



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 04:19 PM UTC

PDB ID : 6XU6 / pdb_00006xu6
EMDB ID : EMD-10622
Title : Drosophila melanogaster Testis 80S 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 : 3.50 Å(reported)
Based on initial model : 4V6W

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

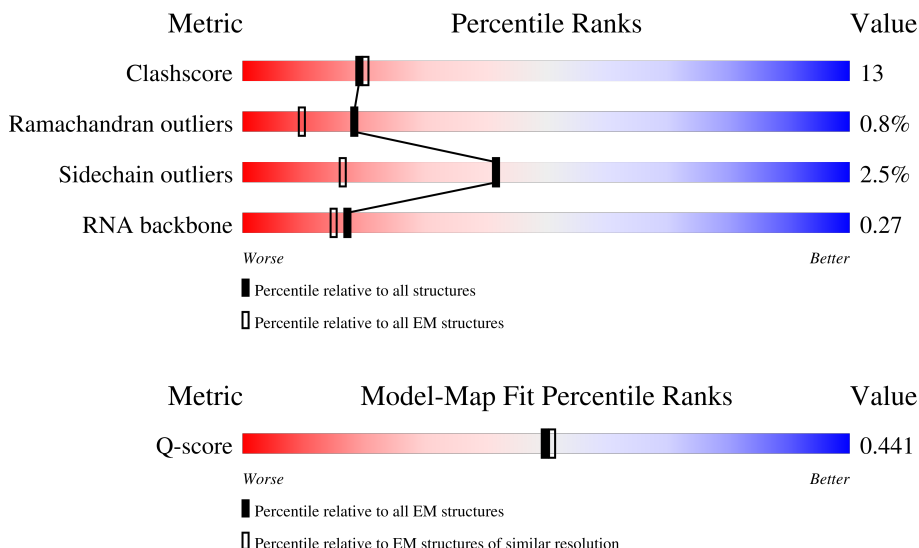
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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.



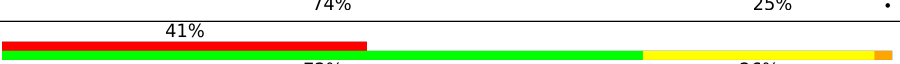
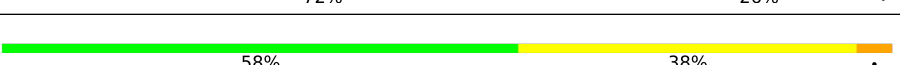
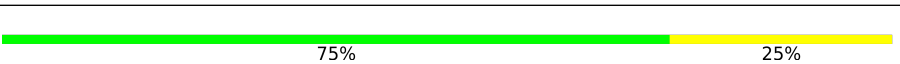
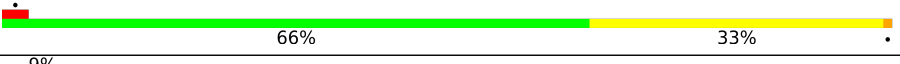
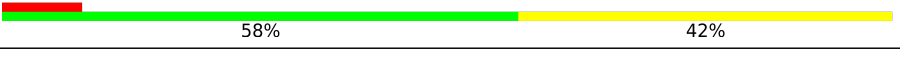
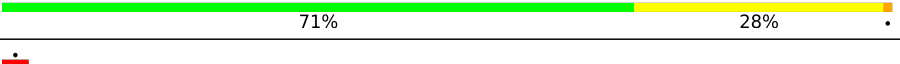
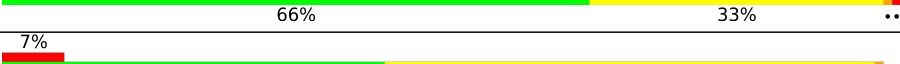
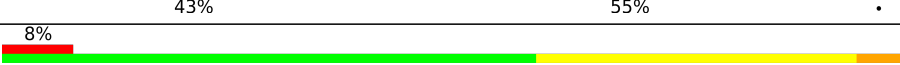
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13950 (3.00 - 4.00)

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	7% 67% 32% .
2	CA	253	70% 26% ..
3	AB	220	62% 37% .

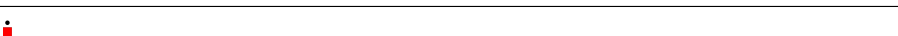
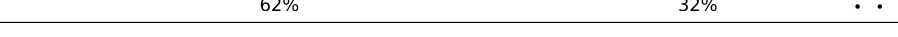
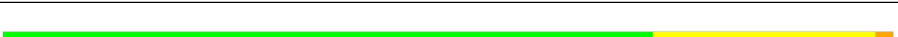
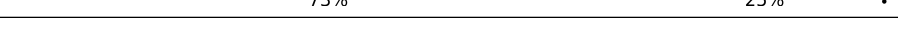
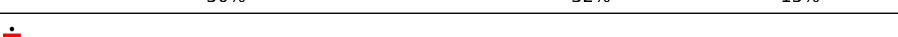
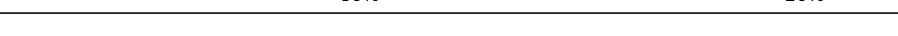
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Mol	Chain	Length	Quality of chain
4	CB	414	
5	AC	227	
6	CC	392	
7	Ag	318	
8	AU	102	
9	AX	143	
10	AM	119	
11	Ad	52	
12	AN	150	
13	AL	155	
14	AR	120	
15	AP	124	
16	AV	82	
17	AY	126	
18	AZ	74	
19	Aa	107	
20	Ab	84	
21	AD	227	
22	Ae	58	
23	Af	80	
24	AJ	181	
25	Ca	149	
26	CN	203	
27	CI	217	
28	CD	290	

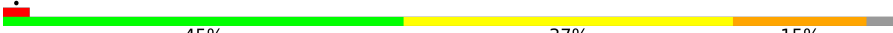
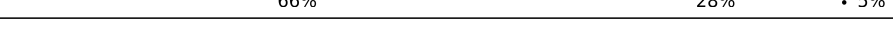
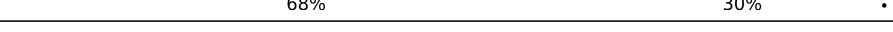
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Mol	Chain	Length	Quality of chain
29	CQ	187	
30	CR	203	
31	CS	173	
32	CT	158	
33	CP	185	
34	CX	120	
35	CY	131	
36	CZ	134	
37	Cr	134	
38	Ch	123	
39	Cb	75	
40	Cc	100	
41	Ce	132	
42	Cf	157	
43	Ci	113	
44	Ck	70	
45	Cl	50	
46	Cm	52	
47	Cn	25	
48	Cp	91	
49	Co	104	
50	CJ	182	
51	CH	190	
52	CE	228	
53	CG	241	

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Mol	Chain	Length	Quality of chain
54	A9	30	
55	A7	120	
56	A8	123	
57	Cz	217	
58	B2	1995	
59	A5	3974	
60	AE	261	
61	AG	231	
62	AH	194	
63	AI	207	
64	AQ	148	
65	CO	205	
66	CL	210	
67	CV	134	
68	CM	159	
69	DA	370	
70	AK	90	
71	AT	143	
72	AF	189	
73	AO	127	
74	Ac	62	
75	AW	129	
76	CW	58	
77	Cg	103	
78	CU	96	

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Mol	Chain	Length	Quality of chain
79	Cj	87	 52% 39% 9%
80	CF	223	 74% 23% •
81	Cd	108	 55% 39% 6%
82	AS	134	 54% 46% •

2 Entry composition

There are 82 unique types of molecules in this entry. The entry contains 219765 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 S23.

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

- Molecule 10 is a protein called 40S ribosomal protein S12.

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

- Molecule 11 is a protein called 40S ribosomal protein S29.

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

- Molecule 12 is a protein called 40S ribosomal protein S13.

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

- Molecule 13 is a protein called 40S ribosomal protein S11.

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

- Molecule 14 is a protein called 40S ribosomal protein S17.

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

- Molecule 15 is a protein called GEO07301p1.

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

- Molecule 16 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	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
AV	80	SER	THR	conflict	UNP O76927

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

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

- Molecule 18 is a protein called 40S ribosomal protein S25.

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

- Molecule 19 is a protein called 40S ribosomal protein S26.

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

- Molecule 20 is a protein called 40S ribosomal protein S27.

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

- Molecule 21 is a protein called 40S ribosomal protein S3.

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

- Molecule 22 is a protein called 40S ribosomal protein S30.

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

- Molecule 23 is a protein called Ubiquitin-40S ribosomal protein S27a.

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

- Molecule 24 is a protein called 40S ribosomal protein S9.

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

- Molecule 25 is a protein called 60S ribosomal protein L27a.

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

- Molecule 26 is a protein called 60S ribosomal protein L15.

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

- Molecule 27 is a protein called 60S ribosomal protein L10.

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

- Molecule 28 is a protein called 60S ribosomal protein L5.

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

- Molecule 29 is a protein called 60S ribosomal protein L18.

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

- Molecule 30 is a protein called 60S ribosomal protein L19.

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

- Molecule 31 is a protein called 60S ribosomal protein L18a.

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

- Molecule 32 is a protein called RE62581p.

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

- Molecule 33 is a protein called 60S ribosomal protein L17.

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

- Molecule 34 is a protein called IP17216p.

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

- Molecule 35 is a protein called GEO07453p1.

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

- Molecule 36 is a protein called 60S ribosomal protein L27.

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

- Molecule 37 is a protein called 60S ribosomal protein L28.

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

- Molecule 38 is a protein called FI02809p.

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

- Molecule 39 is a protein called 60S ribosomal protein L29.

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

- Molecule 40 is a protein called RE25263p.

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

- Molecule 41 is a protein called 60S ribosomal protein L32.

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

- Molecule 42 is a protein called GEO07455p1.

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

- Molecule 43 is a protein called 60S ribosomal protein L36.

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

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

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

- Molecule 45 is a protein called 60S ribosomal protein L39.

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

- Molecule 46 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 47 is a protein called 60S ribosomal protein L41.

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

- Molecule 48 is a protein called 60S ribosomal protein L37a.

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

- Molecule 49 is a protein called TA01007p.

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

- Molecule 50 is a protein called 60S ribosomal protein L11.

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

- Molecule 51 is a protein called 60S ribosomal protein L9.

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

- Molecule 52 is a protein called Ribosomal protein L6, isoform A.

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

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

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

- Molecule 54 is a RNA chain called 2S ribosomal RNA.

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

- Molecule 55 is a RNA chain called 5S ribosomal RNA.

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

- Molecule 56 is a RNA chain called 5.8S ribosomal RNA.

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

- Molecule 57 is a protein called 60S ribosomal protein L10a-2.

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

- Molecule 58 is a RNA chain called 18S ribosomal RNA.

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

- Molecule 59 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	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

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Chain	Residue	Modelled	Actual	Comment	Reference
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 60 is a protein called 40S ribosomal protein S4.

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

- Molecule 61 is a protein called 40S ribosomal protein S6.

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

- Molecule 62 is a protein called 40S ribosomal protein S7.

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

- Molecule 63 is a protein called 40S ribosomal protein S8.

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

- Molecule 64 is a protein called 40S ribosomal protein S16.

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

- Molecule 65 is a protein called 60S ribosomal protein L13a.

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

- Molecule 66 is a protein called 60S ribosomal protein L13.

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

- Molecule 67 is a protein called 60S ribosomal protein L23.

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

- Molecule 68 is a protein called 60S ribosomal protein L14.

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

- Molecule 69 is a protein called LP04564p.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	DA	350	Total	C	N	O	S	0	0
			2756	1730	483	525	18		

- Molecule 70 is a protein called 40S ribosomal protein S10b.

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

- Molecule 71 is a protein called 40S ribosomal protein S19a.

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

- Molecule 72 is a protein called 40S ribosomal protein S5a.

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

- Molecule 73 is a protein called 40S ribosomal protein S14a.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	AO	127	Total	C	N	O	S	0	0
			953	587	185	177	4		

- Molecule 74 is a protein called 40S ribosomal protein S28.

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

- Molecule 75 is a protein called 40S ribosomal protein S15Aa.

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

- Molecule 76 is a protein called 60S ribosomal protein L24.

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

- Molecule 77 is a protein called RH48056p.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Cg	103	Total	C	N	O	S	0	0
			844	525	176	138	5		

- Molecule 78 is a protein called Ribosomal protein L22-like protein.

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

- Molecule 79 is a protein called Probable 60S ribosomal protein L37-B.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
80	CF	223	Total	C	N	O	S	0	0
			1869	1199	363	304	3		

- Molecule 81 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Cd	108	Total	C	N	O	S	0	0
			899	559	177	161	2		

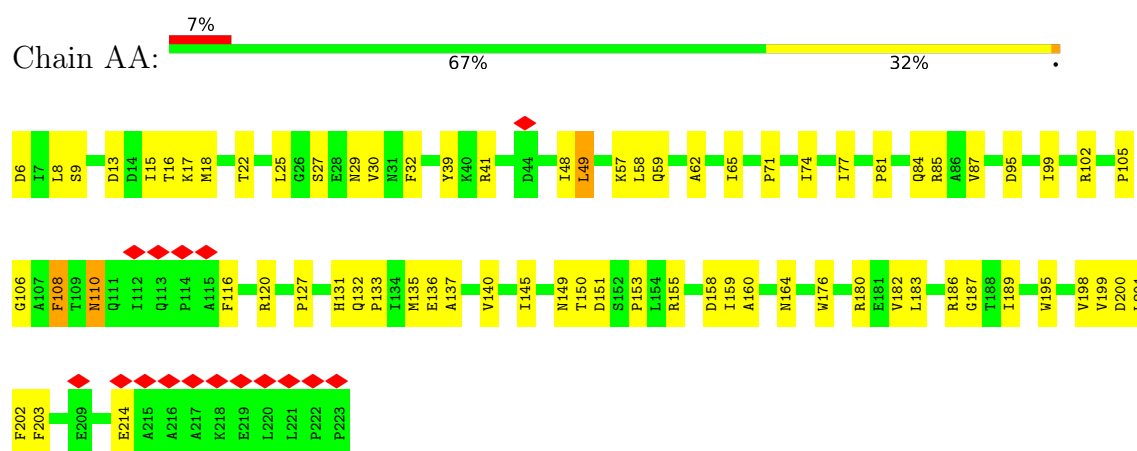
- Molecule 82 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	AS	134	Total	C	N	O	S	0	0
			1101	691	214	193	3		

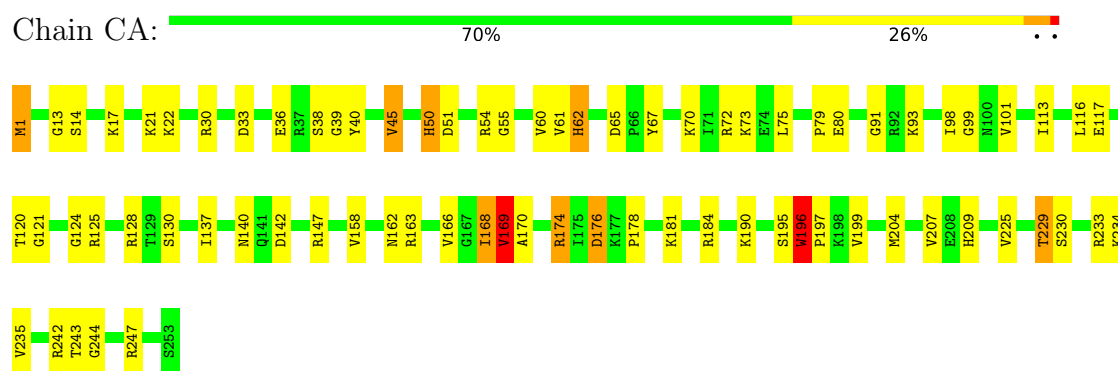
3 Residue-property plots

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.

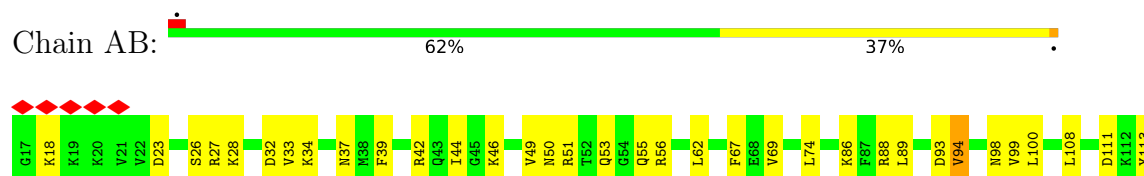
• Molecule 1: 40S ribosomal protein SA

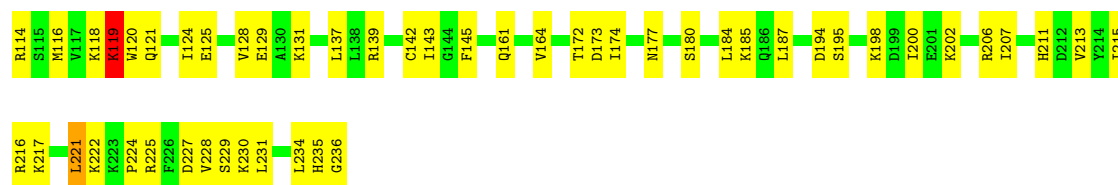


• Molecule 2: 60S ribosomal protein L8

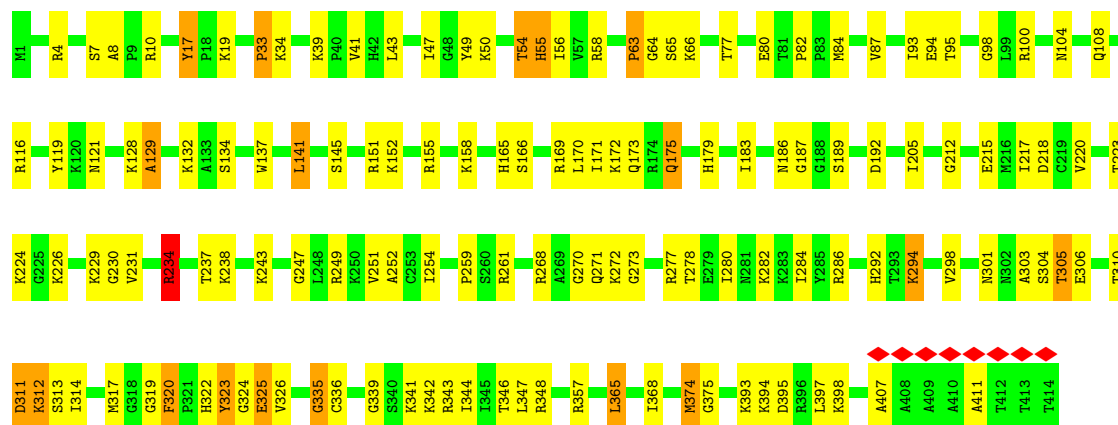


• Molecule 3: 40S ribosomal protein S3a

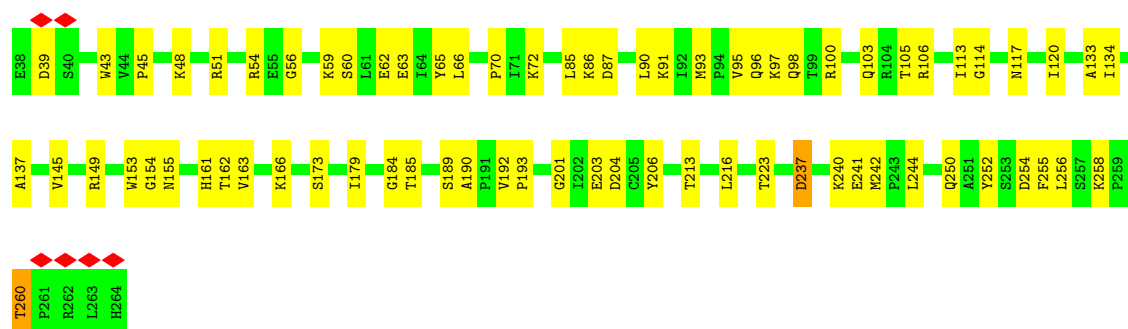




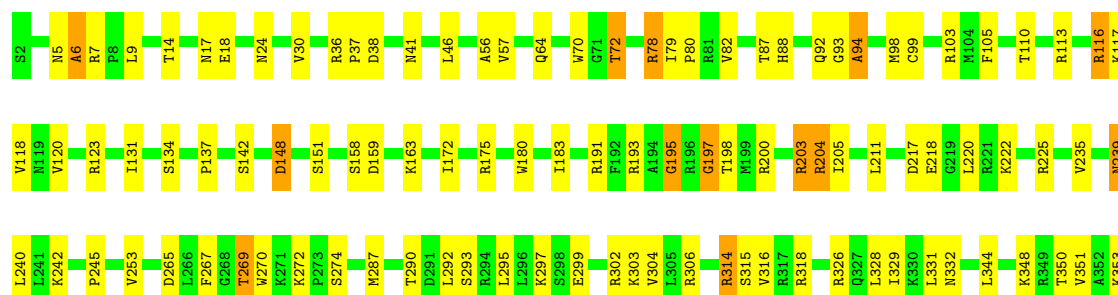
• Molecule 4: 60S ribosomal protein L3



• Molecule 5: 40S ribosomal protein S2

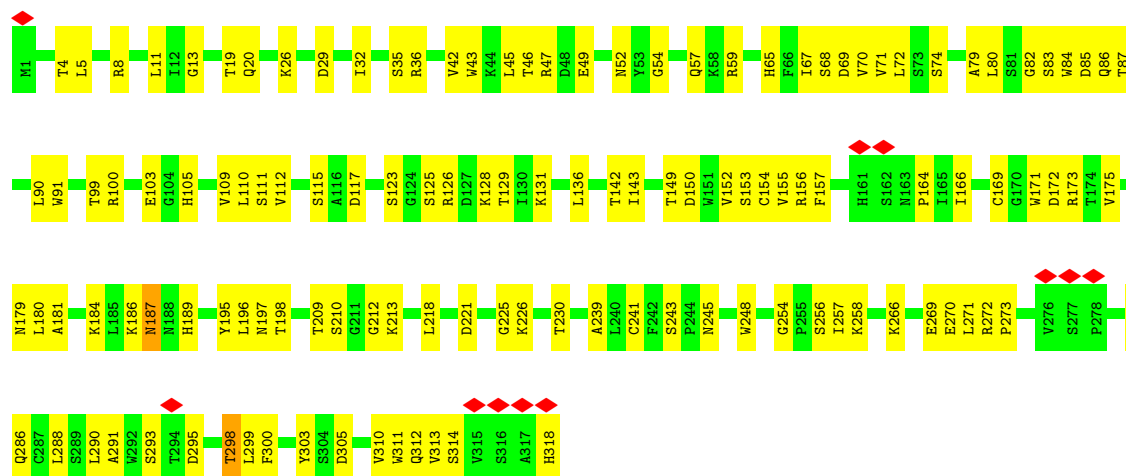


• Molecule 6: 60S ribosomal protein L4

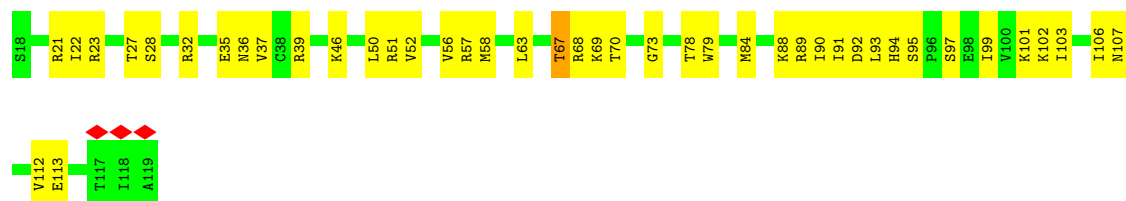




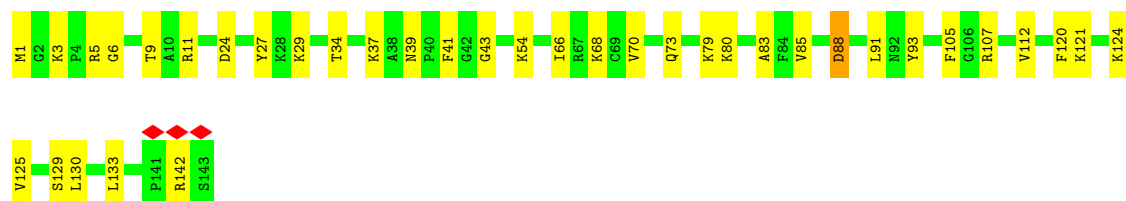
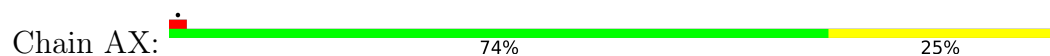
- Molecule 7: Guanine nucleotide-binding protein subunit beta-like protein



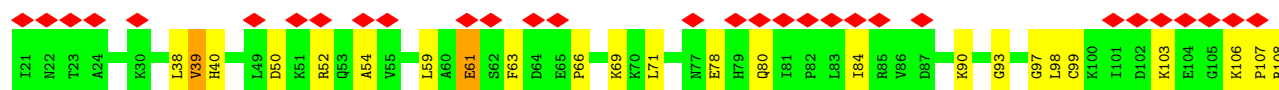
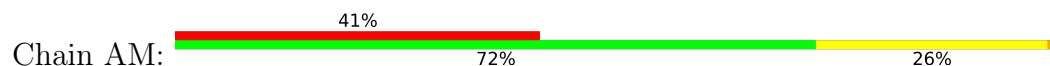
- Molecule 8: 40S ribosomal protein S20

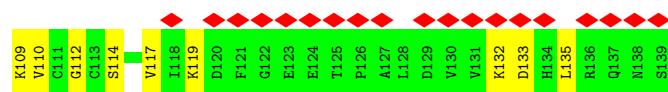


- Molecule 9: 40S ribosomal protein S23



- Molecule 10: 40S ribosomal protein S12

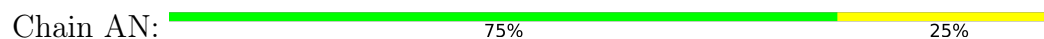




- Molecule 11: 40S ribosomal protein S29



- Molecule 12: 40S ribosomal protein S13



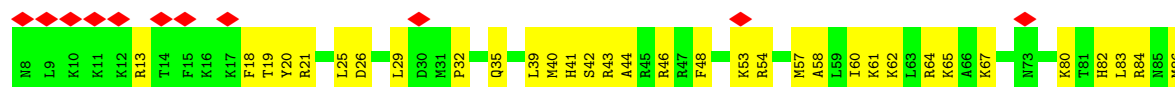
- Molecule 13: 40S ribosomal protein S11



- Molecule 14: 40S ribosomal protein S17



- Molecule 15: GEO07301p1





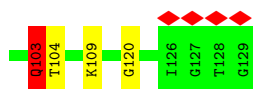
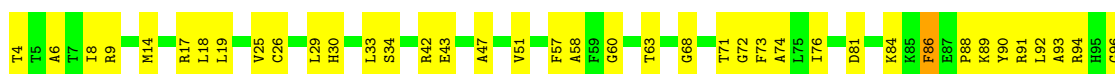
- Molecule 16: 40S ribosomal protein S21

Chain AV: 71% 28%



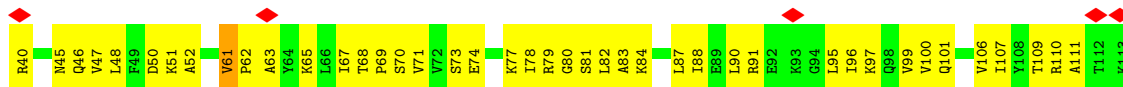
- Molecule 17: 40S ribosomal protein S24

Chain AY: 66% 33%



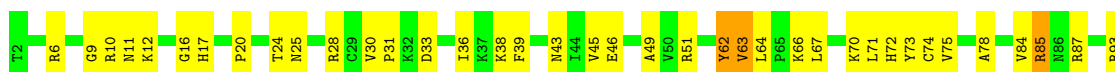
- Molecule 18: 40S ribosomal protein S25

Chain AZ: 7% 43% 55%



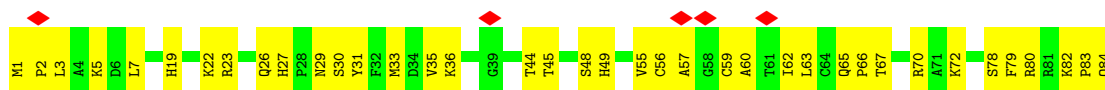
- Molecule 19: 40S ribosomal protein S26

Chain Aa: 8% 60% 36% 5%



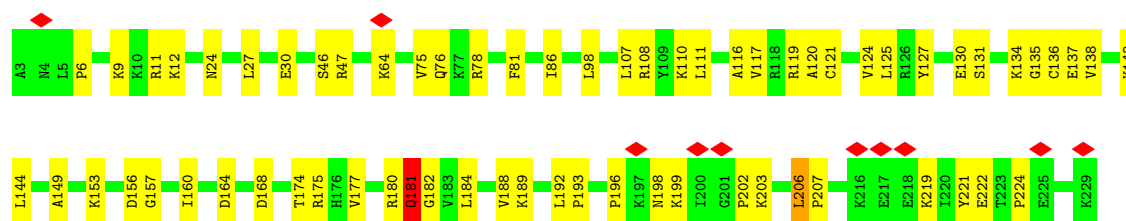
- Molecule 20: 40S ribosomal protein S27

Chain Ab: 6% 55% 45%

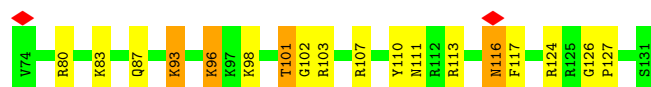


- Molecule 21: 40S ribosomal protein S3

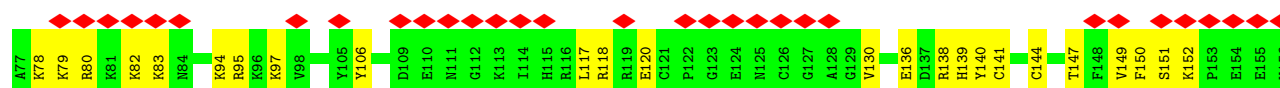
Chain AD: 71% 28%



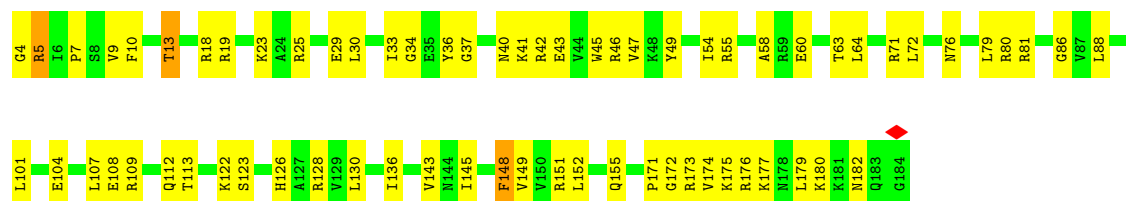
- Molecule 22: 40S ribosomal protein S30



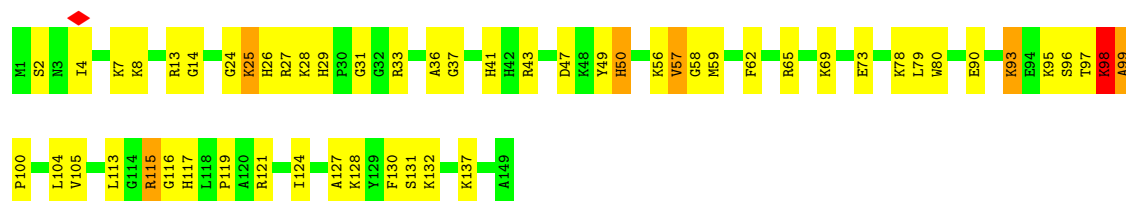
- Molecule 23: Ubiquitin-40S ribosomal protein S27a



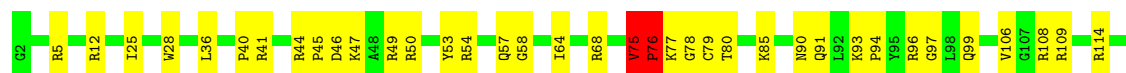
- Molecule 24: 40S ribosomal protein S9

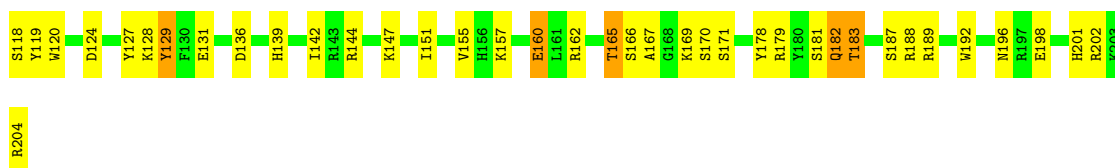


- Molecule 25: 60S ribosomal protein L27a



- Molecule 26: 60S ribosomal protein L15

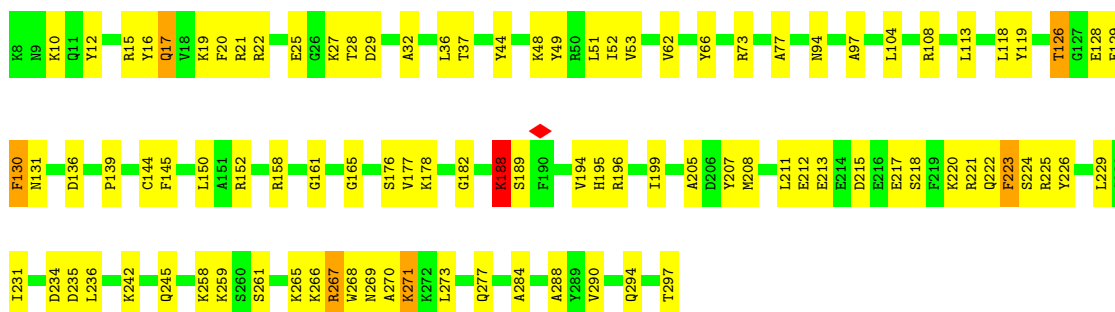




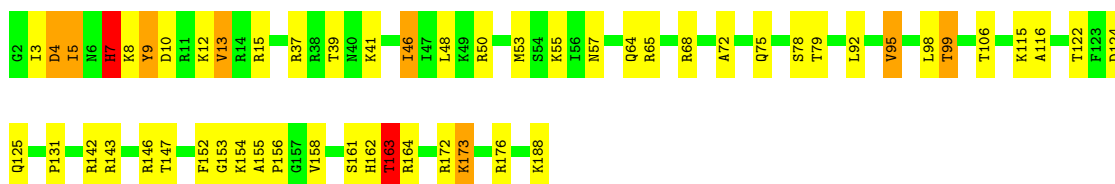
• Molecule 27: 60S ribosomal protein L10



• Molecule 28: 60S ribosomal protein L5

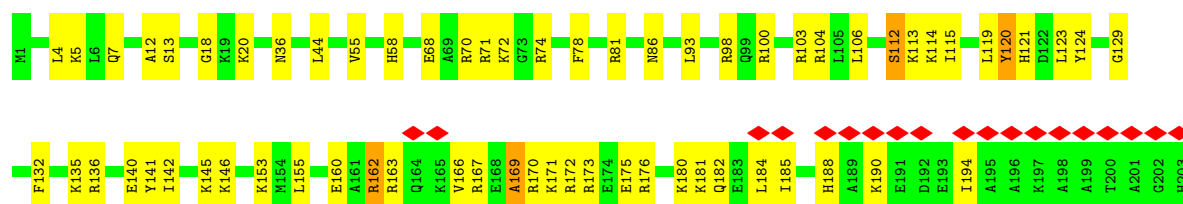


• Molecule 29: 60S ribosomal protein L18

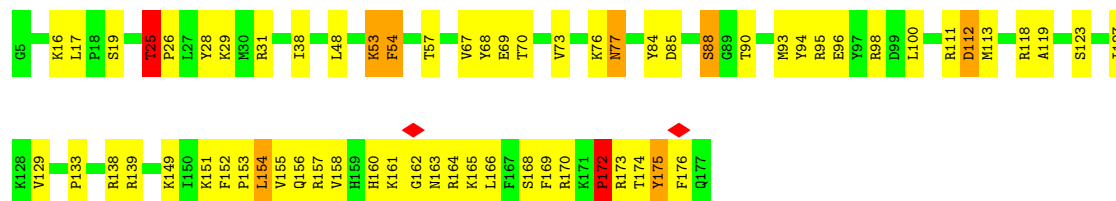


• Molecule 30: 60S ribosomal protein L19

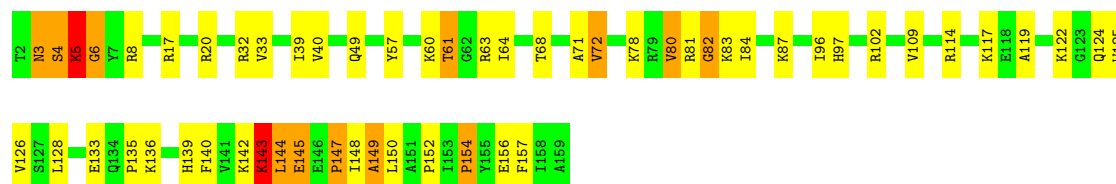




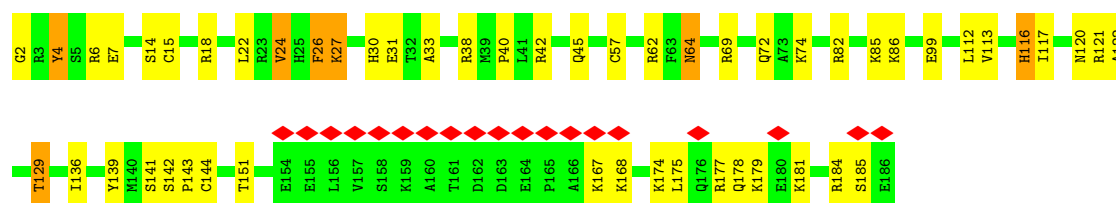
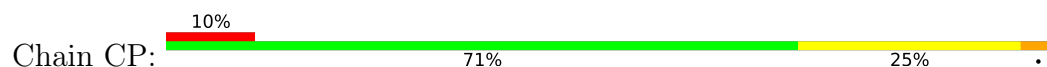
• Molecule 31: 60S ribosomal protein L18a



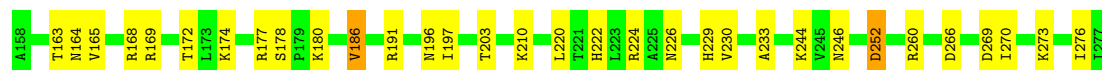
• Molecule 32: RE62581p



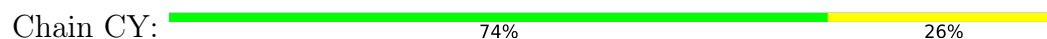
• Molecule 33: 60S ribosomal protein L17



• Molecule 34: IP17216p

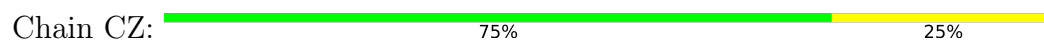


• Molecule 35: GEO07453p1

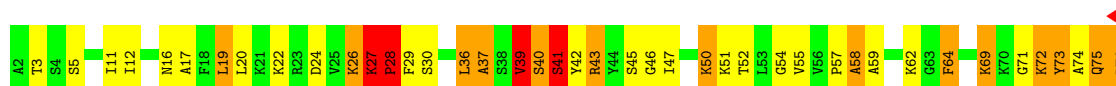




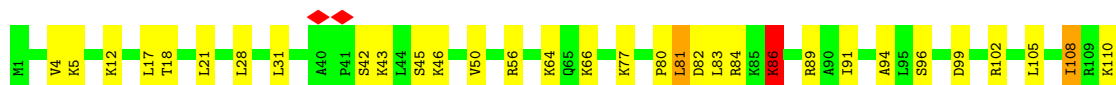
- Molecule 36: 60S ribosomal protein L27



- Molecule 37: 60S ribosomal protein L28



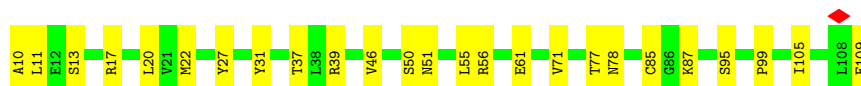
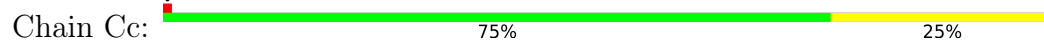
- Molecule 38: FI02809p



- Molecule 39: 60S ribosomal protein L29

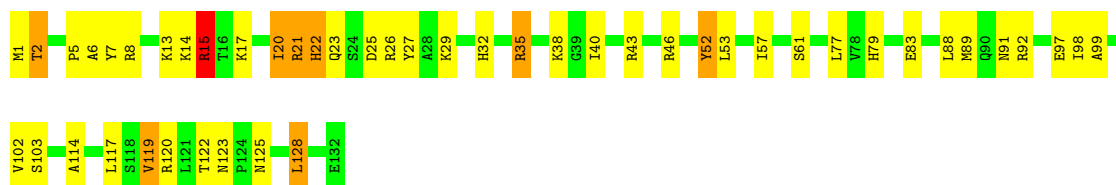


- Molecule 40: RE25263p

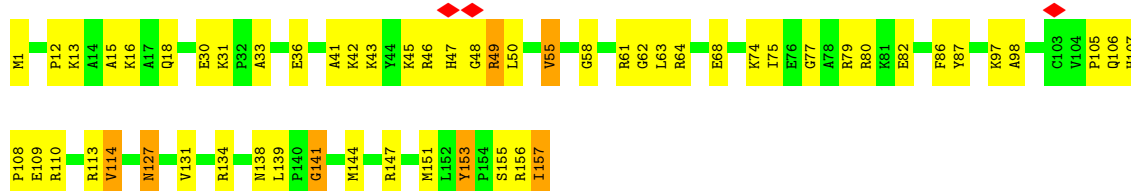


- Molecule 41: 60S ribosomal protein L32

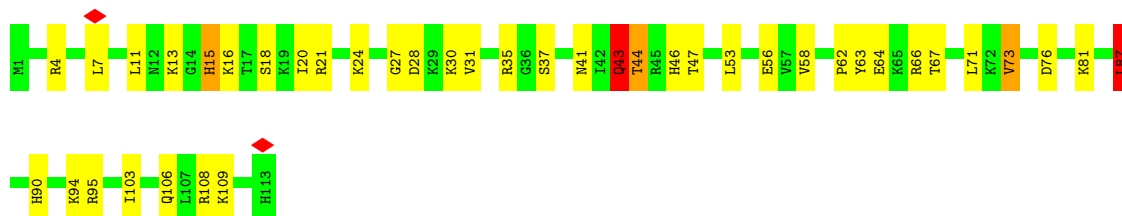




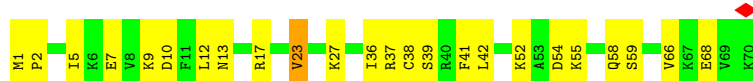
- Molecule 42: GEO07455p1



- Molecule 43: 60S ribosomal protein L36



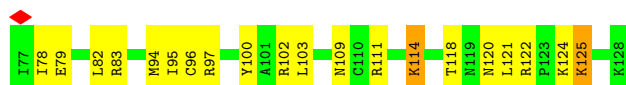
- Molecule 44: 60S ribosomal protein L38



- Molecule 45: 60S ribosomal protein L39

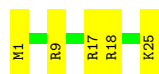


- Molecule 46: Ubiquitin-60S ribosomal protein L40



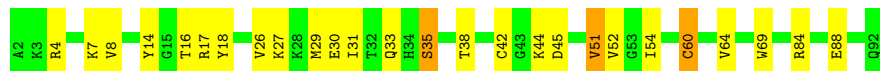
- Molecule 47: 60S ribosomal protein L41

Chain Cn:  80% 20%



- Molecule 48: 60S ribosomal protein L37a

Chain Cp:  71% 25% .



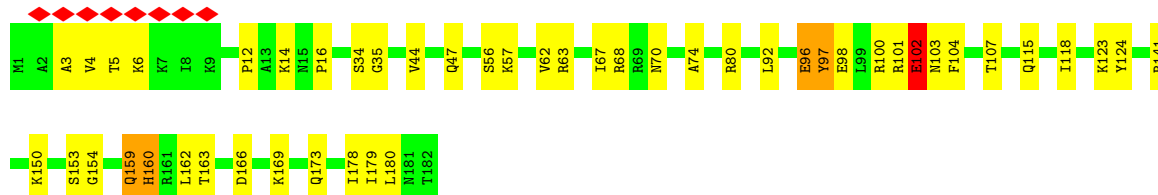
- Molecule 49: TA01007p

Chain Co:  73% 26% .



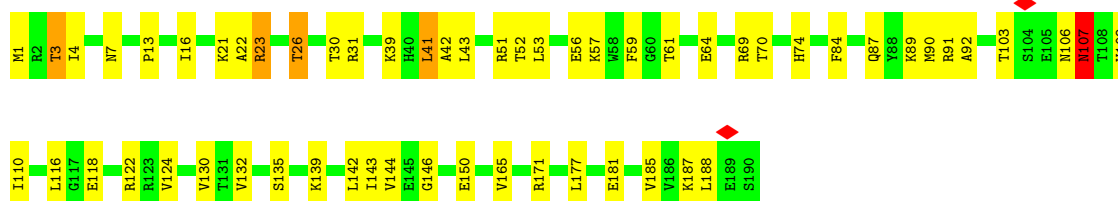
- Molecule 50: 60S ribosomal protein L11

Chain CJ:  74% 24% ..



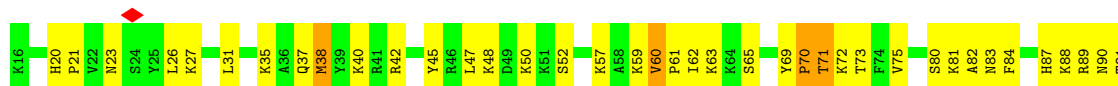
- Molecule 51: 60S ribosomal protein L9

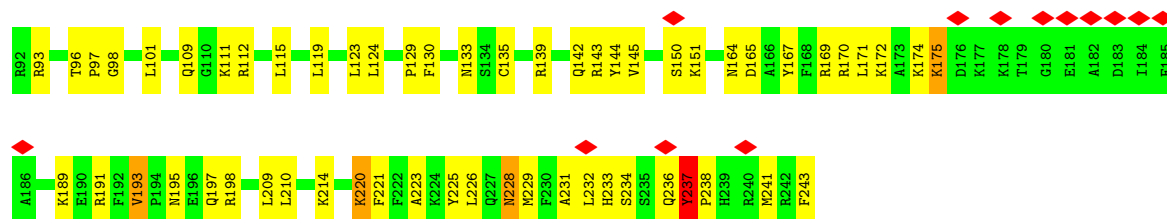
Chain CH:  69% 28% ..



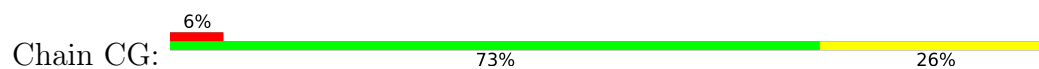
- Molecule 52: Ribosomal protein L6, isoform A

Chain CE:  6% 58% 38% .

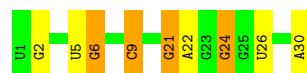




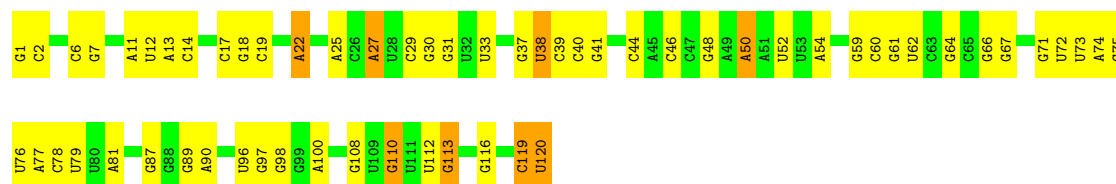
• Molecule 53: 60S ribosomal protein L7a



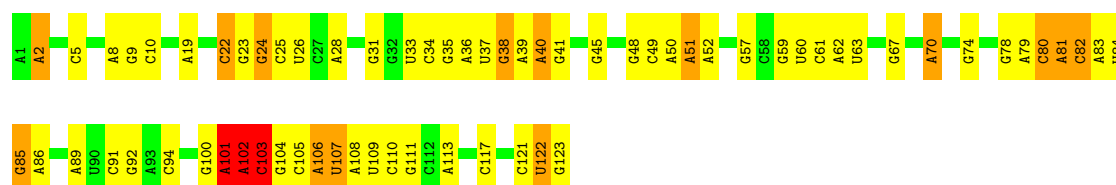
• Molecule 54: 2S ribosomal RNA



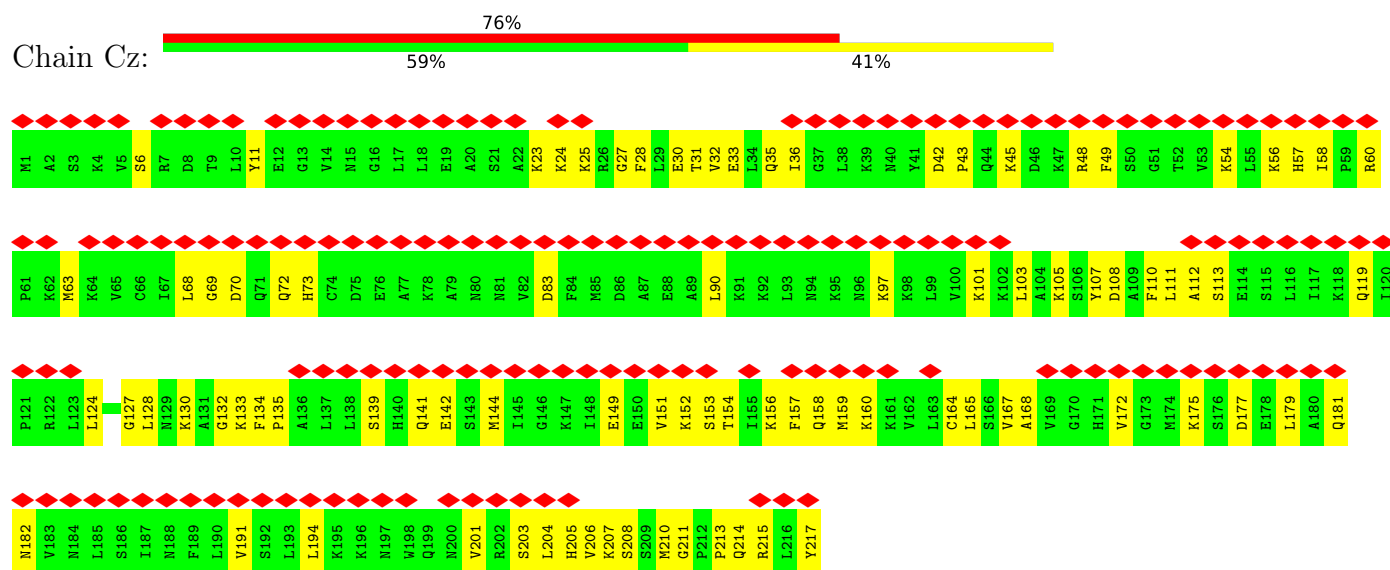
• Molecule 55: 5S ribosomal RNA



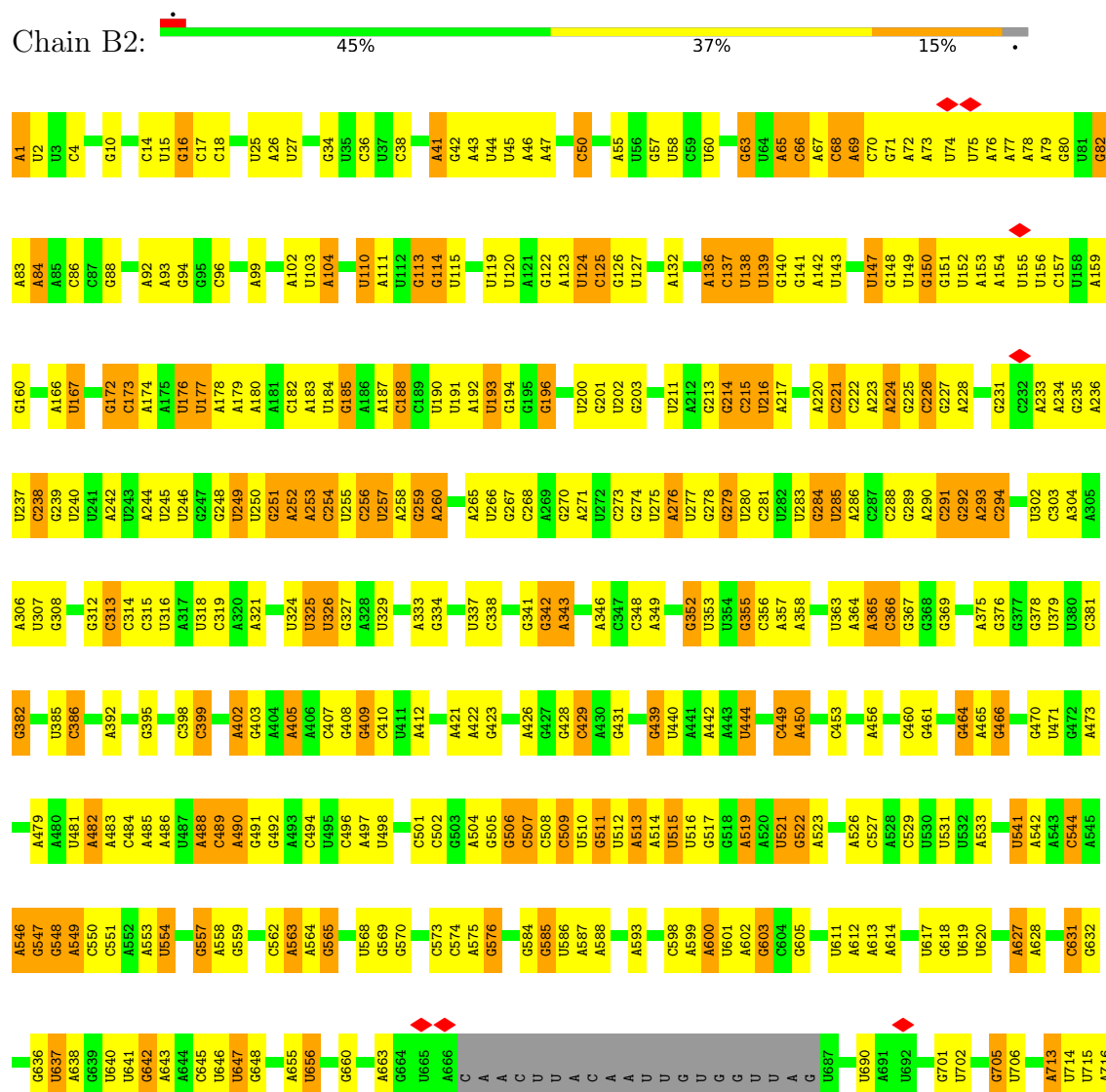
• Molecule 56: 5.8S ribosomal RNA

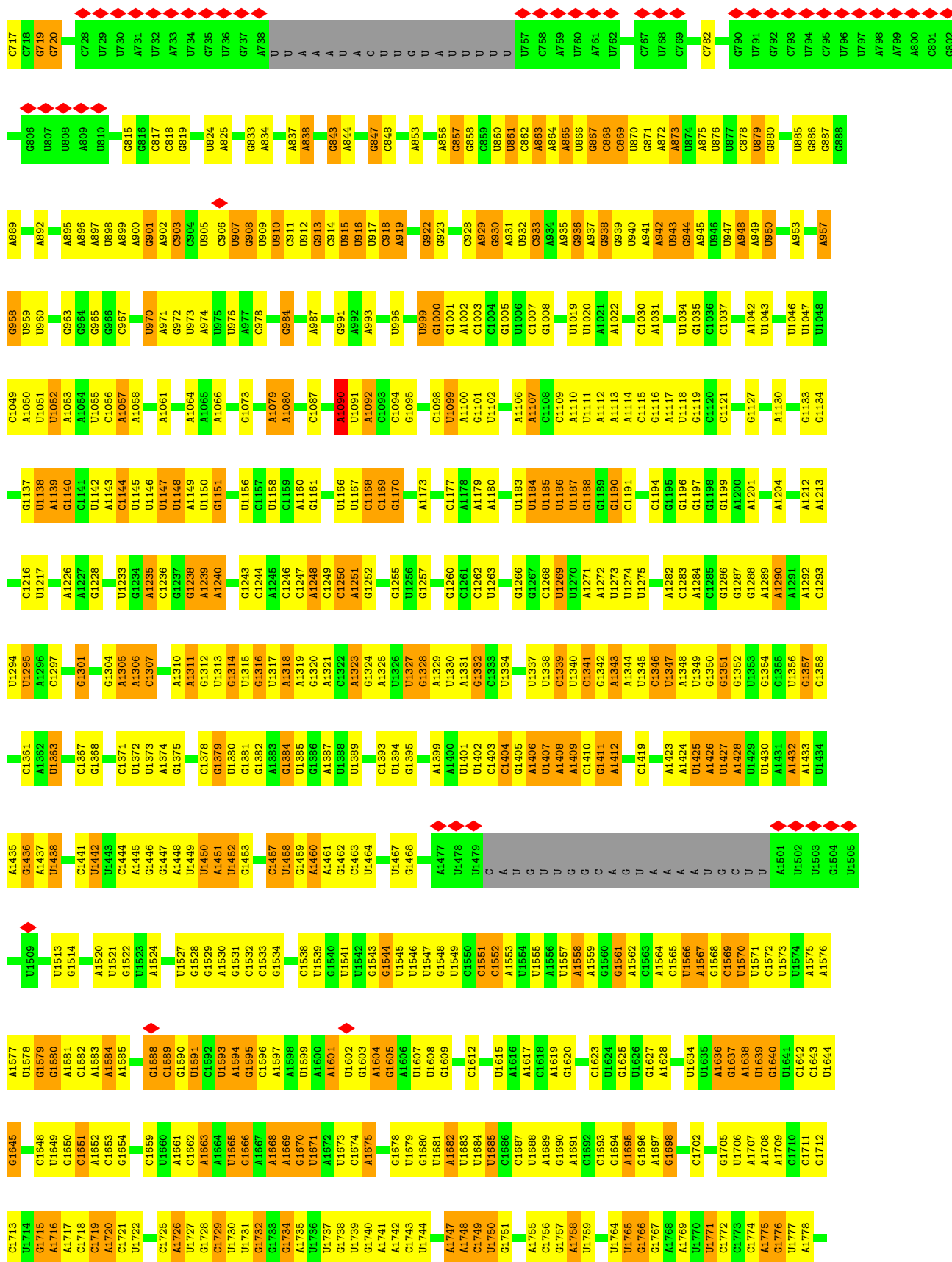


• Molecule 57: 60S ribosomal protein L10a-2



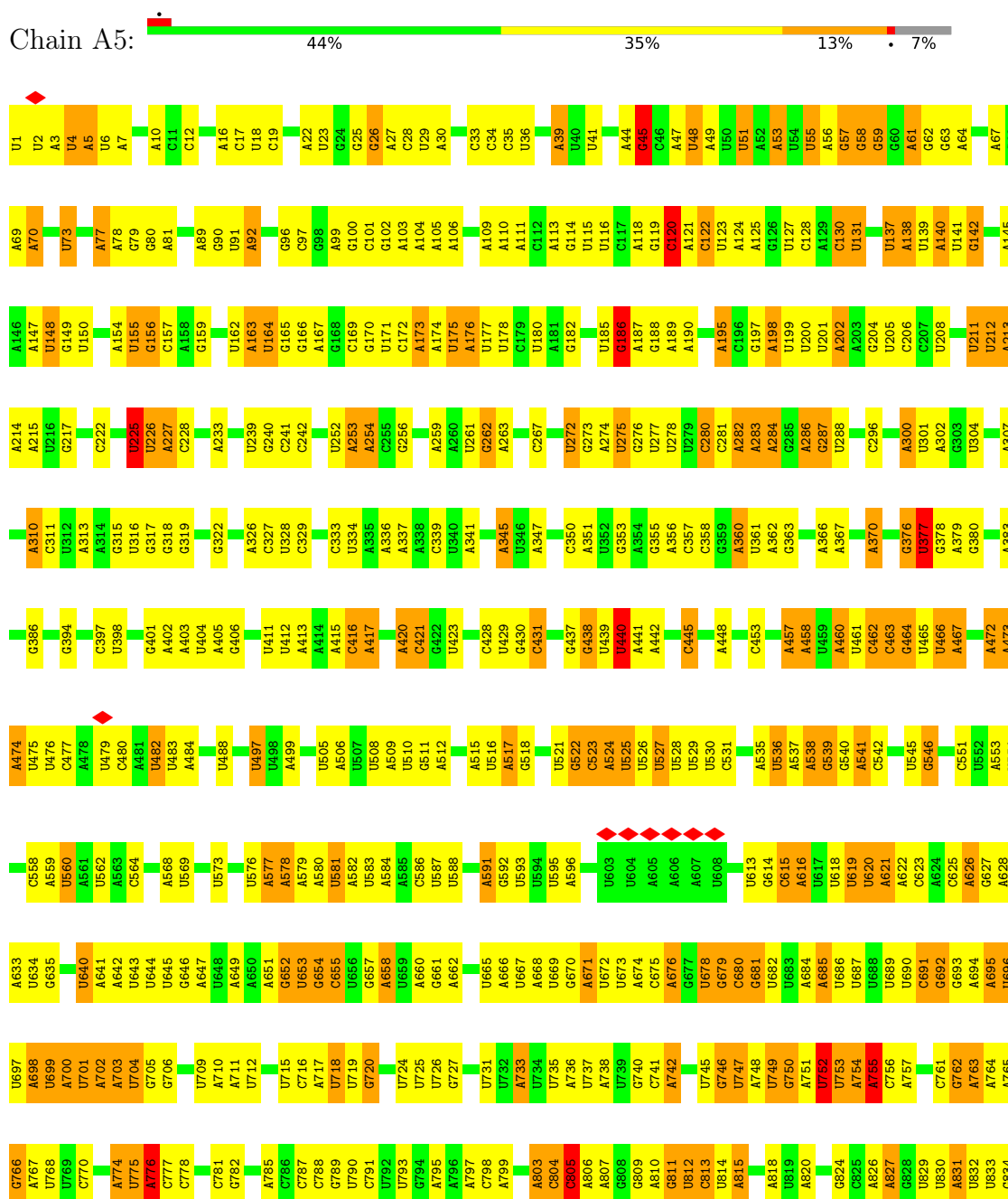
• Molecule 58: 18S ribosomal RNA





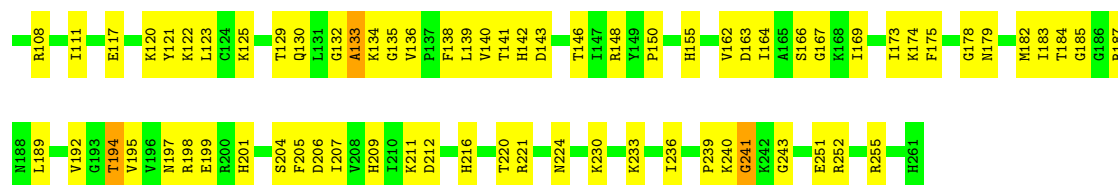


• Molecule 59: 28S ribosomal RNA



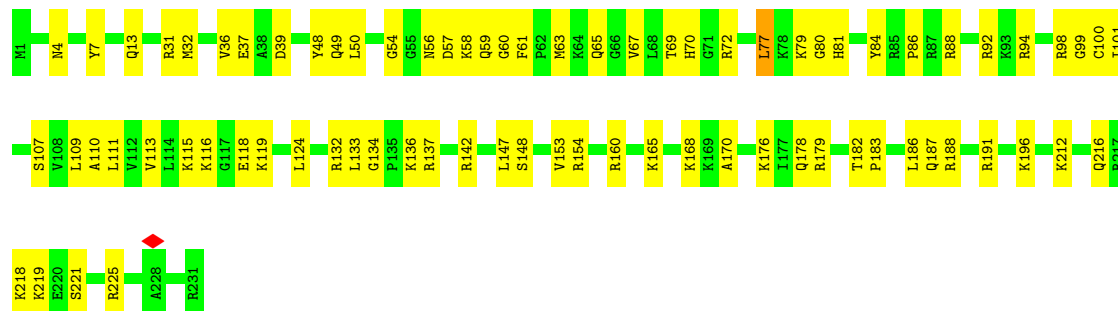
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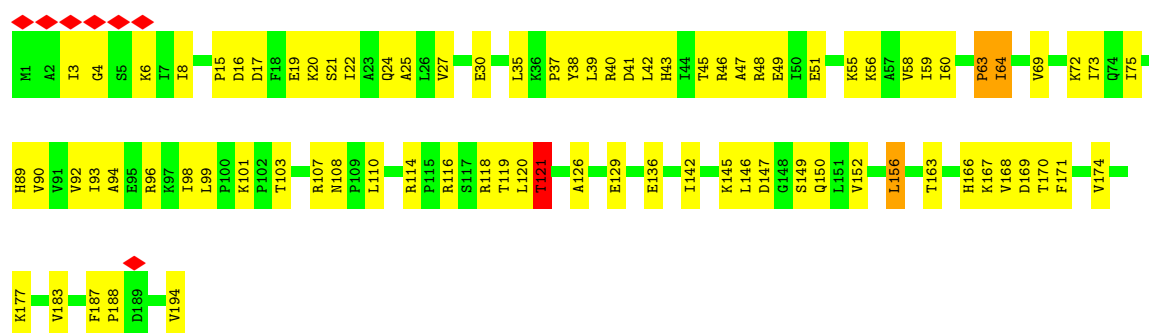
- Molecule 61: 40S ribosomal protein S6

Chain AG: 67% 33%



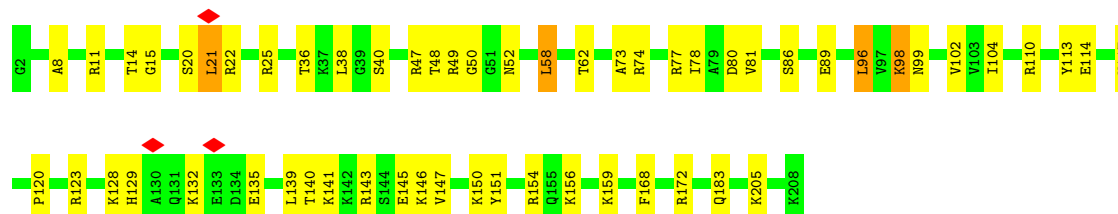
- Molecule 62: 40S ribosomal protein S7

Chain AH: 57% 41%



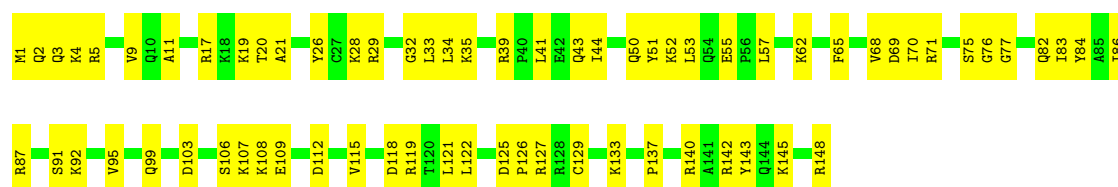
- Molecule 63: 40S ribosomal protein S8

Chain AI: 72% 26%

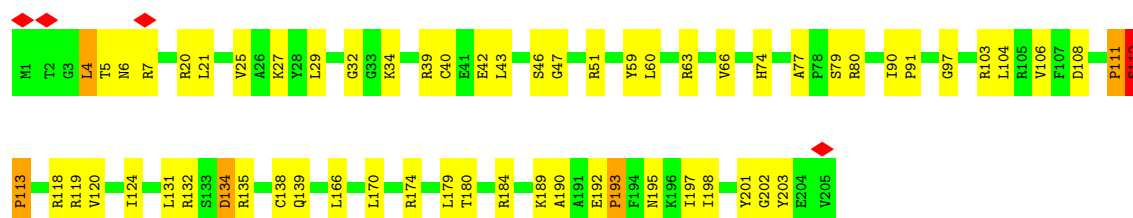
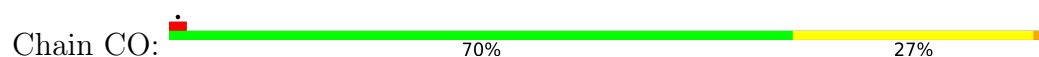


- Molecule 64: 40S ribosomal protein S16

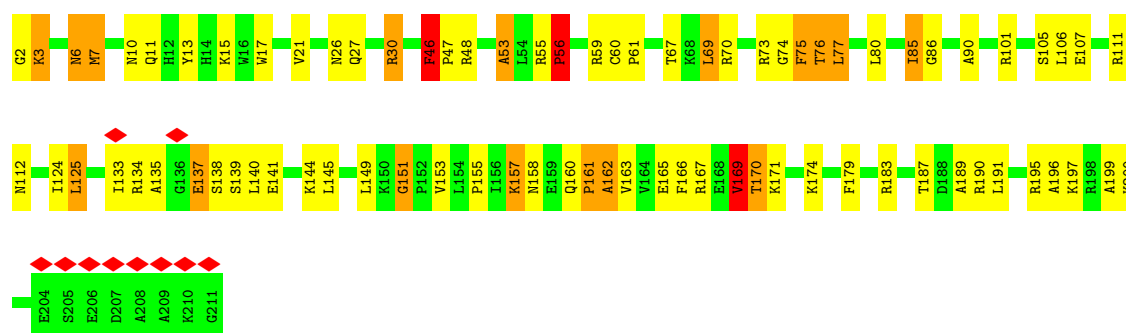
Chain AQ: 54% 46%



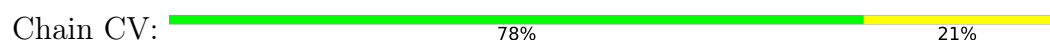
- Molecule 65: 60S ribosomal protein L13a



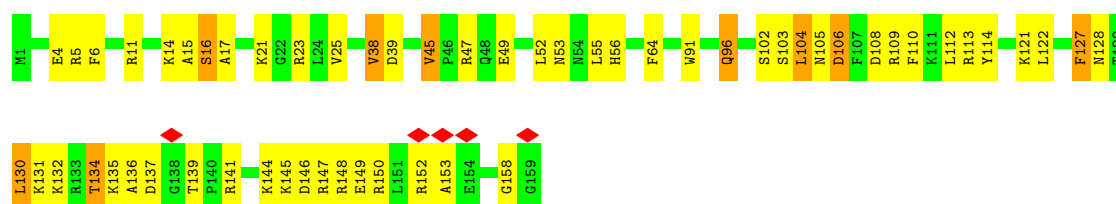
- Molecule 66: 60S ribosomal protein L13



- Molecule 67: 60S ribosomal protein L23

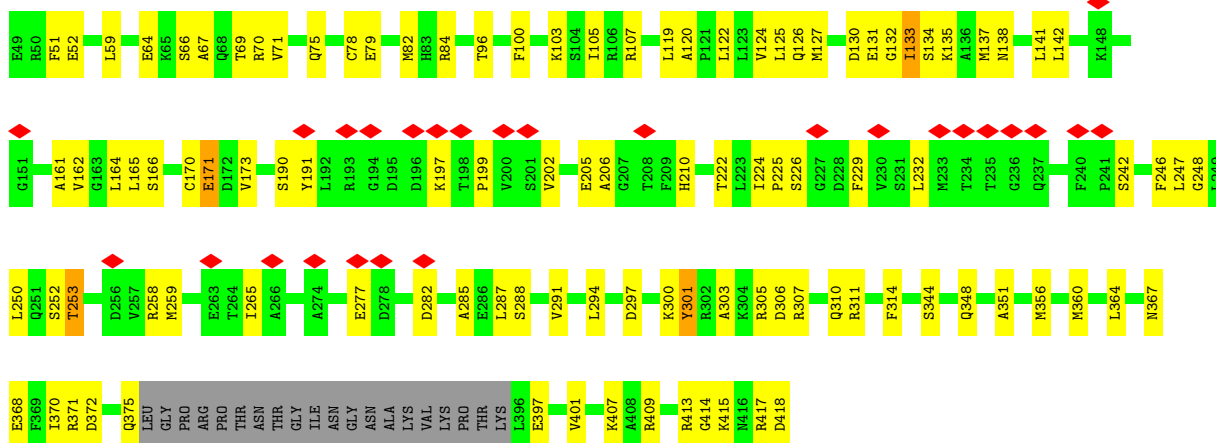


- Molecule 68: 60S ribosomal protein L14



- Molecule 69: LP04564p

Chain DA: 



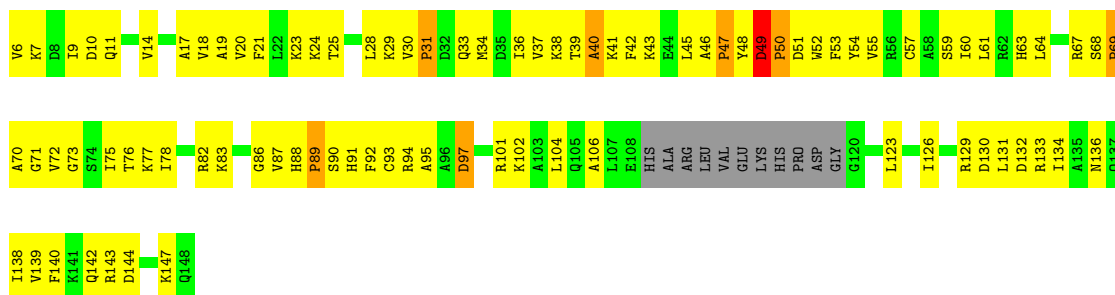
- Molecule 70: 40S ribosomal protein S10b

Chain AK: 



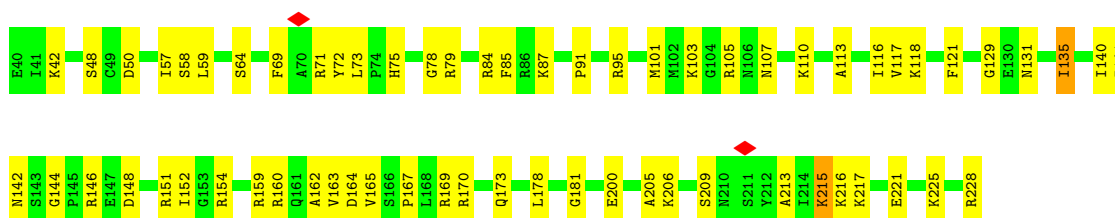
- Molecule 71: 40S ribosomal protein S19a

Chain AT: 



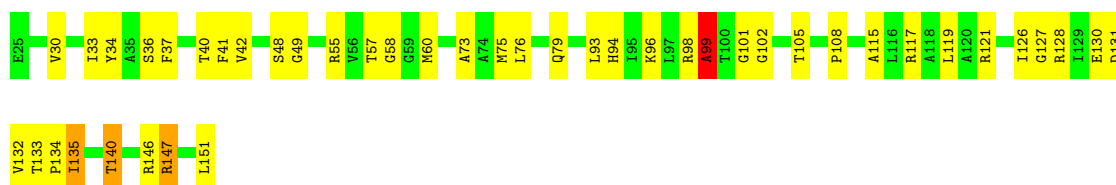
- Molecule 72: 40S ribosomal protein S5a

Chain AF: 



- Molecule 73: 40S ribosomal protein S14a

Chain AO:  65% 31% ..



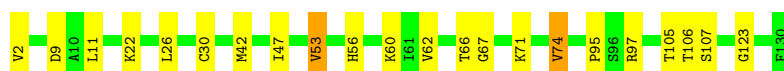
- Molecule 74: 40S ribosomal protein S28

Chain Ac:  55% 42% .



- Molecule 75: 40S ribosomal protein S15Aa

Chain AW:  83% 16% .



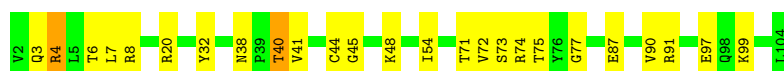
- Molecule 76: 60S ribosomal protein L24

Chain CW:  86% 10% ..



- Molecule 77: RH48056p

Chain Cg:  76% 22% .



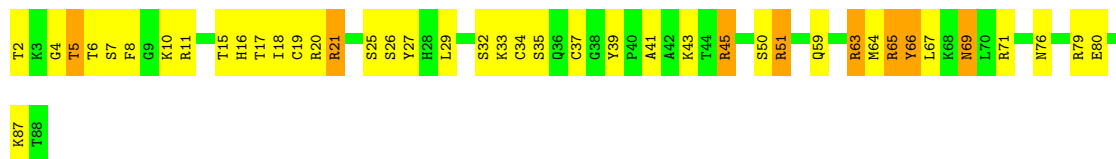
- Molecule 78: Ribosomal protein L22-like protein

Chain CU:  59% 38% .



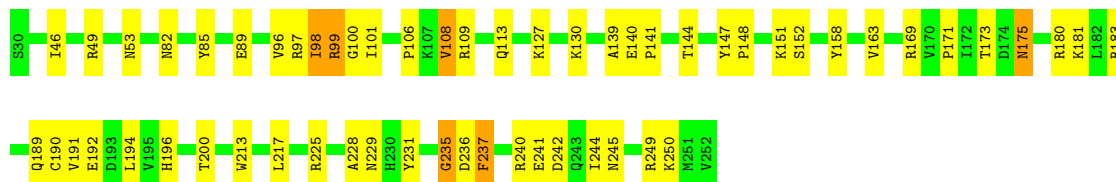
- Molecule 79: Probable 60S ribosomal protein L37-B

Chain Cj:  52% 39% 9%



- Molecule 80: 60S ribosomal protein L7

Chain CF:  74% 23% 3%



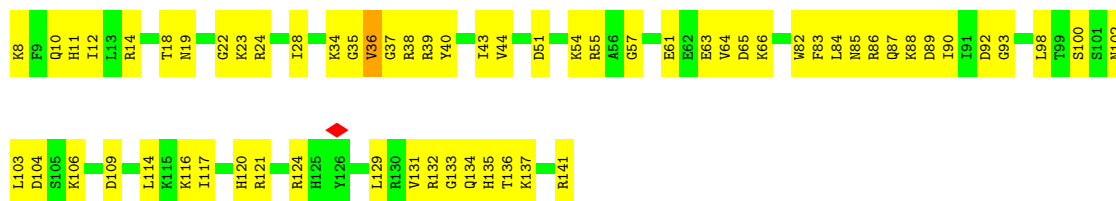
- Molecule 81: 60S ribosomal protein L31

Chain Cd:  55% 39% 6%



- Molecule 82: 40S ribosomal protein S18

Chain AS:  54% 46% 0%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	46878	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	0.459	Depositor
Minimum map value	-0.223	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.025	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	0.46	0/1777	0.75	1/2422 (0.0%)
2	CA	1.31	5/1970 (0.3%)	1.17	7/2635 (0.3%)
3	AB	0.52	0/1825	0.76	2/2448 (0.1%)
4	CB	1.20	4/3356 (0.1%)	1.15	11/4494 (0.2%)
5	AC	0.64	0/1785	0.81	2/2415 (0.1%)
6	CC	1.21	0/3163	1.15	14/4253 (0.3%)
7	Ag	0.26	0/2574	0.53	0/3506
8	AU	0.37	0/825	0.60	0/1111
9	AX	0.78	0/1152	0.95	0/1540
10	AM	0.28	0/937	0.79	3/1260 (0.2%)
11	Ad	0.46	0/443	0.82	0/589
12	AN	0.75	0/1225	0.79	2/1641 (0.1%)
13	AL	0.77	0/1296	0.88	1/1725 (0.1%)
14	AR	0.36	0/993	0.71	2/1333 (0.2%)
15	AP	0.32	0/1036	0.71	0/1383
16	AV	0.57	0/622	0.73	0/835
17	AY	0.42	0/1032	0.84	2/1373 (0.1%)
18	AZ	0.31	0/616	0.73	0/826
19	Aa	0.78	0/883	1.10	6/1184 (0.5%)
20	Ab	0.49	0/668	0.78	0/898
21	AD	0.35	0/1808	0.69	0/2427
22	Ae	0.43	0/475	0.96	4/625 (0.6%)
23	Af	0.27	0/672	0.78	2/887 (0.2%)
24	AJ	0.51	0/1526	0.82	2/2037 (0.1%)
25	Ca	1.37	1/1235 (0.1%)	1.27	13/1640 (0.8%)
26	CN	1.46	3/1750 (0.2%)	1.25	5/2335 (0.2%)
27	CI	0.65	0/1827	0.82	1/2447 (0.0%)
28	CD	0.68	0/2379	0.83	6/3196 (0.2%)
29	CQ	1.24	1/1544 (0.1%)	1.16	9/2069 (0.4%)
30	CR	0.99	1/1703 (0.1%)	0.92	2/2255 (0.1%)
31	CS	1.02	0/1491	1.13	2/1998 (0.1%)
32	CT	1.06	1/1326 (0.1%)	1.21	10/1773 (0.6%)
33	CP	1.30	2/1529 (0.1%)	1.11	4/2042 (0.2%)
34	CX	0.90	0/1001	0.96	3/1348 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	CY	0.99	0/1094	0.92	0/1456
36	CZ	0.72	0/1141	0.76	1/1517 (0.1%)
37	Cr	1.09	0/1069	1.36	12/1432 (0.8%)
38	Ch	0.84	0/1024	0.90	2/1353 (0.1%)
39	Cb	0.97	0/628	1.11	3/832 (0.4%)
40	Cc	0.89	0/779	0.76	0/1048
41	Ce	1.49	5/1132 (0.4%)	1.31	10/1508 (0.7%)
42	Cf	1.15	1/1270 (0.1%)	1.22	6/1696 (0.4%)
43	Ci	0.82	1/944 (0.1%)	1.12	7/1250 (0.6%)
44	Ck	0.69	0/583	0.86	1/774 (0.1%)
45	Cl	1.23	0/445	1.31	5/589 (0.8%)
46	Cm	0.70	0/435	0.92	2/575 (0.3%)
47	Cn	1.40	0/237	1.31	1/300 (0.3%)
48	Cp	1.29	0/719	1.04	0/954
49	Co	0.93	0/887	1.09	0/1162
50	CJ	0.51	0/1494	0.84	4/2001 (0.2%)
51	CH	0.79	0/1519	0.90	4/2042 (0.2%)
52	CE	0.76	1/1883 (0.1%)	1.11	11/2514 (0.4%)
53	CG	0.71	0/1968	0.85	2/2637 (0.1%)
54	A9	1.04	0/714	0.74	1/1112 (0.1%)
55	A7	1.00	0/2854	0.66	0/4447
56	A8	1.34	0/2932	0.99	11/4568 (0.2%)
57	Cz	0.25	0/1727	0.65	0/2308
58	B2	0.75	0/43887	0.63	5/68161 (0.0%)
59	A5	1.32	20/86239 (0.0%)	0.92	101/134149 (0.1%)
60	AE	0.54	0/2096	0.76	2/2819 (0.1%)
61	AG	0.37	0/1891	0.65	0/2519
62	AH	0.44	0/1593	0.76	3/2145 (0.1%)
63	AI	0.69	0/1689	0.88	2/2250 (0.1%)
64	AQ	0.36	0/1202	0.87	4/1608 (0.2%)
65	CO	1.21	0/1700	1.06	6/2277 (0.3%)
66	CL	1.02	1/1726 (0.1%)	1.30	15/2308 (0.6%)
67	CV	1.18	0/1014	1.00	2/1362 (0.1%)
68	CM	0.81	0/1326	1.01	6/1780 (0.3%)
69	DA	0.44	0/2800	0.76	4/3765 (0.1%)
70	AK	0.33	0/786	0.79	3/1064 (0.3%)
71	AT	0.38	0/1060	0.98	10/1421 (0.7%)
72	AF	0.43	1/1510 (0.1%)	0.78	2/2026 (0.1%)
73	AO	0.67	0/965	0.97	3/1295 (0.2%)
74	Ac	0.42	0/502	0.76	0/670
75	AW	0.80	0/1046	0.87	1/1402 (0.1%)
76	CW	1.12	0/495	1.02	0/658
77	Cg	1.23	0/855	1.04	2/1142 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	CU	0.53	0/828	0.82	0/1110
79	Cj	0.84	0/706	1.16	0/929
80	CF	1.24	1/1905 (0.1%)	1.07	4/2553 (0.2%)
81	Cd	0.41	0/914	0.54	0/1229
82	AS	0.23	0/1118	0.69	2/1498 (0.1%)
All	All	1.04	49/235775 (0.0%)	0.88	376/345165 (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
1	AA	0	2
2	CA	0	3
3	AB	0	2
4	CB	0	11
5	AC	0	1
6	CC	0	11
9	AX	0	1
11	Ad	0	1
13	AL	0	2
17	AY	0	1
19	Aa	0	5
21	AD	0	2
22	Ae	0	3
24	AJ	0	2
25	Ca	0	4
26	CN	0	8
27	CI	0	4
28	CD	0	4
29	CQ	0	8
30	CR	0	5
31	CS	0	10
32	CT	0	11
33	CP	0	2
35	CY	0	3
36	CZ	0	1
37	Cr	0	20
38	Ch	0	4
39	Cb	0	4
40	Cc	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
41	Ce	0	5
42	Cf	0	5
43	Ci	0	6
44	Ck	0	1
46	Cm	0	2
48	Cp	0	2
49	Co	0	3
50	CJ	0	3
51	CH	0	2
52	CE	0	13
53	CG	0	4
59	A5	0	1
60	AE	0	3
61	AG	0	1
62	AH	0	4
63	AI	0	5
64	AQ	0	2
65	CO	0	6
66	CL	0	15
67	CV	0	1
68	CM	0	6
69	DA	0	2
71	AT	0	2
73	AO	0	6
74	Ac	0	1
75	AW	0	1
76	CW	0	2
77	Cg	0	1
78	CU	0	1
80	CF	0	2
81	Cd	0	1
All	All	0	245

The worst 5 of 49 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	A5	1382	U	O3'-P	7.72	1.72	1.61
72	AF	165	VAL	C-N	-6.98	1.23	1.33
26	CN	183	THR	CA-CB	-6.52	1.42	1.53
59	A5	1382	U	C3'-O3'	6.50	1.51	1.42
41	Ce	46	ARG	CB-CG	-6.21	1.33	1.52

The worst 5 of 376 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	A8	100	G	OP2-P-O3'	-13.81	66.58	108.00
52	CE	237	TYR	N-CA-C	11.07	127.63	109.58
32	CT	144	LEU	CA-C-N	10.20	140.05	121.70
32	CT	144	LEU	C-N-CA	10.20	140.05	121.70
44	Ck	59	SER	N-CA-C	9.80	124.51	111.28

There are no chirality outliers.

5 of 245 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	108	PHE	Peptide
1	AA	29	ASN	Peptide
2	CA	13	GLY	Peptide
2	CA	196	TRP	Peptide
2	CA	229	THR	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	51	0
2	CA	1935	0	2036	53	0
3	AB	1798	0	1867	60	0
4	CB	3287	0	3432	102	0
5	AC	1746	0	1827	53	0
6	CC	3109	0	3298	85	0
7	Ag	2511	0	2438	85	0
8	AU	815	0	871	35	0
9	AX	1131	0	1190	25	0
10	AM	924	0	960	24	0
11	Ad	433	0	424	20	0
12	AN	1202	0	1291	28	0
13	AL	1274	0	1351	41	0
14	AR	981	0	1038	33	0
15	AP	1016	0	1085	100	0
16	AV	617	0	613	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	AY	1016	0	1073	29	0
18	AZ	608	0	658	54	0
19	Aa	867	0	920	25	0
20	Ab	653	0	680	28	0
21	AD	1782	0	1862	43	0
22	Ae	469	0	503	15	0
23	Af	659	0	695	22	0
24	AJ	1503	0	1620	46	0
25	Ca	1204	0	1260	40	0
26	CN	1710	0	1777	53	0
27	CI	1785	0	1805	56	0
28	CD	2334	0	2354	73	0
29	CQ	1518	0	1626	35	0
30	CR	1683	0	1827	55	0
31	CS	1454	0	1503	47	0
32	CT	1297	0	1364	36	0
33	CP	1505	0	1556	47	0
34	CX	984	0	1058	25	0
35	CY	1078	0	1159	21	0
36	CZ	1115	0	1199	27	0
37	Cr	1051	0	1148	50	0
38	Ch	1015	0	1163	31	0
39	Cb	619	0	650	14	0
40	Cc	770	0	802	19	0
41	Ce	1110	0	1181	32	0
42	Cf	1244	0	1316	54	0
43	Ci	934	0	1029	26	0
44	Ck	576	0	634	16	0
45	Cl	437	0	483	9	0
46	Cm	429	0	472	15	0
47	Cn	236	0	286	3	0
48	Cp	710	0	756	21	0
49	Co	874	0	956	16	0
50	CJ	1468	0	1507	39	0
51	CH	1499	0	1569	37	0
52	CE	1845	0	1981	74	0
53	CG	1936	0	2103	39	0
54	A9	639	0	321	8	0
55	A7	2554	0	1295	35	0
56	A8	2621	0	1318	33	0
57	Cz	1702	0	1814	67	0
58	B2	39355	0	19519	865	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	A5	77175	0	38072	894	0
60	AE	2054	0	2165	73	0
61	AG	1866	0	2029	60	0
62	AH	1566	0	1664	61	0
63	AI	1665	0	1746	39	0
64	AQ	1183	0	1255	54	0
65	CO	1668	0	1783	41	0
66	CL	1695	0	1790	55	0
67	CV	998	0	1046	16	0
68	CM	1302	0	1388	55	0
69	DA	2756	0	2737	68	0
70	AK	760	0	757	20	0
71	AT	1041	0	1064	401	0
72	AF	1490	0	1548	57	0
73	AO	953	0	988	27	0
74	Ac	498	0	525	23	0
75	AW	1028	0	1071	16	0
76	CW	483	0	510	3	0
77	Cg	844	0	924	13	0
78	CU	811	0	838	26	0
79	Cj	696	0	722	52	0
80	CF	1869	0	1980	41	0
81	Cd	899	0	923	74	0
82	AS	1101	0	1129	332	0
All	All	219765	0	162927	4341	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 13.

The worst 5 of 4341 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)
71:AT:42:PHE:CG	71:AT:83:LYS:HD3	1.28	1.64
15:AP:114:MET:HG2	82:AS:117:ILE:CD1	1.15	1.62
71:AT:42:PHE:CD2	71:AT:83:LYS:HD3	1.25	1.61
71:AT:83:LYS:HD2	71:AT:93:CYS:SG	1.37	1.60
58:B2:1750:U:C5	82:AS:124:ARG:NH2	1.71	1.55

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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%)	187 (87%)	28 (13%)	1 (0%)	24	57
2	CA	251/253 (99%)	214 (85%)	36 (14%)	1 (0%)	30	62
3	AB	218/220 (99%)	178 (82%)	38 (17%)	2 (1%)	14	47
4	CB	412/414 (100%)	339 (82%)	68 (16%)	5 (1%)	10	41
5	AC	225/227 (99%)	198 (88%)	27 (12%)	0	100	100
6	CC	390/392 (100%)	323 (83%)	65 (17%)	2 (0%)	24	57
7	Ag	316/318 (99%)	276 (87%)	40 (13%)	0	100	100
8	AU	100/102 (98%)	92 (92%)	8 (8%)	0	100	100
9	AX	141/143 (99%)	117 (83%)	23 (16%)	1 (1%)	18	51
10	AM	117/119 (98%)	93 (80%)	24 (20%)	0	100	100
11	Ad	50/52 (96%)	28 (56%)	21 (42%)	1 (2%)	6	32
12	AN	148/150 (99%)	138 (93%)	10 (7%)	0	100	100
13	AL	153/155 (99%)	125 (82%)	28 (18%)	0	100	100
14	AR	118/120 (98%)	105 (89%)	13 (11%)	0	100	100
15	AP	122/124 (98%)	102 (84%)	20 (16%)	0	100	100
16	AV	80/82 (98%)	65 (81%)	15 (19%)	0	100	100
17	AY	124/126 (98%)	102 (82%)	22 (18%)	0	100	100
18	AZ	72/74 (97%)	65 (90%)	7 (10%)	0	100	100
19	Aa	105/107 (98%)	78 (74%)	26 (25%)	1 (1%)	12	44
20	Ab	82/84 (98%)	63 (77%)	19 (23%)	0	100	100
21	AD	225/227 (99%)	191 (85%)	30 (13%)	4 (2%)	6	34
22	Ae	56/58 (97%)	38 (68%)	18 (32%)	0	100	100
23	Af	78/80 (98%)	62 (80%)	16 (20%)	0	100	100
24	AJ	179/181 (99%)	148 (83%)	28 (16%)	3 (2%)	7	35
25	Ca	147/149 (99%)	118 (80%)	27 (18%)	2 (1%)	9	38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	CN	201/203 (99%)	159 (79%)	40 (20%)	2 (1%)	12	44
27	CI	215/217 (99%)	182 (85%)	32 (15%)	1 (0%)	24	57
28	CD	288/290 (99%)	244 (85%)	43 (15%)	1 (0%)	36	67
29	CQ	185/187 (99%)	164 (89%)	21 (11%)	0	100	100
30	CR	201/203 (99%)	179 (89%)	22 (11%)	0	100	100
31	CS	171/173 (99%)	121 (71%)	43 (25%)	7 (4%)	2	19
32	CT	156/158 (99%)	128 (82%)	26 (17%)	2 (1%)	9	39
33	CP	183/185 (99%)	153 (84%)	30 (16%)	0	100	100
34	CX	118/120 (98%)	95 (80%)	22 (19%)	1 (1%)	16	49
35	CY	129/131 (98%)	115 (89%)	14 (11%)	0	100	100
36	CZ	132/134 (98%)	113 (86%)	18 (14%)	1 (1%)	16	49
37	Cr	132/134 (98%)	95 (72%)	31 (24%)	6 (4%)	2	17
38	Ch	121/123 (98%)	108 (89%)	13 (11%)	0	100	100
39	Cb	73/75 (97%)	57 (78%)	15 (20%)	1 (1%)	9	38
40	Cc	98/100 (98%)	92 (94%)	6 (6%)	0	100	100
41	Ce	130/132 (98%)	112 (86%)	15 (12%)	3 (2%)	5	30
42	Cf	155/157 (99%)	121 (78%)	32 (21%)	2 (1%)	9	39
43	Ci	111/113 (98%)	82 (74%)	27 (24%)	2 (2%)	6	34
44	Ck	68/70 (97%)	61 (90%)	7 (10%)	0	100	100
45	Cl	48/50 (96%)	37 (77%)	11 (23%)	0	100	100
46	Cm	50/52 (96%)	38 (76%)	12 (24%)	0	100	100
47	Cn	23/25 (92%)	23 (100%)	0	0	100	100
48	Cp	89/91 (98%)	78 (88%)	11 (12%)	0	100	100
49	Co	102/104 (98%)	77 (76%)	22 (22%)	3 (3%)	3	26
50	CJ	180/182 (99%)	148 (82%)	31 (17%)	1 (1%)	21	54
51	CH	188/190 (99%)	162 (86%)	23 (12%)	3 (2%)	7	36
52	CE	226/228 (99%)	167 (74%)	55 (24%)	4 (2%)	6	34
53	CG	239/241 (99%)	207 (87%)	31 (13%)	1 (0%)	30	62
57	Cz	215/217 (99%)	196 (91%)	19 (9%)	0	100	100
60	AE	259/261 (99%)	217 (84%)	40 (15%)	2 (1%)	16	49
61	AG	229/231 (99%)	207 (90%)	22 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
62	AH	192/194 (99%)	156 (81%)	35 (18%)	1 (0%)	24	57
63	AI	205/207 (99%)	157 (77%)	47 (23%)	1 (0%)	24	57
64	AQ	146/148 (99%)	123 (84%)	23 (16%)	0	100	100
65	CO	203/205 (99%)	172 (85%)	27 (13%)	4 (2%)	6	32
66	CL	208/210 (99%)	147 (71%)	49 (24%)	12 (6%)	1	13
67	CV	132/134 (98%)	120 (91%)	12 (9%)	0	100	100
68	CM	157/159 (99%)	130 (83%)	26 (17%)	1 (1%)	21	54
69	DA	346/370 (94%)	308 (89%)	37 (11%)	1 (0%)	36	67
70	AK	88/90 (98%)	72 (82%)	16 (18%)	0	100	100
71	AT	128/143 (90%)	100 (78%)	26 (20%)	2 (2%)	7	36
72	AF	187/189 (99%)	145 (78%)	41 (22%)	1 (0%)	24	57
73	AO	125/127 (98%)	100 (80%)	25 (20%)	0	100	100
74	Ac	60/62 (97%)	51 (85%)	9 (15%)	0	100	100
75	AW	127/129 (98%)	116 (91%)	11 (9%)	0	100	100
76	CW	56/58 (97%)	47 (84%)	7 (12%)	2 (4%)	2	22
77	Cg	101/103 (98%)	88 (87%)	13 (13%)	0	100	100
78	CU	94/96 (98%)	71 (76%)	23 (24%)	0	100	100
79	Cj	83/87 (95%)	67 (81%)	14 (17%)	2 (2%)	4	29
80	CF	221/223 (99%)	191 (86%)	26 (12%)	4 (2%)	6	34
81	Cd	106/108 (98%)	92 (87%)	14 (13%)	0	100	100
82	AS	132/134 (98%)	116 (88%)	16 (12%)	0	100	100
All	All	11937/12128 (98%)	9952 (83%)	1888 (16%)	97 (1%)	18	49

5 of 97 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	CA	196	TRP
3	AB	120	TRP
25	Ca	79	LEU
63	AI	99	ASN
65	CO	112	SER

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%)	188 (99%)	2 (1%)	65	74
2	CA	195/195 (100%)	185 (95%)	10 (5%)	21	48
3	AB	199/199 (100%)	196 (98%)	3 (2%)	57	71
4	CB	349/349 (100%)	342 (98%)	7 (2%)	48	67
5	AC	188/188 (100%)	182 (97%)	6 (3%)	34	59
6	CC	323/323 (100%)	312 (97%)	11 (3%)	32	57
7	Ag	280/280 (100%)	278 (99%)	2 (1%)	76	78
8	AU	95/95 (100%)	94 (99%)	1 (1%)	65	74
9	AX	116/116 (100%)	113 (97%)	3 (3%)	40	62
10	AM	104/104 (100%)	103 (99%)	1 (1%)	68	75
11	Ad	45/45 (100%)	44 (98%)	1 (2%)	45	65
12	AN	130/130 (100%)	129 (99%)	1 (1%)	73	77
13	AL	138/138 (100%)	137 (99%)	1 (1%)	76	78
14	AR	108/108 (100%)	107 (99%)	1 (1%)	70	76
15	AP	111/111 (100%)	111 (100%)	0	100	100
16	AV	67/67 (100%)	65 (97%)	2 (3%)	36	60
17	AY	105/106 (99%)	102 (97%)	3 (3%)	37	60
18	AZ	67/67 (100%)	66 (98%)	1 (2%)	57	71
19	Aa	94/94 (100%)	92 (98%)	2 (2%)	47	66
20	Ab	72/72 (100%)	70 (97%)	2 (3%)	38	61
21	AD	192/192 (100%)	190 (99%)	2 (1%)	68	75
22	Ae	47/47 (100%)	47 (100%)	0	100	100
23	Af	70/70 (100%)	70 (100%)	0	100	100
24	AJ	161/161 (100%)	158 (98%)	3 (2%)	50	68
25	Ca	122/122 (100%)	121 (99%)	1 (1%)	73	77
26	CN	174/174 (100%)	169 (97%)	5 (3%)	37	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	CI	187/187 (100%)	182 (97%)	5 (3%)	39	62
28	CD	241/241 (100%)	237 (98%)	4 (2%)	53	70
29	CQ	164/164 (100%)	154 (94%)	10 (6%)	17	43
30	CR	176/176 (100%)	173 (98%)	3 (2%)	53	70
31	CS	156/156 (100%)	147 (94%)	9 (6%)	18	44
32	CT	137/137 (100%)	132 (96%)	5 (4%)	31	57
33	CP	160/160 (100%)	153 (96%)	7 (4%)	25	51
34	CX	106/106 (100%)	103 (97%)	3 (3%)	38	61
35	CY	116/116 (100%)	110 (95%)	6 (5%)	21	47
36	CZ	121/121 (100%)	120 (99%)	1 (1%)	73	77
37	Cr	112/112 (100%)	105 (94%)	7 (6%)	16	42
38	Ch	112/112 (100%)	110 (98%)	2 (2%)	51	69
39	Cb	67/67 (100%)	64 (96%)	3 (4%)	24	50
40	Cc	84/84 (100%)	84 (100%)	0	100	100
41	Ce	120/120 (100%)	117 (98%)	3 (2%)	42	63
42	Cf	123/123 (100%)	119 (97%)	4 (3%)	33	58
43	Ci	100/100 (100%)	97 (97%)	3 (3%)	36	60
44	Ck	65/65 (100%)	63 (97%)	2 (3%)	35	59
45	Cl	45/45 (100%)	44 (98%)	1 (2%)	45	65
46	Cm	48/48 (100%)	46 (96%)	2 (4%)	26	52
47	Cn	23/23 (100%)	22 (96%)	1 (4%)	26	51
48	Cp	74/74 (100%)	70 (95%)	4 (5%)	20	46
49	Co	94/94 (100%)	93 (99%)	1 (1%)	65	74
50	CJ	155/155 (100%)	154 (99%)	1 (1%)	78	79
51	CH	169/169 (100%)	163 (96%)	6 (4%)	31	57
52	CE	197/197 (100%)	194 (98%)	3 (2%)	57	71
53	CG	210/210 (100%)	205 (98%)	5 (2%)	43	64
57	Cz	190/190 (100%)	189 (100%)	1 (0%)	81	80
60	AE	220/220 (100%)	218 (99%)	2 (1%)	70	76
61	AG	200/200 (100%)	198 (99%)	2 (1%)	68	75
62	AH	175/175 (100%)	171 (98%)	4 (2%)	44	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
63	AI	175/175 (100%)	172 (98%)	3 (2%)	53	70
64	AQ	122/122 (100%)	121 (99%)	1 (1%)	73	77
65	CO	175/175 (100%)	170 (97%)	5 (3%)	37	60
66	CL	173/173 (100%)	169 (98%)	4 (2%)	44	64
67	CV	101/101 (100%)	98 (97%)	3 (3%)	36	60
68	CM	138/138 (100%)	133 (96%)	5 (4%)	31	57
69	DA	294/310 (95%)	288 (98%)	6 (2%)	48	67
70	AK	81/81 (100%)	81 (100%)	0	100	100
71	AT	107/116 (92%)	107 (100%)	0	100	100
72	AF	160/160 (100%)	159 (99%)	1 (1%)	78	79
73	AO	98/98 (100%)	95 (97%)	3 (3%)	35	59
74	Ac	54/54 (100%)	52 (96%)	2 (4%)	30	56
75	AW	113/113 (100%)	110 (97%)	3 (3%)	39	62
76	CW	52/52 (100%)	50 (96%)	2 (4%)	29	55
77	Cg	95/95 (100%)	88 (93%)	7 (7%)	13	37
78	CU	90/90 (100%)	87 (97%)	3 (3%)	33	58
79	Cj	71/71 (100%)	56 (79%)	15 (21%)	1	6
80	CF	197/197 (100%)	192 (98%)	5 (2%)	42	63
81	Cd	100/100 (100%)	93 (93%)	7 (7%)	14	39
82	AS	120/120 (100%)	119 (99%)	1 (1%)	73	77
All	All	10405/10431 (100%)	10148 (98%)	257 (2%)	42	63

5 of 257 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
79	Cj	21	ARG
79	Cj	63	ARG
31	CS	77	ASN
31	CS	38	ILE
79	Cj	71	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 88 such sidechains are listed below:

Mol	Chain	Res	Type
51	CH	40	HIS
69	DA	275	HIS
51	CH	107	ASN
63	AI	162	GLN
71	AT	85	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
54	A9	29/30 (96%)	6 (20%)	1 (3%)
55	A7	119/120 (99%)	30 (25%)	1 (0%)
56	A8	122/123 (99%)	53 (43%)	5 (4%)
58	B2	1788/1995 (89%)	673 (37%)	37 (2%)
59	A5	3561/3974 (89%)	1379 (38%)	108 (3%)
All	All	5619/6242 (90%)	2141 (38%)	152 (2%)

5 of 2141 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
54	A9	6	G
54	A9	9	C
54	A9	21	G
54	A9	22	A
54	A9	24	G

5 of 152 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
59	A5	2126	A
59	A5	3708	U
59	A5	2166	U
59	A5	3235	A
59	A5	3891	U

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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
59	A5	2
58	B2	2
79	Cj	1
33	CP	1
26	CN	1

The worst 5 of 7 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A5	2896:U	O3'	2897:G	P	6.34
1	B2	1236:C	O3'	1237:G	P	6.15
1	B2	1817:C	O3'	1818:U	P	4.73
1	Cj	29:LEU	C	30:GLN	N	4.63
1	A5	2819:A	O3'	2820:G	P	3.28

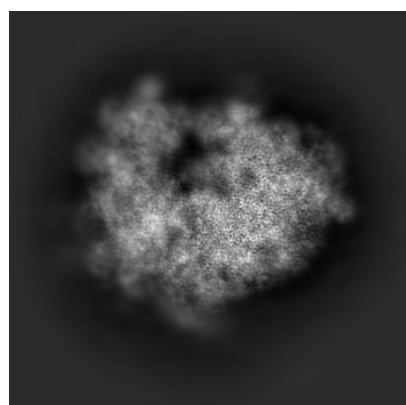
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10622. These allow visual inspection of the internal detail of the map and identification of artifacts.

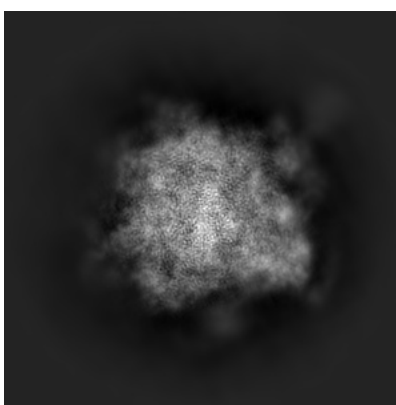
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

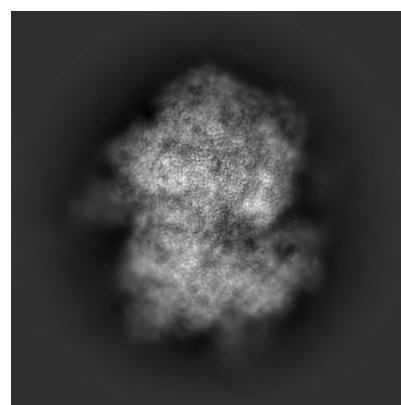
6.1.1 Primary map



X



Y

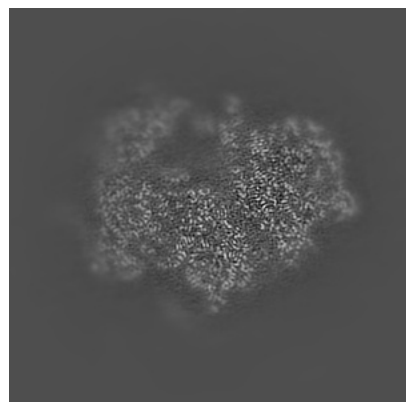


Z

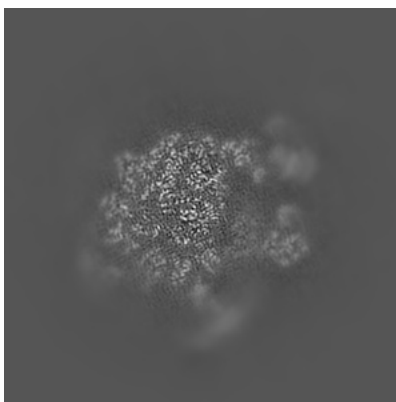
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

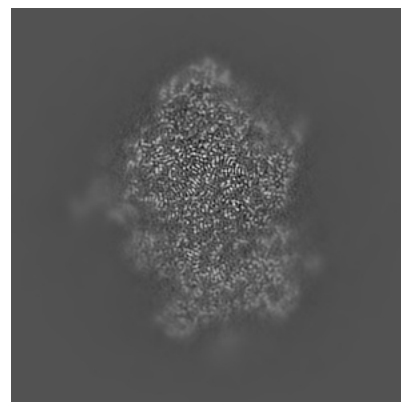
6.2.1 Primary map



X Index: 200



Y Index: 200

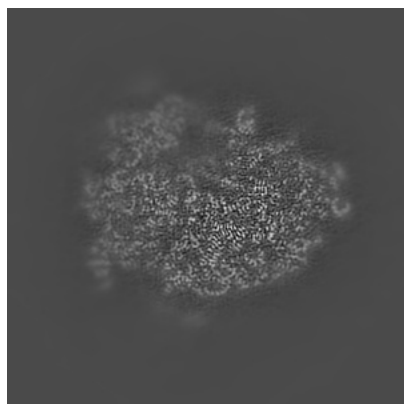


Z Index: 200

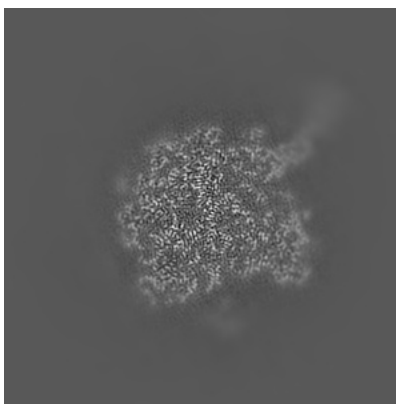
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

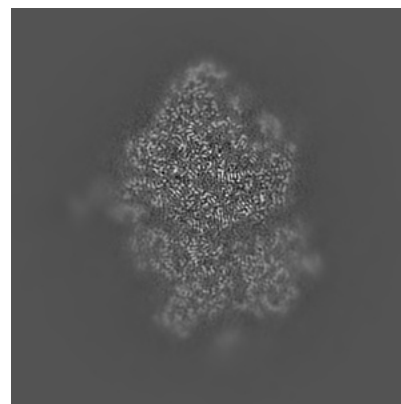
6.3.1 Primary map



X Index: 182



Y Index: 233

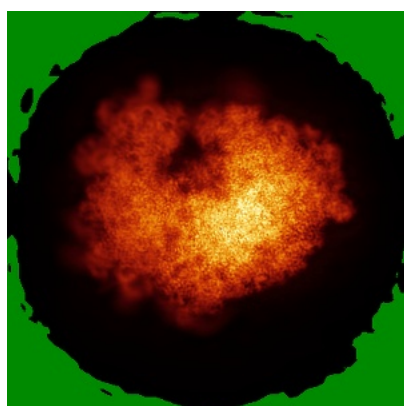


Z Index: 195

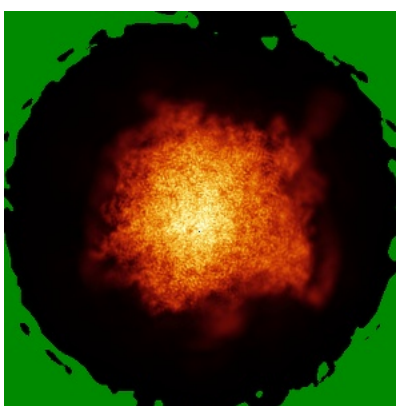
The images above show the largest variance slices of the map in three orthogonal directions.

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

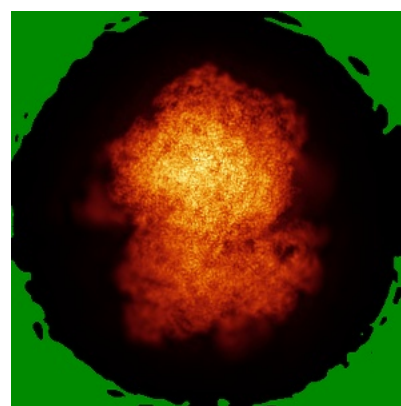
6.4.1 Primary map



X



Y

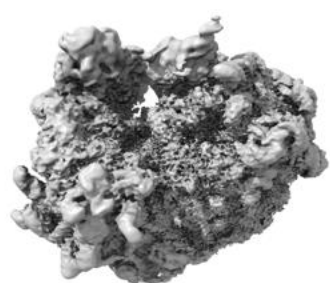


Z

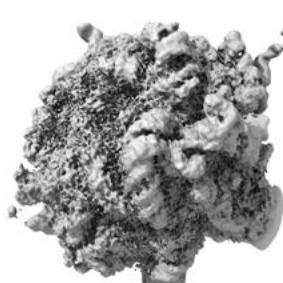
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

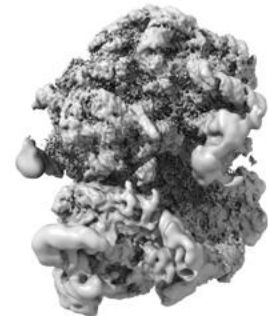
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.025. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

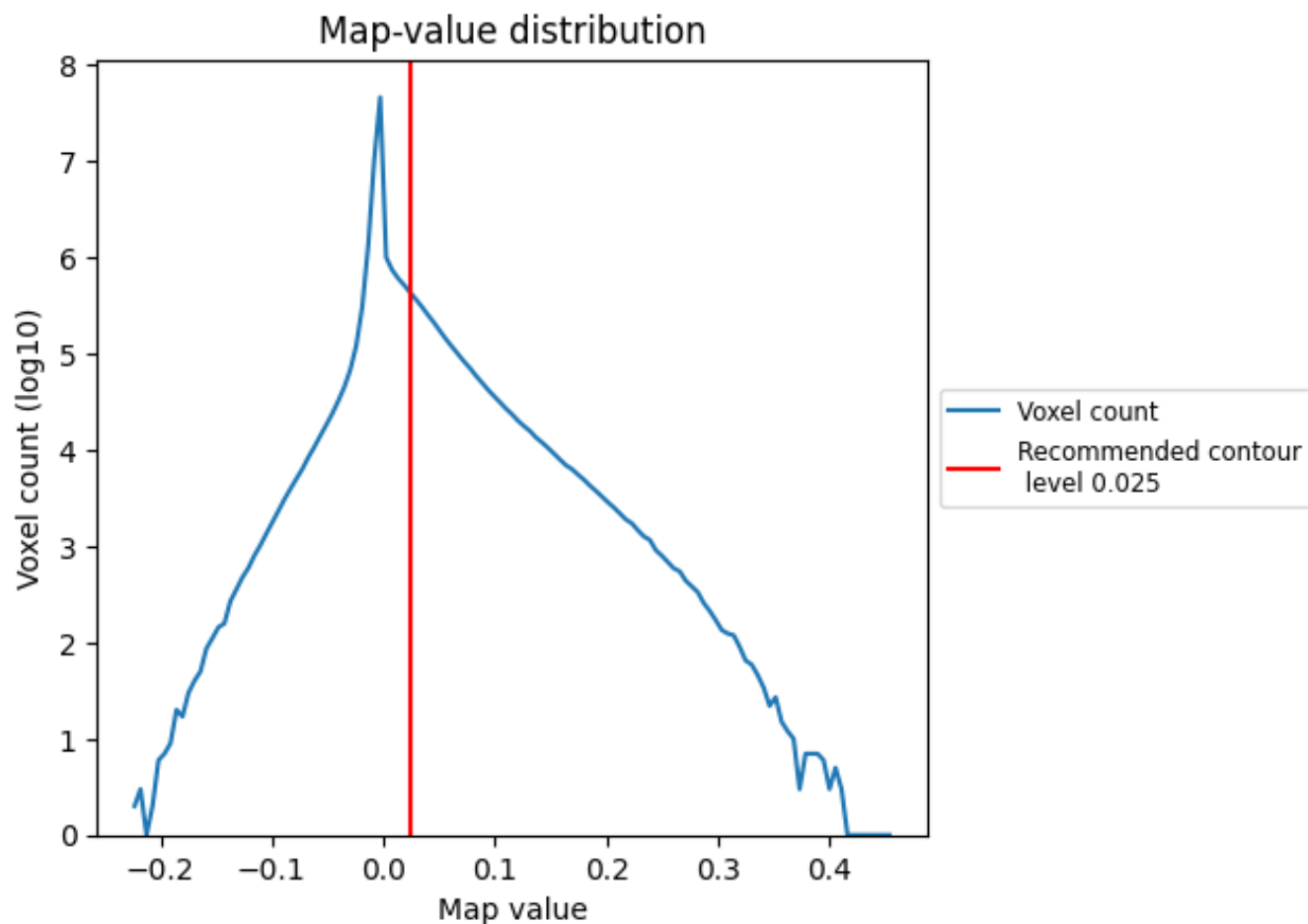
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

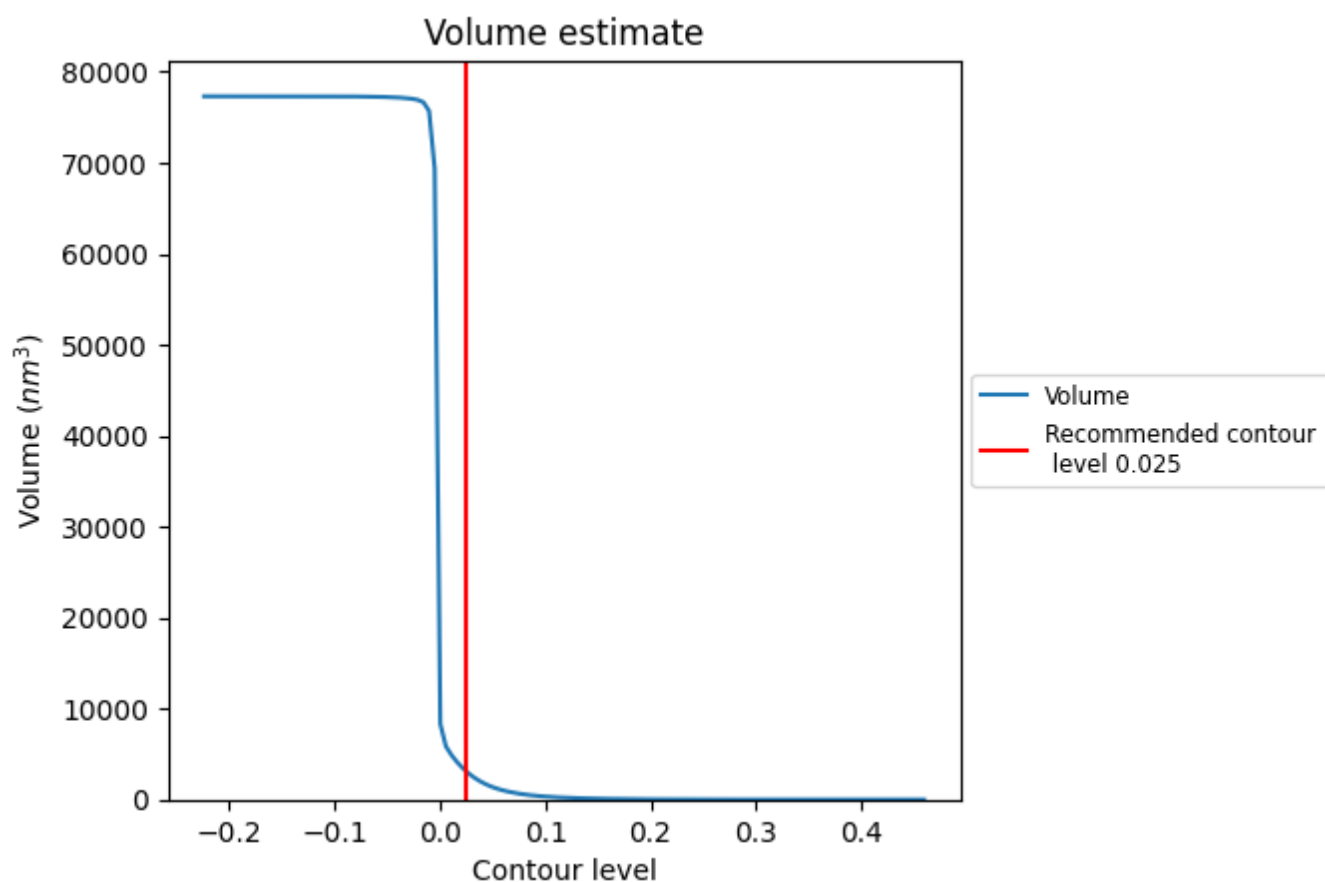
This section contains the results of statistical analysis of the map.

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.

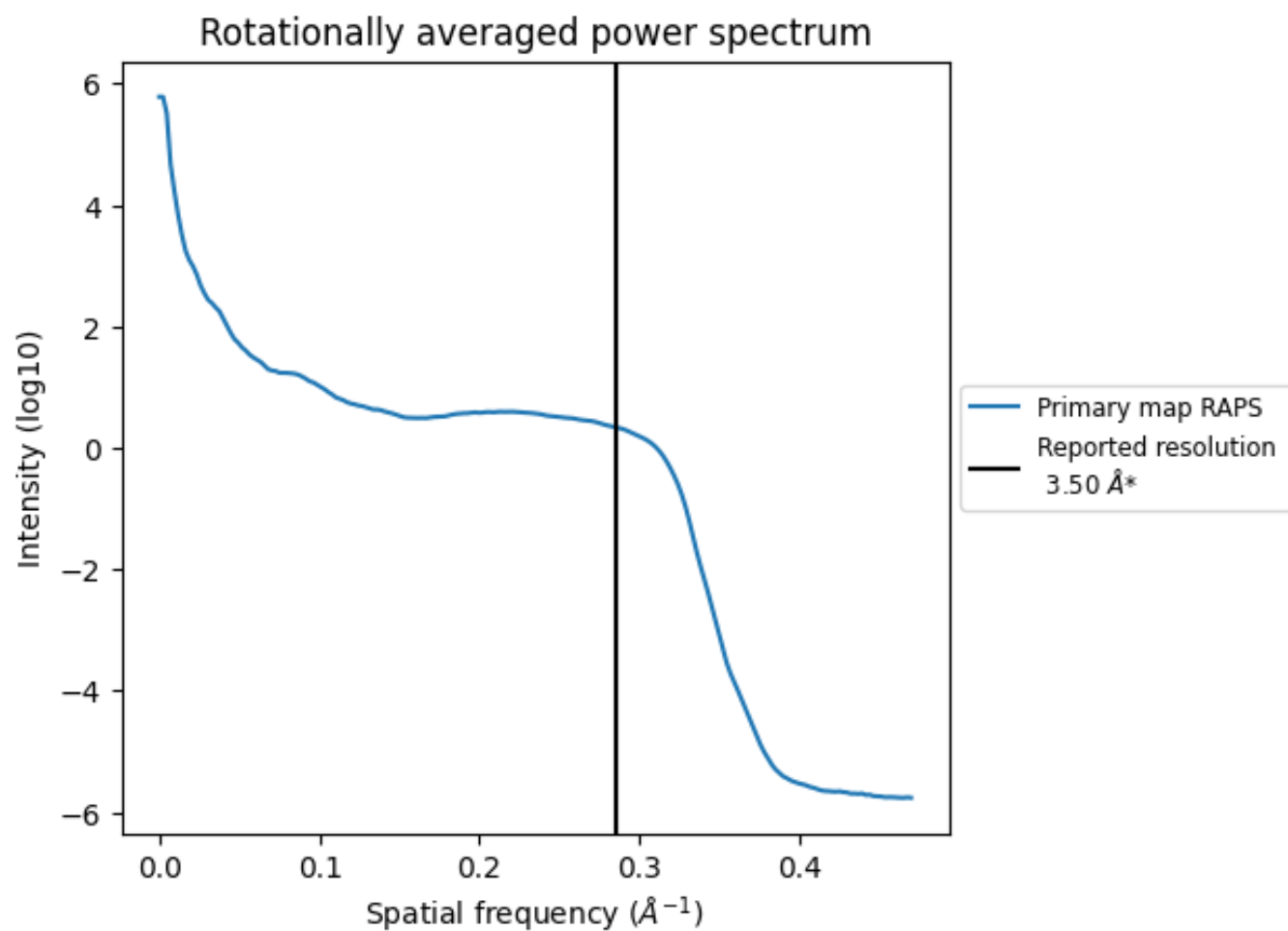
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3140 nm³; this corresponds to an approximate mass of 2836 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 ⓘ

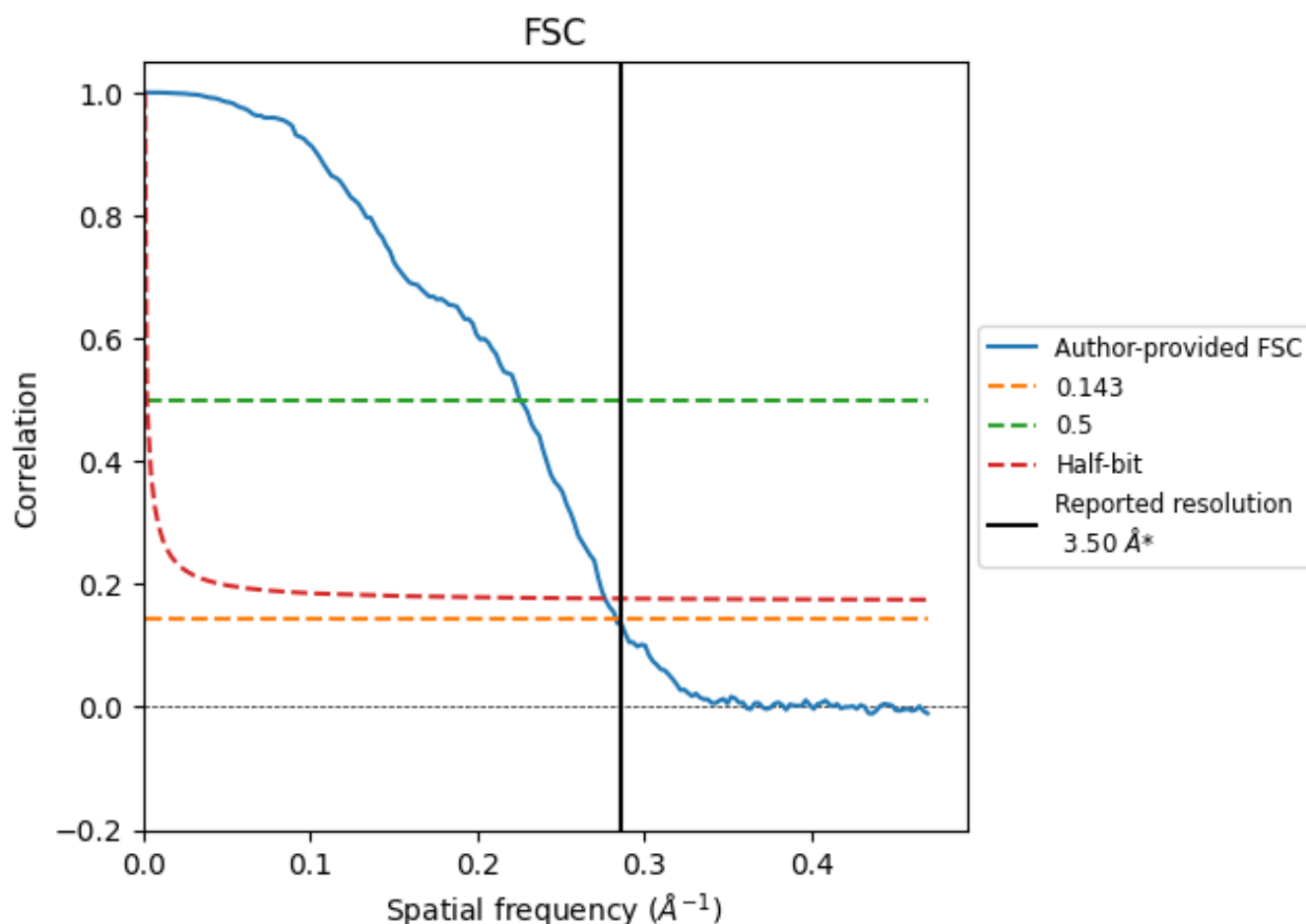


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

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 0.286 Å⁻¹

8.2 Resolution estimates [i](#)

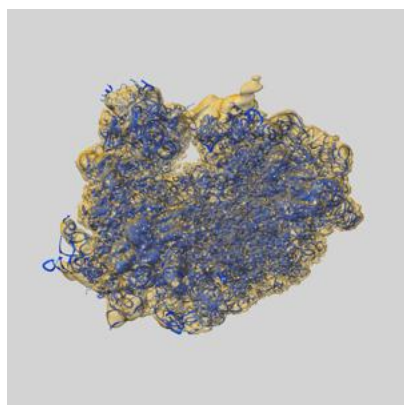
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.53	4.43	3.62
Unmasked-calculated*	-	-	-

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

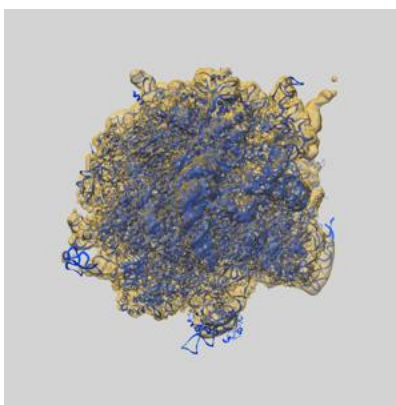
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10622 and PDB model 6XU6. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

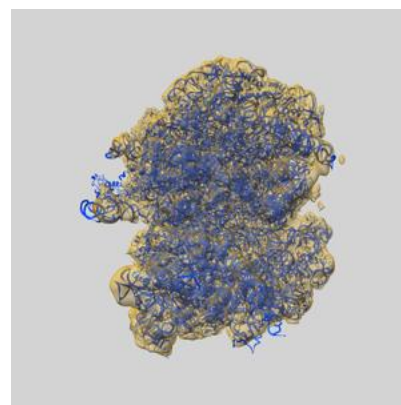
9.1 Map-model overlay [i](#)



X



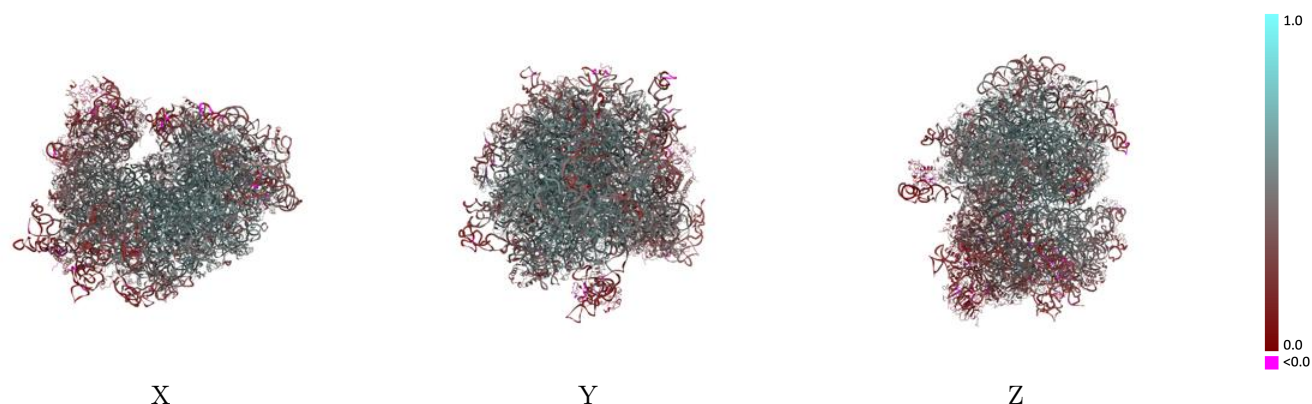
Y



Z

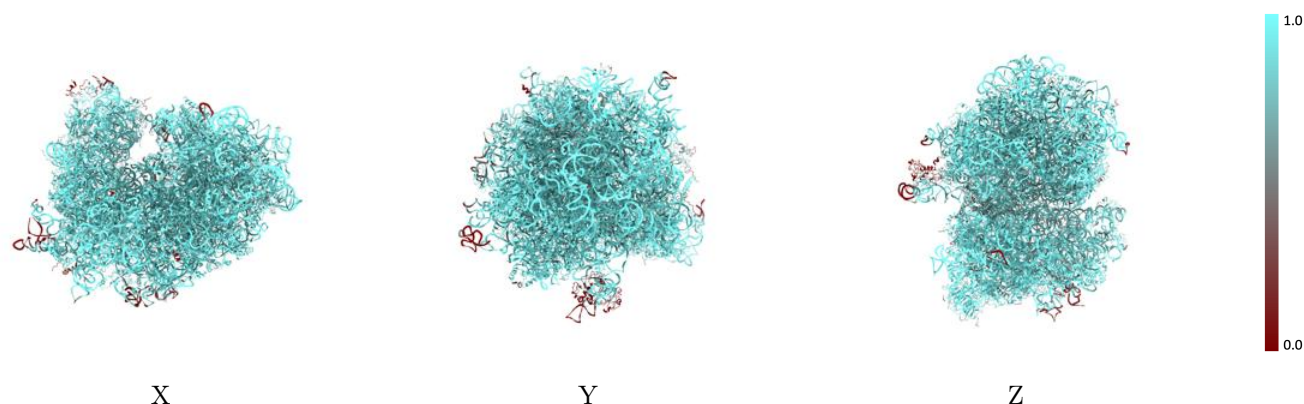
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



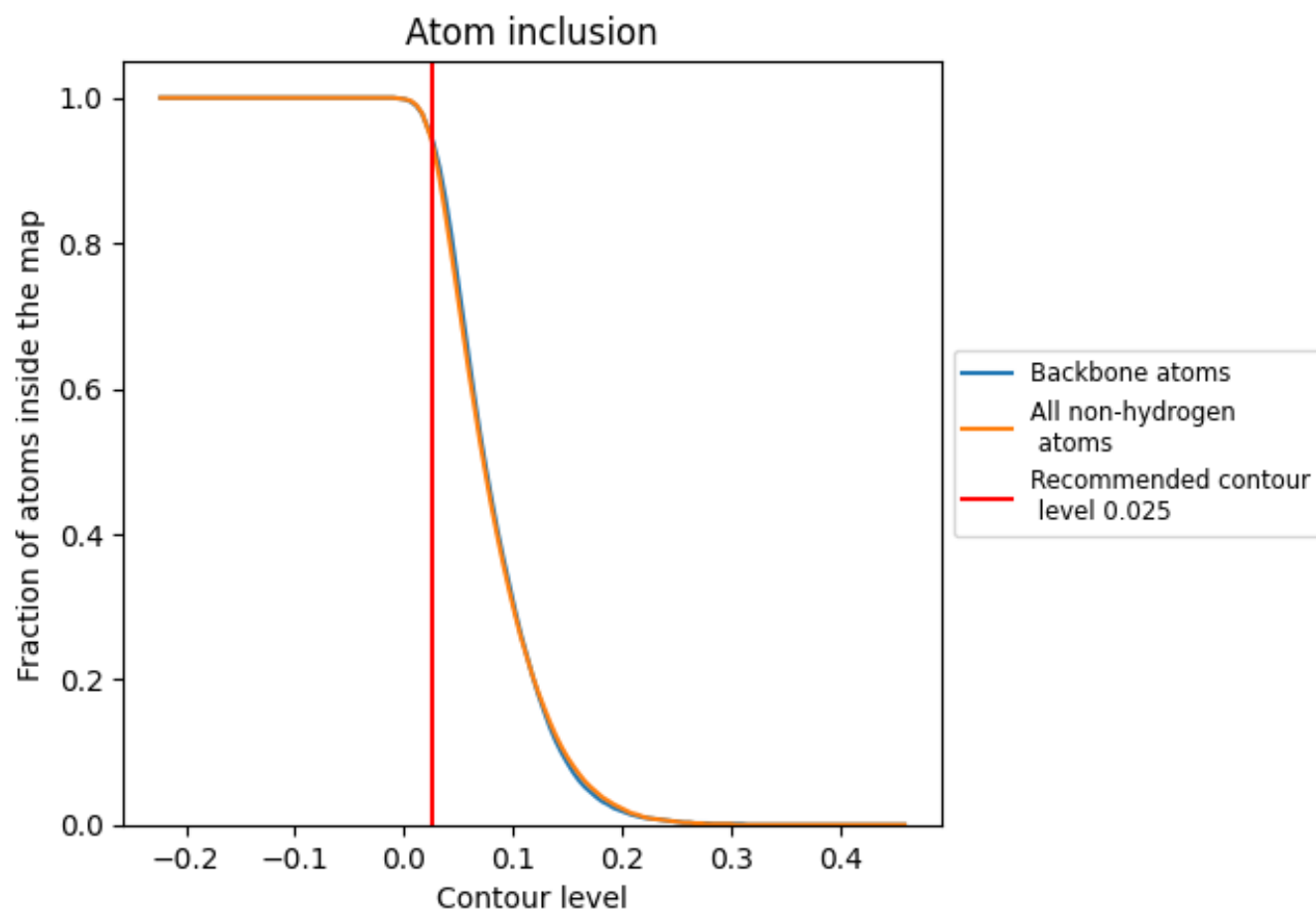
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.025).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 94% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9440	 0.4410
A5	 0.9640	 0.4840
A7	 0.9990	 0.4850
A8	 0.9870	 0.5210
A9	 0.9940	 0.4940
AA	 0.8870	 0.3470
AB	 0.9190	 0.4380
AC	 0.9360	 0.4480
AD	 0.8880	 0.2990
AE	 0.9630	 0.4490
AF	 0.9160	 0.2840
AG	 0.9540	 0.3220
AH	 0.9030	 0.3240
AI	 0.9390	 0.4290
AJ	 0.9450	 0.3940
AK	 0.9340	 0.2060
AL	 0.8610	 0.4770
AM	 0.5280	 0.1170
AN	 0.9620	 0.5010
AO	 0.9670	 0.4680
AP	 0.8310	 0.2200
AQ	 0.9470	 0.2530
AR	 0.9110	 0.2830
AS	 0.9310	 0.2540
AT	 0.9130	 0.2040
AU	 0.9270	 0.2790
AV	 0.9520	 0.4260
AW	 0.9770	 0.5070
AX	 0.9350	 0.5100
AY	 0.9360	 0.3400
AZ	 0.8780	 0.2170
Aa	 0.8890	 0.4820
Ab	 0.9080	 0.3750
Ac	 0.9080	 0.3330
Ad	 0.9690	 0.3290



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Chain	Atom inclusion	Q-score
Ae	 0.9310	 0.3510
Af	 0.5690	 0.1060
Ag	 0.9310	 0.1580
B2	 0.9700	 0.3840
CA	 0.9710	 0.5730
CB	 0.9560	 0.5360
CC	 0.9660	 0.5180
CD	 0.9700	 0.4290
CE	 0.8890	 0.3810
CF	 0.9920	 0.5550
CG	 0.9070	 0.4440
CH	 0.9580	 0.4830
CI	 0.8790	 0.4360
CJ	 0.9260	 0.3830
CL	 0.9140	 0.4660
CM	 0.9270	 0.4120
CN	 0.9830	 0.5740
CO	 0.9610	 0.5380
CP	 0.8780	 0.5160
CQ	 0.9790	 0.5650
CR	 0.8830	 0.4670
CS	 0.9550	 0.5180
CT	 0.9640	 0.5210
CU	 0.9420	 0.3730
CV	 0.9770	 0.5750
CW	 0.9810	 0.5670
CX	 0.9630	 0.5110
CY	 0.9830	 0.5240
CZ	 0.9640	 0.4670
Ca	 0.9790	 0.5580
Cb	 0.9670	 0.4480
Cc	 0.9640	 0.4970
Cd	 0.9180	 0.4220
Ce	 0.9740	 0.5700
Cf	 0.9480	 0.4770
Cg	 0.9830	 0.5590
Ch	 0.9700	 0.5100
Ci	 0.9360	 0.4540
Cj	 0.9130	 0.4700
Ck	 0.9500	 0.4440
Cl	 0.9760	 0.5700
Cm	 0.9640	 0.4880

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Chain	Atom inclusion	Q-score
Cn	 0.9670	 0.5820
Co	 0.9470	 0.5330
Cp	 0.9690	 0.5670
Cr	 0.9060	 0.4720
Cz	 0.2310	 0.0950
DA	 0.7690	 0.4250