



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 03:32 AM UTC

PDB ID : 7OYA / pdb_00007oya
EMDB ID : EMD-13111
Title : Cryo-EM structure of the 1 hpf zebrafish embryo 80S ribosome
Authors : Leesch, F.; Lorenzo-Orts, L.; Grishkovskaya, I.; Kandolf, S.; Belacic, K.; Meinhart, A.; Haselbach, D.; Pauli, A.
Deposited on : 2021-06-24
Resolution : 3.20 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

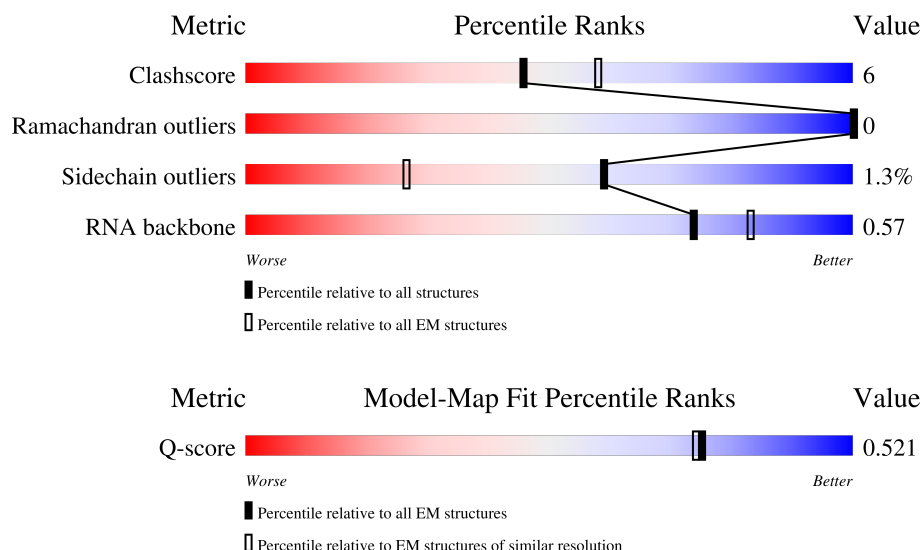
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.20 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	15020 (2.70 - 3.70)

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	22	1939	
2	A2	308	
3	B2	267	

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Mol	Chain	Length	Quality of chain
4	C2	280	
5	E2	263	
6	G2	249	
7	H2	194	
8	I2	208	
9	J2	194	
10	L2	159	
11	N2	151	
12	O2	151	
13	R2	134	
14	V2	81	
15	W2	130	
16	X2	143	
17	Y2	132	
18	a2	115	
19	b2	84	
20	e2	133	
21	D2	245	
22	F2	204	
23	K2	166	
24	P2	145	
25	Q2	146	
26	U2	119	
27	c2	69	
28	d2	56	

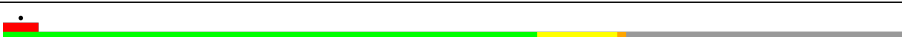
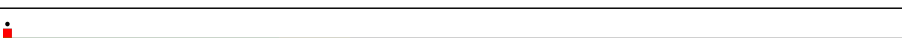
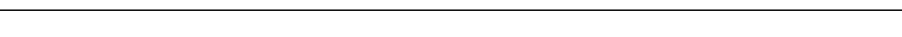
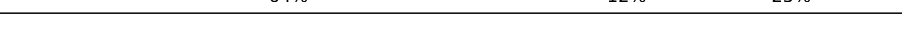
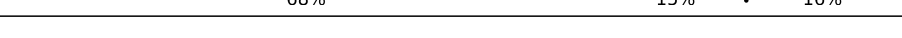
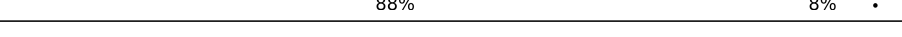
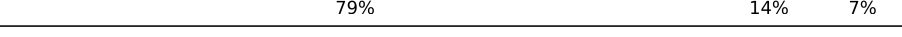
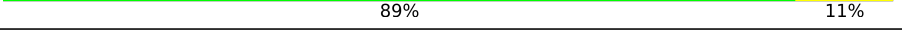
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Mol	Chain	Length	Quality of chain
29	g2	317	
30	Z2	124	
31	T2	146	
32	S2	152	
33	i2	347	
34	Z1	136	
35	b1	64	
36	c1	117	
37	d1	123	
38	e1	135	
39	f1	110	
40	g1	117	
41	h1	123	
42	i1	105	
43	j1	97	
44	k1	70	
45	o1	106	
46	p1	92	
47	A1	257	
48	B1	403	
49	C1	375	
50	D1	296	
51	E1	265	
52	F1	246	
53	G1	266	

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Mol	Chain	Length	Quality of chain
54	H1	192	
55	J1	178	
56	L1	211	
57	M1	139	
58	N1	204	
59	O1	205	
60	P1	184	
61	Q1	182	
62	R1	196	
63	T1	160	
64	U1	141	
65	V1	140	
66	W1	157	
67	X1	155	
68	Y1	145	
69	l1	51	
70	n1	25	
71	r1	138	
72	I1	215	
73	S1	176	
74	m1	128	
75	a1	148	
76	51	4269	
77	71	120	
78	81	158	

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Mol	Chain	Length	Quality of chain
79	q1	392	16%26%70% .
80	v2	858	13%11%87% .
81	11	155	81%74%14%11% .
82	s1	109	13%13%84% .

2 Entry composition

There are 84 unique types of molecules in this entry. The entry contains 199905 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	22	1531	Total	C	N	O	P	0	0
			32731	14610	5931	10660	1530		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A2	210	Total	C	N	O	S	0	0
			1665	1061	290	305	9		

- Molecule 3 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B2	213	Total	C	N	O	S	0	0
			1730	1097	310	309	14		

- Molecule 4 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C2	215	Total	C	N	O	S	0	0
			1669	1080	286	294	9		

- Molecule 5 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E2	261	Total	C	N	O	S	0	0
			2073	1322	385	357	9		

- Molecule 6 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G2	237	Total	C	N	O	S	0	0
			1925	1199	391	328	7		

- Molecule 7 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	H2	186	Total	C	N	O	0	0
			1492	952	276	264		

- Molecule 8 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I2	188	Total	C	N	O	S	0	0
			1531	964	305	257	5		

- Molecule 9 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J2	180	Total	C	N	O	S	0	0
			1492	952	295	243	2		

- Molecule 10 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L2	136	Total	C	N	O	S	0	0
			1110	703	215	186	6		

- Molecule 11 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	N2	149	Total	C	N	O	S	0	0
			1200	767	230	202	1		

- Molecule 12 is a protein called Ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	O2	133	Total	C	N	O	S	0	0
			993	609	194	184	6		

- Molecule 13 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	R2	130	Total	C	N	O	S	0	0
			1053	662	194	193	4		

- Molecule 14 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	V2	81	Total	C	N	O	S	0	0
			623	384	116	119	4		

- Molecule 15 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	W2	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 16 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	X2	139	Total	C	N	O	S	0	0
			1083	684	215	181	3		

- Molecule 17 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Y2	124	Total	C	N	O	S	0	0
			1011	643	193	170	5		

- Molecule 18 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	a2	98	Total	C	N	O	S	0	0
			782	486	161	130	5		

- Molecule 19 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	b2	82	Total	C	N	O	S	0	0
			645	403	122	113	7		

- Molecule 20 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	e2	50	Total	C	N	O	0	0
			399	244	88	67		

- Molecule 21 is a protein called DNA-(apurinic or apyrimidinic site) lyase.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	D2	218	Total	C	N	O	S	0	0
			1668	1061	298	302	7		

- Molecule 22 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	F2	157	Total	C	N	O	S	0	0
			1234	770	229	230	5		

- Molecule 23 is a protein called Ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	K2	94	Total	C	N	O	S	0	0
			771	506	132	128	5		

- Molecule 24 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	P2	112	Total	C	N	O	S	0	0
			927	589	170	161	7		

- Molecule 25 is a protein called Ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Q2	139	Total	C	N	O	S	0	0
			1104	703	207	191	3		

- Molecule 26 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	U2	97	Total	C	N	O	S	0	0
			754	473	139	138	4		

- Molecule 27 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	c2	62	Total	C	N	O	S	0	0
			482	293	95	92	2		

- Molecule 28 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	d2	49	Total	C	N	O	S	0	0
			406	255	83	63	5		

- Molecule 29 is a protein called Guanine nucleotide-binding protein subunit beta-2-like 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	g2	309	Total	C	N	O	S	0	0
			2388	1505	416	455	12		

- Molecule 30 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Z2	71	Total	C	N	O	S	0	0
			566	365	103	98			

- Molecule 31 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	T2	137	Total	C	N	O	S	0	0
			1058	667	202	185	4		

- Molecule 32 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	S2	139	Total	C	N	O	S	0	0
			1139	716	226	196	1		

- Molecule 33 is a protein called Zgc:103482.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	i2	36	Total	C	N	O	S	0	0
			292	168	65	58	1		

- Molecule 34 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Z1	135	Total	C	N	O	S	0	0
			1105	714	208	179	4		

- Molecule 35 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	b1	49	Total	C	N	O	S	0	0
			419	259	92	67	1		

- Molecule 36 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	c1	93	Total	C	N	O	S	0	0
			721	457	127	131	6		

- Molecule 37 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	d1	107	Total	C	N	O	S	0	0
			888	558	172	156	2		

- Molecule 38 is a protein called Ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	e1	125	Total	C	N	O	S	0	0
			1030	649	212	163	6		

- Molecule 39 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	f1	107	Total	C	N	O	S	0	0
			861	550	171	137	3		

- Molecule 40 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	g1	104	Total	C	N	O	S	0	0
			833	519	172	136	6		

- Molecule 41 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	h1	120	Total	C	N	O	S	0	0
			991	627	197	165	2		

- Molecule 42 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	i1	98	Total	C	N	O	S	0	0
			801	502	170	125	4		

- Molecule 43 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	j1	86	Total	C	N	O	S	0	0
			701	430	155	110	6		

- Molecule 44 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	k1	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 45 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o1	102	Total	C	N	O	S	0	0
			840	526	172	136	6		

- Molecule 46 is a protein called Zgc:171772.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	p1	91	Total	C	N	O	S	0	0
			703	444	132	120	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
47	A1	245	Total	C	N	O	S	0	0
			1879	1181	381	310	7		

- Molecule 48 is a protein called Ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	B1	394	Total	C	N	O	S	0	0
			3181	2021	600	544	16		

- Molecule 49 is a protein called Ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	C1	348	Total	C	N	O	S	0	0
			2774	1741	551	464	18		

- Molecule 50 is a protein called Ribosomal protein L5b.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	D1	288	Total	C	N	O	S	0	0
			2337	1482	429	415	11		

- Molecule 51 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	E1	206	Total	C	N	O	S	0	0
			1672	1064	327	274	7		

- Molecule 52 is a protein called Ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	F1	222	Total	C	N	O	S	0	0
			1811	1160	346	298	7		

- Molecule 53 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	G1	207	Total	C	N	O	S	0	0
			1683	1076	322	281	4		

- Molecule 54 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	H1	190	Total	C	N	O	S	0	0
			1505	949	279	271	6		

- Molecule 55 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	J1	167	Total	C	N	O	S	0	0
			1348	854	254	235	5		

- Molecule 56 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	L1	197	Total	C	N	O	S	0	0
			1603	1003	335	260	5		

- Molecule 57 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	M1	134	Total	C	N	O	S	0	0
			1094	702	207	180	5		

- Molecule 58 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	N1	202	Total	C	N	O	S	0	0
			1689	1065	352	267	5		

- Molecule 59 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	O1	204	Total	C	N	O	S	0	0
			1662	1073	318	266	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	P1	152	Total	C	N	O	S	0	0
			1235	770	243	213	9		

- Molecule 61 is a protein called Ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Q1	180	Total	C	N	O	S	0	0
			1459	917	302	236	4		

- Molecule 62 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	R1	166	Total	C	N	O	S	0	0
			1381	856	300	215	10		

- Molecule 63 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	T1	157	Total	C	N	O	S	0	0
			1283	816	250	213	4		

- Molecule 64 is a protein called Ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	U1	97	Total	C	N	O	S	0	0
			792	508	138	144	2		

- Molecule 65 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	V1	129	Total	C	N	O	S	0	0
			970	613	182	170	5		

- Molecule 66 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	W1	60	Total	C	N	O	S	0	0
			503	323	98	80	2		

- Molecule 67 is a protein called Ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	X1	117	Total	C	N	O	S	0	0
			959	614	179	165	1		

- Molecule 68 is a protein called ATPase H⁺ transporting V0 subunit e1.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Y1	122	Total	C	N	O	S	0	0
			1024	643	209	169	3		

- Molecule 69 is a protein called Ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	l1	49	Total	C	N	O	S	0	0
			434	275	97	61	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
70	n1	24	Total	C	N	O	S	0	0
			231	140	63	26	2		

- Molecule 71 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	r1	118	Total	C	N	O	S	0	0
			943	589	193	159	2		

- Molecule 72 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	I1	201	Total	C	N	O	S	0	0
			1630	1037	315	264	14		

- Molecule 73 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	S1	176	Total	C	N	O	S	0	0
			1457	934	284	230	9		

- Molecule 74 is a protein called 60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	m1	50	Total	C	N	O	S	0	0
			413	256	87	64	6		

- Molecule 75 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	a1	147	Total	C	N	O	S	0	0
			1164	740	233	188	3		

- Molecule 76 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	51	3321	Total	C	N	O	P	0	0
			71140	31690	12986	23144	3320		

- Molecule 77 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	71	120	Total	C	N	O	P	0	0
			2563	1145	465	834	119		

- Molecule 78 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	81	158	Total	C	N	O	P	0	0
			3363	1501	600	1104	158		

- Molecule 79 is a protein called Novel protein similar to human proliferation-associated 2G4 protein (PA2G4).

Mol	Chain	Residues	Atoms					AltConf	Trace
79	q1	118	Total	C	N	O	S	0	0
			943	599	165	169	10		

- Molecule 80 is a protein called Eukaryotic translation elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	v2	110	Total	C	N	O	S	0	0
			885	569	147	164	5		

- Molecule 81 is a protein called Eukaryotic translation initiation factor 5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	11	138	Total	C	N	O	S	0	0
			1055	656	183	205	11		

- Molecule 82 is a protein called Dap1b.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	s1	17	Total	C	N	O	S	0	0
			139	87	29	22	1		

- Molecule 83 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
83	a2	1	Total	Zn	0
			1	1	
83	d2	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
83	g1	1	Total 1	Zn 1	0
83	j1	1	Total 1	Zn 1	0
83	o1	1	Total 1	Zn 1	0
83	p1	1	Total 1	Zn 1	0
83	m1	1	Total 1	Zn 1	0

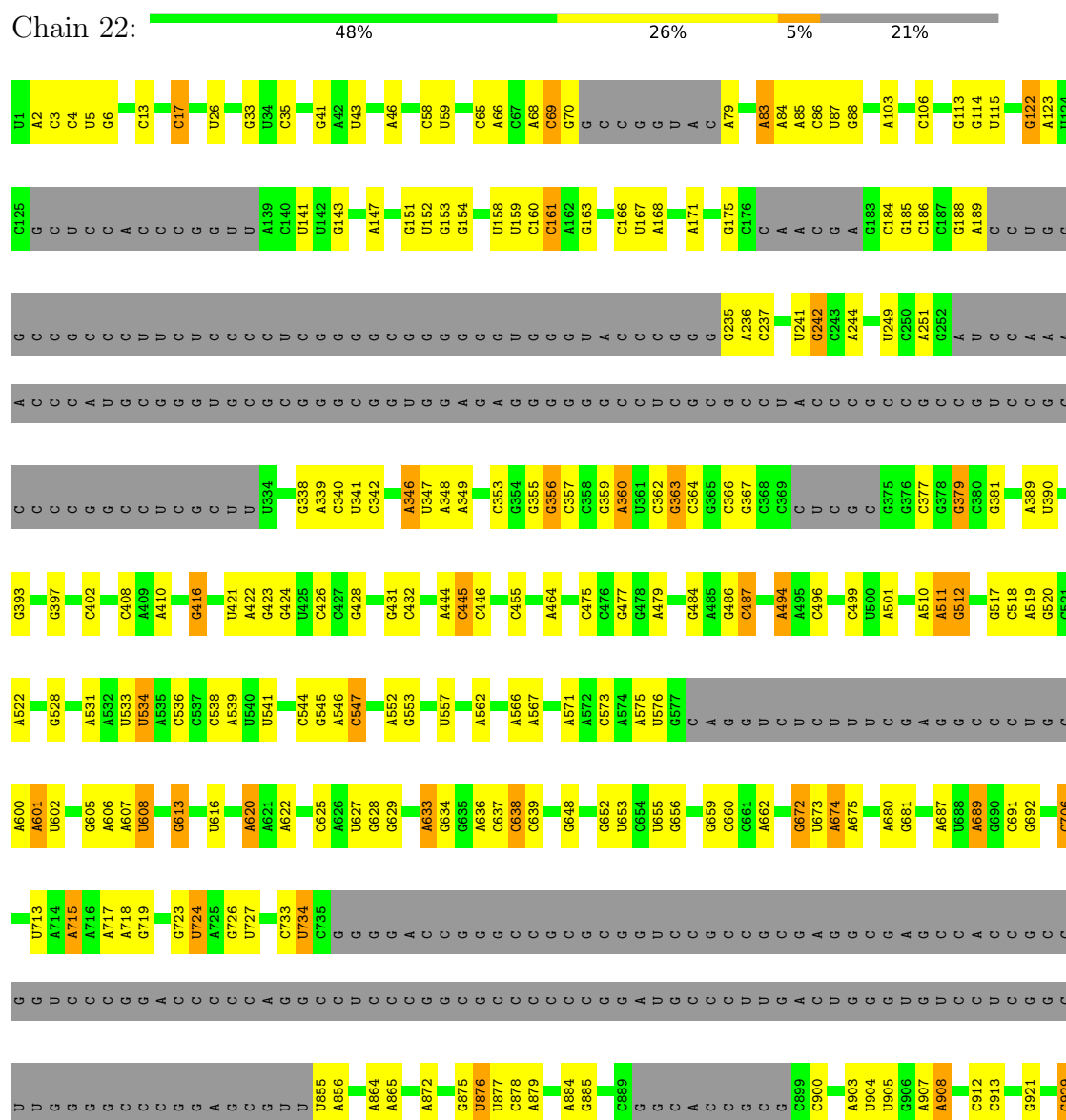
- Molecule 84 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

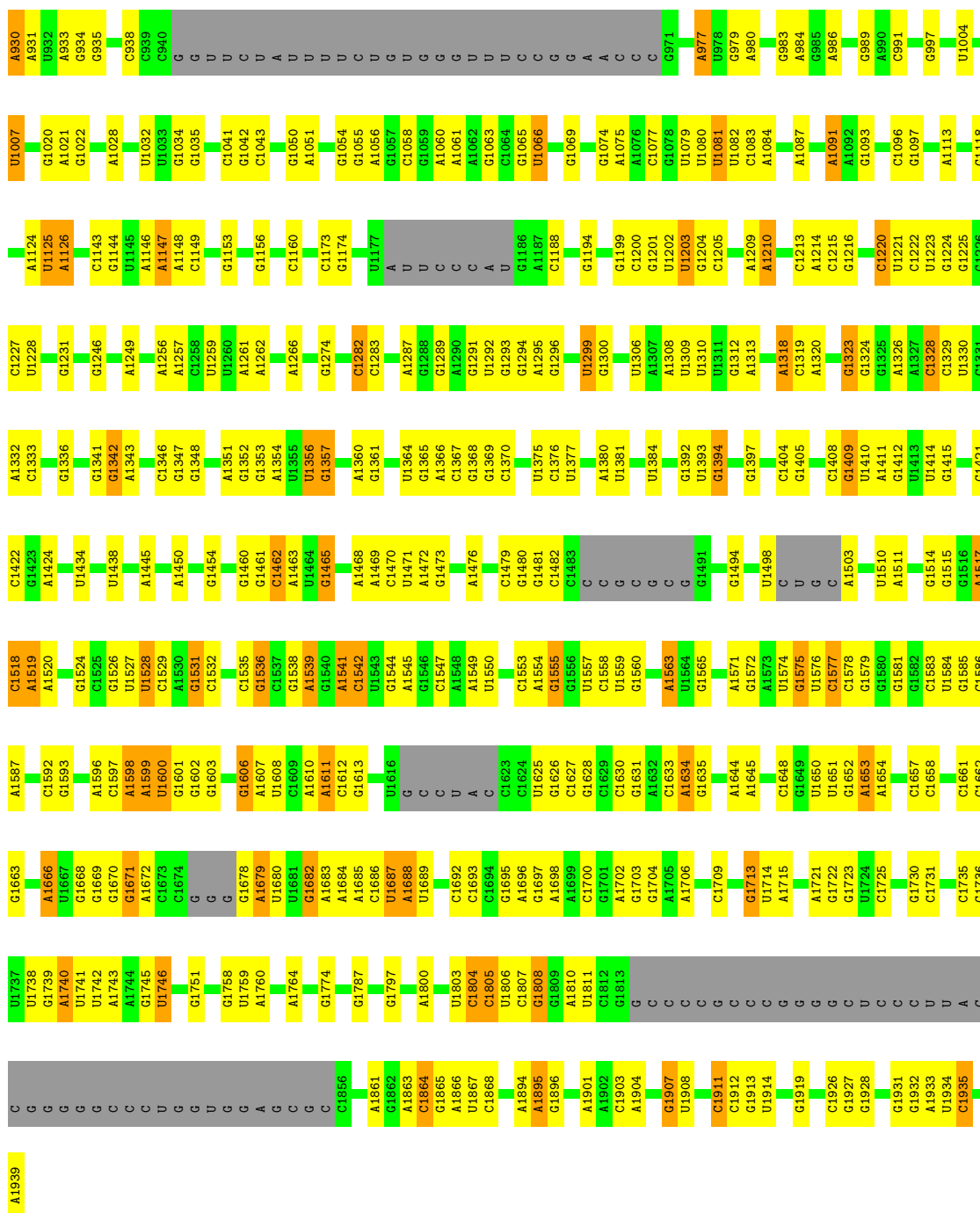
Mol	Chain	Residues	Atoms		AltConf
84	b1	1	Total 1	Mg 1	0
84	A1	1	Total 1	Mg 1	0
84	B1	1	Total 1	Mg 1	0
84	V1	1	Total 1	Mg 1	0
84	S1	1	Total 1	Mg 1	0
84	m1	1	Total 1	Mg 1	0
84	51	186	Total 186	Mg 186	0
84	71	5	Total 5	Mg 5	0
84	81	5	Total 5	Mg 5	0

3 Residue-property plots [i](#)

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

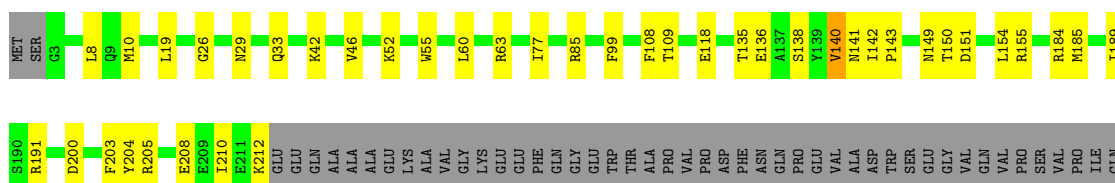
• Molecule 1: 18S rRNA



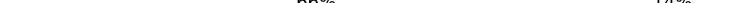


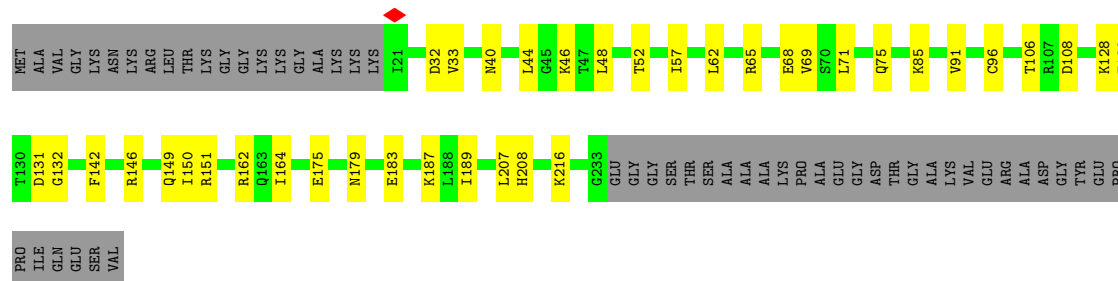
• Molecule 2: 40S ribosomal protein SA

Chain A2: 55% 13% 32%

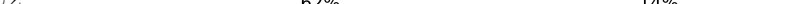


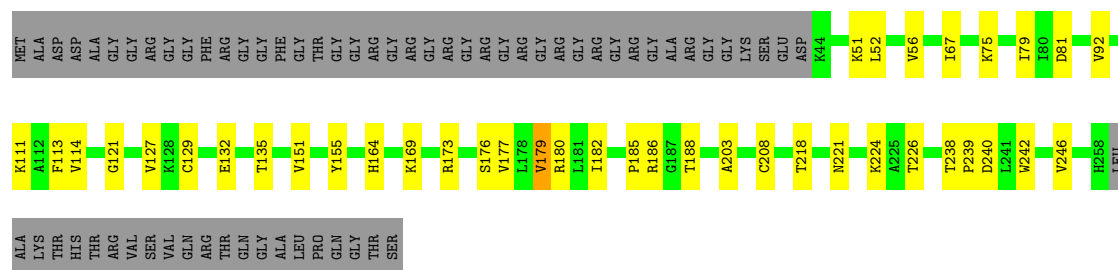
- Molecule 3: 40S ribosomal protein S3a

Chain B2:  66% 14% 20%



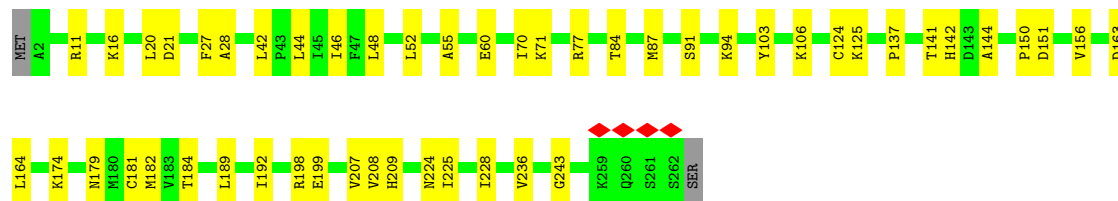
- Molecule 4: 40S ribosomal protein S2

Chain C2:  62% 14% 23%

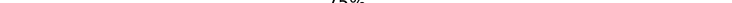


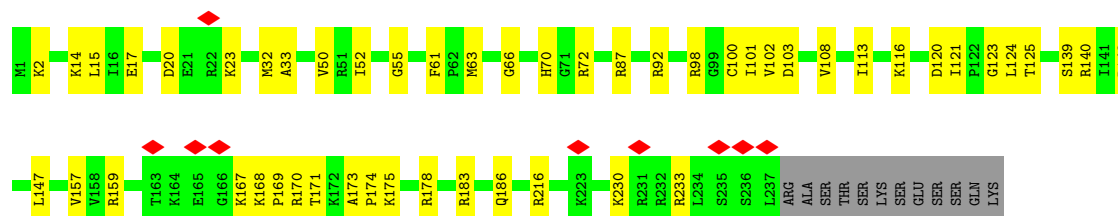
- Molecule 5: 40S ribosomal protein S4, X isoform

Chain E2:  80% 19%

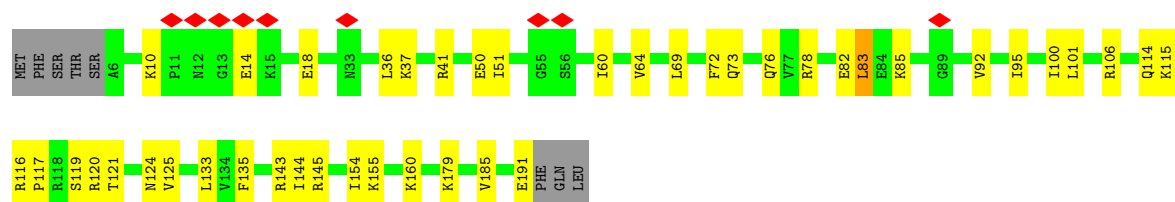
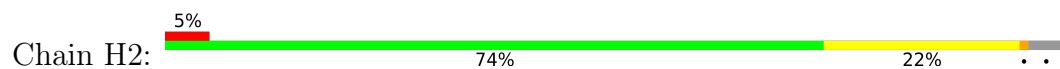


- Molecule 6: 40S ribosomal protein S6

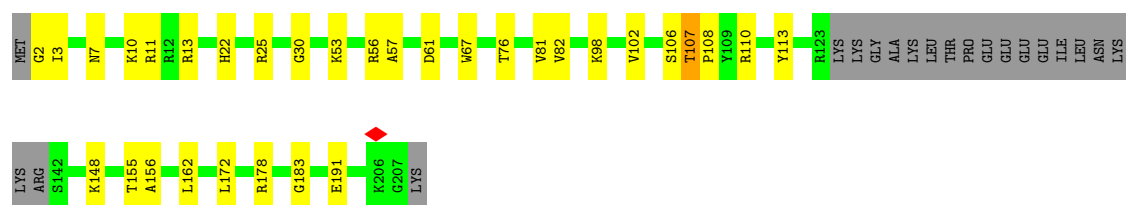
Chain G2:  75% 20% 5%



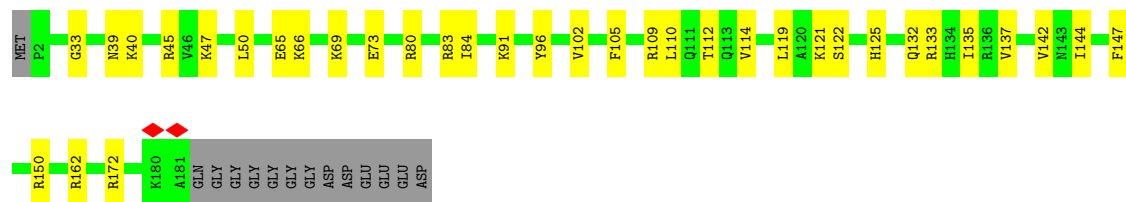
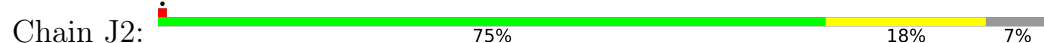
- Molecule 7: 40S ribosomal protein S7



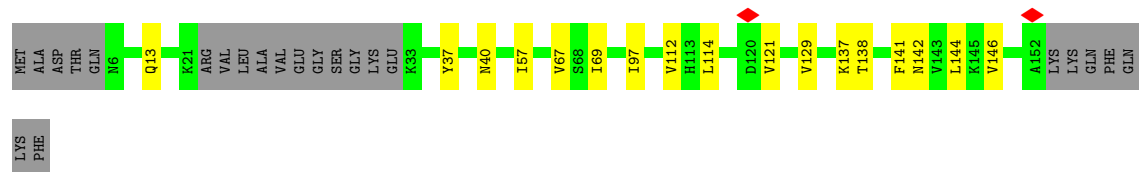
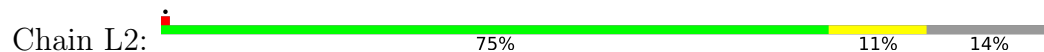
- Molecule 8: 40S ribosomal protein S8



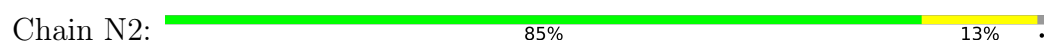
- Molecule 9: 40S ribosomal protein S9



- Molecule 10: 40S ribosomal protein S11



- Molecule 11: 40S ribosomal protein S13



- Molecule 12: Ribosomal protein S14



- Molecule 18: 40S ribosomal protein S26

Chain a2: 



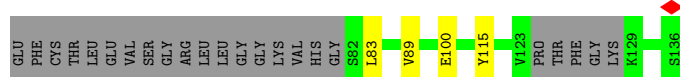
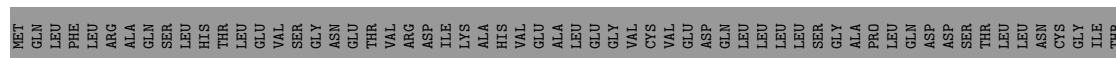
- Molecule 19: 40S ribosomal protein S27

Chain b2: 



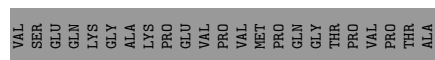
- Molecule 20: 40S ribosomal protein S30

Chain e2: 



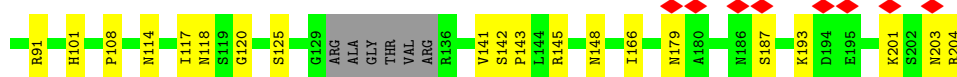
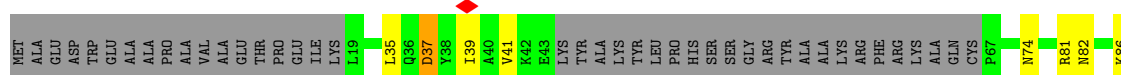
- Molecule 21: DNA-(apurinic or apyrimidinic site) lyase

Chain D2: 

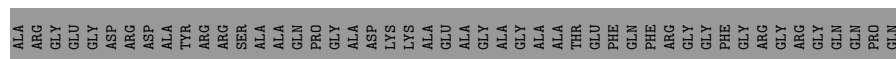
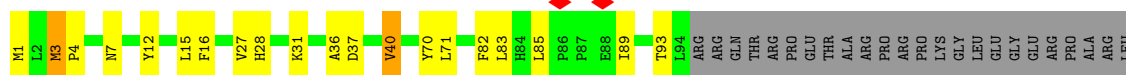


- Molecule 22: Ribosomal protein S5

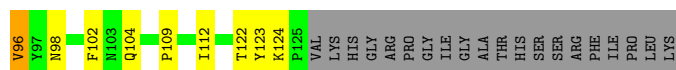
Chain F2: 



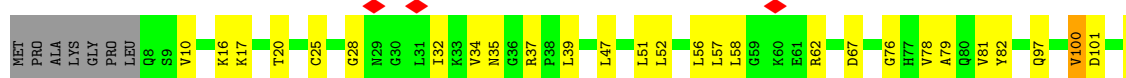
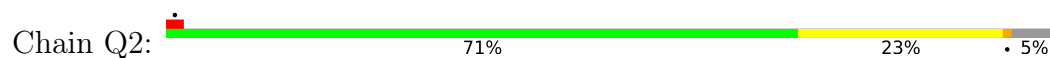
- Molecule 23: Ribosomal protein S10



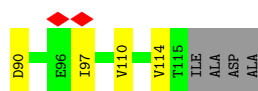
- Molecule 24: 40S ribosomal protein S15



- Molecule 25: Ribosomal protein S16



- Molecule 26: 40S ribosomal protein S20



- Molecule 27: 40S ribosomal protein S28

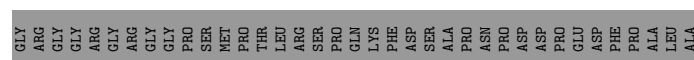
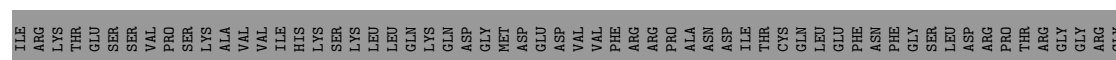
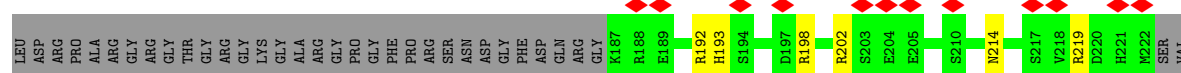
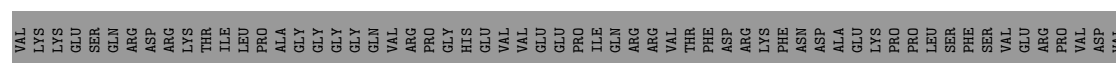
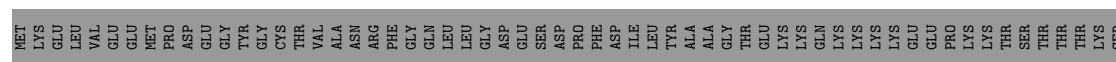


- Molecule 28: 40S ribosomal protein S29



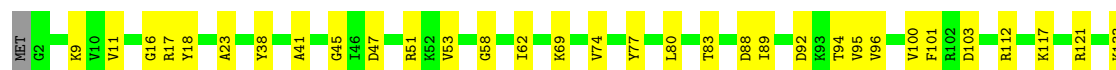
- Molecule 33: Zgc:103482

Chain i2: 9% 90%



- Molecule 34: 60S ribosomal protein L27

Chain Z1: 76% 24%



- Molecule 35: 60S ribosomal protein L29

Chain b1: 69% 8% 23%



- Molecule 36: 60S ribosomal protein L30

Chain c1: 74% 6% 21%



- Molecule 37: 60S ribosomal protein L31

Chain d1: 



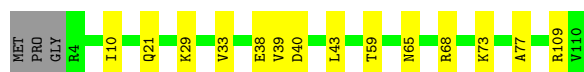
- Molecule 38: Ribosomal protein L32

Chain e1: 



- Molecule 39: 60S ribosomal protein L35a

Chain f1: 



- Molecule 40: 60S ribosomal protein L34

Chain g1: 



- Molecule 41: 60S ribosomal protein L35

Chain h1: 



- Molecule 42: 60S ribosomal protein L36

Chain i1: 



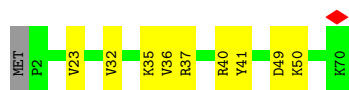
- Molecule 43: Ribosomal protein L37

Chain j1: 



- Molecule 44: 60S ribosomal protein L38

Chain k1: 



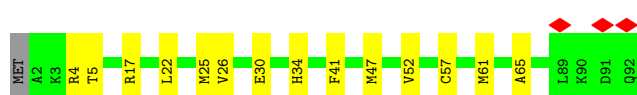
- Molecule 45: 60S ribosomal protein L36a

Chain o1: 



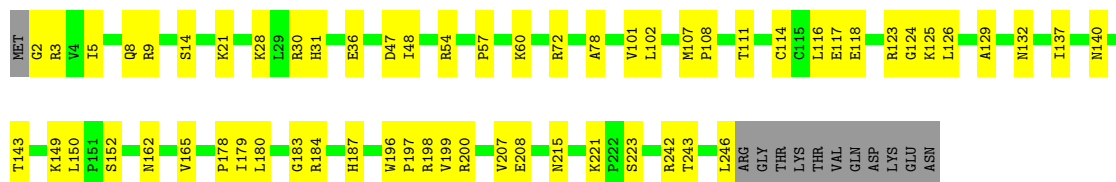
- Molecule 46: Zgc:171772

Chain p1: 



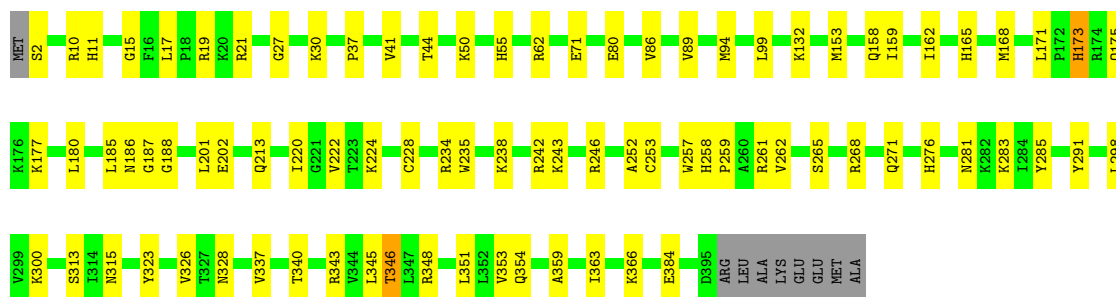
- Molecule 47: 60S ribosomal protein L8

Chain A1: 



- Molecule 48: Ribosomal protein L3

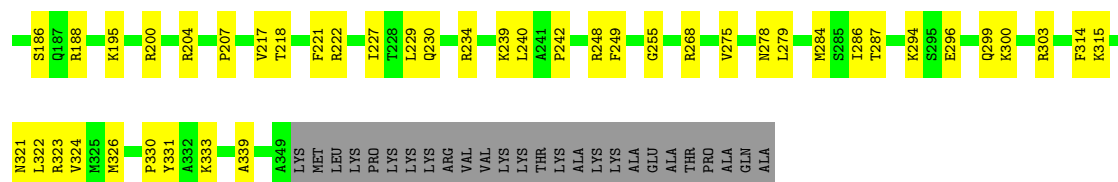
Chain B1: 



- Molecule 49: Ribosomal protein L4

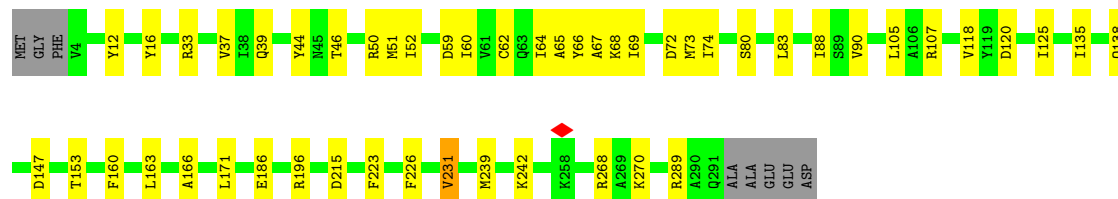
Chain C1: 





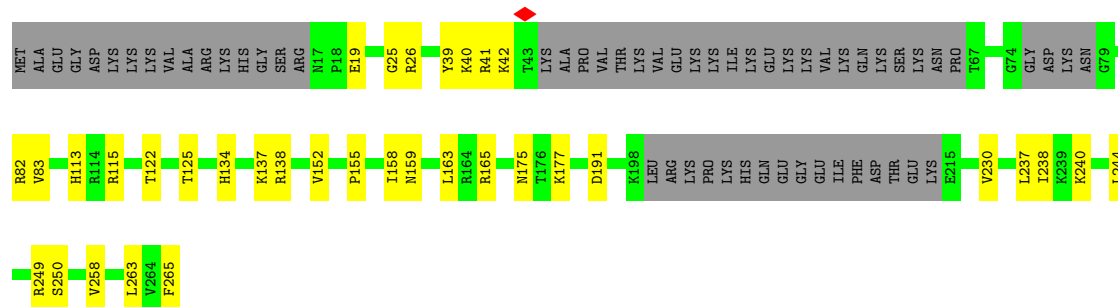
- Molecule 50: Ribosomal protein L5b

Chain D1: 80% 17% .



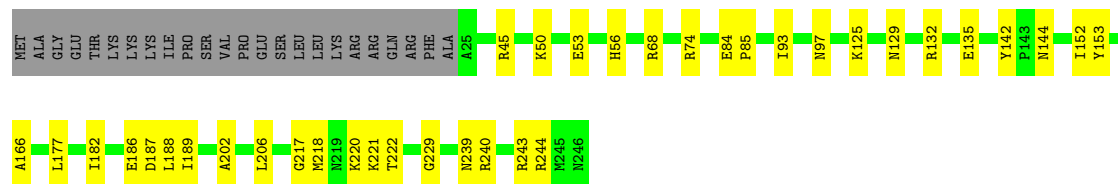
- Molecule 51: 60S ribosomal protein L6

Chain E1: 65% 13% 22%



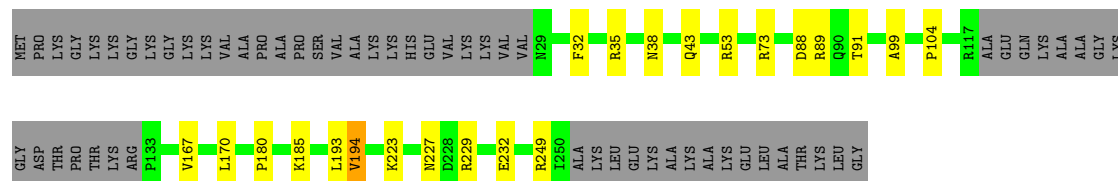
- Molecule 52: Ribosomal protein L7

Chain F1: 75% 15% 10%

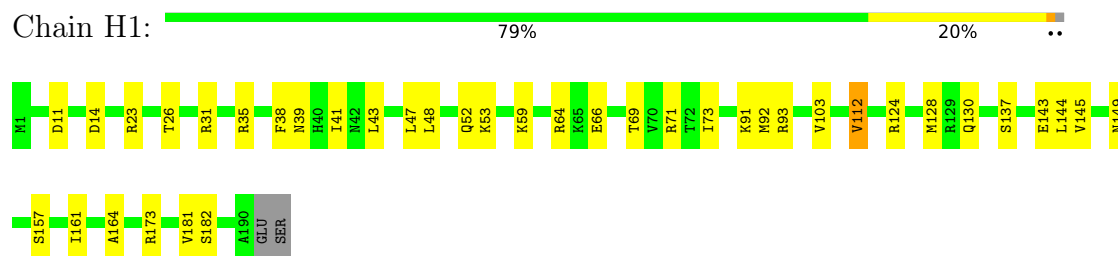


- Molecule 53: 60S ribosomal protein L7a

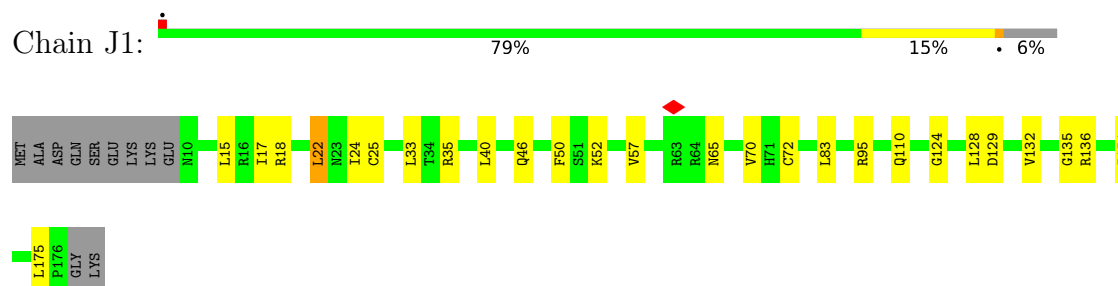
Chain G1: 70% 8% 22%



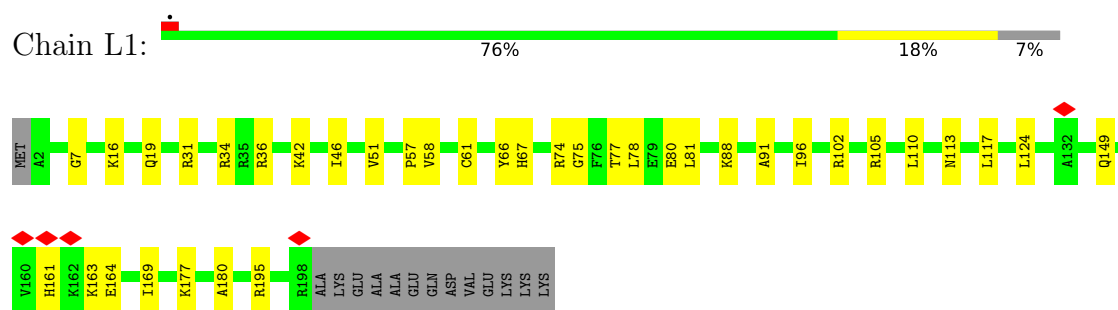
- Molecule 54: 60S ribosomal protein L9



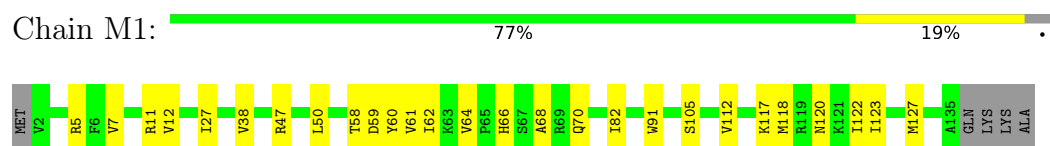
- Molecule 55: 60S ribosomal protein L11



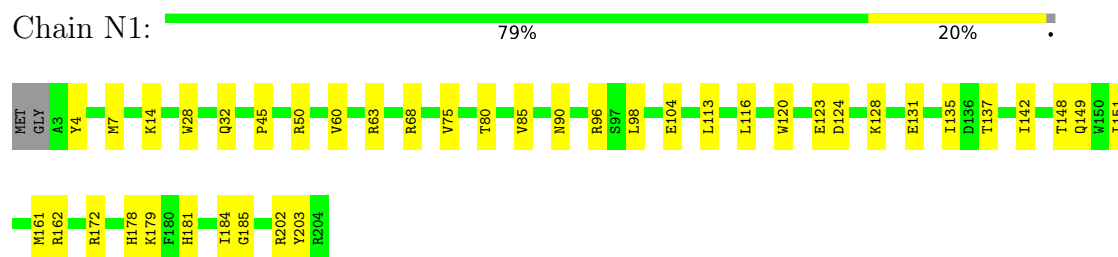
- Molecule 56: 60S ribosomal protein L13



- Molecule 57: 60S ribosomal protein L14

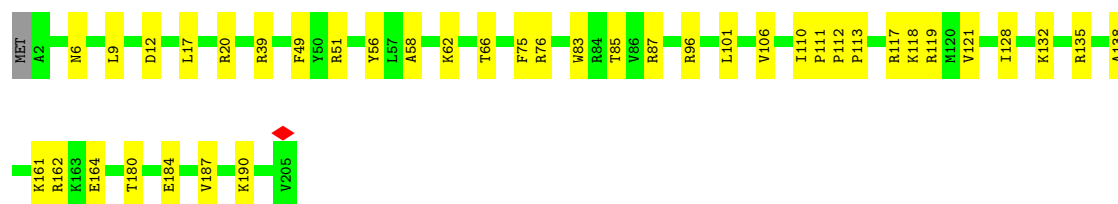


- Molecule 58: Ribosomal protein L15



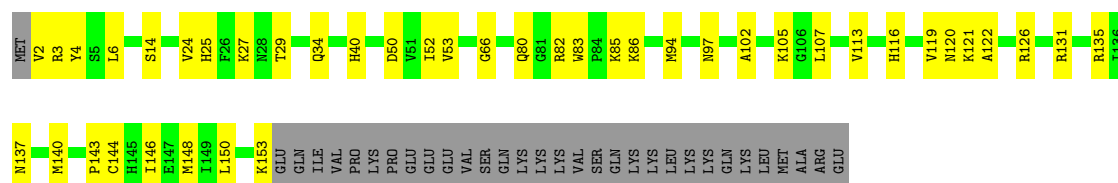
- Molecule 59: 60S ribosomal protein L13a

Chain O1:  80% 19%



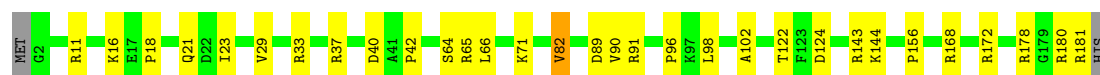
- Molecule 60: 60S ribosomal protein L17

Chain P1:  60% 23% 17%



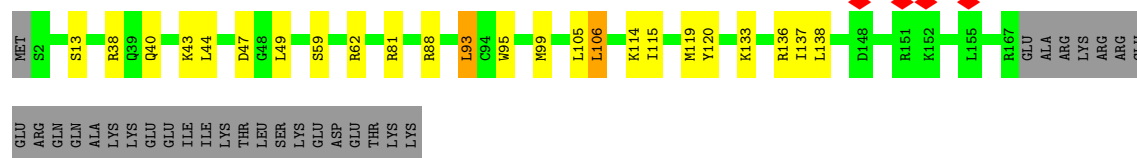
- Molecule 61: Ribosomal protein L18

Chain Q1:  82% 16% ..



- Molecule 62: 60S ribosomal protein L19

Chain R1:  72% 11% 15%



- Molecule 63: 60S ribosomal protein L21

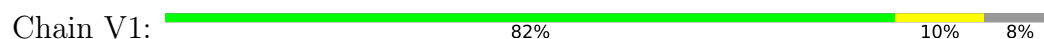
Chain T1:  88% 9% ..



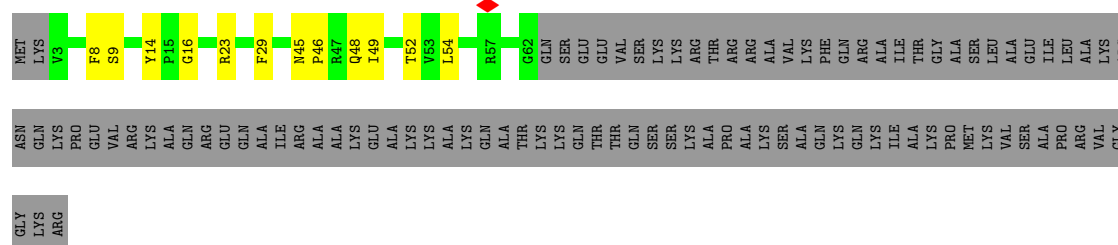
- Molecule 64: Ribosomal protein L22

Chain U1:  60% 9% 31%

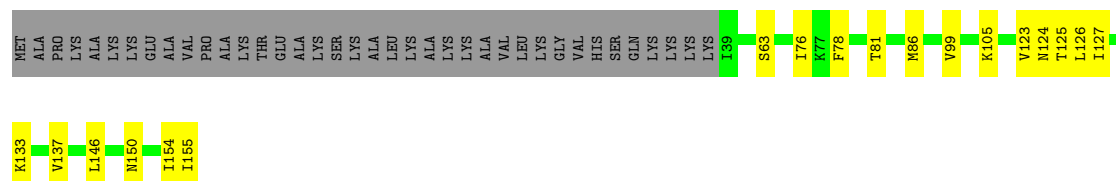
- Molecule 65: 60S ribosomal protein L23



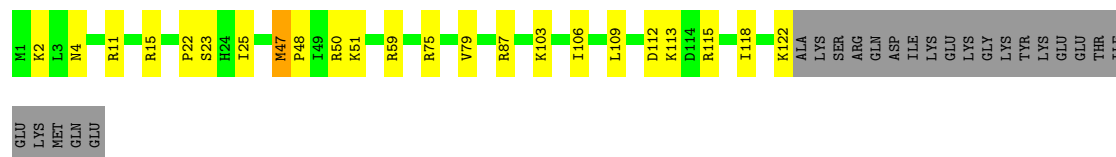
- Molecule 66: 60S ribosomal protein L24



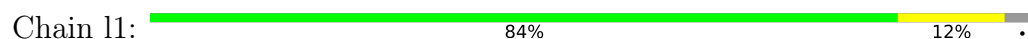
- Molecule 67: Ribosomal protein L23a



- Molecule 68: ATPase H⁺ transporting V0 subunit e1



- Molecule 69: Ribosomal protein L39





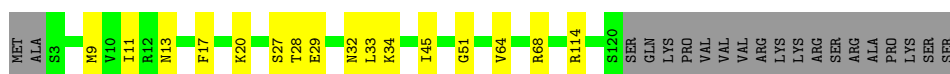
- Molecule 70: 60S ribosomal protein L41

Chain n1: 88% 8%



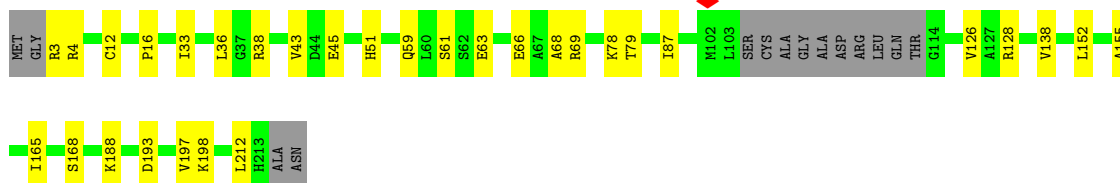
- Molecule 71: 60S ribosomal protein L28

Chain r1: 74% 12% 14%



- Molecule 72: 60S ribosomal protein L10

Chain l1: 79% 14% 7%



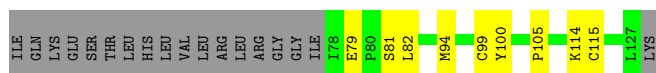
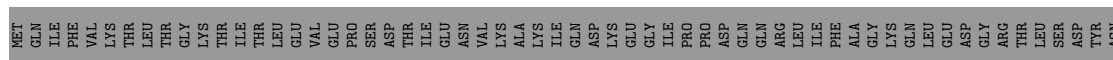
- Molecule 73: 60S ribosomal protein L18a

Chain S1: 89% 11%



- Molecule 74: 60S ribosomal protein L40

Chain m1: 32% 7% 61%

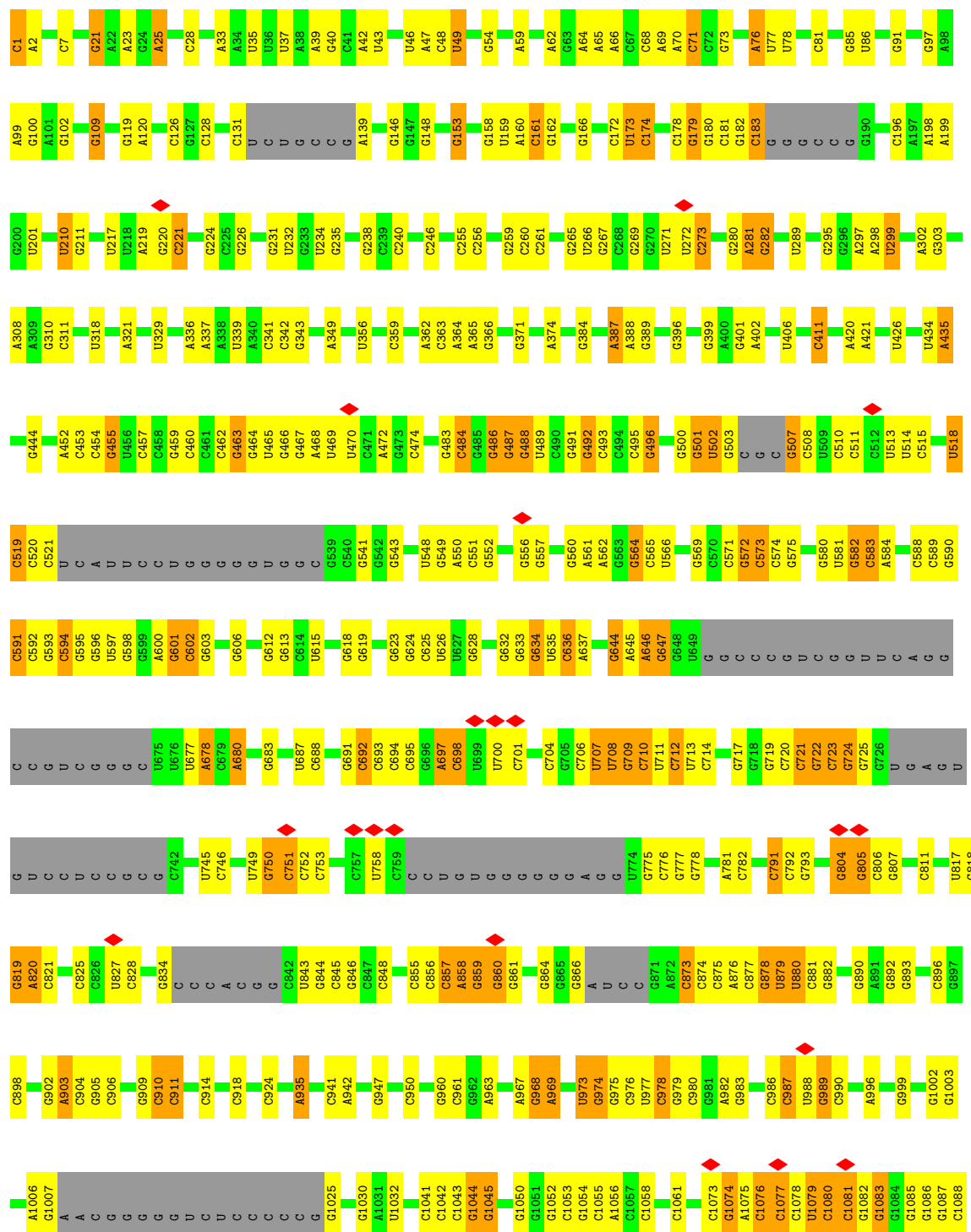


- Molecule 75: 60S ribosomal protein L27a

Chain a1: 79% 20%



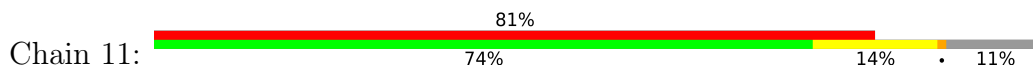
• Molecule 76: 28S rRNA

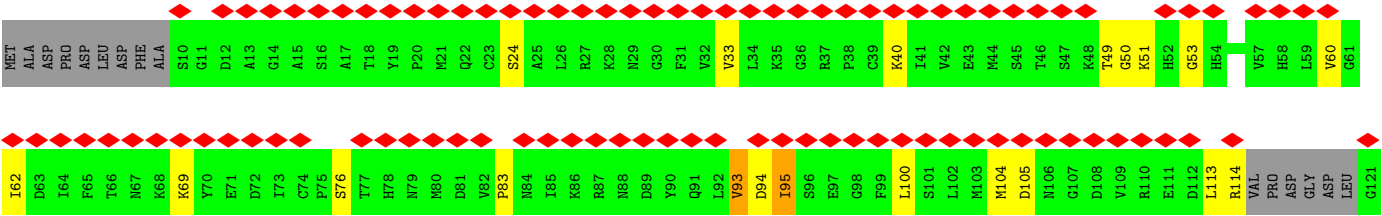




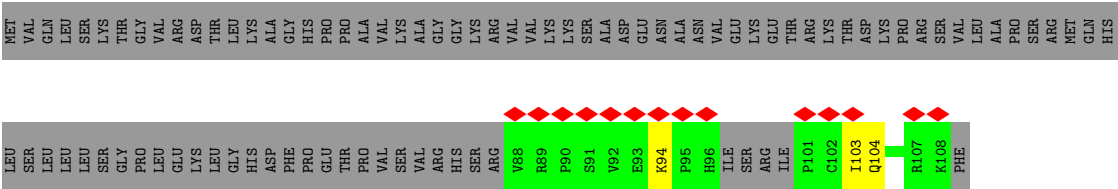
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C4019	U3890	G3784	A3647	G3518	C	C	C	C	C3156	G3036	A2906	G	G	A	C	G	G
C4020	C3891	A3785	A3648	A3519	A	A	U	C	G3157	G3037	C2910	C	C	C	G	G	G
A4022	G3893	A3786	U3651	C3520	C	C	C	C	G3160	A3044	A2913	U	C	C	U	C	U
G4025	U3003	C3787	C3655	A3521	C	C	C	C	A3161	U3046	C2914	C	C	C	U	C	U
G4026	C3904	G3788	A3656	G3522	C	C	C	C	A3165	G3047	A3045	G	G	C	U	C	U
C4027	U3789	A3790	A3657	A3523	C	C	C	C	A3166	C3048	C2921	C	C	C	U	C	U
C4028	U3906	A3791	G3659	A3524	C	C	C	C	A3167	C3049	A2922	C	C	C	G	G	G
C4029	G3907	C3792	U3528	U3528	U	U	G	G	A3168	C3059	A2923	C	C	C	C	C	C
C4030	C3908	C3793	C3529	C3529	C	C	C	C	C3169	U3074	C2924	C	C	C	C	U	C
G4031	G3909	U3794	U3533	U3533	C	C	C	C	G3069	U3077	G2932	C	C	C	C	U	C
G4032	G3795	G3796	A3536	A3536	G	G	G	G	G3070	A3077	G2939	C	C	C	C	G	G
G4033	C3914	G3797	C3669	C3669	C	C	C	C	G3071	U3078	U2940	C	C	C	C	C	C
U4034	C3915	U3800	C3670	U3670	C	C	U	G	C3072	G3079	G2941	C	C	C	C	G	G
A4035	G3928	U3672	U3672	G3540	C	C	C	U	G3182	A3073	A2942	G	C	C	C	C	C
A4036	G3809	C3673	A3541	A3541	C	C	C	C	A3188	U3074	A2942	U	C	C	C	A	C
A4042	G3933	G3673	C3673	C	C	C	C	A	A	U3074	U2948	C	C	C	C	C	C
A	A3812	G3684	G3684	A3549	G	G	C	A	A3207	A3077	G2949	C	C	C	C	C	C
G	G3813	G3684	G3684	A3550	C	C	C	A	A3207	U3078	G2949	C	C	C	C	C	C
C	C3814	G3684	G3684	A3550	C	C	C	U	A	G3079	A2952	C	C	C	C	A	A
C	C3815	U3688	U3688	C3556	C	C	C	C	A	U3079	U2953	C	C	C	C	U	U
C	A3816	C3689	C3689	U3557	C	C	C	C	G	G3083	U2953	C	C	C	C	C	C
C	G3817	A3690	A3690	U3558	C	C	C	C	U	C3083	C2960	C	C	C	C	C	C
U	C3828	U3699	U3699	G3559	C	C	C	C	G	A3088	C2960	C	C	C	C	C	C
C	U3955	C3829	C3829	C3571	G	G	C	C	A	A3088	C2970	C	C	C	C	C	C
U	G3956	G3708	G3708	A3572	C	C	U	U	G	U3098	C2971	C	C	C	C	C	C
C	C3830	U3713	U3713	G3573	A	A	C	C	G	G3099	A2972	U	C	C	C	C	C
C	U3834	U3716	U3716	U3574	C	C	C	C	U	U3100	U2973	C	C	C	C	C	C
G	G3835	C3420	C3420	C3574	C	C	C	C	G	C3103	C2974	C	C	C	C	C	C
G	A3836	C3430	C3430	C3582	C	C	C	C	U	U3113	G2982	C	C	C	C	C	C
G	U3837	C3431	C3431	C3586	C	C	C	C	U	U3113	G2982	C	C	C	C	C	C
G	G3838	C3437	C3437	C3587	C	C	C	C	A	A3116	A2986	C	C	C	C	C	C
C	A3841	U3725	U3725	G3588	C	C	C	C	A	G3117	U3005	C	C	C	C	C	C
C	G3842	C3732	C3732	C3589	C	C	C	C	U	C3118	A3006	C	C	C	C	C	C
C	C3843	A3732	A3732	G3590	C	C	C	C	A	A3119	A3007	C	C	C	C	C	C
C	G3844	C3734	C3734	A3593	C	C	C	C	A	A3120	C3009	C	C	C	C	C	C
C	G3845	G3451	G3451	G3594	C	C	C	C	U	A3121	C3009	C	C	C	C	C	C
G	G3851	G3452	G3452	C3595	C	C	C	C	U	A3122	G3010	C	C	C	C	C	C
C	C3852	G3459	G3459	G3596	C	C	C	C	G	A3127	G3011	C	C	C	C	C	C
C	A3856	G3471	G3471	G3597	C	C	C	C	U	G3128	C3012	C	C	C	C	C	C
C	G3857	A3471	A3471	C3598	U	U	C	C	A	C3129	G3013	C	C	C	C	C	C
C	U3858	C3740	C3740	G3599	C	C	C	C	G	C3130	A3020	C	C	C	C	C	C
C	A3859	C3753	C3753	C3600	C	C	C	C	G	C3137	C3021	C	C	C	C	C	C
C	G3860	U3760	U3760	C3610	C	C	C	C	C	C3138	U3024	C	C	C	C	C	C
C	U3861	G3762	G3762	U3611	G	G	C	C	C	G3139	G3025	C	C	C	C	C	C
C	C3862	U3768	U3768	U3612	G	G	C	C	C	G3140	A3026	C	C	C	C	C	C
C	U3870	C3774	C3774	C3617	G	G	C	C	C	G3141	G2885	C	C	C	C	C	C
C	A3871	A3501	A3501	U3618	U	U	C	C	G	C3147	G2886	C	C	C	C	C	C
C	G3872	C3775	C3775	U3618	C	C	C	C	G	A3150	A2995	C	C	C	C	C	C
C	U3887	G3634	G3634	G3617	G	G	C	C	U	U3151	U2901	C	C	C	C	C	C
C	G3888	G3645	G3645	G3645	C	C	C	C	U	U3152	U2904	C	C	C	C	C	C

Chain v2: 13% 11% 87%





• Molecule 82: Dap1b



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	535633	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	43	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	8.712	Depositor
Minimum map value	-0.551	Depositor
Average map value	0.089	Depositor
Map value standard deviation	0.284	Depositor
Recommended contour level	0.9	Depositor
Map size (Å)	508.8, 508.8, 508.8	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 5CT, MG, ZN

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	22	0.08	0/36607	0.16	0/57041
2	A2	0.08	0/1703	0.23	0/2313
3	B2	0.09	0/1757	0.23	0/2353
4	C2	0.09	0/1705	0.23	0/2304
5	E2	0.09	0/2113	0.27	0/2842
6	G2	0.09	0/1948	0.29	0/2595
7	H2	0.08	0/1515	0.25	0/2033
8	I2	0.10	0/1558	0.28	0/2081
9	J2	0.10	0/1517	0.28	0/2028
10	L2	0.10	0/1130	0.26	0/1513
11	N2	0.09	0/1223	0.25	0/1644
12	O2	0.09	0/1006	0.27	0/1348
13	R2	0.08	0/1067	0.23	0/1433
14	V2	0.09	0/629	0.25	0/842
15	W2	0.10	0/1051	0.25	0/1406
16	X2	0.10	0/1100	0.27	0/1468
17	Y2	0.08	0/1027	0.26	0/1364
18	a2	0.10	0/795	0.26	0/1066
19	b2	0.09	0/658	0.25	0/884
20	e2	0.09	0/401	0.28	0/526
21	D2	0.09	0/1694	0.25	0/2286
22	F2	0.08	0/1247	0.25	0/1676
23	K2	0.08	0/793	0.21	0/1073
24	P2	0.09	0/943	0.26	0/1260
25	Q2	0.09	0/1121	0.27	0/1501
26	U2	0.08	0/763	0.27	0/1027
27	c2	0.09	0/484	0.29	0/649
28	d2	0.10	0/416	0.28	0/553
29	g2	0.08	0/2445	0.26	0/3335
30	Z2	0.08	0/573	0.25	0/770
31	T2	0.09	0/1076	0.26	0/1445
32	S2	0.09	0/1157	0.29	0/1554

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	i2	0.09	0/296	0.29	0/389
34	Z1	0.11	0/1128	0.26	0/1504
35	b1	0.10	0/429	0.27	0/568
36	c1	0.09	0/731	0.21	0/981
37	d1	0.11	0/903	0.29	0/1217
38	e1	0.11	0/1048	0.29	0/1396
39	f1	0.12	0/880	0.28	0/1175
40	g1	0.11	0/843	0.29	0/1123
41	h1	0.10	0/998	0.27	0/1318
42	i1	0.11	0/812	0.29	0/1074
43	j1	0.12	0/715	0.32	0/944
44	k1	0.08	0/575	0.23	0/761
45	o1	0.10	0/853	0.27	0/1125
46	p1	0.09	0/713	0.22	0/945
47	A1	0.11	0/1918	0.27	0/2569
48	B1	0.11	0/3251	0.27	0/4351
49	C1	0.11	0/2828	0.28	0/3797
50	D1	0.09	0/2380	0.25	0/3185
51	E1	0.10	0/1698	0.28	0/2265
52	F1	0.11	0/1842	0.27	0/2460
53	G1	0.10	0/1717	0.28	0/2316
54	H1	0.10	0/1523	0.26	0/2048
55	J1	0.09	0/1371	0.27	0/1833
56	L1	0.11	0/1631	0.30	0/2178
57	M1	0.10	0/1115	0.25	0/1488
58	N1	0.12	0/1731	0.30	0/2314
59	O1	0.11	0/1694	0.27	0/2267
60	P1	0.11	0/1261	0.29	0/1691
61	Q1	0.11	0/1484	0.31	0/1985
62	R1	0.10	0/1397	0.29	0/1849
63	T1	0.10	0/1312	0.26	0/1756
64	U1	0.08	0/806	0.26	0/1081
65	V1	0.11	0/984	0.26	0/1320
66	W1	0.11	0/516	0.29	0/688
67	X1	0.10	0/978	0.24	0/1318
68	Y1	0.10	0/1039	0.28	0/1383
69	l1	0.11	0/444	0.29	0/587
70	n1	0.13	0/232	0.37	0/295
71	r1	0.10	0/956	0.29	0/1279
72	I1	0.10	0/1668	0.26	0/2229
73	S1	0.12	0/1496	0.29	0/2009
74	m1	0.11	0/419	0.30	0/555
75	a1	0.11	0/1196	0.27	0/1601

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	51	0.14	5/79560 (0.0%)	0.19	11/124065 (0.0%)
77	71	0.09	0/2867	0.13	0/4469
78	81	0.09	0/3757	0.15	0/5853
79	q1	0.08	0/960	0.24	0/1280
80	v2	0.06	0/904	0.22	0/1224
81	11	0.09	0/1053	0.28	0/1411
82	s1	0.43	0/142	1.25	1/189 (0.5%)
All	All	0.11	5/214276 (0.0%)	0.22	12/313921 (0.0%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
76	51	3166	A	O3'-P	-10.29	1.45	1.61
76	51	3168	A	O3'-P	-9.36	1.47	1.61
76	51	3169	C	O3'-P	-8.90	1.47	1.61
76	51	3716	G	O3'-P	-8.01	1.49	1.61
76	51	3656	A	O3'-P	-7.64	1.49	1.61

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
76	51	3716	G	P-O3'-C3'	12.47	138.91	120.20
76	51	3656	A	C1'-C2'-O2'	-11.96	90.46	108.40
82	s1	104	GLN	N-CA-C	10.86	126.14	112.24
76	51	3168	A	C4'-C3'-O3'	-8.68	99.98	113.00
76	51	3168	A	C3'-C2'-O2'	6.57	120.55	110.70

There are no chirality outliers.

There are no planarity outliers.

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	22	32731	0	16535	344	0
2	A2	1665	0	1667	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B2	1730	0	1802	25	0
4	C2	1669	0	1752	25	0
5	E2	2073	0	2187	29	0
6	G2	1925	0	2089	39	0
7	H2	1492	0	1583	28	0
8	I2	1531	0	1618	23	0
9	J2	1492	0	1610	26	0
10	L2	1110	0	1166	13	0
11	N2	1200	0	1285	19	0
12	O2	993	0	1019	16	0
13	R2	1053	0	1105	28	0
14	V2	623	0	630	14	0
15	W2	1034	0	1080	19	0
16	X2	1083	0	1150	16	0
17	Y2	1011	0	1085	18	0
18	a2	782	0	828	15	0
19	b2	645	0	667	10	0
20	e2	399	0	434	4	0
21	D2	1668	0	1719	39	0
22	F2	1234	0	1274	21	0
23	K2	771	0	788	14	0
24	P2	927	0	971	33	0
25	Q2	1104	0	1170	25	0
26	U2	754	0	805	16	0
27	c2	482	0	500	14	0
28	d2	406	0	403	11	0
29	g2	2388	0	2326	54	0
30	Z2	566	0	617	13	0
31	T2	1058	0	1100	20	0
32	S2	1139	0	1177	29	0
33	i2	292	0	271	6	0
34	Z1	1105	0	1182	22	0
35	b1	419	0	430	4	0
36	c1	721	0	751	4	0
37	d1	888	0	927	13	0
38	e1	1030	0	1116	13	0
39	f1	861	0	912	9	0
40	g1	833	0	910	19	0
41	h1	991	0	1122	20	0
42	i1	801	0	881	6	0
43	j1	701	0	733	19	0
44	k1	569	0	637	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
45	o1	840	0	911	11	0
46	p1	703	0	755	12	0
47	A1	1879	0	1974	50	0
48	B1	3181	0	3303	65	0
49	C1	2774	0	2909	59	0
50	D1	2337	0	2389	31	0
51	E1	1672	0	1814	25	0
52	F1	1811	0	1937	26	0
53	G1	1683	0	1787	17	0
54	H1	1505	0	1589	23	0
55	J1	1348	0	1393	14	0
56	L1	1603	0	1726	29	0
57	M1	1094	0	1161	17	0
58	N1	1689	0	1744	31	0
59	O1	1662	0	1806	30	0
60	P1	1235	0	1261	29	0
61	Q1	1459	0	1580	29	0
62	R1	1381	0	1520	17	0
63	T1	1283	0	1355	13	0
64	U1	792	0	814	9	0
65	V1	970	0	1031	9	0
66	W1	503	0	512	8	0
67	X1	959	0	1022	13	0
68	Y1	1024	0	1112	23	0
69	l1	434	0	472	5	0
70	n1	231	0	277	2	0
71	r1	943	0	1013	11	0
72	l1	1630	0	1689	22	0
73	S1	1457	0	1518	17	0
74	m1	413	0	446	6	0
75	a1	1164	0	1205	27	0
76	51	71140	0	35974	613	0
77	71	2563	0	1297	12	0
78	81	3363	0	1707	42	0
79	q1	943	0	958	10	0
80	v2	885	0	864	8	0
81	11	1055	0	1059	14	0
82	s1	139	0	147	5	0
83	a2	1	0	0	0	0
83	d2	1	0	0	0	0
83	g1	1	0	0	0	0
83	j1	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
83	m1	1	0	0	0	0
83	o1	1	0	0	0	0
83	p1	1	0	0	0	0
84	51	186	0	0	0	0
84	71	5	0	0	0	0
84	81	5	0	0	0	0
84	A1	1	0	0	0	0
84	B1	1	0	0	0	0
84	S1	1	0	0	0	0
84	V1	1	0	0	0	0
84	b1	1	0	0	0	0
84	m1	1	0	0	0	0
All	All	199905	0	150045	1981	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 6.

The worst 5 of 1981 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:22:1097:G:H1	1:22:1144:G:HO2'	1.21	0.87
76:51:460:C:H42	76:51:596:G:H1	1.25	0.84
76:51:989:G:H21	76:51:990:C:H41	1.27	0.81
1:22:1526:G:H2'	1:22:1528:U:H3	1.43	0.81
76:51:1383:A:H5'	76:51:1384:G:H5'	1.64	0.80

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	
2	A2	208/308 (68%)	206 (99%)	2 (1%)	0	100	100
3	B2	211/267 (79%)	203 (96%)	8 (4%)	0	100	100
4	C2	213/280 (76%)	211 (99%)	2 (1%)	0	100	100
5	E2	259/263 (98%)	249 (96%)	10 (4%)	0	100	100
6	G2	235/249 (94%)	228 (97%)	7 (3%)	0	100	100
7	H2	184/194 (95%)	173 (94%)	11 (6%)	0	100	100
8	I2	184/208 (88%)	180 (98%)	4 (2%)	0	100	100
9	J2	178/194 (92%)	177 (99%)	1 (1%)	0	100	100
10	L2	132/159 (83%)	127 (96%)	5 (4%)	0	100	100
11	N2	147/151 (97%)	145 (99%)	2 (1%)	0	100	100
12	O2	131/151 (87%)	127 (97%)	4 (3%)	0	100	100
13	R2	128/134 (96%)	126 (98%)	2 (2%)	0	100	100
14	V2	79/81 (98%)	78 (99%)	1 (1%)	0	100	100
15	W2	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
16	X2	137/143 (96%)	130 (95%)	7 (5%)	0	100	100
17	Y2	122/132 (92%)	118 (97%)	4 (3%)	0	100	100
18	a2	96/115 (84%)	96 (100%)	0	0	100	100
19	b2	80/84 (95%)	78 (98%)	2 (2%)	0	100	100
20	e2	46/133 (35%)	46 (100%)	0	0	100	100
21	D2	216/245 (88%)	208 (96%)	8 (4%)	0	100	100
22	F2	151/204 (74%)	144 (95%)	7 (5%)	0	100	100
23	K2	92/166 (55%)	87 (95%)	5 (5%)	0	100	100
24	P2	110/145 (76%)	107 (97%)	3 (3%)	0	100	100
25	Q2	137/146 (94%)	131 (96%)	6 (4%)	0	100	100
26	U2	95/119 (80%)	92 (97%)	3 (3%)	0	100	100
27	c2	60/69 (87%)	60 (100%)	0	0	100	100
28	d2	47/56 (84%)	47 (100%)	0	0	100	100
29	g2	307/317 (97%)	292 (95%)	15 (5%)	0	100	100
30	Z2	69/124 (56%)	67 (97%)	2 (3%)	0	100	100
31	T2	135/146 (92%)	130 (96%)	5 (4%)	0	100	100
32	S2	137/152 (90%)	131 (96%)	6 (4%)	0	100	100
33	i2	34/347 (10%)	30 (88%)	4 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	Z1	133/136 (98%)	128 (96%)	5 (4%)	0	100	100
35	b1	47/64 (73%)	44 (94%)	3 (6%)	0	100	100
36	c1	91/117 (78%)	90 (99%)	1 (1%)	0	100	100
37	d1	105/123 (85%)	98 (93%)	7 (7%)	0	100	100
38	e1	123/135 (91%)	120 (98%)	3 (2%)	0	100	100
39	f1	105/110 (96%)	103 (98%)	2 (2%)	0	100	100
40	g1	102/117 (87%)	99 (97%)	3 (3%)	0	100	100
41	h1	118/123 (96%)	116 (98%)	2 (2%)	0	100	100
42	i1	96/105 (91%)	93 (97%)	3 (3%)	0	100	100
43	j1	84/97 (87%)	82 (98%)	2 (2%)	0	100	100
44	k1	67/70 (96%)	67 (100%)	0	0	100	100
45	o1	100/106 (94%)	97 (97%)	3 (3%)	0	100	100
46	p1	89/92 (97%)	88 (99%)	1 (1%)	0	100	100
47	A1	243/257 (95%)	234 (96%)	9 (4%)	0	100	100
48	B1	392/403 (97%)	379 (97%)	13 (3%)	0	100	100
49	C1	346/375 (92%)	338 (98%)	8 (2%)	0	100	100
50	D1	286/296 (97%)	283 (99%)	3 (1%)	0	100	100
51	E1	198/265 (75%)	191 (96%)	7 (4%)	0	100	100
52	F1	220/246 (89%)	216 (98%)	4 (2%)	0	100	100
53	G1	203/266 (76%)	196 (97%)	7 (3%)	0	100	100
54	H1	188/192 (98%)	184 (98%)	4 (2%)	0	100	100
55	J1	165/178 (93%)	162 (98%)	3 (2%)	0	100	100
56	L1	195/211 (92%)	191 (98%)	4 (2%)	0	100	100
57	M1	132/139 (95%)	126 (96%)	6 (4%)	0	100	100
58	N1	200/204 (98%)	194 (97%)	6 (3%)	0	100	100
59	O1	202/205 (98%)	201 (100%)	1 (0%)	0	100	100
60	P1	150/184 (82%)	142 (95%)	8 (5%)	0	100	100
61	Q1	178/182 (98%)	169 (95%)	9 (5%)	0	100	100
62	R1	164/196 (84%)	162 (99%)	2 (1%)	0	100	100
63	T1	155/160 (97%)	148 (96%)	7 (4%)	0	100	100
64	U1	95/141 (67%)	93 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
65	V1	127/140 (91%)	123 (97%)	4 (3%)	0	100	100
66	W1	58/157 (37%)	57 (98%)	1 (2%)	0	100	100
67	X1	115/155 (74%)	113 (98%)	2 (2%)	0	100	100
68	Y1	120/145 (83%)	118 (98%)	2 (2%)	0	100	100
69	l1	47/51 (92%)	47 (100%)	0	0	100	100
70	n1	22/25 (88%)	22 (100%)	0	0	100	100
71	r1	116/138 (84%)	116 (100%)	0	0	100	100
72	l1	197/215 (92%)	195 (99%)	2 (1%)	0	100	100
73	S1	174/176 (99%)	170 (98%)	4 (2%)	0	100	100
74	m1	48/128 (38%)	48 (100%)	0	0	100	100
75	a1	145/148 (98%)	136 (94%)	9 (6%)	0	100	100
79	q1	114/392 (29%)	110 (96%)	4 (4%)	0	100	100
80	v2	106/858 (12%)	104 (98%)	2 (2%)	0	100	100
81	l1	133/155 (86%)	116 (87%)	17 (13%)	0	100	100
82	s1	13/109 (12%)	12 (92%)	1 (8%)	0	100	100
All	All	10994/14099 (78%)	10667 (97%)	327 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	
2	A2	179/250 (72%)	178 (99%)	1 (1%)	78	84
3	B2	194/231 (84%)	194 (100%)	0	100	100
4	C2	181/220 (82%)	177 (98%)	4 (2%)	45	71
5	E2	227/229 (99%)	225 (99%)	2 (1%)	70	81
6	G2	208/219 (95%)	207 (100%)	1 (0%)	81	85
7	H2	165/176 (94%)	161 (98%)	4 (2%)	43	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	I2	163/181 (90%)	161 (99%)	2 (1%)	63	79
9	J2	160/168 (95%)	159 (99%)	1 (1%)	78	84
10	L2	122/141 (86%)	122 (100%)	0	100	100
11	N2	129/130 (99%)	128 (99%)	1 (1%)	73	82
12	O2	103/119 (87%)	102 (99%)	1 (1%)	68	80
13	R2	118/121 (98%)	117 (99%)	1 (1%)	73	82
14	V2	65/65 (100%)	64 (98%)	1 (2%)	57	76
15	W2	112/113 (99%)	112 (100%)	0	100	100
16	X2	111/115 (96%)	111 (100%)	0	100	100
17	Y2	108/116 (93%)	107 (99%)	1 (1%)	70	81
18	a2	86/99 (87%)	85 (99%)	1 (1%)	63	79
19	b2	74/76 (97%)	70 (95%)	4 (5%)	20	53
20	e2	41/112 (37%)	41 (100%)	0	100	100
21	D2	176/204 (86%)	174 (99%)	2 (1%)	65	79
22	F2	135/170 (79%)	131 (97%)	4 (3%)	36	66
23	K2	82/132 (62%)	79 (96%)	3 (4%)	30	63
24	P2	102/130 (78%)	99 (97%)	3 (3%)	37	67
25	Q2	114/119 (96%)	112 (98%)	2 (2%)	51	74
26	U2	87/105 (83%)	85 (98%)	2 (2%)	44	70
27	c2	54/61 (88%)	53 (98%)	1 (2%)	50	73
28	d2	42/49 (86%)	42 (100%)	0	100	100
29	g2	263/274 (96%)	249 (95%)	14 (5%)	20	53
30	Z2	61/105 (58%)	59 (97%)	2 (3%)	33	65
31	T2	110/117 (94%)	110 (100%)	0	100	100
32	S2	119/132 (90%)	116 (98%)	3 (2%)	42	69
33	i2	32/296 (11%)	31 (97%)	1 (3%)	35	66
34	Z1	115/116 (99%)	114 (99%)	1 (1%)	70	81
35	b1	45/56 (80%)	44 (98%)	1 (2%)	45	71
36	c1	78/98 (80%)	78 (100%)	0	100	100
37	d1	98/110 (89%)	97 (99%)	1 (1%)	68	80
38	e1	113/121 (93%)	112 (99%)	1 (1%)	70	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	f1	86/88 (98%)	86 (100%)	0	100	100
40	g1	91/102 (89%)	91 (100%)	0	100	100
41	h1	108/110 (98%)	105 (97%)	3 (3%)	38	68
42	i1	83/88 (94%)	83 (100%)	0	100	100
43	j1	73/80 (91%)	72 (99%)	1 (1%)	59	77
44	k1	64/65 (98%)	61 (95%)	3 (5%)	23	57
45	o1	91/95 (96%)	91 (100%)	0	100	100
46	p1	74/75 (99%)	73 (99%)	1 (1%)	59	77
47	A1	189/200 (94%)	188 (100%)	1 (0%)	81	85
48	B1	346/353 (98%)	343 (99%)	3 (1%)	70	81
49	C1	291/313 (93%)	287 (99%)	4 (1%)	59	77
50	D1	244/249 (98%)	240 (98%)	4 (2%)	55	75
51	E1	182/234 (78%)	179 (98%)	3 (2%)	55	75
52	F1	189/210 (90%)	188 (100%)	1 (0%)	81	85
53	G1	181/224 (81%)	180 (99%)	1 (1%)	78	84
54	H1	167/169 (99%)	164 (98%)	3 (2%)	51	74
55	J1	141/150 (94%)	136 (96%)	5 (4%)	32	64
56	L1	167/178 (94%)	165 (99%)	2 (1%)	63	79
57	M1	113/117 (97%)	112 (99%)	1 (1%)	70	81
58	N1	171/172 (99%)	170 (99%)	1 (1%)	78	84
59	O1	175/176 (99%)	175 (100%)	0	100	100
60	P1	134/165 (81%)	132 (98%)	2 (2%)	57	76
61	Q1	158/160 (99%)	156 (99%)	2 (1%)	61	78
62	R1	145/173 (84%)	143 (99%)	2 (1%)	59	77
63	T1	138/140 (99%)	137 (99%)	1 (1%)	76	83
64	U1	87/127 (68%)	85 (98%)	2 (2%)	44	70
65	V1	101/108 (94%)	101 (100%)	0	100	100
66	W1	52/129 (40%)	52 (100%)	0	100	100
67	X1	105/134 (78%)	105 (100%)	0	100	100
68	Y1	115/136 (85%)	113 (98%)	2 (2%)	53	75
69	l1	45/47 (96%)	45 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
70	n1	23/24 (96%)	23 (100%)	0	100	100
71	r1	102/120 (85%)	101 (99%)	1 (1%)	68	80
72	l1	173/182 (95%)	173 (100%)	0	100	100
73	S1	155/155 (100%)	155 (100%)	0	100	100
74	m1	46/116 (40%)	46 (100%)	0	100	100
75	a1	121/122 (99%)	121 (100%)	0	100	100
79	q1	105/329 (32%)	100 (95%)	5 (5%)	23	56
80	v2	97/731 (13%)	97 (100%)	0	100	100
81	l1	115/129 (89%)	110 (96%)	5 (4%)	26	59
82	s1	17/97 (18%)	17 (100%)	0	100	100
All	All	9632/12048 (80%)	9507 (99%)	125 (1%)	59	78

5 of 125 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	Z2	54	THR
64	U1	54	GLU
44	k1	32	VAL
63	T1	72	VAL
79	q1	246	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 180 such sidechains are listed below:

Mol	Chain	Res	Type
50	D1	229	ASN
60	P1	64	ASN
52	F1	56	HIS
55	J1	167	GLN
62	R1	34	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	22	1515/1939 (78%)	282 (18%)	10 (0%)
76	51	3300/4269 (77%)	585 (17%)	36 (1%)
77	71	119/120 (99%)	7 (5%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
78	81	157/158 (99%)	27 (17%)	2 (1%)
All	All	5091/6486 (78%)	901 (17%)	48 (0%)

5 of 901 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	22	3	C
1	22	4	C
1	22	17	C
1	22	26	U
1	22	33	G

5 of 48 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
76	51	1080	C
76	51	2205	C
76	51	1231	G
76	51	1795	G
76	51	3044	A

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
81	5CT	11	51	81	13,14,15	0.71	0	8,15,17	1.02	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
81	5CT	11	51	81	-	6/13/14/16	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
81	11	51	5CT	C1-C2-C3-C4
81	11	51	5CT	O1-C2-C3-C4
81	11	51	5CT	C2-C1-NZ-CE
81	11	51	5CT	CG-CD-CE-NZ
81	11	51	5CT	N-CA-CB-CG

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
81	11	51	5CT	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 209 ligands modelled in this entry, 209 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](#)

There are no chain breaks in this entry.

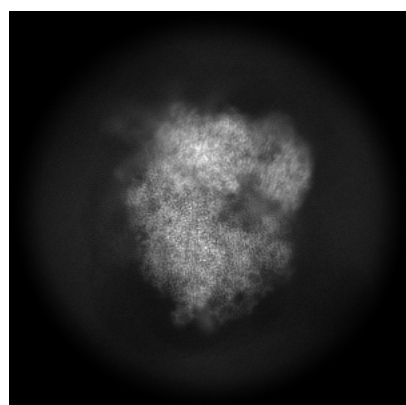
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13111. These allow visual inspection of the internal detail of the map and identification of artifacts.

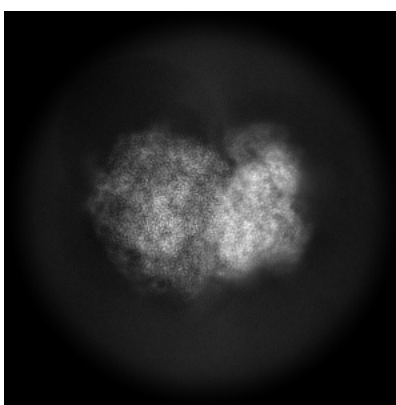
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

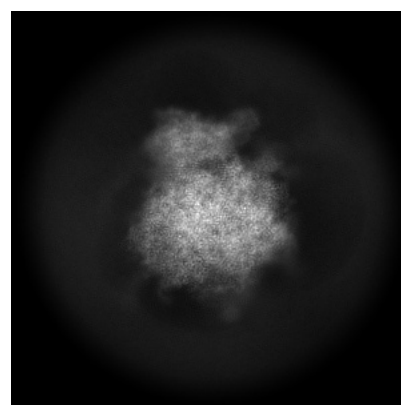
6.1.1 Primary map



X



Y

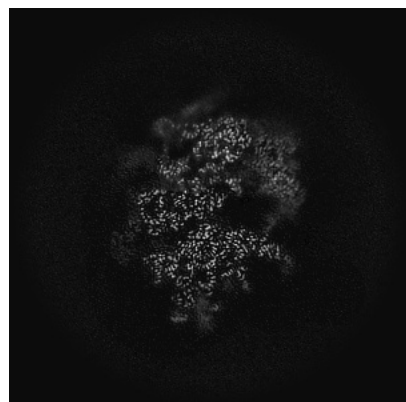


Z

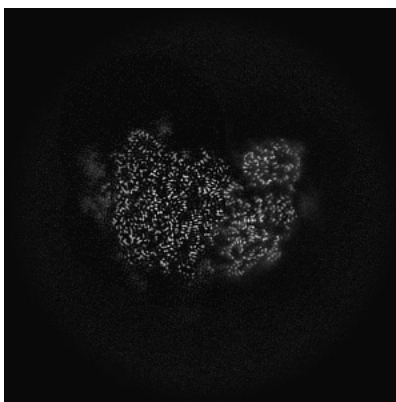
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

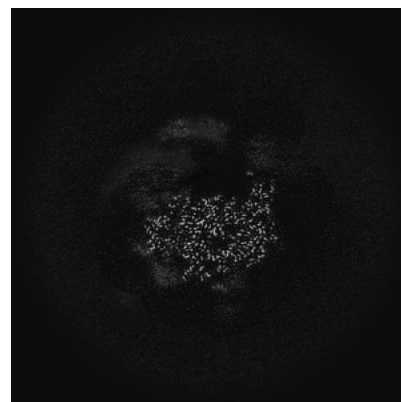
6.2.1 Primary map



X Index: 240



Y Index: 240

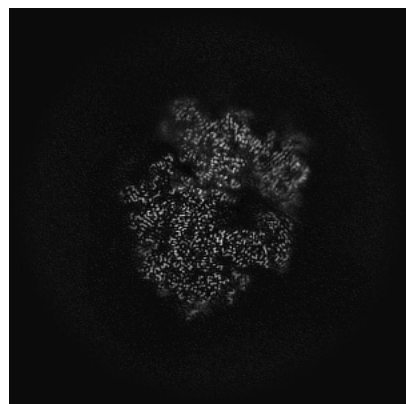


Z Index: 240

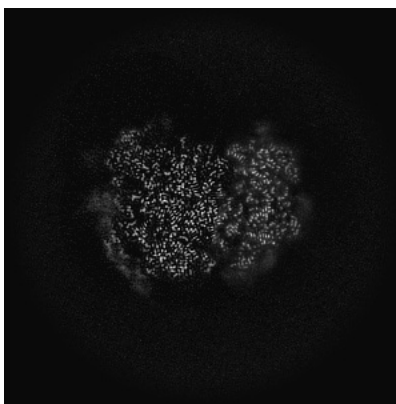
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

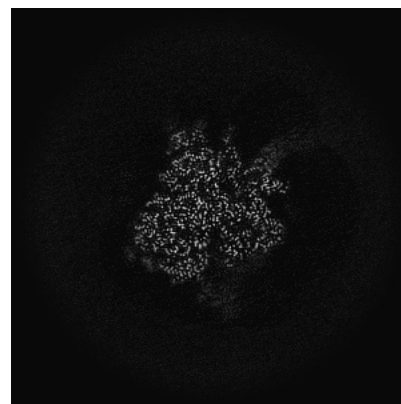
6.3.1 Primary map



X Index: 221



Y Index: 228



Z Index: 202

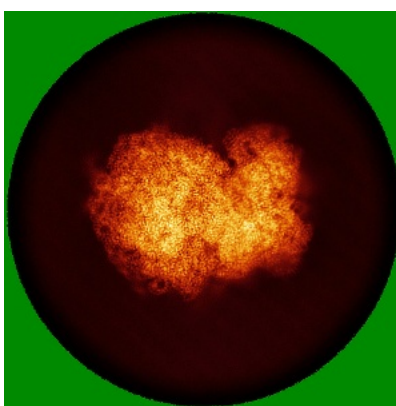
The images above show the largest variance slices of the map in three orthogonal directions.

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

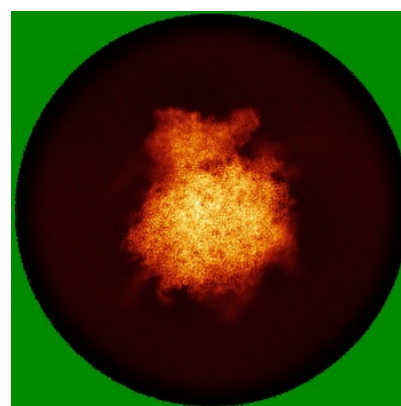
6.4.1 Primary map



X



Y

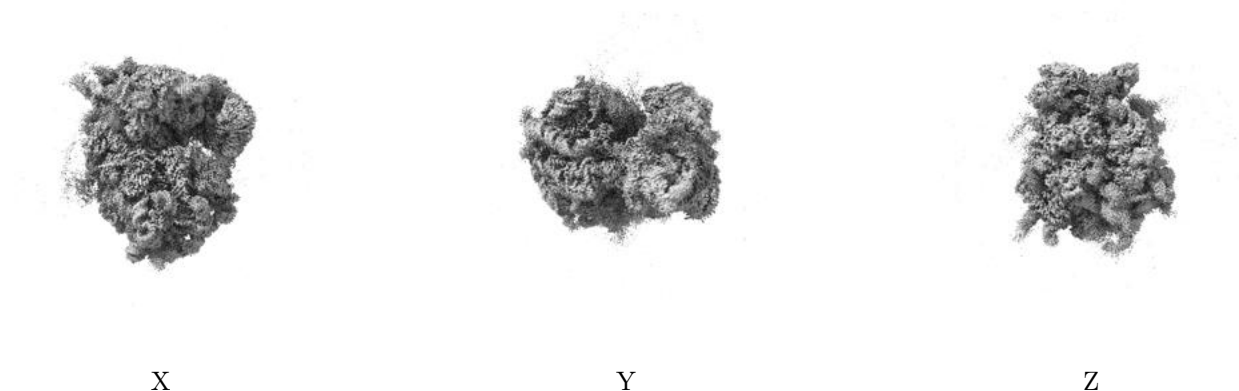


Z

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 0.9. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

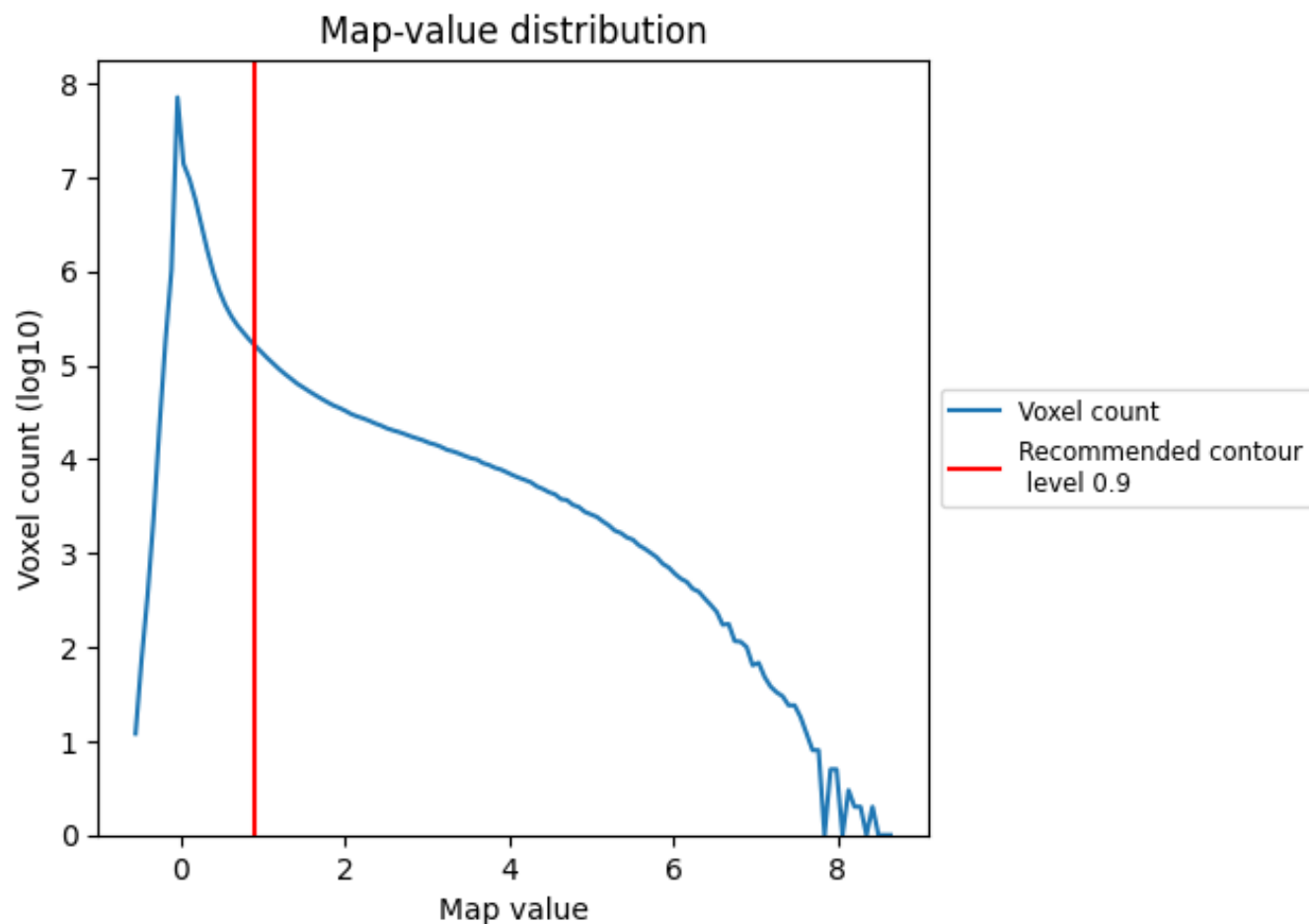
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

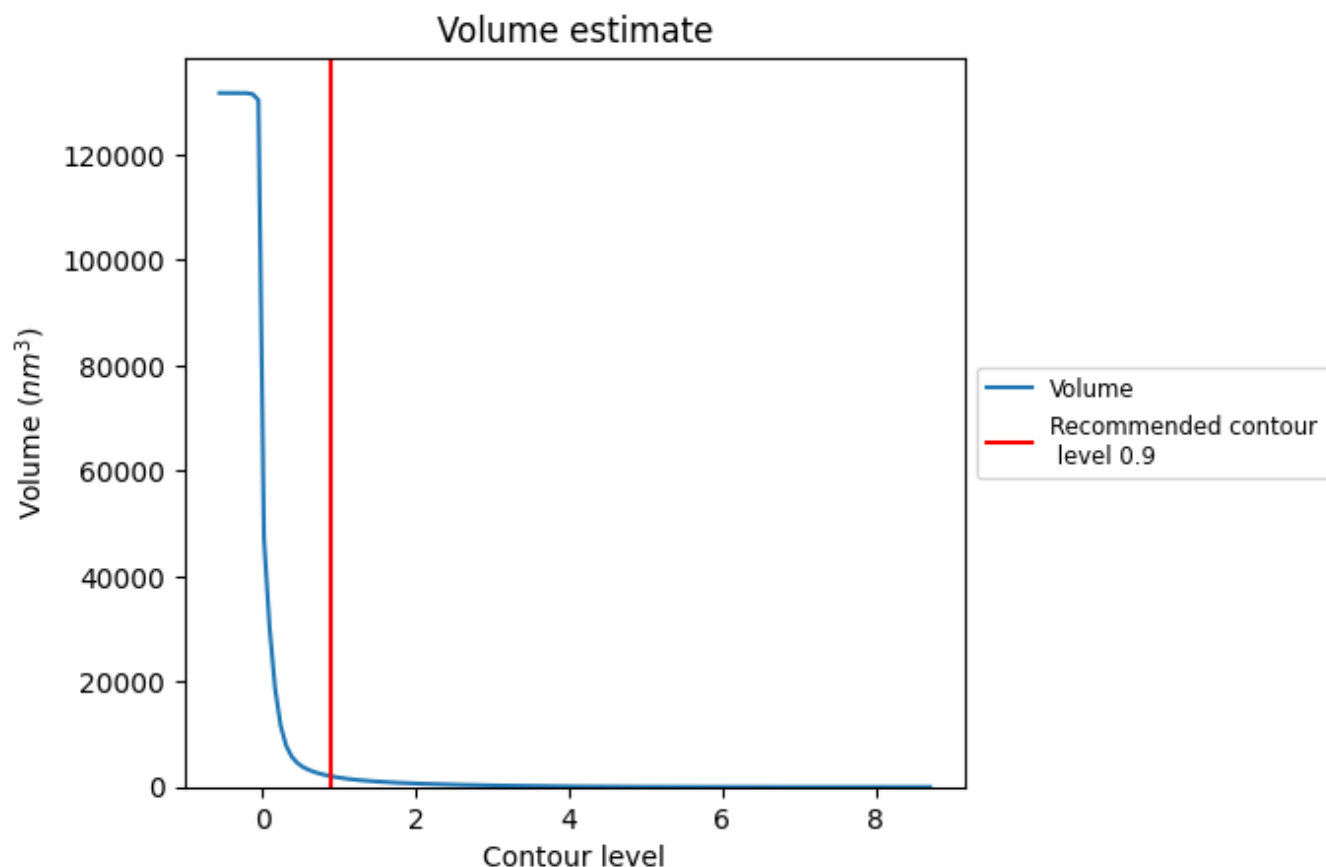
This section contains the results of statistical analysis of the map.

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.

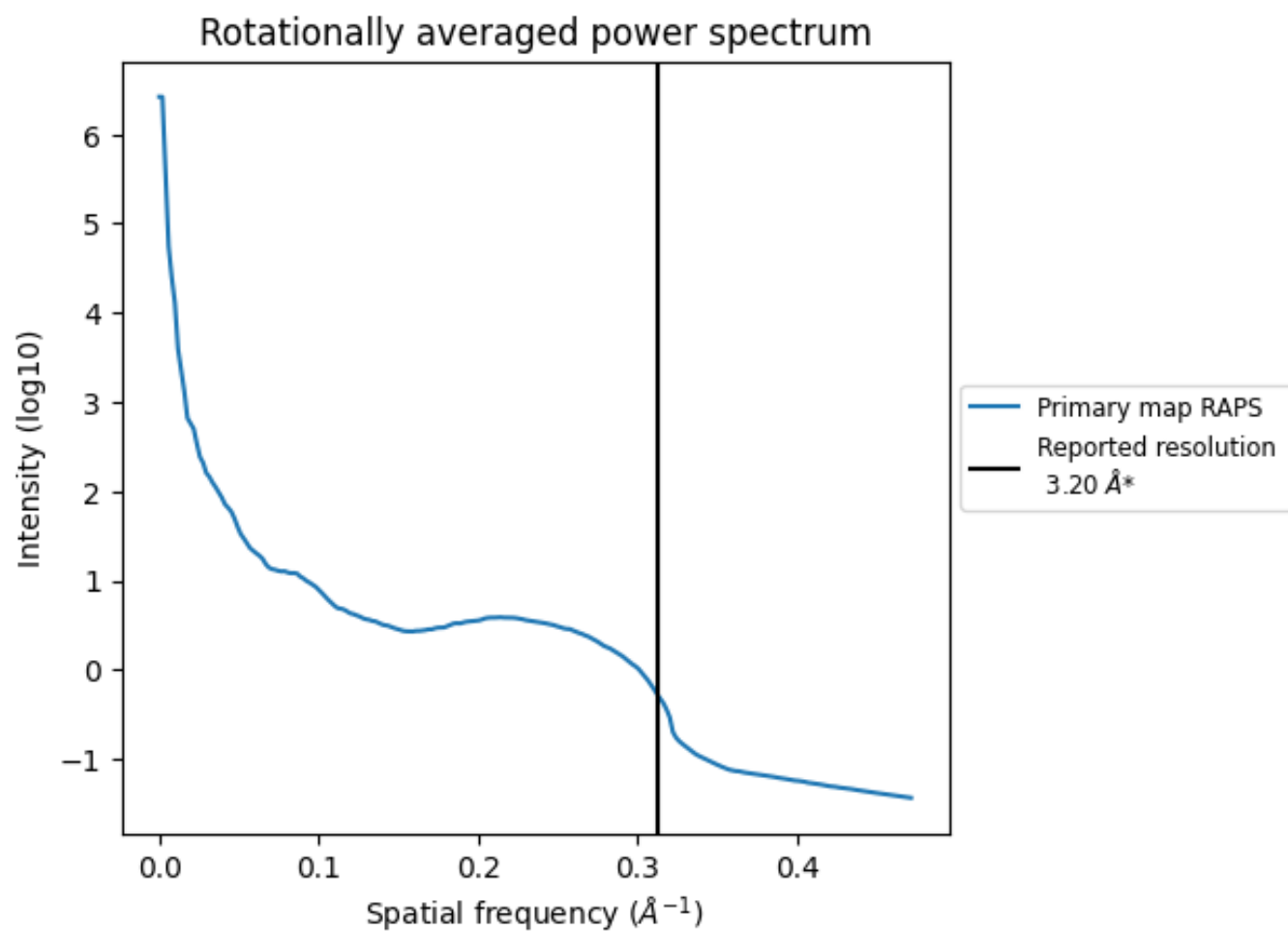
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2042 nm^3 ; this corresponds to an approximate mass of 1844 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 0.312 Å⁻¹

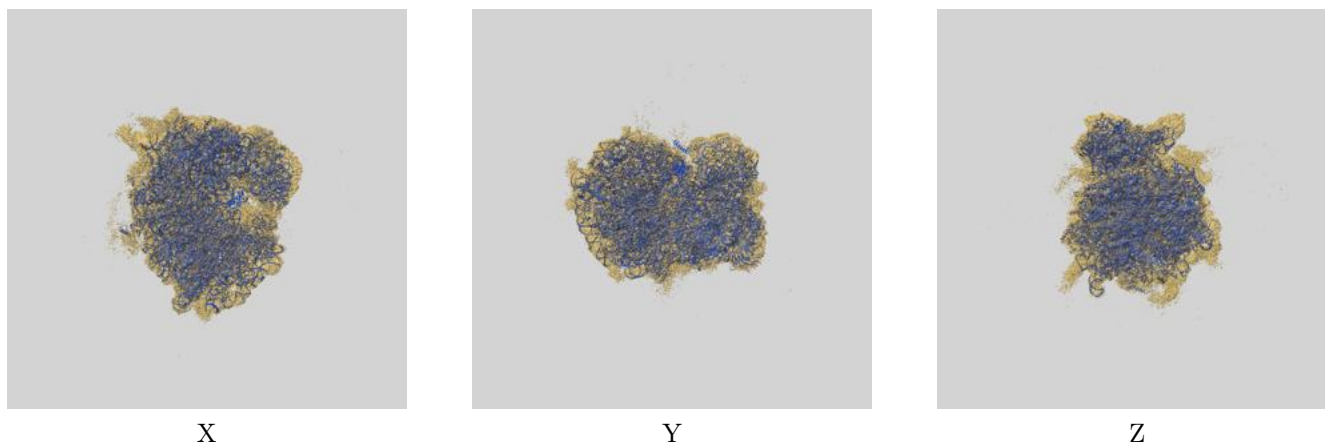
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

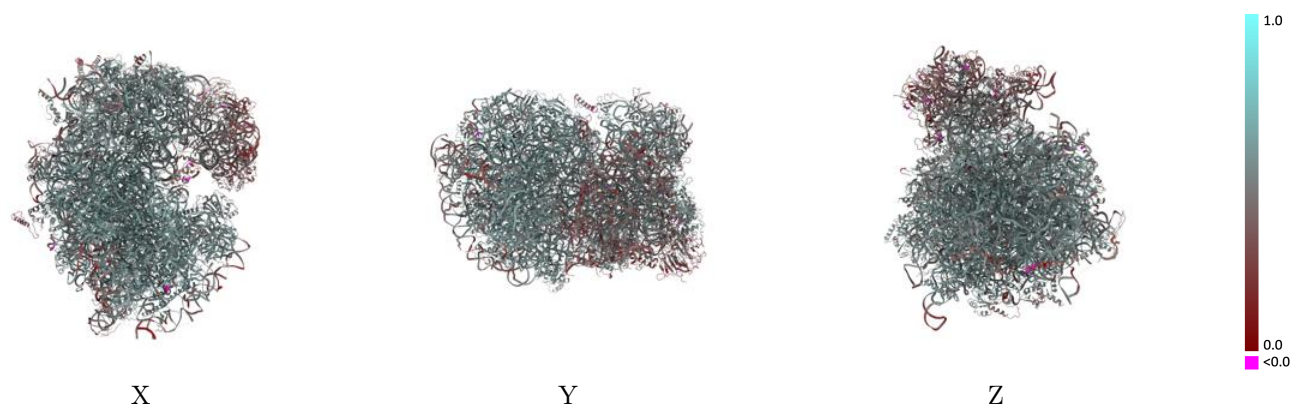
This section contains information regarding the fit between EMDB map EMD-13111 and PDB model 7OYA. Per-residue inclusion information can be found in section [3](#) on page [20](#).

9.1 Map-model overlay [i](#)



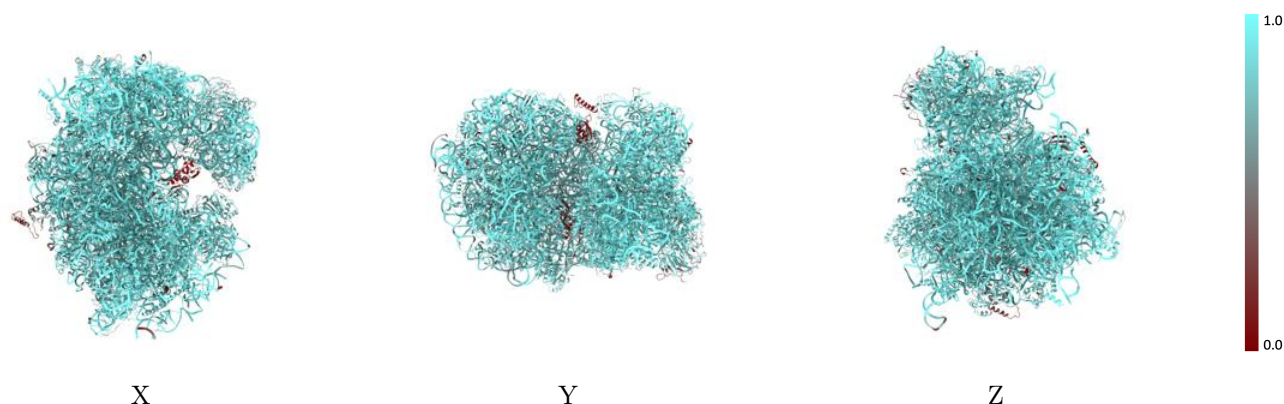
The images above show the 3D surface view of the map at the recommended contour level 0.9 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



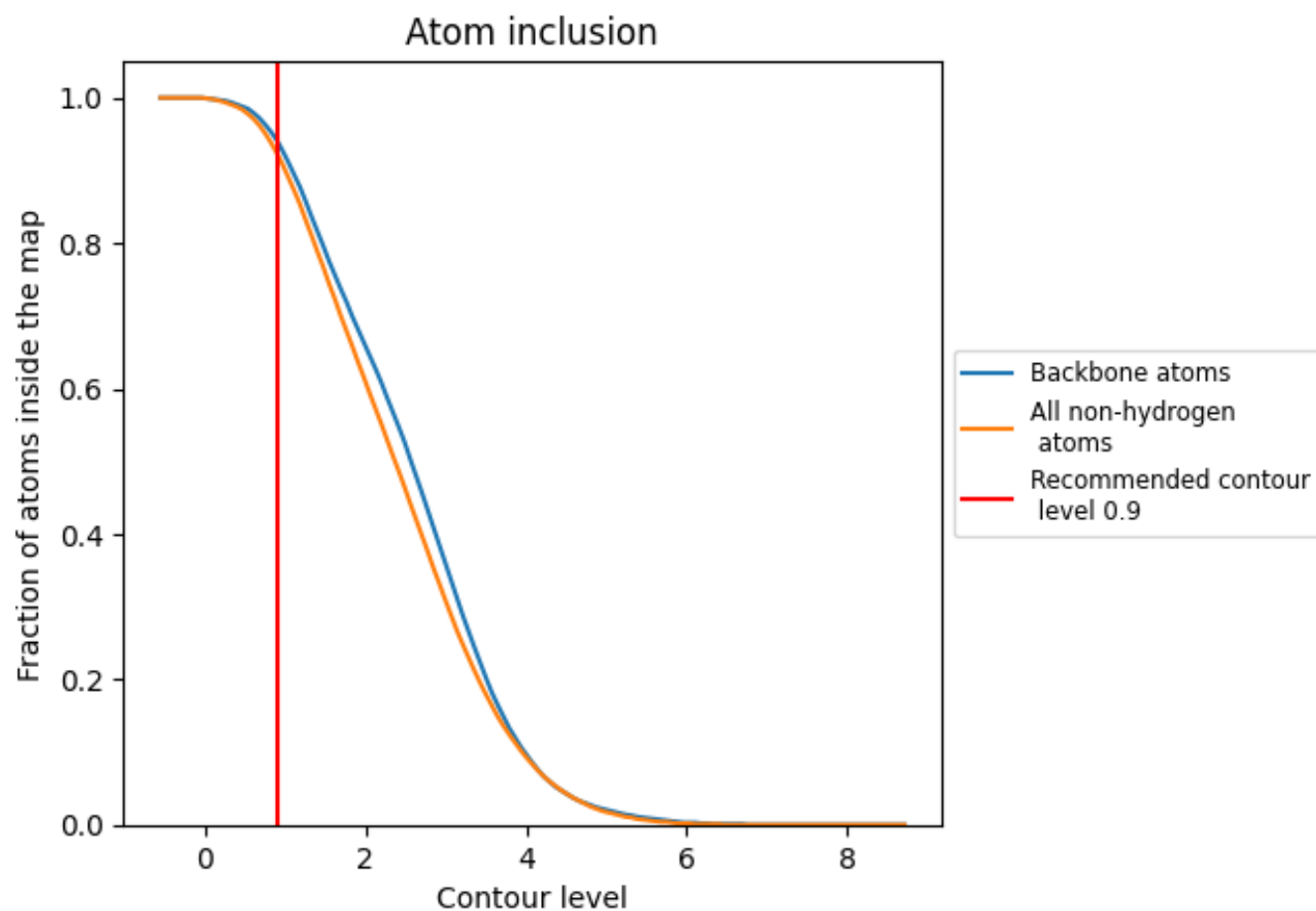
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.9).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 92% 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 (0.9) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9230	 0.5210
11	 0.1370	 0.3190
22	 0.9840	 0.5000
51	 0.9470	 0.5380
71	 0.9840	 0.5730
81	 0.9230	 0.5250
A1	 0.9600	 0.5880
A2	 0.9570	 0.5180
B1	 0.9240	 0.5780
B2	 0.9450	 0.5290
C1	 0.9310	 0.5700
C2	 0.9780	 0.5270
D1	 0.8940	 0.5480
D2	 0.8410	 0.3980
E1	 0.8900	 0.5400
E2	 0.9510	 0.5320
F1	 0.9170	 0.5710
F2	 0.8560	 0.3750
G1	 0.8870	 0.5400
G2	 0.8790	 0.4630
H1	 0.8940	 0.5660
H2	 0.8590	 0.4800
I1	 0.9090	 0.5710
I2	 0.9510	 0.5310
J1	 0.8410	 0.5020
J2	 0.9470	 0.5140
K2	 0.8520	 0.3610
L1	 0.8700	 0.5500
L2	 0.9420	 0.5440
M1	 0.9200	 0.5730
N1	 0.9530	 0.5920
N2	 0.9490	 0.5390
O1	 0.9240	 0.5760
O2	 0.9440	 0.5250
P1	 0.9150	 0.5700



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Chain	Atom inclusion	Q-score
P2	 0.8980	 0.3430
Q1	 0.9230	 0.5730
Q2	 0.8980	 0.3990
R1	 0.8950	 0.5390
R2	 0.8160	 0.4380
S1	 0.9460	 0.5840
S2	 0.8610	 0.3120
T1	 0.8990	 0.5630
T2	 0.9150	 0.4080
U1	 0.8000	 0.4610
U2	 0.8660	 0.3840
V1	 0.8970	 0.5800
V2	 0.9570	 0.5300
W1	 0.8820	 0.5580
W2	 0.9750	 0.5560
X1	 0.8970	 0.5620
X2	 0.9610	 0.5360
Y1	 0.9090	 0.5540
Y2	 0.9090	 0.5030
Z1	 0.9000	 0.5590
Z2	 0.7790	 0.3020
a1	 0.9140	 0.5700
a2	 0.9720	 0.5370
b1	 0.8940	 0.5640
b2	 0.9170	 0.5140
c1	 0.9380	 0.5470
c2	 0.9030	 0.3910
d1	 0.8830	 0.5460
d2	 0.9250	 0.4520
e1	 0.9260	 0.5770
e2	 0.9040	 0.4930
f1	 0.9460	 0.5910
g1	 0.9490	 0.5690
g2	 0.6830	 0.3100
h1	 0.8690	 0.5460
i1	 0.8800	 0.5550
i2	 0.4870	 0.3380
j1	 0.9340	 0.5810
k1	 0.8220	 0.5330
l1	 0.8840	 0.5480
m1	 0.9350	 0.5810
n1	 0.9330	 0.5280

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Chain	Atom inclusion	Q-score
o1	 0.9020	 0.5640
p1	 0.9030	 0.5410
q1	 0.3980	 0.3790
r1	 0.9220	 0.5640
s1	 0.2220	 0.3240
v2	 0.0840	 0.3140