



wwPDB EM Validation Summary Report ⓘ

Oct 13, 2024 – 12:11 pm BST

PDB ID : 6XU7
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:

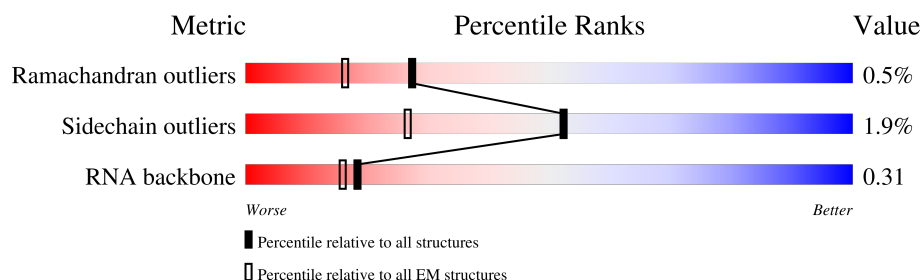
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

1 Overall quality at a glance

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

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

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

Mol	Chain	Length	Quality of chain
1	AA	218	
2	CA	253	
3	AB	220	
4	CB	414	
5	AC	227	
6	CC	392	
7	Ag	318	
8	AU	102	

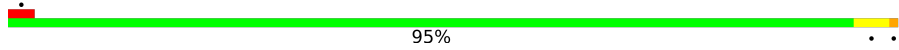
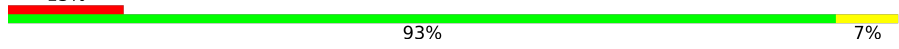
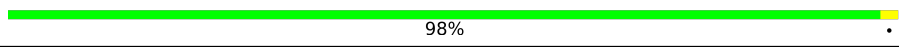
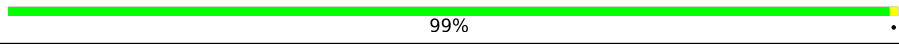
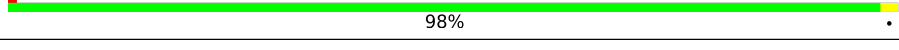

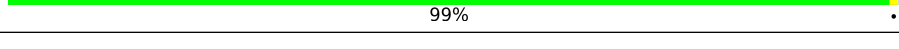
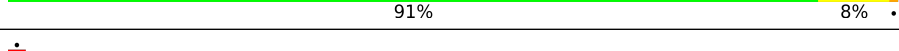
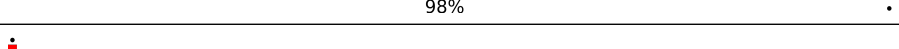
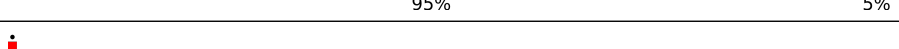
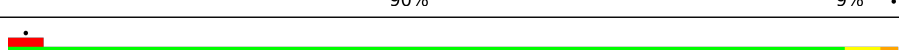
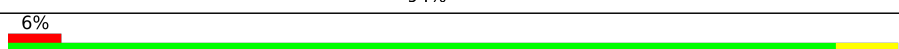
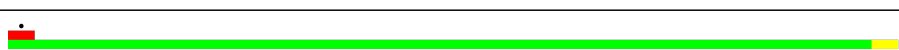

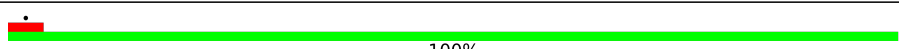
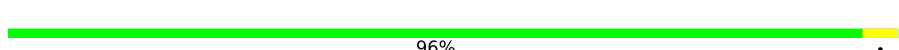

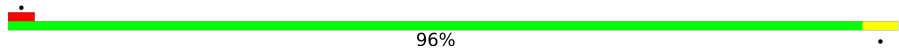
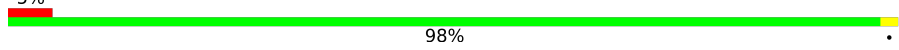
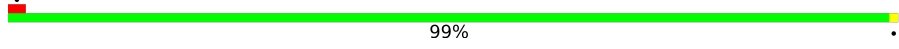
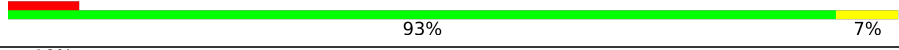
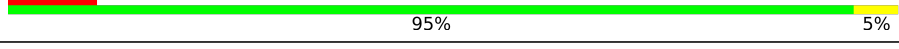



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Mol	Chain	Length	Quality of chain
9	AO	134	13% 97% .
10	AX	143	. 97% .
11	AM	119	61% 98% .
12	AS	137	. 96% .
13	Ad	52	. 92% 8%
14	AN	150	. 99% .
15	AL	155	24% 99% .
16	AR	120	11% 100%
17	AP	124	19% 98% .
18	AV	82	7% 99% .
19	AY	126	7% 100%
20	AZ	74	15% 95% 5%
21	Aa	107	10% 95% ..
22	Ab	84	15% 99% .
23	AD	227	14% 99% .
24	Ae	58	16% 95% ..
25	Af	80	44% 99% .
26	AJ	181	. 97% .
27	Ca	149	. 92% 7% .
28	CN	203	90% 10%
29	CI	217	. 97% .
30	CD	290	. 97% .
31	CQ	187	95% ..
32	CR	203	10% 95% 5%
33	CS	173	91% 9% .

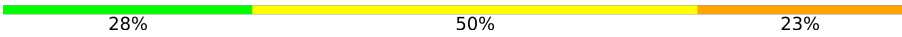
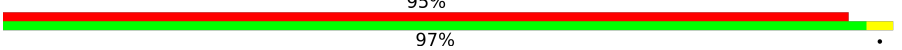

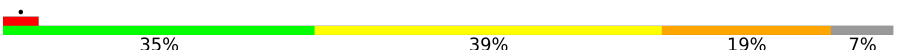
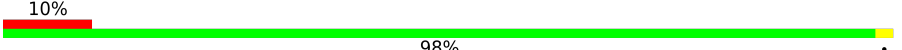
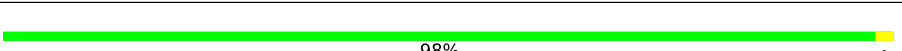
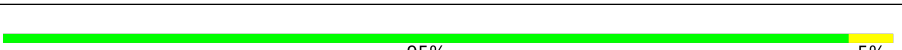
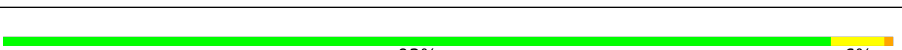
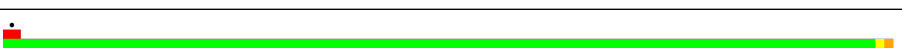
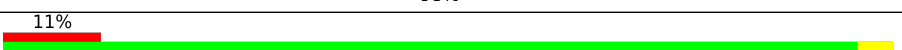
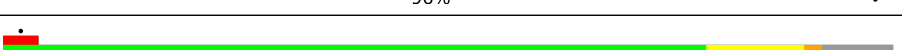
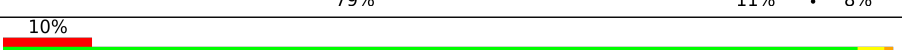
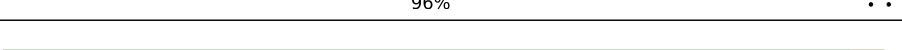
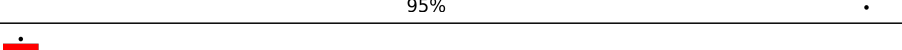
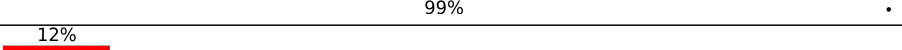
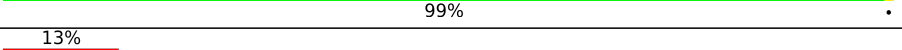
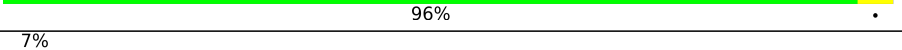
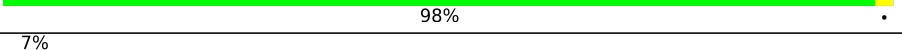
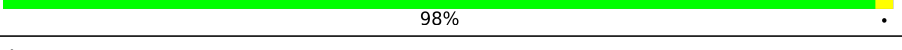
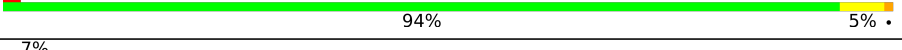
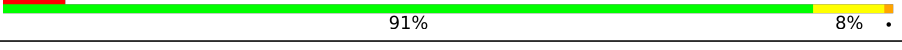
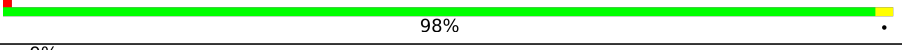
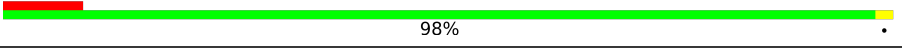


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Mol	Chain	Length	Quality of chain
34	CT	158	
35	CP	185	
36	CX	120	
37	CY	131	
38	CZ	134	
39	Cr	134	
40	Ch	123	
41	Cb	75	
42	Cc	100	
43	Cd	111	
44	Ce	132	
45	Cf	157	
46	Ci	113	
47	Ck	70	
48	Cl	50	
49	Cm	52	
50	Cn	25	
51	Cp	91	
52	Co	104	
53	CJ	182	
54	CH	190	
55	CE	228	
56	CG	241	
57	A9	30	
58	A7	120	

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Mol	Chain	Length	Quality of chain
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	
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		

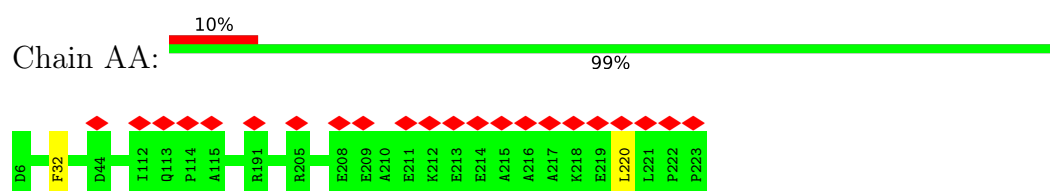
- Molecule 83 is a protein called Probable 60S ribosomal protein L37-B.

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

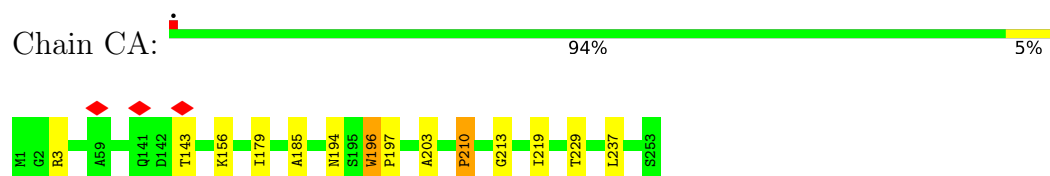
3 Residue-property plots [i](#)

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.

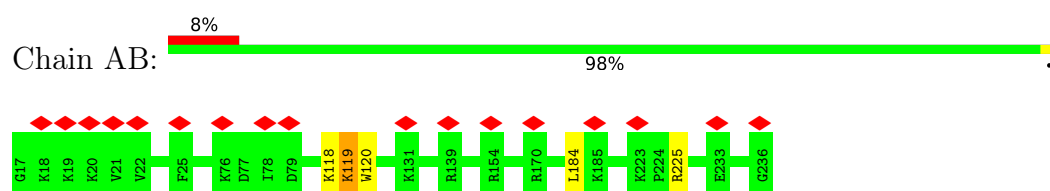
- Molecule 1: 40S ribosomal protein SA



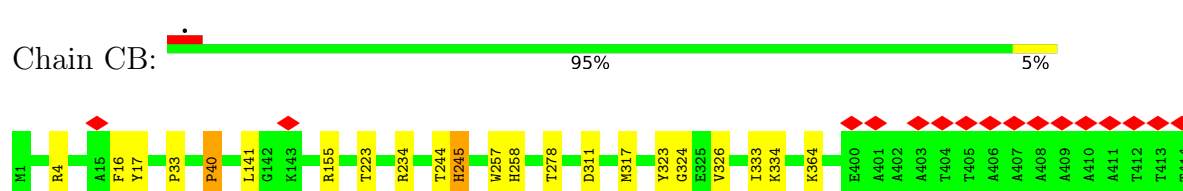
- Molecule 2: 60S ribosomal protein L8



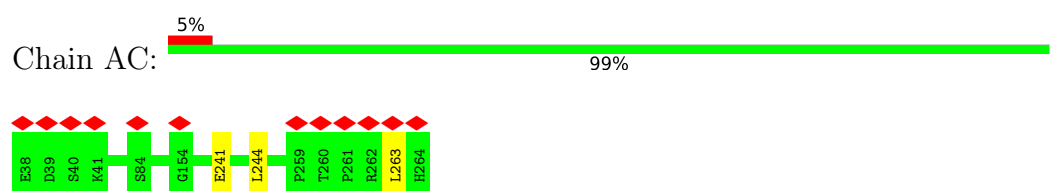
- Molecule 3: 40S ribosomal protein S3a



- Molecule 4: 60S ribosomal protein L3



- Molecule 5: 40S ribosomal protein S2



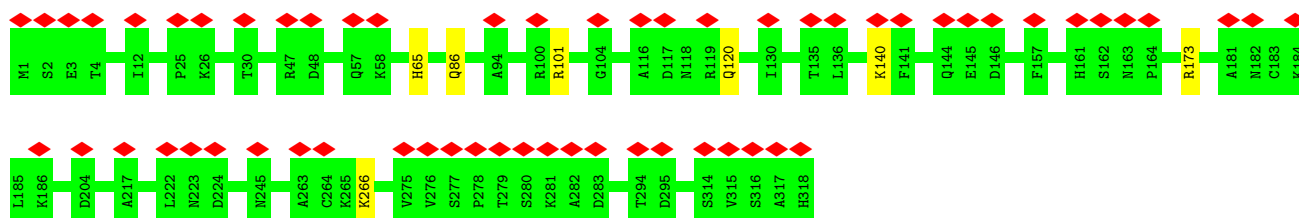
- Molecule 6: 60S ribosomal protein L4

Chain CC:  95% 5%



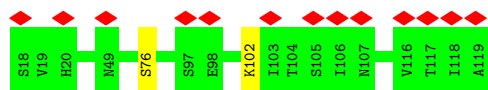
- Molecule 7: Guanine nucleotide-binding protein subunit beta-like protein

Chain Ag:  19% 98%



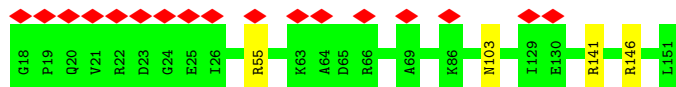
- Molecule 8: 40S ribosomal protein S20

Chain AU:  13% 98%



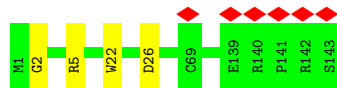
- Molecule 9: 40S ribosomal protein S14a

Chain AO:  13% 97%



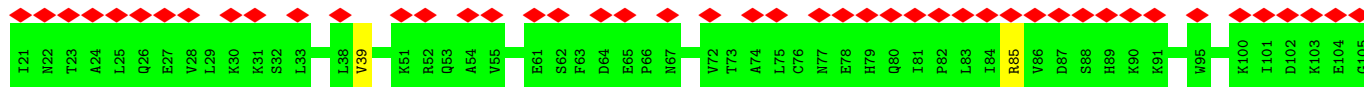
- Molecule 10: 40S ribosomal protein S23

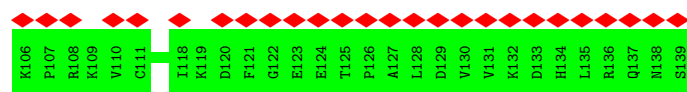
Chain AX:  97%



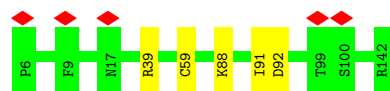
- Molecule 11: 40S ribosomal protein S12

Chain AM:  61% 98%





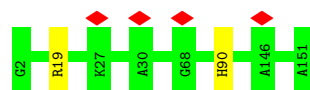
- Molecule 12: 40S ribosomal protein S18



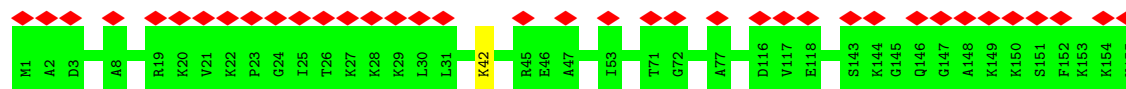
- Molecule 13: 40S ribosomal protein S29



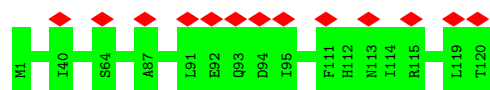
- Molecule 14: 40S ribosomal protein S13



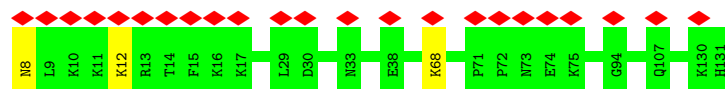
- Molecule 15: 40S ribosomal protein S11



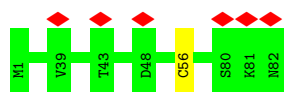
- Molecule 16: 40S ribosomal protein S17



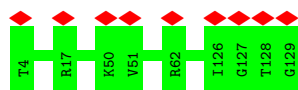
- Molecule 17: GEO07301p1



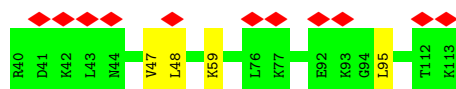
- Molecule 18: 40S ribosomal protein S21



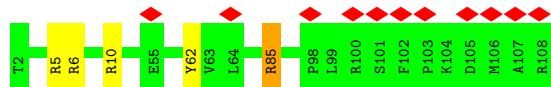
- Molecule 19: 40S ribosomal protein S24



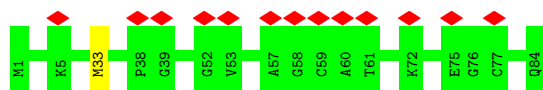
- Molecule 20: 40S ribosomal protein S25



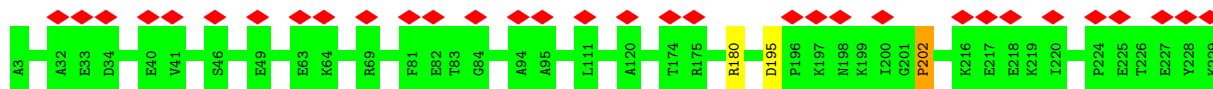
- Molecule 21: 40S ribosomal protein S26



- Molecule 22: 40S ribosomal protein S27



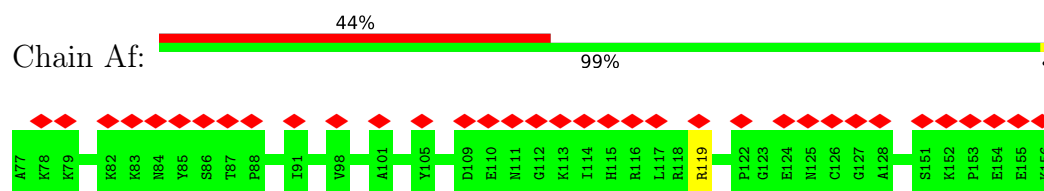
- Molecule 23: 40S ribosomal protein S3



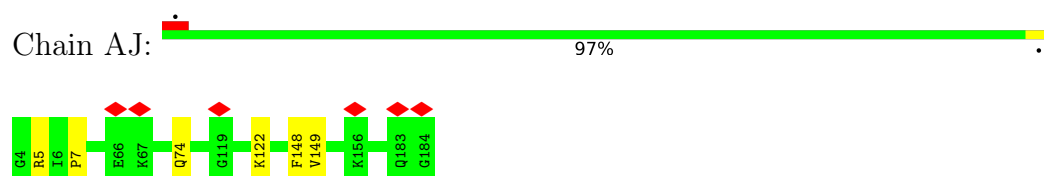
- Molecule 24: 40S ribosomal protein S30



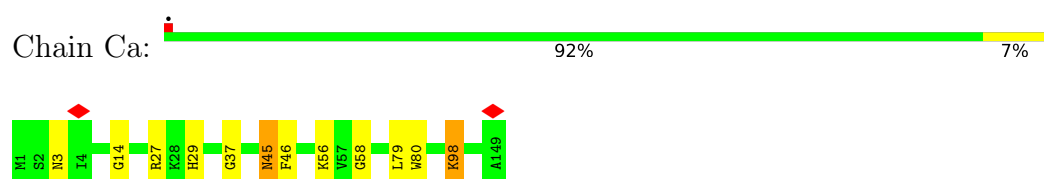
- Molecule 25: Ubiquitin-40S ribosomal protein S27a



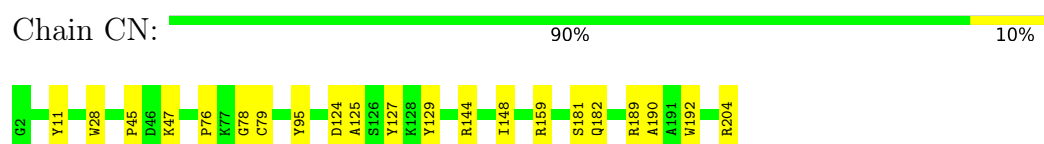
- Molecule 26: 40S ribosomal protein S9



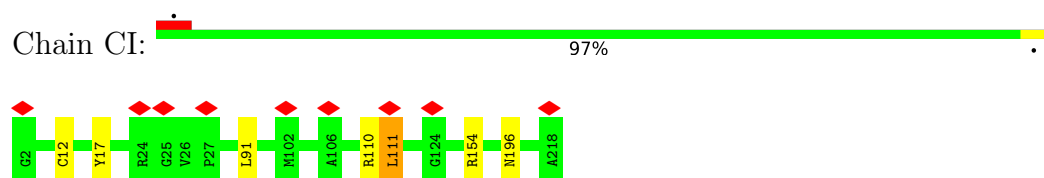
- Molecule 27: 60S ribosomal protein L27a

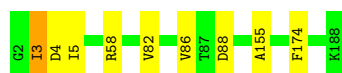


- Molecule 28: 60S ribosomal protein L15

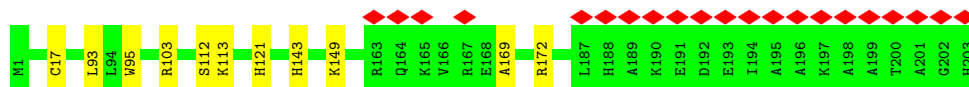


- Molecule 29: 60S ribosomal protein L10





- Molecule 32: 60S ribosomal protein L19



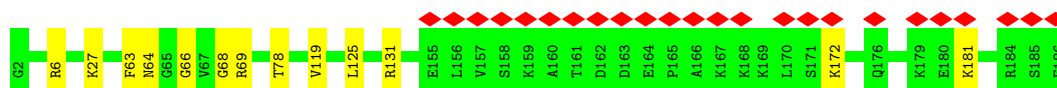
- Molecule 33: 60S ribosomal protein L18a



- Molecule 34: RE62581p



- Molecule 35: 60S ribosomal protein L17



- Molecule 36: IP17216p



- Molecule 37: GEO07453p1

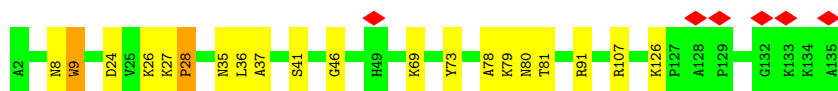
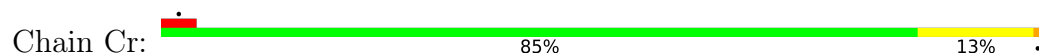


- Molecule 38: 60S ribosomal protein L27

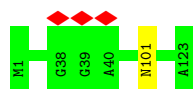




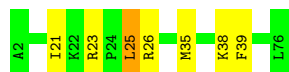
- Molecule 39: 60S ribosomal protein L28



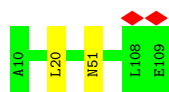
- Molecule 40: FI02809p



- Molecule 41: 60S ribosomal protein L29



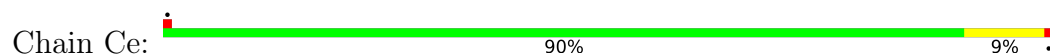
- Molecule 42: RE25263p



- Molecule 43: 60S ribosomal protein L31



- Molecule 44: 60S ribosomal protein L32



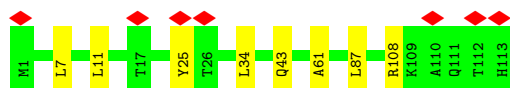
- Molecule 45: GEO07455p1

Chain Cf:  94% . .



- Molecule 46: 60S ribosomal protein L36

Chain Ci:  93% 7%



- Molecule 47: 60S ribosomal protein L38

Chain Ck:  97% .



- Molecule 48: 60S ribosomal protein L39

Chain Cl:  90% 8% .



- Molecule 49: Ubiquitin-60S ribosomal protein L40

Chain Cm:  100%



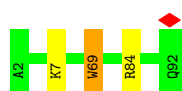
- Molecule 50: 60S ribosomal protein L41

Chain Cn:  96% .



- Molecule 51: 60S ribosomal protein L37a

Chain Cp:  97% . .



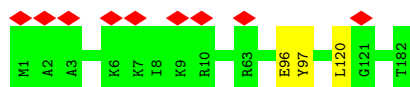
- Molecule 52: TA01007p

Chain Co:  96%



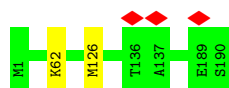
- Molecule 53: 60S ribosomal protein L11

Chain CJ:  98%



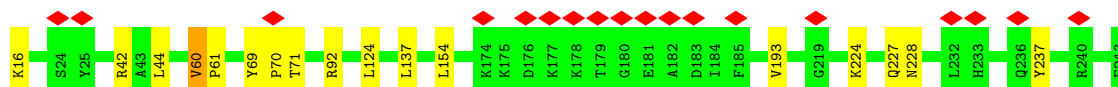
- Molecule 54: 60S ribosomal protein L9

Chain CH:  99%



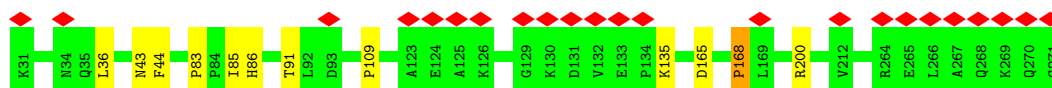
- Molecule 55: Ribosomal protein L6, isoform A

Chain CE:  93% 7%



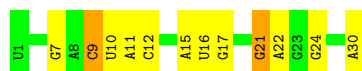
- Molecule 56: 60S ribosomal protein L7a

Chain CG:  95% 5%



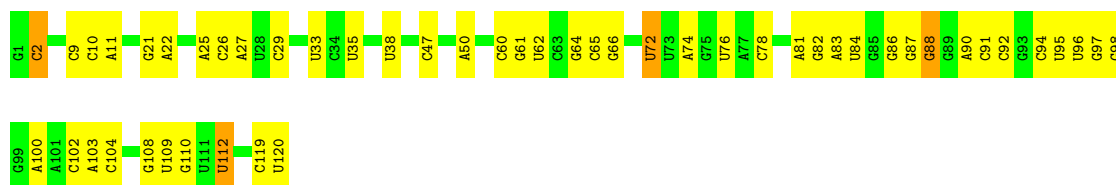
- Molecule 57: 2S ribosomal RNA

Chain A9:  60% 33% 7%



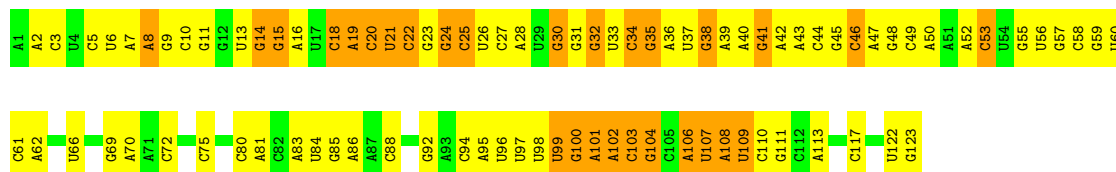
- Molecule 58: 5S ribosomal RNA

Chain A7:  58% 38%



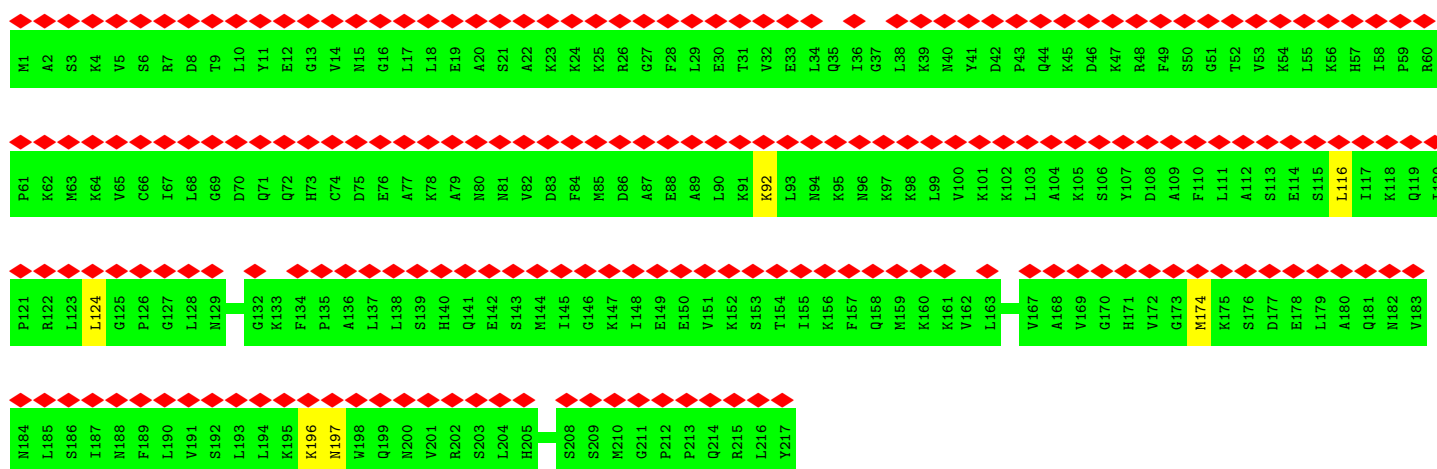
• Molecule 59: 5.8S ribosomal RNA

Chain A8: 28% 50% 23%



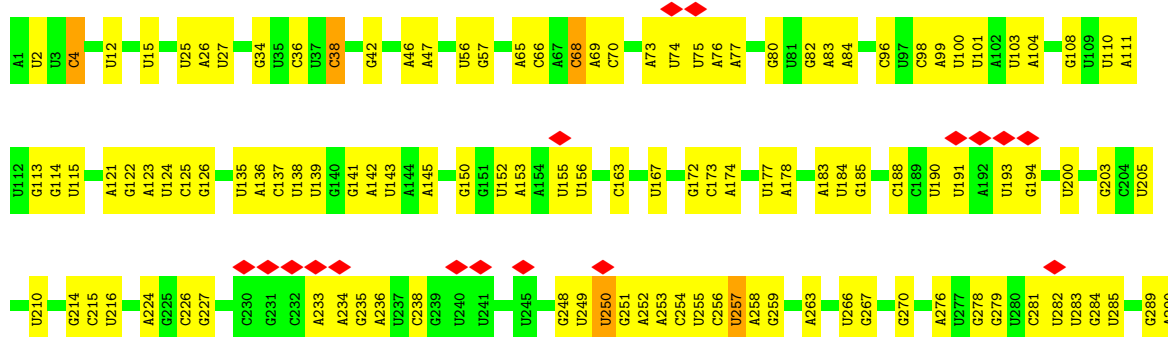
• Molecule 60: 60S ribosomal protein L10a-2

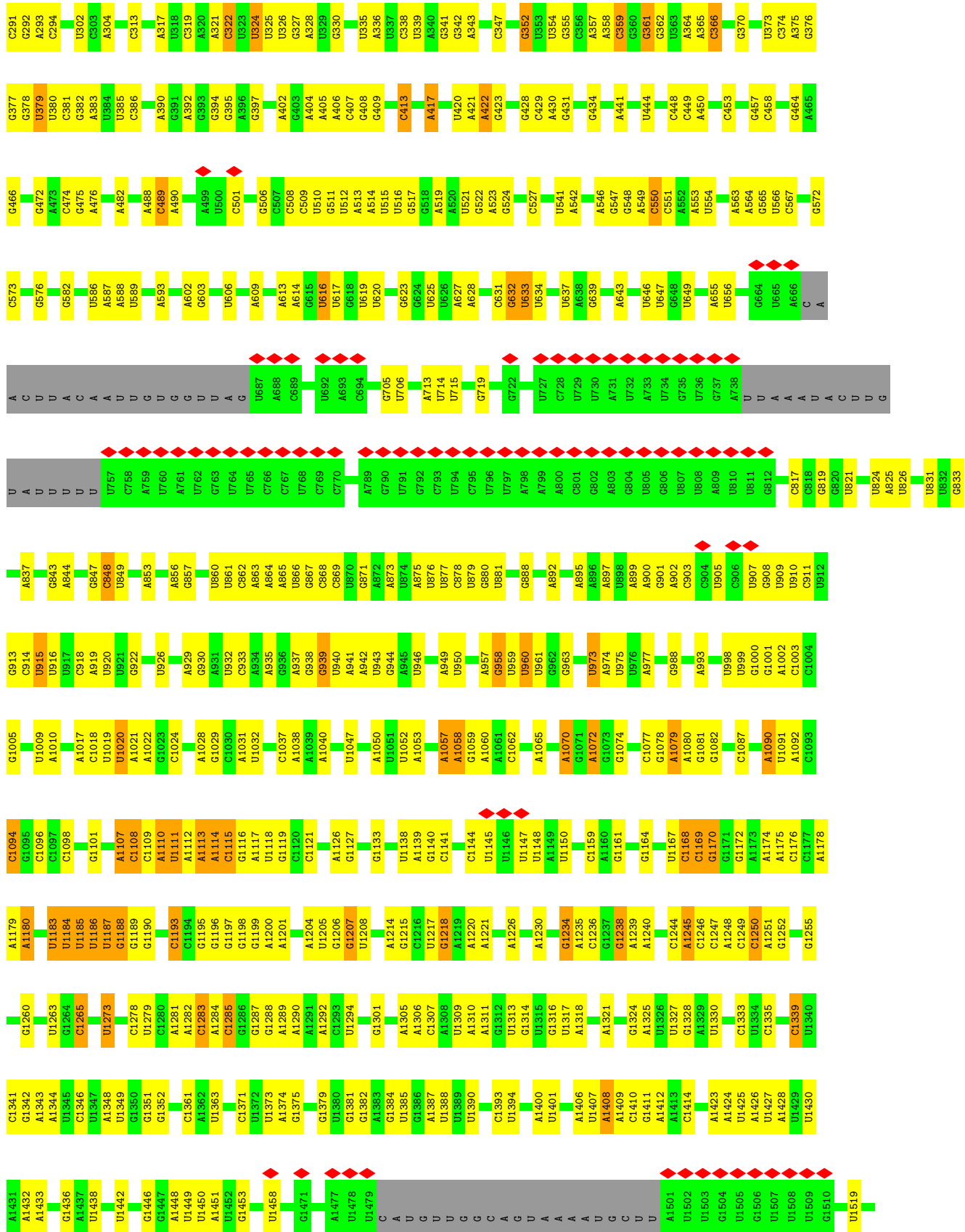
Chain Cz: 95% 97%



• Molecule 61: 18S ribosomal RNA

Chain B2: 6% 56% 36% 5%







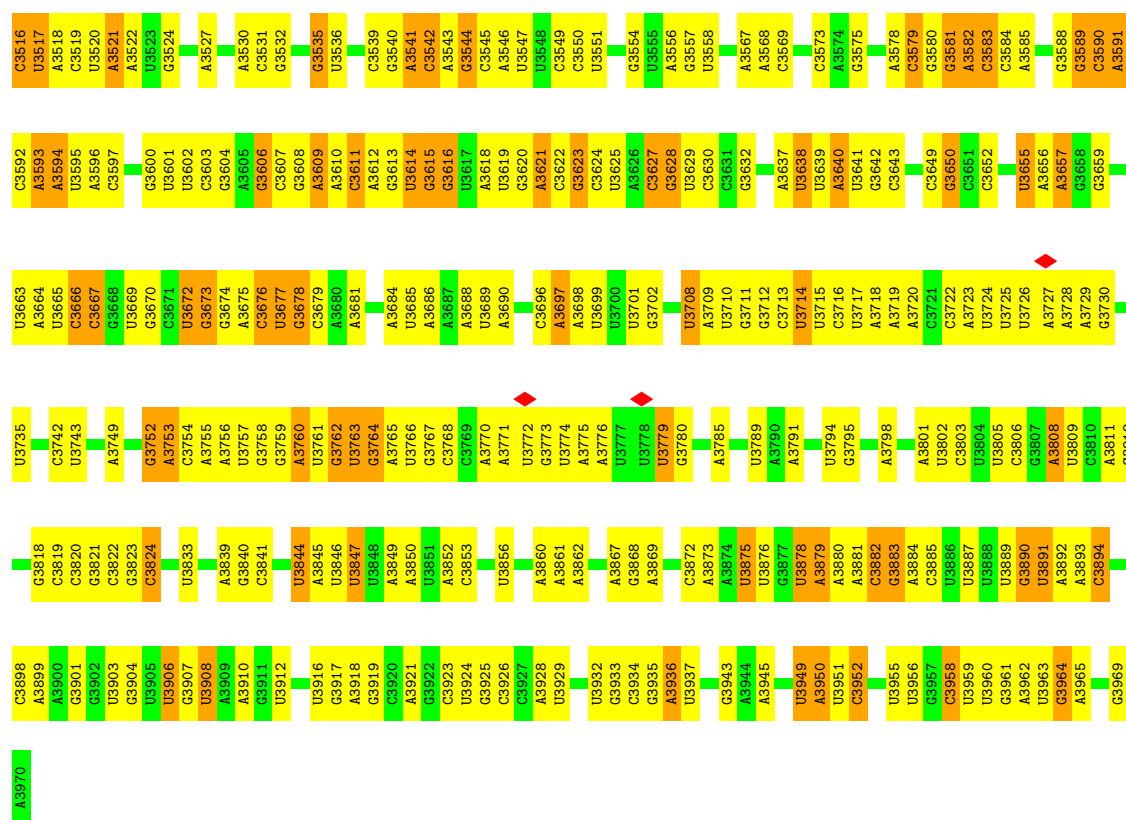
Frequency	Percentage
Daily	35%
Weekly	39%
Monthly	19%
Never	7%



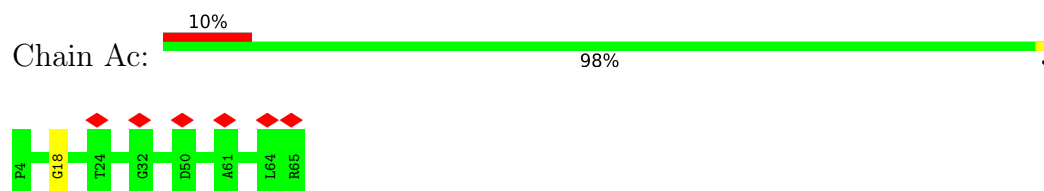
G1510	A1435	C1370	A1298	U1143	A1083	C1018	A931	A856	C791	U620	U527
C1511	A1436	A1371	A1301	C1144	A1084	C1018	A948	U857	U792	A621	U530
C1512	A1437	A1372	A1301	C1145	U1085	U1019	U949	U858	U793	A622	U536
U1513	A1438	A1373	A1301	C1146	C1086	A1020	U950	U859	U794	C623	U537
U1515	A1439	C1374	A1307	C1147	G1087	A1021	U951	C861	A796	C625	A538
A1516	C1442	U1376	A1308	C1148	A1088	A1022	U952	U862	U797	A626	A539
A1517	A1443	U1377	U1309	C1149	U1089	C1023	U953	U863	U798	A632	G540
A1518	C1447	A1378	A1310	C1150	U1090	U1024	U954	U864	U799	A633	A541
A1519	G1448	U1379	U1311	A1151	C1091	U1025	U955	U865	C800	U640	C542
A1520	G1449	U1380	C1312	A1152	U1092	A1026	U956	U866	U796	A641	A543
G1521	U1450	U1381	A1315	U1154	C1093	U1027	C964	U867	A733	A642	U647
A1522	G1451	A1382	U1316	U1155	G1094	C1028	C965	U868	U739	U643	U648
A1523	A1452	A1383	A1317	U1156	G1095	A1030	U966	U869	G740	U644	C551
U1524	U1453	G	A1317	C1157	A1096	G1031	C967	U870	U741	U645	A552
G1525	C1454	U1384	U1317	C1158	A1097	U1032	U968	A871	U742	U646	A553
G1526	A1455	U1385	U1320	C1159	U1098	U1033	A969	A872	U743	U647	U654
C1527	U1456	G1386	G1321	U1160	G1100	U1034	G974	U873	U744	G652	A559
G1528	A1457	C1387	U1322	C1161	A1101	G1035	A975	G874	U745	G654	U562
C1529	G1457	C1388	C1323	A1162	G1102	G1038	A976	G875	U746	G657	C565
U1530	G1458	C1389	C1324	C1163	U1103	A1041	A977	G876	U747	A660	A568
U1531	A1459	C1390	A1326	G1164	A1104	U1046	C977	U877	U748	G661	U569
A1532	A1460	A1391	A1327	A1165	U1105	A1047	U978	U878	U749	U665	U576
G1533	G1461	A1392	U1328	U1166	A1106	A1048	A979	U879	U750	U667	A577
U1534	A1462	C1393	U1329	C1167	G1107	A1049	A980	C890	A751	U668	A578
U1535	C1463	G1394	G1330	C1168	G1108	U1050	A981	U894	U752	U669	A579
U1536	G1464	C1395	C1331	U1170	G1109	C1049	U982	U895	U753	A670	U581
G1537	A1465	A1396	A1332	U1171	C1110	C1050	U983	A896	U754	A671	U582
U1538	A1466	C1397	C1332	C1172	G1111	C1051	U984	U897	A755	U672	U583
A1539	U1467	A1398	U1339	U1173	C1112	G1052	U985	U898	A756	U673	A584
U1540	C1468	C1400	U1340	C1174	A1113	U1053	A986	U899	A757	A674	C586
A1541	U1469	C1401	U1341	C1175	A1114	G1054	U987	A902	A758	U675	U587
C1542	G1470	U1402	A1342	U1176	A1115	U1055	U988	U905	A759	G681	U588
C1543	U1471	C1403	A1343	U1177	G1116	G1056	U989	A906	A760	A685	A591
U1544	U1472	A1404	A1344	C1178	A1117	A1059	U990	A907	A761	U686	G592
U1545	U1473	U1405	G1345	U1179	C1118	A1060	U991	C908	A762	U687	U593
U1546	U1474	C1406	C1346	U1180	C1119	A1061	U992	A909	A763	A674	A585
A1547	G1477	G1407	A1347	U1181	A1120	A1062	U993	C910	A764	A675	C586
C1548	A1478	A1408	G1348	U1182	A1121	A1063	U994	A911	A765	U676	U588
A1549	G1479	G1409	A1349	U1183	U1122	C1064	U995	A912	A766	G681	A591
U1550	U1480	A1410	C1350	A1192	C1123	A1065	C996	C913	A767	A685	G592
U1551	G1481	U1411	C1351	A1193	G1124	A1066	U997	C914	A768	U690	U593
A1552	U1482	A1412	U1352	A1194	A1125	A1067	C998	C915	A769	U696	A596
C1553	G1483	C1413	G1353	U1195	C1126	A1068	U999	C916	A770	U697	U603
C1554	U1484	C1414	C1354	A1196	C1127	A1069	U1000	C917	A771	A698	U604
G1555	A1485	U1415	G1355	A1197	C1128	A1070	A1001	C918	A772	A699	A605
C1556	A1486	A1416	C1356	U1198	A1129	U1071	C1002	G919	A773	A700	A606
U1557	A1487	U1417	U1357	C1199	U1130	U1072	C1003	G917	A774	A701	A607
A1563	C1488	A1418	G1358	U1200	C1131	U1073	C1004	G918	A775	A702	U608
G1564	U1489	U1419	U1359	U1201	U1132	C1074	U1005	G919	A776	A703	U609
A1565	C1490	A1420	U1360	U1202	A1133	U1075	A1006	G920	A777	U704	C615
U1566	U1491	C1421	G1361	U1203	G1134	G1076	A1007	C921	A778	U713	A616
G1567	A1492	G1422	U1362	U1204	U1135	A1077	A1008	C922	A779		
U1570	C1493	U1423	G1363	U1205	U1136	G1078	A1009	C923			
U1571	U1494	A1424	A1364	G1206	U1137	C1079	U1010	U924			
A1572	G1500	G1425	U1365	G1207	G1138	U1079	U1011	C925			
U1573	A1501	U1426	G1366	U1208	C1139	G1080	G1012	U926			
A1574	A1502	U1427	A1367	U1209	U1140	C1081	G1013	U927			
	U1506	C1428	A1368	A1210	U1141	G1082	U1014	U928			
	C1507	U1429	U1369	G1211	U1142	C1083	U1015	U929			
	U1508	U1430	A1369	G1212	U1143	C1084	G1016	U930			
	A1509	C1431		G1213	U1144	C1085					
		C1432			U1145	C1086					
					U1146	C1087					
					U1147	C1088					
					U1148	C1089					
					U1149	C1090					
					U1150	C1091					
					U1151	C1092					
					U1152	C1093					
					U1153	C1094					
					U1154	C1095					
					U1155	C1096					
					U1156	C1097					
					U1157	C1098					
					U1158	C1099					
					U1159	C1100					
					U1160	C1101					
					U1161	C1102					
					U1162	C1103					
					U1163	C1104					
					U1164	C1105					
					U1165	C1106					
					U1166	C1107					
					U1167	C1108					
					U1168	C1109					
					U1169	C1110					
					U1170	C1111					
					U1171	C1112					
					U1172	C1113					
					U1173	C1114					
					U1174	C1115					
					U1175	C1116					
					U1176	C1117					
					U1177	C1118					
					U1178	C1119					
					U1179	C1120					
					U1180	C1121					
					U1181	C1122					
					U1182	C1123					
					U1183	C1124					
					U1184	C1125					
					U1185	C1126					
					U1186	C1127					
					U1187	C1128					
					U1188	C1129					
					U1189	C1130					
					U1190	C1131					
					U1191	C1132					
					U1192	C1133					
					U1193	C1134					
					U1194	C1135					
					U1195	C1136					
					U1196	C1137					
					U1197	C1138					
					U1198	C1139					
					U1199	C1140					
					U1200	C1141					
					U1201	C1142					
					U1202	C1143					
					U1203	C1144					
					U1204	C1145					
					U1205	C1146					
					U1206	C1147					
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					U1214	C1155					
					U1215	C1156					
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					U1219	C1160					
					U1220	C1161					
					U1221	C1162					
					U1222	C1163					
					U1223	C1164					
					U1224	C1165					
					U1225	C1166					
					U1226	C1167					
					U1227	C1168					
					U1228	C1169					
					U1229	C1170					
					U1230	C1171					
					U1231	C1172					
					U1232	C1173					
					U1233	C1174					







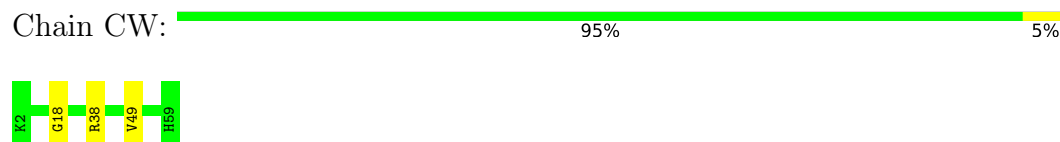
- Molecule 63: 40S ribosomal protein S28



- Molecule 64: 40S ribosomal protein S15Aa

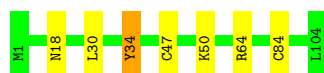


- Molecule 65: 60S ribosomal protein L24

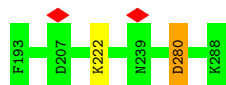


- Molecule 66: RH48056p





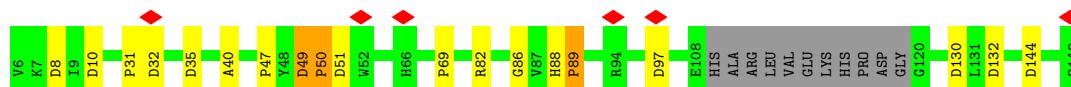
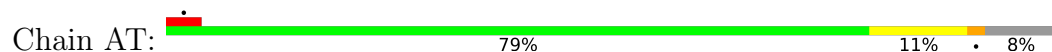
- Molecule 67: Ribosomal protein L22-like protein



- Molecule 68: 40S ribosomal protein S10b



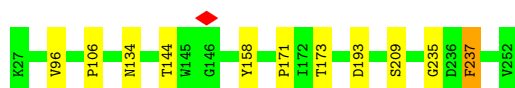
- Molecule 69: 40S ribosomal protein S19a



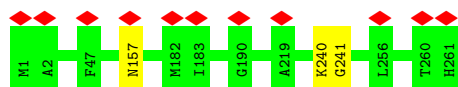
- Molecule 70: 40S ribosomal protein S5a



- Molecule 71: 60S ribosomal protein L7

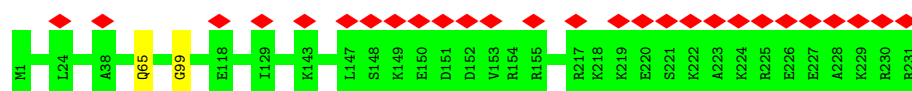


- Molecule 72: 40S ribosomal protein S4



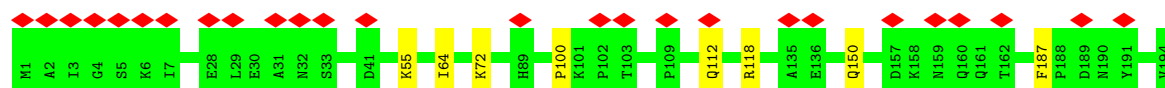
- Molecule 73: 40S ribosomal protein S6

Chain AG:  12% 99%



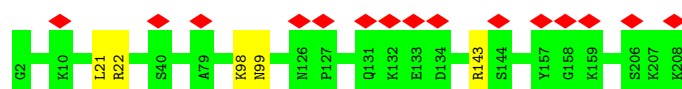
- Molecule 74: 40S ribosomal protein S7

Chain AH:  13% 96%



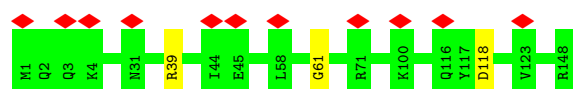
- Molecule 75: 40S ribosomal protein S8

Chain AI:  7% 98%



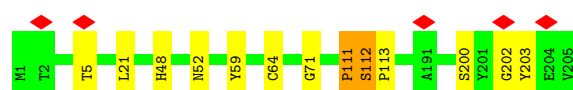
- Molecule 76: 40S ribosomal protein S16

Chain AQ:  7% 98%



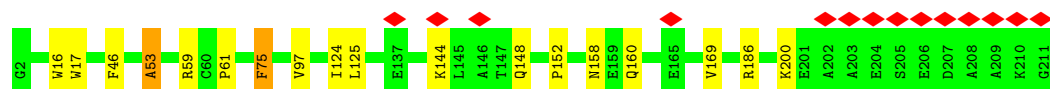
- Molecule 77: 60S ribosomal protein L13a

Chain CO:  94% 5%



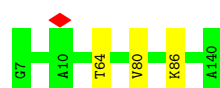
- Molecule 78: 60S ribosomal protein L13

Chain CL:  7% 91% 8%

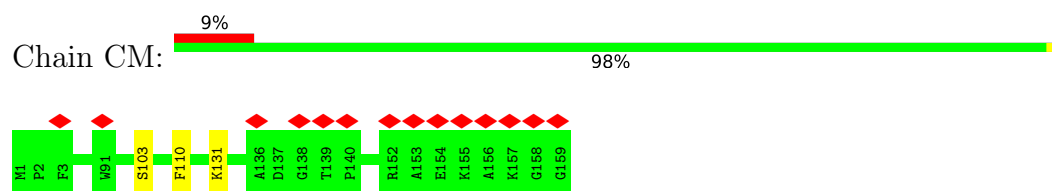


- Molecule 79: 60S ribosomal protein L23

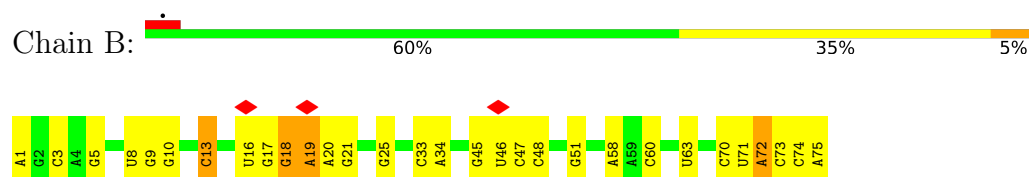
Chain CV:  98%



- Molecule 80: 60S ribosomal protein L14



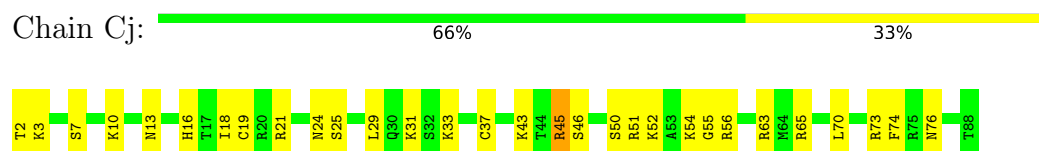
- Molecule 81: P-tRNA



- Molecule 82: mRNA



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



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 (\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 (\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	0.33	0/1777	0.62	1/2422 (0.0%)
2	CA	0.78	2/1970 (0.1%)	0.81	0/2635
3	AB	0.31	0/1825	0.64	0/2448
4	CB	0.69	0/3356	0.84	4/4494 (0.1%)
5	AC	0.34	0/1785	0.66	2/2415 (0.1%)
6	CC	0.70	4/3163 (0.1%)	0.83	7/4253 (0.2%)
7	Ag	0.30	0/2574	0.58	0/3506
8	AU	0.31	0/825	0.57	0/1111
9	AO	0.35	0/1016	0.71	0/1364
10	AX	0.42	0/1152	0.66	0/1540
11	AM	0.29	0/937	0.65	1/1260 (0.1%)
12	AS	0.31	0/1146	0.71	3/1535 (0.2%)
13	Ad	0.37	0/443	0.71	0/589
14	AN	0.38	0/1225	0.63	0/1641
15	AL	0.40	0/1296	0.60	0/1725
16	AR	0.31	0/993	0.63	0/1333
17	AP	0.31	0/1036	0.65	0/1383
18	AV	0.34	0/622	0.61	0/835
19	AY	0.31	0/1032	0.62	0/1373
20	AZ	0.31	0/616	0.67	2/826 (0.2%)
21	Aa	0.43	0/883	0.68	0/1184
22	Ab	0.30	0/668	0.61	0/898
23	AD	0.34	0/1808	0.66	0/2427
24	Ae	0.33	0/475	0.68	1/625 (0.2%)
25	Af	0.32	0/672	0.62	0/887
26	AJ	0.33	0/1526	0.65	1/2037 (0.0%)
27	Ca	0.73	1/1235 (0.1%)	0.87	2/1640 (0.1%)
28	CN	0.89	3/1750 (0.2%)	0.91	1/2335 (0.0%)
29	CI	0.41	0/1827	0.63	2/2447 (0.1%)
30	CD	0.38	0/2379	0.62	2/3196 (0.1%)
31	CQ	0.65	1/1544 (0.1%)	0.76	0/2069
32	CR	0.48	1/1703 (0.1%)	0.62	0/2255
33	CS	0.54	0/1491	0.75	1/1998 (0.1%)
34	CT	0.61	0/1326	0.87	6/1773 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	CP	0.76	0/1529	0.80	2/2042 (0.1%)
36	CX	0.44	0/1001	0.67	1/1348 (0.1%)
37	CY	0.50	0/1094	0.63	0/1456
38	CZ	0.39	1/1141 (0.1%)	0.60	2/1517 (0.1%)
39	Cr	0.55	1/1069 (0.1%)	0.94	2/1432 (0.1%)
40	Ch	0.40	0/1024	0.64	0/1353
41	Cb	0.49	0/628	0.89	2/832 (0.2%)
42	Cc	0.38	0/779	0.65	1/1048 (0.1%)
43	Cd	0.69	0/939	0.76	0/1262
44	Ce	0.94	2/1132 (0.2%)	0.98	3/1508 (0.2%)
45	Cf	0.66	0/1270	0.86	2/1696 (0.1%)
46	Ci	0.38	0/944	0.73	0/1250
47	Ck	0.37	0/583	0.66	1/774 (0.1%)
48	Cl	0.74	0/445	0.95	1/589 (0.2%)
49	Cm	0.37	0/435	0.60	0/575
50	Cn	0.55	0/237	0.80	0/300
51	Cp	0.70	1/719 (0.1%)	0.74	0/954
52	Co	0.53	0/887	0.69	0/1162
53	CJ	0.32	0/1494	0.67	1/2001 (0.0%)
54	CH	0.39	0/1519	0.66	1/2042 (0.0%)
55	CE	0.38	0/1883	0.75	3/2514 (0.1%)
56	CG	0.38	0/1968	0.66	1/2637 (0.0%)
57	A9	1.05	0/714	1.39	7/1112 (0.6%)
58	A7	1.05	9/2854 (0.3%)	1.38	41/4447 (0.9%)
59	A8	1.58	29/2932 (1.0%)	2.00	170/4568 (3.7%)
60	Cz	0.31	0/1727	0.70	2/2308 (0.1%)
61	B2	1.30	34/43887 (0.1%)	1.20	319/68161 (0.5%)
62	A5	1.62	1753/86239 (2.0%)	1.90	4119/134149 (3.1%)
63	Ac	0.29	0/502	0.61	0/670
64	AW	0.37	0/1046	0.59	1/1402 (0.1%)
65	CW	0.60	0/495	0.72	0/658
66	Cg	0.60	0/863	0.84	3/1152 (0.3%)
67	CU	0.33	0/828	0.62	1/1110 (0.1%)
68	AK	0.35	0/786	0.64	2/1064 (0.2%)
69	AT	0.35	0/1060	0.87	15/1421 (1.1%)
70	AF	1.95	2/1510 (0.1%)	0.75	5/2026 (0.2%)
71	CF	0.71	0/1931	0.81	2/2587 (0.1%)
72	AE	0.30	0/2096	0.58	0/2819
73	AG	0.28	0/1891	0.54	0/2519
74	AH	0.32	0/1593	0.68	1/2145 (0.0%)
75	AI	0.35	0/1689	0.67	1/2250 (0.0%)
76	AQ	0.33	0/1202	0.70	1/1608 (0.1%)
77	CO	0.69	0/1700	0.80	1/2277 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
78	CL	0.60	2/1726 (0.1%)	0.86	1/2308 (0.0%)
79	CV	0.61	0/1014	0.71	0/1362
80	CM	0.39	0/1326	0.67	0/1780
81	B	0.56	0/1796	1.21	11/2800 (0.4%)
82	v	0.52	0/283	1.10	0/439
83	Cj	0.57	0/707	0.68	0/932
All	All	1.20	1846/235193 (0.8%)	1.41	4762/344825 (1.4%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
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 1846 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
61	B2	1727	U	C2-N3	115.56	2.18	1.37
61	B2	1727	U	N1-C2	91.04	2.20	1.38
61	B2	1727	U	N3-C4	90.77	2.20	1.38
61	B2	1727	U	N1-C6	84.49	2.13	1.38
61	B2	1727	U	C4-C5	80.97	2.16	1.43

The worst 5 of 4762 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	A5	1366	G	N1-C6-O6	18.38	130.93	119.90
59	A8	34	C	C6-N1-C2	-17.41	113.34	120.30
62	A5	1526	G	C6-C5-N7	-17.19	120.09	130.40
62	A5	3143	U	N3-C2-O2	-16.65	110.55	122.20
62	A5	3408	C	C6-N1-C2	-16.63	113.65	120.30

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](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AA	216/218 (99%)	188 (87%)	27 (12%)	1 (0%)	25	64
2	CA	251/253 (99%)	197 (78%)	52 (21%)	2 (1%)	16	54
3	AB	218/220 (99%)	186 (85%)	29 (13%)	3 (1%)	9	40
4	CB	412/414 (100%)	327 (79%)	84 (20%)	1 (0%)	44	78
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	54
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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	68
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%)	22	59
27	Ca	147/149 (99%)	112 (76%)	34 (23%)	1 (1%)	19	56
28	CN	201/203 (99%)	153 (76%)	46 (23%)	2 (1%)	13	48
29	CI	215/217 (99%)	184 (86%)	31 (14%)	0	100	100
30	CD	288/290 (99%)	247 (86%)	40 (14%)	1 (0%)	37	72
31	CQ	185/187 (99%)	152 (82%)	32 (17%)	1 (0%)	25	64
32	CR	201/203 (99%)	182 (90%)	19 (10%)	0	100	100
33	CS	171/173 (99%)	127 (74%)	41 (24%)	3 (2%)	7	34
34	CT	156/158 (99%)	118 (76%)	37 (24%)	1 (1%)	22	59
35	CP	183/185 (99%)	153 (84%)	30 (16%)	0	100	100
36	CX	118/120 (98%)	94 (80%)	23 (20%)	1 (1%)	16	54
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%)	10	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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	30
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%)	22	59
54	CH	188/190 (99%)	165 (88%)	23 (12%)	0	100	100
55	CE	226/228 (99%)	178 (79%)	46 (20%)	2 (1%)	14	50
56	CG	239/241 (99%)	205 (86%)	31 (13%)	3 (1%)	10	42
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%)	12	46
69	AT	128/143 (90%)	104 (81%)	20 (16%)	4 (3%)	3	22
70	AF	187/189 (99%)	158 (84%)	28 (15%)	1 (0%)	25	64
71	CF	224/226 (99%)	188 (84%)	32 (14%)	4 (2%)	7	34
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	39
76	AQ	146/148 (99%)	117 (80%)	28 (19%)	1 (1%)	19	56
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	40
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	11610/11775 (99%)	9628 (83%)	1926 (17%)	56 (0%)	27 64

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%)	190 (100%)	0	100 100
2	CA	195/195 (100%)	192 (98%)	3 (2%)	60 75
3	AB	199/199 (100%)	198 (100%)	1 (0%)	86 89
4	CB	349/349 (100%)	339 (97%)	10 (3%)	37 57
5	AC	188/188 (100%)	188 (100%)	0	100 100
6	CC	323/323 (100%)	317 (98%)	6 (2%)	52 70
7	Ag	280/280 (100%)	273 (98%)	7 (2%)	42 62
8	AU	95/95 (100%)	94 (99%)	1 (1%)	70 80
9	AO	103/103 (100%)	100 (97%)	3 (3%)	37 57
10	AX	116/116 (100%)	114 (98%)	2 (2%)	56 72
11	AM	104/104 (100%)	103 (99%)	1 (1%)	73 82
12	AS	123/123 (100%)	122 (99%)	1 (1%)	79 85
13	Ad	45/45 (100%)	43 (96%)	2 (4%)	24 46
14	AN	130/130 (100%)	128 (98%)	2 (2%)	60 75
15	AL	138/138 (100%)	137 (99%)	1 (1%)	81 87
16	AR	108/108 (100%)	108 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	AP	111/111 (100%)	108 (97%)	3 (3%)	40	59
18	AV	67/67 (100%)	66 (98%)	1 (2%)	60	75
19	AY	105/106 (99%)	105 (100%)	0	100	100
20	AZ	67/67 (100%)	65 (97%)	2 (3%)	36	56
21	Aa	94/94 (100%)	91 (97%)	3 (3%)	34	54
22	Ab	72/72 (100%)	71 (99%)	1 (1%)	62	76
23	AD	192/192 (100%)	191 (100%)	1 (0%)	86	89
24	Ae	47/47 (100%)	46 (98%)	1 (2%)	48	67
25	Af	70/70 (100%)	69 (99%)	1 (1%)	62	76
26	AJ	161/161 (100%)	159 (99%)	2 (1%)	67	79
27	Ca	122/122 (100%)	120 (98%)	2 (2%)	58	74
28	CN	174/174 (100%)	169 (97%)	5 (3%)	37	57
29	CI	187/187 (100%)	183 (98%)	4 (2%)	48	67
30	CD	241/241 (100%)	238 (99%)	3 (1%)	67	79
31	CQ	164/164 (100%)	161 (98%)	3 (2%)	54	71
32	CR	176/176 (100%)	171 (97%)	5 (3%)	38	58
33	CS	156/156 (100%)	153 (98%)	3 (2%)	52	70
34	CT	137/137 (100%)	137 (100%)	0	100	100
35	CP	160/160 (100%)	155 (97%)	5 (3%)	35	55
36	CX	106/106 (100%)	105 (99%)	1 (1%)	75	83
37	CY	116/116 (100%)	115 (99%)	1 (1%)	75	83
38	CZ	121/121 (100%)	121 (100%)	0	100	100
39	Cr	112/112 (100%)	107 (96%)	5 (4%)	23	45
40	Ch	112/112 (100%)	111 (99%)	1 (1%)	75	83
41	Cb	67/67 (100%)	66 (98%)	1 (2%)	60	75
42	Cc	84/84 (100%)	83 (99%)	1 (1%)	67	79
43	Cd	103/103 (100%)	101 (98%)	2 (2%)	52	70
44	Ce	120/120 (100%)	117 (98%)	3 (2%)	42	62
45	Cf	123/123 (100%)	118 (96%)	5 (4%)	26	48
46	Ci	100/100 (100%)	96 (96%)	4 (4%)	27	48
47	Ck	65/65 (100%)	65 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
48	Cl	45/45 (100%)	43 (96%)	2 (4%)	24	46
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%)	72 (97%)	2 (3%)	40	59
52	Co	94/94 (100%)	93 (99%)	1 (1%)	70	80
53	CJ	155/155 (100%)	155 (100%)	0	100	100
54	CH	169/169 (100%)	168 (99%)	1 (1%)	84	88
55	CE	197/197 (100%)	191 (97%)	6 (3%)	36	56
56	CG	210/210 (100%)	208 (99%)	2 (1%)	73	82
60	Cz	190/190 (100%)	186 (98%)	4 (2%)	48	67
63	Ac	54/54 (100%)	54 (100%)	0	100	100
64	AW	113/113 (100%)	111 (98%)	2 (2%)	54	71
65	CW	52/52 (100%)	51 (98%)	1 (2%)	52	70
66	Cg	96/96 (100%)	93 (97%)	3 (3%)	35	55
67	CU	90/90 (100%)	88 (98%)	2 (2%)	47	65
68	AK	81/81 (100%)	80 (99%)	1 (1%)	67	79
69	AT	107/116 (92%)	107 (100%)	0	100	100
70	AF	160/160 (100%)	156 (98%)	4 (2%)	42	62
71	CF	200/200 (100%)	197 (98%)	3 (2%)	60	75
72	AE	220/220 (100%)	219 (100%)	1 (0%)	86	89
73	AG	200/200 (100%)	199 (100%)	1 (0%)	86	89
74	AH	175/175 (100%)	171 (98%)	4 (2%)	45	64
75	AI	175/175 (100%)	175 (100%)	0	100	100
76	AQ	122/122 (100%)	121 (99%)	1 (1%)	79	85
77	CO	175/175 (100%)	173 (99%)	2 (1%)	70	80
78	CL	173/173 (100%)	167 (96%)	6 (4%)	31	52
79	CV	101/101 (100%)	98 (97%)	3 (3%)	36	56
80	CM	138/138 (100%)	136 (99%)	2 (1%)	62	76
83	Cj	71/71 (100%)	43 (61%)	28 (39%)	0	0
All	All	10126/10136 (100%)	9935 (98%)	191 (2%)	52	70

5 of 191 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
55	CE	16	LYS
72	AE	157	ASN
55	CE	193	VAL
66	Cg	34	TYR
77	CO	48	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
69	AT	88	HIS
69	AT	128	GLN
83	Cj	30	GLN
79	CV	135	ASN
22	Ab	49	HIS

5.3.3 RNA [i](#)

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%)
59	A8	122/123 (99%)	58 (47%)	2 (1%)
61	B2	1792/1995 (89%)	726 (40%)	26 (1%)
62	A5	3566/3974 (89%)	1650 (46%)	86 (2%)
81	B	74/75 (98%)	27 (36%)	1 (1%)
82	v	11/12 (91%)	6 (54%)	0
All	All	5713/6329 (90%)	2507 (43%)	117 (2%)

5 of 2507 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

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Mol	Chain	Res	Type
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

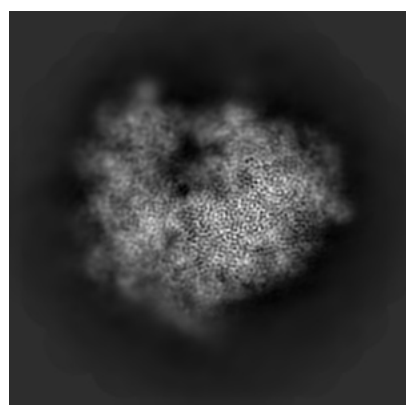
6 Map visualisation [i](#)

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.

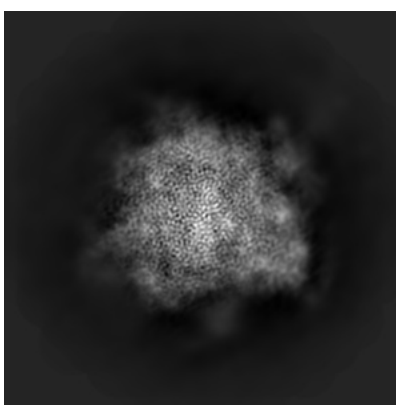
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

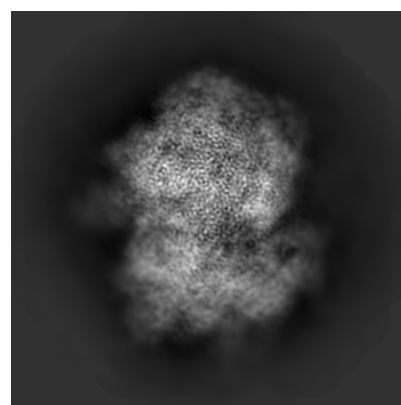
6.1.1 Primary map



X



Y

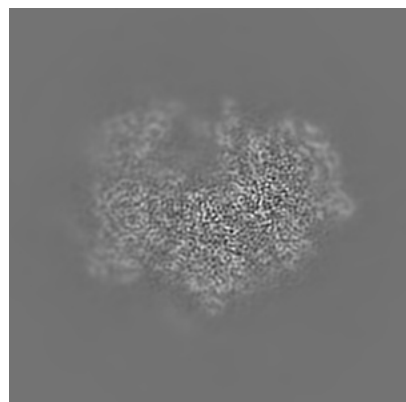


Z

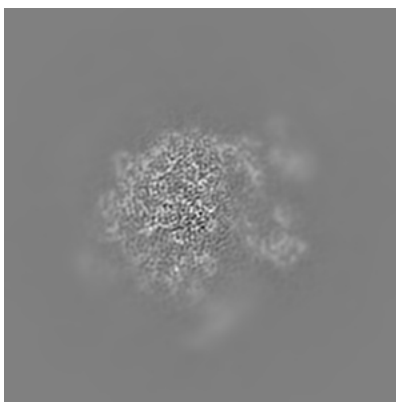
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

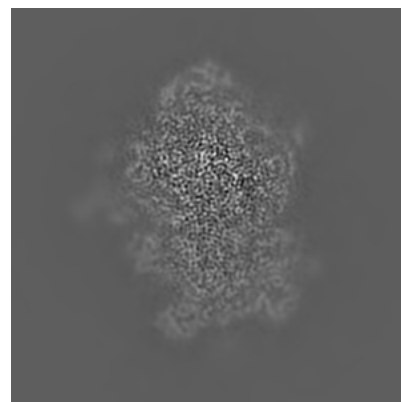
6.2.1 Primary map



X Index: 200



Y Index: 200

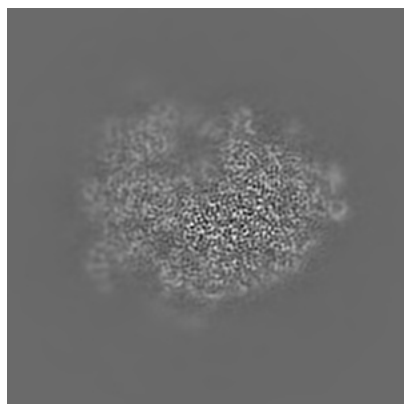


Z Index: 200

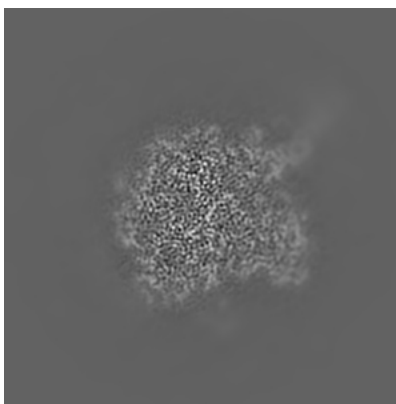
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

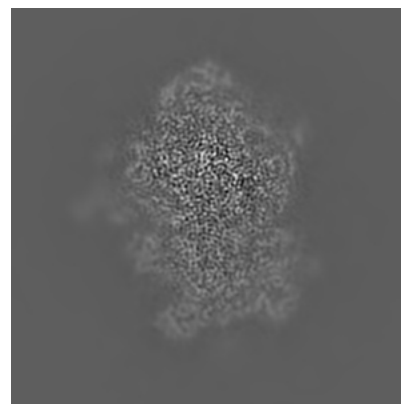
6.3.1 Primary map



X Index: 185



Y Index: 230

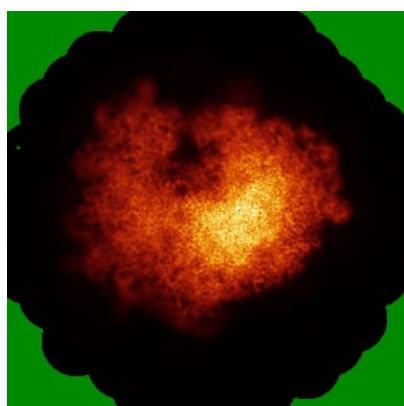


Z Index: 200

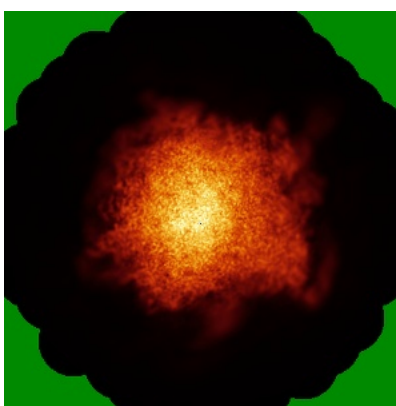
The images above show the largest variance slices of the map in three orthogonal directions.

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

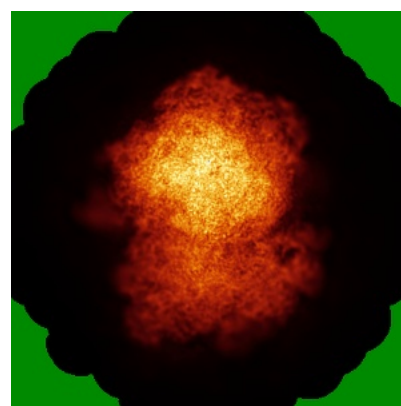
6.4.1 Primary map



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.

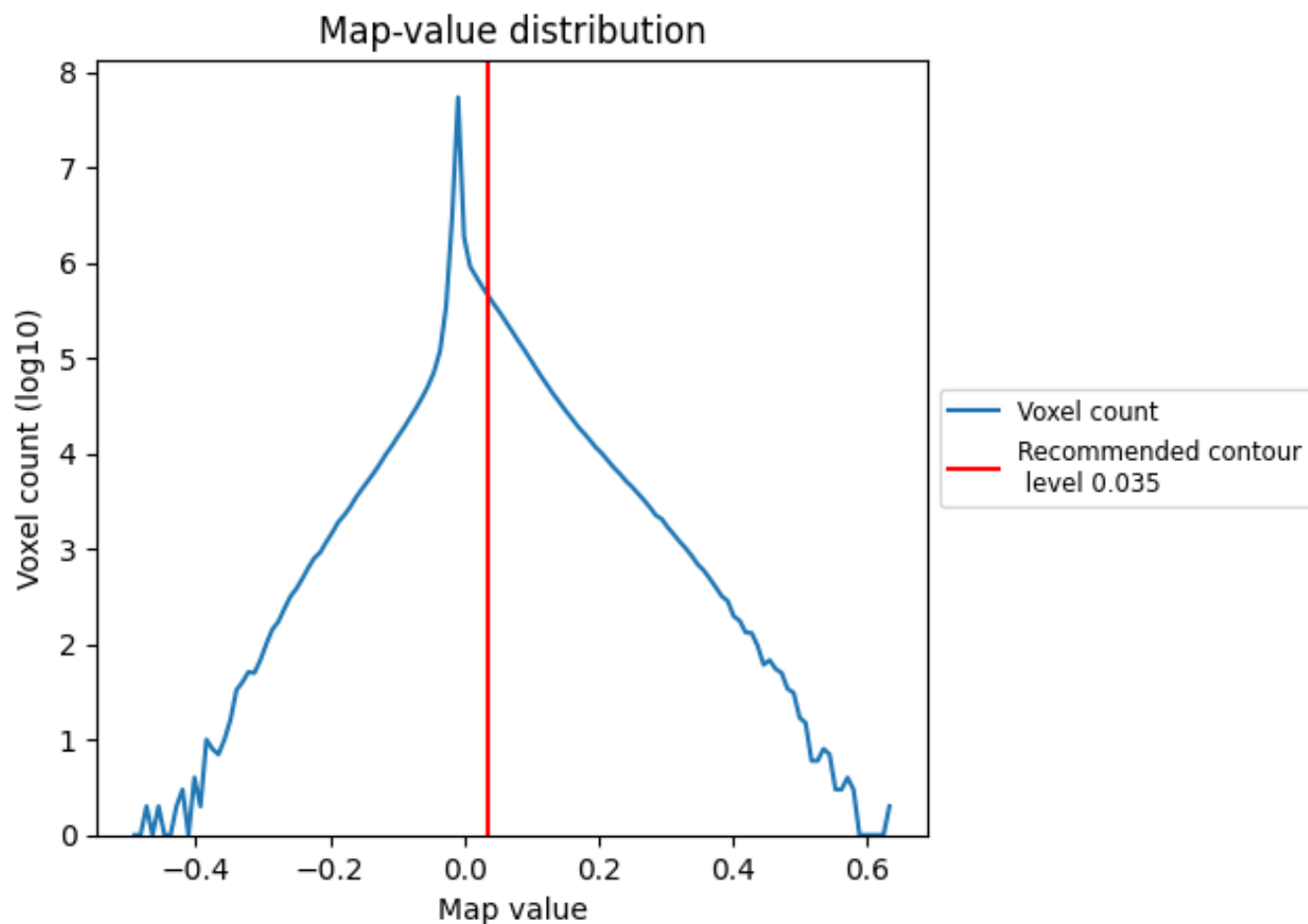
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

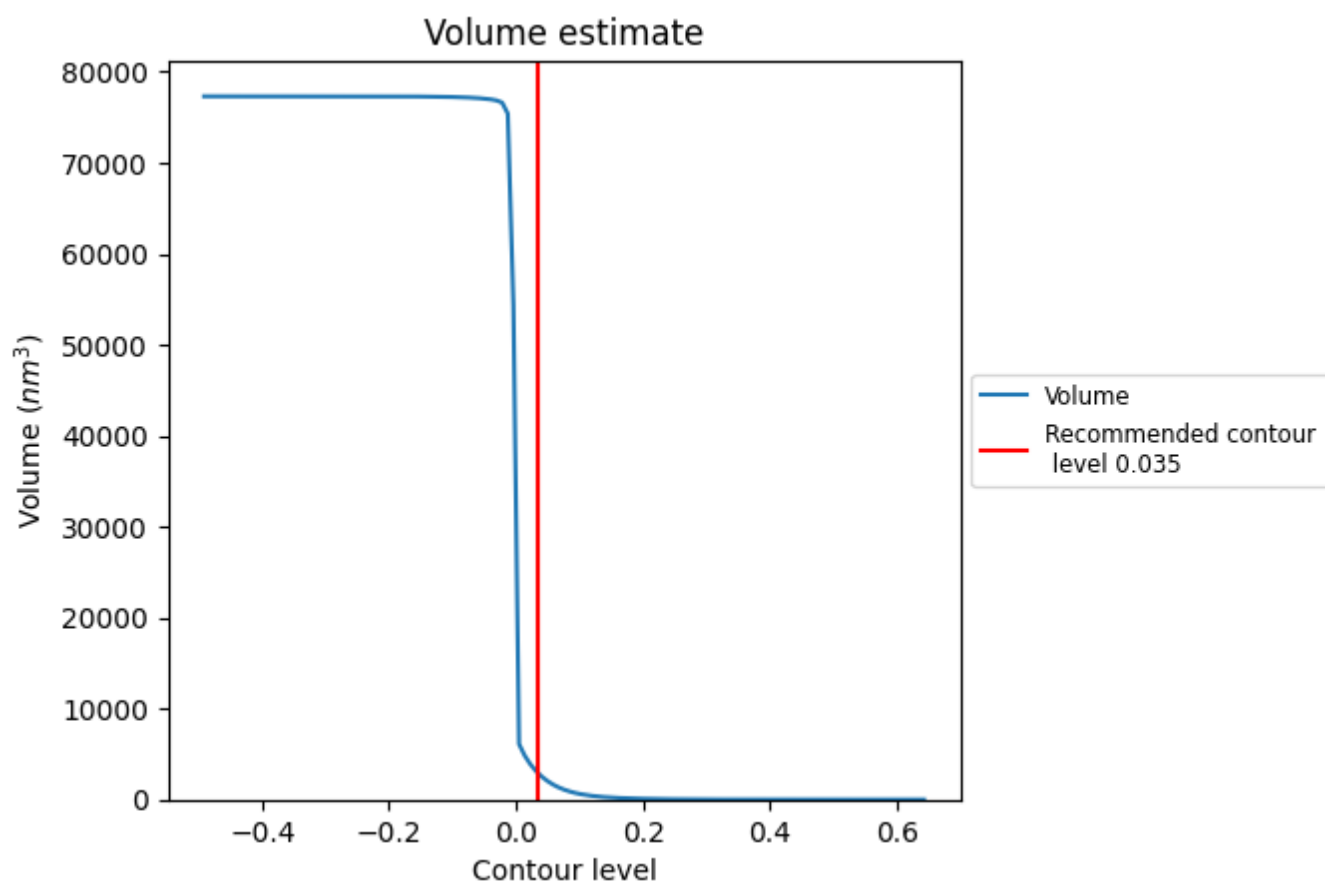
This section contains the results of statistical analysis of the map.

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.

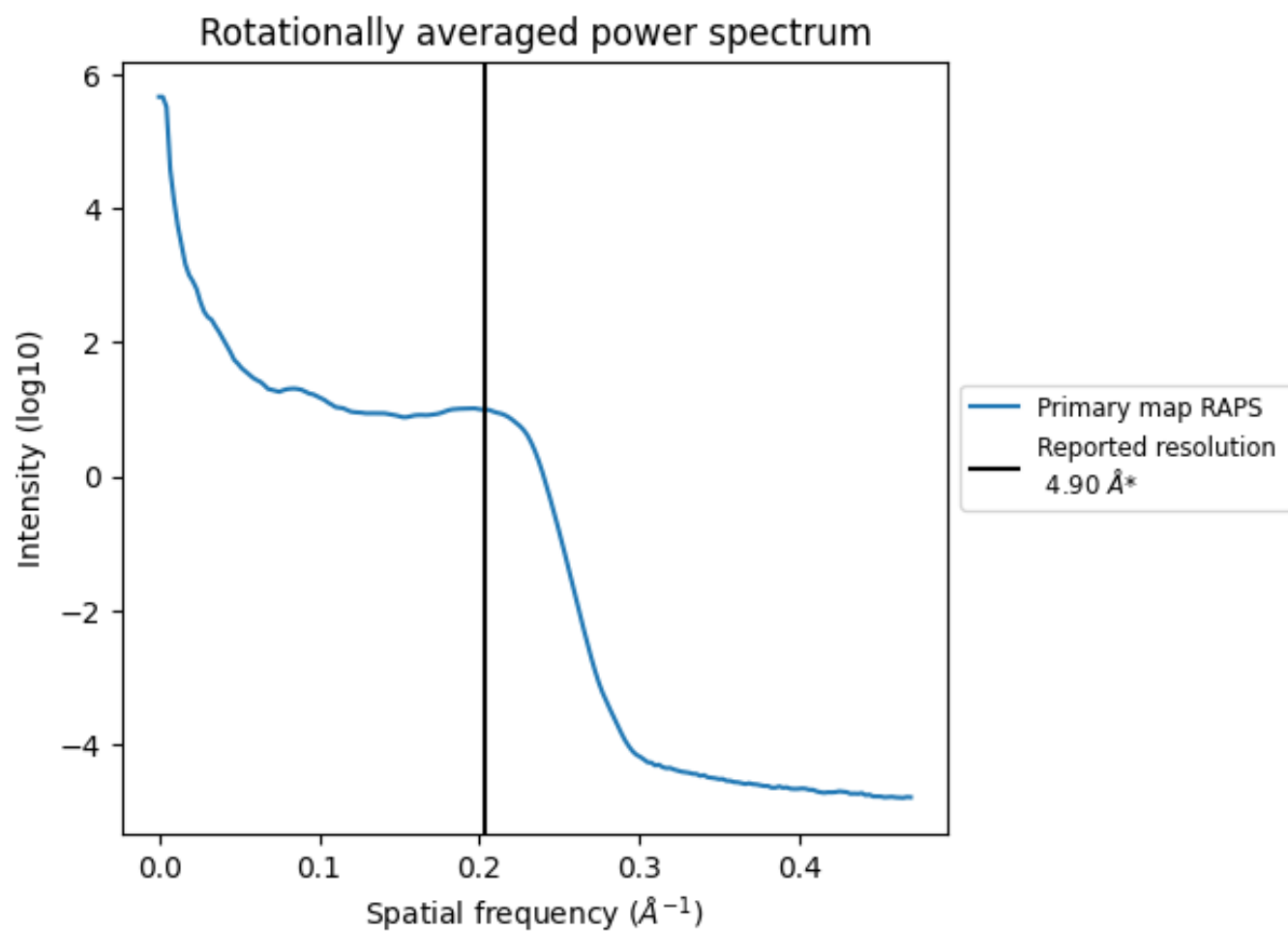
7.2 Volume estimate [i](#)



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 ⓘ

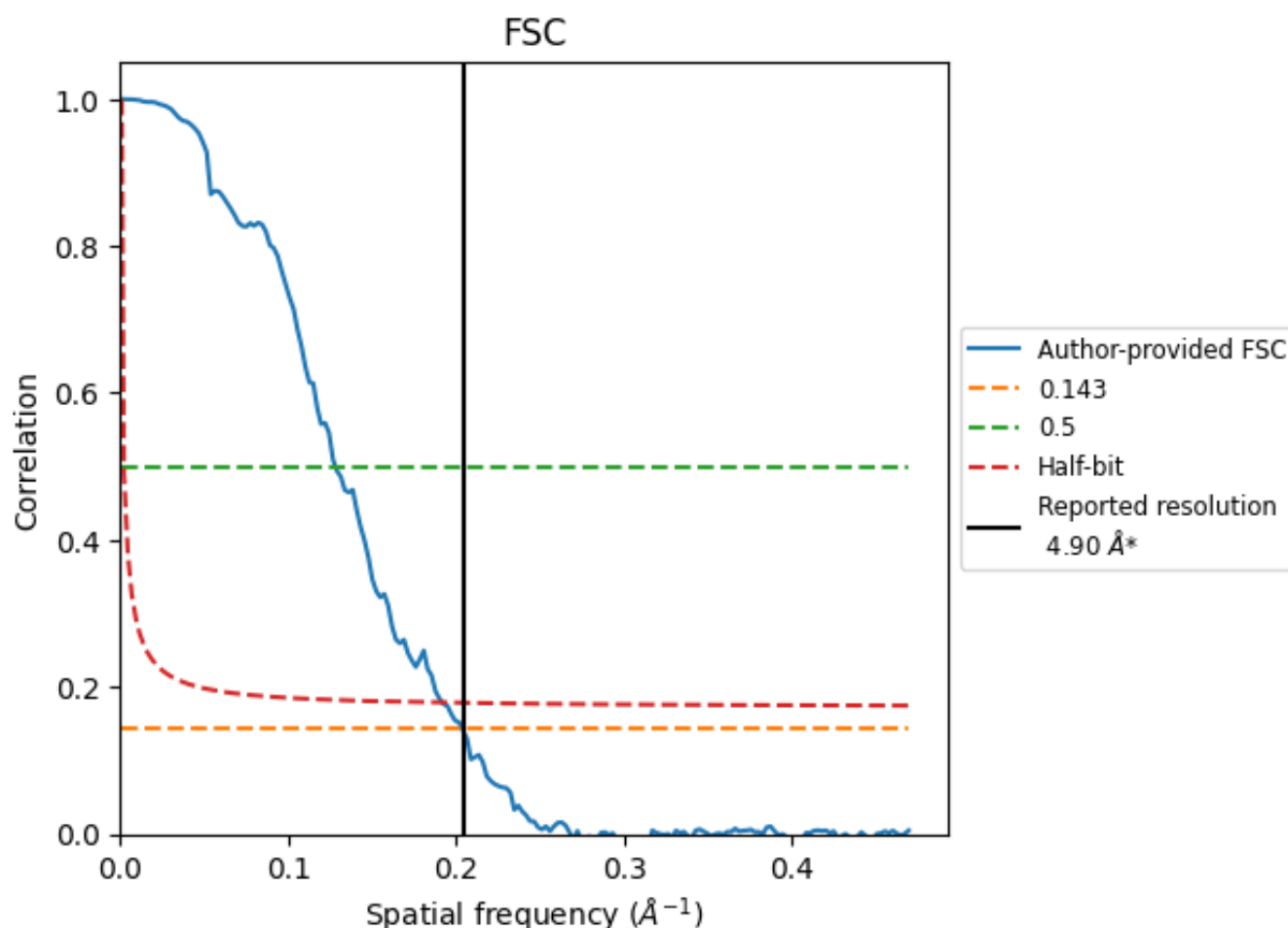


*Reported resolution corresponds to spatial frequency of 0.204 Å⁻¹

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](#)

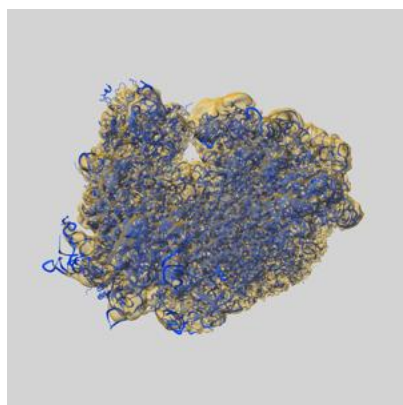
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.90	-	-
Author-provided FSC curve	4.91	7.80	5.21
Unmasked-calculated*	-	-	-

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

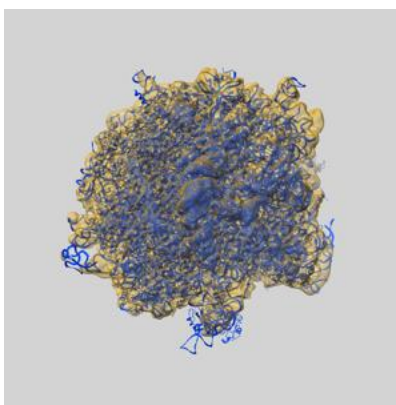
9 Map-model fit [i](#)

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 [19](#).

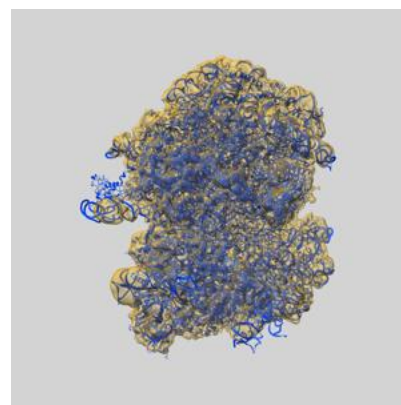
9.1 Map-model overlay [i](#)



X



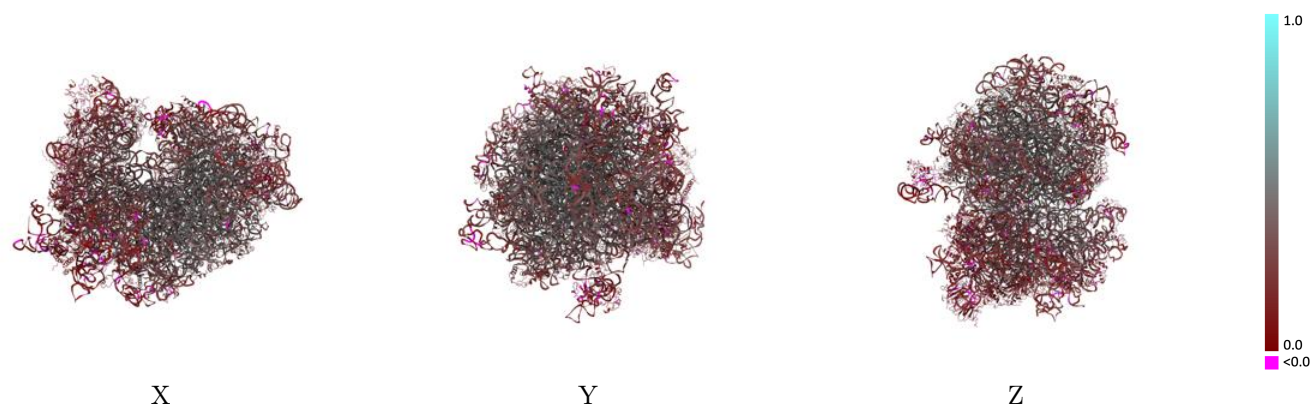
Y



Z

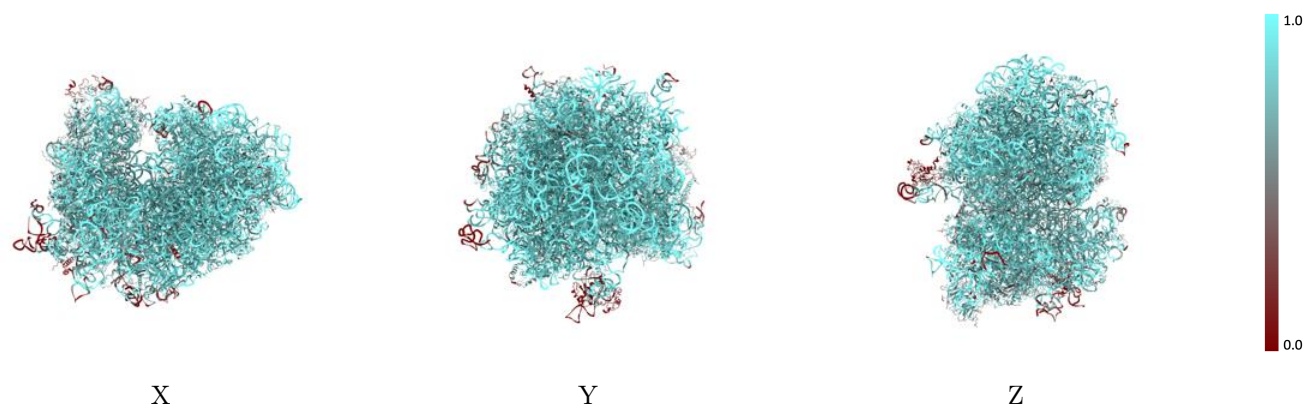
The images above show the 3D surface view of the map at the recommended contour level 0.035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



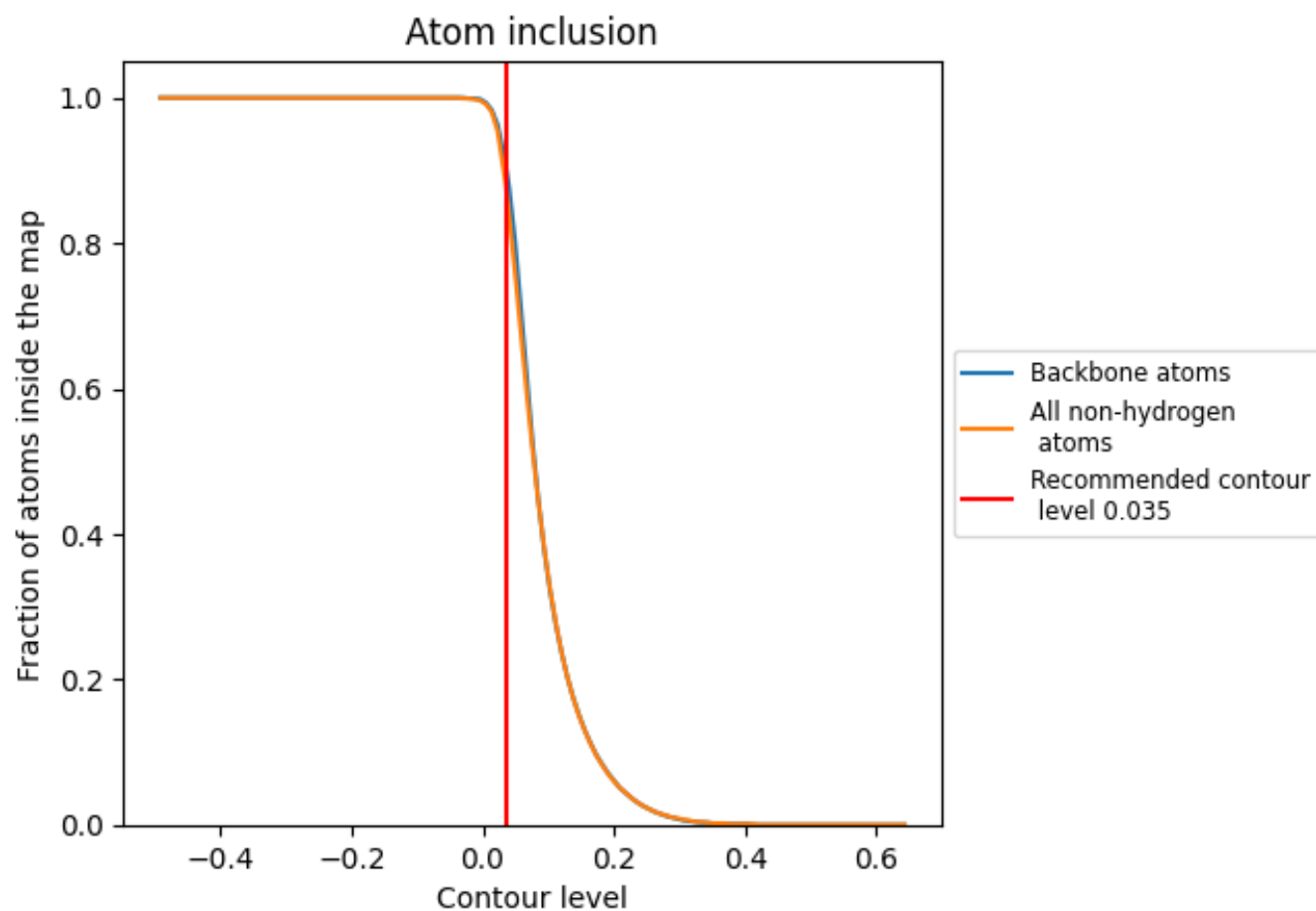
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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