



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 10:00 AM UTC

PDB ID : 6XU7 / pdb_00006xu7
EMDB ID : EMD-10623
Title : Drosophila melanogaster Testis polysome ribosome
Authors : Hopes, T.; Agapiou, M.; Norris, K.; McCarthy, C.G.P.; OConnell, M.J.;
Fontana, J.; Aspden, J.L.
Deposited on : 2020-01-17
Resolution : 4.90 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:

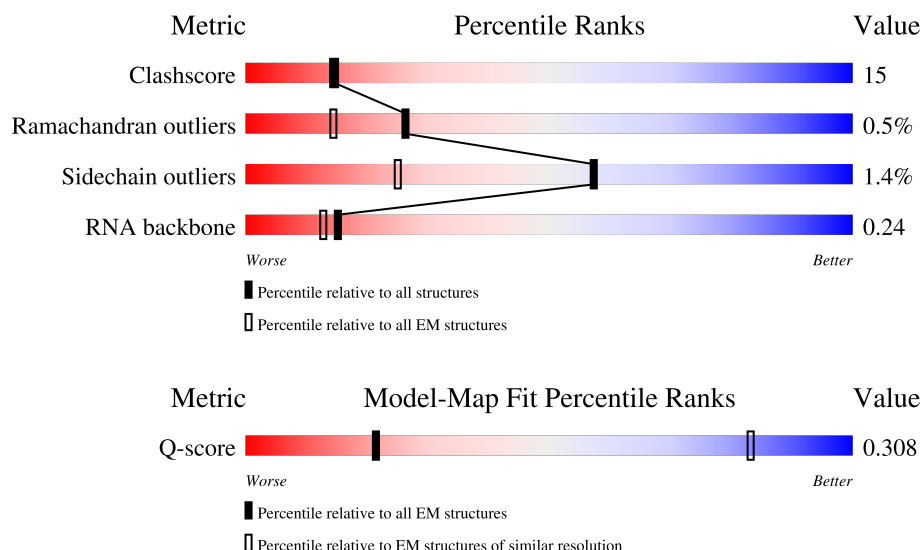
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 4.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



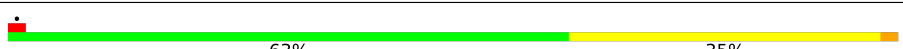
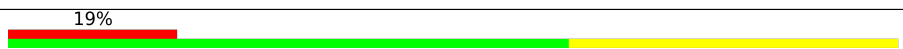
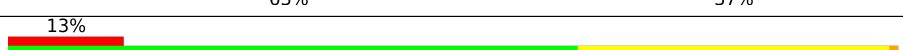
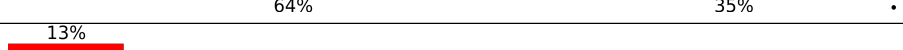
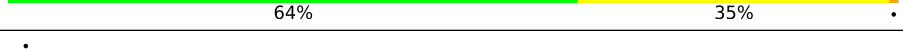
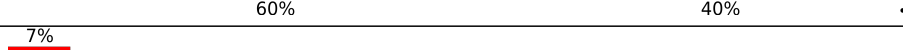
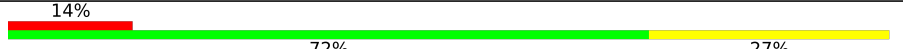
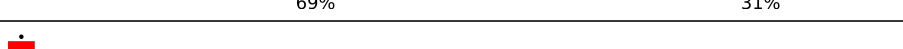
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	1274 (4.40 - 5.40)

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

Mol	Chain	Length	Quality of chain
1	AA	218	
2	CA	253	
3	AB	220	

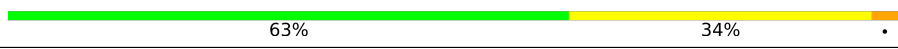
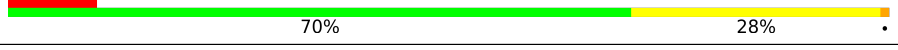
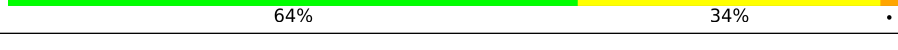
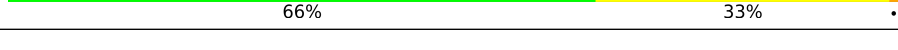
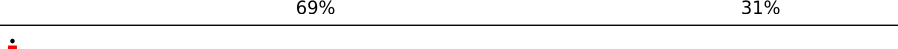
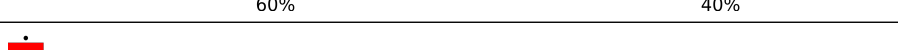
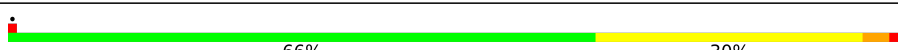
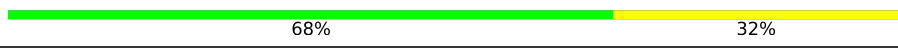
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Mol	Chain	Length	Quality of chain
4	CB	414	
5	AC	227	
6	CC	392	
7	Ag	318	
8	AU	102	
9	AO	134	
10	AX	143	
11	AM	119	
12	AS	137	
13	Ad	52	
14	AN	150	
15	AL	155	
16	AR	120	
17	AP	124	
18	AV	82	
19	AY	126	
20	AZ	74	
21	Aa	107	
22	Ab	84	
23	AD	227	
24	Ae	58	
25	Af	80	
26	AJ	181	
27	Ca	149	
28	CN	203	

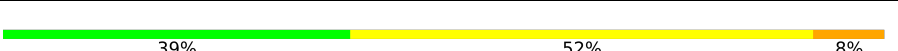
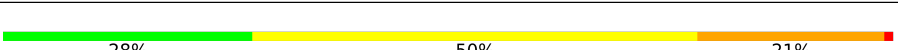
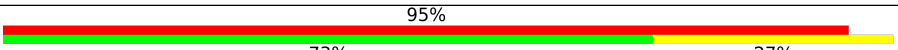
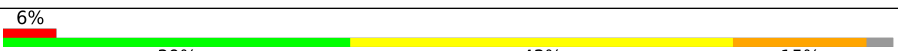
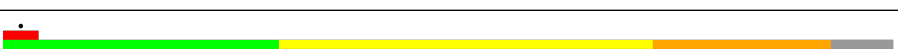
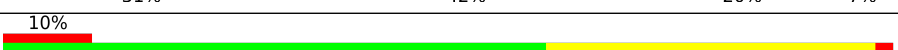
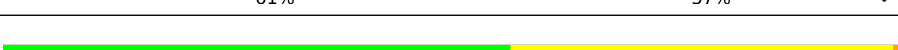
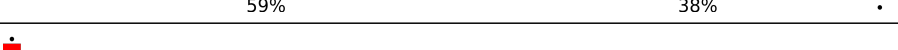
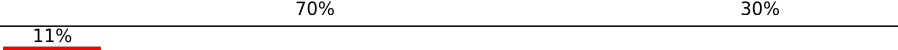
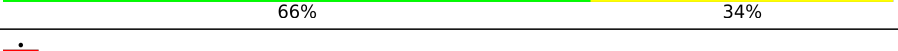
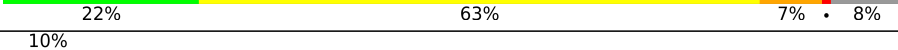
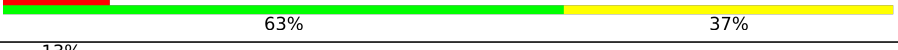
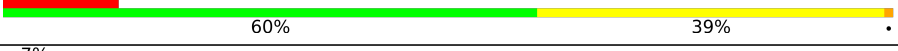
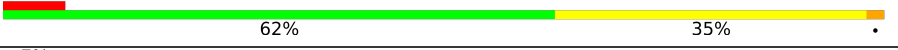
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Mol	Chain	Length	Quality of chain
29	CI	217	
30	CD	290	
31	CQ	187	
32	CR	203	
33	CS	173	
34	CT	158	
35	CP	185	
36	CX	120	
37	CY	131	
38	CZ	134	
39	Cr	134	
40	Ch	123	
41	Cb	75	
42	Cc	100	
43	Cd	111	
44	Ce	132	
45	Cf	157	
46	Ci	113	
47	Ck	70	
48	Cl	50	
49	Cm	52	
50	Cn	25	
51	Cp	91	
52	Co	104	
53	CJ	182	

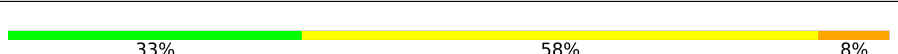
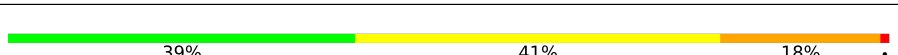
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Mol	Chain	Length	Quality of chain
54	CH	190	
55	CE	228	
56	CG	241	
57	A9	30	
58	A7	120	
59	A8	123	
60	Cz	217	
61	B2	1995	
62	A5	3974	
63	Ac	62	
64	AW	129	
65	CW	58	
66	Cg	104	
67	CU	96	
68	AK	90	
69	AT	143	
70	AF	189	
71	CF	226	
72	AE	261	
73	AG	231	
74	AH	194	
75	AI	207	
76	AQ	148	
77	CO	205	
78	CL	210	

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Mol	Chain	Length	Quality of chain
79	CV	134	
80	CM	159	
81	B	75	
82	v	12	
83	Cj	87	

2 Entry composition

There are 83 unique types of molecules in this entry. The entry contains 219005 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 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	218	Total	C	N	O	S	0	0
			1737	1113	298	321	5		

- Molecule 2 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	CA	253	Total	C	N	O	S	0	0
			1935	1206	395	326	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AB	220	Total	C	N	O	S	0	0
			1798	1138	328	324	8		

- Molecule 4 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	CB	414	Total	C	N	O	S	0	0
			3287	2083	621	565	18		

- Molecule 5 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AC	227	Total	C	N	O	S	0	0
			1746	1126	302	311	7		

- Molecule 6 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	CC	392	Total	C	N	O	S	0	0
			3109	1959	622	522	6		

- Molecule 7 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Ag	318	Total	C	N	O	S	0	0
			2511	1577	444	480	10		

- Molecule 8 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AU	102	Total	C	N	O	S	0	0
			815	505	161	145	4		

- Molecule 9 is a protein called 40S ribosomal protein S14a.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AO	134	Total	C	N	O	S	0	0
			1003	616	196	187	4		

- Molecule 10 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AX	143	Total	C	N	O	S	0	0
			1131	712	226	191	2		

- Molecule 11 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AM	119	Total	C	N	O	S	0	0
			924	582	165	171	6		

- Molecule 12 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AS	137	Total	C	N	O	S	0	0
			1128	707	220	198	3		

- Molecule 13 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Ad	52	Total	C	N	O	S	0	0
			433	269	87	72	5		

- Molecule 14 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AN	150	Total	C	N	O	S	0	0
			1202	767	229	203	3		

- Molecule 15 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AL	155	Total	C	N	O	S	0	0
			1274	803	254	211	6		

- Molecule 16 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AR	120	Total	C	N	O	S	0	0
			981	618	183	176	4		

- Molecule 17 is a protein called GEO07301p1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AP	124	Total	C	N	O	S	0	0
			1016	652	189	169	6		

- Molecule 18 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AV	82	Total	C	N	O	S	0	0
			617	373	114	125	5		

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AV	2	GLN	GLU	conflict	UNP O76927
AV	8	PHE	ASN	conflict	UNP O76927
AV	25	GLY	HIS	conflict	UNP O76927
AV	32	ILE	VAL	conflict	UNP O76927
AV	34	MET	LEU	conflict	UNP O76927
AV	35	ASN	SER	conflict	UNP O76927
AV	36	VAL	ILE	conflict	UNP O76927
AV	58	ALA	GLU	conflict	UNP O76927
AV	68	SER	CYS	conflict	UNP O76927
AV	70	LEU	VAL	conflict	UNP O76927
AV	75	ALA	LYS	conflict	UNP O76927
AV	79	VAL	ILE	conflict	UNP O76927

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Chain	Residue	Modelled	Actual	Comment	Reference
AV	80	SER	THR	conflict	UNP O76927

- Molecule 19 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AY	126	Total	C	N	O	S	0	0
			1016	644	196	171	5		

- Molecule 20 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AZ	74	Total	C	N	O	S	0	0
			608	390	112	106			

- Molecule 21 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Aa	107	Total	C	N	O	S	0	0
			867	539	182	140	6		

- Molecule 22 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Ab	84	Total	C	N	O	S	0	0
			653	412	123	110	8		

- Molecule 23 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AD	227	Total	C	N	O	S	0	0
			1782	1127	319	326	10		

- Molecule 24 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Ae	58	Total	C	N	O	S	0	0
			469	289	105	75			

- Molecule 25 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Af	80	Total	C	N	O	S	0	0
			659	417	128	109	5		

- Molecule 26 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AJ	181	Total	C	N	O	S	0	0
			1503	957	298	247	1		

- Molecule 27 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Ca	149	Total	C	N	O	S	0	0
			1204	769	242	189	4		

- Molecule 28 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	CN	203	Total	C	N	O	S	0	0
			1710	1072	362	271	5		

- Molecule 29 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	CI	217	Total	C	N	O	S	0	0
			1785	1125	343	304	13		

- Molecule 30 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	CD	290	Total	C	N	O	S	0	0
			2334	1471	434	423	6		

- Molecule 31 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	CQ	187	Total	C	N	O	S	0	0
			1518	957	306	251	4		

- Molecule 32 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	CR	203	Total	C	N	O	S	0	0
			1683	1047	350	277	9		

- Molecule 33 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	CS	173	Total	C	N	O	S	0	0
			1454	935	275	240	4		

- Molecule 34 is a protein called RE62581p.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	CT	158	Total	C	N	O	S	0	0
			1297	829	253	212	3		

- Molecule 35 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	CP	185	Total	C	N	O	S	0	0
			1505	928	305	263	9		

- Molecule 36 is a protein called IP17216p.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	CX	120	Total	C	N	O	S	0	0
			984	625	192	165	2		

- Molecule 37 is a protein called GEO07453p1.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	CY	131	Total	C	N	O	S	0	0
			1078	676	224	176	2		

- Molecule 38 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	CZ	134	Total	C	N	O	S	0	0
			1115	723	209	180	3		

- Molecule 39 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	Cr	134	Total	C	N	O	0	0
			1051	670	205	176		

- Molecule 40 is a protein called FI02809p.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Ch	123	Total	C	N	O	S	0	0
			1015	646	202	164	3		

- Molecule 41 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Cb	75	Total	C	N	O	S	0	0
			619	378	133	107	1		

- Molecule 42 is a protein called RE25263p.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Cc	100	Total	C	N	O	S	0	0
			770	486	132	147	5		

- Molecule 43 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Cd	111	Total	C	N	O	S	0	0
			924	573	180	169	2		

- Molecule 44 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Ce	132	Total	C	N	O	S	0	0
			1110	698	230	177	5		

- Molecule 45 is a protein called GEO07455p1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Cf	157	Total	C	N	O	S	0	0
			1244	781	255	203	5		

- Molecule 46 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Ci	113	Total	C	N	O	S	0	0
			934	585	193	153	3		

- Molecule 47 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Ck	70	Total	C	N	O	S	0	0
			576	366	108	100	2		

- Molecule 48 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	Cl	50	Total	C	N	O	0	0
			437	276	98	63		

- Molecule 49 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Cm	52	Total	C	N	O	S	0	0
			429	267	89	67	6		

- Molecule 50 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Cn	25	Total	C	N	O	S	0	0
			236	143	63	27	3		

- Molecule 51 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Cp	91	Total	C	N	O	S	0	0
			710	441	140	122	7		

- Molecule 52 is a protein called TA01007p.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Co	104	Total	C	N	O	S	0	0
			874	548	180	138	8		

- Molecule 53 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	CJ	182	Total	C	N	O	S	0	0
			1468	926	278	258	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
54	CH	190	Total	C	N	O	S	0	0
			1499	947	265	278	9		

- Molecule 55 is a protein called Ribosomal protein L6, isoform A.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	CE	228	Total	C	N	O	S	0	0
			1845	1185	351	305	4		

- Molecule 56 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	CG	241	Total	C	N	O	S	0	0
			1936	1237	368	327	4		

- Molecule 57 is a RNA chain called 2S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	A9	30	Total	C	N	O	P	0	0
			639	286	111	213	29		

- Molecule 58 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	A7	120	Total	C	N	O	P	0	0
			2554	1141	456	838	119		

- Molecule 59 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	A8	123	Total	C	N	O	P	0	0
			2621	1173	474	852	122		

- Molecule 60 is a protein called 60S ribosomal protein L10a-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Cz	217	Total	C	N	O	S	0	0
			1702	1084	303	305	10		

- Molecule 61 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	B2	1936	Total	C	N	O	P	0	0
			39355	17526	6780	13114	1935		

- Molecule 62 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	A5	3707	Total	C	N	O	P	0	0
			77175	34473	13566	25431	3705		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A5	1301	A	U	conflict	GB NR_133562.1
A5	1319	A	U	conflict	GB NR_133562.1
A5	1320	U	G	conflict	GB NR_133562.1
A5	1321	G	U	conflict	GB NR_133562.1
A5	1322	U	G	conflict	GB NR_133562.1
A5	1686	A	-	insertion	GB NR_133562.1
A5	1710	G	-	insertion	GB NR_133562.1
A5	2158A	C	-	insertion	GB NR_133562.1
A5	2279	C	G	conflict	GB NR_133562.1
A5	3569	C	-	insertion	GB NR_133562.1

- Molecule 63 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Ac	62	Total	C	N	O	S	0	0
			498	307	100	89	2		

- Molecule 64 is a protein called 40S ribosomal protein S15Aa.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AW	129	Total	C	N	O	S	0	0
			1028	656	189	176	7		

- Molecule 65 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	CW	58	Total	C	N	O	S	0	0
			483	314	89	76	4		

- Molecule 66 is a protein called RH48056p.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Cg	104	Total	C	N	O	S	0	0
			852	530	177	139	6		

- Molecule 67 is a protein called Ribosomal protein L22-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	CU	96	Total	C	N	O	S	0	0
			811	531	137	139	4		

- Molecule 68 is a protein called 40S ribosomal protein S10b.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	AK	90	Total	C	N	O	S	0	0
			760	500	130	127	3		

- Molecule 69 is a protein called 40S ribosomal protein S19a.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	AT	132	Total	C	N	O	S	0	0
			1041	659	200	179	3		

- Molecule 70 is a protein called 40S ribosomal protein S5a.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	AF	189	Total	C	N	O	S	0	0
			1490	929	284	268	9		

- Molecule 71 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	CF	226	Total	C	N	O	S	0	0
			1895	1216	368	308	3		

- Molecule 72 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	AE	261	Total	C	N	O	S	0	0
			2054	1314	380	353	7		

- Molecule 73 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	AG	231	Total	C	N	O	S	0	0
			1866	1172	372	315	7		

- Molecule 74 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	AH	194	Total	C	N	O	S	0	0
			1566	1006	278	281	1		

- Molecule 75 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	AI	207	Total	C	N	O	S	0	0
			1665	1037	329	296	3		

- Molecule 76 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	AQ	148	Total	C	N	O	S	0	0
			1183	753	223	204	3		

- Molecule 77 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	CO	205	Total	C	N	O	S	0	0
			1668	1063	331	268	6		

- Molecule 78 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	CL	210	Total	C	N	O	S	0	0
			1695	1066	342	284	3		

- Molecule 79 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	CV	134	Total	C	N	O	S	0	0
			998	629	190	173	6		

- Molecule 80 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	CM	159	Total	C	N	O	S	0	0
			1302	826	256	218	2		

- Molecule 81 is a RNA chain called P-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	B	75	Total	C	N	O	P	0	0
			1605	717	296	518	74		

- Molecule 82 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	v	12	Total	C	N	O	P	0	0
			255	113	43	87	12		

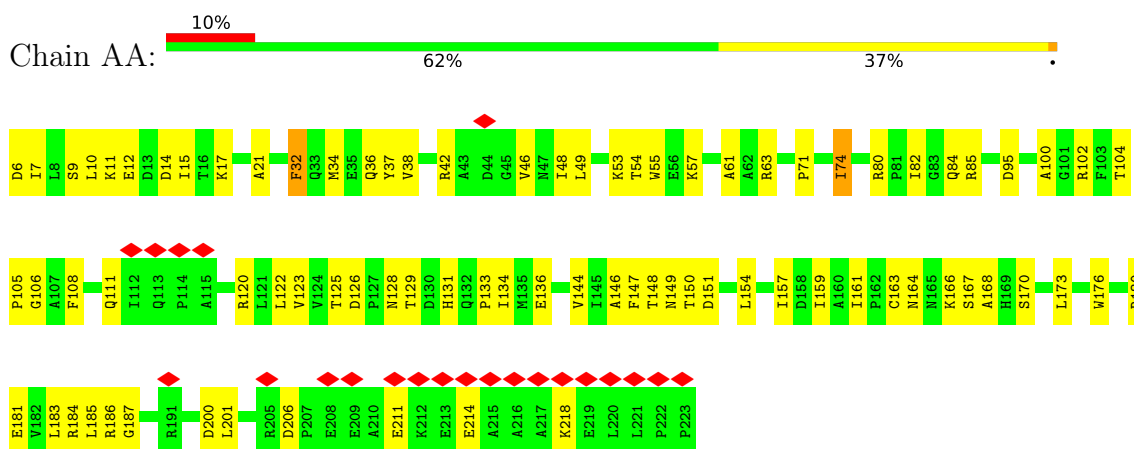
- Molecule 83 is a protein called Probable 60S ribosomal protein L37-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Cj	87	Total	C	N	O	S	0	0
			696	422	154	115	5		

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.

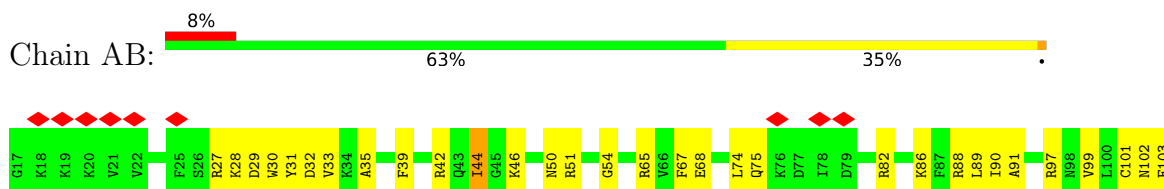
• Molecule 1: 40S ribosomal protein SA

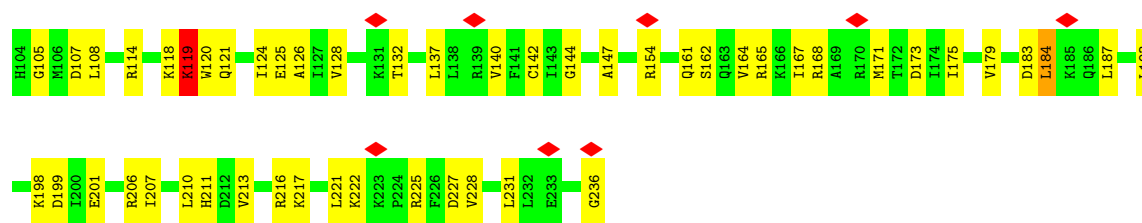


• Molecule 2: 60S ribosomal protein L8



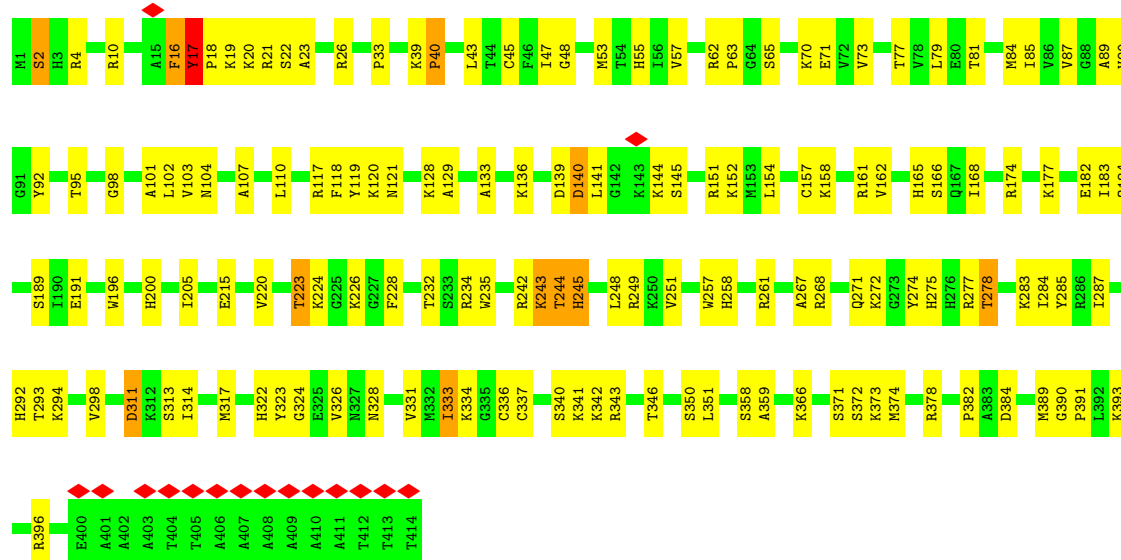
• Molecule 3: 40S ribosomal protein S3a





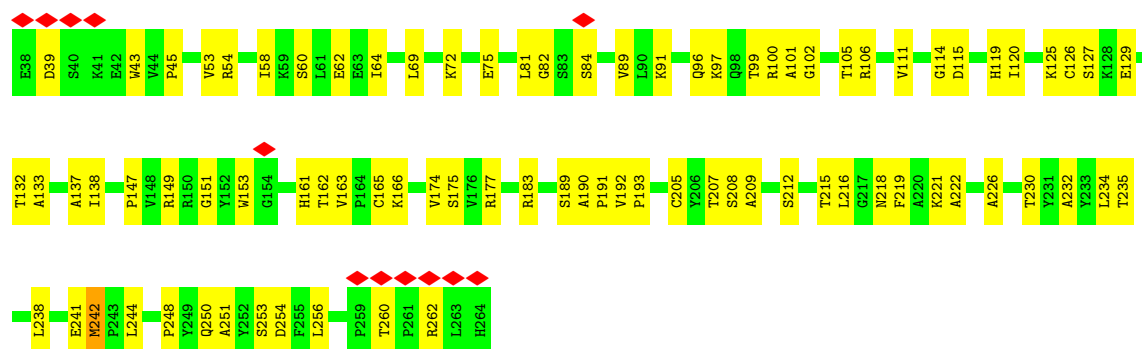
• Molecule 4: 60S ribosomal protein L3

Chain CB: 64% 33%



• Molecule 5: 40S ribosomal protein S2

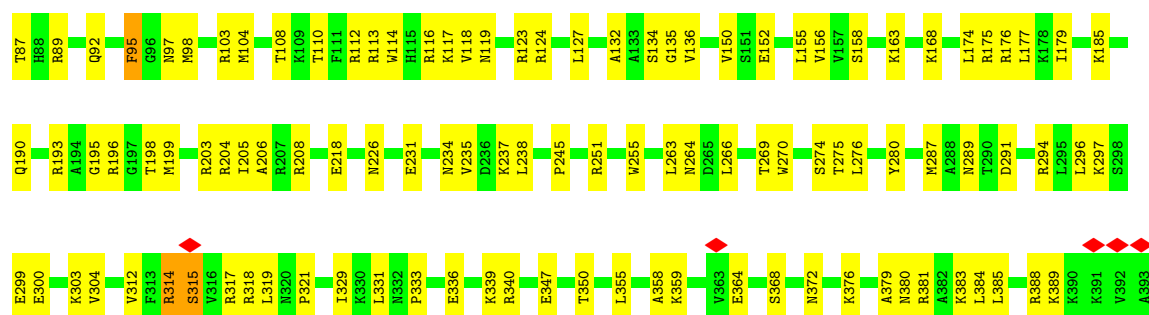
Chain AC: 5% 63% 37%



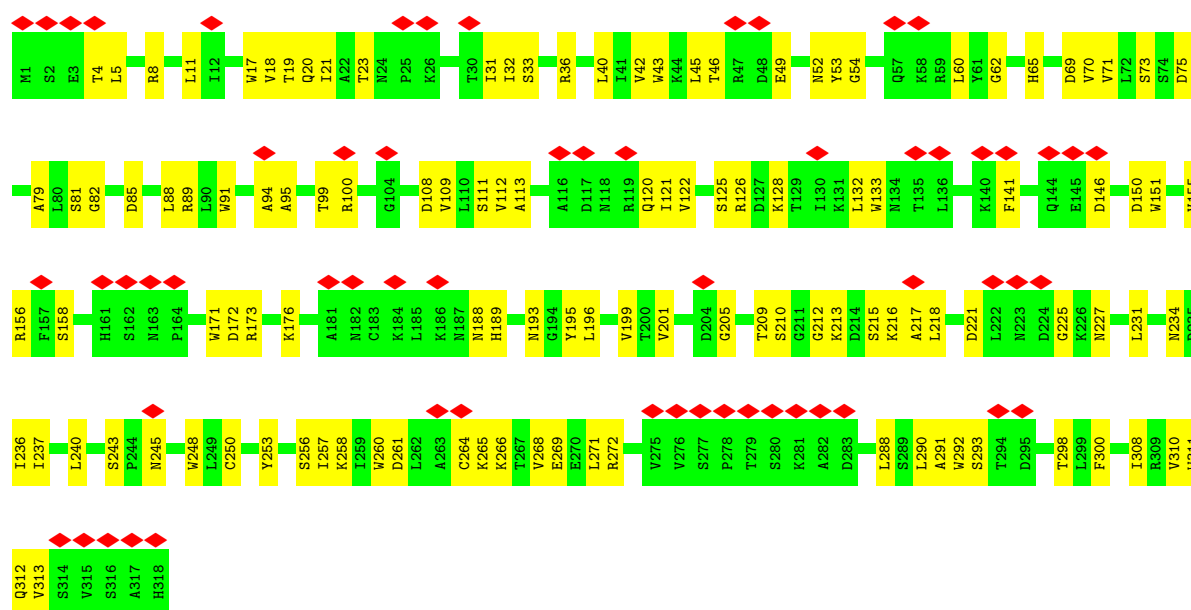
• Molecule 6: 60S ribosomal protein L4

Chain CC: 63% 35%

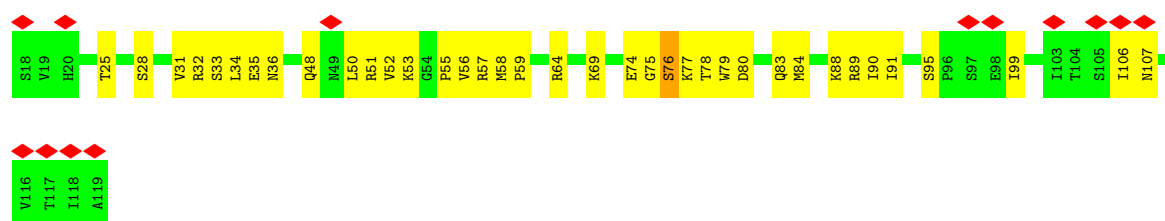




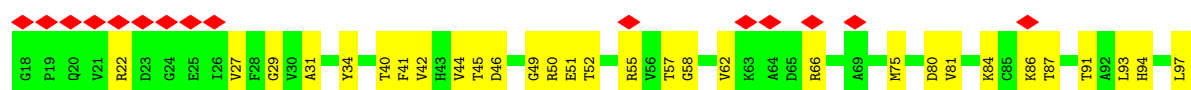
• Molecule 7: Guanine nucleotide-binding protein subunit beta-like protein

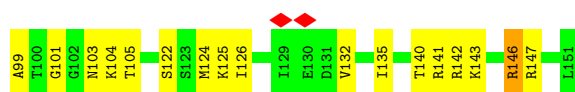


• Molecule 8: 40S ribosomal protein S20



• Molecule 9: 40S ribosomal protein S14a





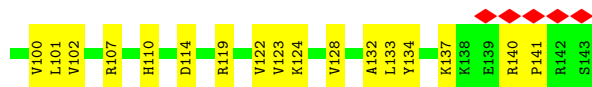
- Molecule 10: 40S ribosomal protein S23

Chain AX: 62% 38%



- Molecule 11: 40S ribosomal protein S12

Chain AM: 61% 38%



- Molecule 12: 40S ribosomal protein S18

Chain AS: 58% 42%



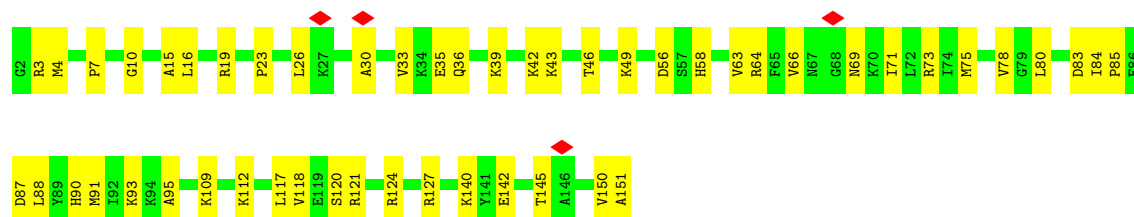
- Molecule 13: 40S ribosomal protein S29

Chain Ad: 58% 38%

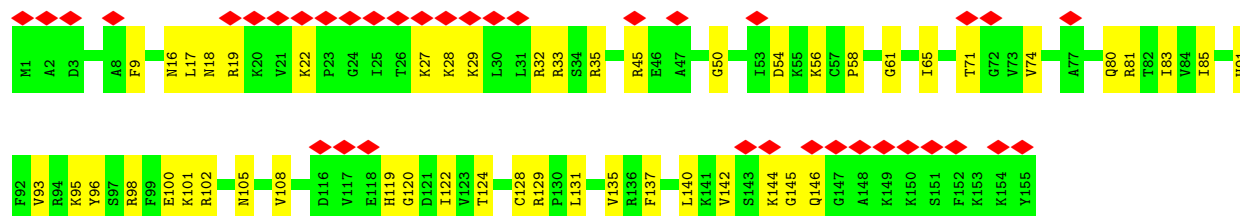


- Molecule 14: 40S ribosomal protein S13

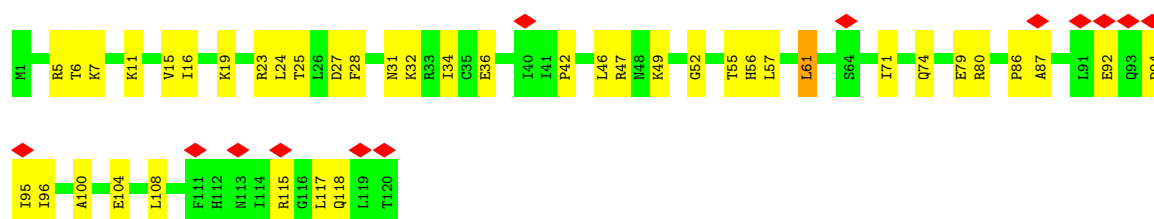
Chain AN: 66% 34%



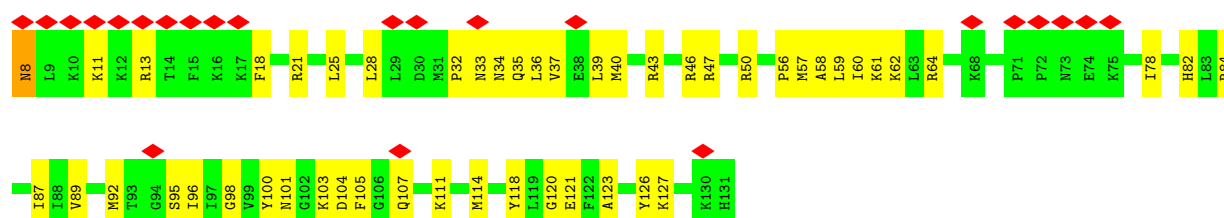
• Molecule 15: 40S ribosomal protein S11



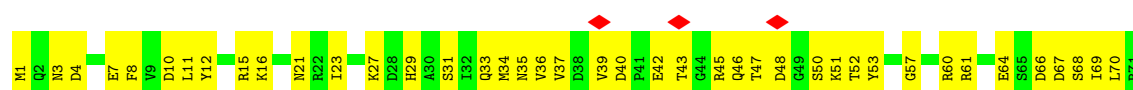
• Molecule 16: 40S ribosomal protein S17

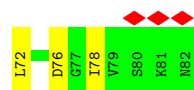


• Molecule 17: GEO07301p1

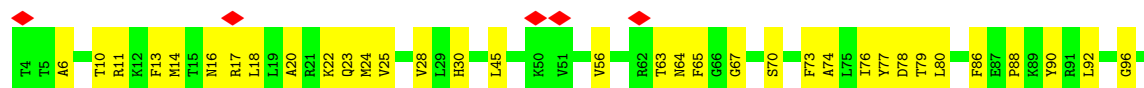


• Molecule 18: 40S ribosomal protein S21





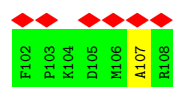
- Molecule 19: 40S ribosomal protein S24



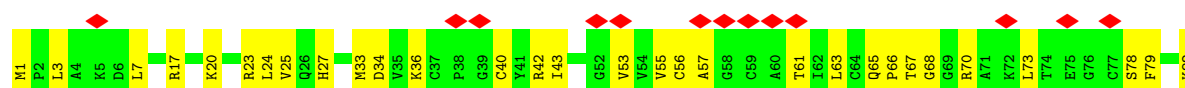
- Molecule 20: 40S ribosomal protein S25



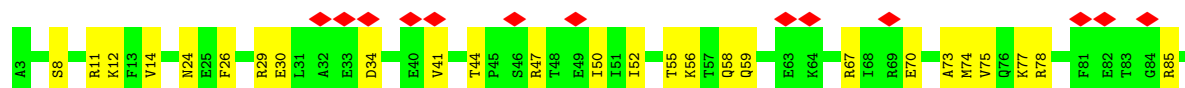
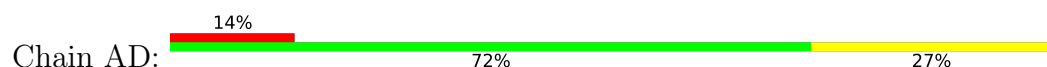
- Molecule 21: 40S ribosomal protein S26

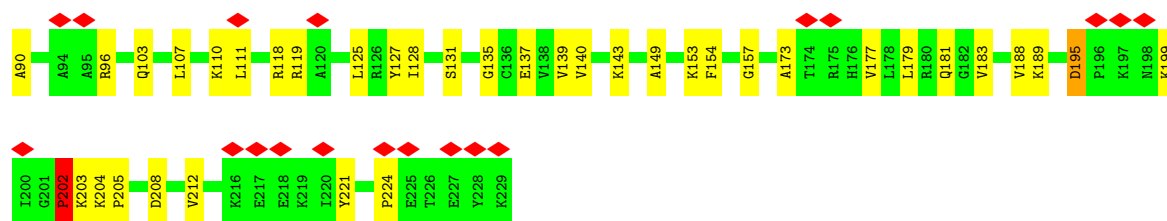


- Molecule 22: 40S ribosomal protein S27

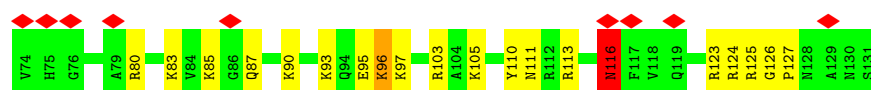


- Molecule 23: 40S ribosomal protein S3

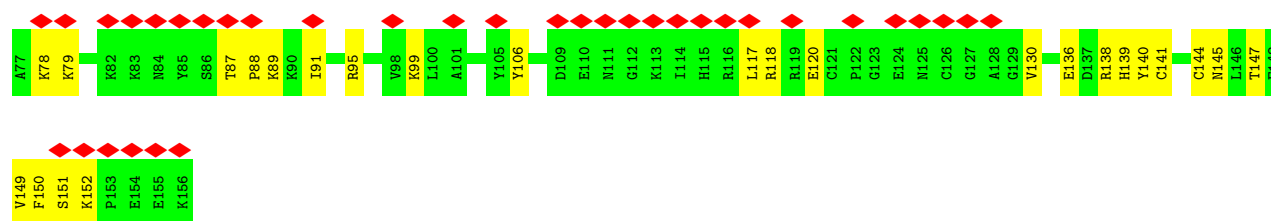




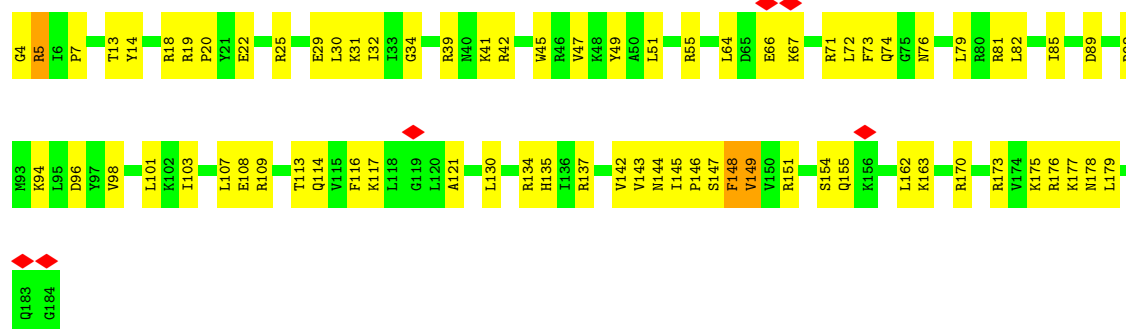
- Molecule 24: 40S ribosomal protein S30



- Molecule 25: Ubiquitin-40S ribosomal protein S27a

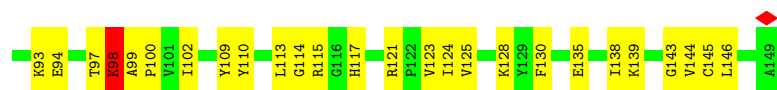


- Molecule 26: 40S ribosomal protein S9

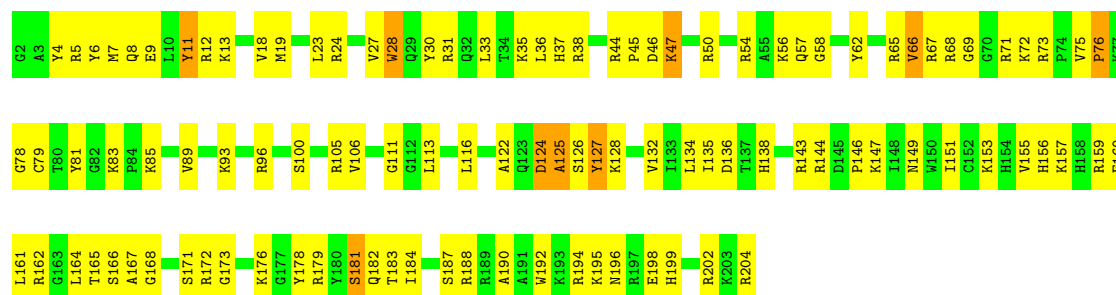


- Molecule 27: 60S ribosomal protein L27a

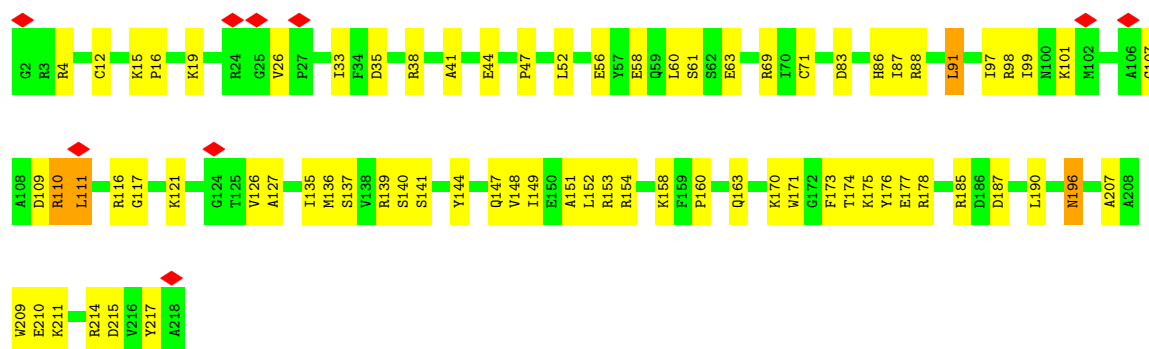




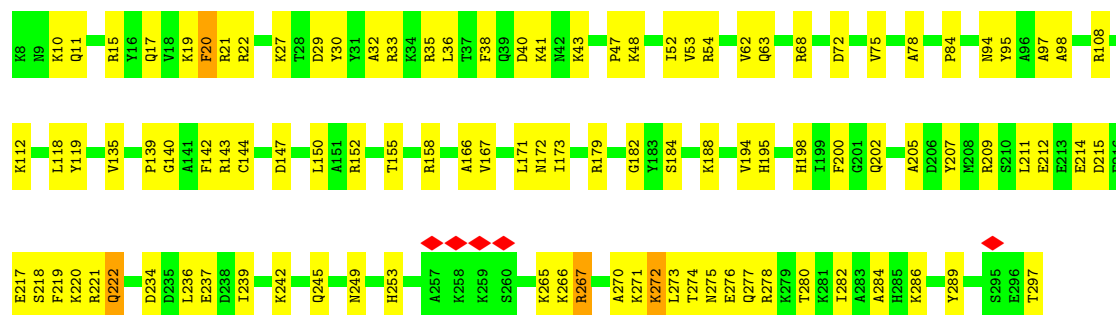
• Molecule 28: 60S ribosomal protein L15



• Molecule 29: 60S ribosomal protein L10

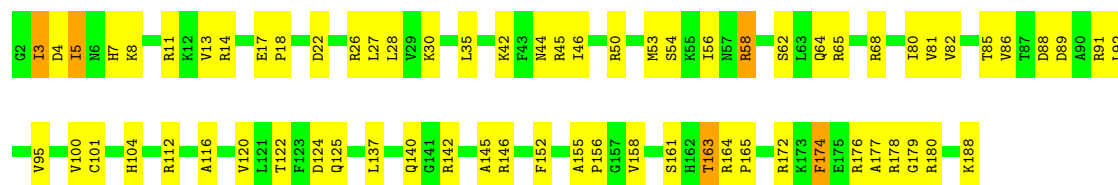


• Molecule 30: 60S ribosomal protein L5

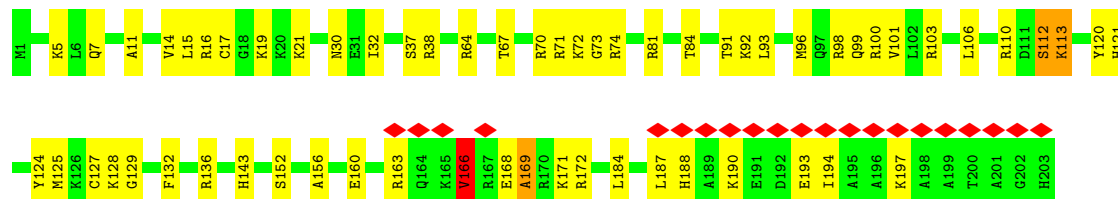
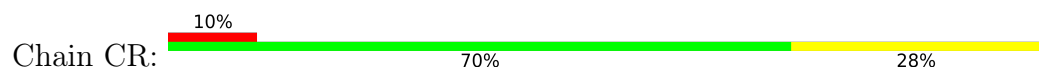


• Molecule 31: 60S ribosomal protein L18

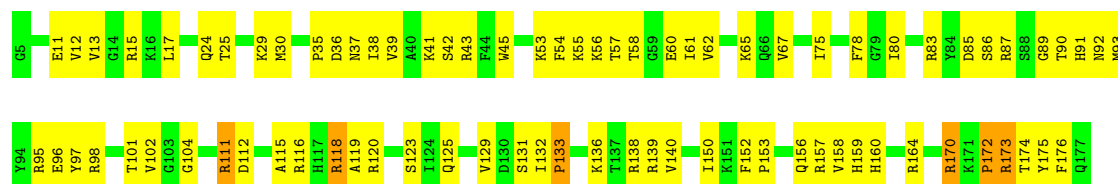




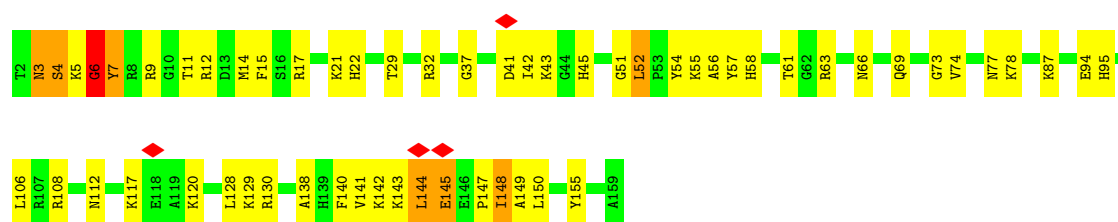
• Molecule 32: 60S ribosomal protein L19



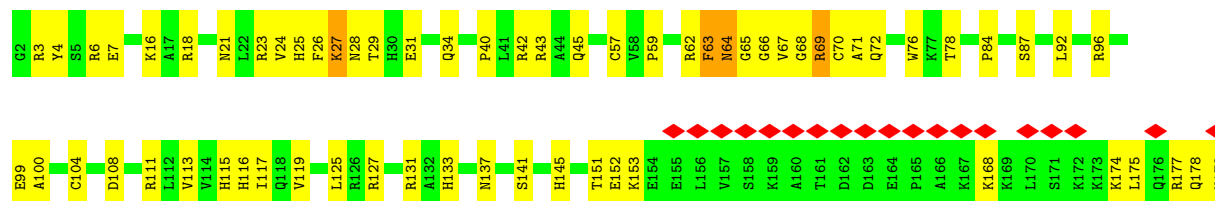
• Molecule 33: 60S ribosomal protein L18a

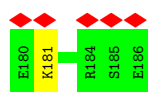


• Molecule 34: RE62581p



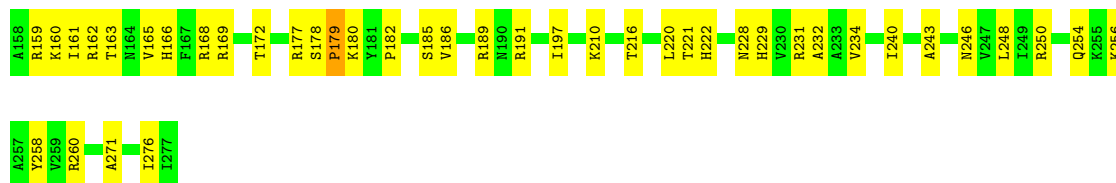
• Molecule 35: 60S ribosomal protein L17





• Molecule 36: IP17216p

Chain CX: 66% 33%



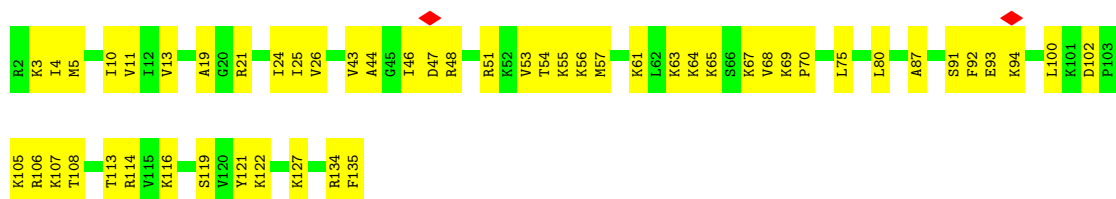
• Molecule 37: GEO07453p1

Chain CY: 69% 31%



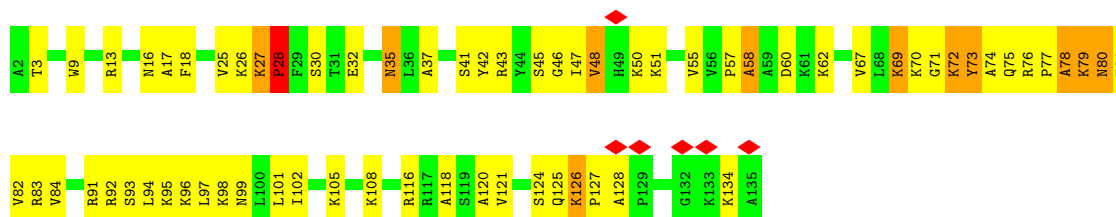
• Molecule 38: 60S ribosomal protein L27

Chain CZ: 60% 40%



• Molecule 39: 60S ribosomal protein L28

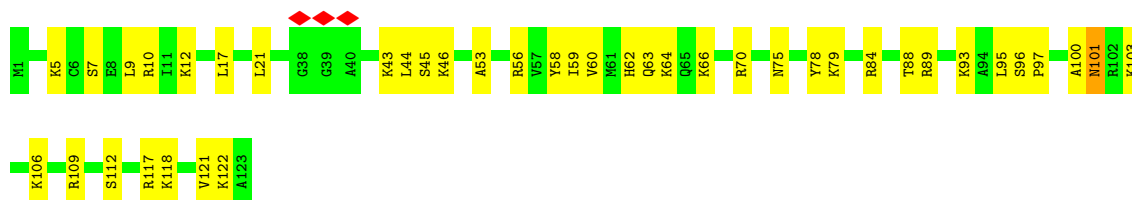
Chain Cr: 49% 42% 8%



• Molecule 40: FI02809p

Chain Ch: 67% 33%





- Molecule 41: 60S ribosomal protein L29

Chain Cb: 71% 25% ..



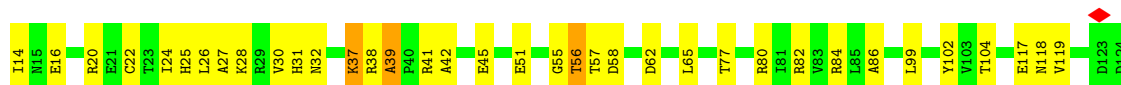
- Molecule 42: RE25263p

Chain Cc: 69% 30% .



- Molecule 43: 60S ribosomal protein L31

Chain Cd: 68% 30% .



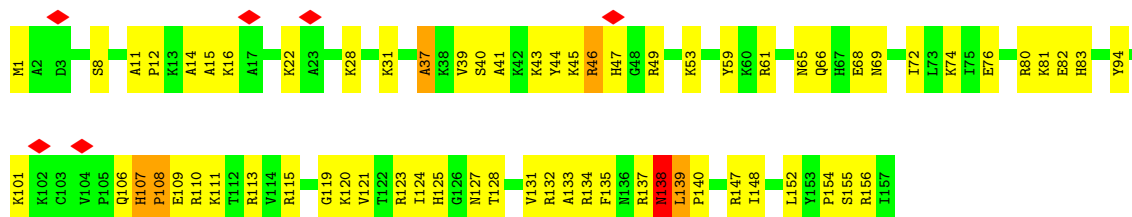
- Molecule 44: 60S ribosomal protein L32

Chain Ce: 66% 30% ..

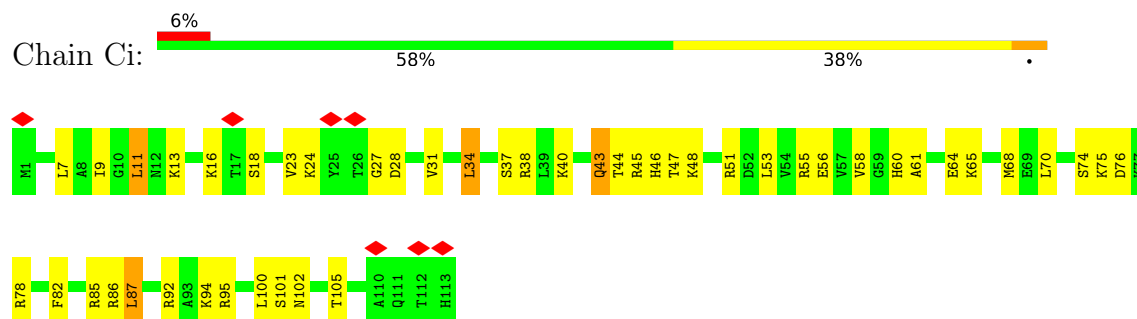


- Molecule 45: GEO07455p1

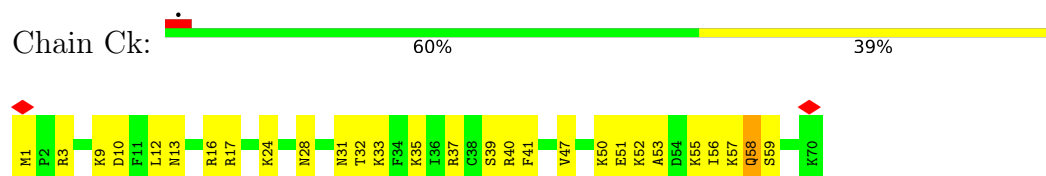
Chain Cf: 57% 39% ..



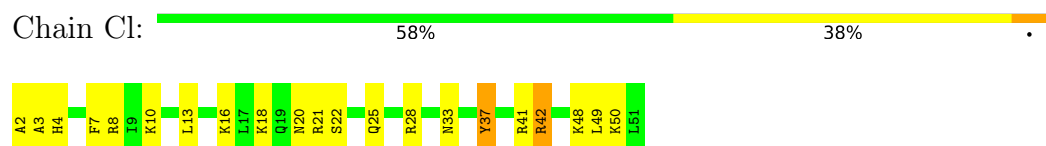
- Molecule 46: 60S ribosomal protein L36



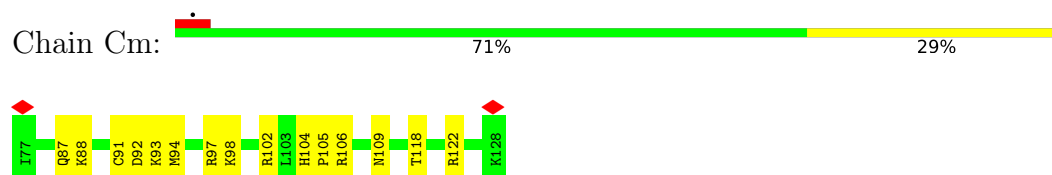
- Molecule 47: 60S ribosomal protein L38



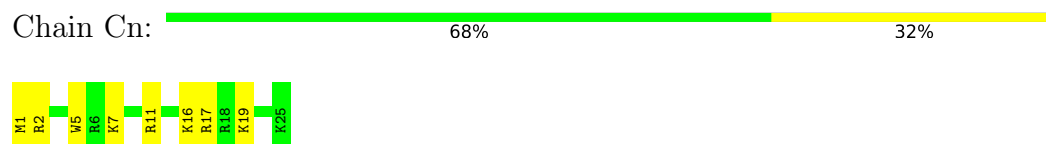
- Molecule 48: 60S ribosomal protein L39



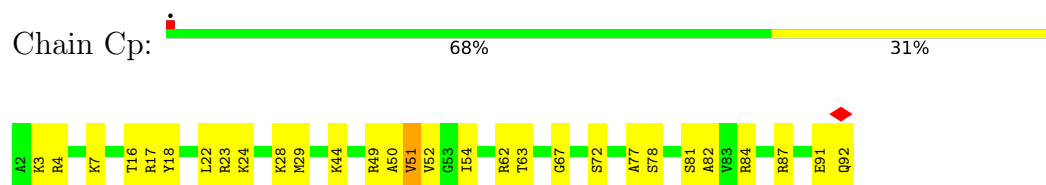
- Molecule 49: Ubiquitin-60S ribosomal protein L40



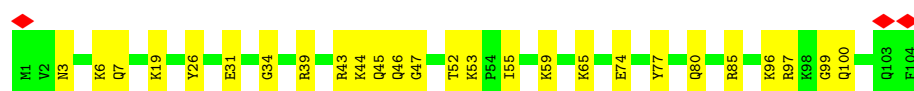
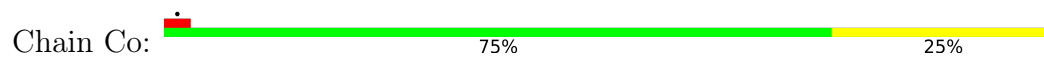
- Molecule 50: 60S ribosomal protein L41



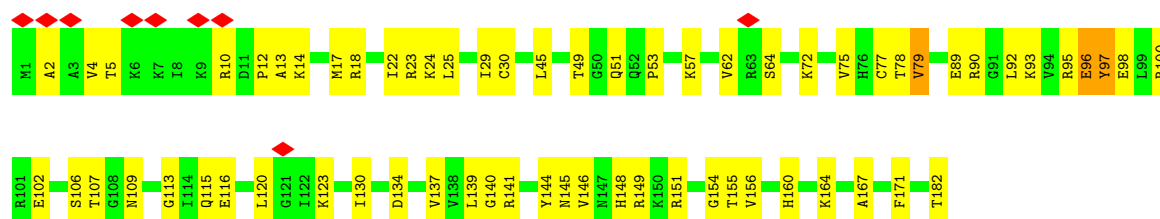
- Molecule 51: 60S ribosomal protein L37a



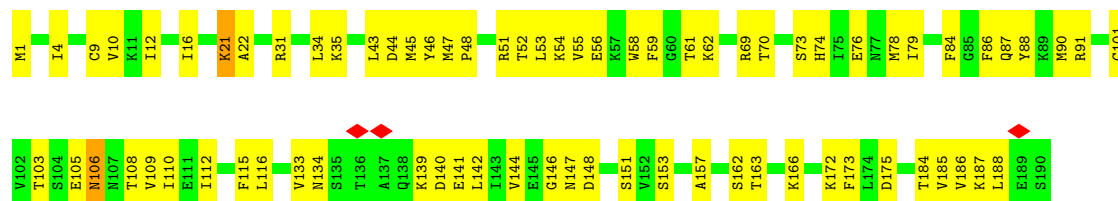
- Molecule 52: TA01007p



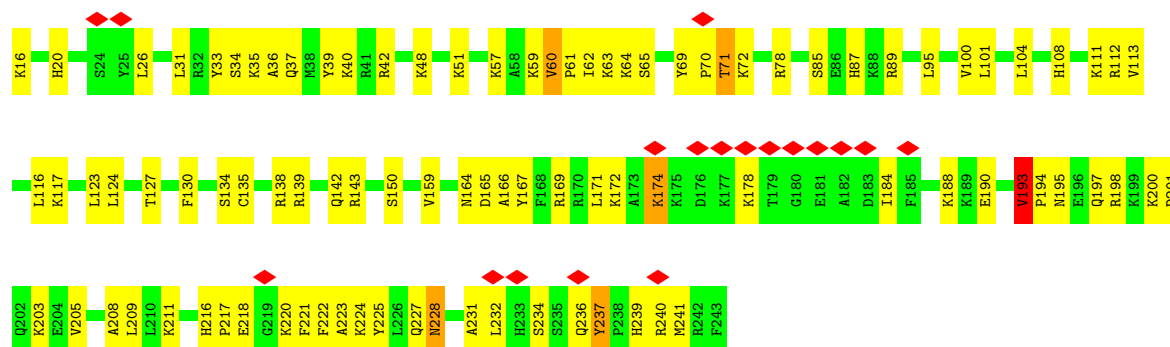
• Molecule 53: 60S ribosomal protein L11



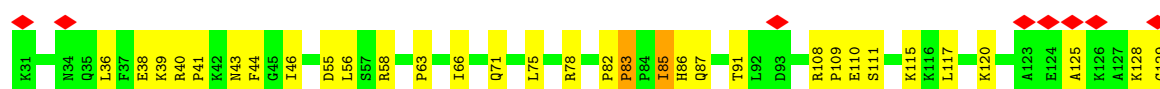
• Molecule 54: 60S ribosomal protein L9

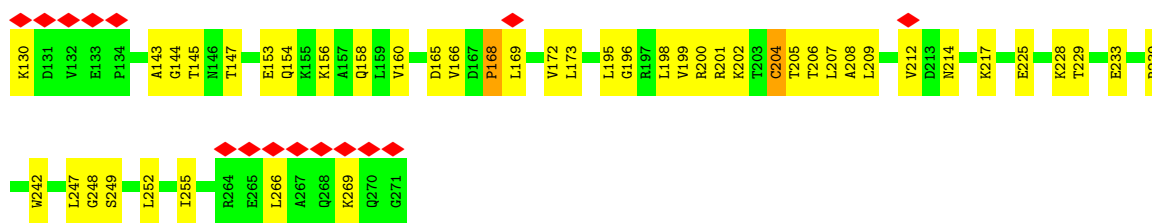


• Molecule 55: Ribosomal protein L6, isoform A



• Molecule 56: 60S ribosomal protein L7a





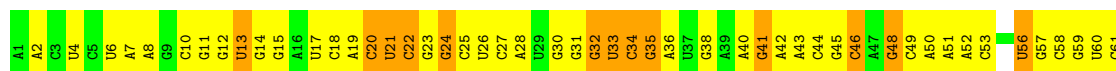
• Molecule 57: 2S ribosomal RNA



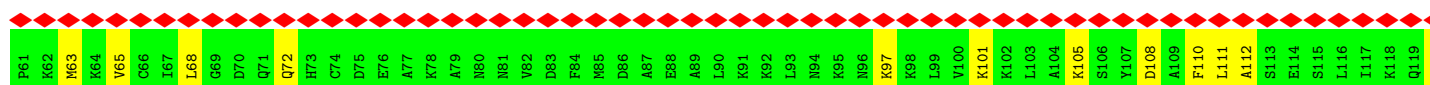
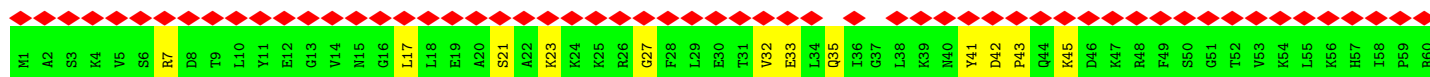
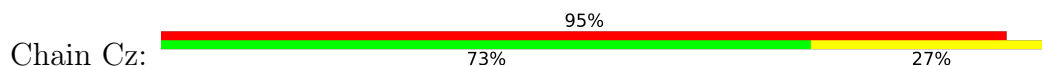
• Molecule 58: 5S ribosomal RNA



• Molecule 59: 5.8S ribosomal RNA

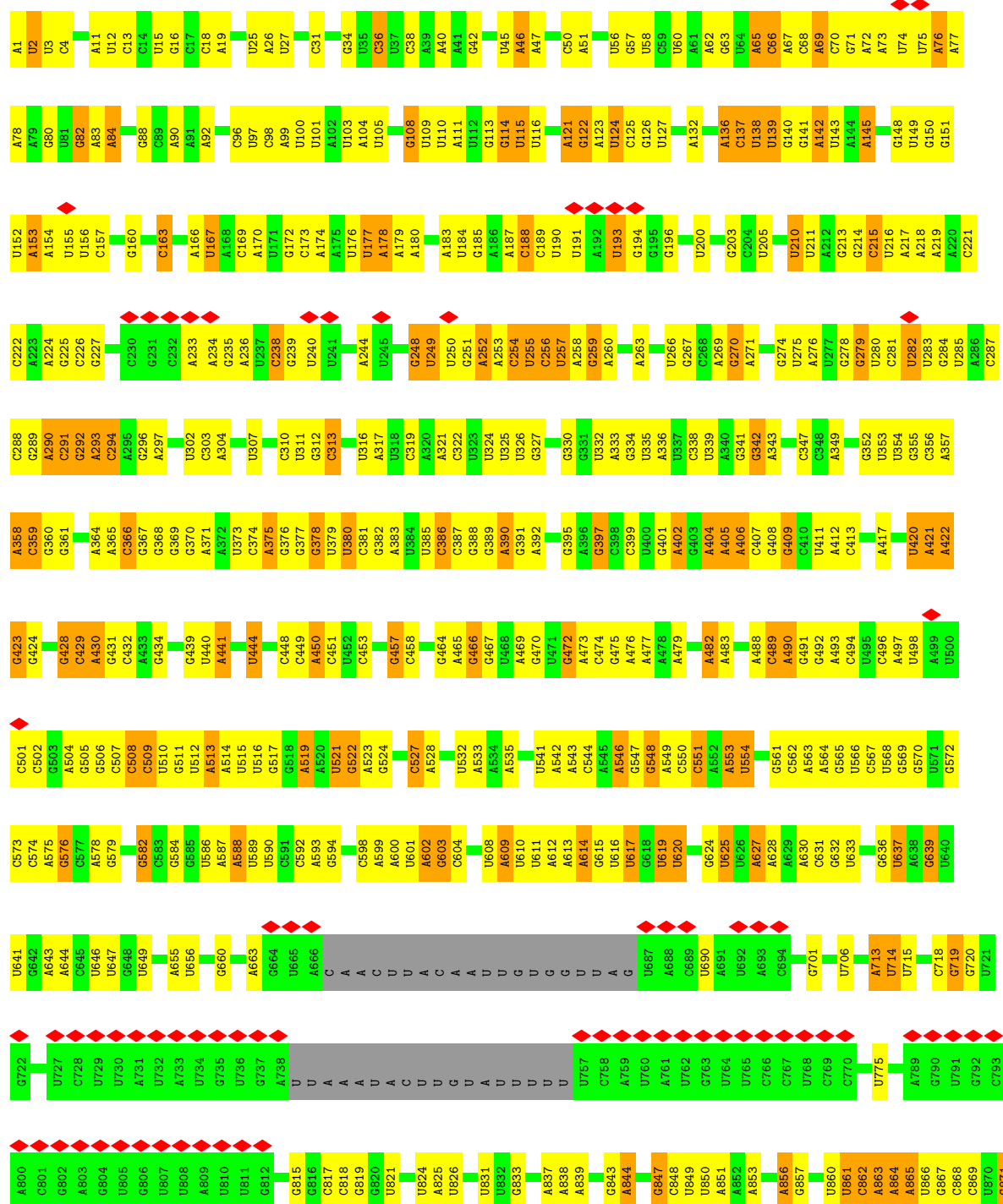


• Molecule 60: 60S ribosomal protein L10a-2

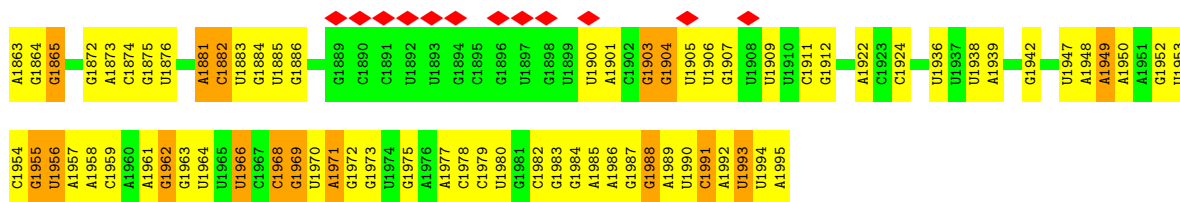




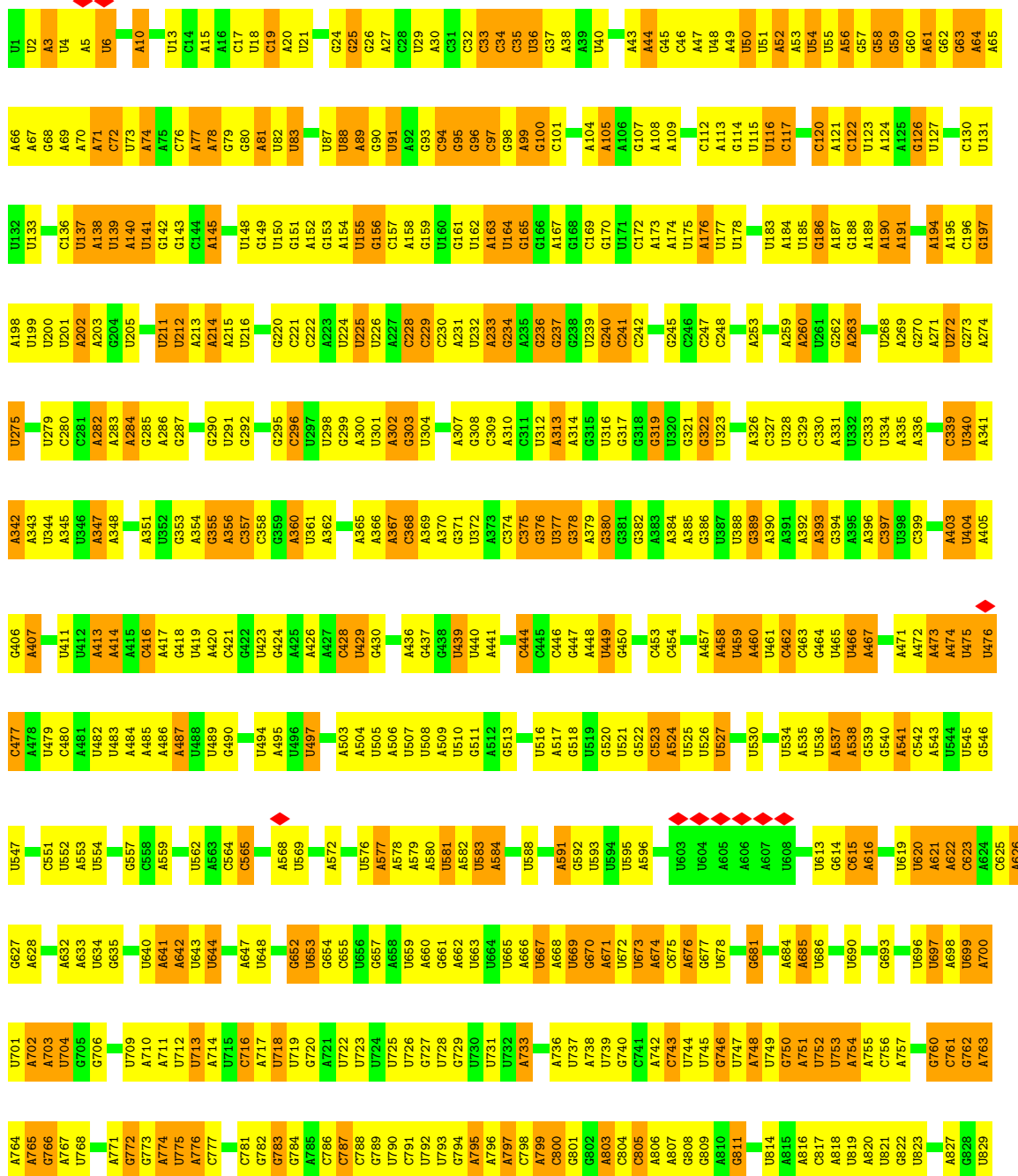
• Molecule 61: 18S ribosomal RNA



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G1786	C1718	A1583	U1508	A1435	G1354	A1291	A1220	G1152	G1089	A1018	G936	A873
U1787	C1719	A1584	U1509	G1436	A1362	A1292	A1221	C1157	G1090	U1019	A937	U874
C1788	U1720	U1585	U1510	U1438	U1363	C1293	C1222	U1158	U1091	C1018	G938	A875
	U1721	U1586				U1294	U1224	C1159	A1092	U1020	G939	U876
	U1722	U1587				U1295	U1225	U1160	A1022	A1021	U940	U877
A1793	U1723	G1588	U1513	C1441	C1367	A1296	A1226	G1161	G1093	A1022	A941	C878
C1794	U1724	C1589	G1514	U1442	G1368		A1227	G1162	C1094	C1023	A942	U879
U1795	C1725	G1590	A1520	U1443	U1371			G1164	G1095	C1024	U943	G880
C1797	U1726	U1591		A1445	U1372	C1302	A1230	C1165	C1096	G1025	A944	U881
	U1727	C1592		G1446	U1373	G1303	A1231	U1166	C1097	A1026	A945	G882
A1798	G1728	U1593	U1527	G1447	A1374	A1304	G1234	U1167	A1028	A1027	U946	U885
C1799	U1729	G1594	G1528	A1448	G1375	A1305	A1235	C1168	G1029	A1028	A946	G886
U1800	U1730	G1595	G1529	U1449		A1306	A1236	C1169	C1030	A1030	A949	G887
U1801	C1731	A1596	A1530	U1450	C1378	A1307	G1237	G1170	A1031	U1032	U950	G888
G1802	U1732	A1597	G1531	A1451	C1379	A1308	G1238	G1171	A1066	U1032	A951	A889
A1803	G1733	A1598	C1532	U1452	U1380	U1309	A1239	G1172	A1107	A1037	G952	U890
U1804	U1734	U1599	G1533	G1453	U1381	A1310	A1240	A1173	A1108	C1037	A953	A891
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	U1736	A1601	U1535	C1457	A1383	A1312		A1175	A1110	A1039		
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U1809	C1674	G1603		A1459	U1385	G1314	A1245	A1178	U1112	A1041	G958	A896
C1810	A1741	U1604	U1539	A1460	G1386	U1315	A1246	A1179	A1113	A1042	U959	A897
G1812	C1743	G1605	U1541		U1387	G1316	C1247	A1180	A1114	U1043	U960	U898
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G1814	G1745		G1543	G1468		A1318	A1249		G1116	U1046	G962	A900
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G1821	C1686	A1616	U1549	U1479	A1400	U1325	G1257	G1190	A1054	U976	U977	U907
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A1823	U1688	G1618	C1551	C		U1328	A1259	U1192	A1057	A1058	G982	U909
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A1825	G1690	U1620	U1557	U	G1405	U1330	C1261	C1194			G984	U912
C1826	U1691	G1621	A1558	G	A1406	A1331	C1262		C1062	G1063	A987	G913
A1827	C1692	U1622	A1559	U	U1407	G1332	U1263	G1198	C1063		G988	C914
C1828	G1693	C1623	G1560	U	A1408	A1333	G1264	A1200	A1066	A1067	U998	U915
G1829	U1694	U1624	G1561	C	A1409	U1334	C1265	A1201	G1067		A992	U916
C1830	G1695	G1625	A1564	G	C1410	G1335		G1202	A1067	A993	A994	U917
C1831	A1697	U1626	A1565	A	G1411	U1336	U1270	G1203	A1070	A994		C918
C1832	U1698	G1627	C1566	U	A1412	U1337	U1273	A1204	G1071	U998	U999	U920
C1833		A1628	A1567	A	G1415	G1338	U1274	U1205	A1072	U998	G1000	G922
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	G1703	G1637	G1568	A	A1422	C1341	G1278	U1209	A1080	A1081	G1002	
U1839	U1704	A1638	C1569	A	A1423	G1342	U1279	G1210	A1079	G1082	G1005	U926
A1847	U1705	U1639	U1570	A	A1424	A1343	U1280	G1141	G1083	G1084	A1010	A931
U1848	C1773	G1640	U1571	U	U1425	A1344	A1281	U1142	C1083	G1012	A1011	A932
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G1850	A1707	C1642	U1573	U	U1427	C1346	G1283	U1145	G1004			
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	G1712	C1713	A1577	A1501	A1431	U1350	G1287	U1149				
	U1714	U1578	U1579	U1502	A1432	G1352	G1288	U1150				
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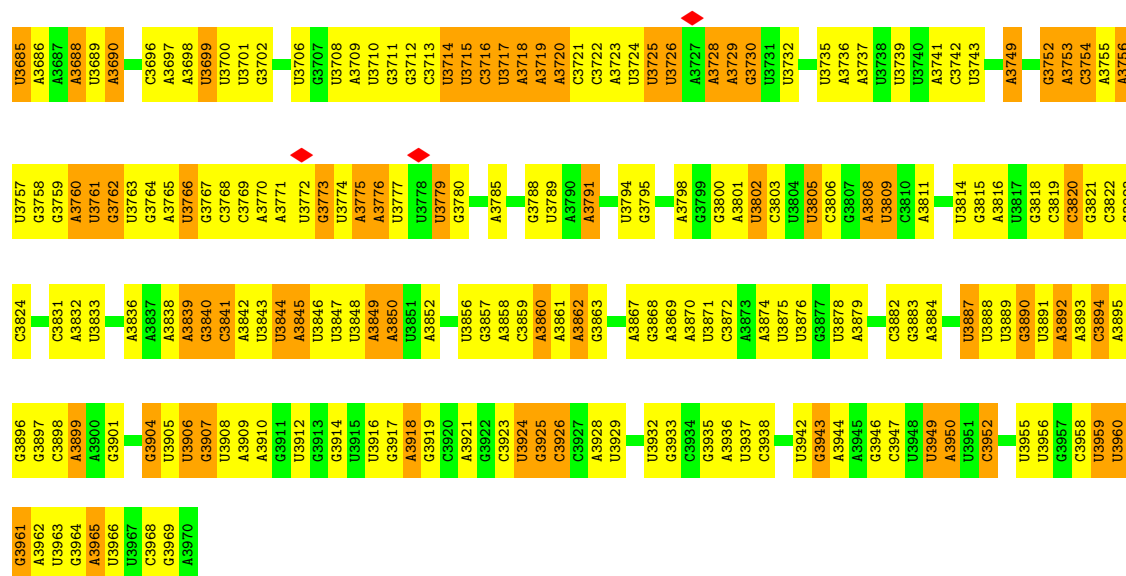
• Molecule 62: 28S ribosomal RNA



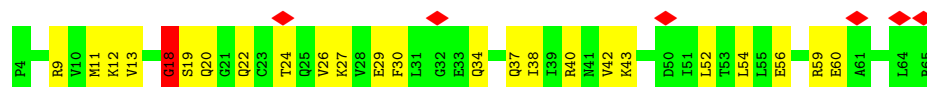
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A902	U905	U906	U907	U908	U909	U910	U911	U912	U913	U914	U994	U995	U999	U1000	U1001	U1002	U1003	U1004	U1005	U1006	U1007	U1008	U1009	U1010	U1011	U1012	U1013	U1014	U1015	U1016	U1017	U1018	U1019	U1020	U1021	U1022	U1023	U1091	U1092	U1093	U1094	U1095	U1096	U1097	U1100	U1101	U1102	U1103	U1104	U1105	U1106	U1107	U1108	U1109	U1110	U1111	U1112		
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C2641	A2560	A2496	C2234	C2165	G2103	U2033	G1967	U1900	C	U1780
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G2651	G2502	U	C2239	C2172	A2110	G2039	G1973	A1905	U	G1786
G2652	G2503	U	U2240	C2173	A2111	A2040	U1907	U1906	A	C1787
A2505	A2504	U	U2241	A2174	A2112	G2041	A1908	U1907	A	G1788
	C	C	G	A2175	A2113	A2042	C1975	A1909	A	A1789
	G	G	U	G2176	U2114	G2043	G1978	C1910	U	A1790
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	A	A	U	U2178	U2116		G1980	G1912	C	G1792
	U	U	U	U2179	A2117	U2047	A1981	U1913	C	C
	C	C	C	A2180	U2118	G2048	U1982	U1914	A	C1793
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	U	U	U	A2182	G2120	U2050	U1984	U1918	U	A1795
	C	C	U	A2183	U2121	A2051	C1985	A1919	G	A1796
	G	G	U	G	G2122	G2052	G1986	U1920	A	A1797
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	C	C	U	C2188	G2124	U2054	A1988	A1922	U	U1799
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	U	U	U	A2190	A2126		A1990	A1924	U	U1801
	U	U	U	G2191	C2127	A2060	A1991	U1925	U	C1802
	U	U	U	U2192	A2128	G2061		A1926	U	C1803
	G	G	U	C2193	C2129	A2062	U1994	U1927	U	A1804
	A	A	U	G2194	G2130	G2063	U1995	A1928	U	A1805
	G	G	U	A2195	C2131	G2064		G1930	U	G1806
	U	U	U	G2196	A2132	A2065	U2000	G1931	U	U1807
	U	U	U	U2199	A2133	G2066	U2001	C1934	U	A1808
	C	C	U	A2200	A2134	G2067	U2002	G1935	U	A1809
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	G	G	U	G2203	U2138	G2070	U2004	U1937	U	C1812
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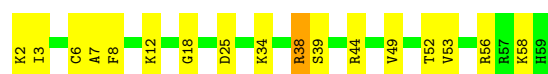
• Molecule 63: 40S ribosomal protein S28



• Molecule 64: 40S ribosomal protein S15Aa



• Molecule 65: 60S ribosomal protein L24



• Molecule 66: RH48056p

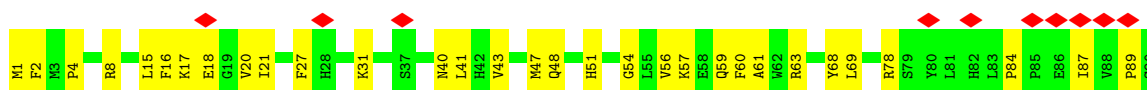




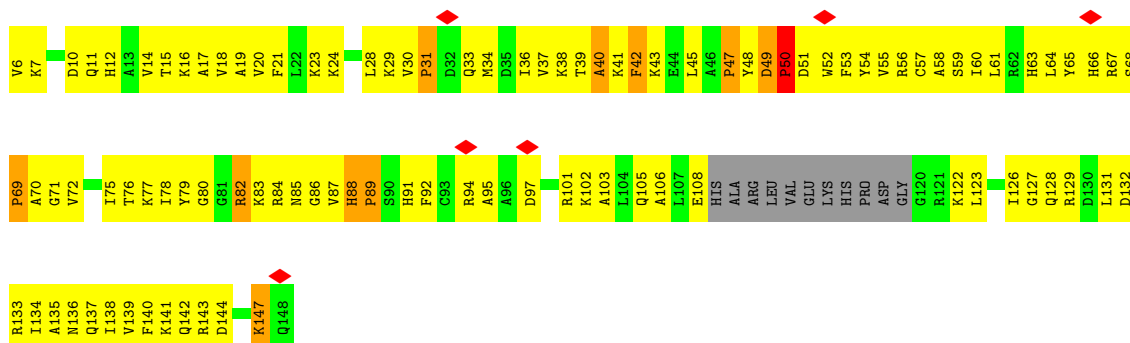
- Molecule 67: Ribosomal protein L22-like protein



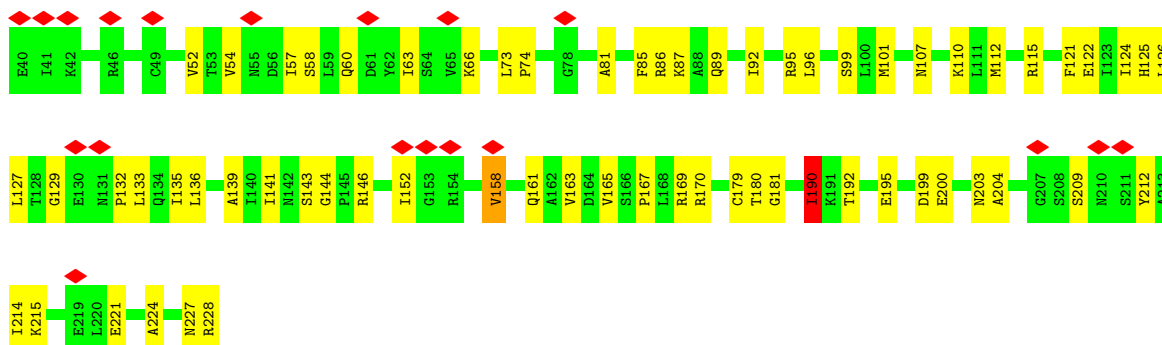
- Molecule 68: 40S ribosomal protein S10b



- Molecule 69: 40S ribosomal protein S19a

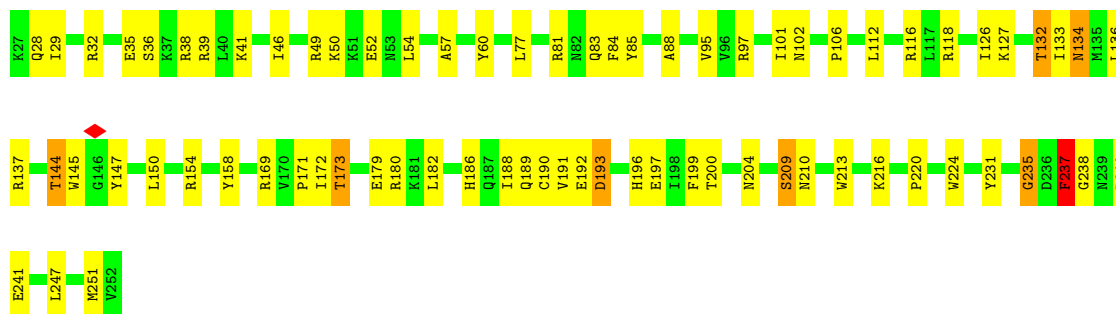


- Molecule 70: 40S ribosomal protein S5a



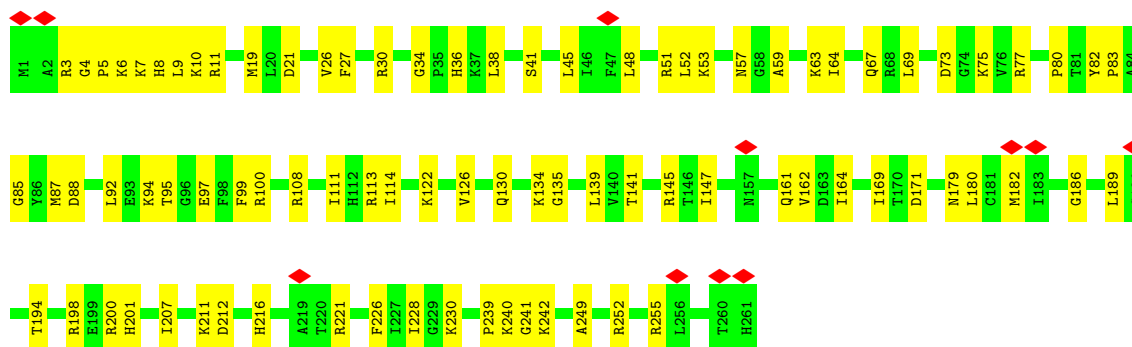
- Molecule 71: 60S ribosomal protein L7

Chain CF:  67% 30% .



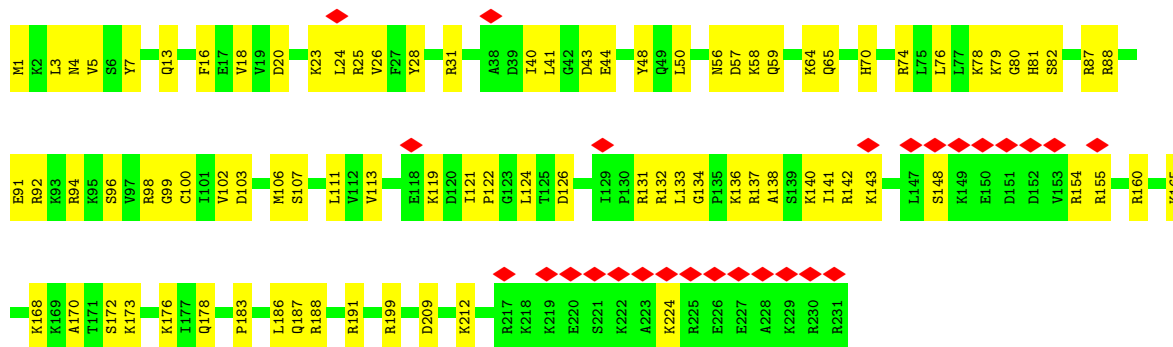
- Molecule 72: 40S ribosomal protein S4

Chain AE:  67% 33%



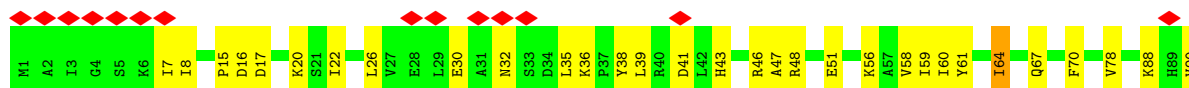
- Molecule 73: 40S ribosomal protein S6

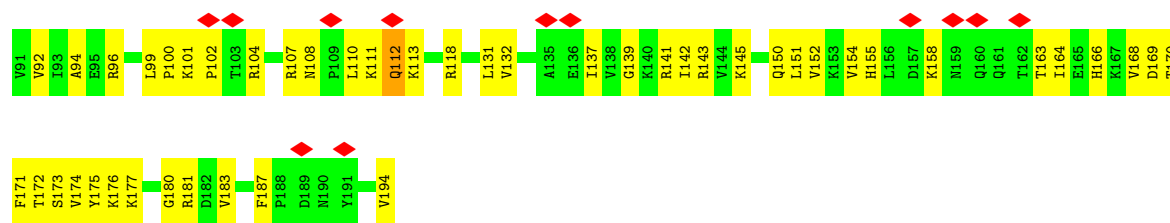
Chain AG:  12% 63% 37%



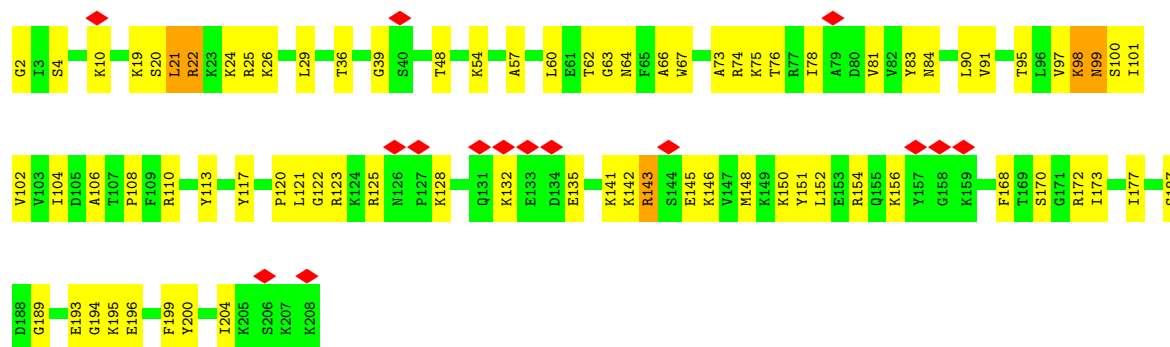
- Molecule 74: 40S ribosomal protein S7

Chain AH:  13% 60% 39%

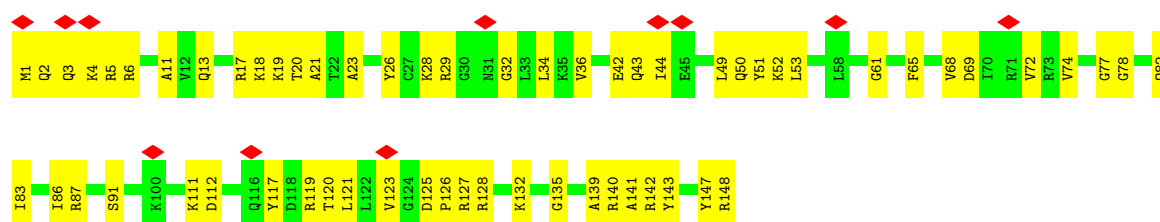




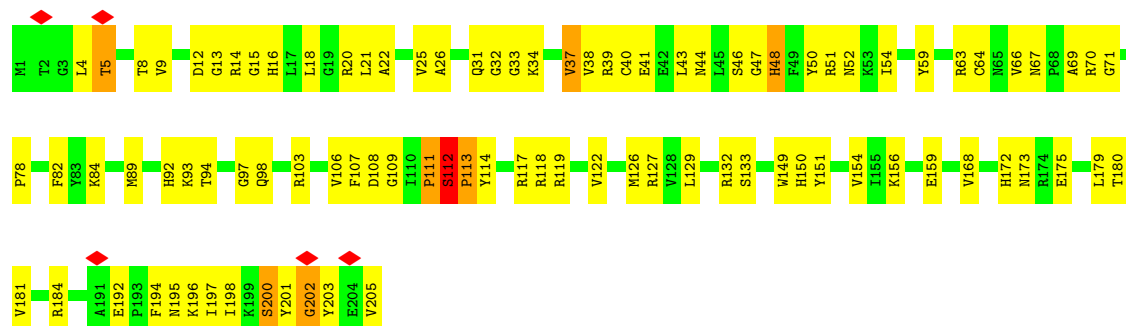
- Molecule 75: 40S ribosomal protein S8



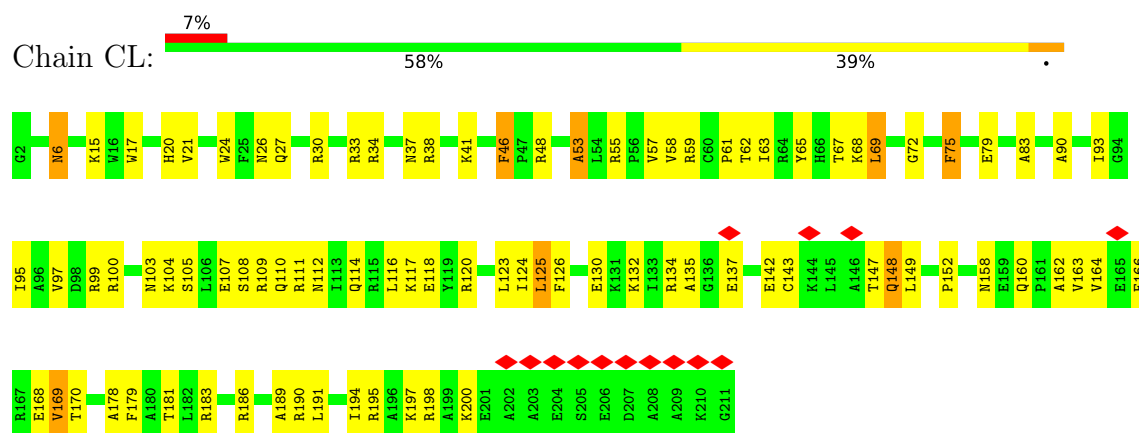
- Molecule 76: 40S ribosomal protein S16



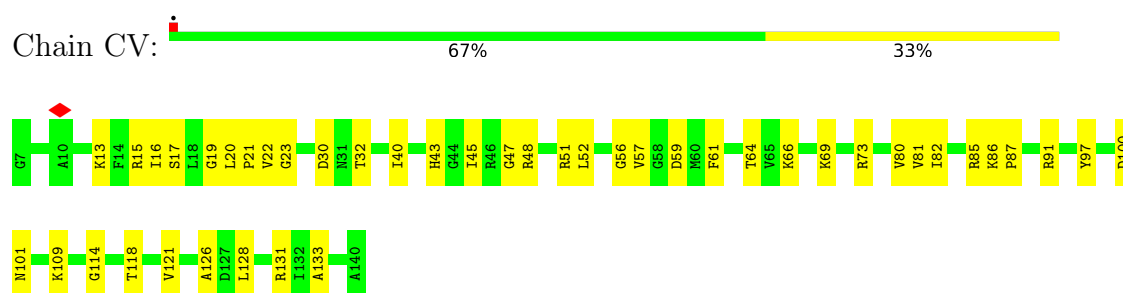
- Molecule 77: 60S ribosomal protein L13a



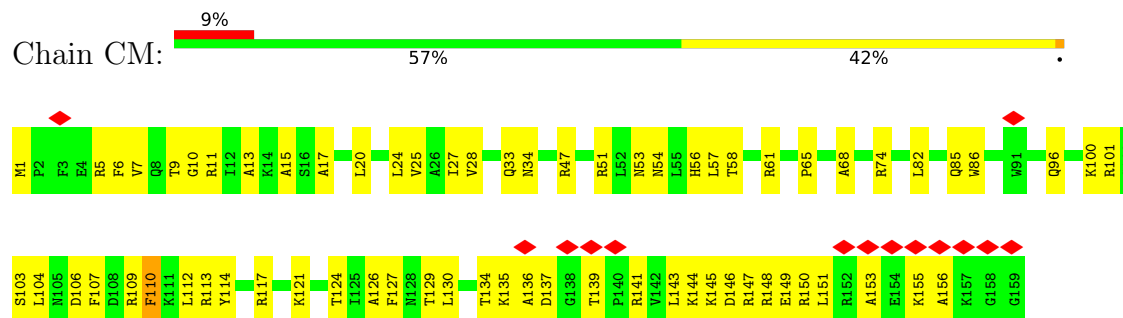
- Molecule 78: 60S ribosomal protein L13



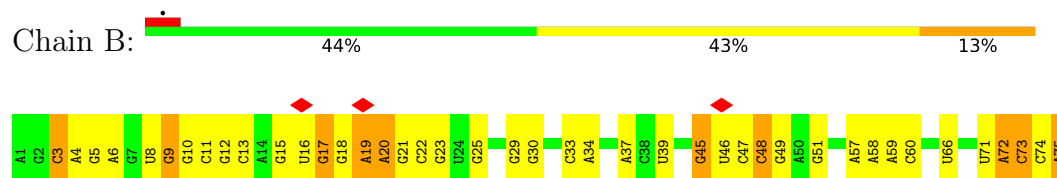
- Molecule 79: 60S ribosomal protein L23



- Molecule 80: 60S ribosomal protein L14



- Molecule 81: P-tRNA

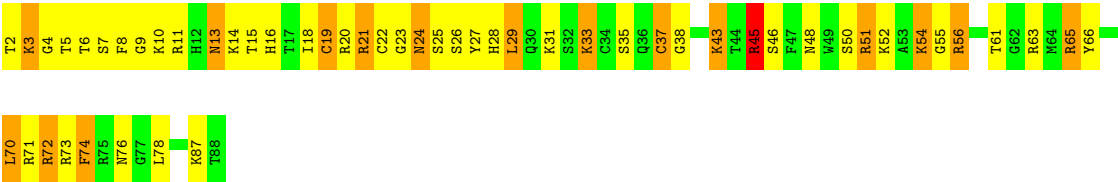


- Molecule 82: mRNA



- Molecule 83: Probable 60S ribosomal protein L37-B

Chain Cj: 39% 41% 18% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	10392	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	80	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.643	Depositor
Minimum map value	-0.491	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.020	Depositor
Recommended contour level	0.035	Depositor
Map size ($\text{\AA}$)	426.00003, 426.00003, 426.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.065, 1.065, 1.065	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	AA	0.28	0/1777	0.67	0/2422
2	CA	0.74	1/1970 (0.1%)	0.93	1/2635 (0.0%)
3	AB	0.26	0/1825	0.65	0/2448
4	CB	0.70	5/3356 (0.1%)	0.97	7/4494 (0.2%)
5	AC	0.31	0/1785	0.72	3/2415 (0.1%)
6	CC	0.68	1/3163 (0.0%)	0.95	10/4253 (0.2%)
7	Ag	0.21	0/2574	0.52	0/3506
8	AU	0.26	0/825	0.57	0/1111
9	AO	0.36	0/1016	0.84	4/1364 (0.3%)
10	AX	0.38	0/1152	0.74	0/1540
11	AM	0.25	0/937	0.68	2/1260 (0.2%)
12	AS	0.25	0/1146	0.70	3/1535 (0.2%)
13	Ad	0.30	0/443	0.77	0/589
14	AN	0.34	0/1225	0.68	2/1641 (0.1%)
15	AL	0.32	0/1296	0.65	0/1725
16	AR	0.26	0/993	0.67	2/1333 (0.2%)
17	AP	0.27	0/1036	0.66	0/1383
18	AV	0.28	0/622	0.62	0/835
19	AY	0.28	0/1032	0.70	2/1373 (0.1%)
20	AZ	0.24	0/616	0.62	0/826
21	Aa	0.40	0/883	0.88	4/1184 (0.3%)
22	Ab	0.22	0/668	0.60	0/898
23	AD	0.30	1/1808 (0.1%)	0.65	0/2427
24	Ae	0.30	0/475	0.85	2/625 (0.3%)
25	Af	0.25	0/672	0.76	4/887 (0.5%)
26	AJ	0.27	0/1526	0.70	2/2037 (0.1%)
27	Ca	0.73	0/1235	1.00	5/1640 (0.3%)
28	CN	0.85	0/1750	1.04	0/2335
29	CI	0.34	0/1827	0.77	4/2447 (0.2%)
30	CD	0.33	0/2379	0.68	4/3196 (0.1%)
31	CQ	0.63	1/1544 (0.1%)	0.89	3/2069 (0.1%)
32	CR	0.45	0/1703	0.69	1/2255 (0.0%)
33	CS	0.51	0/1491	0.92	1/1998 (0.1%)
34	CT	0.57	1/1326 (0.1%)	1.00	8/1773 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	CP	0.72	0/1529	0.89	1/2042 (0.0%)
36	CX	0.42	0/1001	0.80	5/1348 (0.4%)
37	CY	0.48	0/1094	0.71	0/1456
38	CZ	0.31	0/1141	0.58	0/1517
39	Cr	0.57	1/1069 (0.1%)	1.15	8/1432 (0.6%)
40	Ch	0.38	0/1024	0.71	0/1353
41	Cb	0.53	0/628	1.11	6/832 (0.7%)
42	Cc	0.34	0/779	0.63	1/1048 (0.1%)
43	Cd	0.66	0/939	0.87	0/1262
44	Ce	0.86	0/1132	1.11	3/1508 (0.2%)
45	Cf	0.62	0/1270	1.00	4/1696 (0.2%)
46	Ci	0.37	0/944	0.86	2/1250 (0.2%)
47	Ck	0.30	0/583	0.70	2/774 (0.3%)
48	Cl	0.78	0/445	1.06	1/589 (0.2%)
49	Cm	0.34	0/435	0.65	0/575
50	Cn	0.61	0/237	0.80	0/300
51	Cp	0.63	0/719	0.87	0/954
52	Co	0.47	0/887	0.81	1/1162 (0.1%)
53	CJ	0.26	0/1494	0.72	3/2001 (0.1%)
54	CH	0.34	0/1519	0.72	4/2042 (0.2%)
55	CE	0.35	0/1883	0.86	8/2514 (0.3%)
56	CG	0.34	0/1968	0.75	4/2637 (0.2%)
57	A9	0.51	0/714	0.63	0/1112
58	A7	0.48	0/2854	0.49	0/4447
59	A8	0.75	0/2932	0.82	2/4568 (0.0%)
60	Cz	0.25	0/1727	0.66	0/2308
61	B2	0.57	6/43887 (0.0%)	0.47	3/68161 (0.0%)
62	A5	0.75	2/86239 (0.0%)	0.76	20/134149 (0.0%)
63	Ac	0.23	0/502	0.66	1/670 (0.1%)
64	AW	0.35	1/1046 (0.1%)	0.65	1/1402 (0.1%)
65	CW	0.55	0/495	0.81	2/658 (0.3%)
66	Cg	0.57	0/863	0.95	2/1152 (0.2%)
67	CU	0.27	0/828	0.62	0/1110
68	AK	0.31	0/786	0.74	2/1064 (0.2%)
69	AT	0.34	0/1060	0.90	8/1421 (0.6%)
70	AF	2.71	2/1510 (0.1%)	0.80	4/2026 (0.2%)
71	CF	0.66	0/1931	0.96	1/2587 (0.0%)
72	AE	0.24	0/2096	0.60	0/2819
73	AG	0.21	0/1891	0.54	0/2519
74	AH	0.28	0/1593	0.70	1/2145 (0.0%)
75	AI	0.32	0/1689	0.80	5/2250 (0.2%)
76	AQ	0.30	0/1202	0.79	4/1608 (0.2%)
77	CO	0.64	0/1700	0.93	2/2277 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	CL	0.55	0/1726	1.08	6/2308 (0.3%)
79	CV	0.59	0/1014	0.82	0/1362
80	CM	0.37	0/1326	0.77	4/1780 (0.2%)
81	B	0.28	0/1796	0.49	0/2800
82	v	0.29	0/283	0.47	0/439
83	Cj	0.85	0/707	1.11	1/932 (0.1%)
All	All	0.64	22/235193 (0.0%)	0.72	196/344825 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	CA	0	9
3	AB	0	2
4	CB	0	9
5	AC	0	1
6	CC	0	6
8	AU	0	1
10	AX	0	2
12	AS	0	1
13	Ad	0	2
21	Aa	0	3
23	AD	0	2
24	Ae	0	2
26	AJ	0	2
27	Ca	0	8
28	CN	0	11
29	CI	0	2
30	CD	0	4
31	CQ	0	5
32	CR	0	5
33	CS	0	10
34	CT	0	5
35	CP	0	6
39	Cr	0	11
41	Cb	0	5
43	Cd	0	4
44	Ce	0	7
45	Cf	0	4
46	Ci	0	4

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Mol	Chain	#Chirality outliers	#Planarity outliers
47	Ck	0	1
48	Cl	0	3
50	Cn	0	1
51	Cp	0	1
52	Co	0	3
53	CJ	0	1
55	CE	0	7
56	CG	0	7
63	Ac	0	1
65	CW	0	2
66	Cg	0	2
69	AT	0	3
70	AF	0	1
71	CF	0	3
72	AE	0	2
73	AG	0	1
74	AH	0	3
75	AI	0	1
77	CO	0	8
78	CL	0	9
80	CM	0	1
All	All	0	194

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
70	AF	190	ILE	CB-CG1	104.44	3.62	1.53
61	B2	1727	U	N1-C2	40.97	2.20	1.38
61	B2	1727	U	N3-C4	40.84	2.20	1.38
61	B2	1727	U	C2-N3	40.45	2.18	1.37
61	B2	1727	U	N1-C6	38.02	2.13	1.38

The worst 5 of 196 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	CI	91	LEU	CA-C-N	13.65	140.59	121.61
29	CI	91	LEU	C-N-CA	13.65	140.59	121.61
70	AF	190	ILE	CA-CB-CG1	11.76	130.39	110.40
59	A8	100	G	OP1-P-O3'	-10.73	75.80	108.00
70	AF	190	ILE	CB-CG1-CD1	10.00	134.79	113.80

There are no chirality outliers.

5 of 194 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	CA	179	ILE	Peptide
2	CA	185	ALA	Peptide
2	CA	196	TRP	Peptide
2	CA	197	PRO	Peptide
2	CA	3	ARG	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	1737	0	1750	59	0
2	CA	1935	0	2037	91	0
3	AB	1798	0	1867	58	0
4	CB	3287	0	3432	110	0
5	AC	1746	0	1827	61	0
6	CC	3109	0	3298	125	0
7	Ag	2511	0	2438	72	0
8	AU	815	0	871	30	0
9	AO	1003	0	1035	39	0
10	AX	1131	0	1190	47	0
11	AM	924	0	960	30	0
12	AS	1128	0	1177	64	0
13	Ad	433	0	424	19	0
14	AN	1202	0	1291	38	0
15	AL	1274	0	1351	40	0
16	AR	981	0	1038	30	0
17	AP	1016	0	1086	47	0
18	AV	617	0	613	33	0
19	AY	1016	0	1073	34	0
20	AZ	608	0	658	20	0
21	Aa	867	0	920	30	0
22	Ab	653	0	680	24	0
23	AD	1782	0	1862	46	0
24	Ae	469	0	503	19	0
25	Af	659	0	695	19	0
26	AJ	1503	0	1620	56	0
27	Ca	1204	0	1260	59	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	CN	1710	0	1778	106	0
29	CI	1785	0	1805	59	0
30	CD	2334	0	2354	75	0
31	CQ	1518	0	1626	54	0
32	CR	1683	0	1827	43	0
33	CS	1454	0	1503	66	0
34	CT	1297	0	1364	54	0
35	CP	1505	0	1556	50	0
36	CX	984	0	1058	37	0
37	CY	1078	0	1159	34	0
38	CZ	1115	0	1199	44	0
39	Cr	1051	0	1148	42	0
40	Ch	1015	0	1163	36	0
41	Cb	619	0	650	15	0
42	Cc	770	0	802	23	0
43	Cd	924	0	942	23	0
44	Ce	1110	0	1181	33	0
45	Cf	1244	0	1316	60	0
46	Ci	934	0	1029	44	0
47	Ck	576	0	634	23	0
48	Cl	437	0	483	24	0
49	Cm	429	0	472	11	0
50	Cn	236	0	286	6	0
51	Cp	710	0	756	23	0
52	Co	874	0	956	20	0
53	CJ	1468	0	1507	47	0
54	CH	1499	0	1569	52	0
55	CE	1845	0	1981	79	0
56	CG	1936	0	2103	50	0
57	A9	639	0	321	13	0
58	A7	2554	0	1296	52	0
59	A8	2621	0	1327	79	0
60	Cz	1702	0	1814	37	0
61	B2	39355	0	19531	807	0
62	A5	77175	0	38515	1442	0
63	Ac	498	0	525	19	0
64	AW	1028	0	1071	47	0
65	CW	483	0	510	9	0
66	Cg	852	0	933	39	0
67	CU	811	0	838	22	0
68	AK	760	0	757	20	0
69	AT	1041	0	1061	409	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
70	AF	1490	0	1548	60	0
71	CF	1895	0	2012	54	0
72	AE	2054	0	2165	70	0
73	AG	1866	0	2029	62	0
74	AH	1566	0	1664	59	0
75	AI	1665	0	1746	61	0
76	AQ	1183	0	1255	46	0
77	CO	1668	0	1783	70	0
78	CL	1695	0	1790	71	0
79	CV	998	0	1046	32	0
80	CM	1302	0	1388	65	0
81	B	1605	0	814	22	0
82	v	255	0	130	2	0
83	Cj	696	0	720	102	0
All	All	219005	0	161752	5054	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 15.

The worst 5 of 5054 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)
61:B2:1717:A:H4'	69:AT:92:PHE:CE1	1.20	1.70
62:A5:1017:A:C8	83:Cj:15:THR:HG22	1.21	1.70
59:A8:107:U:C5	83:Cj:20:ARG:HD2	1.25	1.69
69:AT:29:LYS:CD	69:AT:106:ALA:HA	1.24	1.67
62:A5:1017:A:H8	83:Cj:15:THR:CG2	1.15	1.59

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AA	216/218 (99%)	188 (87%)	27 (12%)	1 (0%)	24	63
2	CA	251/253 (99%)	197 (78%)	52 (21%)	2 (1%)	16	52
3	AB	218/220 (99%)	186 (85%)	29 (13%)	3 (1%)	9	39
4	CB	412/414 (100%)	327 (79%)	84 (20%)	1 (0%)	43	77
5	AC	225/227 (99%)	200 (89%)	25 (11%)	0	100	100
6	CC	390/392 (100%)	308 (79%)	82 (21%)	0	100	100
7	Ag	316/318 (99%)	276 (87%)	40 (13%)	0	100	100
8	AU	100/102 (98%)	93 (93%)	7 (7%)	0	100	100
9	AO	132/134 (98%)	112 (85%)	19 (14%)	1 (1%)	16	52
10	AX	141/143 (99%)	112 (79%)	29 (21%)	0	100	100
11	AM	117/119 (98%)	100 (86%)	17 (14%)	0	100	100
12	AS	135/137 (98%)	120 (89%)	15 (11%)	0	100	100
13	Ad	50/52 (96%)	38 (76%)	12 (24%)	0	100	100
14	AN	148/150 (99%)	137 (93%)	11 (7%)	0	100	100
15	AL	153/155 (99%)	127 (83%)	26 (17%)	0	100	100
16	AR	118/120 (98%)	107 (91%)	11 (9%)	0	100	100
17	AP	122/124 (98%)	108 (88%)	14 (12%)	0	100	100
18	AV	80/82 (98%)	67 (84%)	13 (16%)	0	100	100
19	AY	124/126 (98%)	106 (86%)	18 (14%)	0	100	100
20	AZ	72/74 (97%)	59 (82%)	13 (18%)	0	100	100
21	Aa	105/107 (98%)	85 (81%)	20 (19%)	0	100	100
22	Ab	82/84 (98%)	66 (80%)	16 (20%)	0	100	100
23	AD	225/227 (99%)	191 (85%)	33 (15%)	1 (0%)	30	67
24	Ae	56/58 (97%)	39 (70%)	17 (30%)	0	100	100
25	Af	78/80 (98%)	64 (82%)	14 (18%)	0	100	100
26	AJ	179/181 (99%)	156 (87%)	22 (12%)	1 (1%)	21	58
27	Ca	147/149 (99%)	112 (76%)	34 (23%)	1 (1%)	18	55
28	CN	201/203 (99%)	153 (76%)	46 (23%)	2 (1%)	12	47
29	CI	215/217 (99%)	184 (86%)	31 (14%)	0	100	100
30	CD	288/290 (99%)	247 (86%)	40 (14%)	1 (0%)	36	71
31	CQ	185/187 (99%)	152 (82%)	32 (17%)	1 (0%)	24	63
32	CR	201/203 (99%)	182 (90%)	19 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	CS	171/173 (99%)	127 (74%)	41 (24%)	3 (2%)	6	33
34	CT	156/158 (99%)	118 (76%)	37 (24%)	1 (1%)	21	58
35	CP	183/185 (99%)	153 (84%)	30 (16%)	0	100	100
36	CX	118/120 (98%)	94 (80%)	23 (20%)	1 (1%)	16	52
37	CY	129/131 (98%)	111 (86%)	18 (14%)	0	100	100
38	CZ	132/134 (98%)	112 (85%)	20 (15%)	0	100	100
39	Cr	132/134 (98%)	92 (70%)	37 (28%)	3 (2%)	5	28
40	Ch	121/123 (98%)	107 (88%)	14 (12%)	0	100	100
41	Cb	73/75 (97%)	56 (77%)	17 (23%)	0	100	100
42	Cc	98/100 (98%)	94 (96%)	4 (4%)	0	100	100
43	Cd	109/111 (98%)	89 (82%)	20 (18%)	0	100	100
44	Ce	130/132 (98%)	99 (76%)	31 (24%)	0	100	100
45	Cf	155/157 (99%)	119 (77%)	34 (22%)	2 (1%)	9	41
46	Ci	111/113 (98%)	82 (74%)	29 (26%)	0	100	100
47	Ck	68/70 (97%)	63 (93%)	5 (7%)	0	100	100
48	Cl	48/50 (96%)	33 (69%)	14 (29%)	1 (2%)	5	29
49	Cm	50/52 (96%)	41 (82%)	9 (18%)	0	100	100
50	Cn	23/25 (92%)	21 (91%)	2 (9%)	0	100	100
51	Cp	89/91 (98%)	72 (81%)	17 (19%)	0	100	100
52	Co	102/104 (98%)	79 (78%)	23 (22%)	0	100	100
53	CJ	180/182 (99%)	147 (82%)	32 (18%)	1 (1%)	21	58
54	CH	188/190 (99%)	165 (88%)	23 (12%)	0	100	100
55	CE	226/228 (99%)	178 (79%)	46 (20%)	2 (1%)	14	49
56	CG	239/241 (99%)	205 (86%)	31 (13%)	3 (1%)	9	41
60	Cz	215/217 (99%)	192 (89%)	23 (11%)	0	100	100
63	Ac	60/62 (97%)	53 (88%)	7 (12%)	0	100	100
64	AW	127/129 (98%)	109 (86%)	18 (14%)	0	100	100
65	CW	56/58 (97%)	45 (80%)	11 (20%)	0	100	100
66	Cg	102/104 (98%)	88 (86%)	14 (14%)	0	100	100
67	CU	94/96 (98%)	76 (81%)	18 (19%)	0	100	100
68	AK	88/90 (98%)	68 (77%)	19 (22%)	1 (1%)	11	45

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
69	AT	128/143 (90%)	104 (81%)	20 (16%)	4 (3%)	3	21
70	AF	187/189 (99%)	158 (84%)	28 (15%)	1 (0%)	24	63
71	CF	224/226 (99%)	188 (84%)	32 (14%)	4 (2%)	6	33
72	AE	259/261 (99%)	225 (87%)	34 (13%)	0	100	100
73	AG	229/231 (99%)	211 (92%)	18 (8%)	0	100	100
74	AH	192/194 (99%)	161 (84%)	31 (16%)	0	100	100
75	AI	205/207 (99%)	162 (79%)	40 (20%)	3 (2%)	8	38
76	AQ	146/148 (99%)	117 (80%)	28 (19%)	1 (1%)	18	55
77	CO	203/205 (99%)	161 (79%)	38 (19%)	4 (2%)	6	31
78	CL	208/210 (99%)	151 (73%)	54 (26%)	3 (1%)	9	39
79	CV	132/134 (98%)	115 (87%)	17 (13%)	0	100	100
80	CM	157/159 (99%)	131 (83%)	26 (17%)	0	100	100
83	Cj	85/87 (98%)	57 (67%)	25 (29%)	3 (4%)	3	20
All	All	11610/11775 (99%)	9628 (83%)	1926 (17%)	56 (0%)	26	63

5 of 56 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	AB	120	TRP
69	AT	40	ALA
71	CF	237	PHE
77	CO	113	PRO
30	CD	20	PHE

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	AA	190/190 (100%)	189 (100%)	1 (0%)	81	82
2	CA	195/195 (100%)	190 (97%)	5 (3%)	40	61
3	AB	199/199 (100%)	198 (100%)	1 (0%)	81	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	CB	349/349 (100%)	342 (98%)	7 (2%)	48	66
5	AC	188/188 (100%)	188 (100%)	0	100	100
6	CC	323/323 (100%)	315 (98%)	8 (2%)	42	62
7	Ag	280/280 (100%)	277 (99%)	3 (1%)	65	74
8	AU	95/95 (100%)	95 (100%)	0	100	100
9	AO	103/103 (100%)	101 (98%)	2 (2%)	50	66
10	AX	116/116 (100%)	115 (99%)	1 (1%)	70	77
11	AM	104/104 (100%)	104 (100%)	0	100	100
12	AS	123/123 (100%)	123 (100%)	0	100	100
13	Ad	45/45 (100%)	44 (98%)	1 (2%)	45	64
14	AN	130/130 (100%)	128 (98%)	2 (2%)	57	71
15	AL	138/138 (100%)	137 (99%)	1 (1%)	76	79
16	AR	108/108 (100%)	107 (99%)	1 (1%)	70	77
17	AP	111/111 (100%)	110 (99%)	1 (1%)	70	77
18	AV	67/67 (100%)	67 (100%)	0	100	100
19	AY	105/106 (99%)	105 (100%)	0	100	100
20	AZ	67/67 (100%)	66 (98%)	1 (2%)	57	71
21	Aa	94/94 (100%)	93 (99%)	1 (1%)	65	74
22	Ab	72/72 (100%)	71 (99%)	1 (1%)	59	72
23	AD	192/192 (100%)	192 (100%)	0	100	100
24	Ae	47/47 (100%)	47 (100%)	0	100	100
25	Af	70/70 (100%)	70 (100%)	0	100	100
26	AJ	161/161 (100%)	159 (99%)	2 (1%)	63	74
27	Ca	122/122 (100%)	120 (98%)	2 (2%)	55	69
28	CN	174/174 (100%)	172 (99%)	2 (1%)	65	74
29	CI	187/187 (100%)	185 (99%)	2 (1%)	65	74
30	CD	241/241 (100%)	240 (100%)	1 (0%)	84	83
31	CQ	164/164 (100%)	160 (98%)	4 (2%)	43	63
32	CR	176/176 (100%)	172 (98%)	4 (2%)	44	63
33	CS	156/156 (100%)	154 (99%)	2 (1%)	61	72
34	CT	137/137 (100%)	135 (98%)	2 (2%)	57	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	CP	160/160 (100%)	157 (98%)	3 (2%)	50	66
36	CX	106/106 (100%)	105 (99%)	1 (1%)	70	77
37	CY	116/116 (100%)	114 (98%)	2 (2%)	53	68
38	CZ	121/121 (100%)	121 (100%)	0	100	100
39	Cr	112/112 (100%)	111 (99%)	1 (1%)	70	77
40	Ch	112/112 (100%)	110 (98%)	2 (2%)	51	67
41	Cb	67/67 (100%)	67 (100%)	0	100	100
42	Cc	84/84 (100%)	82 (98%)	2 (2%)	43	63
43	Cd	103/103 (100%)	101 (98%)	2 (2%)	50	66
44	Ce	120/120 (100%)	116 (97%)	4 (3%)	33	55
45	Cf	123/123 (100%)	119 (97%)	4 (3%)	33	55
46	Ci	100/100 (100%)	98 (98%)	2 (2%)	48	66
47	Ck	65/65 (100%)	65 (100%)	0	100	100
48	Cl	45/45 (100%)	45 (100%)	0	100	100
49	Cm	48/48 (100%)	48 (100%)	0	100	100
50	Cn	23/23 (100%)	23 (100%)	0	100	100
51	Cp	74/74 (100%)	73 (99%)	1 (1%)	59	72
52	Co	94/94 (100%)	94 (100%)	0	100	100
53	CJ	155/155 (100%)	154 (99%)	1 (1%)	78	81
54	CH	169/169 (100%)	168 (99%)	1 (1%)	78	81
55	CE	197/197 (100%)	194 (98%)	3 (2%)	57	71
56	CG	210/210 (100%)	209 (100%)	1 (0%)	81	82
60	Cz	190/190 (100%)	188 (99%)	2 (1%)	65	74
63	Ac	54/54 (100%)	54 (100%)	0	100	100
64	AW	113/113 (100%)	112 (99%)	1 (1%)	70	77
65	CW	52/52 (100%)	51 (98%)	1 (2%)	50	66
66	Cg	96/96 (100%)	95 (99%)	1 (1%)	68	76
67	CU	90/90 (100%)	90 (100%)	0	100	100
68	AK	81/81 (100%)	81 (100%)	0	100	100
69	AT	107/116 (92%)	107 (100%)	0	100	100
70	AF	160/160 (100%)	159 (99%)	1 (1%)	78	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
71	CF	200/200 (100%)	196 (98%)	4 (2%)	48	66
72	AE	220/220 (100%)	220 (100%)	0	100	100
73	AG	200/200 (100%)	199 (100%)	1 (0%)	81	82
74	AH	175/175 (100%)	174 (99%)	1 (1%)	78	81
75	AI	175/175 (100%)	173 (99%)	2 (1%)	65	74
76	AQ	122/122 (100%)	121 (99%)	1 (1%)	73	78
77	CO	175/175 (100%)	171 (98%)	4 (2%)	44	63
78	CL	173/173 (100%)	169 (98%)	4 (2%)	44	63
79	CV	101/101 (100%)	98 (97%)	3 (3%)	36	57
80	CM	138/138 (100%)	137 (99%)	1 (1%)	76	79
83	Cj	71/71 (100%)	41 (58%)	30 (42%)	0	0
All	All	10126/10136 (100%)	9981 (99%)	145 (1%)	57	72

5 of 145 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
83	Cj	2	THR
83	Cj	73	ARG
83	Cj	13	ASN
83	Cj	43	LYS
31	CQ	86	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 99 such sidechains are listed below:

Mol	Chain	Res	Type
48	Cl	19	GLN
60	Cz	197	ASN
52	Co	3	ASN
55	CE	197	GLN
66	Cg	46	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
57	A9	29/30 (96%)	10 (34%)	1 (3%)
58	A7	119/120 (99%)	30 (25%)	1 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
59	A8	122/123 (99%)	58 (47%)	2 (1%)
61	B2	1787/1995 (89%)	723 (40%)	26 (1%)
62	A5	3560/3974 (89%)	1649 (46%)	86 (2%)
81	B	74/75 (98%)	27 (36%)	1 (1%)
82	v	11/12 (91%)	6 (54%)	0
All	All	5702/6329 (90%)	2503 (43%)	117 (2%)

5 of 2503 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
57	A9	7	G
57	A9	9	C
57	A9	10	U
57	A9	11	A
57	A9	15	A

5 of 117 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
62	A5	1161	C
62	A5	3808	A
62	A5	1594	U
62	A5	3765	A
62	A5	3516	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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
61	B2	2
62	A5	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B2	1236:C	O3'	1237:G	P	6.91
1	A5	2896:U	O3'	2897:G	P	5.92
1	B2	1817:C	O3'	1818:U	P	4.83
1	A5	2819:A	O3'	2820:G	P	3.80

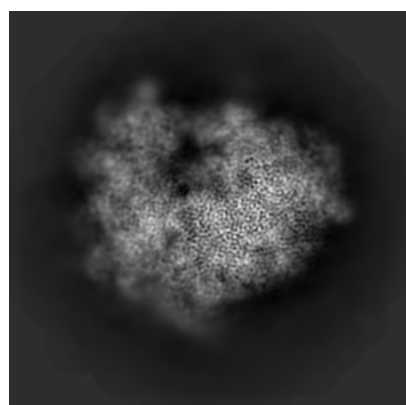
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10623. These allow visual inspection of the internal detail of the map and identification of artifacts.

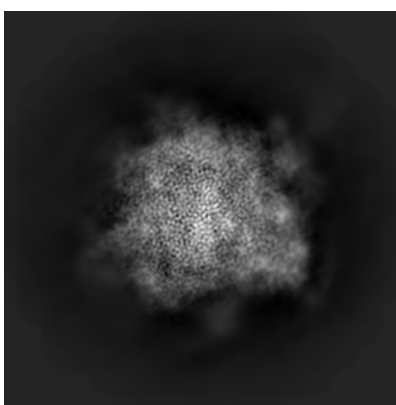
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

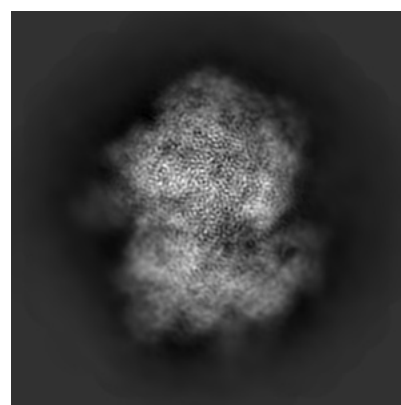
6.1.1 Primary map



X



Y

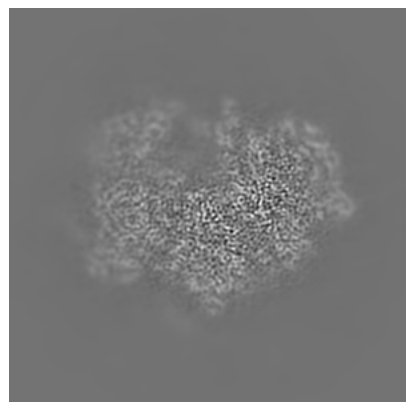


Z

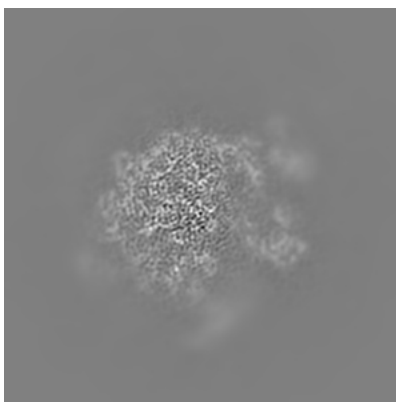
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

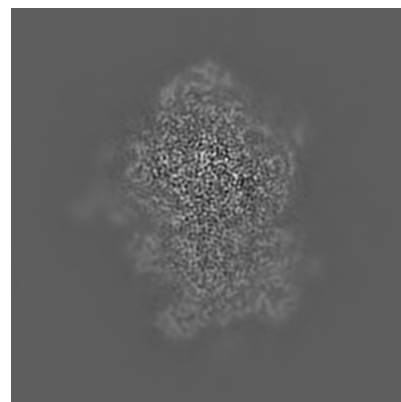
6.2.1 Primary map



X Index: 200



Y Index: 200

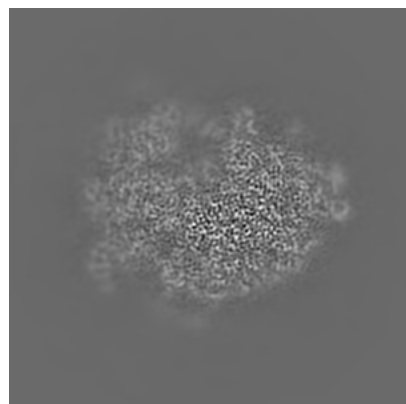


Z Index: 200

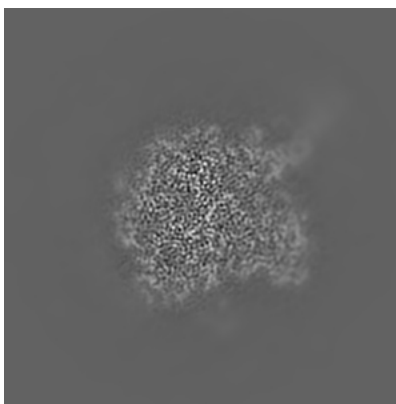
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

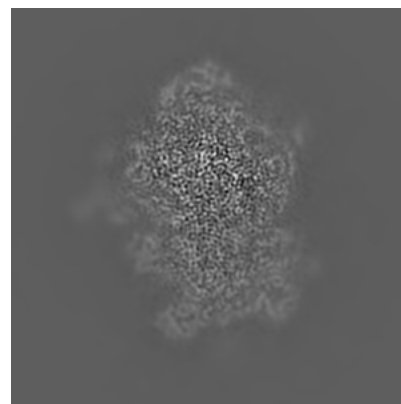
6.3.1 Primary map



X Index: 185



Y Index: 230

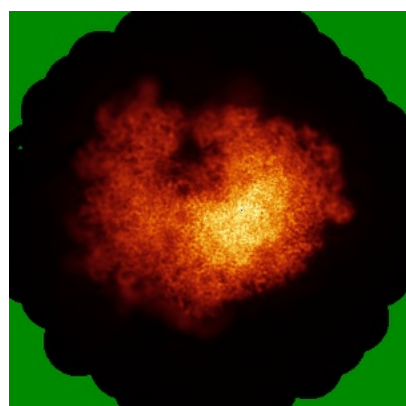


Z Index: 200

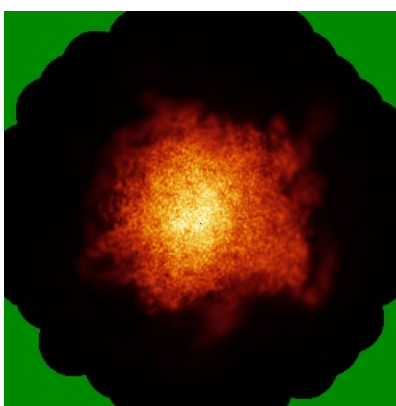
The images above show the largest variance slices of the map in three orthogonal directions.

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

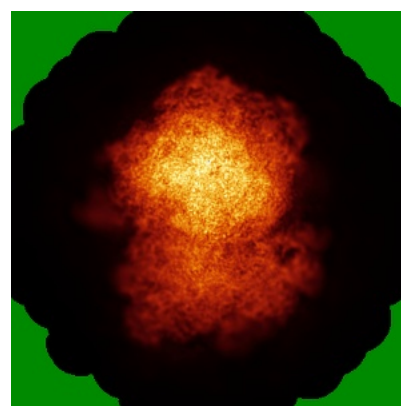
6.4.1 Primary map



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

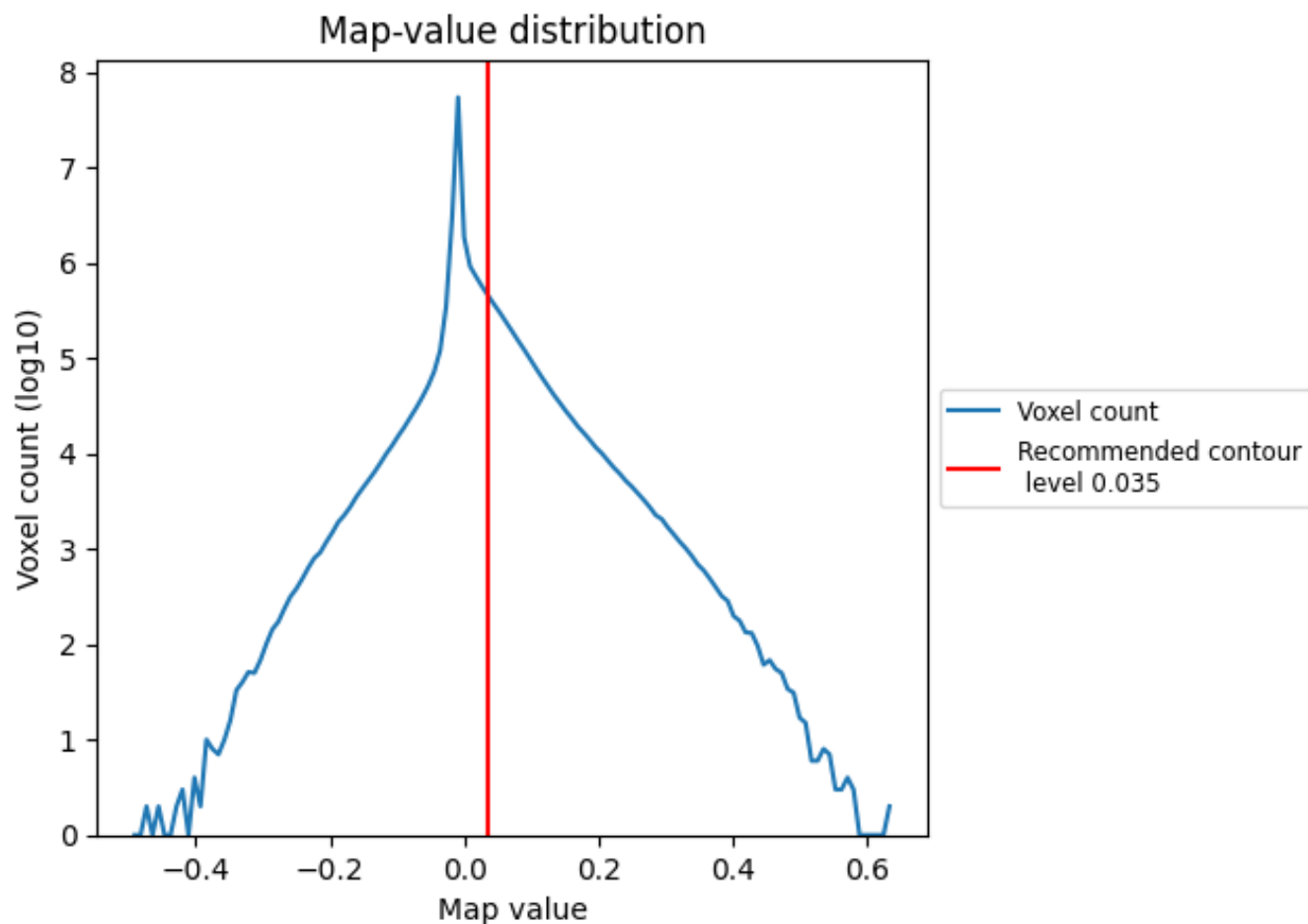
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

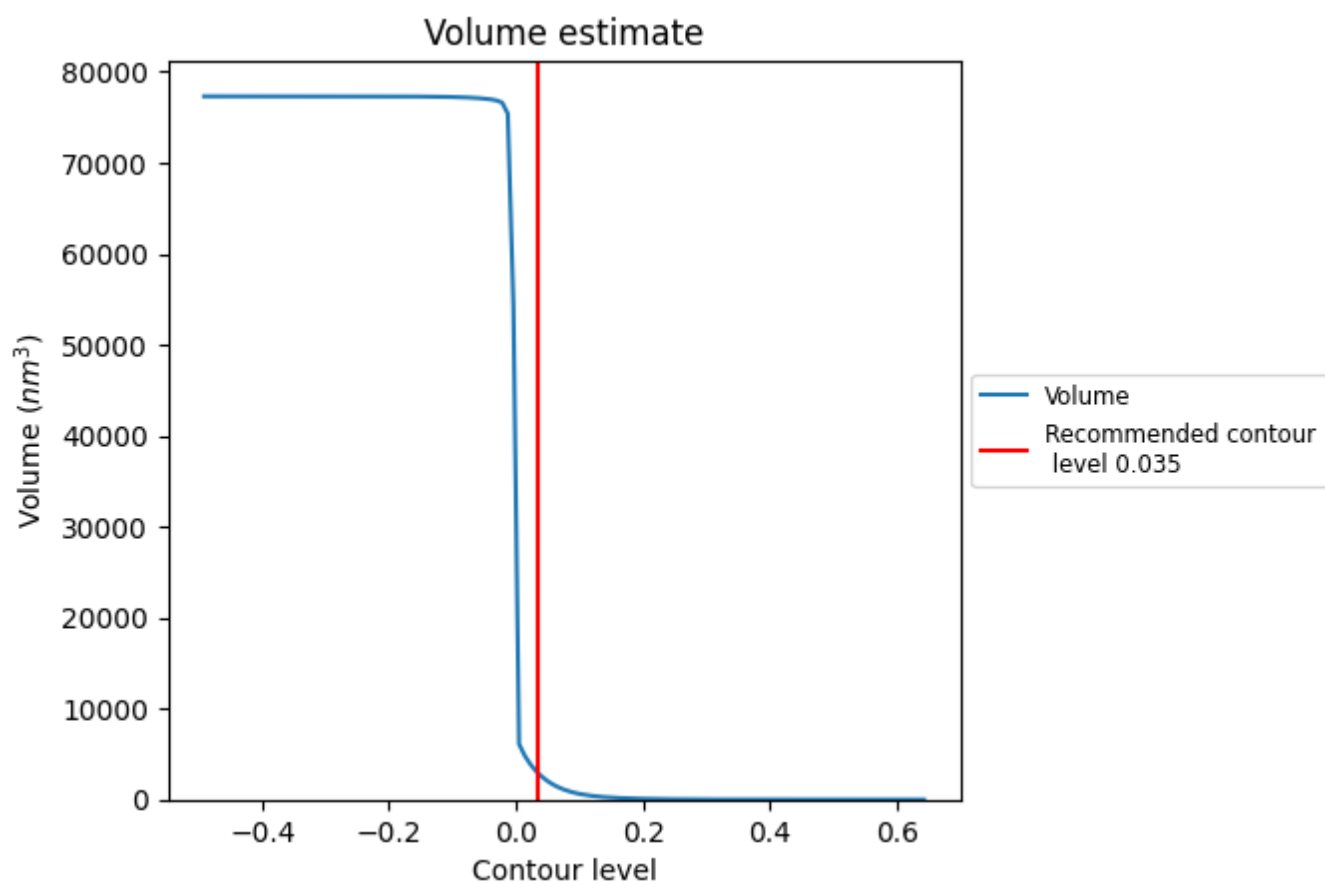
This section contains the results of statistical analysis of the map.

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.

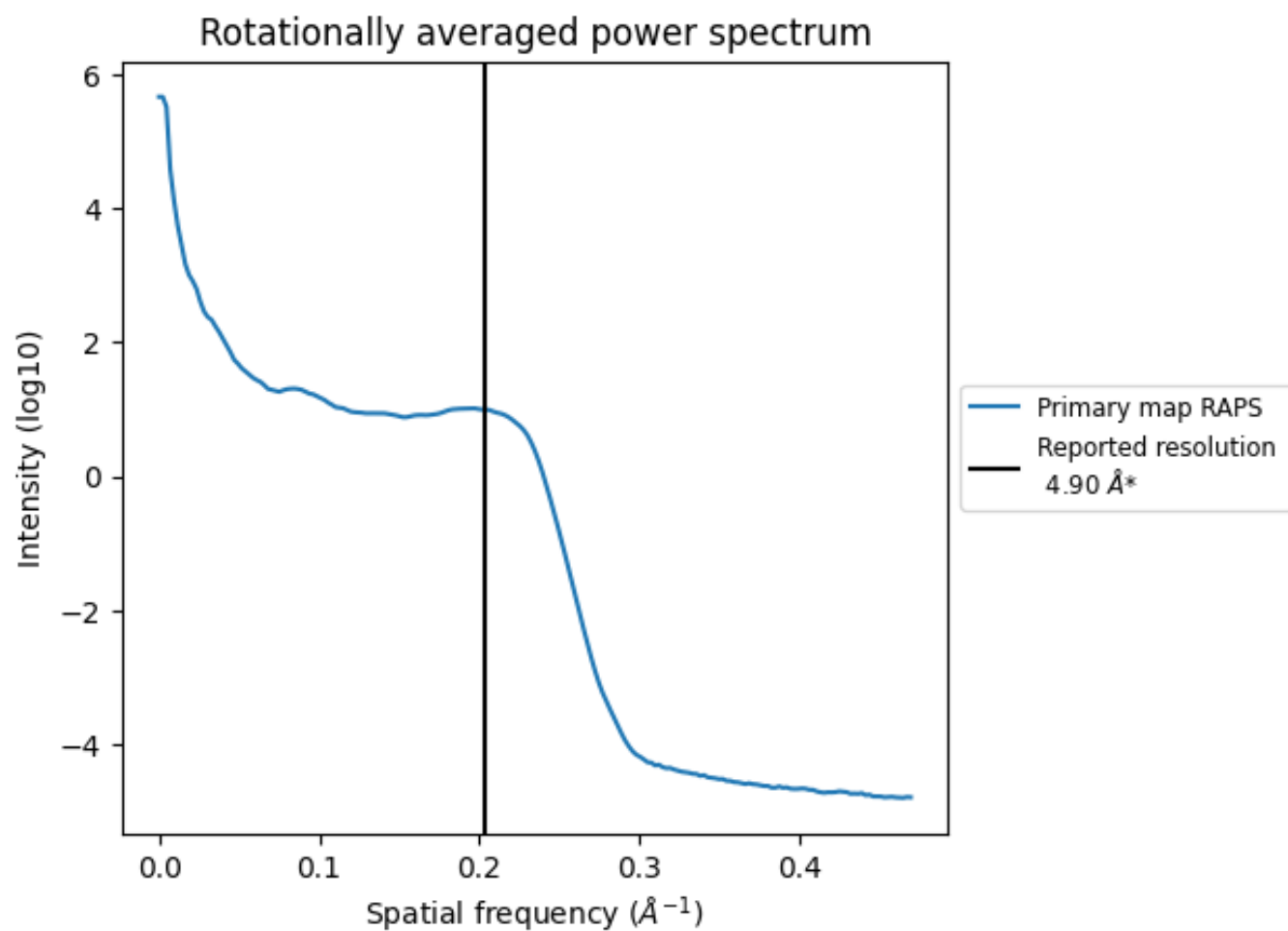
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2920 nm³; this corresponds to an approximate mass of 2638 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

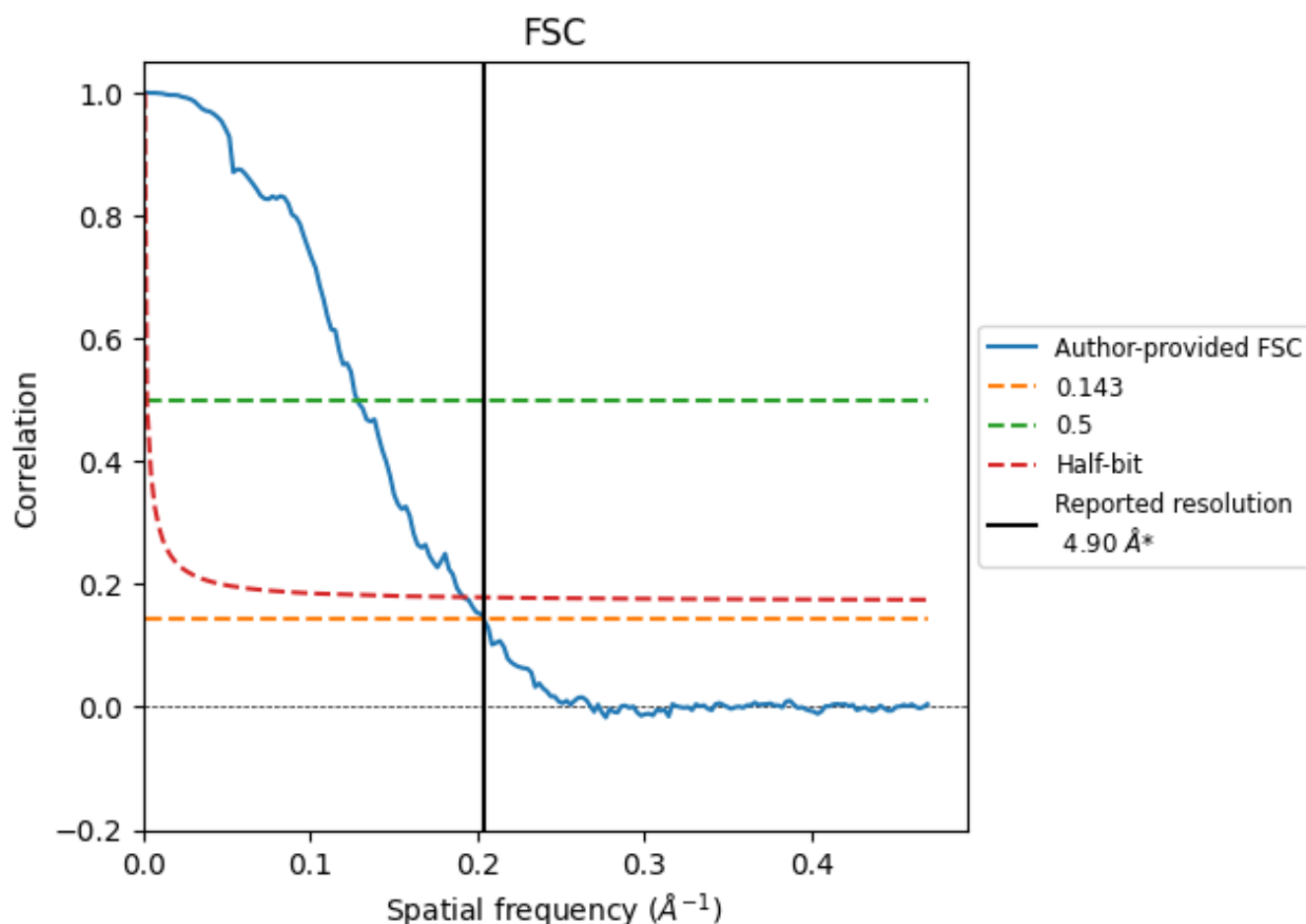


*Reported resolution corresponds to spatial frequency of 0.204 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

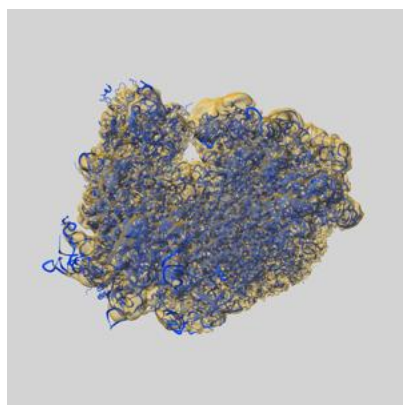
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.90	-	-
Author-provided FSC curve	4.91	7.80	5.21
Unmasked-calculated*	-	-	-

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

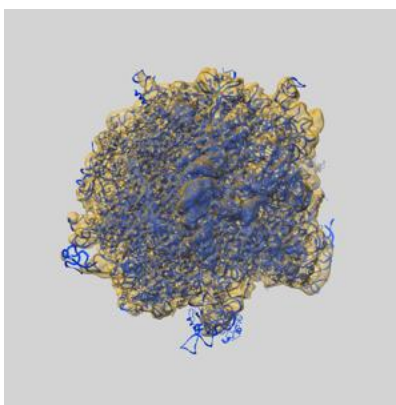
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10623 and PDB model 6XU7. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

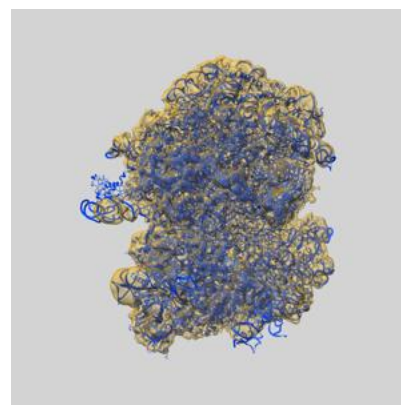
9.1 Map-model overlay [i](#)



X



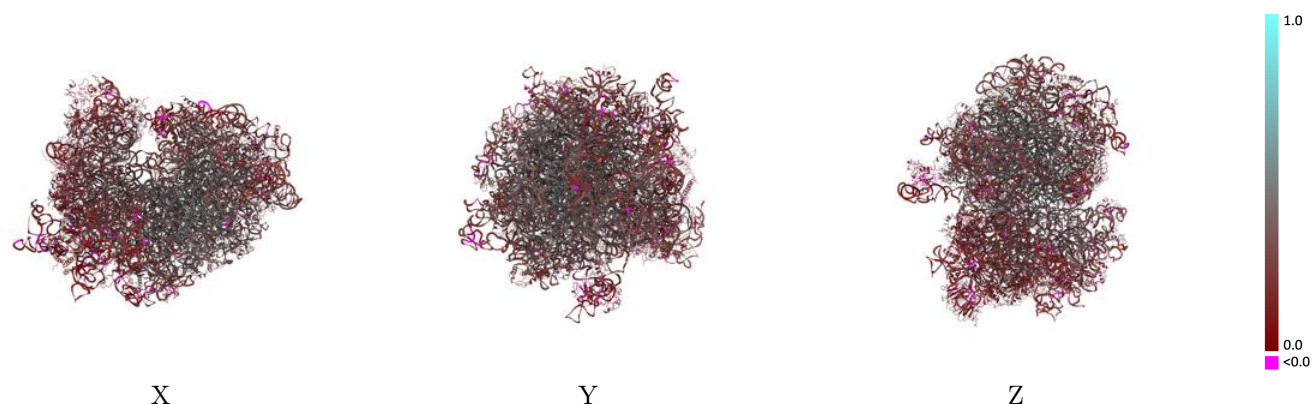
Y



Z

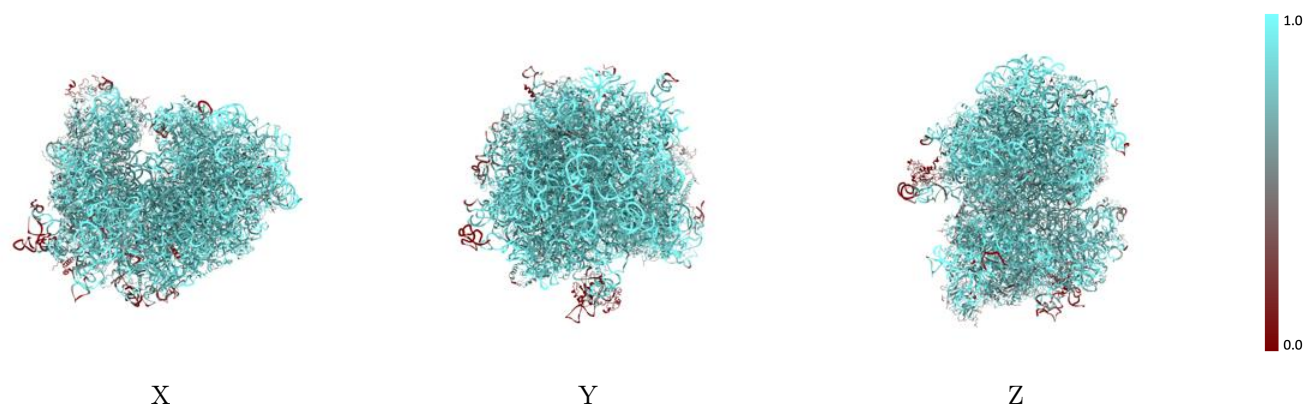
The images above show the 3D surface view of the map at the recommended contour level 0.035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



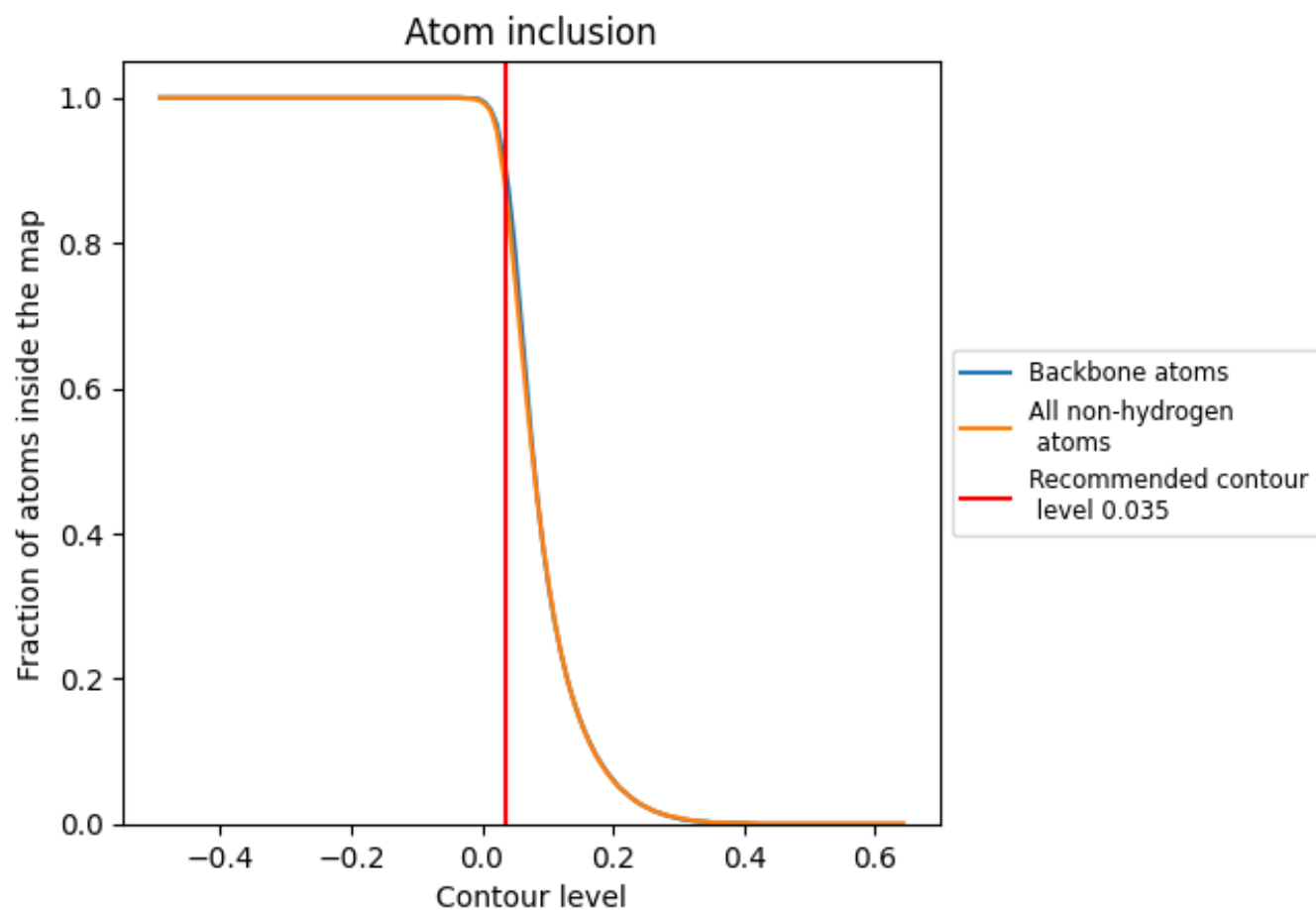
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.035).

9.4 Atom inclusion ⓘ



At the recommended contour level, 91% of all backbone atoms, 88% 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 (0.035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8820	 0.3080
A5	 0.9390	 0.3480
A7	 0.9890	 0.3240
A8	 0.9720	 0.3830
A9	 0.9940	 0.3590
AA	 0.7250	 0.1960
AB	 0.7430	 0.2320
AC	 0.7880	 0.2630
AD	 0.6780	 0.2180
AE	 0.7870	 0.2180
AF	 0.7630	 0.1920
AG	 0.7640	 0.1780
AH	 0.6970	 0.1920
AI	 0.7830	 0.2500
AJ	 0.8010	 0.2180
AK	 0.7470	 0.1760
AL	 0.7060	 0.3020
AM	 0.3330	 0.1230
AN	 0.8460	 0.3200
AO	 0.7320	 0.2370
AP	 0.6860	 0.1630
AQ	 0.7640	 0.1890
AR	 0.7050	 0.2090
AS	 0.7850	 0.1830
AT	 0.8010	 0.1720
AU	 0.7190	 0.2050
AV	 0.7740	 0.2390
AW	 0.8310	 0.2850
AX	 0.8320	 0.3320
AY	 0.8000	 0.1660
AZ	 0.7260	 0.1800
Aa	 0.8040	 0.3290
Ab	 0.7400	 0.2020
Ac	 0.7140	 0.1970
Ad	 0.8330	 0.2120



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Chain	Atom inclusion	Q-score
Ae	 0.7020	 0.2000
Af	 0.5090	 0.1050
Ag	 0.7050	 0.1460
B	 0.8550	 0.2680
B2	 0.9250	 0.2690
CA	 0.8970	 0.4180
CB	 0.8970	 0.3910
CC	 0.9160	 0.3880
CD	 0.8990	 0.2520
CE	 0.8220	 0.2310
CF	 0.9140	 0.3860
CG	 0.7960	 0.2770
CH	 0.8880	 0.3040
CI	 0.8420	 0.2940
CJ	 0.8380	 0.2010
CL	 0.8480	 0.3380
CM	 0.8290	 0.2520
CN	 0.9360	 0.4350
CO	 0.9080	 0.3830
CP	 0.8190	 0.3910
CQ	 0.9350	 0.4110
CR	 0.8130	 0.3440
CS	 0.9050	 0.3690
CT	 0.8940	 0.3790
CU	 0.8670	 0.2630
CV	 0.9170	 0.4190
CW	 0.9320	 0.4200
CX	 0.9050	 0.3560
CY	 0.9490	 0.3710
CZ	 0.8870	 0.2720
Ca	 0.9270	 0.3950
Cb	 0.9280	 0.3540
Cc	 0.8360	 0.3230
Cd	 0.9240	 0.4240
Ce	 0.9310	 0.4550
Cf	 0.8970	 0.3430
Cg	 0.8780	 0.3680
Ch	 0.9160	 0.3560
Ci	 0.8250	 0.3000
Cj	 0.8840	 0.4040
Ck	 0.8620	 0.2850
Cl	 0.9300	 0.4490

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Chain	Atom inclusion	Q-score
Cm	 0.8530	 0.3090
Cn	 0.9440	 0.4660
Co	 0.8880	 0.3730
Cp	 0.9050	 0.4040
Cr	 0.8510	 0.3230
Cz	 0.0410	 0.0690
v	 0.8750	 0.3200