



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 07:09 AM UTC

PDB ID : 3JBN / pdb_00003jbn
EMDB ID : EMD-6456
Title : Cryo-electron microscopy reconstruction of the Plasmodium falciparum 80S ribosome bound to P-tRNA
Authors : Sun, M.; Li, W.; Blomqvist, K.; Das, S.; Hashem, Y.; Dvorin, J.D.; Frank, J.
Deposited on : 2015-09-16
Resolution : 4.70 Å (reported)
Based on initial models : 3J7A, 3J79

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:

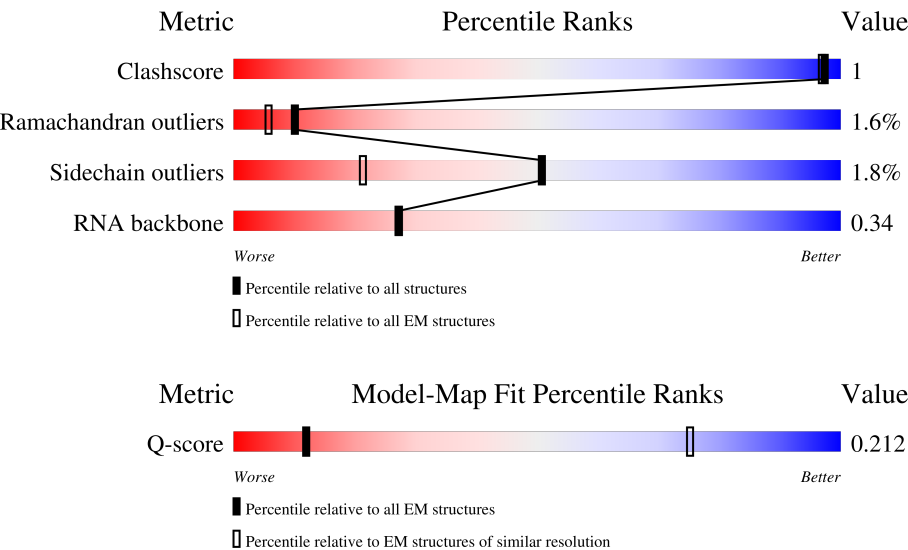
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.70 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	523 (6.20 - 7.20)

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	A	1608	14% 59% 32% 8%
2	7	76	16% 67% 25% 7%
3	D	209	16% 72% 25%

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Mol	Chain	Length	Quality of chain
4	E	185	
5	G	224	
6	I	189	
7	K	129	
8	M	138	
9	W	108	
10	R	114	
11	O	79	
12	Y	154	
13	Z	72	
14	1	120	
15	2	68	
16	3	95	
17	4	76	
18	5	65	
19	6	43	
20	B	210	
21	F	257	
22	H	214	
23	J	188	
24	L	214	
25	N	98	
26	P	127	
27	Q	144	
28	S	128	

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Mol	Chain	Length	Quality of chain
29	T	48	
30	U	149	
31	V	156	
32	X	103	
33	C	195	
34	AA	3193	
35	AC	151	
36	AB	118	
37	AL	211	
38	A1	145	
39	A2	118	
40	A4	66	
41	A6	98	
42	A7	102	
43	AN	146	
44	A8	125	
45	A9	103	
46	Aa	106	
47	Ab	105	
48	Ad	76	
49	Ae	50	
50	Af	51	
51	AP	204	
52	Ah	85	
53	Ai	95	

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Mol	Chain	Length	Quality of chain
54	AI	213	
55	AJ	244	
56	Ac	89	
57	AK	201	
58	AM	132	
59	AS	186	
60	AO	147	
61	AQ	205	
62	AR	289	
63	AW	170	
64	AY	101	
65	AT	181	
66	AZ	121	
67	A3	119	
68	A5	223	
69	AD	247	
70	AE	380	
71	AF	390	
72	AG	159	
73	AU	180	
74	AH	185	
75	AV	155	
76	Ag	37	
77	AX	97	
78	A0	62	

2 Entry composition

There are 78 unique types of molecules in this entry. The entry contains 193061 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1608	Total	C	N	O	P	0	0
			34207	15346	6106	11169	1586		

- Molecule 2 is a RNA chain called P-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	76	Total	C	N	O	P	0	0
			1620	723	295	527	75		

- Molecule 3 is a protein called 40S ribosomal protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	157	Total	C	N	O	S	0	0
			1229	782	225	215	7		

- Molecule 4 is a protein called 40S ribosomal protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	185	Total	C	N	O	S	0	0
			1515	962	290	261	2		

- Molecule 5 is a protein called 40S ribosomal protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	224	Total	C	N	O	S	0	0
			1758	1132	307	310	9		

- Molecule 6 is a protein called 40S ribosomal protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	I	180	Total	C	N	O	S	0	0
			1424	893	263	258	10		

- Molecule 7 is a protein called 40S ribosomal protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	K	129	Total	C	N	O	S	0	0
			1037	665	189	178	5		

- Molecule 8 is a protein called 40S ribosomal protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	M	138	Total	C	N	O	S	0	0
			1099	704	200	194	1		

- Molecule 9 is a protein called 40S ribosomal protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	W	95	Total	C	N	O	S	0	0
			786	498	149	136	3		

- Molecule 10 is a protein called 40S ribosomal protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	R	98	Total	C	N	O	S	0	0
			747	474	123	146	4		

- Molecule 11 is a protein called 40S ribosomal protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	O	79	Total	C	N	O	S	0	0
			687	450	116	119	2		

- Molecule 12 is a protein called 40S ribosomal protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Y	154	Total	C	N	O	S	0	0
			1267	811	239	215	2		

- Molecule 13 is a protein called 40S ribosomal protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Z	72	Total	C	N	O	S	0	0
			557	346	102	105	4		

- Molecule 14 is a protein called 40S ribosomal protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	1	120	Total	C	N	O	S	0	0
			986	632	189	163	2		

- Molecule 15 is a protein called 40S ribosomal protein eS25.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	2	41	Total	C	N	O	0	0
			321	208	56	57		

- Molecule 16 is a protein called 40S ribosomal protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	3	95	Total	C	N	O	S	0	0
			782	478	169	129	6		

- Molecule 17 is a protein called 40S ribosomal protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	4	76	Total	C	N	O	S	0	0
			586	368	102	107	9		

- Molecule 18 is a protein called 40S ribosomal protein eS28.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	5	58	Total	C	N	O	0	0
			458	285	93	80		

- Molecule 19 is a protein called 40S ribosomal protein eS30.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	6	43	Total	C	N	O	0	0
			346	213	75	58		

- Molecule 20 is a protein called 40S ribosomal protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	B	210	Total	C	N	O	S	0	0
			1714	1097	301	304	12		

- Molecule 21 is a protein called 40S ribosomal protein eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	F	257	Total	C	N	O	S	0	0
			2062	1320	377	357	8		

- Molecule 22 is a protein called 40S ribosomal protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	H	204	Total	C	N	O	S	0	0
			1648	1045	313	284	6		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	158	ILE	-	insertion	UNP Q8IDR9
H	195	ASP	GLU	conflict	UNP Q8IDR9

- Molecule 23 is a protein called 40S ribosomal protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	J	188	Total	C	N	O	S	0	0
			1529	982	264	279	4		

- Molecule 24 is a protein called 40S ribosomal protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	L	171	Total	C	N	O	S	0	0
			1383	872	264	243	4		

- Molecule 25 is a protein called 40S ribosomal protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	N	98	Total	C	N	O	S	0	0
			772	484	135	148	5		

- Molecule 26 is a protein called 40S ribosomal protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	P	127	Total	C	N	O	S	0	0
			954	591	184	176	3		

- Molecule 27 is a protein called 40S ribosomal protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Q	144	Total	C	N	O	S	0	0
			1129	712	222	193	2		

- Molecule 28 is a protein called 40S ribosomal protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	S	128	Total	C	N	O	S	0	0
			1047	657	205	181	4		

- Molecule 29 is a protein called 40S ribosomal protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	T	48	Total	C	N	O	S	0	0
			405	252	85	64	4		

- Molecule 30 is a protein called 40S ribosomal protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	U	149	Total	C	N	O	S	0	0
			1202	769	220	210	3		

- Molecule 31 is a protein called 40S ribosomal protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	V	146	Total	C	N	O	S	0	0
			1206	772	227	200	7		

- Molecule 32 is a protein called 40S ribosomal protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	X	96	Total	C	N	O	S	0	0
			777	497	137	139	4		

- Molecule 33 is a protein called 40S ribosomal protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	C	195	Total	C	N	O	S	0	0
			1539	990	266	274	9		

- Molecule 34 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	AA	3193	Total	C	N	O	P	0	0
			67884	30446	12054	22223	3161		

- Molecule 35 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	AC	151	Total	C	N	O	P	0	0
			3215	1444	589	1034	148		

- Molecule 36 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	AB	118	Total	C	N	O	P	0	0
			2522	1128	461	816	117		

- Molecule 37 is a protein called 60S ribosomal protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	AL	211	Total	C	N	O	S	0	0
			1757	1116	346	291	4		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AL	19	HIS	ARG	conflict	UNP Q8IAX6
AL	20	ARG	HIS	conflict	UNP Q8IAX6
AL	201	CYS	ARG	conflict	UNP Q8IAX6

- Molecule 38 is a protein called 60S ribosomal protein eL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	A1	140	Total	C	N	O	S	0	0
			1134	736	204	191	3		

- Molecule 39 is a protein called 60S ribosomal protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	A2	104	Total	C	N	O	S	0	0
			831	529	151	148	3		

- Molecule 40 is a protein called 60S ribosomal protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	A4	66	Total	C	N	O	S	0	0
			555	347	116	90	2		

- Molecule 41 is a protein called 60S ribosomal protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	A6	98	Total	C	N	O	S	0	0
			741	462	132	140	7		

- Molecule 42 is a protein called 60S ribosomal protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	A7	96	Total	C	N	O	S	0	0
			794	508	151	130	5		

- Molecule 43 is a protein called 60S ribosomal protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AN	146	Total	C	N	O	S	0	0
			1202	781	210	205	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AN	?	-	LYS	deletion	UNP Q8ILE8

- Molecule 44 is a protein called 60S ribosomal protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	A8	125	Total	C	N	O	S	0	0
			1037	660	206	164	7		

- Molecule 45 is a protein called 60S ribosomal protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	A9	103	Total	C	N	O	S	0	0
			845	543	163	136	3		

- Molecule 46 is a protein called 60S ribosomal protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Aa	106	Total	C	N	O	S	0	0
			859	530	184	139	6		

- Molecule 47 is a protein called 60S ribosomal protein eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Ab	95	Total	C	N	O	S	0	0
			757	477	150	130			

- Molecule 48 is a protein called 60S ribosomal protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Ad	72	Total	C	N	O	S	0	0
			604	395	107	100	2		

- Molecule 49 is a protein called 60S ribosomal protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Ae	43	Total	C	N	O	S	0	0
			388	243	92	52	1		

- Molecule 50 is a protein called 60S ribosomal protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Af	51	Total	C	N	O	S	0	0
			414	255	87	67	5		

- Molecule 51 is a protein called 60S ribosomal protein eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	AP	204	Total	C	N	O	S	0	0
			1697	1075	351	267	4		

- Molecule 52 is a protein called 60S ribosomal protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Ah	85	Total	C	N	O	S	0	0
			659	417	127	108	7		

- Molecule 53 is a protein called 60S ribosomal protein eL44.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Ai	95	Total	C	N	O	S	0	0
			779	490	152	128	9		

- Molecule 54 is a protein called 60S ribosomal protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	AI	207	Total	C	N	O	S	0	0
			1685	1096	298	286	5		

- Molecule 55 is a protein called 60S ribosomal protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	AJ	222	Total	C	N	O	S	0	0
			1813	1174	323	309	7		

- Molecule 56 is a protein called 60S ribosomal protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Ac	89	Total	C	N	O	S	0	0
			710	441	150	114	5		

- Molecule 57 is a protein called 60S ribosomal protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	AK	201	Total	C	N	O	S	0	0
			1660	1064	311	277	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AK	109	ALA	TYR	conflict	UNP Q8IJZ7

- Molecule 58 is a protein called 60S ribosomal protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AM	132	Total	C	N	O	S	0	0
			996	631	179	178	8		

- Molecule 59 is a protein called 60S ribosomal protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AS	186	Total	C	N	O	S	0	0
			1503	958	299	241	5		

- Molecule 60 is a protein called 60S ribosomal protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	AO	147	Total	C	N	O	S	0	0
			1172	747	232	189	4		

- Molecule 61 is a protein called 60S ribosomal protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AQ	189	Total	C	N	O	S	0	0
			1545	984	291	262	8		

- Molecule 62 is a protein called 60S ribosomal protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AR	252	Total	C	N	O	S	0	0
			2050	1300	385	359	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AR	?	-	LYS	deletion	UNP Q8ILL3

- Molecule 63 is a protein called 60S ribosomal protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	AW	170	Total	C	N	O	S	0	0
			1319	824	266	222	7		

- Molecule 64 is a protein called 60S ribosomal protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AY	101	Total	C	N	O	S	0	0
			797	502	144	145	6		

- Molecule 65 is a protein called 60S ribosomal protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AT	181	Total	C	N	O	S	0	0
			1509	952	309	244	4		

- Molecule 66 is a protein called 60S ribosomal protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	AZ	121	Total	C	N	O	S	0	0
			1001	626	206	166	3		

- Molecule 67 is a protein called 60S ribosomal protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	A3	119	Total	C	N	O	S	0	0
			995	635	194	164	2		

- Molecule 68 is a protein called 60S ribosomal protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	A5	223	Total	C	N	O	S	0	0
			1879	1211	357	306	5		

- Molecule 69 is a protein called 60S ribosomal protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	AD	247	Total	C	N	O	S	0	0
			1867	1166	374	318	9		

- Molecule 70 is a protein called 60S ribosomal protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	AE	380	Total	C	N	O	S	0	0
			3062	1948	575	522	17		

- Molecule 71 is a protein called 60S ribosomal protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	AF	390	Total	C	N	O	S	0	0
			3095	1962	594	528	11		

- Molecule 72 is a protein called 60S ribosomal protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	AG	124	Total	C	N	O	S	0	0
			1011	636	197	172	6		

- Molecule 73 is a protein called 60S ribosomal protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	AU	180	Total	C	N	O	S	0	0
			1497	946	289	255	7		

- Molecule 74 is a protein called 60S ribosomal protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	AH	185	Total	C	N	O	S	0	0
			1476	950	264	256	6		

- Molecule 75 is a protein called 60S ribosomal protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	AV	155	Total	C	N	O	S	0	0
			1276	814	241	215	6		

- Molecule 76 is a protein called 60S ribosomal protein eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Ag	37	Total	C	N	O	S	0	0
			343	210	86	45	2		

- Molecule 77 is a protein called 60S ribosomal protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	AX	97	Total	C	N	O	S	0	0
			825	548	135	140	2		

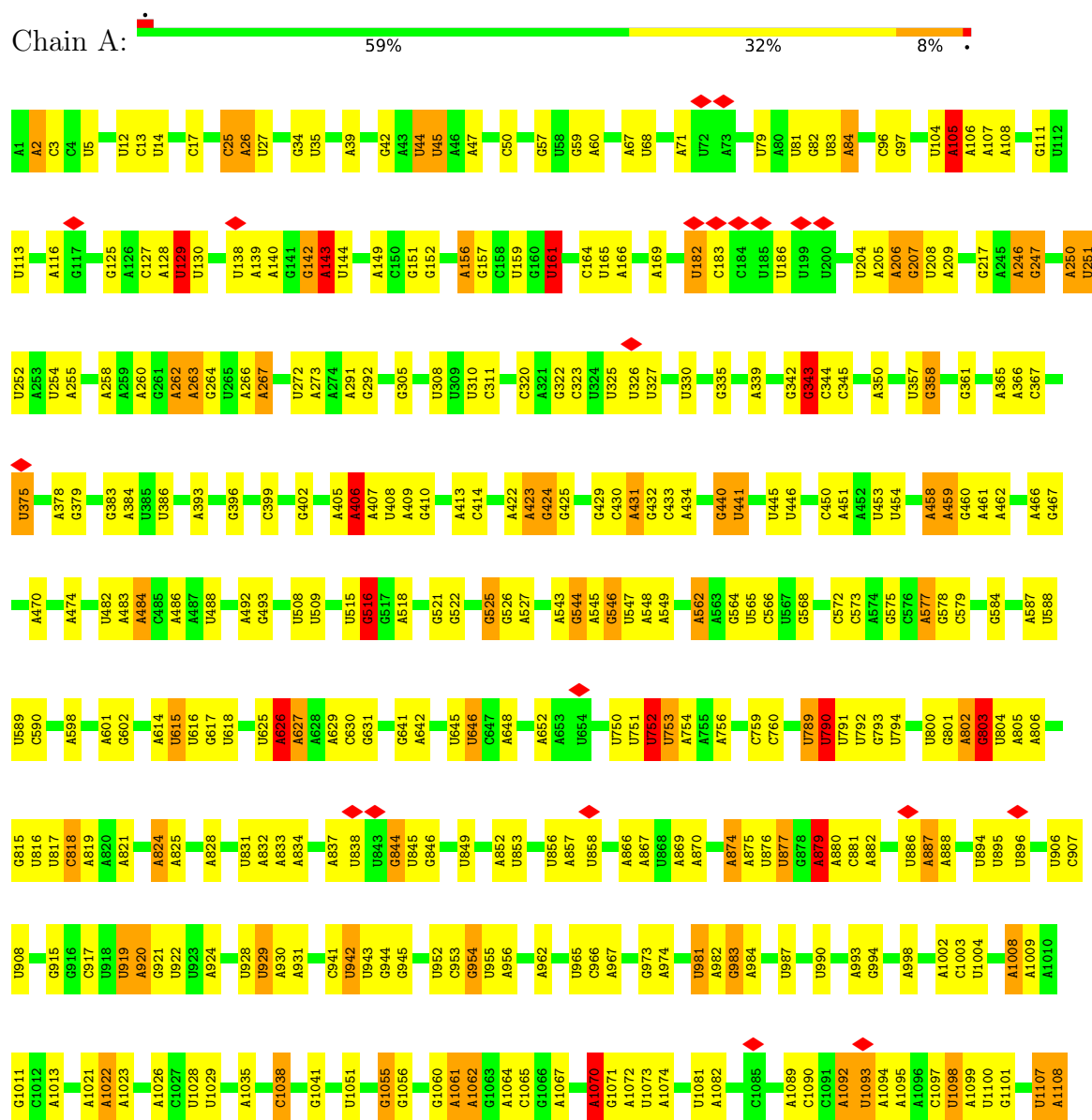
- Molecule 78 is a protein called 60S ribosomal protein eL24.

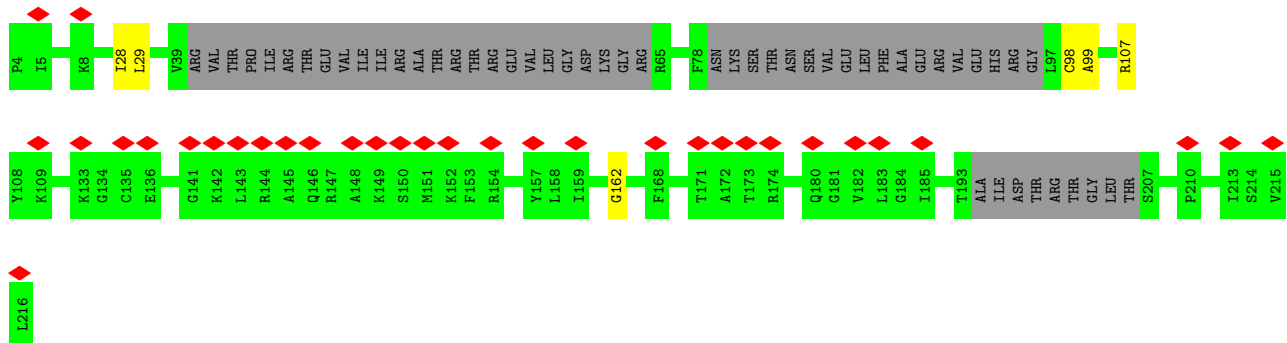
Mol	Chain	Residues	Atoms					AltConf	Trace
78	A0	62	Total	C	N	O	S	0	0
			522	336	97	88	1		

3 Residue-property plots

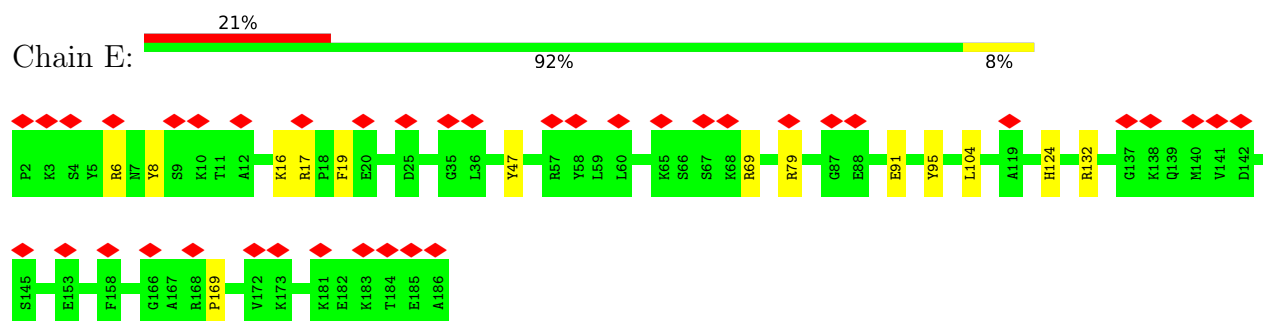
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 18S ribosomal RNA

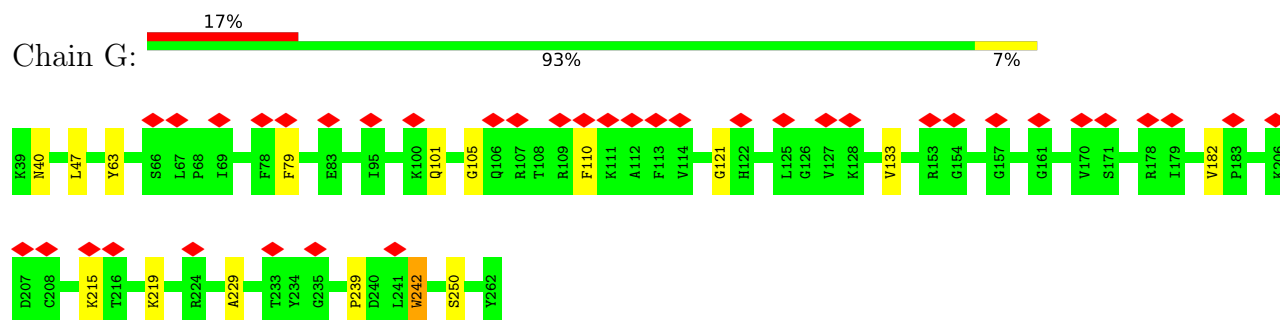




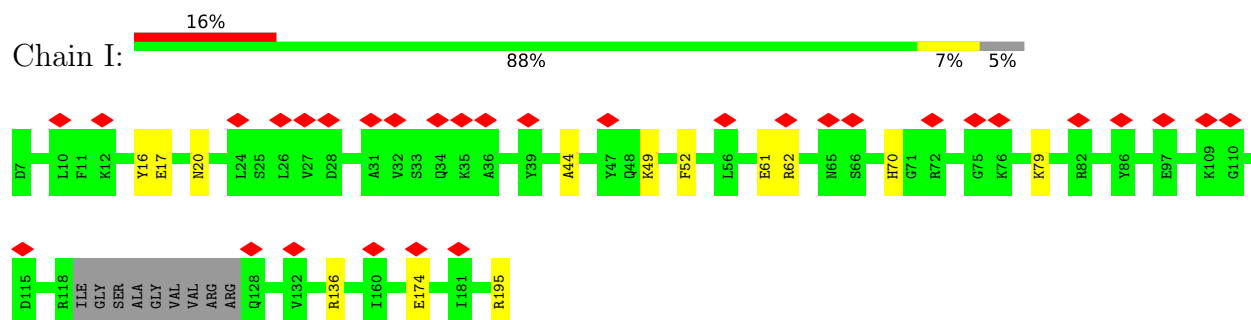
- Molecule 4: 40S ribosomal protein uS4

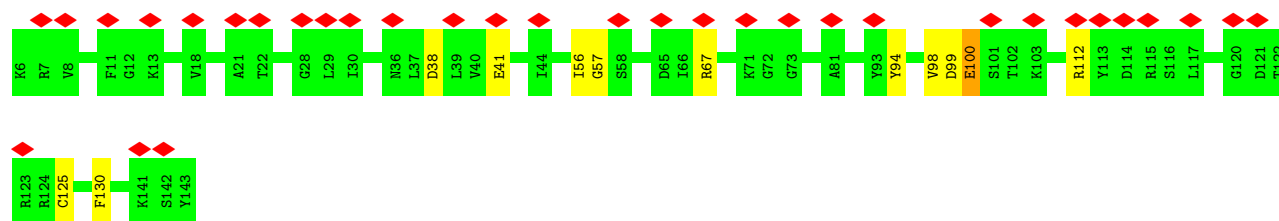


- Molecule 5: 40S ribosomal protein uS5

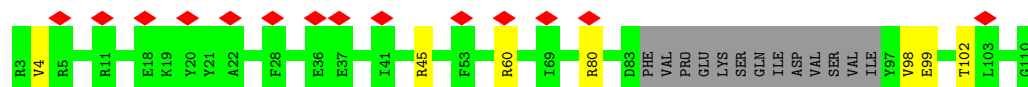
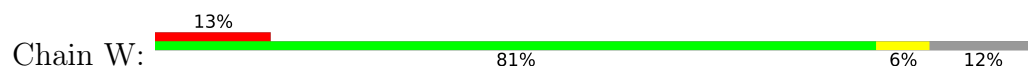


- Molecule 6: 40S ribosomal protein uS7

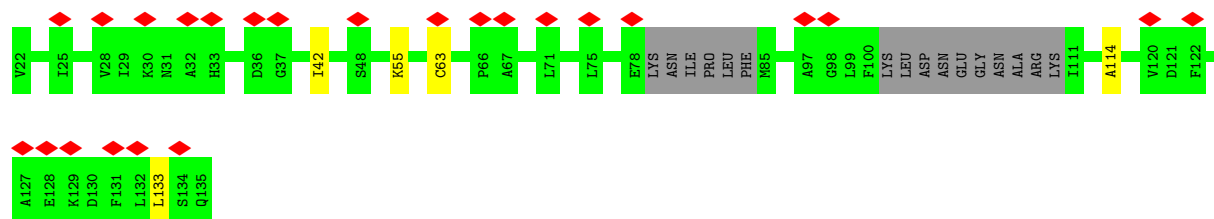
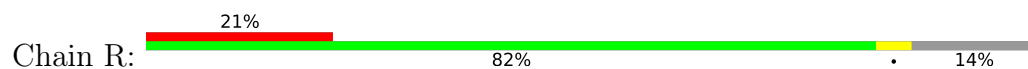




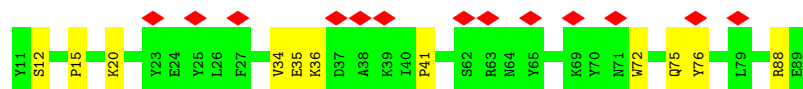
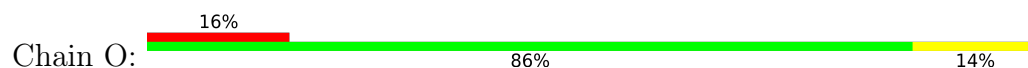
• Molecule 9: 40S ribosomal protein eS17



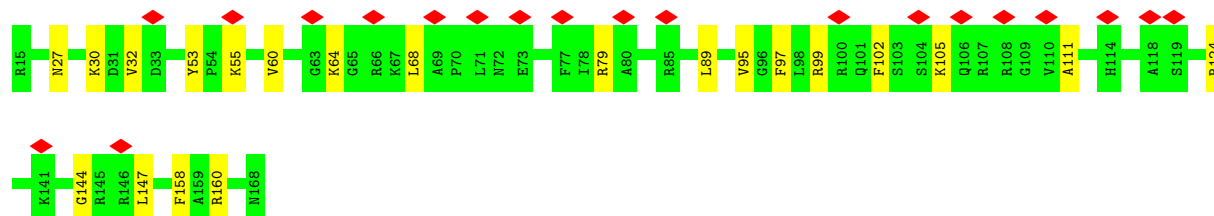
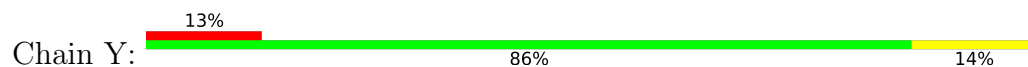
• Molecule 10: 40S ribosomal protein eS12



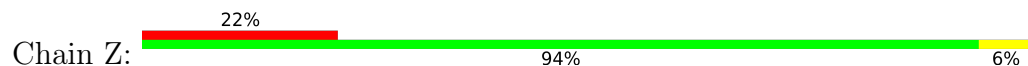
• Molecule 11: 40S ribosomal protein eS10

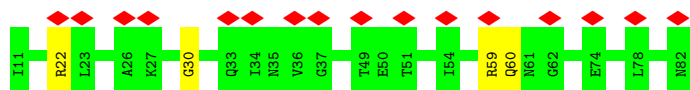


• Molecule 12: 40S ribosomal protein eS19

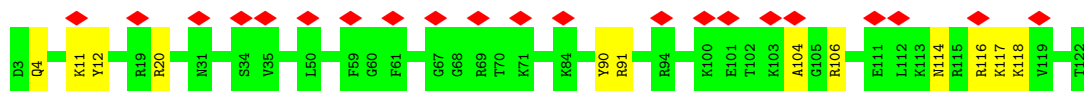
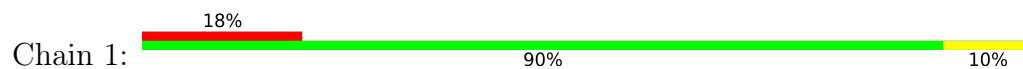


• Molecule 13: 40S ribosomal protein eS21

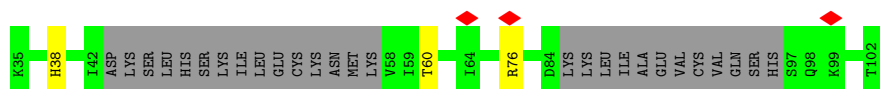




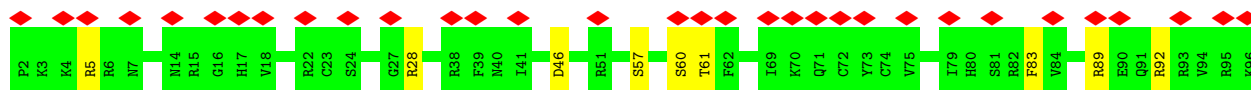
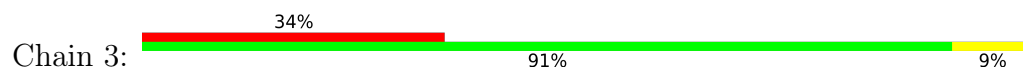
- Molecule 14: 40S ribosomal protein eS24



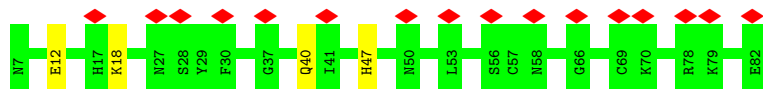
- Molecule 15: 40S ribosomal protein eS25



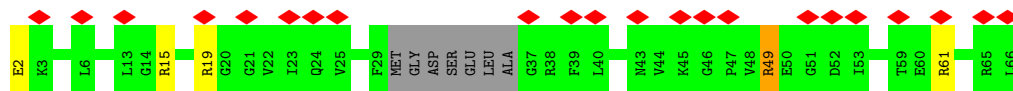
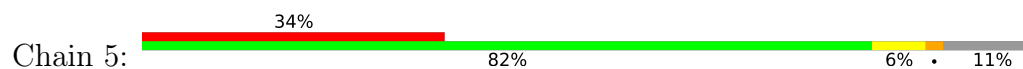
- Molecule 16: 40S ribosomal protein eS26



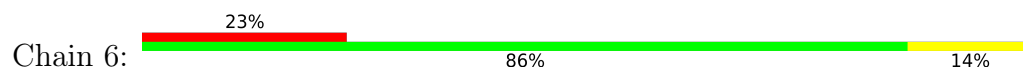
- Molecule 17: 40S ribosomal protein eS27



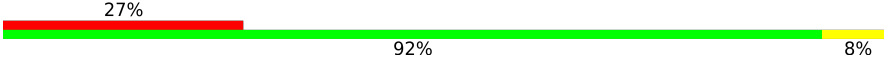
- Molecule 18: 40S ribosomal protein eS28

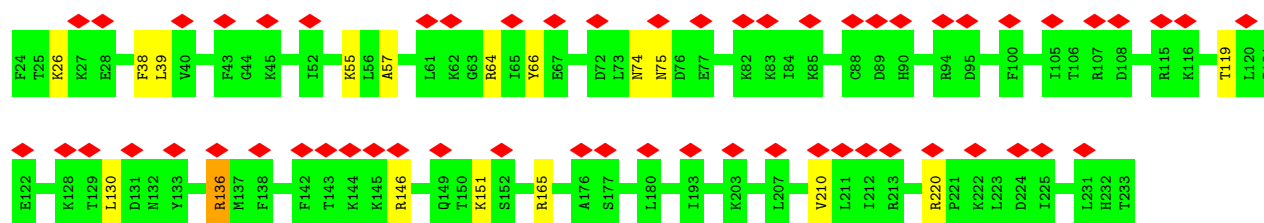


- Molecule 19: 40S ribosomal protein eS30

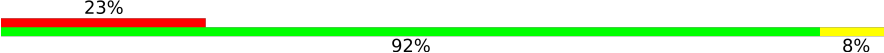


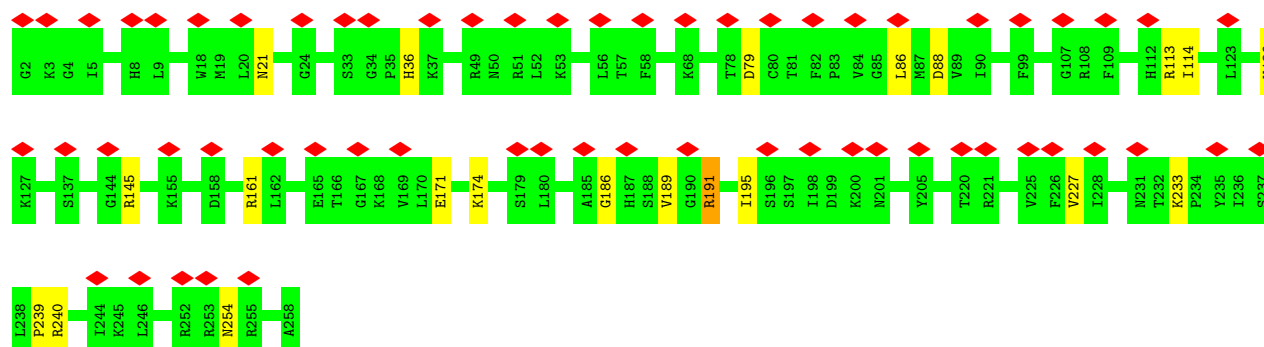
- Molecule 20: 40S ribosomal protein eS1

Chain B: 

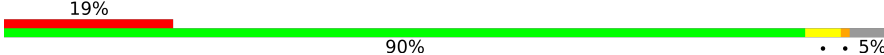


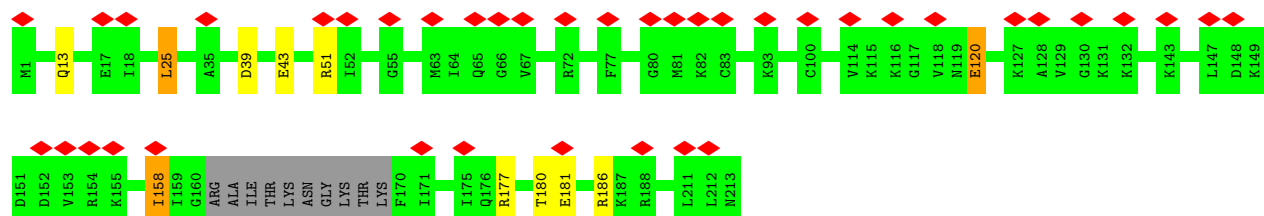
- Molecule 21: 40S ribosomal protein eS4

Chain F: 



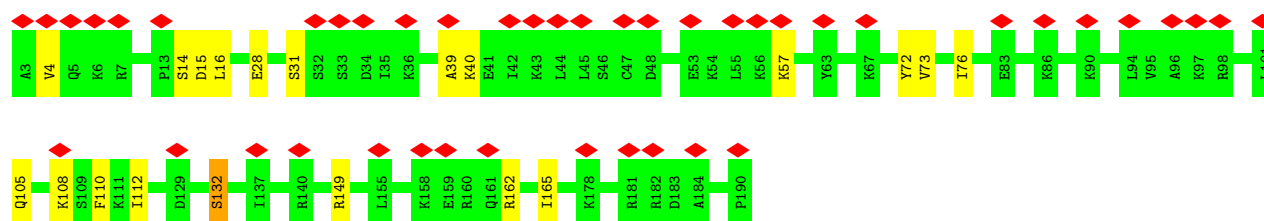
- Molecule 22: 40S ribosomal protein eS6

Chain H: 



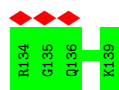
- Molecule 23: 40S ribosomal protein eS7

Chain J: 

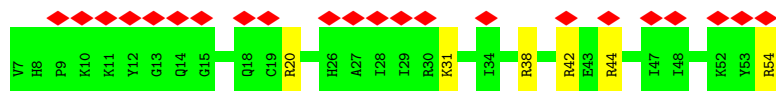
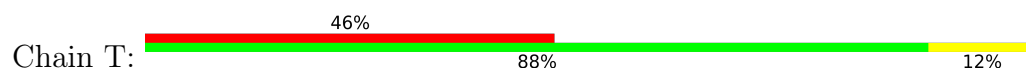


- Molecule 24: 40S ribosomal protein eS8

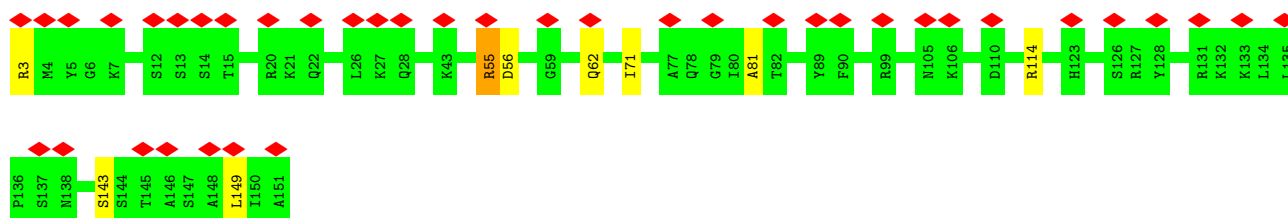
Chain L: 



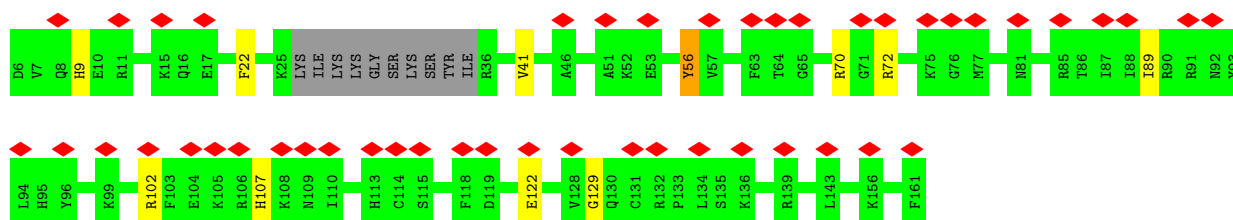
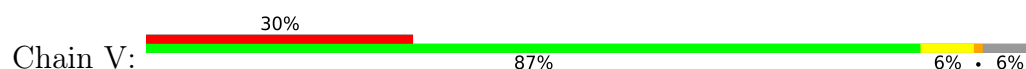
- Molecule 29: 40S ribosomal protein uS14



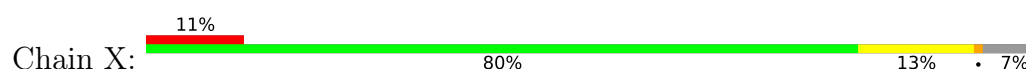
- Molecule 30: 40S ribosomal protein uS15



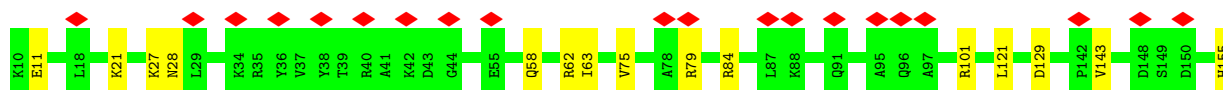
- Molecule 31: 40S ribosomal protein uS17



- Molecule 32: 40S ribosomal protein uS19



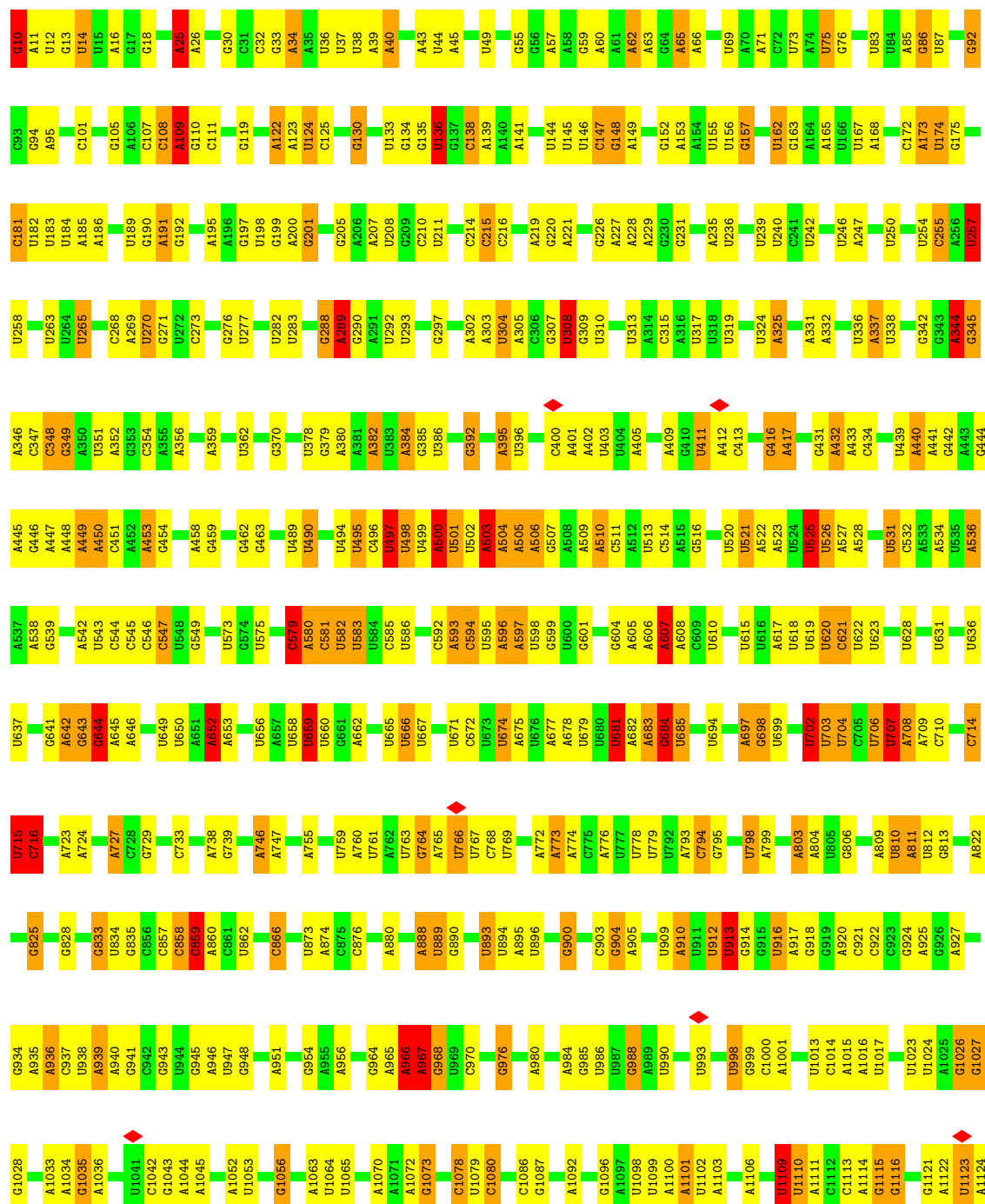
- Molecule 33: 40S ribosomal protein uS2

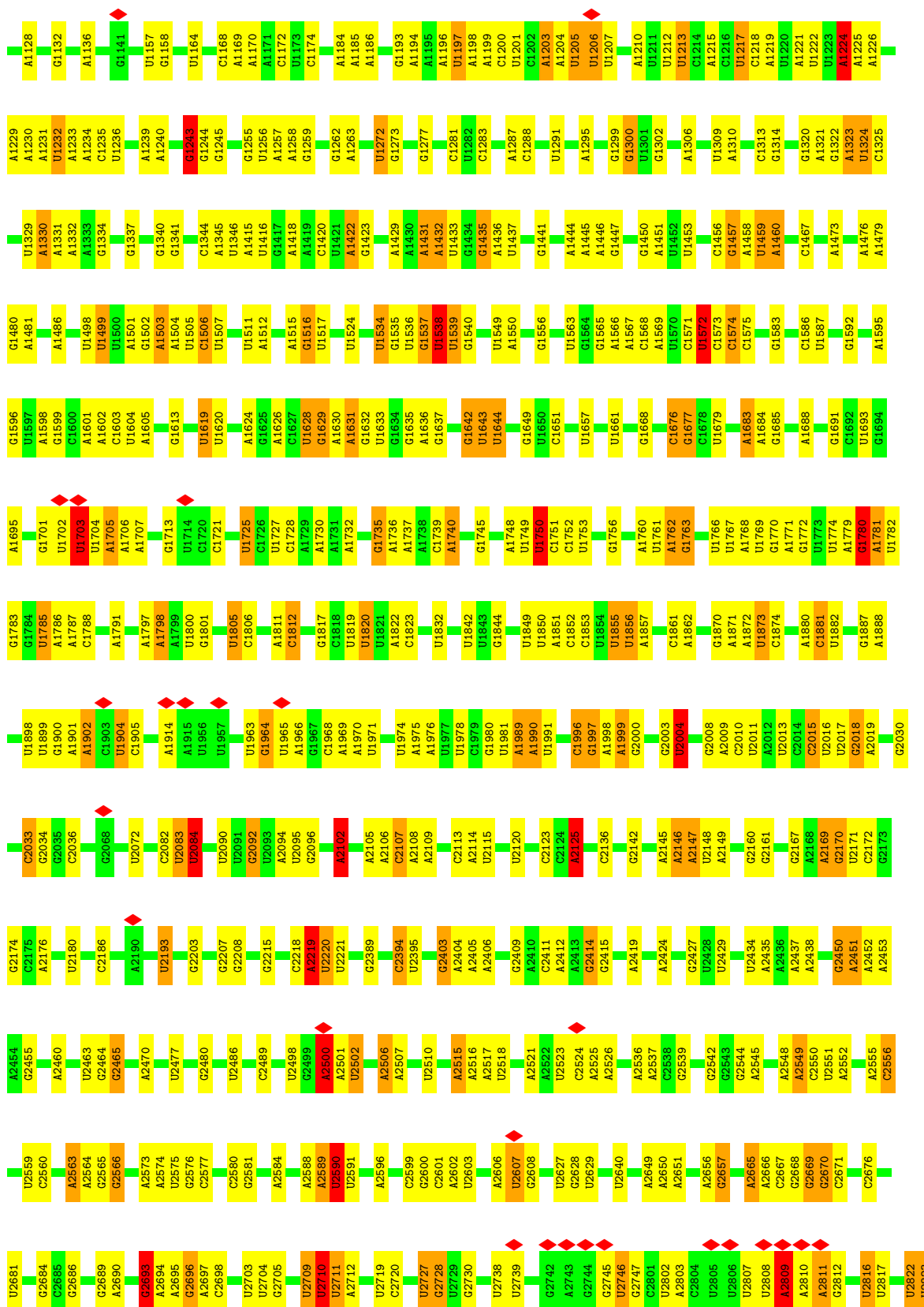


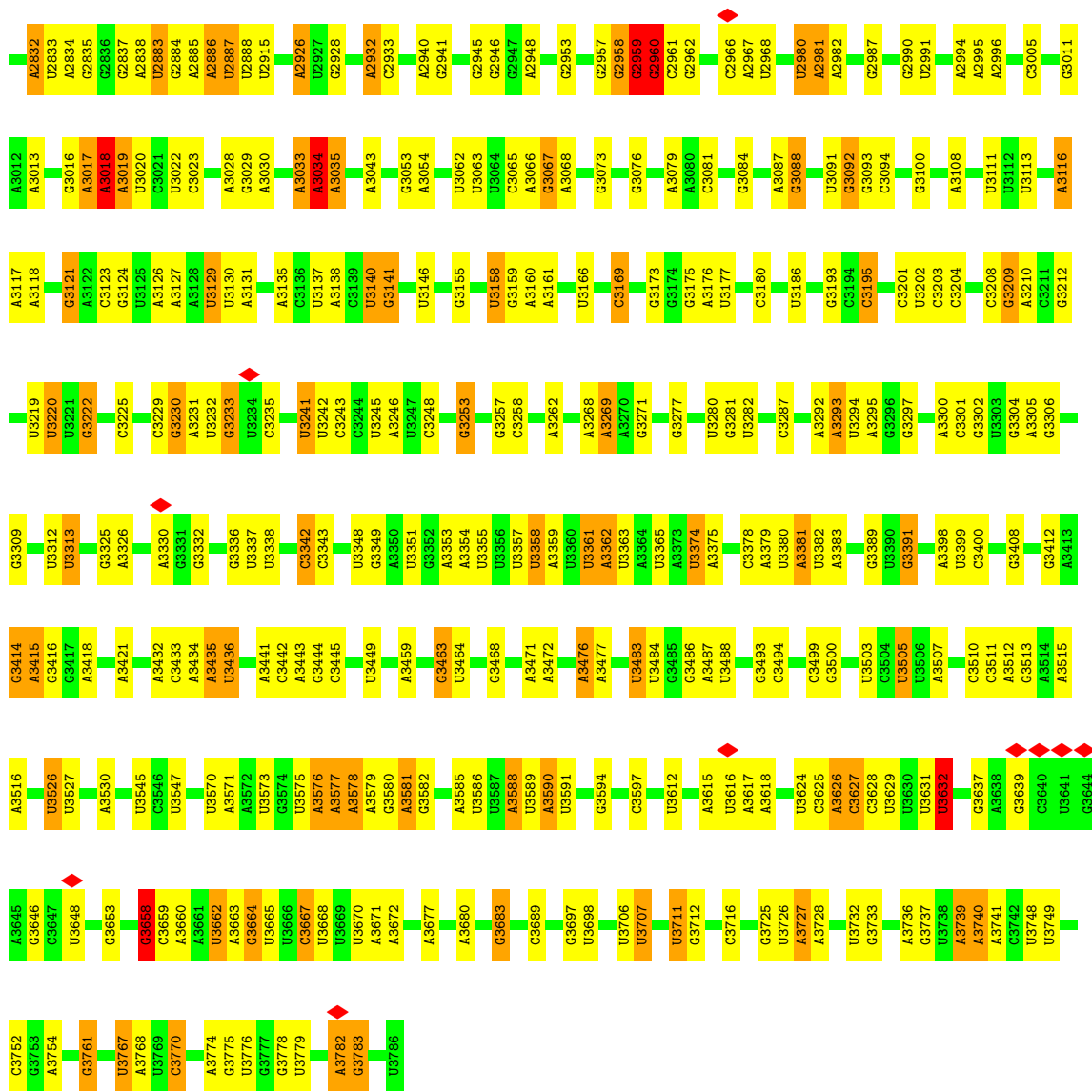


• Molecule 34: 28S ribosomal RNA

Chain AA: 57% 32% 9%

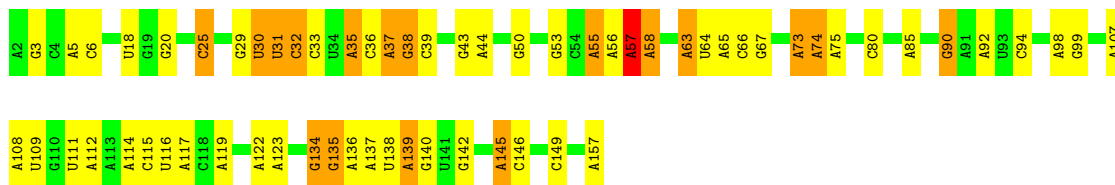






• Molecule 35: 5.8S ribosomal RNA

Chain AC: 58% 30% 11%



• Molecule 36: 5S ribosomal RNA

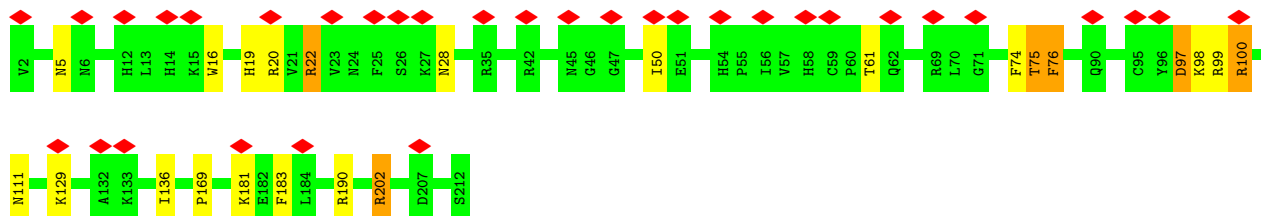
Chain AB: 69% 26%





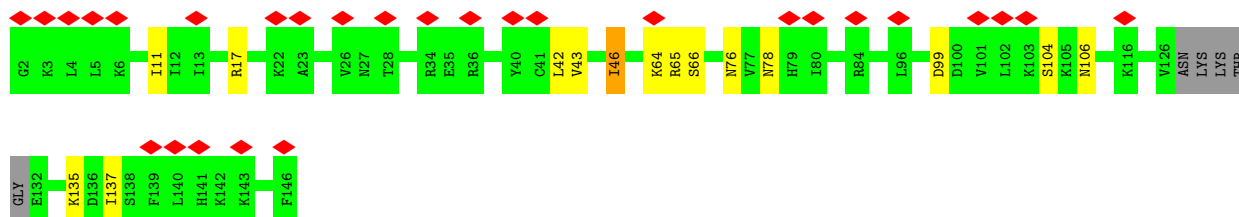
- Molecule 37: 60S ribosomal protein eL13

Chain AL: 16% 89% 8%



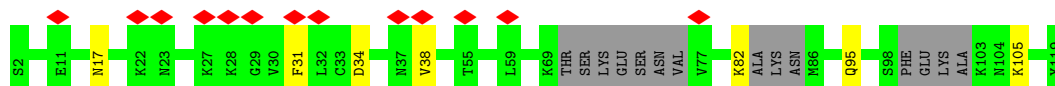
- Molecule 38: 60S ribosomal protein eL27

Chain A1: 19% 86% 10%



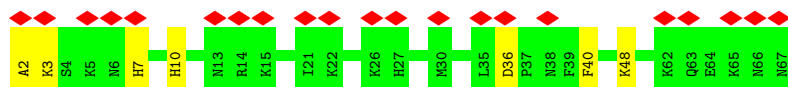
- Molecule 39: 60S ribosomal protein eL28

Chain A2: 11% 82% 6% 12%



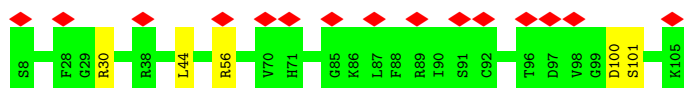
- Molecule 40: 60S ribosomal protein eL29

Chain A4: 32% 89% 11%

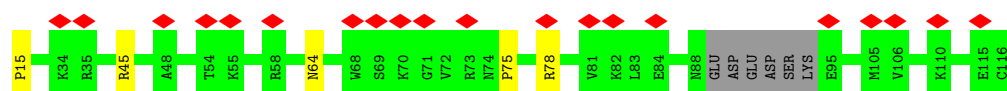
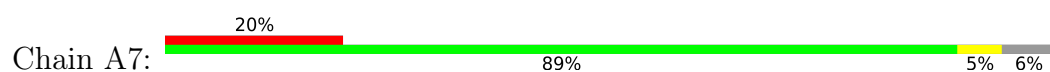


- Molecule 41: 60S ribosomal protein eL30

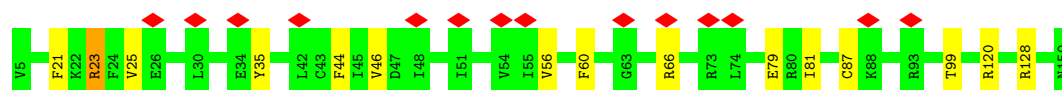
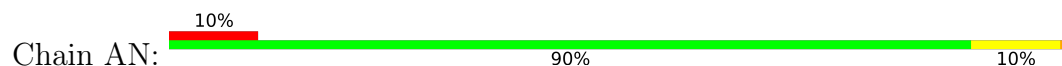
Chain A6: 15% 95% 5%



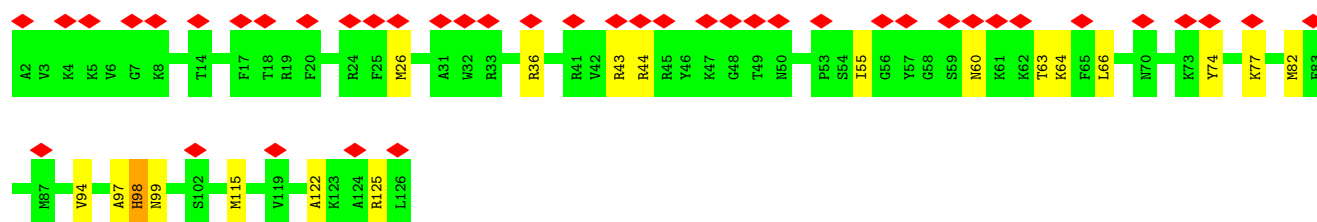
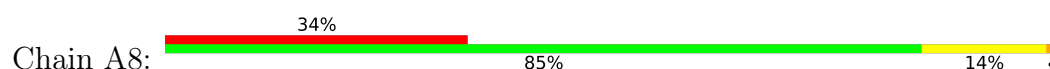
- Molecule 42: 60S ribosomal protein eL31



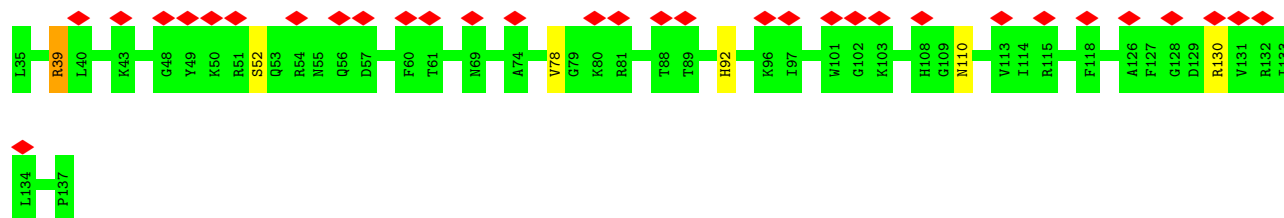
- Molecule 43: 60S ribosomal protein eL14



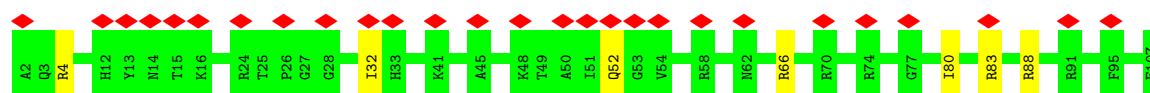
- Molecule 44: 60S ribosomal protein eL32



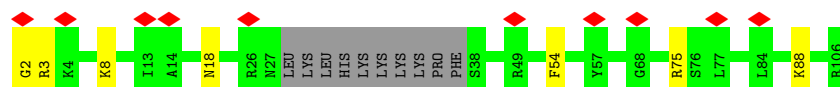
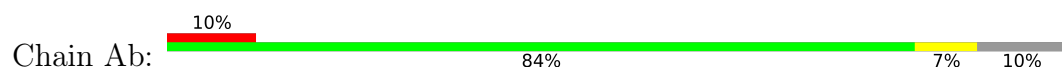
- Molecule 45: 60S ribosomal protein eL33



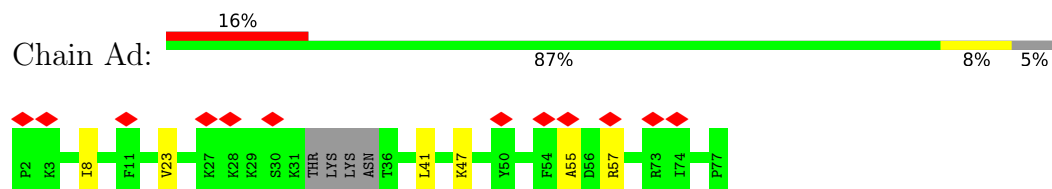
- Molecule 46: 60S ribosomal protein eL34



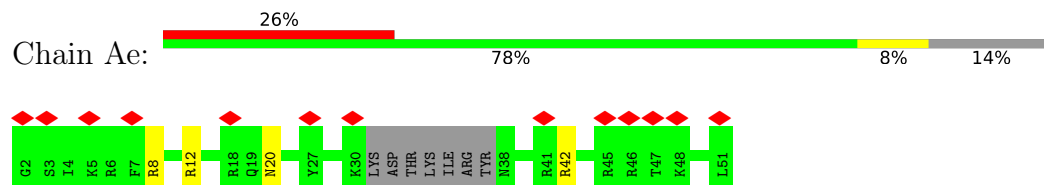
- Molecule 47: 60S ribosomal protein eL36



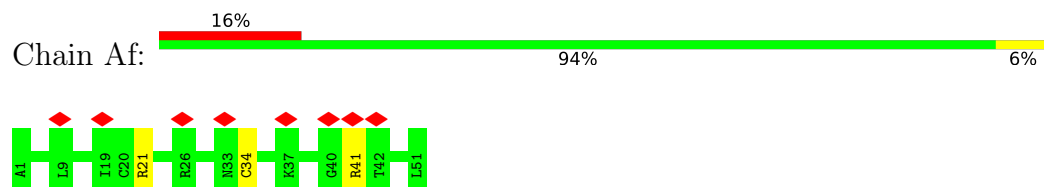
- Molecule 48: 60S ribosomal protein eL38



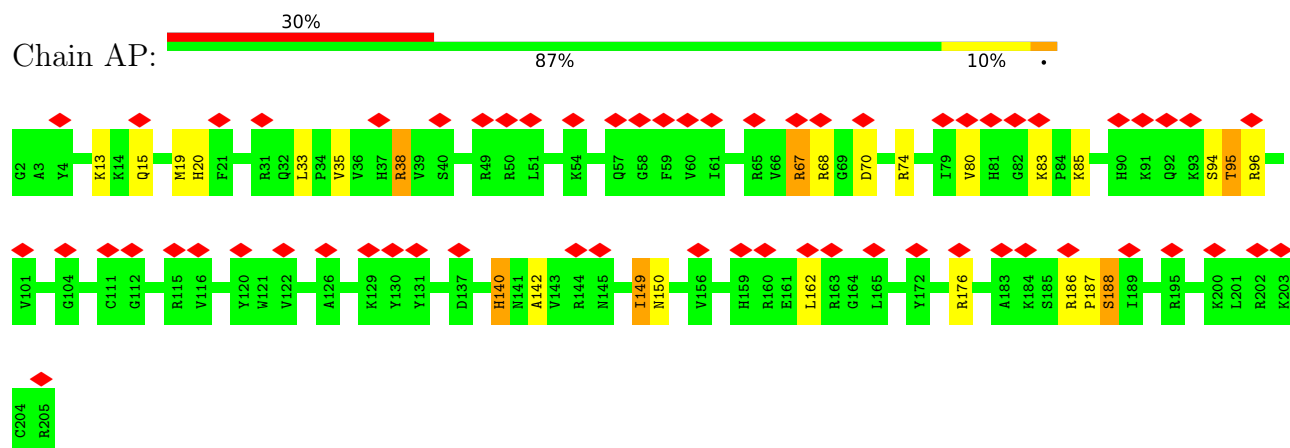
- Molecule 49: 60S ribosomal protein eL39



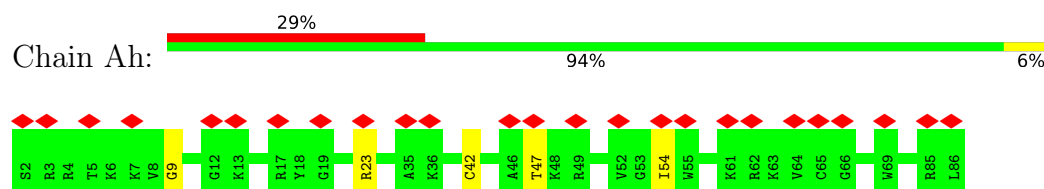
- Molecule 50: 60S ribosomal protein eL40



- Molecule 51: 60S ribosomal protein eL15

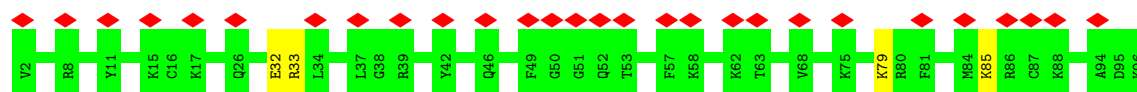


- Molecule 52: 60S ribosomal protein eL43

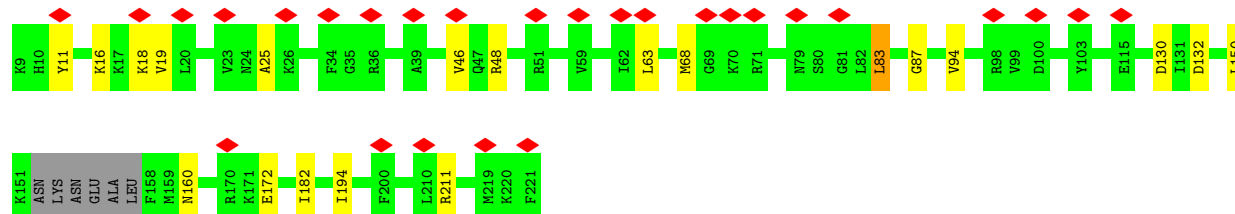
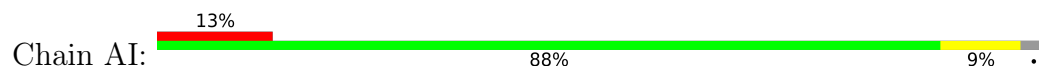


- Molecule 53: 60S ribosomal protein eL44

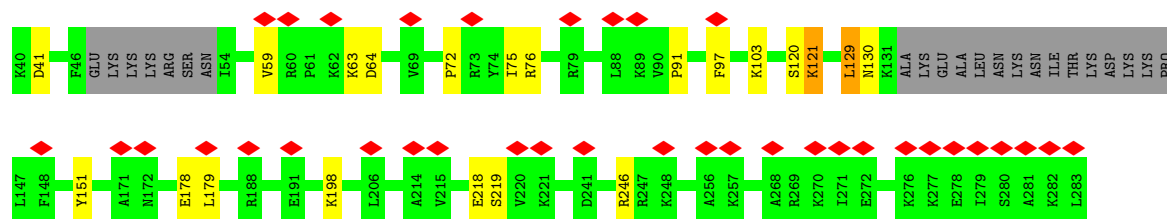
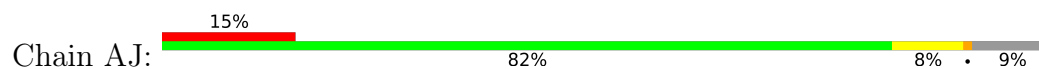




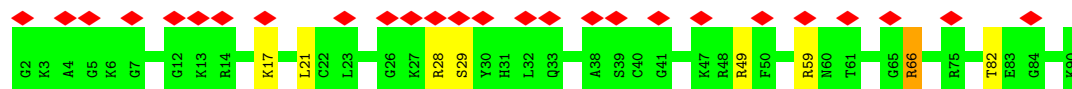
- Molecule 54: 60S ribosomal protein eL6



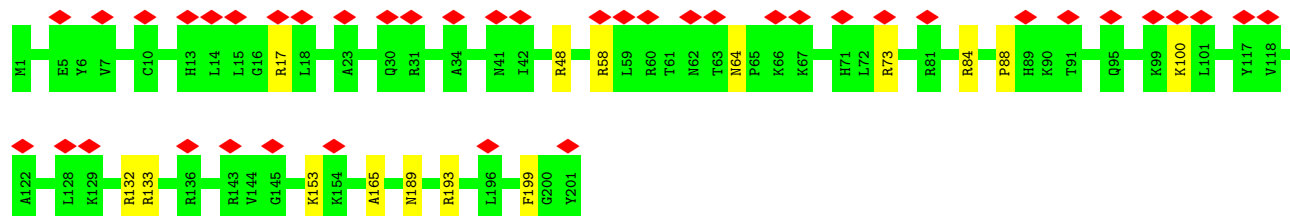
- Molecule 55: 60S ribosomal protein eL8



- Molecule 56: 60S ribosomal protein eL37

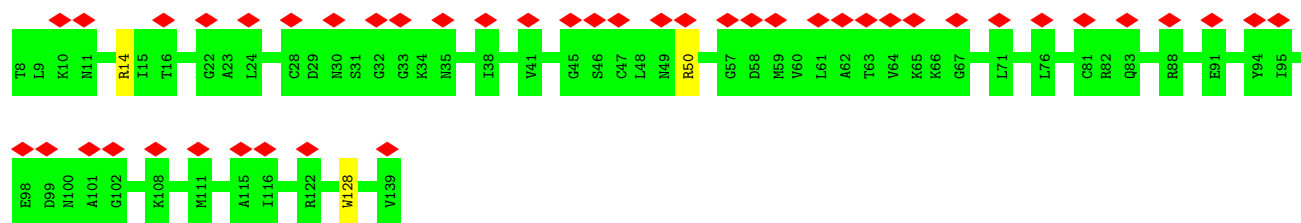


- Molecule 57: 60S ribosomal protein uL13

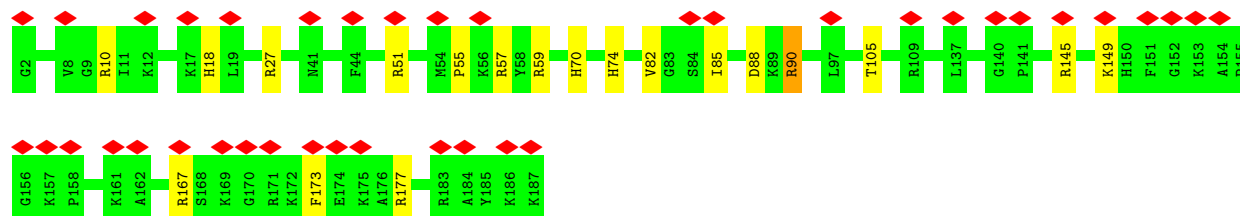
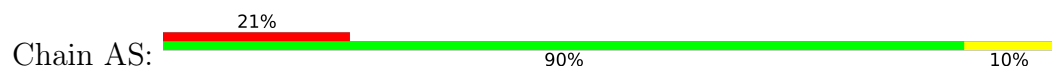


- Molecule 58: 60S ribosomal protein uL14

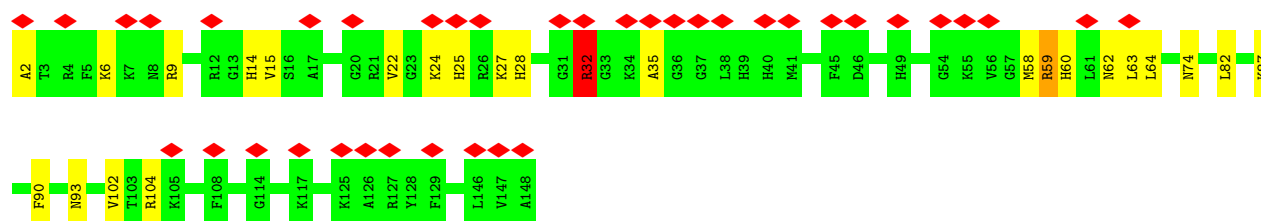
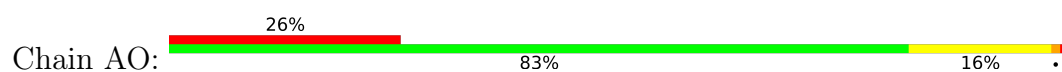




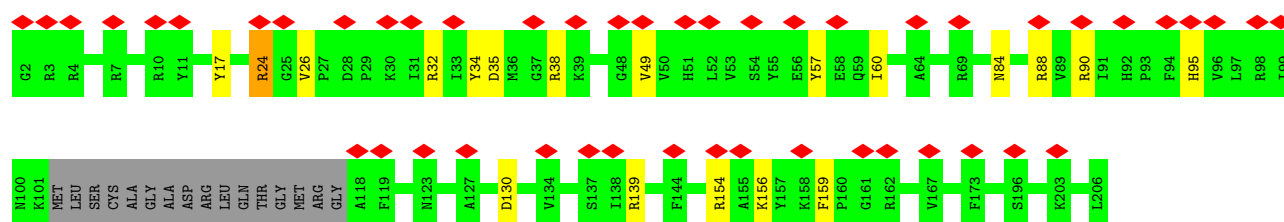
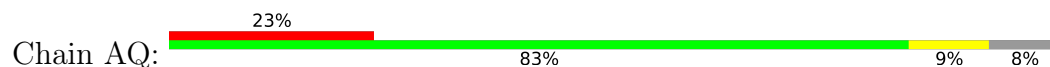
• Molecule 59: 60S ribosomal protein eL18



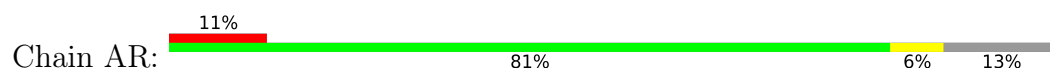
• Molecule 60: 60S ribosomal protein uL15

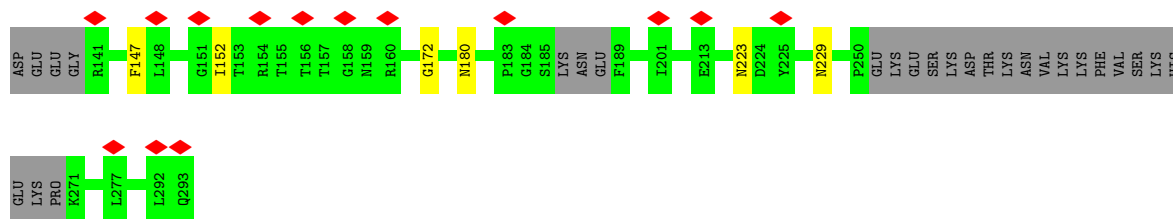


• Molecule 61: 60S ribosomal protein uL16

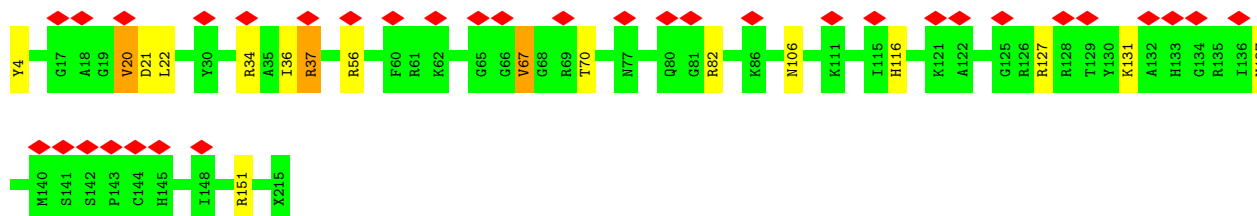


• Molecule 62: 60S ribosomal protein uL18

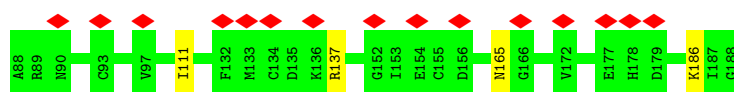




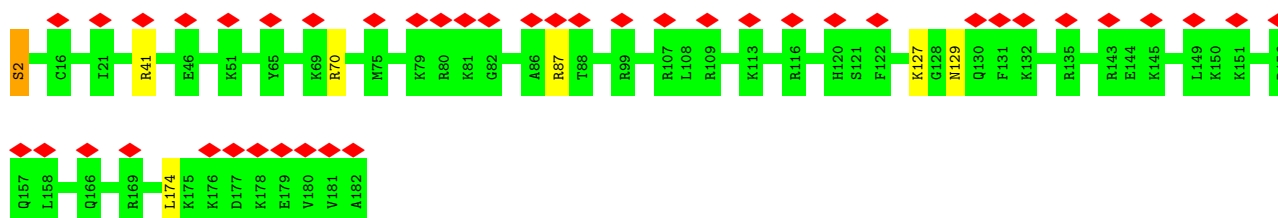
• Molecule 63: 60S ribosomal protein uL22



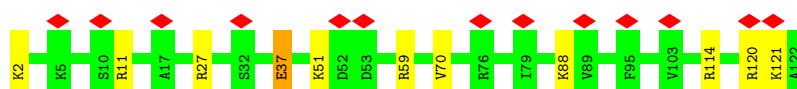
• Molecule 64: 60S ribosomal protein uL23



• Molecule 65: 60S ribosomal protein eL19

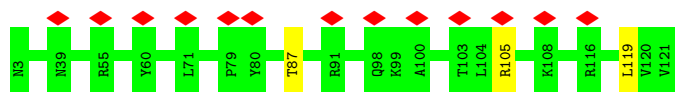


• Molecule 66: 60S ribosomal protein uL24

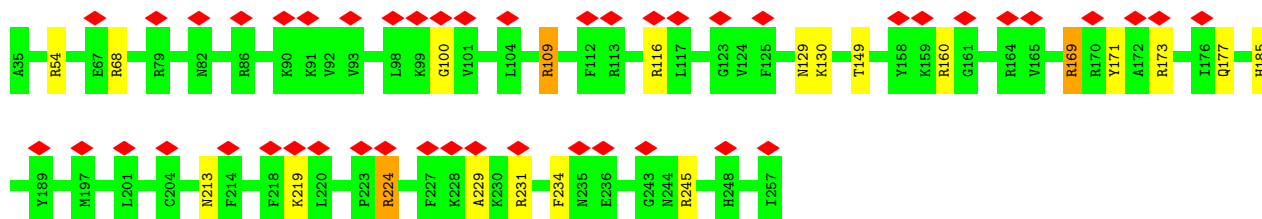


• Molecule 67: 60S ribosomal protein uL29

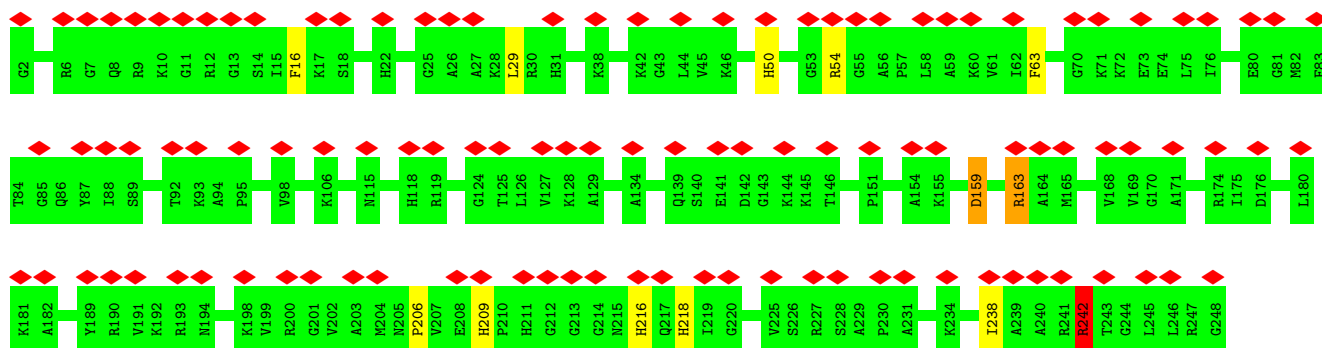




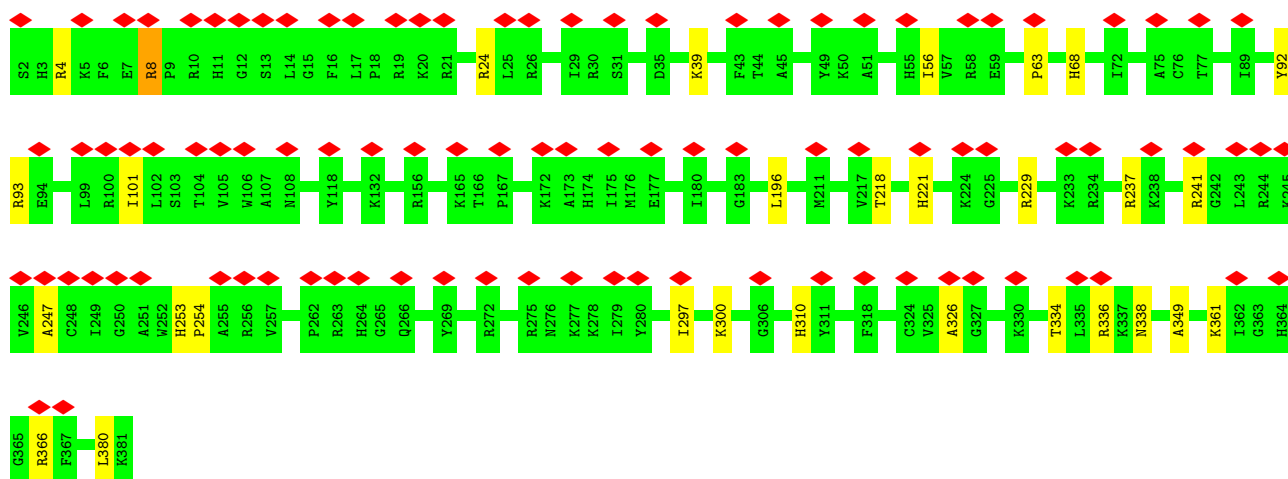
- Molecule 68: 60S ribosomal protein uL30



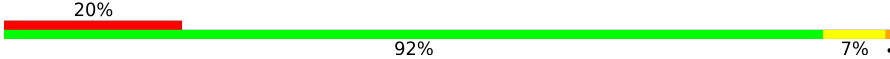
- Molecule 69: 60S ribosomal protein uL2

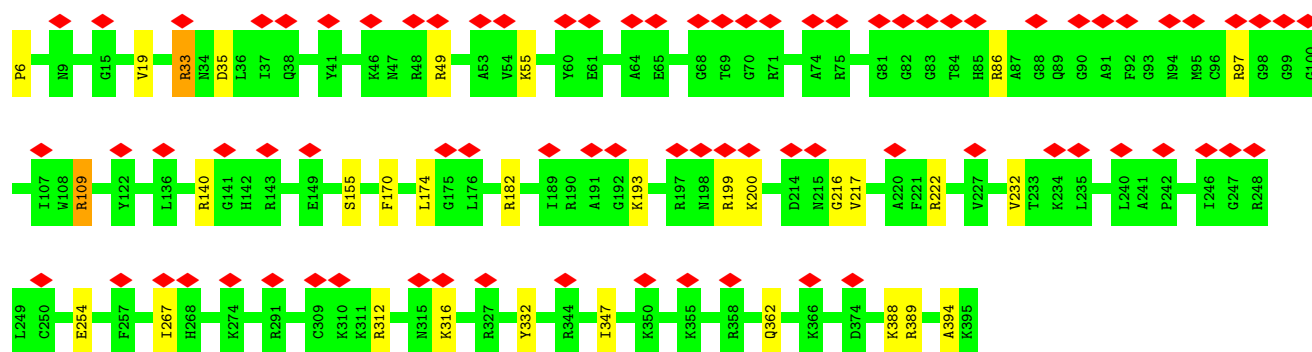


- Molecule 70: 60S ribosomal protein uL3



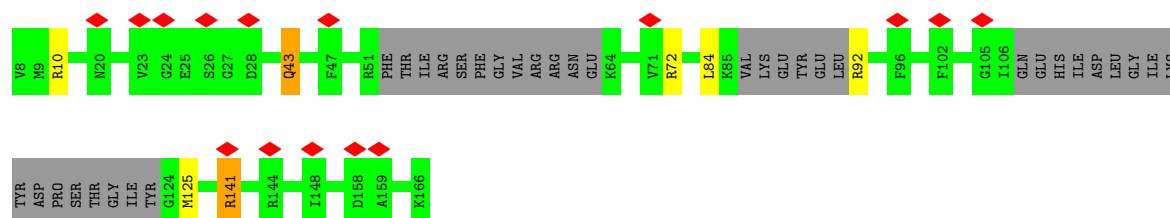
- Molecule 71: 60S ribosomal protein uL4

Chain AF: 



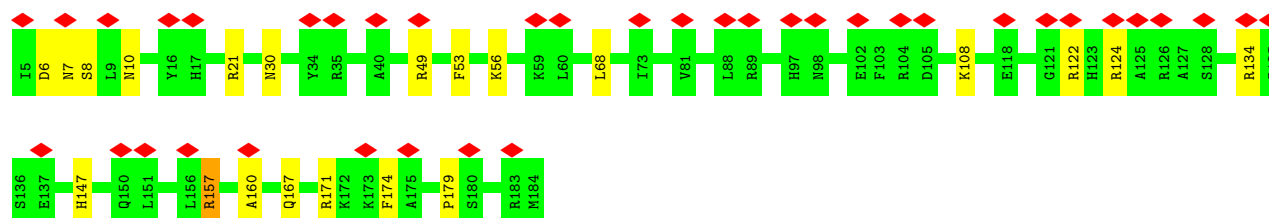
• Molecule 72: 60S ribosomal protein uL5

Chain AG: 

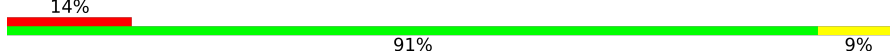


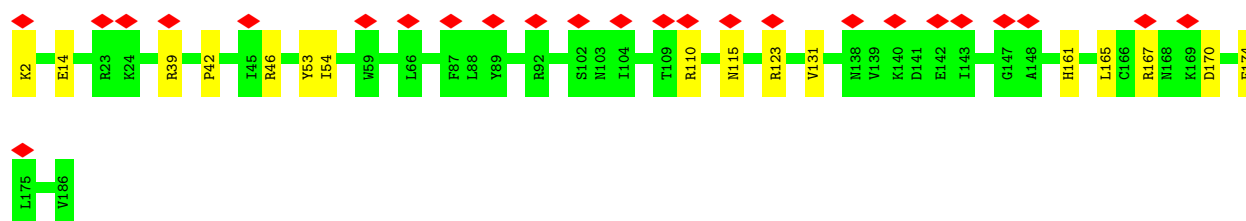
• Molecule 73: 60S ribosomal protein eL20

Chain AU: 

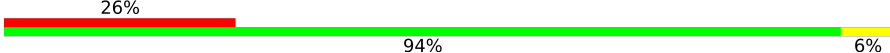


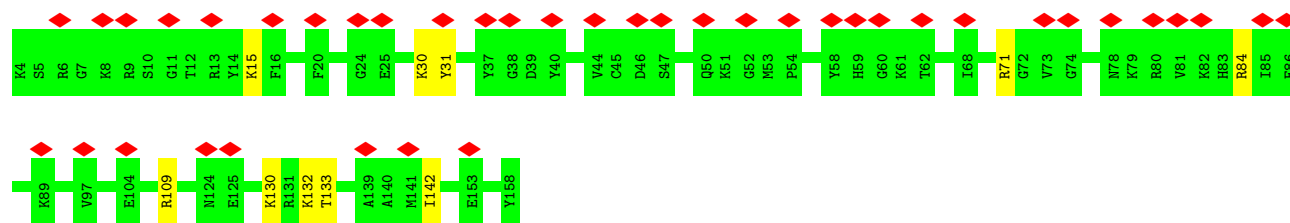
• Molecule 74: 60S ribosomal protein uL6

Chain AH: 

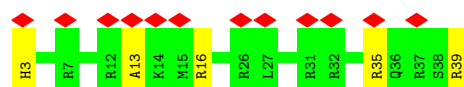
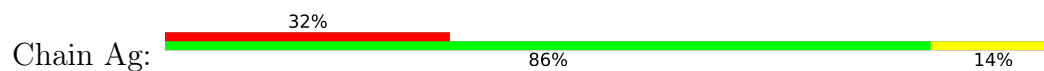


• Molecule 75: 60S ribosomal protein eL21

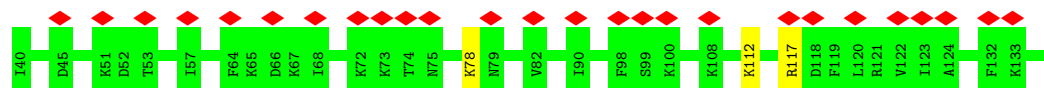
Chain AV: 



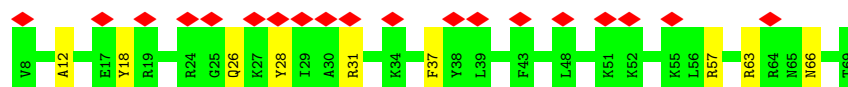
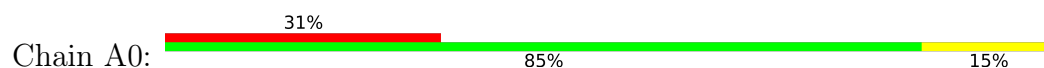
- Molecule 76: 60S ribosomal protein eL41



- Molecule 77: 60S ribosomal protein eL22



- Molecule 78: 60S ribosomal protein eL24



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	14696	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Each micrograph	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	30120	Depositor
Image detector	GATAN K2 (4k x 4k)	Depositor
Maximum map value	0.133	Depositor
Minimum map value	-0.088	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.03	Depositor
Map size ($\text{\AA}$)	491.36, 491.36, 491.36	wwPDB
Map dimensions	296, 296, 296	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.66, 1.66, 1.66	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	A	0.94	0/38275	1.14	120/59596 (0.2%)
2	7	0.95	0/1810	1.19	9/2821 (0.3%)
3	D	0.89	0/1241	1.43	4/1652 (0.2%)
4	E	0.87	0/1539	1.51	3/2055 (0.1%)
5	G	0.82	0/1800	1.48	10/2429 (0.4%)
6	I	0.85	0/1443	1.56	3/1936 (0.2%)
7	K	0.86	0/1054	1.48	3/1411 (0.2%)
8	M	0.83	0/1114	1.43	4/1487 (0.3%)
9	W	0.86	0/793	1.61	8/1053 (0.8%)
10	R	0.91	0/755	1.56	5/1013 (0.5%)
11	O	0.86	0/706	1.50	2/950 (0.2%)
12	Y	0.86	0/1295	1.63	12/1742 (0.7%)
13	Z	0.84	0/565	1.48	2/758 (0.3%)
14	1	0.85	0/999	1.50	3/1321 (0.2%)
15	2	0.90	0/324	1.45	0/435
16	3	0.92	0/794	1.55	7/1055 (0.7%)
17	4	0.81	0/597	1.46	0/801
18	5	0.91	0/459	1.40	4/606 (0.7%)
19	6	0.91	0/349	1.59	2/458 (0.4%)
20	B	0.82	0/1738	1.55	8/2321 (0.3%)
21	F	0.85	0/2098	1.45	9/2819 (0.3%)
22	H	0.82	0/1665	1.46	7/2210 (0.3%)
23	J	0.81	0/1545	1.51	12/2064 (0.6%)
24	L	0.87	0/1407	1.52	10/1879 (0.5%)
25	N	0.83	0/780	1.52	4/1053 (0.4%)
26	P	0.87	0/966	1.60	10/1295 (0.8%)
27	Q	0.86	0/1149	1.51	1/1532 (0.1%)
28	S	0.87	0/1063	1.65	8/1425 (0.6%)
29	T	0.90	0/412	1.40	0/544
30	U	0.83	0/1223	1.53	5/1634 (0.3%)
31	V	0.87	0/1233	1.41	3/1645 (0.2%)
32	X	0.86	0/788	1.62	13/1050 (1.2%)
33	C	0.82	0/1570	1.51	11/2129 (0.5%)
34	AA	0.93	0/75947	1.14	279/118255 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	AC	0.94	0/3599	1.15	14/5603 (0.2%)
36	AB	0.93	0/2823	1.07	8/4400 (0.2%)
37	AL	0.85	0/1789	1.61	12/2381 (0.5%)
38	A1	0.84	0/1151	1.54	11/1531 (0.7%)
39	A2	0.83	0/840	1.47	2/1114 (0.2%)
40	A4	0.85	0/564	1.67	4/737 (0.5%)
41	A6	0.84	0/749	1.49	5/1001 (0.5%)
42	A7	0.89	0/806	1.53	1/1073 (0.1%)
43	AN	0.81	0/1218	1.54	7/1621 (0.4%)
44	A8	0.85	0/1054	1.63	13/1399 (0.9%)
45	A9	0.88	0/865	1.47	5/1160 (0.4%)
46	Aa	0.89	0/872	1.52	0/1161
47	Ab	0.88	0/763	1.52	2/1008 (0.2%)
48	Ad	0.84	0/612	1.51	1/812 (0.1%)
49	Ae	0.99	0/396	1.46	1/521 (0.2%)
50	Af	0.87	0/419	1.46	1/556 (0.2%)
51	AP	0.89	0/1735	1.58	15/2320 (0.6%)
52	Ah	0.83	0/668	1.42	0/887
53	Ai	0.82	0/789	1.36	0/1032
54	AI	0.81	0/1708	1.55	17/2274 (0.7%)
55	AJ	0.83	0/1840	1.55	10/2456 (0.4%)
56	Ac	0.88	0/723	1.55	2/951 (0.2%)
57	AK	0.83	0/1690	1.53	9/2260 (0.4%)
58	AM	0.83	0/1012	1.45	2/1363 (0.1%)
59	AS	0.86	0/1531	1.51	8/2040 (0.4%)
60	AO	0.87	0/1199	1.57	15/1597 (0.9%)
61	AQ	0.87	0/1580	1.52	10/2113 (0.5%)
62	AR	0.86	0/2079	1.54	4/2777 (0.1%)
63	AW	0.88	0/1244	1.51	7/1663 (0.4%)
64	AY	0.80	0/806	1.45	2/1074 (0.2%)
65	AT	0.85	0/1525	1.52	4/2016 (0.2%)
66	AZ	0.86	0/1013	1.49	2/1339 (0.1%)
67	A3	0.83	0/1005	1.55	1/1329 (0.1%)
68	A5	0.86	0/1917	1.53	11/2562 (0.4%)
69	AD	0.85	0/1902	1.51	12/2544 (0.5%)
70	AE	0.84	0/3130	1.50	6/4195 (0.1%)
71	AF	0.86	0/3145	1.56	9/4205 (0.2%)
72	AG	0.90	0/1021	1.59	1/1349 (0.1%)
73	AU	0.87	0/1527	1.51	7/2043 (0.3%)
74	AH	0.84	0/1501	1.50	9/2025 (0.4%)
75	AV	0.84	0/1301	1.48	2/1732 (0.1%)
76	Ag	0.98	0/348	1.67	1/448 (0.2%)
77	AX	0.81	0/842	1.44	5/1125 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	A0	0.84	0/534	1.57	4/711 (0.6%)
All	All	0.90	0/207331	1.30	843/303942 (0.3%)

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	A	0	127
2	7	0	8
4	E	0	7
5	G	0	1
6	I	0	2
7	K	0	3
8	M	0	3
9	W	0	2
12	Y	0	3
14	1	0	3
15	2	0	1
16	3	0	3
18	5	0	2
19	6	0	3
20	B	1	5
21	F	0	3
22	H	0	2
23	J	0	4
24	L	0	4
25	N	0	1
26	P	0	3
27	Q	0	3
28	S	0	1
29	T	0	5
30	U	0	1
31	V	0	4
32	X	0	3
33	C	0	2
34	AA	1	304
35	AC	0	10
36	AB	0	9
37	AL	0	6
38	A1	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
40	A4	0	1
41	A6	0	1
42	A7	0	3
43	AN	0	5
44	A8	0	4
45	A9	0	2
46	Aa	0	3
47	Ab	0	1
48	Ad	0	1
49	Ae	0	2
50	Af	0	2
51	AP	0	7
52	Ah	0	1
53	Ai	0	1
54	AI	0	4
55	AJ	0	2
56	Ac	0	4
57	AK	0	7
58	AM	0	3
59	AS	0	7
60	AO	0	3
61	AQ	0	6
62	AR	0	4
63	AW	0	4
64	AY	0	1
65	AT	0	4
66	AZ	0	5
67	A3	0	1
68	A5	0	5
69	AD	0	1
70	AE	0	7
71	AF	0	10
72	AG	0	3
73	AU	0	5
75	AV	0	3
76	Ag	0	2
78	A0	0	4
All	All	2	668

There are no bond length outliers.

The worst 5 of 843 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	AA	255	C	P-O5'-C5'	13.59	141.29	120.90
36	AB	27	A	O3'-P-O5'	-13.46	83.82	104.00
1	A	1659	U	P-O3'-C3'	12.57	139.06	120.20
1	A	981	U	P-O3'-C3'	12.15	138.43	120.20
34	AA	811	A	P-O3'-C3'	11.88	138.02	120.20

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
20	B	225	ILE	CB
34	AA	3018	A	C3'

5 of 668 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	129	U	Sidechain
1	A	143	A	Sidechain
1	A	39	A	Sidechain
1	A	44	U	Sidechain
1	A	84	A	Sidechain

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	A	34207	0	17266	43	0
2	7	1620	0	827	1	0
3	D	1229	0	1311	0	0
4	E	1515	0	1605	0	0
5	G	1758	0	1811	1	0
6	I	1424	0	1471	0	0
7	K	1037	0	1099	2	0
8	M	1099	0	1183	1	0
9	W	786	0	858	0	0
10	R	747	0	754	0	0
11	O	687	0	695	0	0
12	Y	1267	0	1316	0	0
13	Z	557	0	558	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	1	986	0	1076	0	0
15	2	321	0	338	0	0
16	3	782	0	820	0	0
17	4	586	0	604	0	0
18	5	458	0	496	0	0
19	6	346	0	381	0	0
20	B	1714	0	1838	0	0
21	F	2062	0	2200	2	0
22	H	1648	0	1803	3	0
23	J	1529	0	1680	1	0
24	L	1383	0	1434	1	0
25	N	772	0	813	0	0
26	P	954	0	997	0	0
27	Q	1129	0	1196	1	0
28	S	1047	0	1101	1	0
29	T	405	0	419	0	0
30	U	1202	0	1299	1	0
31	V	1206	0	1239	1	0
32	X	777	0	832	0	0
33	C	1539	0	1600	1	0
34	AA	67884	0	34242	118	0
35	AC	3215	0	1633	4	0
36	AB	2522	0	1275	2	0
37	AL	1757	0	1888	3	0
38	A1	1134	0	1245	2	0
39	A2	831	0	887	1	0
40	A4	555	0	599	1	0
41	A6	741	0	763	0	0
42	A7	794	0	869	0	0
43	AN	1202	0	1316	1	0
44	A8	1037	0	1139	3	0
45	A9	845	0	886	0	0
46	Aa	859	0	912	0	0
47	Ab	757	0	842	1	0
48	Ad	604	0	686	2	0
49	Ae	388	0	421	0	0
50	Af	414	0	452	0	0
51	AP	1697	0	1802	2	0
52	Ah	659	0	727	1	0
53	Ai	779	0	861	0	0
54	AI	1685	0	1849	1	0
55	AJ	1813	0	1985	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	Ac	710	0	761	1	0
57	AK	1660	0	1785	0	0
58	AM	996	0	1044	0	0
59	AS	1503	0	1636	2	0
60	AO	1172	0	1230	5	0
61	AQ	1545	0	1582	1	0
62	AR	2050	0	2140	1	0
63	AW	1319	0	1303	3	0
64	AY	797	0	850	0	0
65	AT	1509	0	1682	1	0
66	AZ	1001	0	1099	2	0
67	A3	995	0	1121	0	0
68	A5	1879	0	2005	1	0
69	AD	1867	0	1964	1	0
70	AE	3062	0	3205	4	0
71	AF	3095	0	3333	3	0
72	AG	1011	0	1073	1	0
73	AU	1497	0	1556	3	0
74	AH	1476	0	1574	1	0
75	AV	1276	0	1355	1	0
76	Ag	343	0	388	1	0
77	AX	825	0	882	0	0
78	A0	522	0	539	0	0
All	All	193061	0	144306	213	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 1.

The worst 5 of 213 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)
34:AA:3770:C:H4'	70:AE:310:HIS:CE1	2.36	0.61
1:A:458:A:H3'	1:A:459:A:C5'	2.32	0.60
34:AA:3117:A:HO2'	47:Ab:2:GLY:N	1.99	0.60
34:AA:445:A:C2	34:AA:702:U:C4	2.91	0.59
34:AA:236:U:HO2'	66:AZ:2:LYS:N	2.01	0.58

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	
3	D	149/209 (71%)	144 (97%)	3 (2%)	2 (1%)	9	41
4	E	183/185 (99%)	175 (96%)	6 (3%)	2 (1%)	11	45
5	G	222/224 (99%)	206 (93%)	14 (6%)	2 (1%)	14	49
6	I	176/189 (93%)	161 (92%)	12 (7%)	3 (2%)	7	35
7	K	127/129 (98%)	118 (93%)	7 (6%)	2 (2%)	7	37
8	M	136/138 (99%)	127 (93%)	5 (4%)	4 (3%)	3	23
9	W	91/108 (84%)	84 (92%)	6 (7%)	1 (1%)	11	45
10	R	92/114 (81%)	80 (87%)	10 (11%)	2 (2%)	5	28
11	O	77/79 (98%)	67 (87%)	4 (5%)	6 (8%)	1	10
12	Y	152/154 (99%)	137 (90%)	11 (7%)	4 (3%)	4	25
13	Z	70/72 (97%)	65 (93%)	4 (6%)	1 (1%)	9	39
14	1	118/120 (98%)	111 (94%)	4 (3%)	3 (2%)	4	26
15	2	35/68 (52%)	31 (89%)	3 (9%)	1 (3%)	3	23
16	3	93/95 (98%)	81 (87%)	11 (12%)	1 (1%)	11	45
17	4	74/76 (97%)	65 (88%)	7 (10%)	2 (3%)	4	25
18	5	54/65 (83%)	53 (98%)	1 (2%)	0	100	100
19	6	41/43 (95%)	35 (85%)	5 (12%)	1 (2%)	4	27
20	B	208/210 (99%)	186 (89%)	19 (9%)	3 (1%)	9	39
21	F	255/257 (99%)	238 (93%)	13 (5%)	4 (2%)	7	37
22	H	200/214 (94%)	191 (96%)	8 (4%)	1 (0%)	24	63
23	J	186/188 (99%)	176 (95%)	5 (3%)	5 (3%)	4	25
24	L	165/214 (77%)	147 (89%)	14 (8%)	4 (2%)	4	27
25	N	96/98 (98%)	91 (95%)	3 (3%)	2 (2%)	5	29
26	P	125/127 (98%)	114 (91%)	8 (6%)	3 (2%)	4	27
27	Q	142/144 (99%)	130 (92%)	7 (5%)	5 (4%)	3	20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	S	126/128 (98%)	108 (86%)	14 (11%)	4 (3%)	3	21
29	T	46/48 (96%)	44 (96%)	2 (4%)	0	100	100
30	U	147/149 (99%)	142 (97%)	4 (3%)	1 (1%)	18	55
31	V	142/156 (91%)	129 (91%)	10 (7%)	3 (2%)	5	29
32	X	92/103 (89%)	78 (85%)	10 (11%)	4 (4%)	2	17
33	C	193/195 (99%)	181 (94%)	9 (5%)	3 (2%)	7	37
37	AL	209/211 (99%)	190 (91%)	16 (8%)	3 (1%)	9	39
38	A1	136/145 (94%)	127 (93%)	7 (5%)	2 (2%)	8	38
39	A2	96/118 (81%)	89 (93%)	5 (5%)	2 (2%)	5	29
40	A4	64/66 (97%)	58 (91%)	4 (6%)	2 (3%)	3	21
41	A6	96/98 (98%)	93 (97%)	3 (3%)	0	100	100
42	A7	92/102 (90%)	89 (97%)	3 (3%)	0	100	100
43	AN	144/146 (99%)	140 (97%)	2 (1%)	2 (1%)	9	39
44	A8	123/125 (98%)	114 (93%)	8 (6%)	1 (1%)	16	53
45	A9	101/103 (98%)	92 (91%)	9 (9%)	0	100	100
46	Aa	104/106 (98%)	99 (95%)	5 (5%)	0	100	100
47	Ab	91/105 (87%)	85 (93%)	5 (6%)	1 (1%)	11	45
48	Ad	68/76 (90%)	68 (100%)	0	0	100	100
49	Ae	39/50 (78%)	39 (100%)	0	0	100	100
50	Af	49/51 (96%)	46 (94%)	3 (6%)	0	100	100
51	AP	202/204 (99%)	183 (91%)	14 (7%)	5 (2%)	4	26
52	Ah	83/85 (98%)	76 (92%)	5 (6%)	2 (2%)	4	27
53	Ai	93/95 (98%)	87 (94%)	5 (5%)	1 (1%)	11	45
54	AI	203/213 (95%)	187 (92%)	14 (7%)	2 (1%)	12	47
55	AJ	216/244 (88%)	196 (91%)	13 (6%)	7 (3%)	3	21
56	Ac	87/89 (98%)	74 (85%)	12 (14%)	1 (1%)	11	45
57	AK	199/201 (99%)	191 (96%)	6 (3%)	2 (1%)	12	47
58	AM	130/132 (98%)	121 (93%)	9 (7%)	0	100	100
59	AS	184/186 (99%)	171 (93%)	12 (6%)	1 (0%)	24	63
60	AO	145/147 (99%)	132 (91%)	10 (7%)	3 (2%)	5	29
61	AQ	185/205 (90%)	170 (92%)	12 (6%)	3 (2%)	7	37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
62	AR	244/289 (84%)	224 (92%)	13 (5%)	7 (3%)	3	23
63	AW	149/170 (88%)	135 (91%)	12 (8%)	2 (1%)	9	41
64	AY	99/101 (98%)	97 (98%)	2 (2%)	0	100	100
65	AT	179/181 (99%)	173 (97%)	5 (3%)	1 (1%)	21	59
66	AZ	119/121 (98%)	113 (95%)	5 (4%)	1 (1%)	16	53
67	A3	117/119 (98%)	108 (92%)	9 (8%)	0	100	100
68	A5	221/223 (99%)	201 (91%)	15 (7%)	5 (2%)	5	28
69	AD	245/247 (99%)	230 (94%)	14 (6%)	1 (0%)	30	67
70	AE	378/380 (100%)	346 (92%)	26 (7%)	6 (2%)	7	37
71	AF	388/390 (100%)	363 (94%)	21 (5%)	4 (1%)	12	47
72	AG	116/159 (73%)	107 (92%)	6 (5%)	3 (3%)	4	25
73	AU	178/180 (99%)	167 (94%)	9 (5%)	2 (1%)	11	45
74	AH	183/185 (99%)	168 (92%)	12 (7%)	3 (2%)	7	37
75	AV	153/155 (99%)	141 (92%)	9 (6%)	3 (2%)	6	31
76	Ag	35/37 (95%)	29 (83%)	5 (14%)	1 (3%)	3	23
77	AX	95/97 (98%)	90 (95%)	4 (4%)	1 (1%)	11	45
78	A0	60/62 (97%)	57 (95%)	2 (3%)	1 (2%)	7	35
All	All	10111/10698 (94%)	9361 (93%)	590 (6%)	160 (2%)	10	37

5 of 160 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	K	120	HIS
8	M	41	GLU
9	W	4	VAL
10	R	42	ILE
12	Y	55	LYS

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	
3	D	132/177 (75%)	131 (99%)	1 (1%)	73	78
4	E	161/164 (98%)	159 (99%)	2 (1%)	63	74
5	G	191/191 (100%)	187 (98%)	4 (2%)	47	65
6	I	154/160 (96%)	149 (97%)	5 (3%)	34	56
7	K	115/115 (100%)	111 (96%)	4 (4%)	32	54
8	M	116/116 (100%)	114 (98%)	2 (2%)	53	68
9	W	86/99 (87%)	86 (100%)	0	100	100
10	R	83/97 (86%)	83 (100%)	0	100	100
11	O	76/76 (100%)	73 (96%)	3 (4%)	28	50
12	Y	137/137 (100%)	133 (97%)	4 (3%)	37	58
13	Z	60/60 (100%)	60 (100%)	0	100	100
14	1	104/104 (100%)	101 (97%)	3 (3%)	37	58
15	2	35/61 (57%)	34 (97%)	1 (3%)	37	58
16	3	87/87 (100%)	87 (100%)	0	100	100
17	4	70/70 (100%)	68 (97%)	2 (3%)	37	58
18	5	47/52 (90%)	45 (96%)	2 (4%)	26	48
19	6	36/36 (100%)	36 (100%)	0	100	100
20	B	195/195 (100%)	192 (98%)	3 (2%)	57	71
21	F	233/233 (100%)	229 (98%)	4 (2%)	53	68
22	H	182/190 (96%)	179 (98%)	3 (2%)	55	69
23	J	177/177 (100%)	176 (99%)	1 (1%)	78	81
24	L	151/190 (80%)	149 (99%)	2 (1%)	61	72
25	N	91/91 (100%)	89 (98%)	2 (2%)	45	64
26	P	99/99 (100%)	96 (97%)	3 (3%)	36	57
27	Q	120/120 (100%)	119 (99%)	1 (1%)	73	78
28	S	114/114 (100%)	109 (96%)	5 (4%)	25	47
29	T	43/43 (100%)	42 (98%)	1 (2%)	44	64
30	U	132/132 (100%)	130 (98%)	2 (2%)	57	71
31	V	131/140 (94%)	129 (98%)	2 (2%)	57	71
32	X	88/94 (94%)	88 (100%)	0	100	100
33	C	167/167 (100%)	162 (97%)	5 (3%)	36	57
37	AL	190/190 (100%)	187 (98%)	3 (2%)	55	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	A1	127/131 (97%)	124 (98%)	3 (2%)	43	63
39	A2	97/109 (89%)	95 (98%)	2 (2%)	47	65
40	A4	60/60 (100%)	60 (100%)	0	100	100
41	A6	83/83 (100%)	82 (99%)	1 (1%)	63	74
42	A7	90/96 (94%)	89 (99%)	1 (1%)	65	74
43	AN	135/135 (100%)	134 (99%)	1 (1%)	76	79
44	A8	114/114 (100%)	110 (96%)	4 (4%)	32	54
45	A9	90/90 (100%)	90 (100%)	0	100	100
46	Aa	89/89 (100%)	85 (96%)	4 (4%)	24	47
47	Ab	82/92 (89%)	80 (98%)	2 (2%)	43	63
48	Ad	69/73 (94%)	68 (99%)	1 (1%)	59	72
49	Ae	40/47 (85%)	39 (98%)	1 (2%)	42	62
50	Af	45/45 (100%)	45 (100%)	0	100	100
51	AP	179/179 (100%)	174 (97%)	5 (3%)	38	59
52	Ah	70/70 (100%)	69 (99%)	1 (1%)	59	72
53	Ai	87/87 (100%)	85 (98%)	2 (2%)	44	64
54	AI	189/195 (97%)	187 (99%)	2 (1%)	65	74
55	AJ	204/224 (91%)	200 (98%)	4 (2%)	48	66
56	Ac	74/74 (100%)	73 (99%)	1 (1%)	59	72
57	AK	181/181 (100%)	180 (99%)	1 (1%)	78	81
58	AM	106/106 (100%)	106 (100%)	0	100	100
59	AS	158/158 (100%)	156 (99%)	2 (1%)	61	72
60	AO	121/121 (100%)	114 (94%)	7 (6%)	18	40
61	AQ	165/176 (94%)	163 (99%)	2 (1%)	63	74
62	AR	215/250 (86%)	213 (99%)	2 (1%)	70	77
63	AW	128/128 (100%)	125 (98%)	3 (2%)	44	64
64	AY	90/90 (100%)	89 (99%)	1 (1%)	65	74
65	AT	162/162 (100%)	162 (100%)	0	100	100
66	AZ	111/111 (100%)	109 (98%)	2 (2%)	51	67
67	A3	110/110 (100%)	109 (99%)	1 (1%)	70	77
68	A5	201/201 (100%)	197 (98%)	4 (2%)	48	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	AD	191/191 (100%)	185 (97%)	6 (3%)	35	56
70	AE	335/335 (100%)	327 (98%)	8 (2%)	43	63
71	AF	336/336 (100%)	329 (98%)	7 (2%)	47	65
72	AG	110/142 (78%)	109 (99%)	1 (1%)	70	77
73	AU	162/162 (100%)	157 (97%)	5 (3%)	35	56
74	AH	168/168 (100%)	164 (98%)	4 (2%)	43	63
75	AV	140/140 (100%)	138 (99%)	2 (1%)	59	72
76	Ag	34/34 (100%)	34 (100%)	0	100	100
77	AX	92/92 (100%)	92 (100%)	0	100	100
78	A0	53/53 (100%)	52 (98%)	1 (2%)	50	66
All	All	9096/9417 (97%)	8932 (98%)	164 (2%)	51	67

5 of 164 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
61	AQ	49	VAL
70	AE	380	LEU
63	AW	22	LEU
69	AD	54	ARG
71	AF	347	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 104 such sidechains are listed below:

Mol	Chain	Res	Type
49	Ae	25	HIS
59	AS	14	HIS
74	AH	40	HIS
50	Af	44	GLN
57	AK	62	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1586/1608 (98%)	487 (30%)	89 (5%)
2	7	75/76 (98%)	13 (17%)	2 (2%)
34	AA	3168/3193 (99%)	993 (31%)	187 (5%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
35	AC	148/151 (98%)	50 (33%)	9 (6%)
36	AB	117/118 (99%)	27 (23%)	1 (0%)
All	All	5094/5146 (98%)	1570 (30%)	288 (5%)

5 of 1570 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	3	C
1	A	5	U
1	A	17	C
1	A	25	C
1	A	26	A

5 of 288 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
34	AA	2966	C
35	AC	145	A
34	AA	3137	U
34	AA	3576	A
34	AA	138	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
63	AW	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AW	154:ASN	C	197:UNK	N	33.92

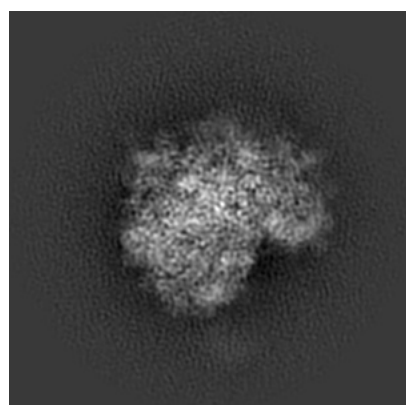
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6456. These allow visual inspection of the internal detail of the map and identification of artifacts.

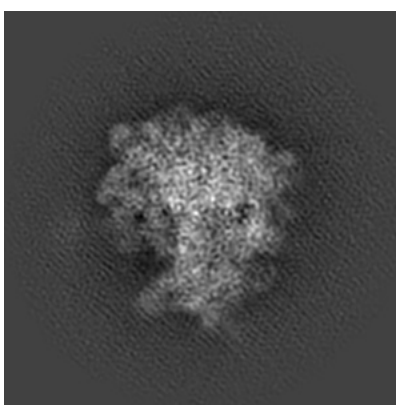
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

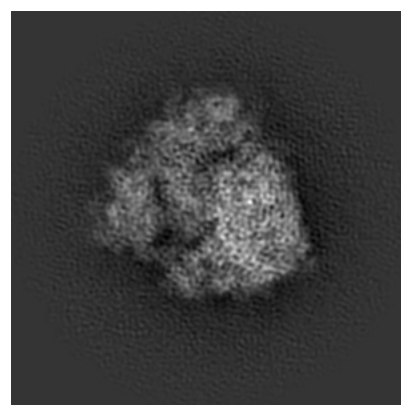
6.1.1 Primary map



X



Y

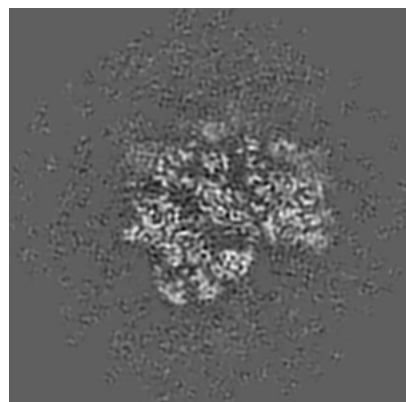


Z

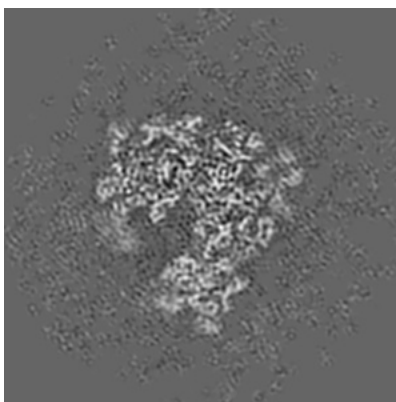
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

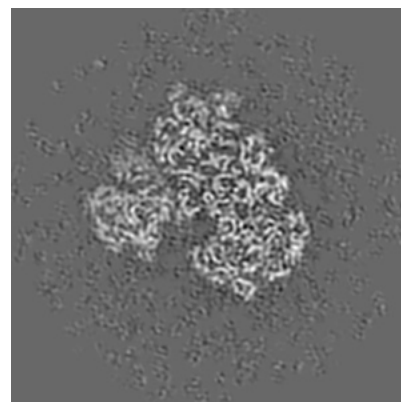
6.2.1 Primary map



X Index: 148



Y Index: 148

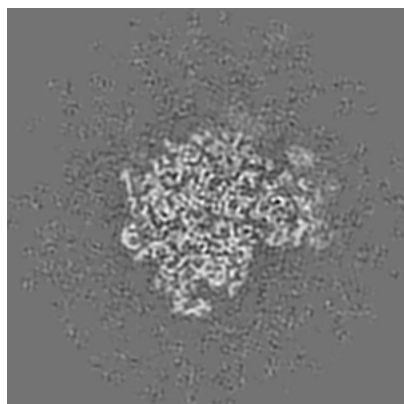


Z Index: 148

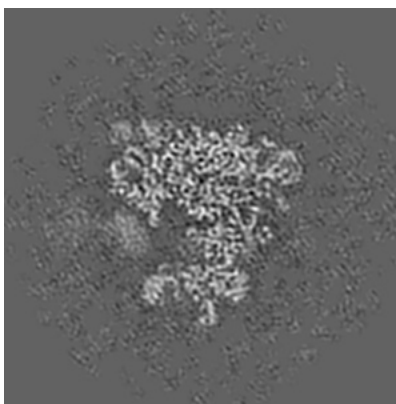
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

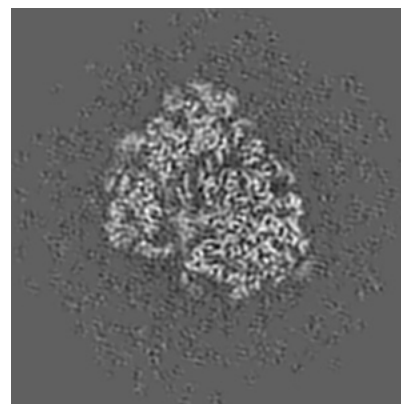
6.3.1 Primary map



X Index: 156



Y Index: 158

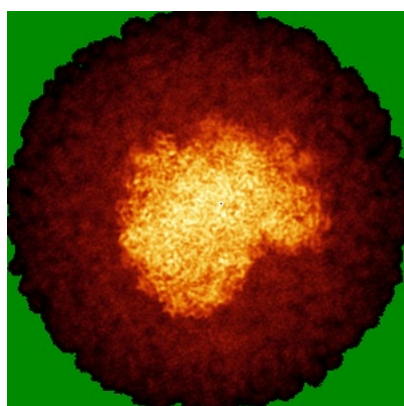


Z Index: 140

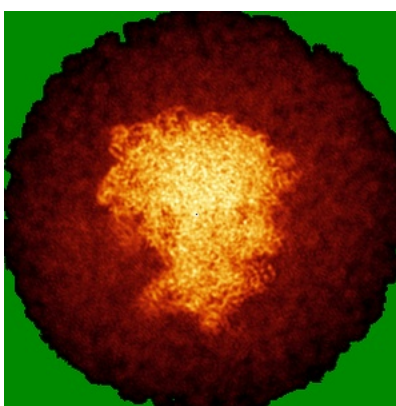
The images above show the largest variance slices of the map in three orthogonal directions.

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

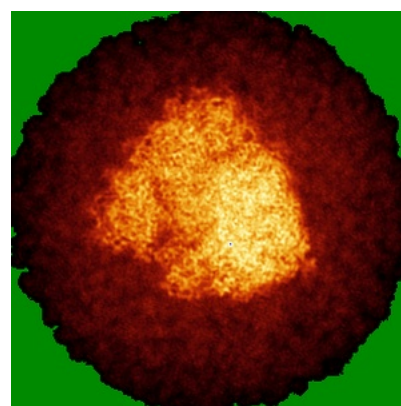
6.4.1 Primary map



X



Y

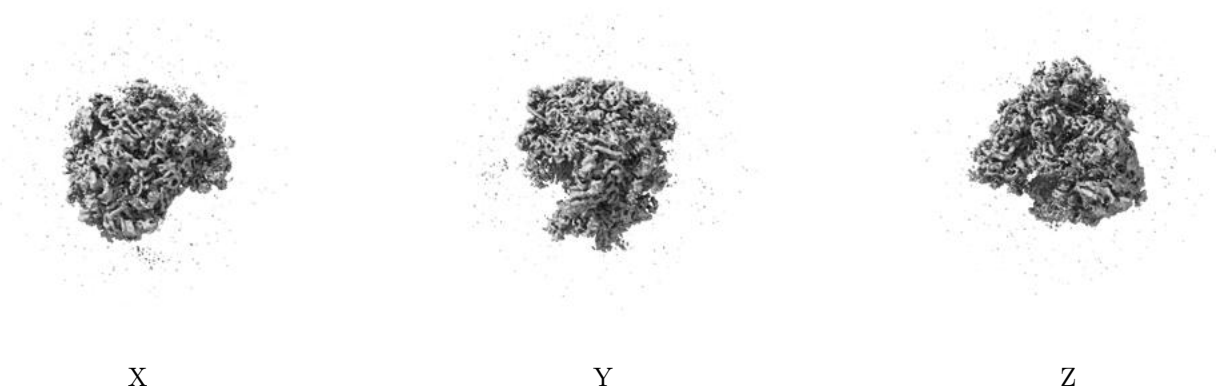


Z

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

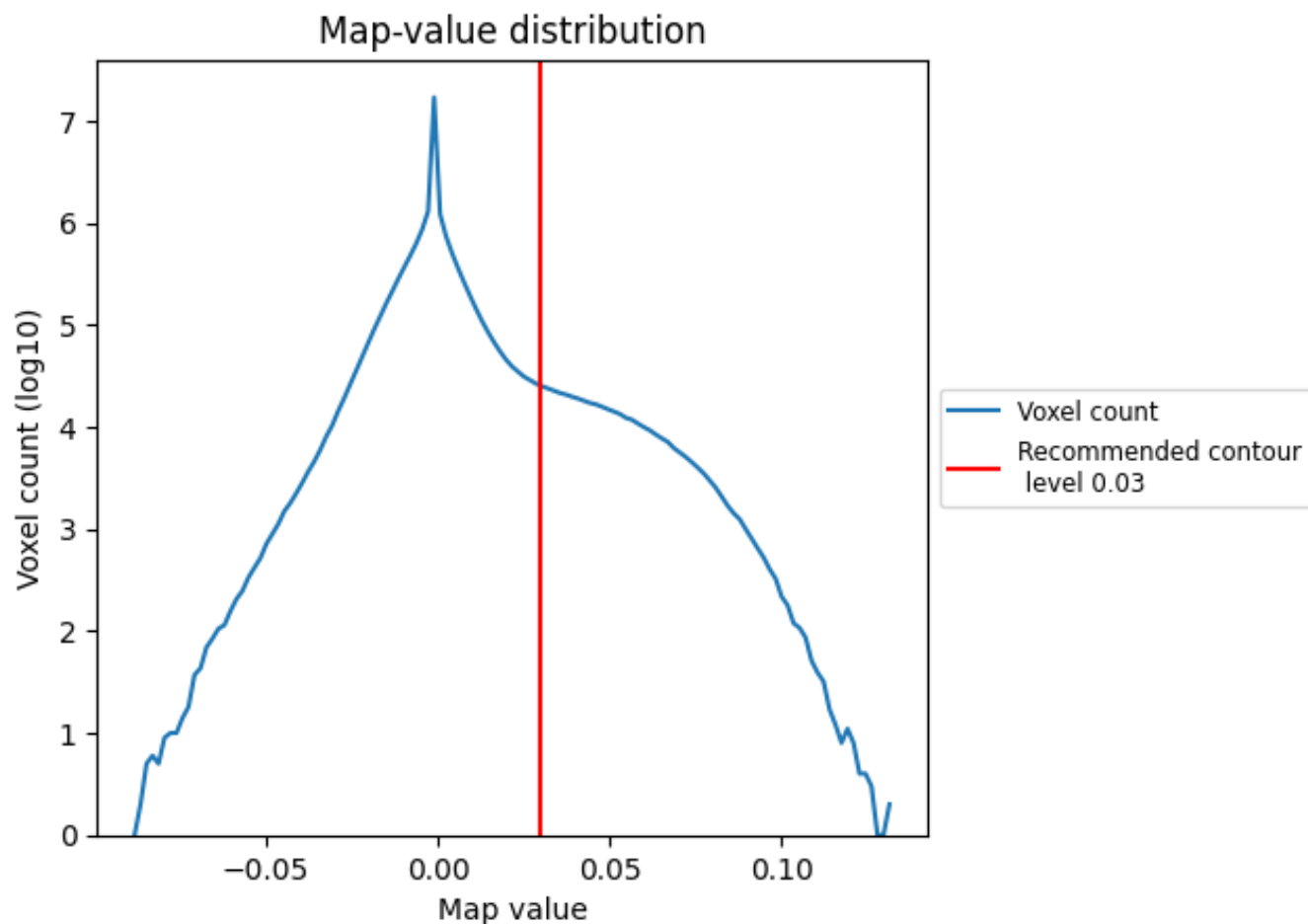
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

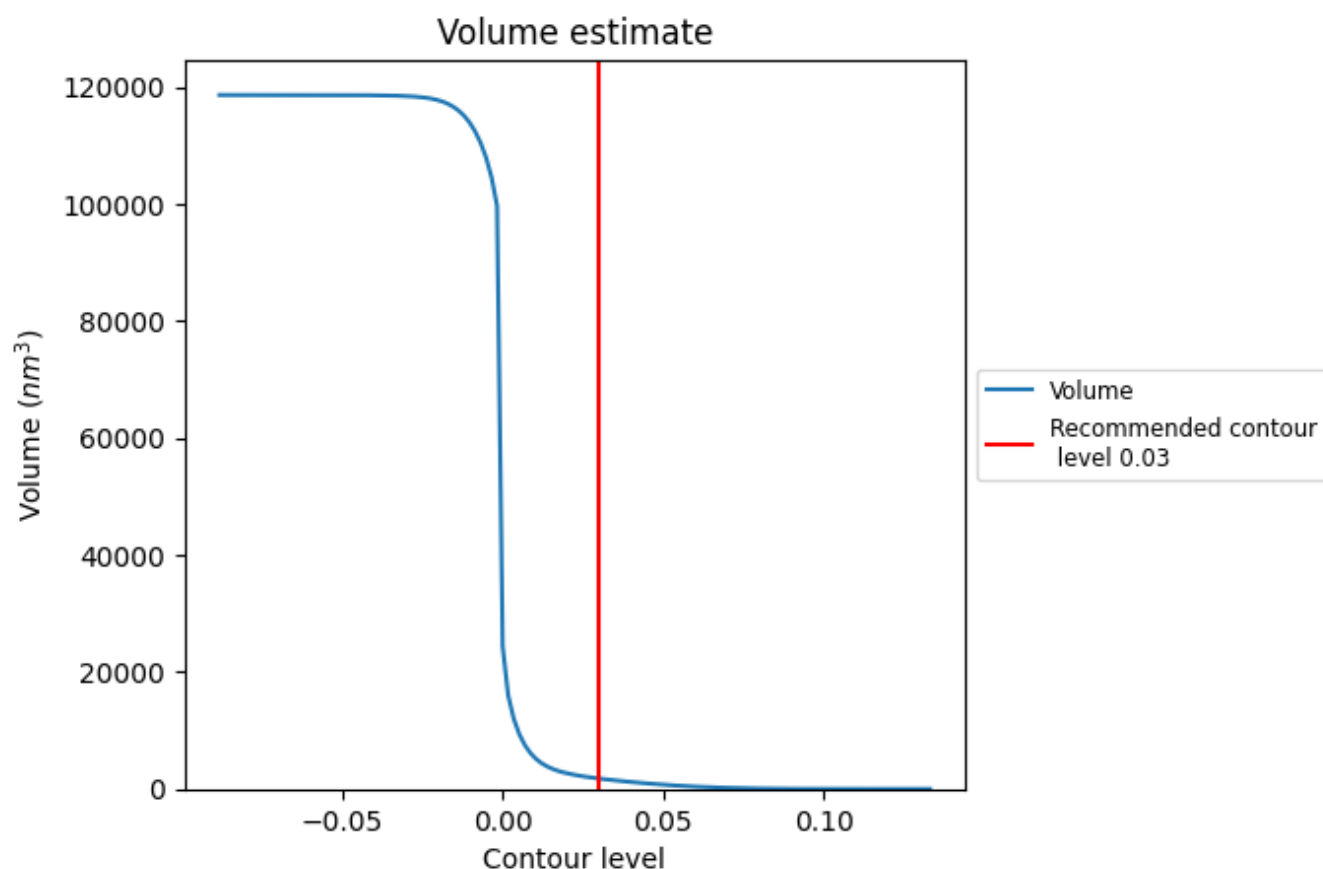
This section contains the results of statistical analysis of the map.

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.

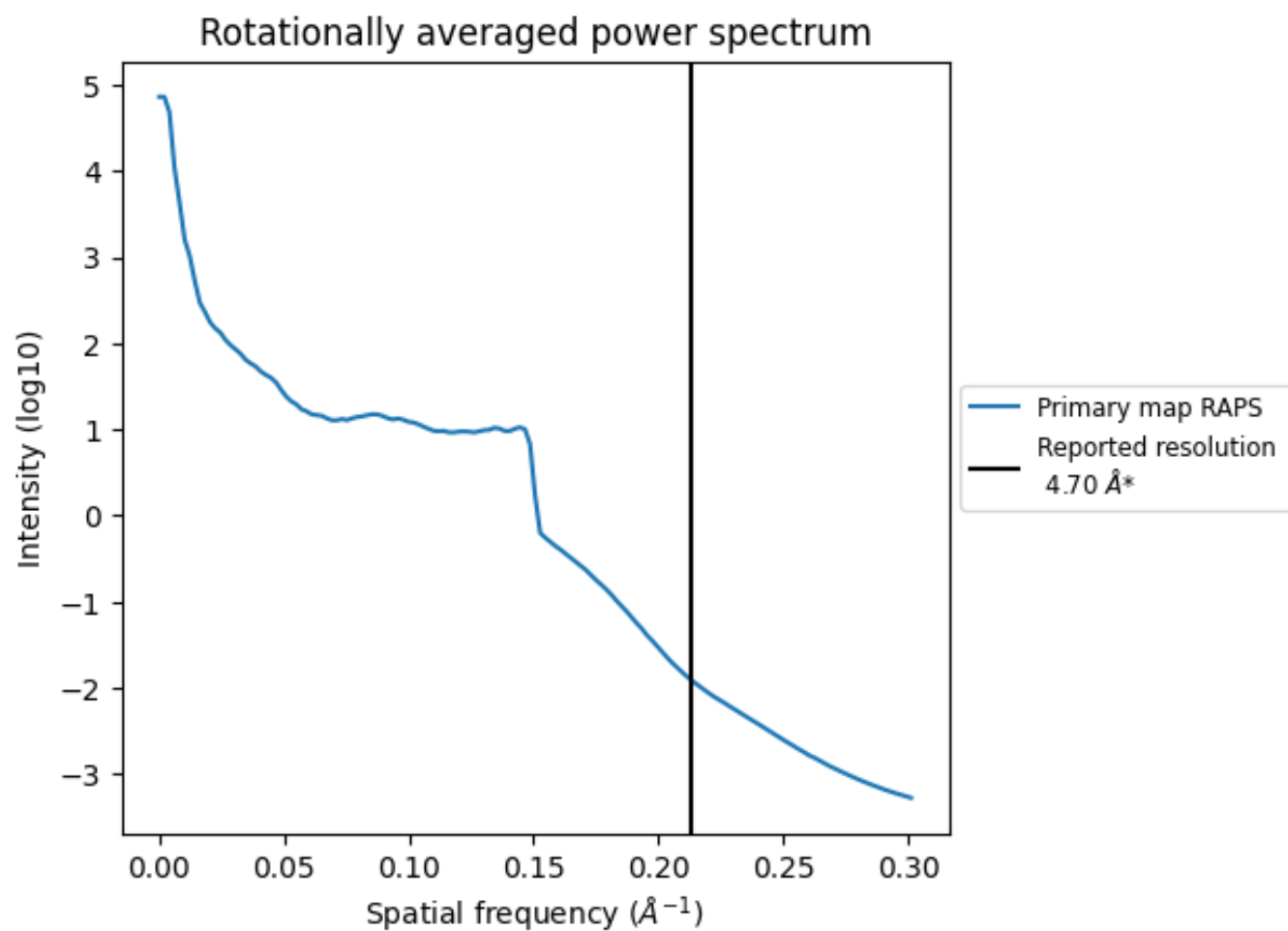
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1785 nm³; this corresponds to an approximate mass of 1612 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 0.213 Å⁻¹

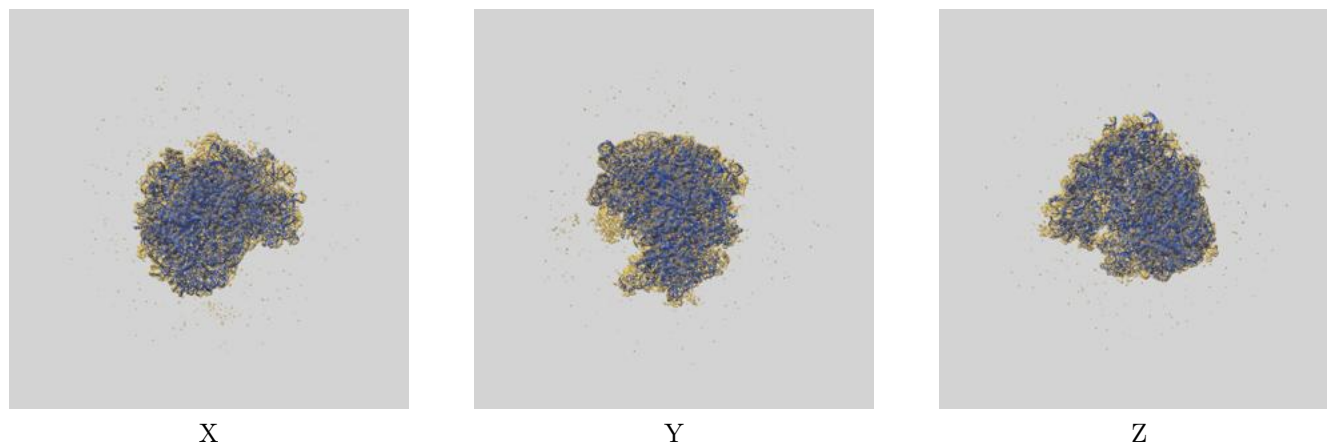
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

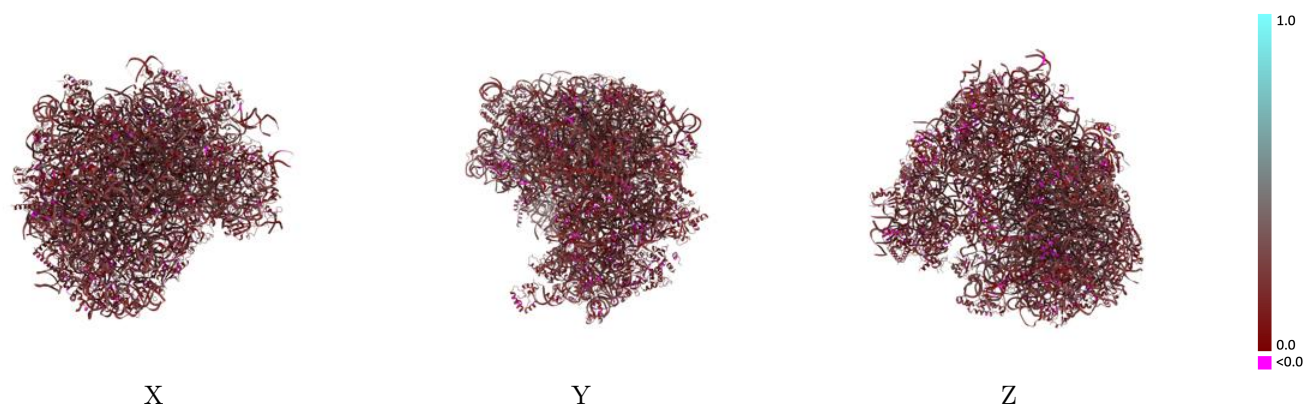
This section contains information regarding the fit between EMDB map EMD-6456 and PDB model 3JBN. Per-residue inclusion information can be found in [section 3](#) on [page 18](#).

9.1 Map-model overlay [i](#)



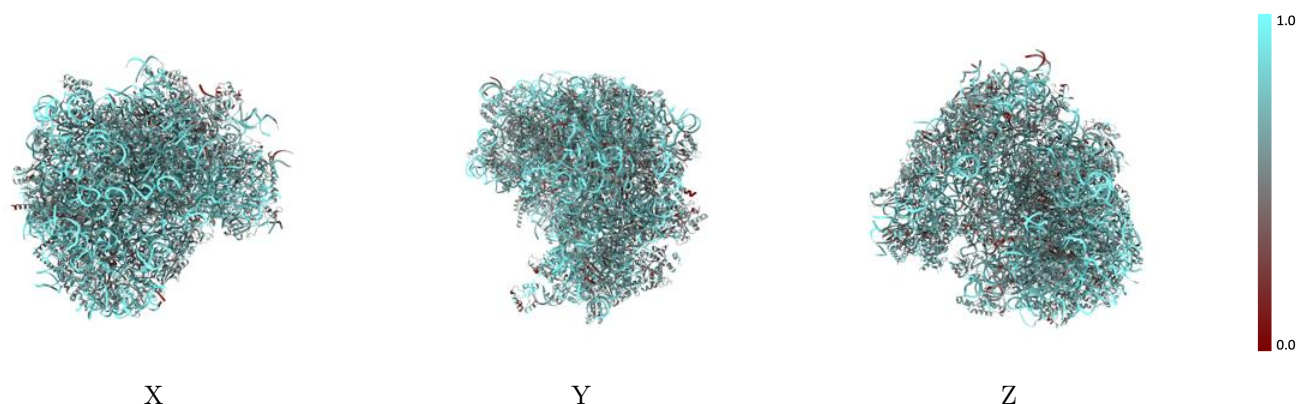
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



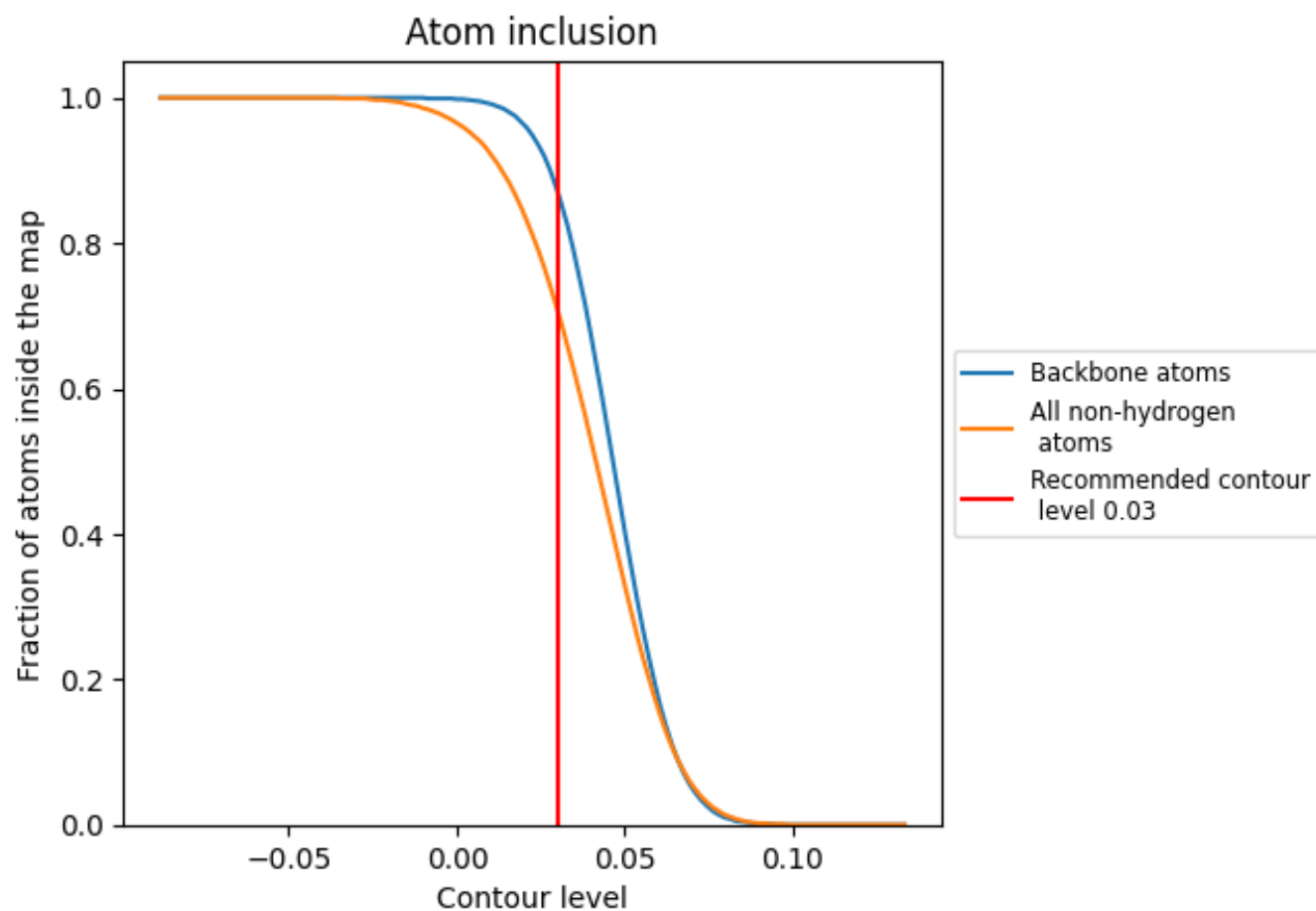
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion ⓘ



At the recommended contour level, 87% of all backbone atoms, 71% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7080	 0.2120
1	 0.5850	 0.1930
2	 0.7290	 0.2350
3	 0.4950	 0.1840
4	 0.5710	 0.2280
5	 0.4950	 0.1860
6	 0.5460	 0.1990
7	 0.6700	 0.2120
A	 0.8290	 0.2330
A0	 0.5330	 0.1800
A1	 0.5520	 0.1910
A2	 0.6370	 0.2100
A3	 0.5860	 0.1640
A4	 0.4910	 0.1830
A5	 0.5400	 0.1560
A6	 0.5510	 0.2030
A7	 0.5580	 0.1850
A8	 0.4910	 0.1730
A9	 0.4950	 0.1550
AA	 0.8210	 0.2360
AB	 0.8970	 0.2400
AC	 0.8610	 0.2440
AD	 0.4260	 0.1490
AE	 0.5310	 0.1710
AF	 0.5550	 0.1790
AG	 0.6190	 0.2110
AH	 0.6090	 0.1900
AI	 0.5930	 0.1790
AJ	 0.5790	 0.2010
AK	 0.5350	 0.1640
AL	 0.5900	 0.1900
AM	 0.4910	 0.1930
AN	 0.6040	 0.1820
AO	 0.5410	 0.1770
AP	 0.5180	 0.1530



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Chain	Atom inclusion	Q-score
AQ	0.5370	0.1970
AR	0.5980	0.1730
AS	0.5480	0.1720
AT	0.5010	0.1720
AU	0.5450	0.1820
AV	0.5240	0.1930
AW	0.5850	0.1890
AX	0.5490	0.1860
AY	0.5510	0.2110
AZ	0.6220	0.1780
Aa	0.5290	0.1780
Ab	0.6080	0.2020
Ac	0.5390	0.1680
Ad	0.5830	0.1920
Ae	0.5450	0.1830
Af	0.5950	0.1760
Ag	0.4750	0.1480
Ah	0.5110	0.1640
Ai	0.5070	0.1740
B	0.5040	0.1720
C	0.5800	0.1910
D	0.5820	0.2060
E	0.5540	0.1730
F	0.5390	0.1770
G	0.5940	0.1880
H	0.5530	0.1770
I	0.5730	0.1790
J	0.5150	0.1920
K	0.5340	0.1530
L	0.5330	0.1870
M	0.5380	0.1580
N	0.5780	0.1910
O	0.6180	0.1990
P	0.4790	0.1660
Q	0.4680	0.1880
R	0.6860	0.2090
S	0.6040	0.1890
T	0.4510	0.1400
U	0.5260	0.1820
V	0.4960	0.1890
W	0.6020	0.1990
X	0.6320	0.2110

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Chain	Atom inclusion	Q-score
Y	 0.5970	 0.1700
Z	 0.5730	 0.1940