



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 03:55 PM UTC

PDB ID : 6XU8 / pdb_00006xu8
EMDB ID : EMD-10624
Title : Drosophila melanogaster Ovary 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 : 3.00 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

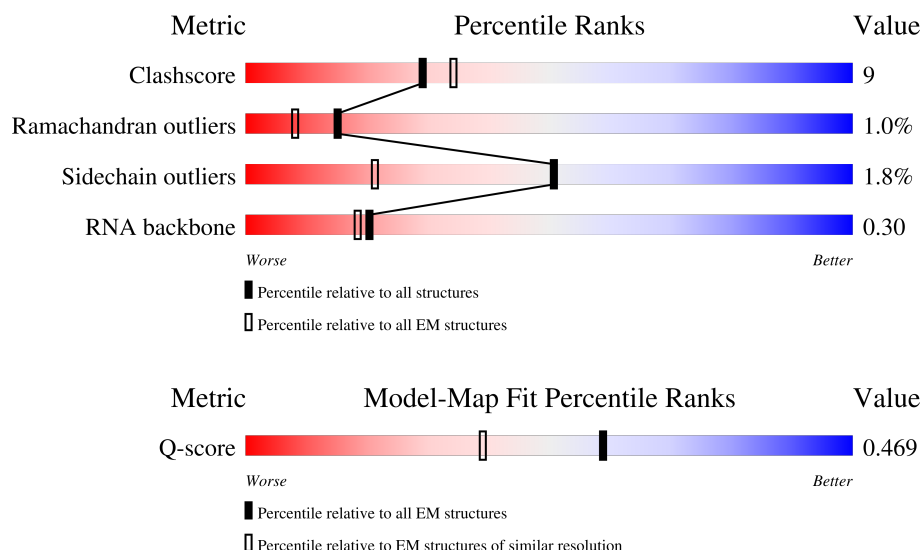
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.00 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.



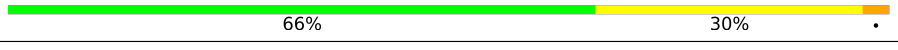
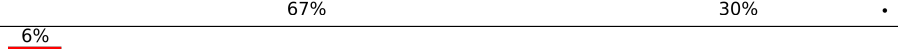
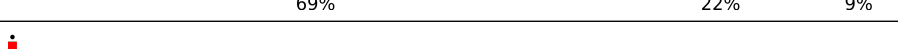
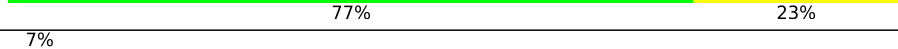
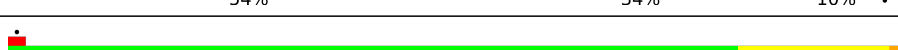
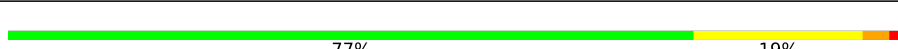
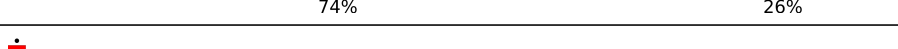
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

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	CO	205	
2	CL	210	
3	CV	134	

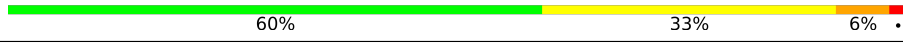
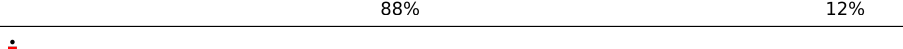
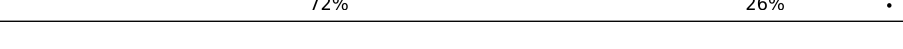
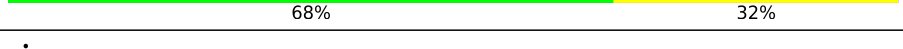
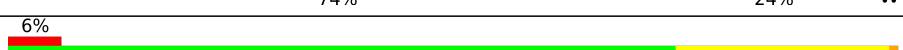
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Mol	Chain	Length	Quality of chain
4	CM	159	
5	Ca	149	
6	CN	203	
7	CI	217	
8	CD	290	
9	CQ	187	
10	CR	203	
11	CA	253	
12	CS	173	
13	CT	158	
14	CP	185	
15	CX	120	
16	CY	131	
17	CZ	134	
18	Cr	134	
19	Ch	123	
20	Cb	75	
21	CB	414	
22	CF	226	
23	Cc	100	
24	Ce	132	
25	Cf	157	
26	Ci	113	
27	Ck	70	
28	Cl	50	

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Mol	Chain	Length	Quality of chain
29	CC	392	
30	Cm	52	
31	Cn	25	
32	Cp	91	
33	Co	104	
34	CJ	182	
35	CH	190	
36	CE	228	
37	CG	241	
38	A9	30	
39	A7	120	
40	A8	123	
41	Ag	318	
42	AU	102	
43	AO	127	
44	AX	143	
45	AM	119	
46	Ad	52	
47	AN	150	
48	AL	155	
49	AR	120	
50	AP	124	
51	AB	220	
52	AA	218	
53	AV	82	

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Mol	Chain	Length	Quality of chain
54	AY	126	
55	AZ	74	
56	Aa	107	
57	Ab	84	
58	AD	227	
59	Ae	58	
60	Af	80	
61	AJ	181	
62	AE	261	
63	AC	227	
64	AG	231	
65	AH	194	
66	AI	207	
67	AQ	148	
68	Cz	217	
69	A5	3703	
70	B2	1936	
71	AW	129	
72	AT	126	
73	AK	90	
74	AF	189	
75	Ac	62	
76	CU	99	
77	Cj	87	
78	CW	60	

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Mol	Chain	Length	Quality of chain
79	Cg	103	 73% 22% 5%
80	Cd	107	 51% 43% 6%
81	AS	136	 18% 50% 50%

2 Entry composition

There are 81 unique types of molecules in this entry. The entry contains 216955 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 60S ribosomal protein L13a.

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

- Molecule 2 is a protein called 60S ribosomal protein L13.

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

- Molecule 3 is a protein called 60S ribosomal protein L23.

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

- Molecule 4 is a protein called 60S ribosomal protein L14.

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

- Molecule 5 is a protein called 60S ribosomal protein L27a.

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

- Molecule 6 is a protein called 60S ribosomal protein L15.

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

- Molecule 7 is a protein called 60S ribosomal protein L10.

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

- Molecule 8 is a protein called 60S ribosomal protein L5.

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

- Molecule 9 is a protein called 60S ribosomal protein L18.

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

- Molecule 10 is a protein called 60S ribosomal protein L19.

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

- Molecule 11 is a protein called 60S ribosomal protein L8.

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

- Molecule 12 is a protein called 60S ribosomal protein L18a.

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

- Molecule 13 is a protein called RE62581p.

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

- Molecule 14 is a protein called 60S ribosomal protein L17.

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

- Molecule 15 is a protein called IP17216p.

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

- Molecule 16 is a protein called GEO07453p1.

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

- Molecule 17 is a protein called 60S ribosomal protein L27.

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

- Molecule 18 is a protein called 60S ribosomal protein L28.

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

- Molecule 19 is a protein called FI02809p.

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

- Molecule 20 is a protein called 60S ribosomal protein L29.

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

- Molecule 21 is a protein called 60S ribosomal protein L3.

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

- Molecule 22 is a protein called 60S ribosomal protein L7.

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

- Molecule 23 is a protein called RE25263p.

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

- Molecule 24 is a protein called 60S ribosomal protein L32.

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

- Molecule 25 is a protein called GEO07455p1.

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

- Molecule 26 is a protein called 60S ribosomal protein L36.

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

- Molecule 27 is a protein called 60S ribosomal protein L38.

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

- Molecule 28 is a protein called 60S ribosomal protein L39.

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

- Molecule 29 is a protein called 60S ribosomal protein L4.

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

- Molecule 30 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 31 is a protein called 60S ribosomal protein L41.

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

- Molecule 32 is a protein called 60S ribosomal protein L37a.

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

- Molecule 33 is a protein called TA01007p.

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

- Molecule 34 is a protein called 60S ribosomal protein L11.

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

- Molecule 35 is a protein called 60S ribosomal protein L9.

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

- Molecule 36 is a protein called Ribosomal protein L6, isoform A.

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

- Molecule 37 is a protein called 60S ribosomal protein L7a.

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

- Molecule 38 is a RNA chain called 2S ribosomal RNA.

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

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

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

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

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

- Molecule 41 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

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

- Molecule 42 is a protein called 40S ribosomal protein S20.

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

- Molecule 43 is a protein called 40S ribosomal protein S14a.

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

- Molecule 44 is a protein called 40S ribosomal protein S23.

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

- Molecule 45 is a protein called 40S ribosomal protein S12.

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

- Molecule 46 is a protein called 40S ribosomal protein S29.

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

- Molecule 47 is a protein called 40S ribosomal protein S13.

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

- Molecule 48 is a protein called 40S ribosomal protein S11.

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

- Molecule 49 is a protein called 40S ribosomal protein S17.

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

- Molecule 50 is a protein called GEO07301p1.

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

- Molecule 51 is a protein called 40S ribosomal protein S3a.

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

- Molecule 52 is a protein called 40S ribosomal protein SA.

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

- Molecule 53 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	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 54 is a protein called 40S ribosomal protein S24.

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

- Molecule 55 is a protein called 40S ribosomal protein S25.

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

- Molecule 56 is a protein called 40S ribosomal protein S26.

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

- Molecule 57 is a protein called 40S ribosomal protein S27.

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

- Molecule 58 is a protein called 40S ribosomal protein S3.

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

- Molecule 59 is a protein called 40S ribosomal protein S30.

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

- Molecule 60 is a protein called Ubiquitin-40S ribosomal protein S27a.

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

- Molecule 61 is a protein called 40S ribosomal protein S9.

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

- Molecule 62 is a protein called 40S ribosomal protein S4.

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

- Molecule 63 is a protein called 40S ribosomal protein S2.

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

- Molecule 64 is a protein called 40S ribosomal protein S6.

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

- Molecule 65 is a protein called 40S ribosomal protein S7.

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

- Molecule 66 is a protein called 40S ribosomal protein S8.

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

- Molecule 67 is a protein called 40S ribosomal protein S16.

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

- Molecule 68 is a protein called 60S ribosomal protein L10a-2.

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

- Molecule 69 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	A5	3703	Total	C	N	O	P	0	0
			77093	34436	13555	25401	3701		

- Molecule 70 is a RNA chain called 18S ribosomal RNA.

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

- Molecule 71 is a protein called 40S ribosomal protein S15Aa.

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

- Molecule 72 is a protein called 40S ribosomal protein S19a.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	AT	126	Total	C	N	O	S	0	0
			1000	635	192	170	3		

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AT	?	-	GLU	deletion	UNP P39018
AT	?	-	HIS	deletion	UNP P39018
AT	?	-	ALA	deletion	UNP P39018
AT	?	-	ARG	deletion	UNP P39018
AT	?	-	LEU	deletion	UNP P39018
AT	?	-	VAL	deletion	UNP P39018

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Chain	Residue	Modelled	Actual	Comment	Reference
AT	?	-	GLU	deletion	UNP P39018
AT	?	-	LYS	deletion	UNP P39018
AT	?	-	HIS	deletion	UNP P39018
AT	?	-	PRO	deletion	UNP P39018
AT	?	-	ASP	deletion	UNP P39018
AT	?	-	GLY	deletion	UNP P39018
AT	?	-	GLY	deletion	UNP P39018

- Molecule 73 is a protein called 40S ribosomal protein S10b.

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

- Molecule 74 is a protein called 40S ribosomal protein S5b.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	AF	189	Total	C	N	O	S	0	0
			1481	925	283	266	7		

- Molecule 75 is a protein called 40S ribosomal protein S28.

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

- Molecule 76 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	CU	99	Total	C	N	O	S	0	0
			825	530	144	149	2		

- Molecule 77 is a protein called Probable 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Cj	87	Total	C	N	O	S	0	0
			704	430	154	115	5		

- Molecule 78 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	CW	60	Total	C	N	O	S	0	0
			503	326	95	78	4		

- Molecule 79 is a protein called 60S ribosomal protein L34.

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

- Molecule 80 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Cd	107	Total	C	N	O	S	0	0
			893	556	176	159	2		

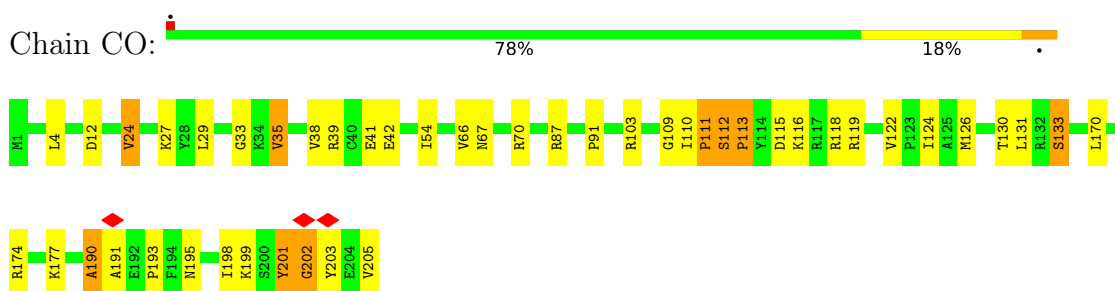
- Molecule 81 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	AS	136	Total	C	N	O	S	0	0
			1117	701	216	197	3		

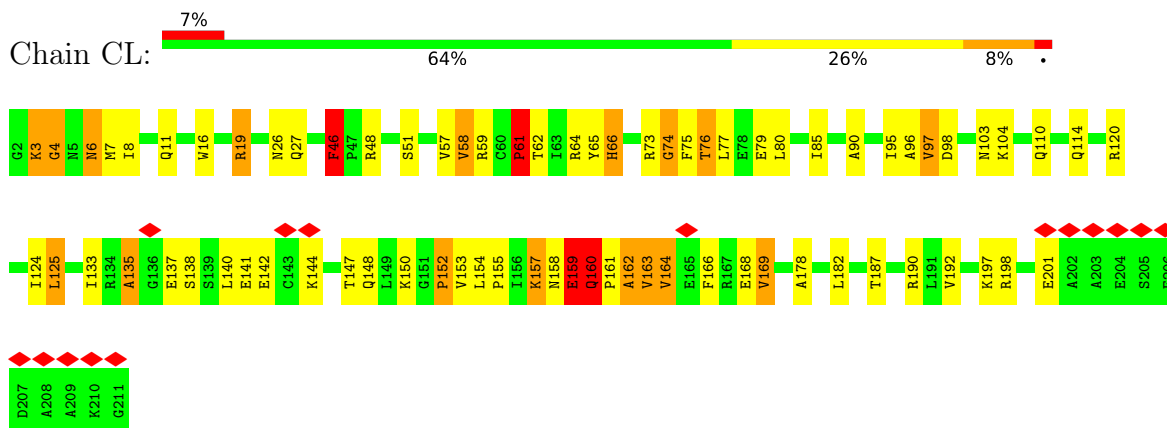
3 Residue-property plots

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.

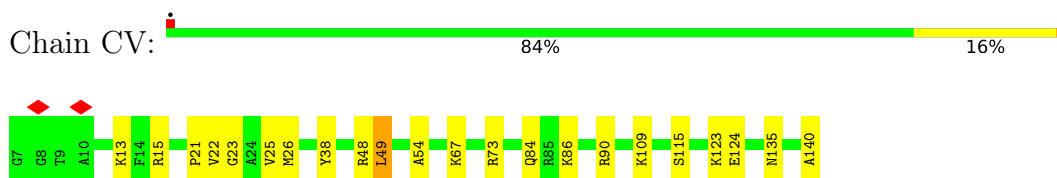
- Molecule 1: 60S ribosomal protein L13a



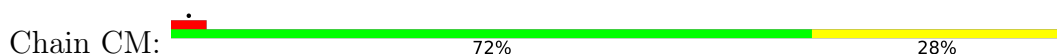
- Molecule 2: 60S ribosomal protein L13

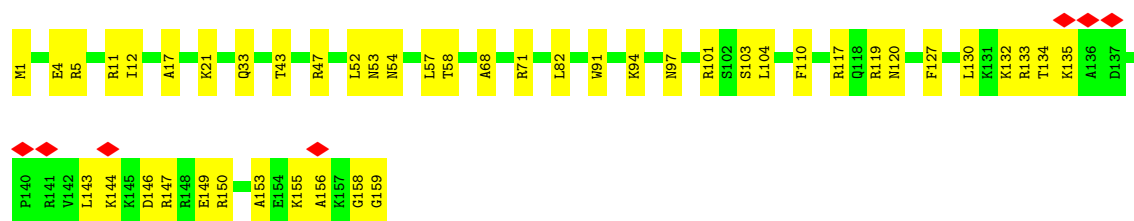


- Molecule 3: 60S ribosomal protein L23

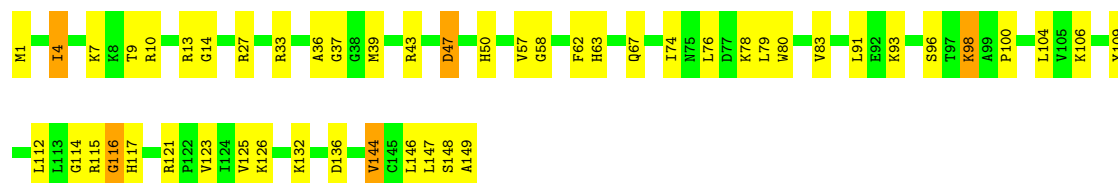


- Molecule 4: 60S ribosomal protein L14

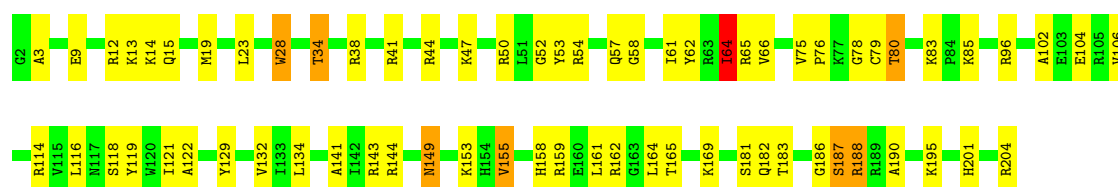




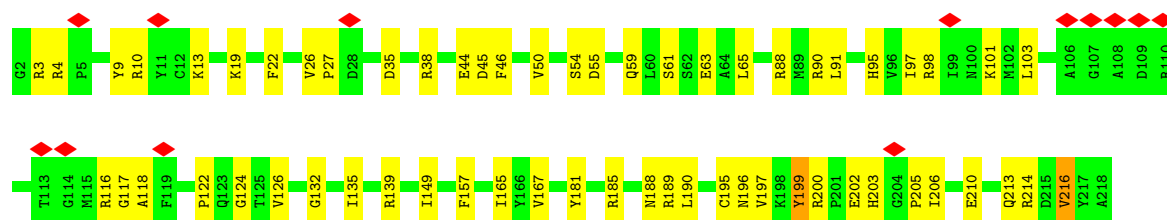
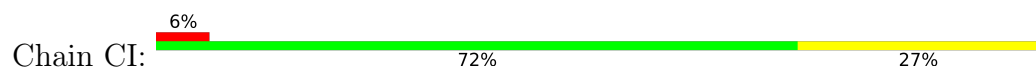
• Molecule 5: 60S ribosomal protein L27a



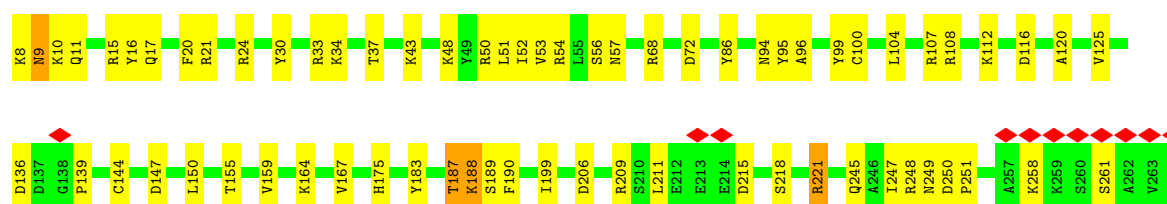
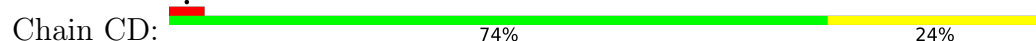
• Molecule 6: 60S ribosomal protein L15



• Molecule 7: 60S ribosomal protein L10



• Molecule 8: 60S ribosomal protein L5





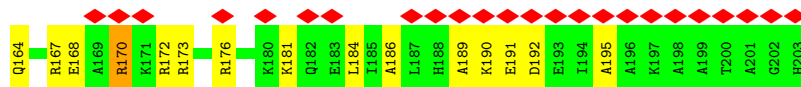
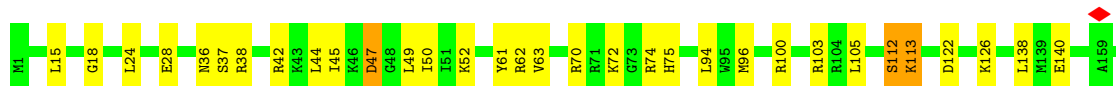
- Molecule 9: 60S ribosomal protein L18

Chain CQ: 68% 29% ..



- Molecule 10: 60S ribosomal protein L19

Chain CR: 12% 77% 21% .



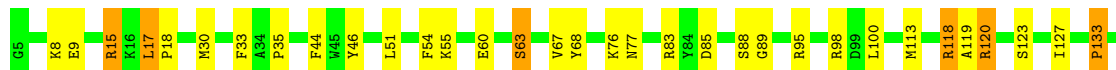
- Molecule 11: 60S ribosomal protein L8

Chain CA: 72% 27% .

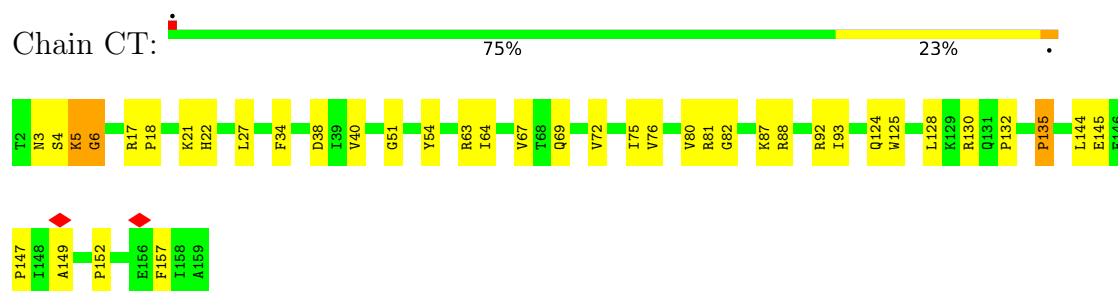


- Molecule 12: 60S ribosomal protein L18a

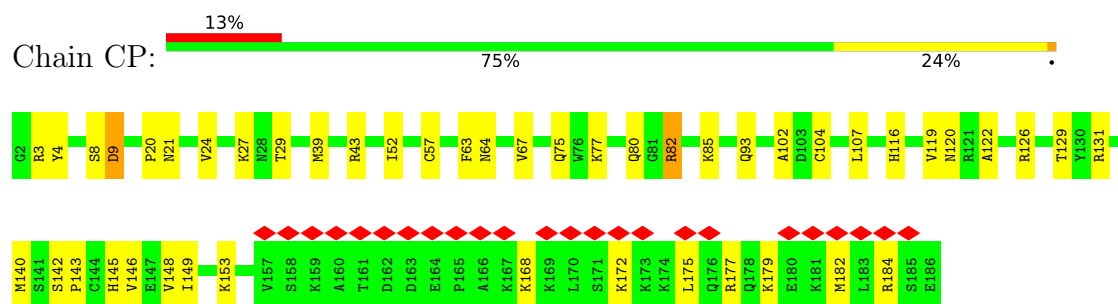
Chain CS: 69% 22% 9% .



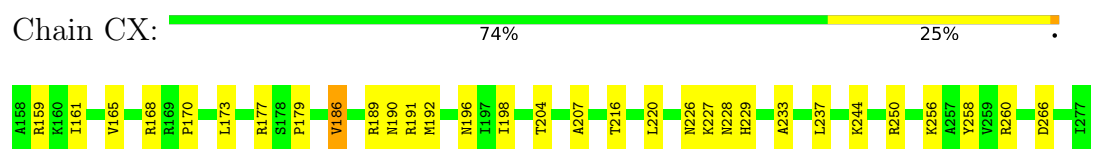
- Molecule 13: RE62581p



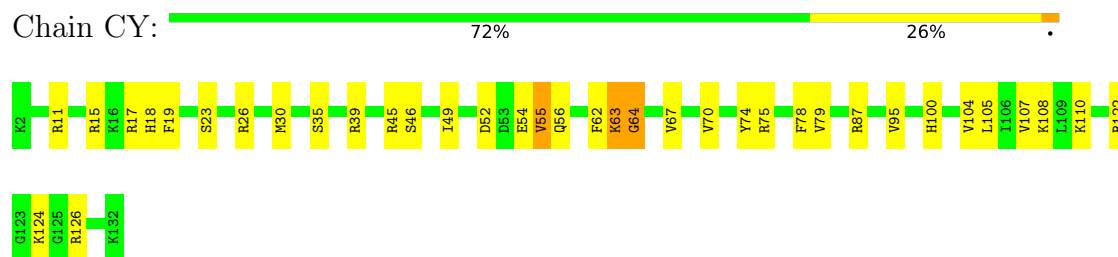
- Molecule 14: 60S ribosomal protein L17



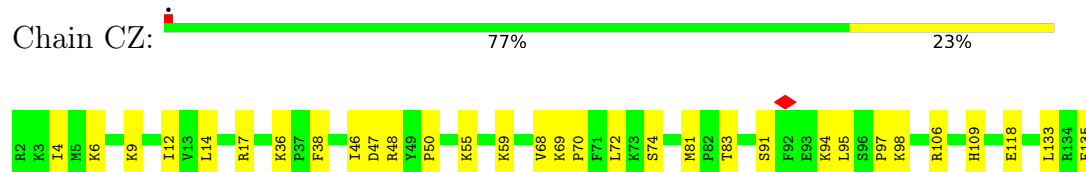
- Molecule 15: IP17216p



- Molecule 16: GEO07453p1

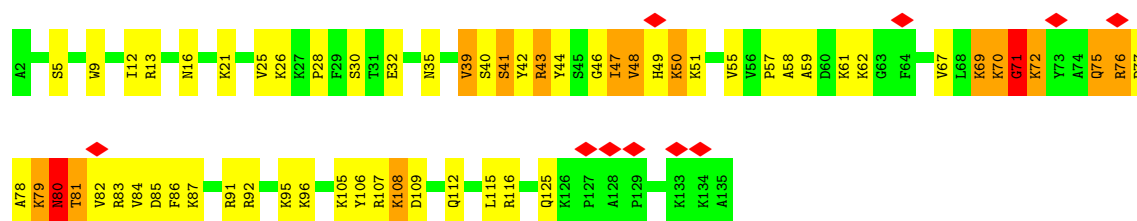


- Molecule 17: 60S ribosomal protein L27

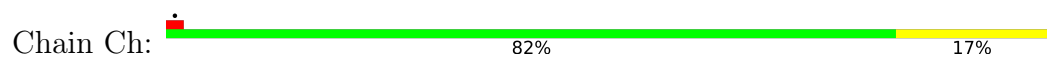


- Molecule 18: 60S ribosomal protein L28

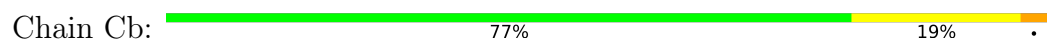




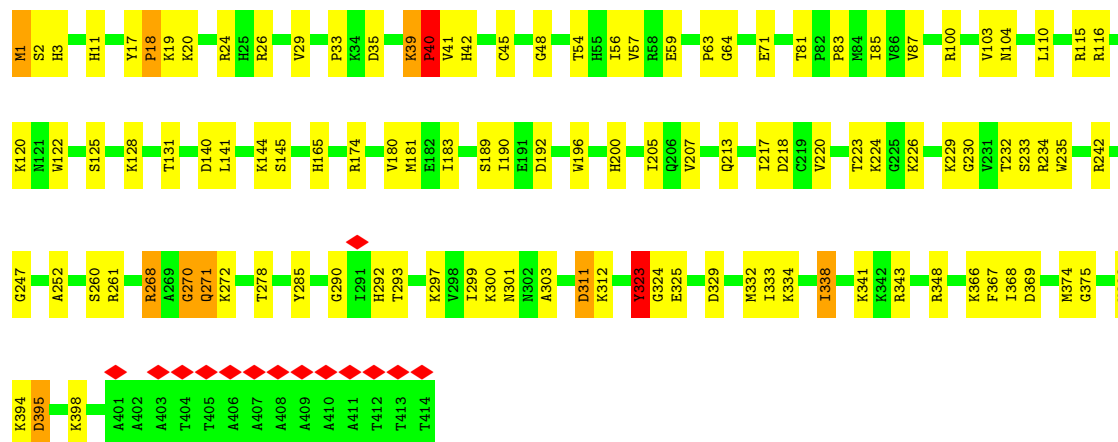
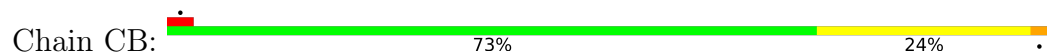
• Molecule 19: FI02809p



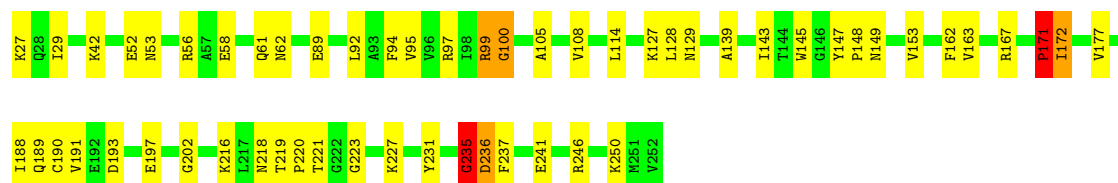
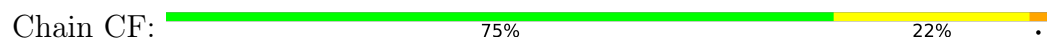
• Molecule 20: 60S ribosomal protein L29



• Molecule 21: 60S ribosomal protein L3



• Molecule 22: 60S ribosomal protein L7



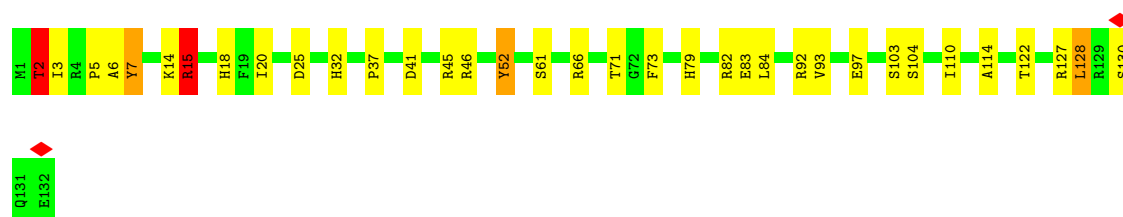
• Molecule 23: RE25263p

Chain Cc:  74% 26%



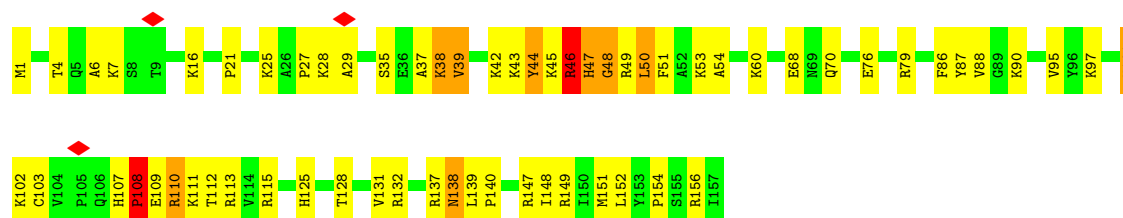
- Molecule 24: 60S ribosomal protein L32

Chain Ce:  73% 23%



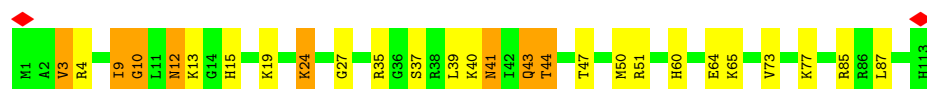
- Molecule 25: GEO07455p1

Chain Cf:  60% 33% 6%



- Molecule 26: 60S ribosomal protein L36

Chain Ci:  76% 17% 7%



- Molecule 27: 60S ribosomal protein L38

Chain Ck:  76% 24%

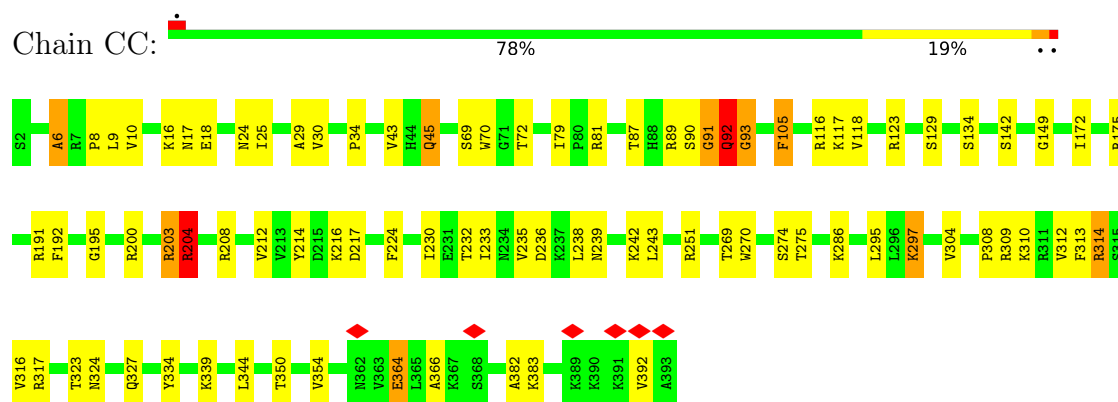


- Molecule 28: 60S ribosomal protein L39

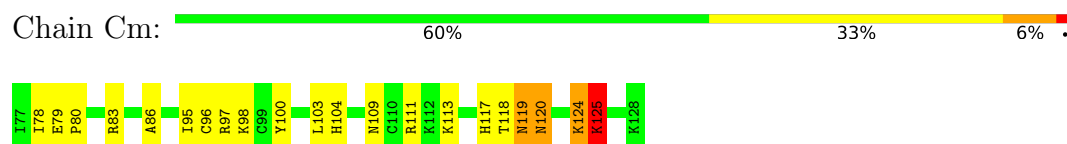
Chain Cl:  86% 14%



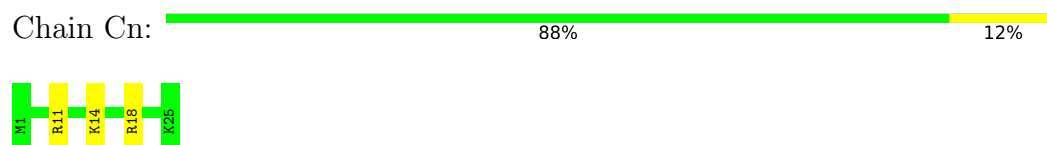
- Molecule 29: 60S ribosomal protein L4



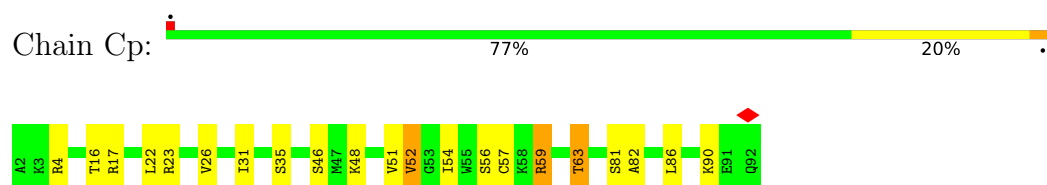
- Molecule 30: Ubiquitin-60S ribosomal protein L40



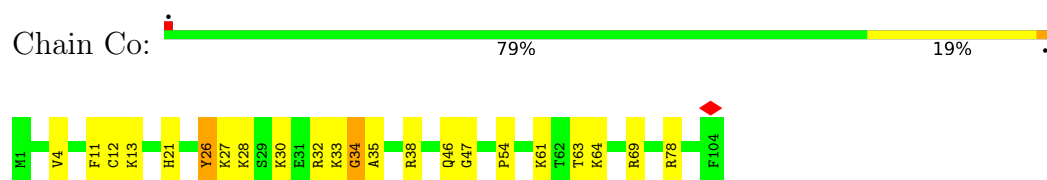
- Molecule 31: 60S ribosomal protein L41



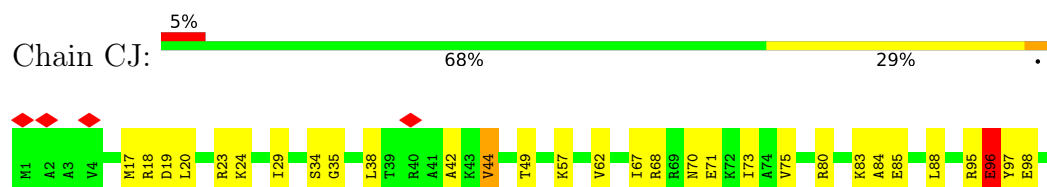
- Molecule 32: 60S ribosomal protein L37a

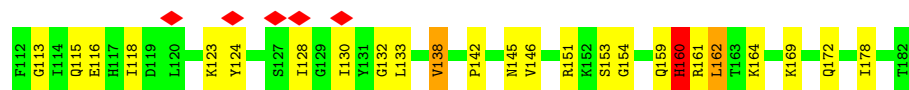


- Molecule 33: TA01007p

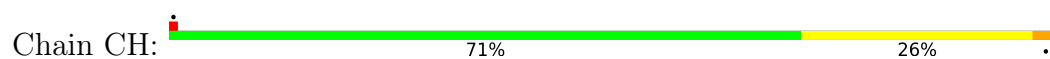


- Molecule 34: 60S ribosomal protein L11

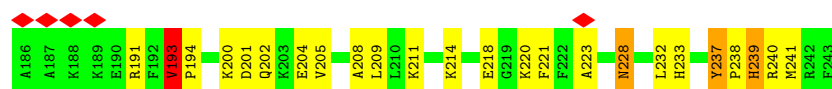
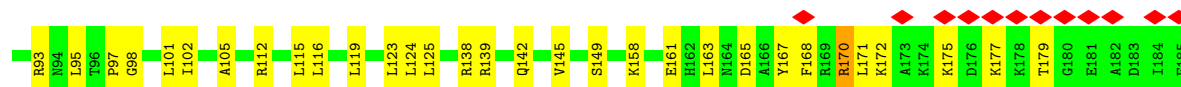
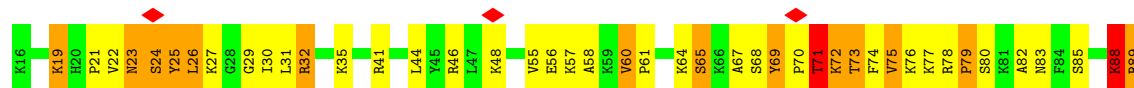




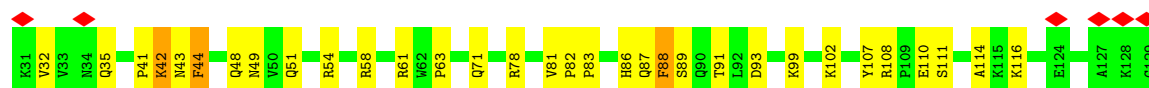
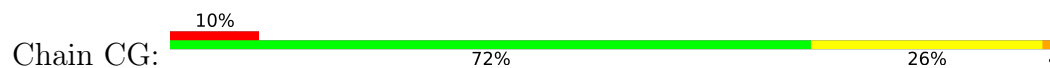
- Molecule 35: 60S ribosomal protein L9



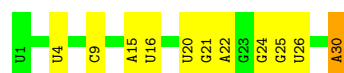
- Molecule 36: Ribosomal protein L6, isoform A



- Molecule 37: 60S ribosomal protein L7a

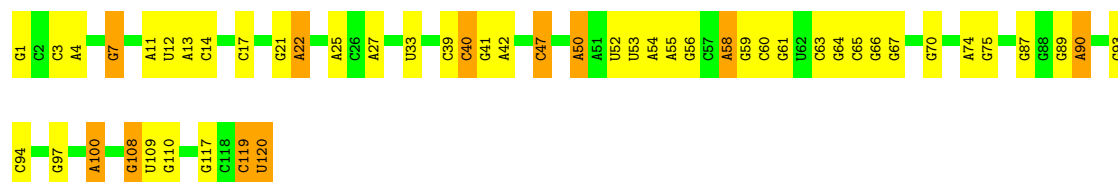


- Molecule 38: 2S ribosomal RNA



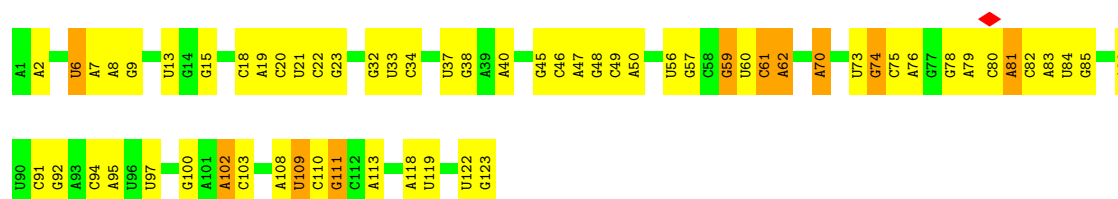
- Molecule 39: 5S ribosomal RNA

Chain A7: 



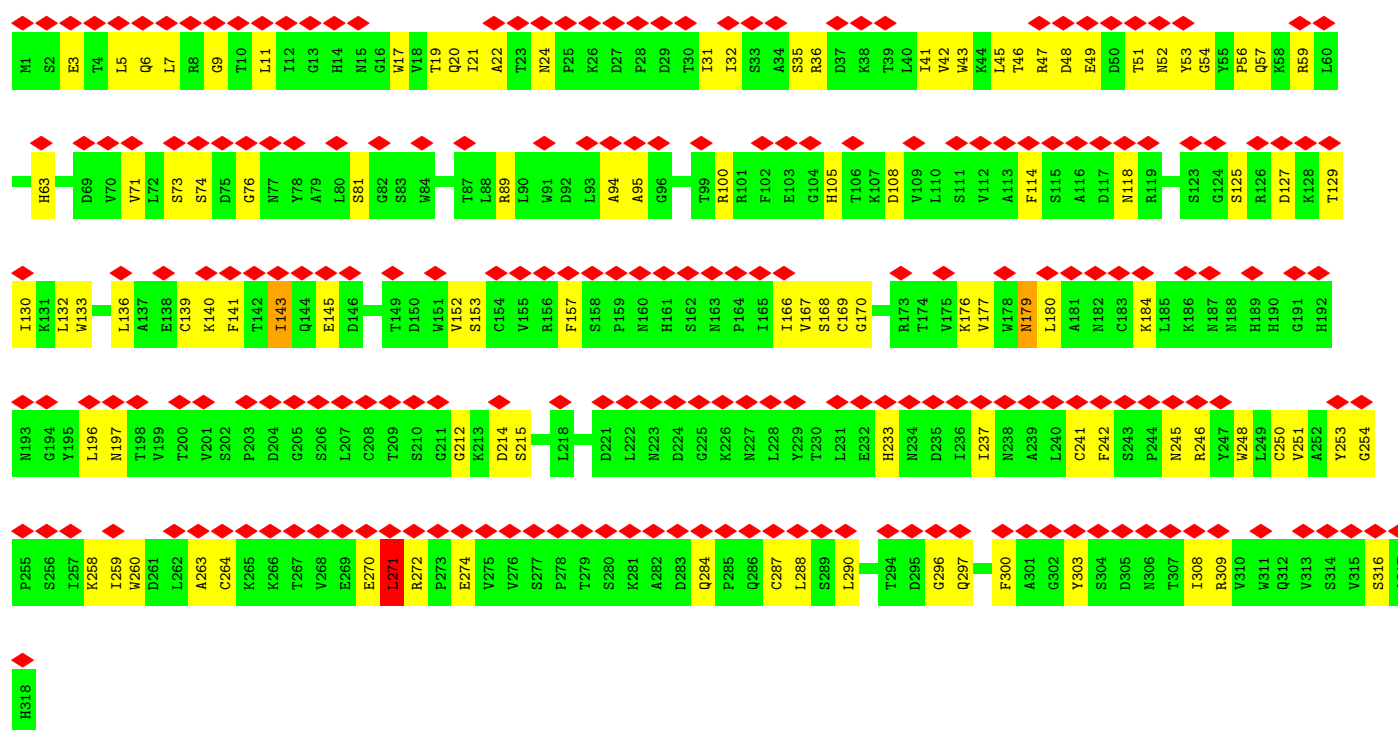
- Molecule 40: 5.8S ribosomal RNA

Chain A8: 



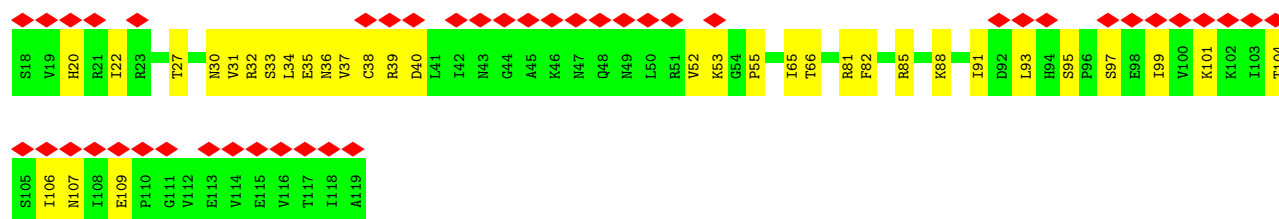
- Molecule 41: Guanine nucleotide-binding protein subunit beta-like protein

Chain Ag: 

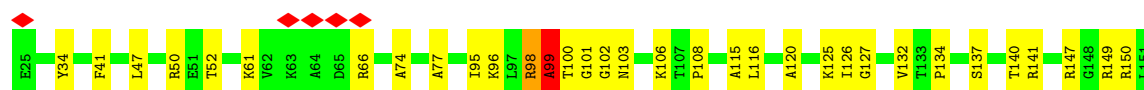
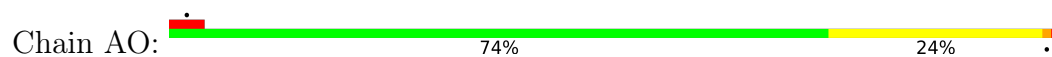


- Molecule 42: 40S ribosomal protein S20

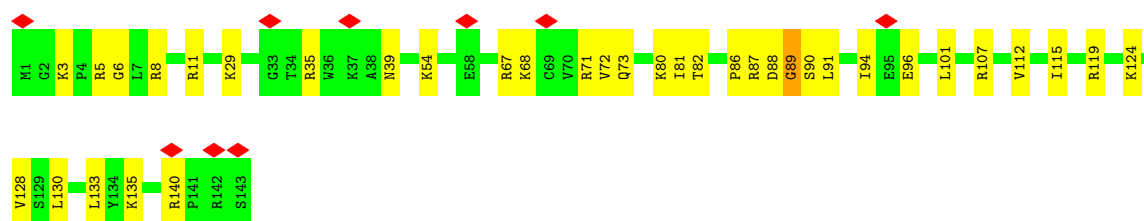
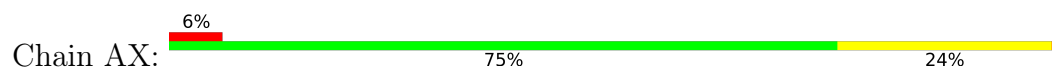
Chain AU: 



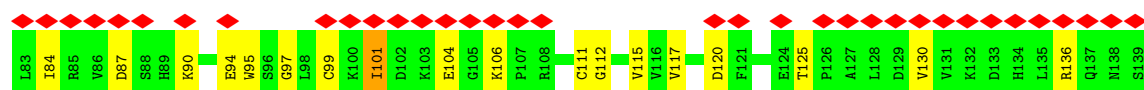
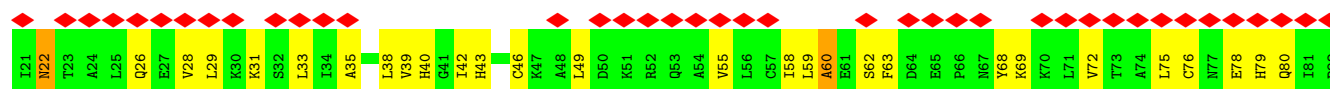
- Molecule 43: 40S ribosomal protein S14a



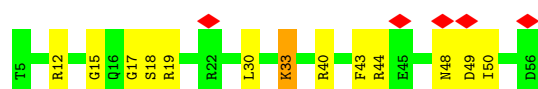
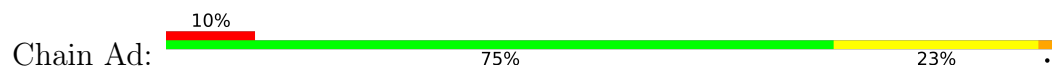
- Molecule 44: 40S ribosomal protein S23



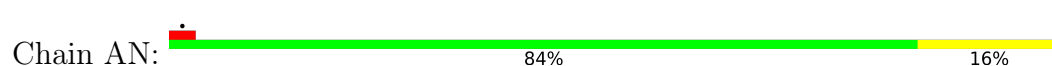
- Molecule 45: 40S ribosomal protein S12



- Molecule 46: 40S ribosomal protein S29

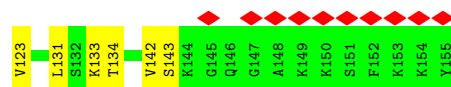
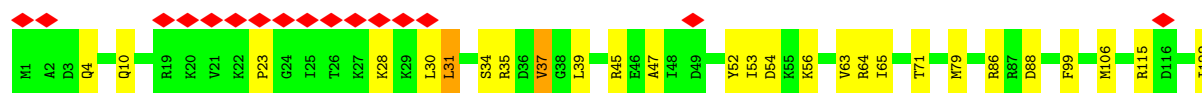
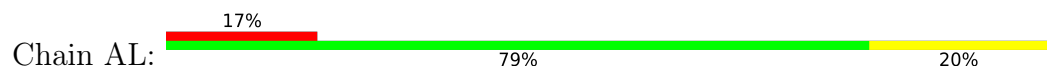


- Molecule 47: 40S ribosomal protein S13

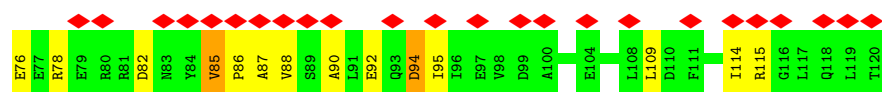
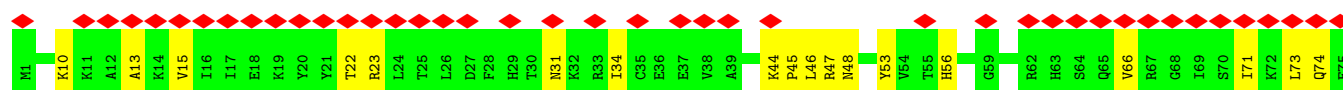
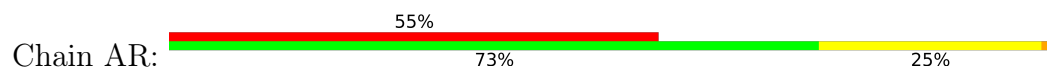




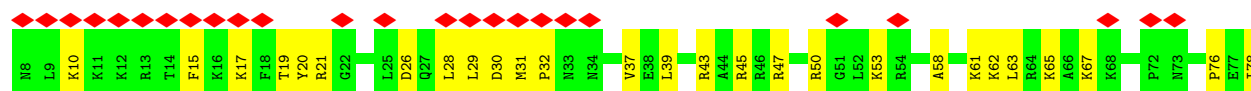
- Molecule 48: 40S ribosomal protein S11



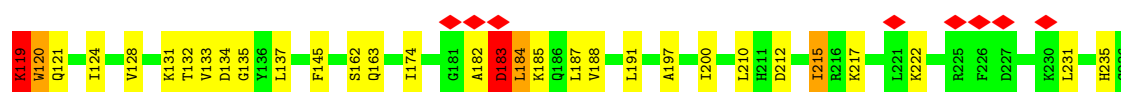
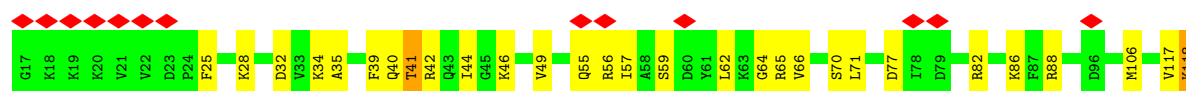
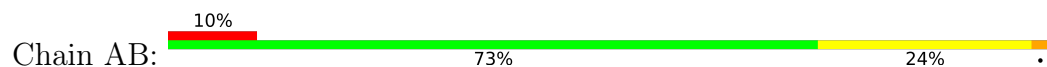
- Molecule 49: 40S ribosomal protein S17



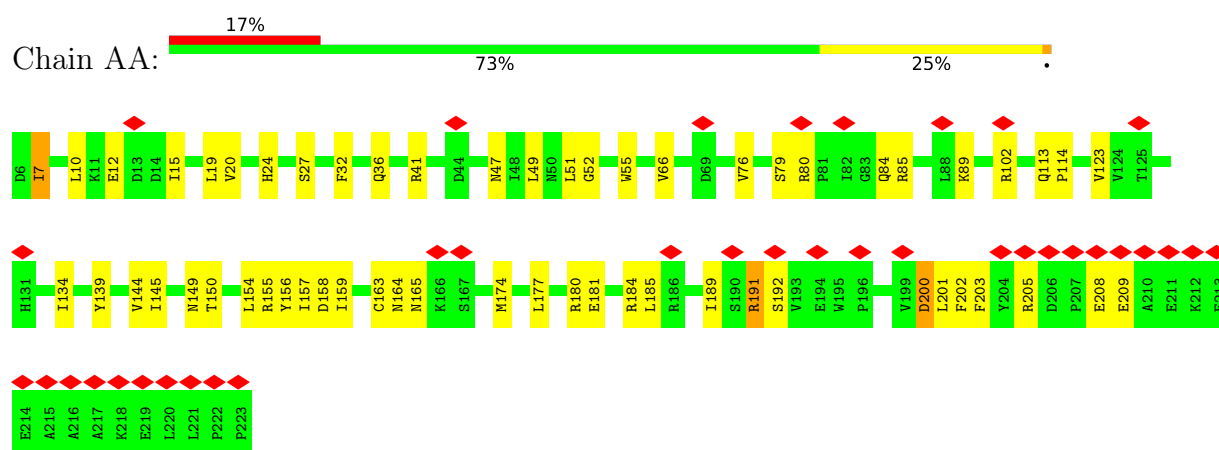
- Molecule 50: GEO07301p1



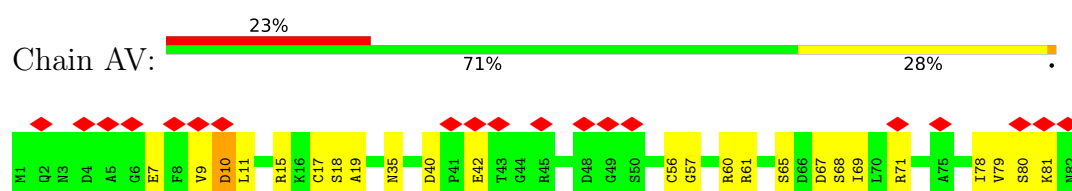
- Molecule 51: 40S ribosomal protein S3a



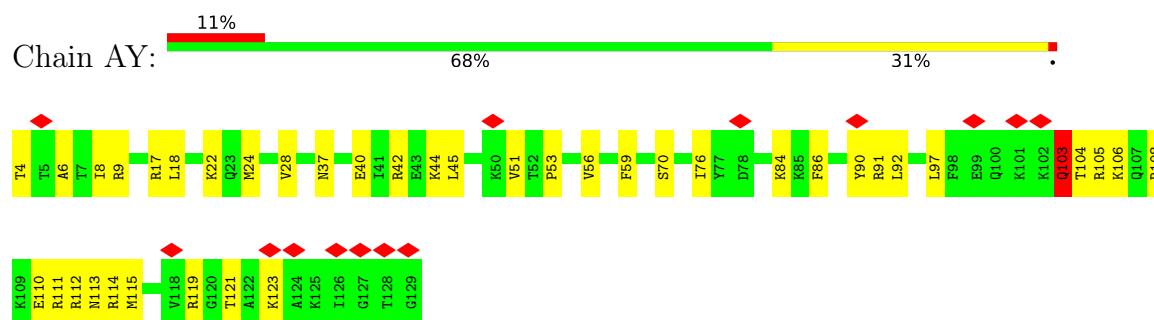
- Molecule 52: 40S ribosomal protein SA



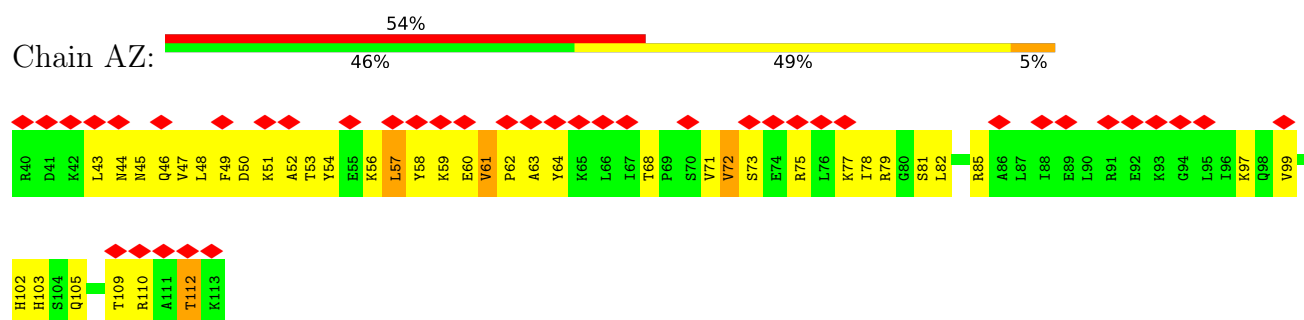
• Molecule 53: 40S ribosomal protein S21



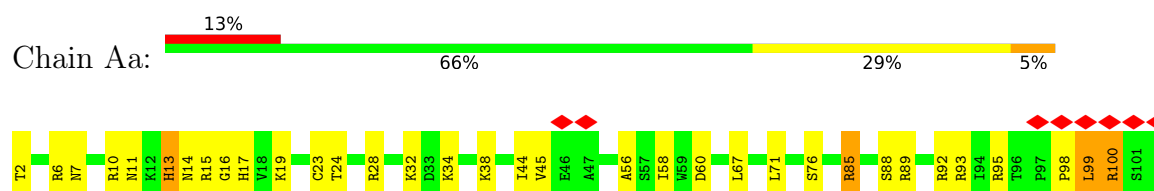
• Molecule 54: 40S ribosomal protein S24



• Molecule 55: 40S ribosomal protein S25

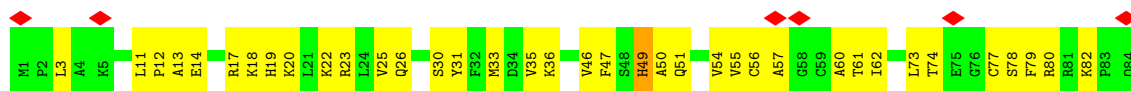


• Molecule 56: 40S ribosomal protein S26

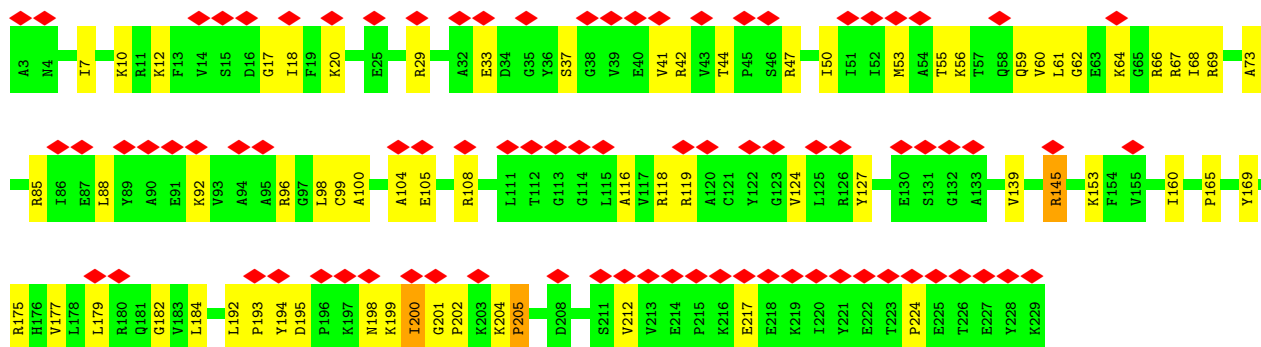
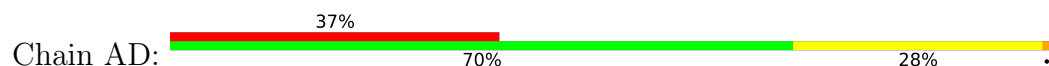




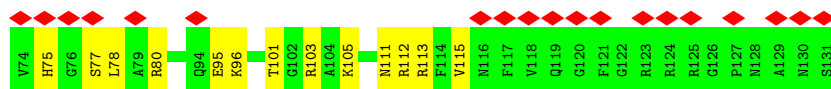
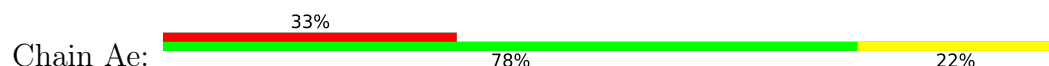
- Molecule 57: 40S ribosomal protein S27



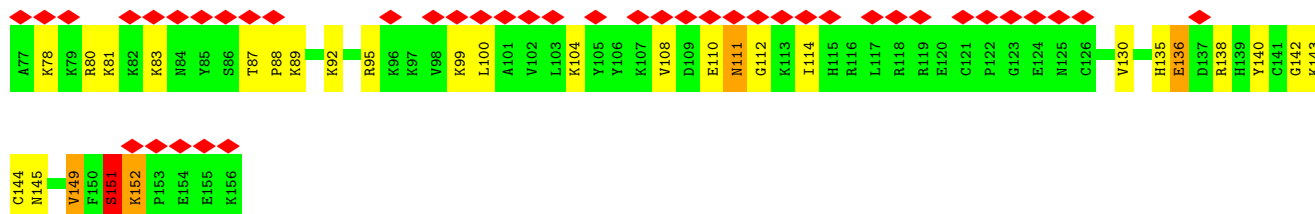
- Molecule 58: 40S ribosomal protein S3



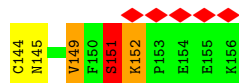
- Molecule 59: 40S ribosomal protein S30

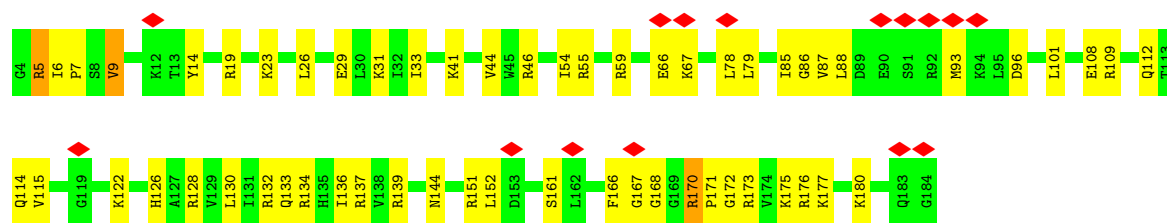


- Molecule 60: Ubiquitin-40S ribosomal protein S27a

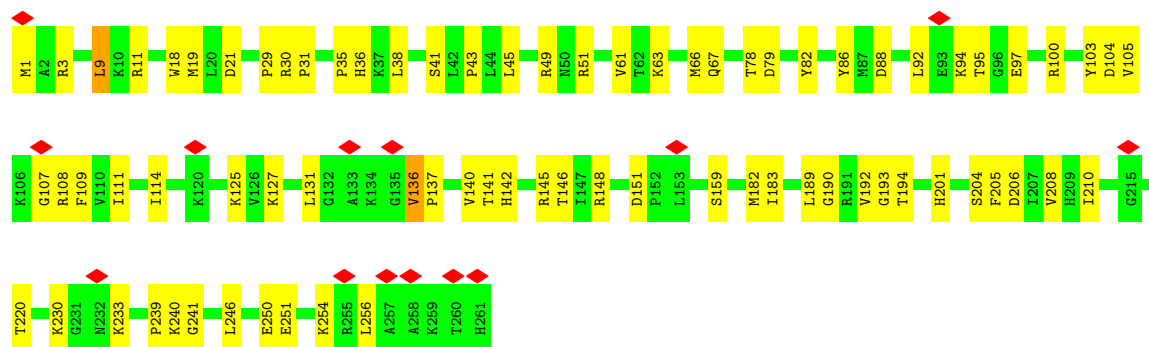
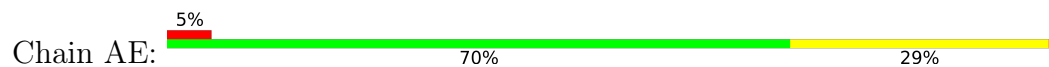


- Molecule 61: 40S ribosomal protein S9

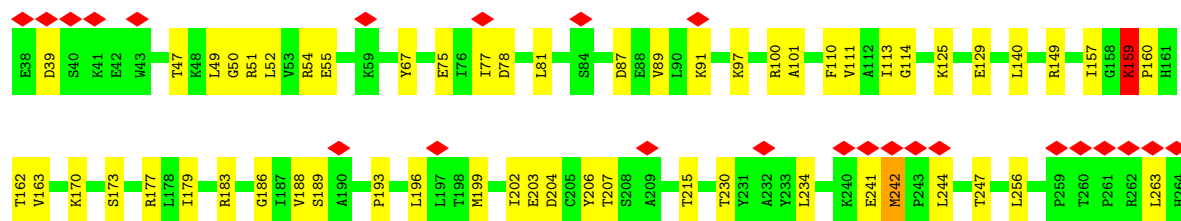
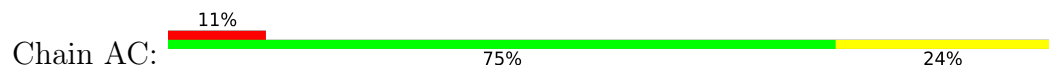




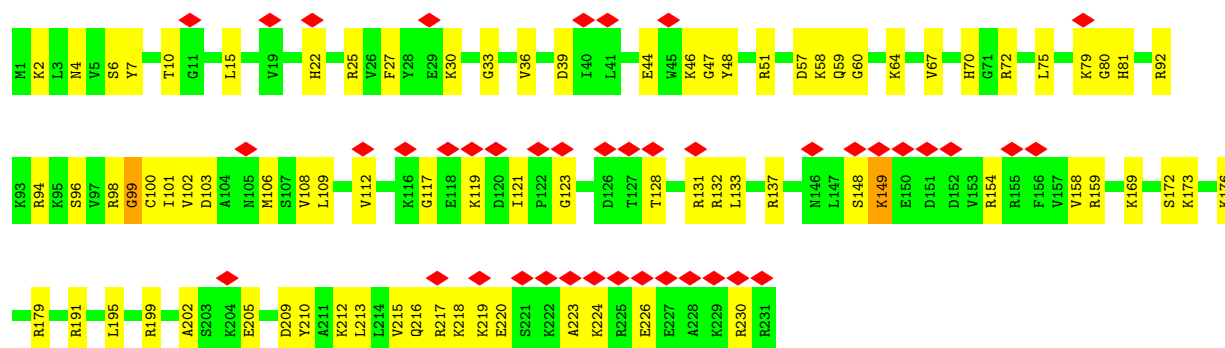
• Molecule 62: 40S ribosomal protein S4



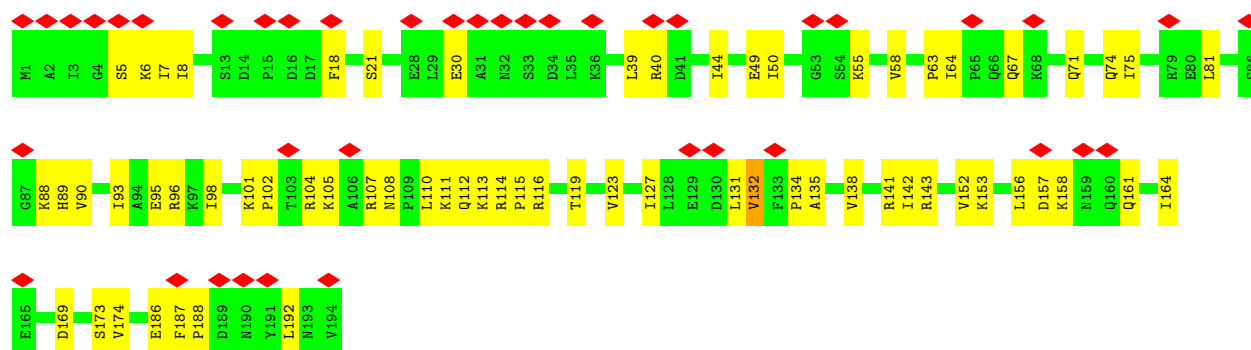
• Molecule 63: 40S ribosomal protein S2



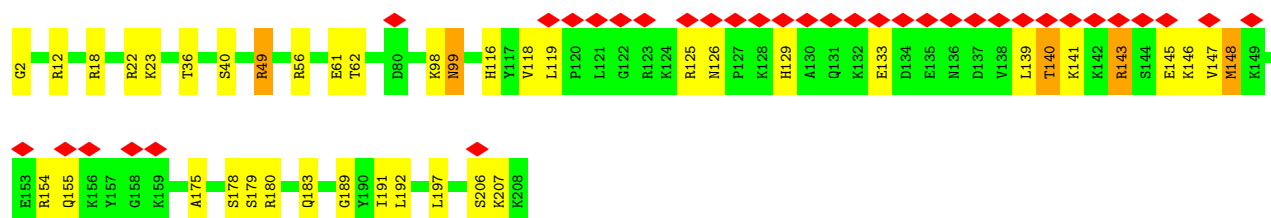
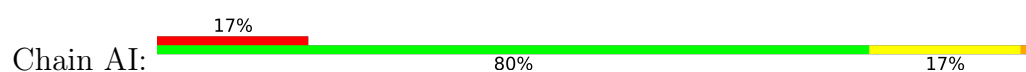
• Molecule 64: 40S ribosomal protein S6



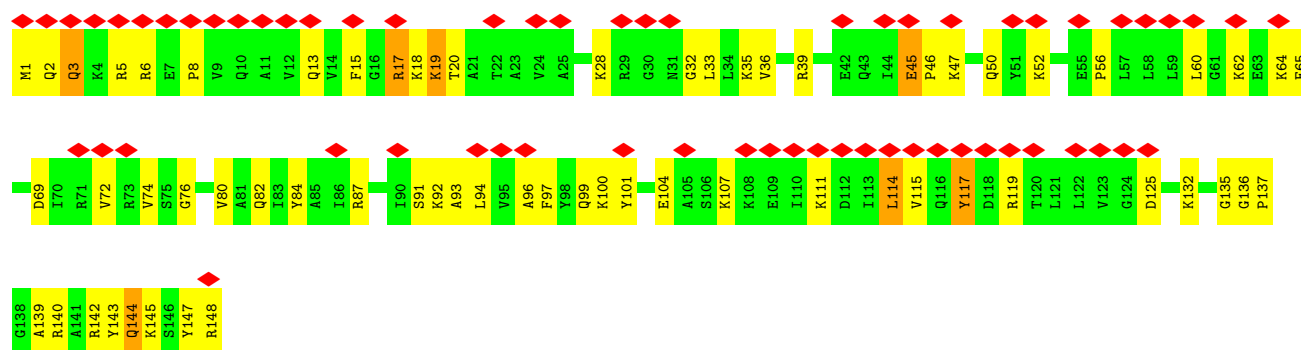
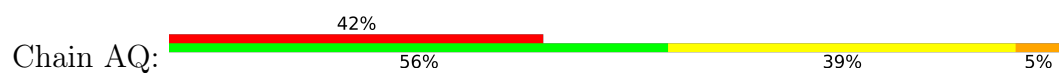
• Molecule 65: 40S ribosomal protein S7



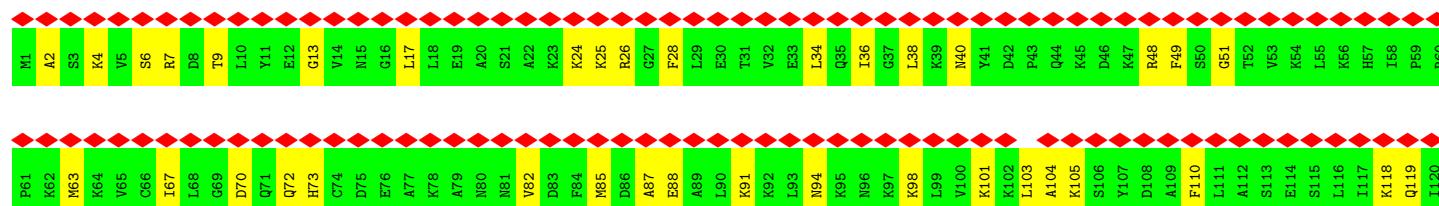
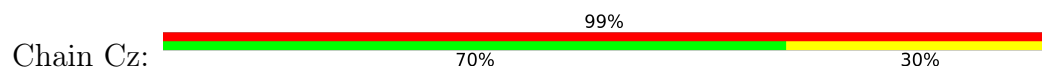
- Molecule 66: 40S ribosomal protein S8



- Molecule 67: 40S ribosomal protein S16

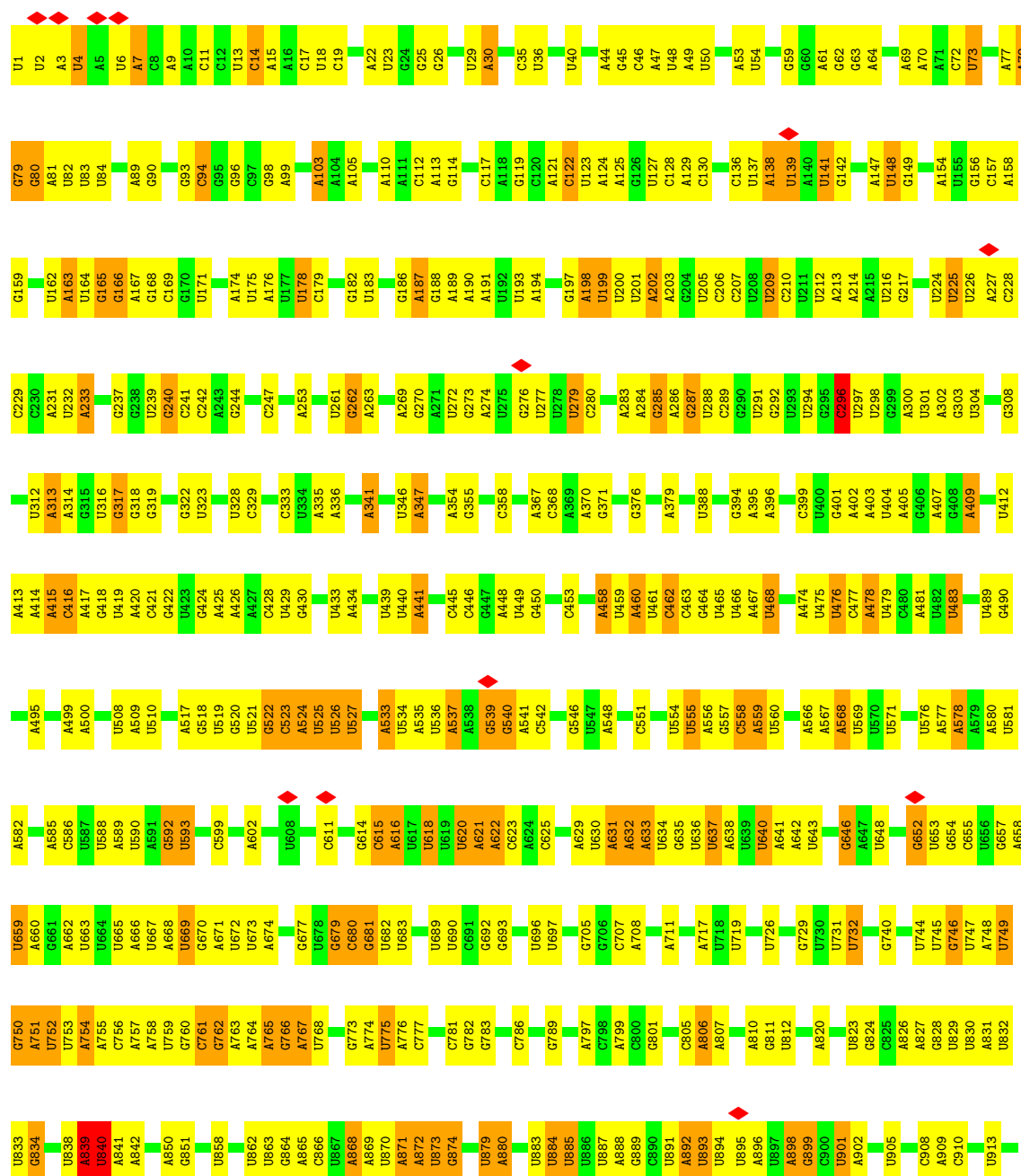


- Molecule 68: 60S ribosomal protein L10a-2



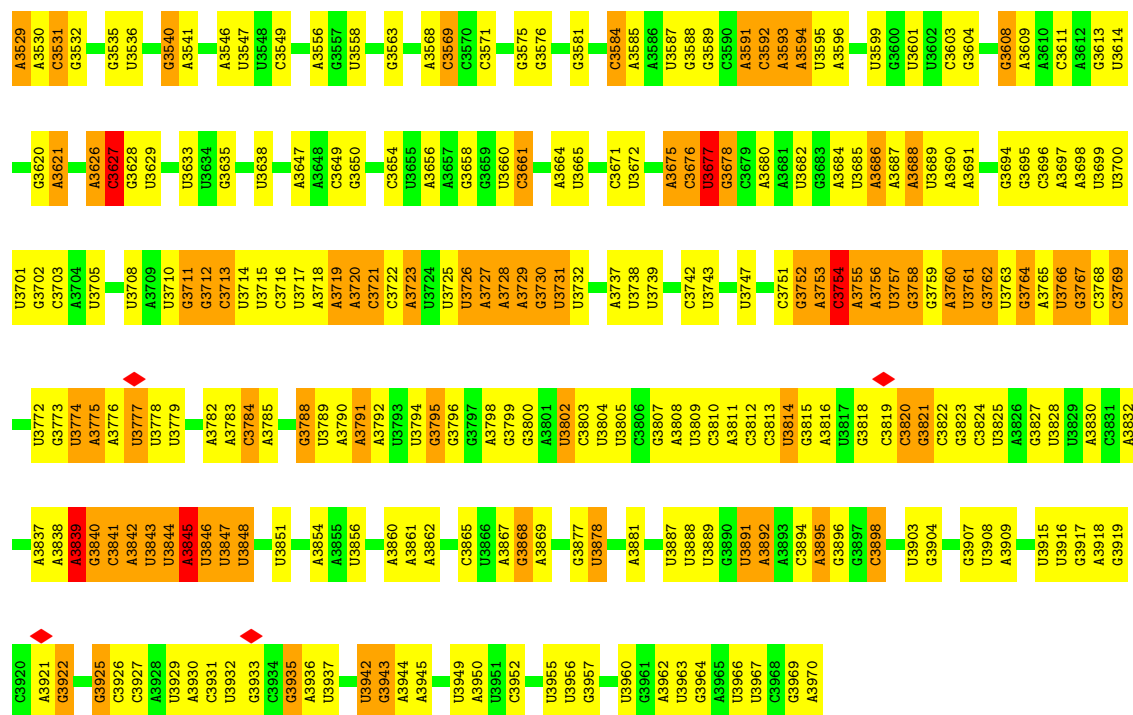


• Molecule 69: 28S ribosomal RNA

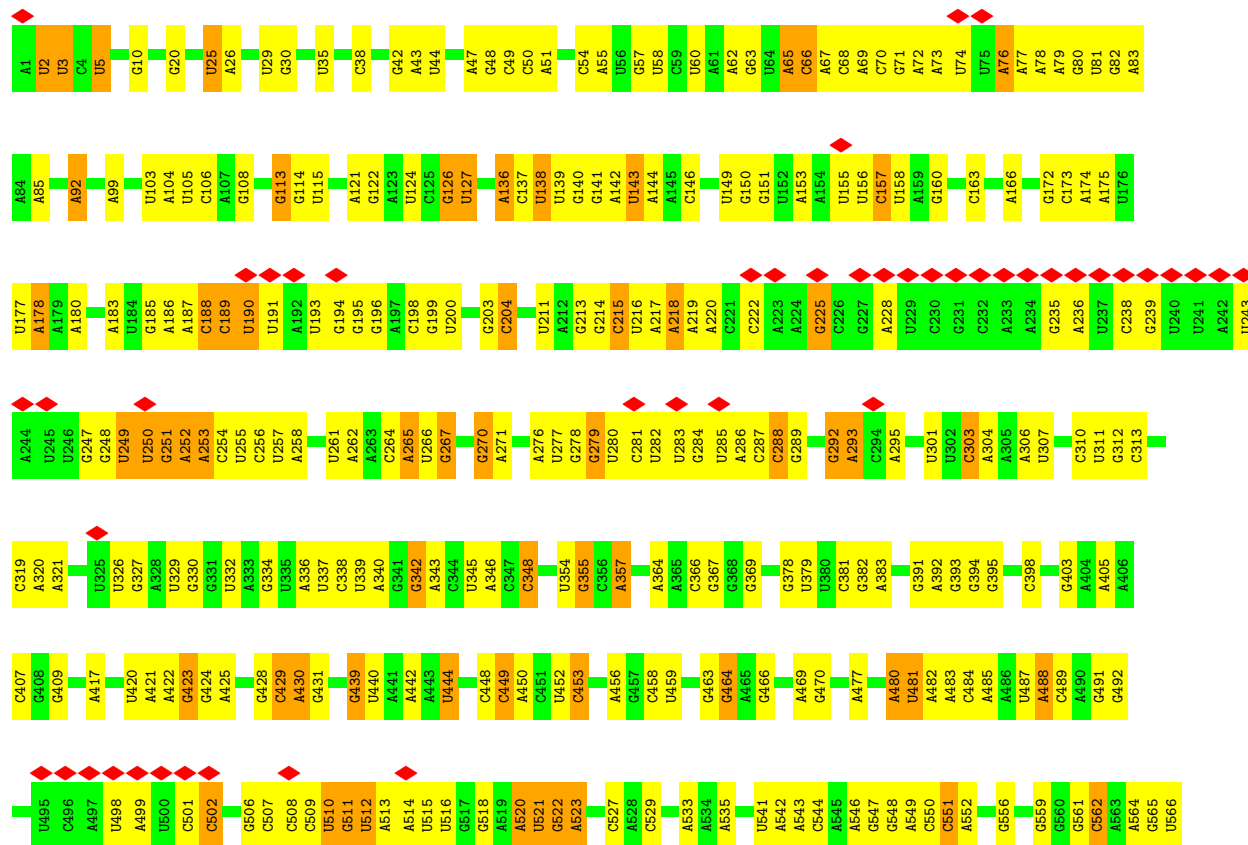


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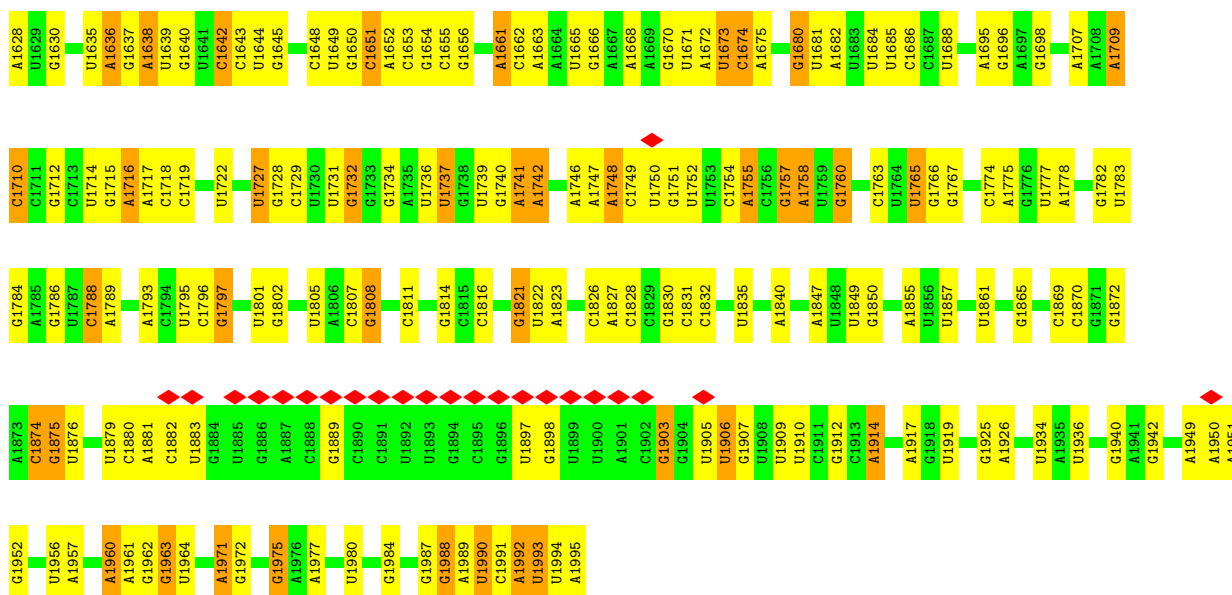
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		A3338			G3086	G2981	C2873	A2875		U2401			U2401	
		A3339			G3087	U2982	A2876	U2876		G2402			G2402	
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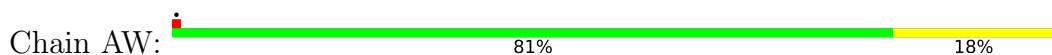
• Molecule 70: 18S ribosomal RNA



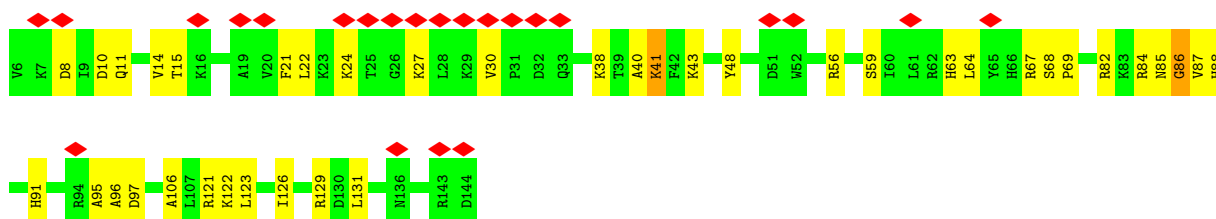




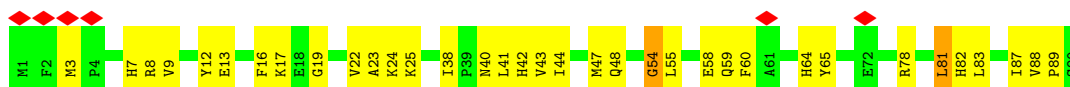
• Molecule 71: 40S ribosomal protein S15Aa



• Molecule 72: 40S ribosomal protein S19a

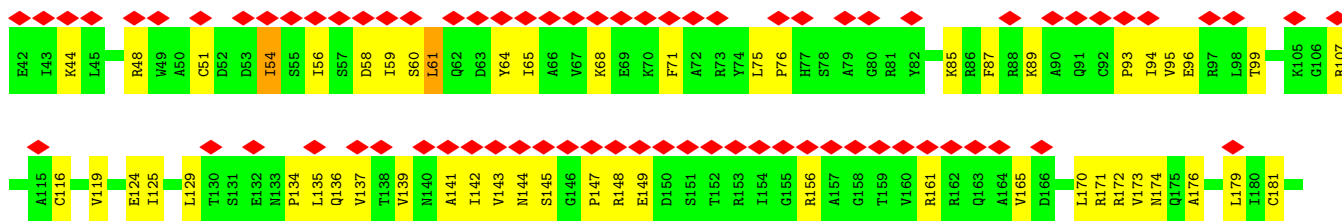


• Molecule 73: 40S ribosomal protein S10b

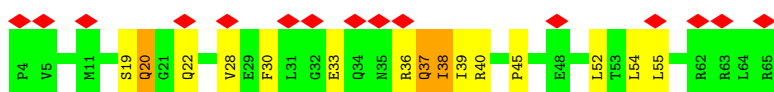
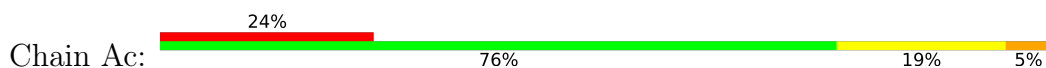


• Molecule 74: 40S ribosomal protein S5b

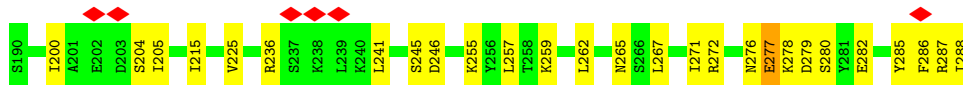
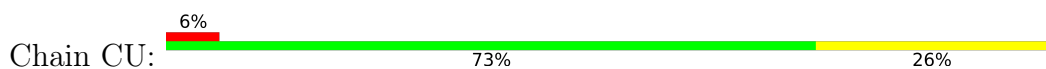




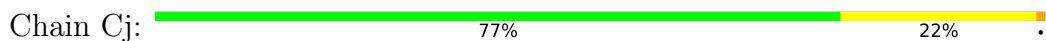
- Molecule 75: 40S ribosomal protein S28



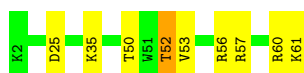
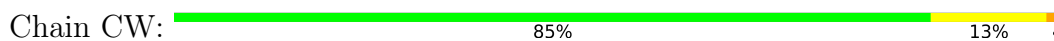
- Molecule 76: 60S ribosomal protein L22



- Molecule 77: Probable 60S ribosomal protein L37-A



- Molecule 78: 60S ribosomal protein L24

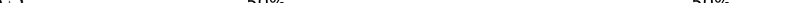


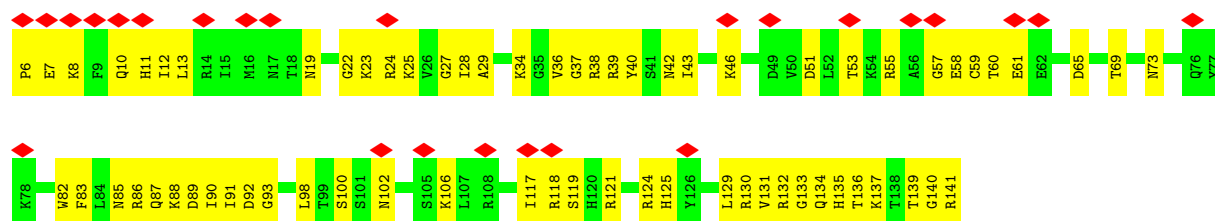
- Molecule 79: 60S ribosomal protein L34



- Molecule 80: 60S ribosomal protein L31

E93	E94	E95	E96	E97	E98	E99	E100	E101	E102	E103	E104	E105	E106	E107	E108	E109	E110	E111	E112	E113	E114	E115	E116	E117	E118	E119	E120	E121	E122	E123	E124	E125	E126	E127	E128	E129	E130	E131	E132	E133	E134	E135	E136	E137	E138	E139	E140	E141	E142	E143	E144	E145	E146	E147	E148	E149	E150	E151	E152	E153	E154	E155	E156	E157	E158	E159	E160	E161	E162	E163	E164	E165	E166	E167	E168	E169	E170	E171	E172	E173	E174	E175	E176	E177	E178	E179	E180	E181	E182	E183	E184	E185	E186	E187	E188	E189	E190	E191	E192	E193	E194	E195	E196	E197	E198	E199	E200	E201	E202	E203	E204	E205	E206	E207	E208	E209	E210	E211	E212	E213	E214	E215	E216	E217	E218	E219	E220	E221	E222	E223	E224	E225	E226	E227	E228	E229	E230	E231	E232	E233	E234	E235	E236	E237	E238	E239	E240	E241	E242	E243	E244	E245	E246	E247	E248	E249	E250	E251	E252	E253	E254	E255	E256	E257	E258	E259	E260	E261	E262	E263	E264	E265	E266	E267	E268	E269	E270	E271	E272	E273	E274	E275	E276	E277	E278	E279	E280	E281	E282	E283	E284	E285	E286	E287	E288	E289	E290	E291	E292	E293	E294	E295	E296	E297	E298	E299	E300	E301	E302	E303	E304	E305	E306	E307	E308	E309	E310	E311	E312	E313	E314	E315	E316	E317	E318	E319	E320	E321	E322	E323	E324	E325	E326	E327	E328	E329	E330	E331	E332	E333	E334	E335	E336	E337	E338	E339	E340	E341	E342	E343	E344	E345	E346	E347	E348	E349	E350	E351	E352	E353	E354	E355	E356	E357	E358	E359	E360	E361	E362	E363	E364	E365	E366	E367	E368	E369	E370	E371	E372	E373	E374	E375	E376	E377	E378	E379	E380	E381	E382	E383	E384	E385	E386	E387	E388	E389	E390	E391	E392	E393	E394	E395	E396	E397	E398	E399	E400	E401	E402	E403	E404	E405	E406	E407	E408	E409	E410	E411	E412	E413	E414	E415	E416	E417	E418	E419	E420	E421	E422	E423	E424	E425	E426	E427	E428	E429	E430	E431	E432	E433	E434	E435	E436	E437	E438	E439	E440	E441	E442	E443	E444	E445	E446	E447	E448	E449	E450	E451	E452	E453	E454	E455	E456	E457	E458	E459	E460	E461	E462	E463	E464	E465	E466	E467	E468	E469	E470	E471	E472	E473	E474	E475	E476	E477	E478	E479	E480	E481	E482	E483	E484	E485	E486	E487	E488	E489	E490	E491	E492	E493	E494	E495	E496	E497	E498	E499	E500	E501	E502	E503	E504	E505	E506	E507	E508	E509	E510	E511	E512	E513	E514	E515	E516	E517	E518	E519	E520	E521	E522	E523	E524	E525	E526	E527	E528	E529	E530	E531	E532	E533	E534	E535	E536	E537	E538	E539	E540	E541	E542	E543	E544	E545	E546	E547	E548	E549	E550	E551	E552	E553	E554	E555	E556	E557	E558	E559	E560	E561	E562	E563	E564	E565	E566	E567	E568	E569	E570	E571	E572	E573	E574	E575	E576	E577	E578	E579	E580	E581	E582	E583	E584	E585	E586	E587	E588	E589	E590	E591	E592	E593	E594	E595	E596	E597	E598	E599	E600	E601	E602	E603	E604</
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- Chain AS: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	185913	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	0.861	Depositor
Minimum map value	-0.593	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.035	Depositor
Map size ($\text{\AA}$)	426.00003, 426.00003, 426.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.065, 1.065, 1.065	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	CO	0.84	0/1700	0.97	5/2277 (0.2%)
2	CL	0.75	0/1726	1.23	26/2308 (1.1%)
3	CV	0.74	0/1014	0.79	2/1362 (0.1%)
4	CM	0.67	0/1326	0.88	2/1780 (0.1%)
5	Ca	0.99	0/1235	1.10	6/1640 (0.4%)
6	CN	0.97	0/1750	1.12	8/2335 (0.3%)
7	CI	0.50	1/1827 (0.1%)	0.78	3/2447 (0.1%)
8	CD	0.53	0/2379	0.75	2/3196 (0.1%)
9	CQ	0.92	0/1544	1.02	4/2069 (0.2%)
10	CR	0.60	0/1703	0.72	0/2255
11	CA	0.81	0/1970	0.91	4/2635 (0.2%)
12	CS	0.79	0/1491	1.18	10/1998 (0.5%)
13	CT	0.74	0/1326	1.01	4/1773 (0.2%)
14	CP	0.84	0/1529	0.92	0/2042
15	CX	0.67	0/1001	0.98	3/1348 (0.2%)
16	CY	0.76	0/1094	0.86	0/1456
17	CZ	0.47	0/1141	0.74	0/1517
18	Cr	0.88	0/1069	1.32	13/1432 (0.9%)
19	Ch	0.65	0/1024	0.86	0/1353
20	Cb	0.67	0/628	1.05	1/832 (0.1%)
21	CB	0.78	0/3356	1.01	9/4494 (0.2%)
22	CF	0.86	0/1931	0.92	3/2587 (0.1%)
23	Cc	0.52	0/779	0.64	0/1048
24	Ce	0.99	0/1132	1.07	5/1508 (0.3%)
25	Cf	0.86	0/1270	1.24	12/1696 (0.7%)
26	Ci	0.59	0/944	1.07	8/1250 (0.6%)
27	Ck	0.54	0/583	0.79	0/774
28	Cl	0.91	0/445	0.89	0/589
29	CC	0.89	1/3163 (0.0%)	1.11	12/4253 (0.3%)
30	Cm	0.55	0/435	0.89	2/575 (0.3%)
31	Cn	0.60	0/237	0.72	0/300
32	Cp	0.78	0/719	0.93	2/954 (0.2%)
33	Co	0.71	0/887	0.97	2/1162 (0.2%)
34	CJ	0.37	0/1494	0.88	7/2001 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	CH	0.57	0/1519	0.83	4/2042 (0.2%)
36	CE	0.63	0/1883	1.13	10/2514 (0.4%)
37	CG	0.55	1/1968 (0.1%)	0.86	2/2637 (0.1%)
38	A9	0.73	0/714	0.70	0/1112
39	A7	0.72	0/2854	0.61	0/4447
40	A8	0.93	0/2932	0.72	0/4568
41	Ag	0.28	0/2574	0.71	1/3506 (0.0%)
42	AU	0.30	0/825	0.71	0/1111
43	AO	0.32	0/965	0.80	2/1295 (0.2%)
44	AX	0.34	0/1152	0.79	1/1540 (0.1%)
45	AM	0.32	0/937	0.93	2/1260 (0.2%)
46	Ad	0.28	0/443	0.75	0/589
47	AN	0.35	0/1225	0.68	3/1641 (0.2%)
48	AL	0.39	0/1296	0.73	2/1725 (0.1%)
49	AR	0.31	0/993	0.83	2/1333 (0.2%)
50	AP	0.29	0/1036	0.82	0/1383
51	AB	0.29	0/1825	0.74	3/2448 (0.1%)
52	AA	0.28	0/1777	0.70	0/2422
53	AV	0.28	0/622	0.67	0/835
54	AY	0.26	0/1032	0.78	4/1373 (0.3%)
55	AZ	0.31	0/616	0.83	0/826
56	Aa	0.38	0/883	0.78	2/1184 (0.2%)
57	Ab	0.25	0/668	0.67	0/898
58	AD	0.26	0/1808	0.77	3/2427 (0.1%)
59	Ae	0.27	0/475	0.80	2/625 (0.3%)
60	Af	0.29	0/672	0.86	4/887 (0.5%)
61	AJ	0.28	0/1526	0.72	2/2037 (0.1%)
62	AE	0.29	0/2096	0.66	0/2819
63	AC	0.32	0/1785	0.74	5/2415 (0.2%)
64	AG	0.28	0/1891	0.70	0/2519
65	AH	0.28	0/1593	0.74	0/2145
66	AI	0.41	0/1689	0.94	5/2250 (0.2%)
67	AQ	0.30	0/1202	0.92	6/1608 (0.4%)
68	Cz	0.31	0/1727	0.80	0/2308
69	A5	0.87	3/86147 (0.0%)	0.75	56/134004 (0.0%)
70	B2	0.34	0/43887	0.44	2/68161 (0.0%)
71	AW	0.33	0/1046	0.58	0/1402
72	AT	0.26	0/1019	0.75	0/1367
73	AK	0.33	0/786	0.90	2/1064 (0.2%)
74	AF	0.29	0/1501	0.73	2/2017 (0.1%)
75	Ac	0.31	0/502	0.82	2/670 (0.3%)
76	CU	0.41	0/838	0.88	4/1123 (0.4%)
77	Cj	1.03	0/717	0.95	0/950

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	CW	0.63	0/515	0.87	2/683 (0.3%)
79	Cg	0.78	0/855	0.89	1/1142 (0.1%)
80	Cd	0.20	0/908	0.46	0/1221
81	AS	0.23	0/1135	0.74	2/1521 (0.1%)
All	All	0.68	6/232911 (0.0%)	0.76	293/341300 (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	CO	0	9
2	CL	0	14
4	CM	0	2
5	Ca	0	5
6	CN	0	7
7	CI	0	5
8	CD	0	5
9	CQ	0	5
10	CR	0	3
11	CA	0	4
12	CS	0	11
13	CT	0	8
14	CP	0	3
16	CY	0	2
18	Cr	0	15
19	Ch	0	5
20	Cb	0	4
21	CB	0	18
22	CF	0	4
24	Ce	0	3
25	Cf	0	11
26	Ci	0	7
27	Ck	0	2
29	CC	0	15
30	Cm	0	2
33	Co	0	3
34	CJ	0	4
35	CH	0	4
36	CE	0	25
37	CG	0	9

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Mol	Chain	#Chirality outliers	#Planarity outliers
43	AO	0	4
44	AX	0	1
45	AM	0	3
46	Ad	0	1
50	AP	0	3
51	AB	0	4
52	AA	0	2
53	AV	0	2
54	AY	0	1
55	AZ	0	4
56	Aa	0	2
57	Ab	0	1
58	AD	0	6
59	Ae	0	1
60	Af	0	10
61	AJ	0	4
62	AE	0	1
63	AC	0	2
64	AG	0	2
65	AH	0	3
66	AI	0	2
67	AQ	0	5
68	Cz	0	2
72	AT	0	3
74	AF	0	2
75	Ac	0	1
76	CU	0	1
78	CW	0	1
79	Cg	0	1
80	Cd	0	1
All	All	0	290

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	CI	132	GLY	C-N	-9.40	1.18	1.33
37	CG	133	GLU	C-N	6.15	1.38	1.33
29	CC	79	ILE	CG1-CD1	-5.77	1.29	1.51
69	A5	1795	A	C5-C6	-5.76	1.29	1.41
69	A5	1383	A	O3'-P	5.18	1.69	1.61

The worst 5 of 293 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	CI	132	GLY	CA-C-N	11.48	137.56	121.61
7	CI	132	GLY	C-N-CA	11.48	137.56	121.61
29	CC	195	GLY	CA-C-N	10.72	140.99	121.70
29	CC	195	GLY	C-N-CA	10.72	140.99	121.70
25	Cf	46	ARG	N-CA-C	10.55	124.89	108.12

There are no chirality outliers.

5 of 290 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	CO	109	GLY	Peptide
1	CO	111	PRO	Peptide
1	CO	112	SER	Peptide
1	CO	177	LYS	Peptide
1	CO	190	ALA	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	CO	1668	0	1783	32	0
2	CL	1695	0	1790	41	0
3	CV	998	0	1046	13	0
4	CM	1302	0	1388	41	0
5	Ca	1204	0	1260	40	0
6	CN	1710	0	1778	41	0
7	CI	1785	0	1804	35	0
8	CD	2334	0	2354	52	0
9	CQ	1518	0	1626	45	0
10	CR	1683	0	1827	35	0
11	CA	1935	0	2037	54	0
12	CS	1454	0	1503	42	0
13	CT	1297	0	1364	24	0
14	CP	1505	0	1556	32	0
15	CX	984	0	1058	25	0
16	CY	1078	0	1159	25	0
17	CZ	1115	0	1199	26	0
18	Cr	1051	0	1148	43	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	Ch	1015	0	1163	12	0
20	Cb	619	0	650	10	0
21	CB	3287	0	3432	67	0
22	CF	1895	0	2012	34	0
23	Cc	770	0	802	20	0
24	Ce	1110	0	1181	29	0
25	Cf	1244	0	1316	47	0
26	Ci	934	0	1029	19	0
27	Ck	576	0	634	10	0
28	Cl	437	0	483	7	0
29	CC	3109	0	3298	50	0
30	Cm	429	0	472	15	0
31	Cn	236	0	286	3	0
32	Cp	710	0	756	15	0
33	Co	874	0	956	12	0
34	CJ	1468	0	1507	33	0
35	CH	1499	0	1569	34	0
36	CE	1845	0	1981	66	0
37	CG	1936	0	2103	38	0
38	A9	639	0	321	4	0
39	A7	2554	0	1296	26	0
40	A8	2621	0	1327	25	0
41	Ag	2511	0	2438	69	0
42	AU	815	0	871	23	0
43	AO	953	0	988	26	0
44	AX	1131	0	1190	24	0
45	AM	924	0	960	27	0
46	Ad	433	0	424	10	0
47	AN	1202	0	1291	17	0
48	AL	1274	0	1351	25	0
49	AR	981	0	1038	25	0
50	AP	1016	0	1086	89	0
51	AB	1798	0	1867	38	0
52	AA	1737	0	1750	44	0
53	AV	617	0	613	17	0
54	AY	1016	0	1073	27	0
55	AZ	608	0	657	133	0
56	Aa	867	0	920	31	0
57	Ab	653	0	680	26	0
58	AD	1782	0	1862	40	0
59	Ae	469	0	503	10	0
60	Af	659	0	695	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	AJ	1503	0	1620	41	0
62	AE	2054	0	2165	52	0
63	AC	1746	0	1827	37	0
64	AG	1866	0	2029	60	0
65	AH	1566	0	1664	42	0
66	AI	1665	0	1746	29	0
67	AQ	1183	0	1255	52	0
68	Cz	1702	0	1814	45	0
69	A5	77093	0	38445	767	0
70	B2	39355	0	19532	519	0
71	AW	1028	0	1071	19	0
72	AT	1000	0	1037	34	0
73	AK	760	0	757	23	0
74	AF	1481	0	1541	45	0
75	Ac	498	0	525	13	0
76	CU	825	0	853	14	0
77	Cj	704	0	733	14	0
78	CW	503	0	536	6	0
79	Cg	844	0	924	18	0
80	Cd	893	0	918	50	0
81	AS	1117	0	1148	290	0
All	All	216955	0	160651	3163	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 9.

The worst 5 of 3163 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)
70:B2:1758:A:P	81:AS:37:GLY:HA3	1.59	1.43
55:AZ:49:PHE:HB3	81:AS:6:PRO:C	1.45	1.41
55:AZ:51:LYS:HE3	81:AS:6:PRO:CG	1.49	1.39
55:AZ:48:LEU:HD11	81:AS:11:HIS:NE2	1.28	1.38
55:AZ:51:LYS:CE	81:AS:6:PRO:HG3	1.53	1.35

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	CO	203/205 (99%)	177 (87%)	24 (12%)	2 (1%)	12	45
2	CL	208/210 (99%)	154 (74%)	42 (20%)	12 (6%)	1	8
3	CV	132/134 (98%)	122 (92%)	10 (8%)	0	100	100
4	CM	157/159 (99%)	129 (82%)	27 (17%)	1 (1%)	21	56
5	Ca	147/149 (99%)	113 (77%)	33 (22%)	1 (1%)	18	53
6	CN	201/203 (99%)	166 (83%)	32 (16%)	3 (2%)	8	35
7	CI	215/217 (99%)	183 (85%)	30 (14%)	2 (1%)	14	48
8	CD	288/290 (99%)	247 (86%)	39 (14%)	2 (1%)	18	53
9	CQ	185/187 (99%)	160 (86%)	25 (14%)	0	100	100
10	CR	201/203 (99%)	183 (91%)	18 (9%)	0	100	100
11	CA	251/253 (99%)	211 (84%)	39 (16%)	1 (0%)	30	65
12	CS	171/173 (99%)	126 (74%)	37 (22%)	8 (5%)	2	11
13	CT	156/158 (99%)	130 (83%)	25 (16%)	1 (1%)	21	56
14	CP	183/185 (99%)	163 (89%)	19 (10%)	1 (0%)	24	60
15	CX	118/120 (98%)	98 (83%)	19 (16%)	1 (1%)	16	50
16	CY	129/131 (98%)	112 (87%)	16 (12%)	1 (1%)	16	50
17	CZ	132/134 (98%)	110 (83%)	21 (16%)	1 (1%)	16	50
18	Cr	132/134 (98%)	81 (61%)	47 (36%)	4 (3%)	3	19
19	Ch	121/123 (98%)	106 (88%)	15 (12%)	0	100	100
20	Cb	73/75 (97%)	59 (81%)	11 (15%)	3 (4%)	2	13
21	CB	412/414 (100%)	346 (84%)	56 (14%)	10 (2%)	4	24
22	CF	224/226 (99%)	199 (89%)	20 (9%)	5 (2%)	5	26
23	Cc	98/100 (98%)	94 (96%)	4 (4%)	0	100	100
24	Ce	130/132 (98%)	118 (91%)	11 (8%)	1 (1%)	16	50
25	Cf	155/157 (99%)	113 (73%)	36 (23%)	6 (4%)	2	14

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	Ci	111/113 (98%)	82 (74%)	28 (25%)	1 (1%)	14	48
27	Ck	68/70 (97%)	61 (90%)	7 (10%)	0	100	100
28	Cl	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
29	CC	390/392 (100%)	318 (82%)	67 (17%)	5 (1%)	9	38
30	Cm	50/52 (96%)	43 (86%)	6 (12%)	1 (2%)	6	28
31	Cn	23/25 (92%)	21 (91%)	2 (9%)	0	100	100
32	Cp	89/91 (98%)	80 (90%)	9 (10%)	0	100	100
33	Co	102/104 (98%)	82 (80%)	18 (18%)	2 (2%)	6	28
34	CJ	180/182 (99%)	149 (83%)	30 (17%)	1 (1%)	21	56
35	CH	188/190 (99%)	164 (87%)	21 (11%)	3 (2%)	7	34
36	CE	226/228 (99%)	157 (70%)	62 (27%)	7 (3%)	3	19
37	CG	239/241 (99%)	194 (81%)	43 (18%)	2 (1%)	16	50
41	Ag	316/318 (99%)	265 (84%)	51 (16%)	0	100	100
42	AU	100/102 (98%)	89 (89%)	11 (11%)	0	100	100
43	AO	125/127 (98%)	100 (80%)	25 (20%)	0	100	100
44	AX	141/143 (99%)	120 (85%)	20 (14%)	1 (1%)	18	53
45	AM	117/119 (98%)	85 (73%)	32 (27%)	0	100	100
46	Ad	50/52 (96%)	33 (66%)	17 (34%)	0	100	100
47	AN	148/150 (99%)	137 (93%)	11 (7%)	0	100	100
48	AL	153/155 (99%)	133 (87%)	19 (12%)	1 (1%)	18	53
49	AR	118/120 (98%)	92 (78%)	25 (21%)	1 (1%)	16	50
50	AP	122/124 (98%)	96 (79%)	26 (21%)	0	100	100
51	AB	218/220 (99%)	176 (81%)	37 (17%)	5 (2%)	5	25
52	AA	216/218 (99%)	179 (83%)	36 (17%)	1 (0%)	24	60
53	AV	80/82 (98%)	67 (84%)	13 (16%)	0	100	100
54	AY	124/126 (98%)	101 (82%)	22 (18%)	1 (1%)	16	50
55	AZ	72/74 (97%)	56 (78%)	16 (22%)	0	100	100
56	Aa	105/107 (98%)	86 (82%)	18 (17%)	1 (1%)	12	45
57	Ab	82/84 (98%)	64 (78%)	18 (22%)	0	100	100
58	AD	225/227 (99%)	179 (80%)	44 (20%)	2 (1%)	14	48
59	Ae	56/58 (97%)	39 (70%)	17 (30%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
60	Af	78/80 (98%)	57 (73%)	21 (27%)	0	100	100
61	AJ	179/181 (99%)	152 (85%)	26 (14%)	1 (1%)	21	56
62	AE	259/261 (99%)	215 (83%)	42 (16%)	2 (1%)	16	50
63	AC	225/227 (99%)	188 (84%)	35 (16%)	2 (1%)	14	48
64	AG	229/231 (99%)	197 (86%)	30 (13%)	2 (1%)	14	48
65	AH	192/194 (99%)	161 (84%)	31 (16%)	0	100	100
66	AI	205/207 (99%)	161 (78%)	41 (20%)	3 (2%)	8	35
67	AQ	146/148 (99%)	116 (80%)	29 (20%)	1 (1%)	18	53
68	Cz	215/217 (99%)	175 (81%)	40 (19%)	0	100	100
71	AW	127/129 (98%)	117 (92%)	10 (8%)	0	100	100
72	AT	122/126 (97%)	92 (75%)	29 (24%)	1 (1%)	16	50
73	AK	88/90 (98%)	64 (73%)	24 (27%)	0	100	100
74	AF	187/189 (99%)	146 (78%)	41 (22%)	0	100	100
75	Ac	60/62 (97%)	49 (82%)	11 (18%)	0	100	100
76	CU	97/99 (98%)	73 (75%)	23 (24%)	1 (1%)	12	45
77	Cj	85/87 (98%)	74 (87%)	10 (12%)	1 (1%)	10	40
78	CW	58/60 (97%)	53 (91%)	5 (9%)	0	100	100
79	Cg	101/103 (98%)	90 (89%)	10 (10%)	1 (1%)	12	45
80	Cd	105/107 (98%)	97 (92%)	8 (8%)	0	100	100
81	AS	134/136 (98%)	117 (87%)	16 (12%)	1 (1%)	18	53
All	All	11596/11750 (99%)	9587 (83%)	1892 (16%)	117 (1%)	15	45

5 of 117 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	CO	112	SER
1	CO	113	PRO
2	CL	7	MET
2	CL	148	GLN
2	CL	160	GLN

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	CO	175/175 (100%)	173 (99%)	2 (1%)	65	83
2	CL	173/173 (100%)	167 (96%)	6 (4%)	32	65
3	CV	101/101 (100%)	101 (100%)	0	100	100
4	CM	138/138 (100%)	137 (99%)	1 (1%)	76	86
5	Ca	122/122 (100%)	120 (98%)	2 (2%)	55	79
6	CN	174/174 (100%)	168 (97%)	6 (3%)	32	66
7	CI	187/187 (100%)	186 (100%)	1 (0%)	81	89
8	CD	241/241 (100%)	240 (100%)	1 (0%)	84	90
9	CQ	164/164 (100%)	160 (98%)	4 (2%)	43	73
10	CR	176/176 (100%)	175 (99%)	1 (1%)	78	88
11	CA	195/195 (100%)	193 (99%)	2 (1%)	68	84
12	CS	156/156 (100%)	152 (97%)	4 (3%)	40	72
13	CT	137/137 (100%)	135 (98%)	2 (2%)	57	80
14	CP	160/160 (100%)	151 (94%)	9 (6%)	19	52
15	CX	106/106 (100%)	105 (99%)	1 (1%)	70	85
16	CY	116/116 (100%)	111 (96%)	5 (4%)	26	60
17	CZ	121/121 (100%)	121 (100%)	0	100	100
18	Cr	112/112 (100%)	111 (99%)	1 (1%)	70	85
19	Ch	112/112 (100%)	110 (98%)	2 (2%)	51	77
20	Cb	67/67 (100%)	66 (98%)	1 (2%)	57	80
21	CB	349/349 (100%)	341 (98%)	8 (2%)	44	74
22	CF	200/200 (100%)	197 (98%)	3 (2%)	57	80
23	Cc	84/84 (100%)	84 (100%)	0	100	100
24	Ce	120/120 (100%)	119 (99%)	1 (1%)	73	86
25	Cf	123/123 (100%)	121 (98%)	2 (2%)	55	79
26	Ci	100/100 (100%)	98 (98%)	2 (2%)	48	76
27	Ck	65/65 (100%)	63 (97%)	2 (3%)	35	68
28	Cl	45/45 (100%)	45 (100%)	0	100	100
29	CC	323/323 (100%)	317 (98%)	6 (2%)	50	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	Cm	48/48 (100%)	45 (94%)	3 (6%)	16	48
31	Cn	23/23 (100%)	23 (100%)	0	100	100
32	Cp	74/74 (100%)	69 (93%)	5 (7%)	14	45
33	Co	94/94 (100%)	93 (99%)	1 (1%)	65	83
34	CJ	155/155 (100%)	151 (97%)	4 (3%)	40	72
35	CH	169/169 (100%)	165 (98%)	4 (2%)	43	73
36	CE	197/197 (100%)	189 (96%)	8 (4%)	27	61
37	CG	210/210 (100%)	205 (98%)	5 (2%)	43	73
41	Ag	280/280 (100%)	276 (99%)	4 (1%)	59	80
42	AU	95/95 (100%)	94 (99%)	1 (1%)	65	83
43	AO	98/98 (100%)	96 (98%)	2 (2%)	48	76
44	AX	116/116 (100%)	115 (99%)	1 (1%)	70	85
45	AM	104/104 (100%)	100 (96%)	4 (4%)	29	63
46	Ad	45/45 (100%)	45 (100%)	0	100	100
47	AN	130/130 (100%)	130 (100%)	0	100	100
48	AL	138/138 (100%)	135 (98%)	3 (2%)	45	74
49	AR	108/108 (100%)	106 (98%)	2 (2%)	50	76
50	AP	111/111 (100%)	111 (100%)	0	100	100
51	AB	199/199 (100%)	198 (100%)	1 (0%)	81	89
52	AA	190/190 (100%)	189 (100%)	1 (0%)	81	89
53	AV	67/67 (100%)	66 (98%)	1 (2%)	57	80
54	AY	105/106 (99%)	103 (98%)	2 (2%)	50	76
55	AZ	67/67 (100%)	64 (96%)	3 (4%)	24	59
56	Aa	94/94 (100%)	92 (98%)	2 (2%)	47	75
57	Ab	72/72 (100%)	72 (100%)	0	100	100
58	AD	192/192 (100%)	191 (100%)	1 (0%)	81	89
59	Ae	47/47 (100%)	47 (100%)	0	100	100
60	Af	70/70 (100%)	69 (99%)	1 (1%)	59	80
61	AJ	161/161 (100%)	161 (100%)	0	100	100
62	AE	220/220 (100%)	218 (99%)	2 (1%)	70	85
63	AC	188/188 (100%)	187 (100%)	1 (0%)	81	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
64	AG	200/200 (100%)	198 (99%)	2 (1%)	68	84
65	AH	175/175 (100%)	173 (99%)	2 (1%)	65	83
66	AI	175/175 (100%)	174 (99%)	1 (1%)	78	88
67	AQ	122/122 (100%)	121 (99%)	1 (1%)	73	86
68	Cz	190/190 (100%)	189 (100%)	1 (0%)	81	89
71	AW	113/113 (100%)	111 (98%)	2 (2%)	51	77
72	AT	104/104 (100%)	102 (98%)	2 (2%)	50	76
73	AK	81/81 (100%)	79 (98%)	2 (2%)	42	72
74	AF	157/157 (100%)	151 (96%)	6 (4%)	29	63
75	Ac	54/54 (100%)	52 (96%)	2 (4%)	30	64
76	CU	92/92 (100%)	90 (98%)	2 (2%)	45	74
77	Cj	74/74 (100%)	72 (97%)	2 (3%)	39	71
78	CW	54/54 (100%)	53 (98%)	1 (2%)	50	76
79	Cg	95/95 (100%)	87 (92%)	8 (8%)	10	37
80	Cd	99/99 (100%)	86 (87%)	13 (13%)	4	19
81	AS	122/122 (100%)	122 (100%)	0	100	100
All	All	10116/10117 (100%)	9932 (98%)	184 (2%)	51	77

5 of 184 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
45	AM	84	ILE
68	Cz	82	VAL
48	AL	71	THR
56	Aa	11	ASN
74	AF	54	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 107 such sidechains are listed below:

Mol	Chain	Res	Type
41	Ag	238	ASN
51	AB	151	GLN
75	Ac	34	GLN
45	AM	80	GLN
48	AL	10	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
38	A9	29/30 (96%)	8 (27%)	1 (3%)
39	A7	119/120 (99%)	30 (25%)	1 (0%)
40	A8	122/123 (99%)	45 (36%)	1 (0%)
69	A5	3555/3703 (96%)	1353 (38%)	81 (2%)
70	B2	1788/1936 (92%)	627 (35%)	32 (1%)
All	All	5613/5912 (94%)	2063 (36%)	116 (2%)

5 of 2063 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
38	A9	4	U
38	A9	9	C
38	A9	20	U
38	A9	21	G
38	A9	22	A

5 of 116 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
69	A5	2125	G
70	B2	1673	U
69	A5	3608	G
70	B2	1595	G
70	B2	1185	U

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
69	A5	7
70	B2	5
72	AT	1
7	CI	1

The worst 5 of 14 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AT	107:LEU	C	121:ARG	N	19.55
1	A5	2293:C	O3'	2390:U	P	18.82
1	A5	2941:G	O3'	2976:A	P	18.19
1	B2	738:A	O3'	757:U	P	14.79
1	A5	2406:A	O3'	2452:A	P	13.09

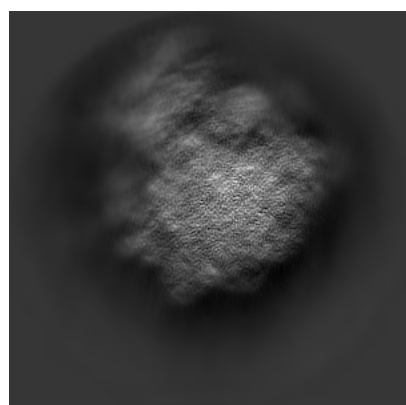
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10624. These allow visual inspection of the internal detail of the map and identification of artifacts.

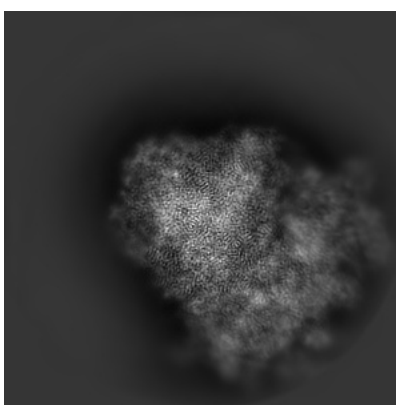
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

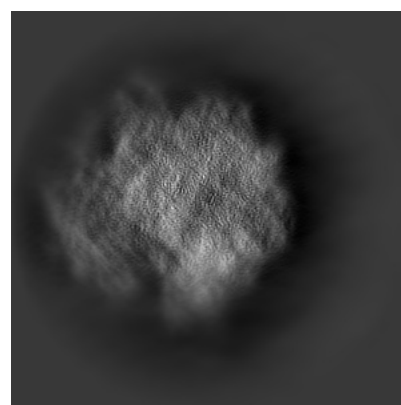
6.1.1 Primary map



X



Y

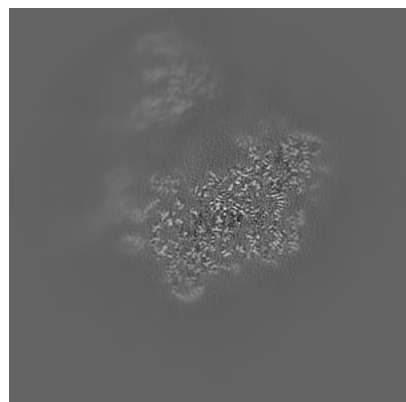


Z

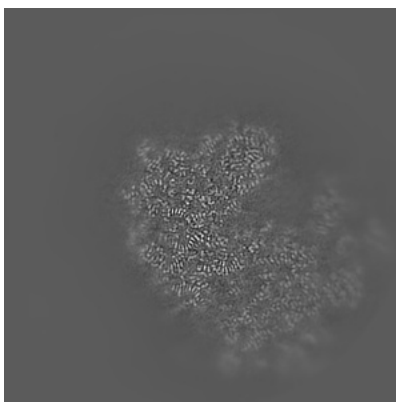
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

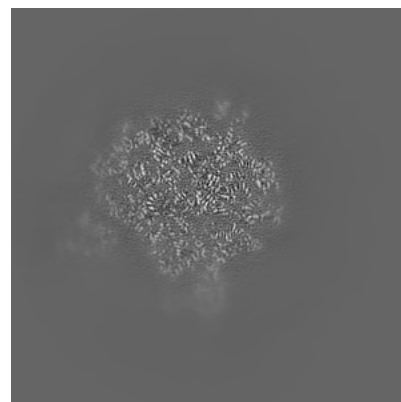
6.2.1 Primary map



X Index: 200



Y Index: 200

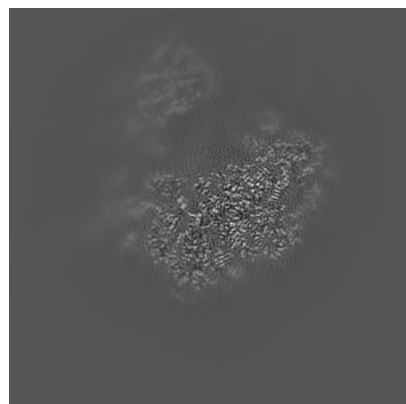


Z Index: 200

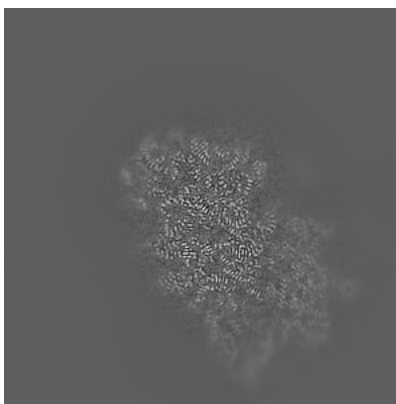
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

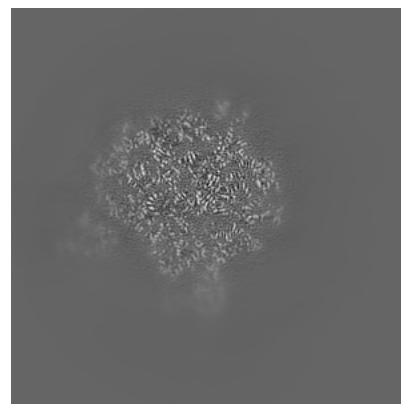
6.3.1 Primary map



X Index: 206



Y Index: 225

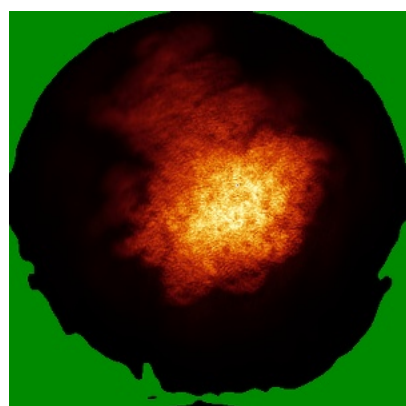


Z Index: 200

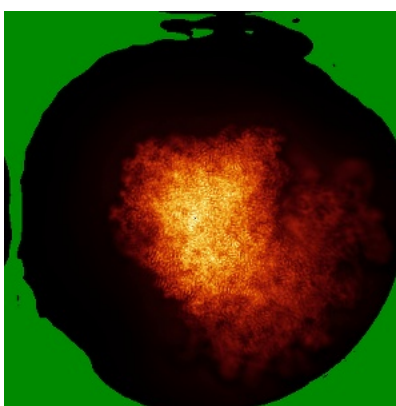
The images above show the largest variance slices of the map in three orthogonal directions.

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

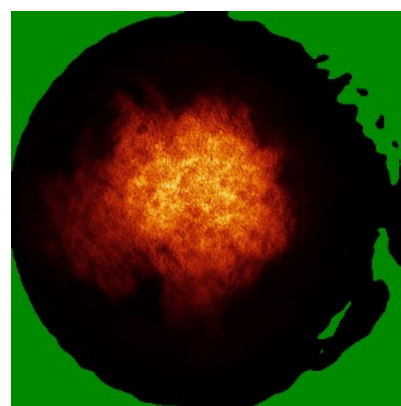
6.4.1 Primary map



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.

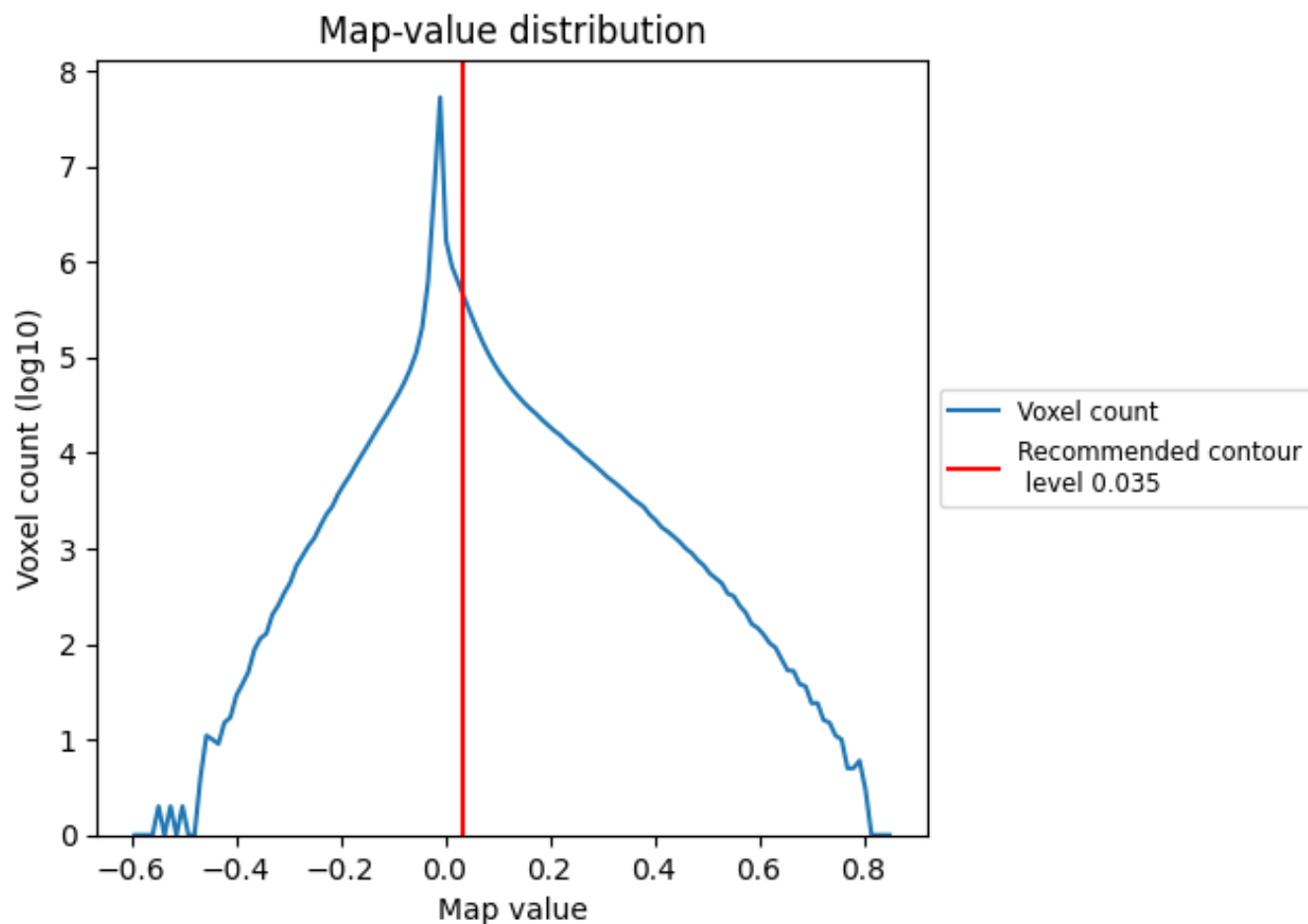
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

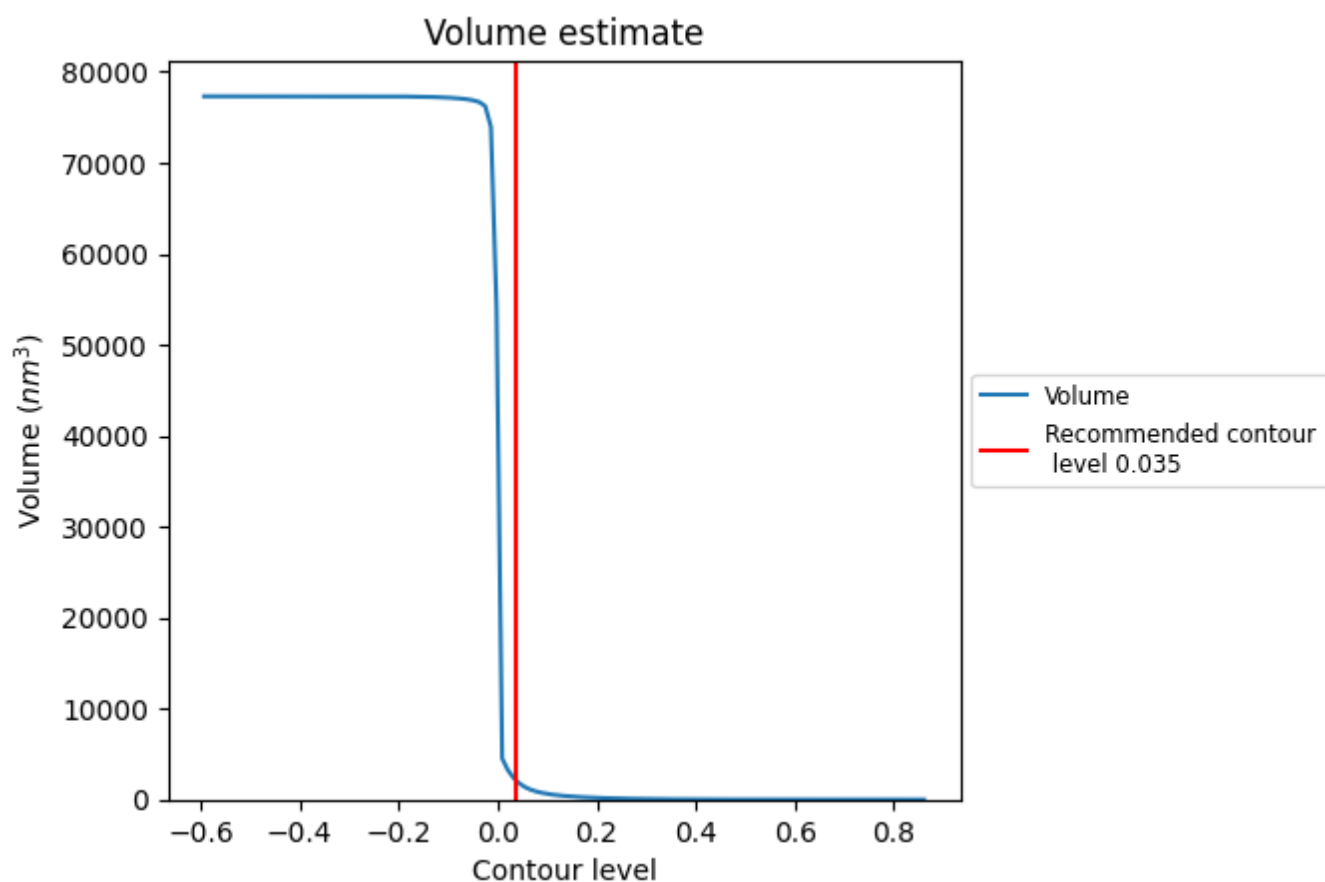
This section contains the results of statistical analysis of the map.

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.

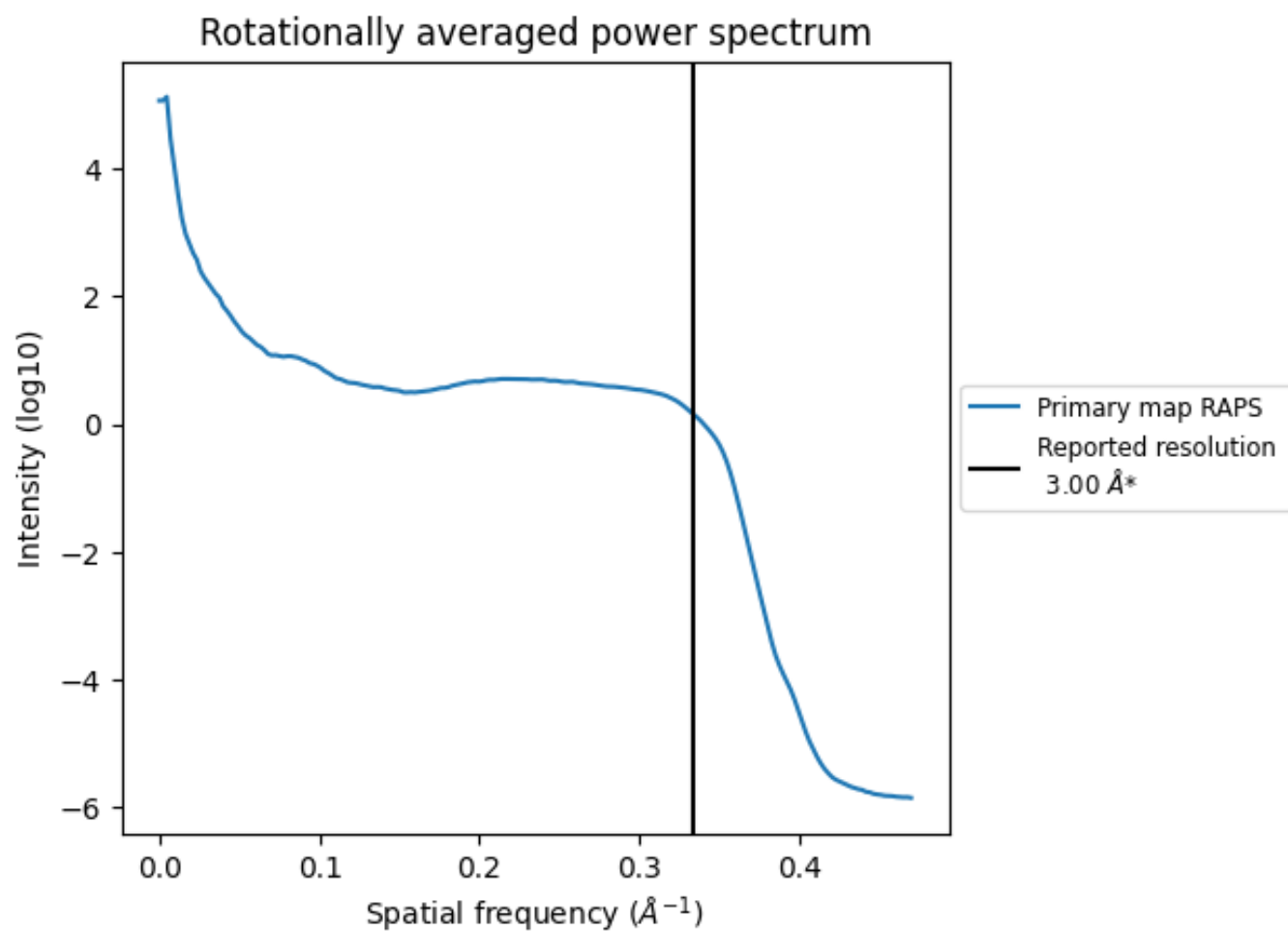
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2221 nm^3 ; this corresponds to an approximate mass of 2007 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 ⓘ

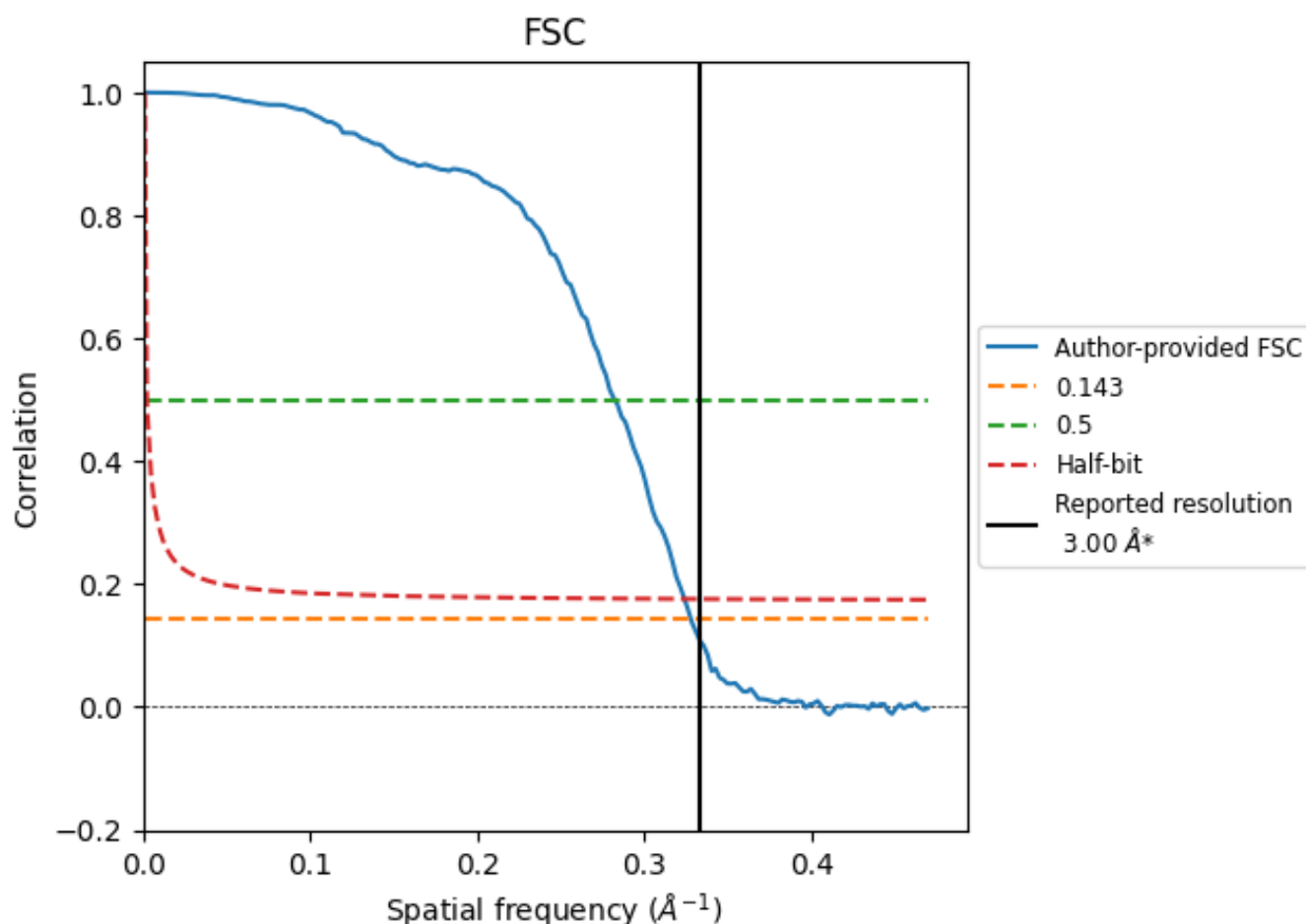


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

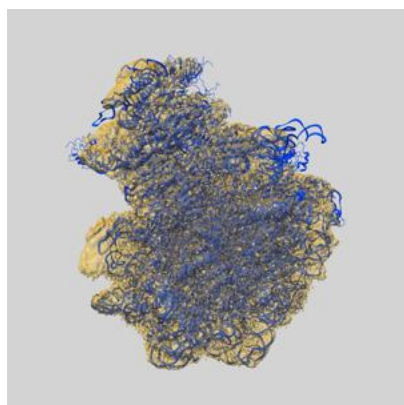
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.05	3.54	3.09
Unmasked-calculated*	-	-	-

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

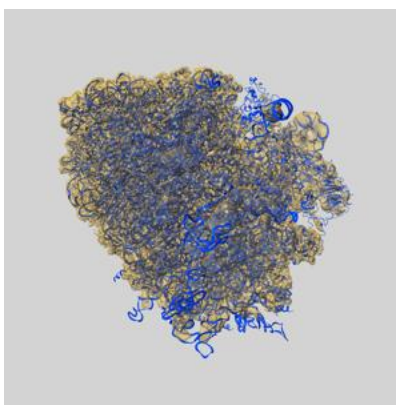
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10624 and PDB model 6XU8. Per-residue inclusion information can be found in section [3](#) on page [20](#).

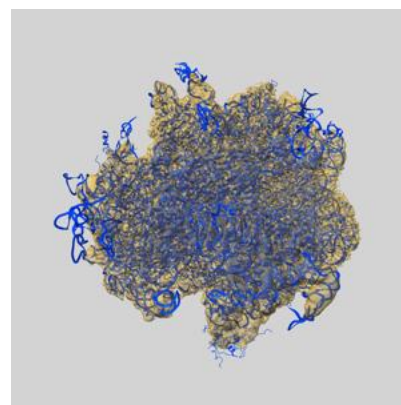
9.1 Map-model overlay [i](#)



X



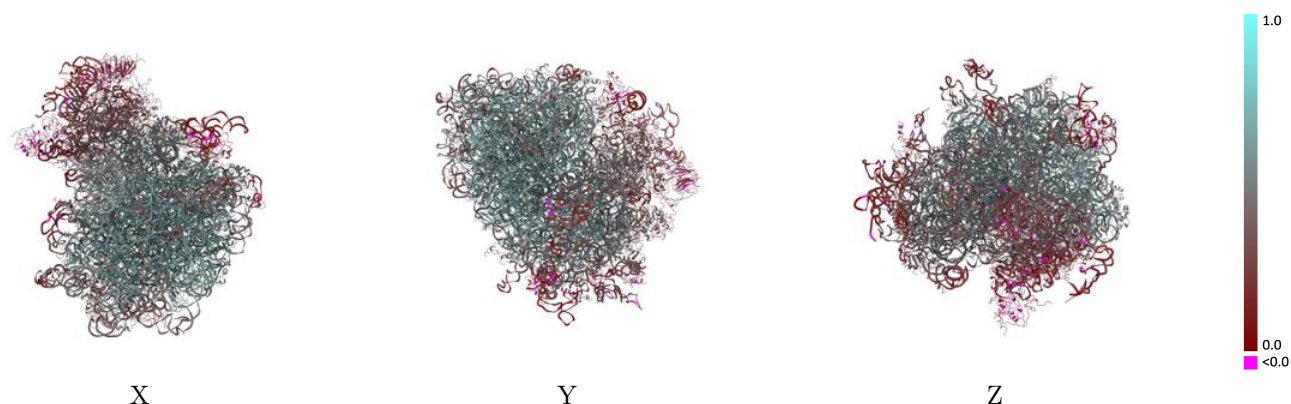
Y



Z

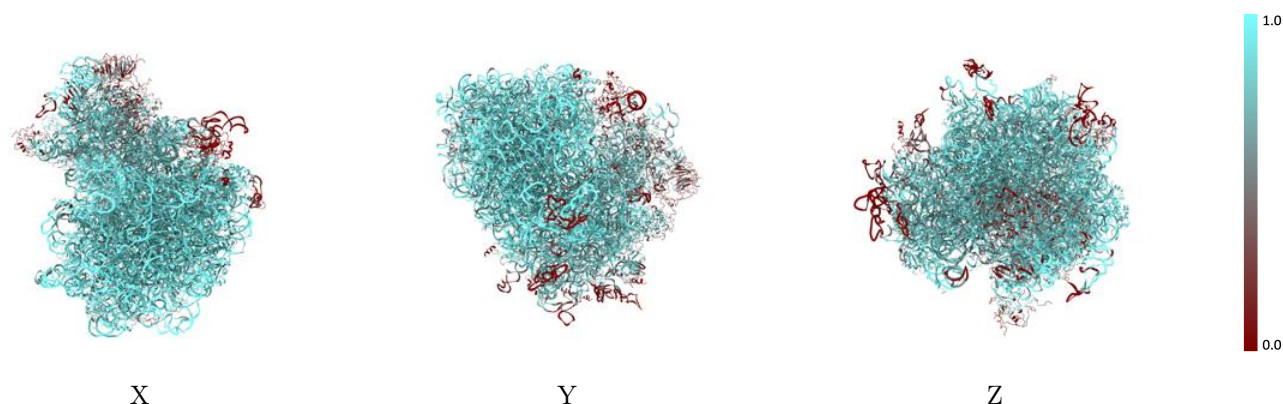
The images above show the 3D surface view of the map at the recommended contour level 0.035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



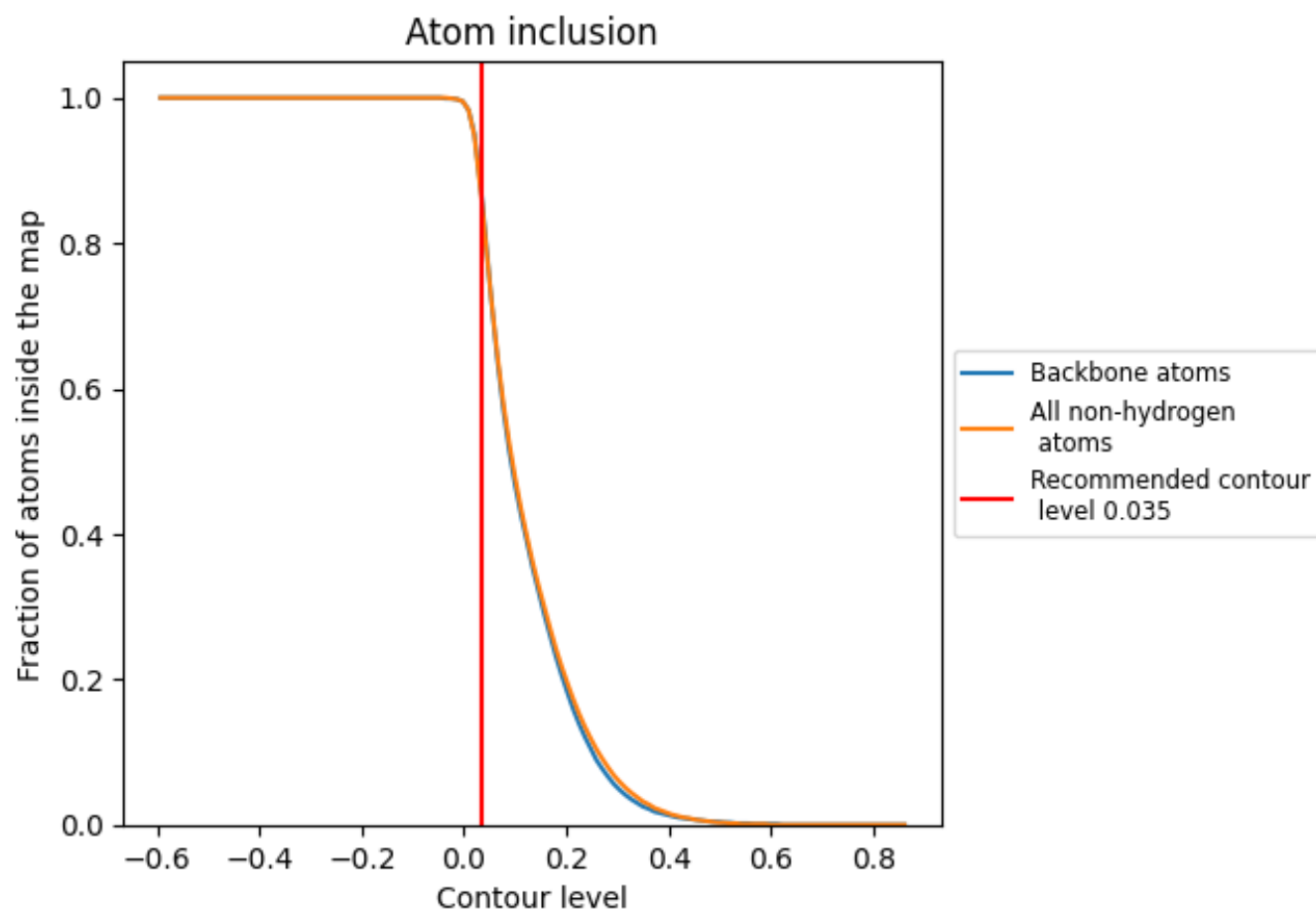
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.035).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 86% 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	 0.8560	 0.4690
A5	 0.9300	 0.5240
A7	 0.9890	 0.5620
A8	 0.9790	 0.5900
A9	 0.9890	 0.5630
AA	 0.6440	 0.3570
AB	 0.7850	 0.4240
AC	 0.7080	 0.4180
AD	 0.4960	 0.2880
AE	 0.7810	 0.4400
AF	 0.4030	 0.2890
AG	 0.6770	 0.3620
AH	 0.6720	 0.3350
AI	 0.7140	 0.4450
AJ	 0.7860	 0.3840
AK	 0.8310	 0.1820
AL	 0.7310	 0.4760
AM	 0.3340	 0.0880
AN	 0.8370	 0.4940
AO	 0.8010	 0.4400
AP	 0.6410	 0.2030
AQ	 0.4760	 0.2430
AR	 0.3860	 0.2720
AS	 0.6640	 0.2790
AT	 0.6780	 0.2540
AU	 0.4620	 0.2850
AV	 0.6100	 0.3970
AW	 0.8340	 0.4890
AX	 0.7800	 0.4840
AY	 0.7450	 0.3580
AZ	 0.3970	 0.2280
Aa	 0.7760	 0.4720
Ab	 0.7900	 0.3890
Ac	 0.5360	 0.3050
Ad	 0.8290	 0.3120



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Chain	Atom inclusion	Q-score
Ae	 0.6000	 0.3500
Af	 0.4230	 0.0970
Ag	 0.2740	 0.1760
B2	 0.8560	 0.3880
CA	 0.9590	 0.5900
CB	 0.9340	 0.5680
CC	 0.9430	 0.5700
CD	 0.8930	 0.4970
CE	 0.8360	 0.4500
CF	 0.9770	 0.5970
CG	 0.8210	 0.4880
CH	 0.9590	 0.5270
CI	 0.8560	 0.4890
CJ	 0.8410	 0.4420
CL	 0.8710	 0.5180
CM	 0.9020	 0.4850
CN	 0.9670	 0.5880
CO	 0.9580	 0.5830
CP	 0.8400	 0.5490
CQ	 0.9720	 0.5970
CR	 0.8270	 0.4900
CS	 0.9540	 0.5590
CT	 0.9520	 0.5600
CU	 0.8200	 0.4670
CV	 0.9580	 0.5910
CW	 0.9510	 0.5770
CX	 0.9120	 0.5480
CY	 0.9670	 0.5800
CZ	 0.9260	 0.5180
Ca	 0.9520	 0.5710
Cb	 0.9330	 0.5120
Cc	 0.9350	 0.5380
Cd	 0.9530	 0.5620
Ce	 0.9680	 0.6060
Cf	 0.9070	 0.5050
Cg	 0.9730	 0.5870
Ch	 0.9340	 0.5600
Ci	 0.8650	 0.4810
Cj	 0.9780	 0.6210
Ck	 0.8650	 0.4890
Cl	 0.9810	 0.6090
Cm	 0.9740	 0.5340

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Chain	Atom inclusion	Q-score
Cn	 0.9350	 0.5760
Co	 0.9480	 0.5650
Cp	 0.9560	 0.5900
Cr	 0.8540	 0.5020
Cz	 0.0230	 0.1440