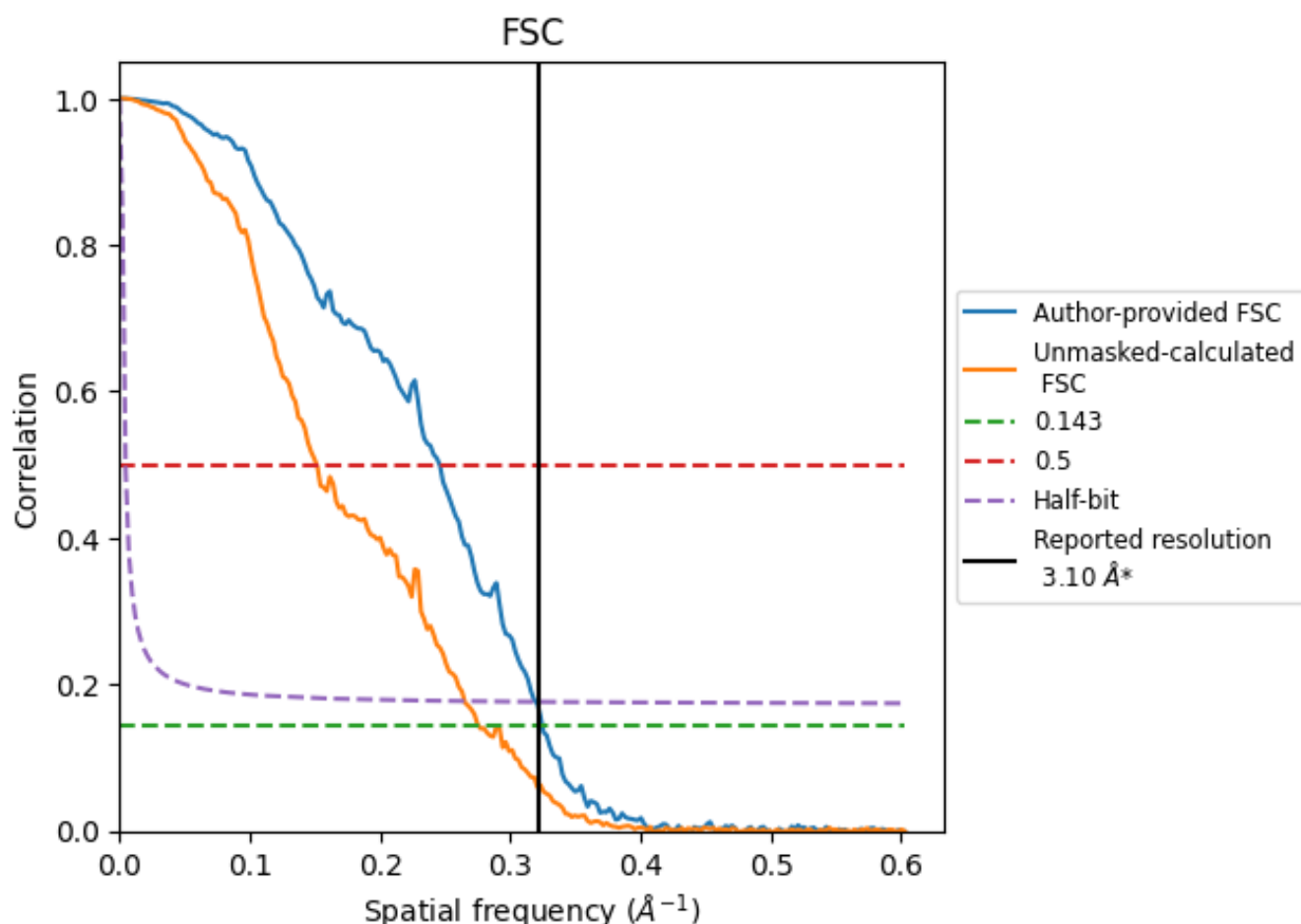


*Reported resolution corresponds to spatial frequency of 0.323 \AA^{-1}

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 0.323 \AA^{-1}

8.2 Resolution estimates [i](#)

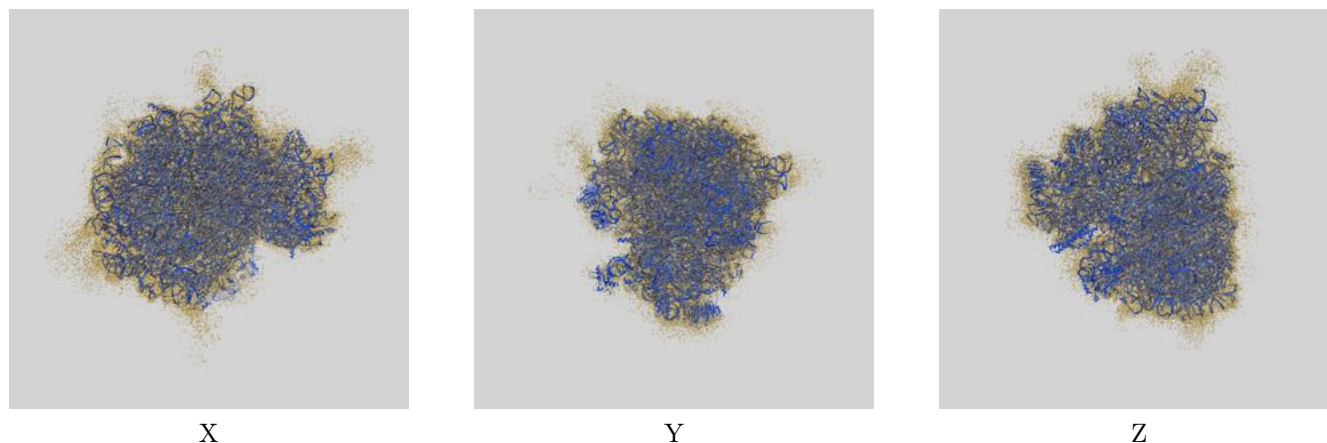
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.08	4.07	3.13
Unmasked-calculated*	3.62	6.61	3.77

*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 3.62 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

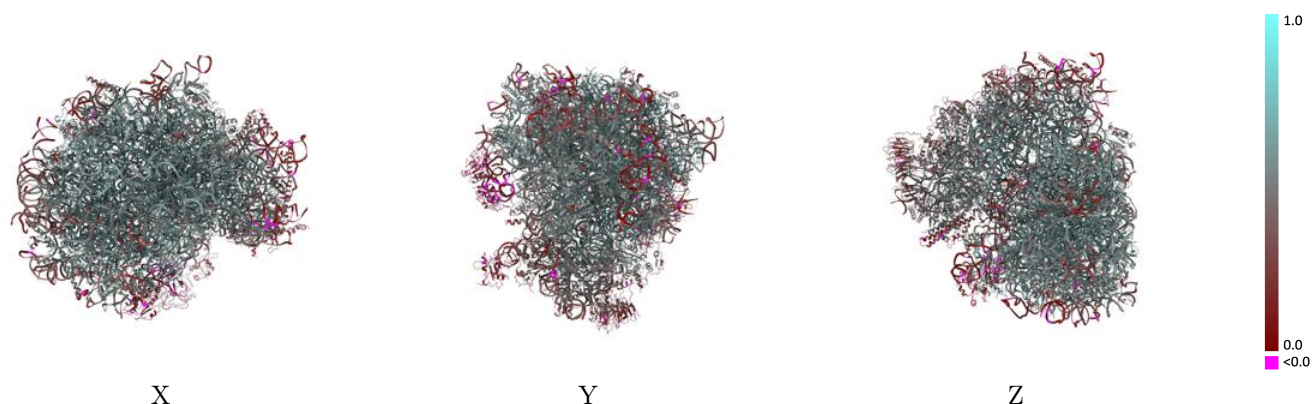
This section contains information regarding the fit between EMDB map EMD-16052 and PDB model 8BHF. Per-residue inclusion information can be found in section [3](#) on page [22](#).

9.1 Map-model overlay [i](#)



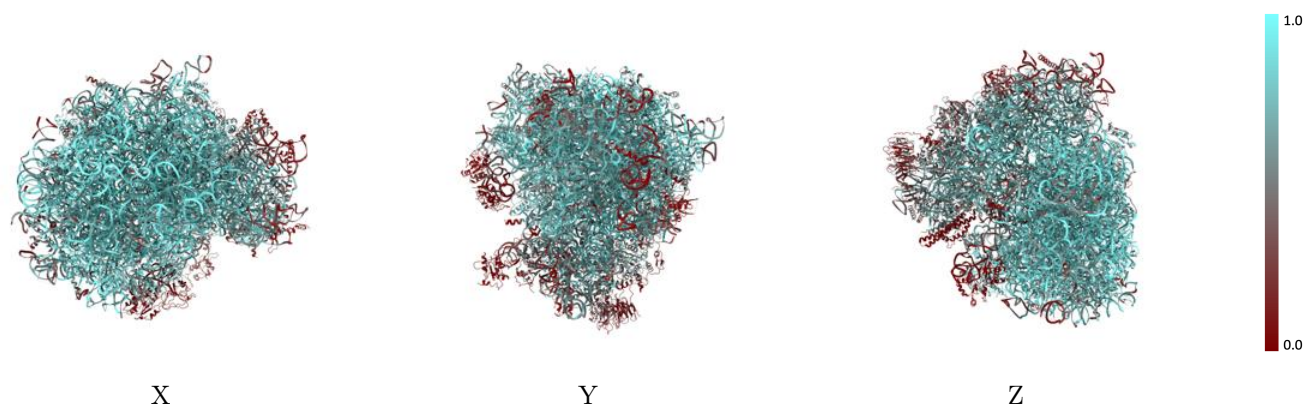
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



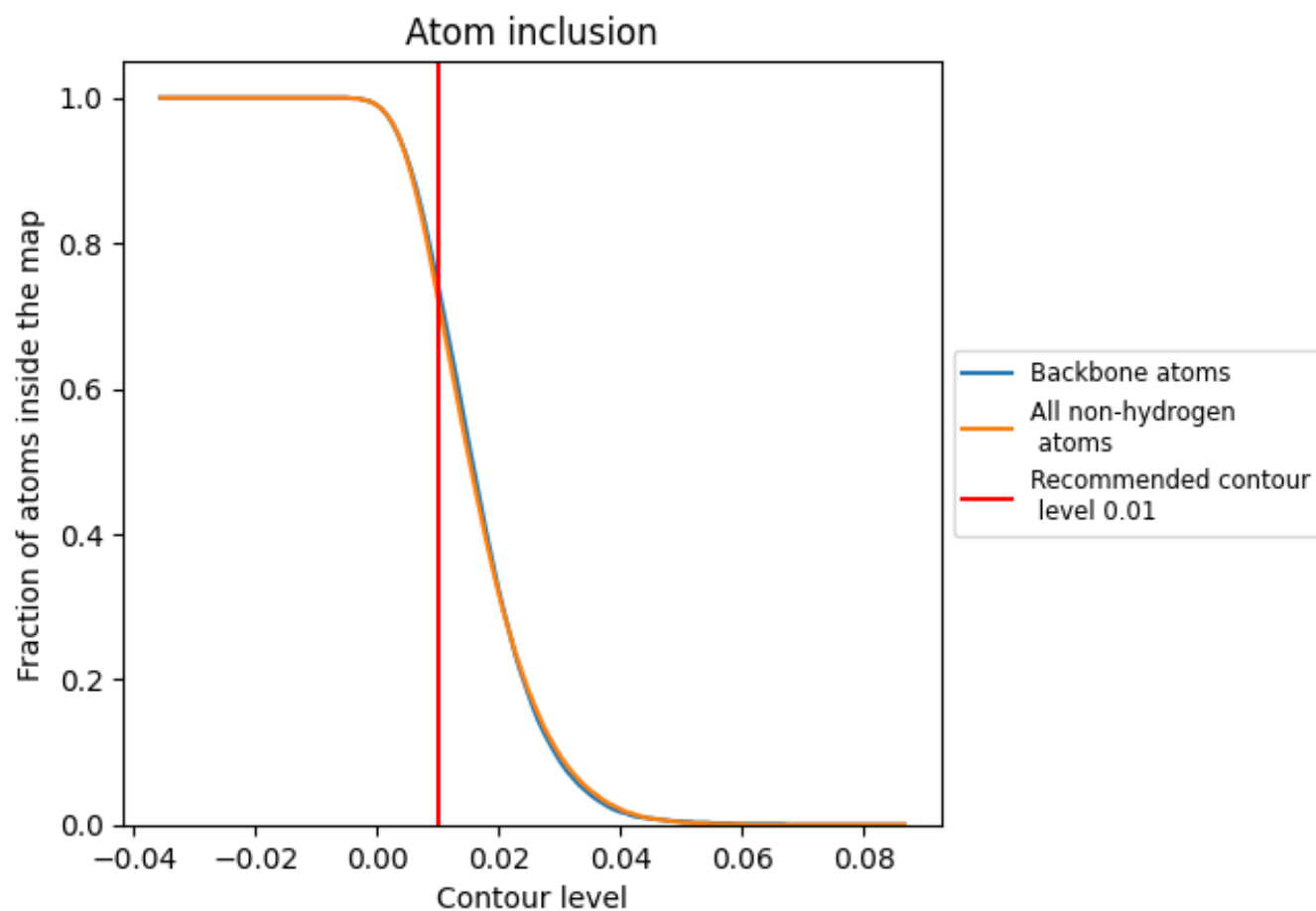
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 72% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7250	 0.4920
11	 0.3240	 0.3870
21	 0.6740	 0.4480
A1	 0.8670	 0.5820
A2	 0.8330	 0.5090
A3	 0.7330	 0.4720
B1	 0.8360	 0.5710
B2	 0.9380	 0.5760
B3	 0.5220	 0.4700
C1	 0.8330	 0.5680
C2	 0.9040	 0.5530
C3	 0.6090	 0.4970
D1	 0.8330	 0.5700
D3	 0.6360	 0.5010
E1	 0.7340	 0.5220
E3	 0.3540	 0.3690
F1	 0.8320	 0.5700
F3	 0.6040	 0.4890
G1	 0.7820	 0.5450
G3	 0.5350	 0.4560
H1	 0.6550	 0.4750
H3	 0.4400	 0.3870
I1	 0.7610	 0.5480
I3	 0.3260	 0.3730
J1	 0.5200	 0.4220
J3	 0.6090	 0.5010
K1	 0.7810	 0.5430
K3	 0.6350	 0.4830
L1	 0.8100	 0.5470
L3	 0.2720	 0.3370
M1	 0.7550	 0.5370
M3	 0.6720	 0.5450
N1	 0.8700	 0.5850
N3	 0.0650	 0.2000
O1	 0.6580	 0.5030























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Chain	Atom inclusion	Q-score
O3	 0.6690	 0.5200
P1	 0.7610	 0.5420
P3	 0.6680	 0.5140
Q1	 0.7600	 0.5370
Q3	 0.4030	 0.3740
R1	 0.8500	 0.5750
R3	 0.5150	 0.4300
S1	 0.8470	 0.5750
S3	 0.3960	 0.3910
T1	 0.7590	 0.5510
T3	 0.4570	 0.4090
U1	 0.7770	 0.5460
U3	 0.4880	 0.4100
V1	 0.7510	 0.5420
V3	 0.3810	 0.4100
W1	 0.9120	 0.5920
W3	 0.5390	 0.4760
X1	 0.6500	 0.4800
X3	 0.7350	 0.5470
Y1	 0.7960	 0.5440
Y3	 0.6650	 0.5310
Z1	 0.8100	 0.5610
Z3	 0.5560	 0.4400
a1	 0.7890	 0.5860
a3	 0.3960	 0.4130
b1	 0.7930	 0.5690
b3	 0.6970	 0.5340
c1	 0.7630	 0.5470
c3	 0.5380	 0.4480
d1	 0.8110	 0.5620
d3	 0.5060	 0.4760
e1	 0.0490	 0.1620
e3	 0.5320	 0.4550
f1	 0.0550	 0.1720
f3	 0.4570	 0.4340
g3	 0.0870	 0.2050
h3	 0.2280	 0.2930
j3	 0.8360	 0.5790
k3	 0.8320	 0.5730
l1	 0.0220	 0.1540
l3	 0.8320	 0.5660
m1	 0.8710	 0.5660

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Chain	Atom inclusion	Q-score
m3	 0.8030	 0.5430
n1	 0.1820	 0.3090
n3	 0.7290	 0.5140
o3	 0.8040	 0.5550
p3	 0.6620	 0.4980
q3	 0.7460	 0.5350
r3	 0.7860	 0.5530
s3	 0.7130	 0.5150
t3	 0.7640	 0.5430
u3	 0.7940	 0.5490