



## wwPDB EM Validation Summary Report ⓘ

Nov 19, 2022 – 10:18 PM EST

PDB ID : 4V4N  
EMDB ID : EMD-5691  
Title : Structure of the Methanococcus jannaschii ribosome-SecYEBeta channel complex  
Authors : Menetret, J.F.; Park, E.; Gumbart, J.C.; Ludtke, S.J.; Li, W.; Whynot, A.; Rapoport, T.A.; Akey, C.W.  
Deposited on : 2013-06-17  
Resolution : 9.00 Å (reported)  
Based on initial models : 3J21, 3J2L, 3J20, 1RHZ

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

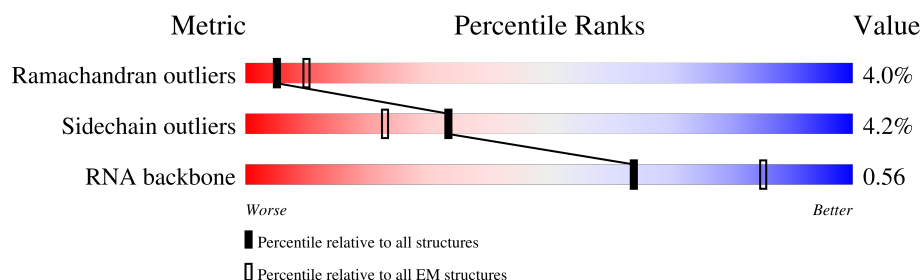
EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.3

# 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 9.00 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)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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  $\geq 3$ , 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	A7	67	
2	A8	52	
3	Af	51	
4	AQ	150	
5	AS	150	
6	AT	84	
7	AU	121	
8	AW	72	

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Mol	Chain	Length	Quality of chain
9	AX	436	
10	B1	77	
11	B2	1495	
12	AG	123	
12	B3	123	
13	BA	190	
14	BB	202	
15	BC	186	
16	BD	172	
17	BE	241	
18	BF	217	
19	BG	125	
20	BH	215	
21	BI	129	
22	BJ	127	
23	BK	135	
24	BL	102	
25	BM	133	
26	BN	145	
27	BO	148	
28	BP	56	
29	BQ	158	
30	BR	113	
31	BS	67	
32	BT	111	

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Mol	Chain	Length	Quality of chain
33	BU	144	
34	BV	99	
35	BW	63	
36	BX	71	
37	BY	50	
38	A1	3049	
39	A3	126	
40	A5	81	
40	AK	81	
41	AA	216	
42	Aa	92	
43	AB	239	
44	Ab	127	
45	AC	365	
46	AD	255	
47	Ad	89	
48	AE	186	
49	Ae	62	
50	AF	184	
51	Ag	45	
52	AH	134	
53	Ah	24	
54	AI	142	
55	Ai	78	
56	AJ	132	

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Mol	Chain	Length	Quality of chain
57	Aj	94	
58	Ak	212	
59	AL	147	
60	AM	194	
61	AN	168	
62	AO	197	
63	AP	120	
64	AR	95	
65	AV	66	
66	AY	155	
67	AZ	99	

## 2 Entry composition [i](#)

There are 67 unique types of molecules in this entry. The entry contains 171094 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 Preprotein translocase subunit SecE.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A7	65	Total	C	N	O	S	0	0
			525	348	85	91	1		

- Molecule 2 is a protein called Preprotein translocase subunit SecG.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	A8	32	Total	C	N	O	0	0
			258	172	42	44		

- Molecule 3 is a protein called 50S ribosomal protein L39E.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Af	51	Total	C	N	O	S	0	0
			445	284	98	62	1		

- Molecule 4 is a protein called 50S ribosomal protein L19E.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AQ	150	Total	C	N	O	S	0	0
			1256	794	255	202	5		

- Molecule 5 is a protein called 50S ribosomal protein L22P.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AS	150	Total	C	N	O	S	0	0
			1200	764	230	202	4		

- Molecule 6 is a protein called 50S ribosomal protein L23P.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	AT	84	Total	C	N	O	0	0
			680	440	118	122		

- Molecule 7 is a protein called 50S ribosomal protein L24P.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AU	121	Total	C	N	O	S	0	0
			1008	637	195	172	4		

- Molecule 8 is a protein called 50S ribosomal protein L29P.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AW	66	Total	C	N	O	S	0	0
			546	338	105	99	4		

- Molecule 9 is a protein called Protein translocase subunit SecY.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AX	432	Total	C	N	O	S	0	0
			3309	2210	521	559	19		

- Molecule 10 is a RNA chain called E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B1	77	Total	C	N	O	P	0	0
			1646	734	303	533	76		

- Molecule 11 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	B2	1495	Total	C	N	O	P	0	0
			32132	14297	5954	10387	1494		

- Molecule 12 is a protein called 30S ribosomal protein L7AE.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	B3	123	Total	C	N	O	S	0	0
			939	599	155	181	4		
12	AG	123	Total	C	N	O	S	0	0
			939	599	155	181	4		

- Molecule 13 is a protein called 30S ribosomal protein S3AE.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	BA	190	Total	C	N	O	S	0	0
			1559	1007	273	274	5		

- Molecule 14 is a protein called 30S ribosomal protein S2P.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	BB	202	Total	C	N	O	S	0	0
			1623	1046	282	290	5		

- Molecule 15 is a protein called 30S ribosomal protein S3P.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	BC	186	Total	C	N	O	S	0	0
			1460	933	271	252	4		

- Molecule 16 is a protein called 30S ribosomal protein S4P.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	BD	172	Total	C	N	O	S	0	0
			1434	902	273	255	4		

- Molecule 17 is a protein called 30S ribosomal protein S4E.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	BE	241	Total	C	N	O	S	0	0
			1976	1277	355	339	5		

- Molecule 18 is a protein called 30S ribosomal protein S5P.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	BF	217	Total	C	N	O	S	0	0
			1717	1084	319	306	8		

- Molecule 19 is a protein called 30S ribosomal protein S6E.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	BG	125	Total	C	N	O	S	0	0
			984	623	180	179	2		

- Molecule 20 is a protein called 30S ribosomal protein S7P.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	BH	215	Total	C	N	O	S	0	0
			1736	1100	326	302	8		

- Molecule 21 is a protein called 30S ribosomal protein S8P.



Mol	Chain	Residues	Atoms					AltConf	Trace
21	BI	129	Total	C	N	O	S	0	0
			1028	668	178	180	2		

- Molecule 22 is a protein called 30S ribosomal protein S8E.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	BJ	127	Total	C	N	O	S	0	0
			1004	622	207	174	1		

- Molecule 23 is a protein called 30S ribosomal protein S9P.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	BK	135	Total	C	N	O	S	0	0
			1072	671	205	190	6		

- Molecule 24 is a protein called 30S ribosomal protein S10P.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	BL	102	Total	C	N	O	S	0	0
			822	507	159	152	4		

- Molecule 25 is a protein called 30S ribosomal protein S11P.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BM	133	Total	C	N	O	S	0	0
			1004	623	200	179	2		

- Molecule 26 is a protein called 30S ribosomal protein S12P.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BN	145	Total	C	N	O	S	0	0
			1141	722	223	193	3		

- Molecule 27 is a protein called 30S ribosomal protein S13P.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BO	148	Total	C	N	O	S	0	0
			1189	746	237	200	6		

- Molecule 28 is a protein called 30S ribosomal protein S14P.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BP	56	Total	C	N	O	S	0	0
			462	292	95	69	6		

- Molecule 29 is a protein called 30S ribosomal protein S15P/S13E.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BQ	158	Total	C	N	O	S	0	0
			1310	834	250	221	5		

- Molecule 30 is a protein called 30S ribosomal protein S17P.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BR	113	Total	C	N	O	S	0	0
			934	592	177	160	5		

- Molecule 31 is a protein called 30S ribosomal protein S17E.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BS	67	Total	C	N	O	S	0	0
			556	353	105	95	3		

- Molecule 32 is a protein called 30S ribosomal protein S19P.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BT	111	Total	C	N	O	S	0	0
			924	594	173	151	6		

- Molecule 33 is a protein called 30S ribosomal protein S19E.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BU	144	Total	C	N	O	S	0	0
			1176	758	212	205	1		

- Molecule 34 is a protein called 30S ribosomal protein S24E.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BV	99	Total	C	N	O	S	0	0
			823	532	134	154	3		

- Molecule 35 is a protein called 30S ribosomal protein S27E.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BW	63	Total	C	N	O	S	0	0
			478	306	85	81	6		

- Molecule 36 is a protein called 30S ribosomal protein S28E.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BX	71	Total	C	N	O	S	0	0
			568	345	115	107	1		

- Molecule 37 is a protein called 30S ribosomal protein S27AE.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BY	50	Total	C	N	O	S	0	0
			409	262	75	66	6		

- Molecule 38 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	A1	2969	Total	C	N	O	P	0	0
			63885	28427	11905	20589	2964		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	A3	126	Total	C	N	O	P	0	0
			2691	1199	492	875	125		

- Molecule 40 is a protein called 50S ribosomal protein L14E.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	A5	81	Total	C	N	O	S	0	0
			614	386	119	108	1		
40	AK	81	Total	C	N	O	S	0	0
			614	386	119	108	1		

- Molecule 41 is a protein called 50S ribosomal protein L1P.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	AA	216	Total	C	N	O	S	0	0
			1677	1068	300	304	5		

- Molecule 42 is a protein called 50S ribosomal protein L31E.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	Aa	82	Total	C	N	O		
			677	444	126	107	0	0

- Molecule 43 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AB	239	Total	C	N	O	S		
			1838	1169	347	317	5	0	0

- Molecule 44 is a protein called 50S ribosomal protein L32E.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Ab	127	Total	C	N	O	S		
			1075	689	217	168	1	0	0

- Molecule 45 is a protein called 50S ribosomal protein L3P.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	AC	342	Total	C	N	O	S		
			2717	1741	495	467	14	0	0

- Molecule 46 is a protein called 50S ribosomal protein L4P.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	AD	255	Total	C	N	O	S		
			2026	1288	391	342	5	0	0

- Molecule 47 is a protein called 50S ribosomal protein L34E.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Ad	89	Total	C	N	O	S		
			740	463	158	108	11	0	0

- Molecule 48 is a protein called 50S ribosomal protein L5P.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	AE	186	Total	C	N	O	S		
			1489	937	278	265	9	0	0

- Molecule 49 is a protein called 50S ribosomal protein L37E.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Ae	62	Total	C	N	O	S	0	0
			506	312	111	78	5		

- Molecule 50 is a protein called 50S ribosomal protein L6P.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	AF	184	Total	C	N	O	S	0	0
			1476	956	252	266	2		

- Molecule 51 is a protein called 50S ribosomal protein L40E.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Ag	45	Total	C	N	O	S	0	0
			372	236	76	56	4		

- Molecule 52 is a protein called 50S ribosomal protein L11P.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	AH	134	Total	C	N	O	S	0	0
			989	635	164	184	6		

- Molecule 53 is a protein called 50S ribosomal protein L41E.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Ah	24	Total	C	N	O	S	0	0
			230	147	54	28	1		

- Molecule 54 is a protein called 50S ribosomal protein L13P.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	AI	142	Total	C	N	O	S	0	0
			1150	737	215	195	3		

- Molecule 55 is a protein called 50S ribosomal protein L37AE.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Ai	78	Total	C	N	O	S	0	0
			590	368	122	95	5		

- Molecule 56 is a protein called 50S ribosomal protein L14P.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	AJ	132	Total	C	N	O	S	0	0
			1014	631	204	176	3		

- Molecule 57 is a protein called 50S ribosomal protein L44E.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Aj	94	Total	C	N	O	S	0	0
			788	499	162	122	5		

- Molecule 58 is a protein called 50S ribosomal protein P0/L10E.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Ak	212	Total	C	N	O	S	0	0
			1633	1051	272	304	6		

- Molecule 59 is a protein called 50S ribosomal protein L15P.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AL	147	Total	C	N	O	S	0	0
			1154	727	227	195	5		

- Molecule 60 is a protein called 50S ribosomal protein L15E.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	AM	194	Total	C	N	O	S	0	0
			1595	1020	316	253	6		

- Molecule 61 is a protein called 50S ribosomal protein L10E/L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AN	168	Total	C	N	O	S	0	0
			1379	872	268	233	6		

- Molecule 62 is a protein called 50S ribosomal protein L18P.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AO	197	Total	C	N	O	S	0	0
			1598	1021	299	275	3		

- Molecule 63 is a protein called 50S ribosomal protein L18E.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	AP	120	Total	C	N	O	S	0	0
			966	606	186	171	3		

- Molecule 64 is a protein called 50S ribosomal protein L21E.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AR	95	Total	C	N	O	S	0	0
			787	501	160	125	1		

- Molecule 65 is a protein called 50S ribosomal protein L24E.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AV	66	Total	C	N	O	S	0	0
			555	351	106	91	7		

- Molecule 66 is a protein called 50S ribosomal protein L30P.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	AY	155	Total	C	N	O	S	0	0
			1243	788	235	213	7		

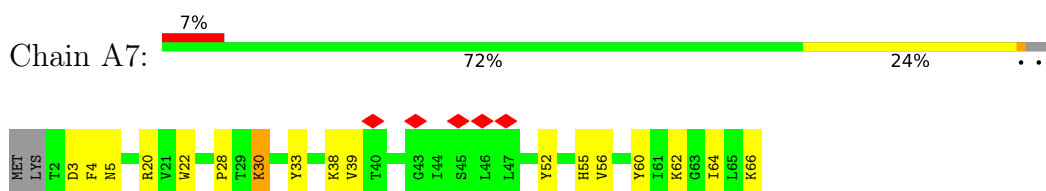
- Molecule 67 is a protein called 50S ribosomal protein L30E.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	AZ	99	Total	C	N	O	S	0	0
			754	489	121	142	2		

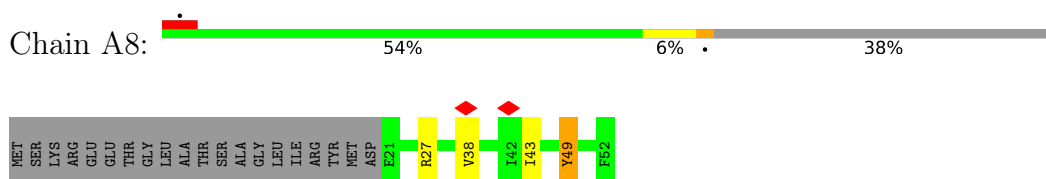
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

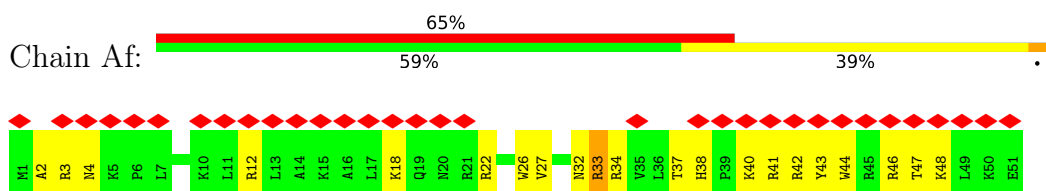
- Molecule 1: Preprotein translocase subunit SecE



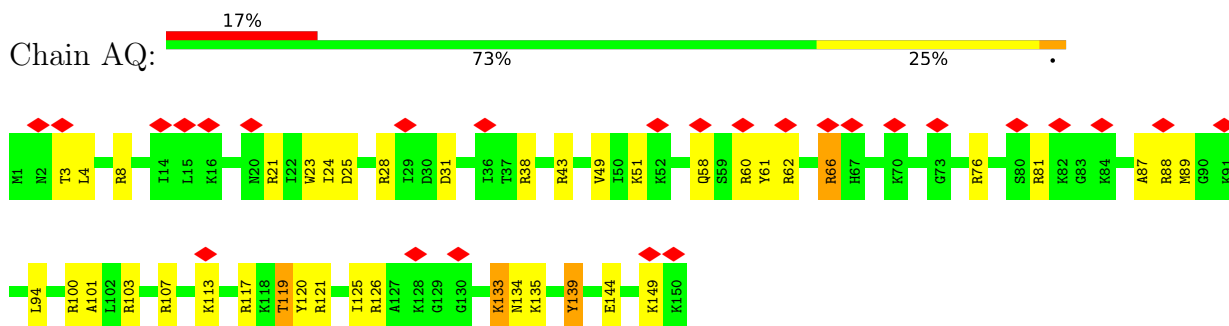
- Molecule 2: Preprotein translocase subunit SecG



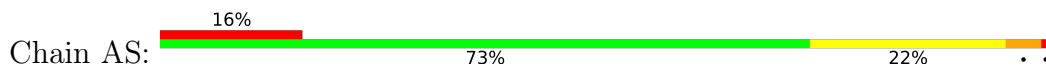
- Molecule 3: 50S ribosomal protein L39E



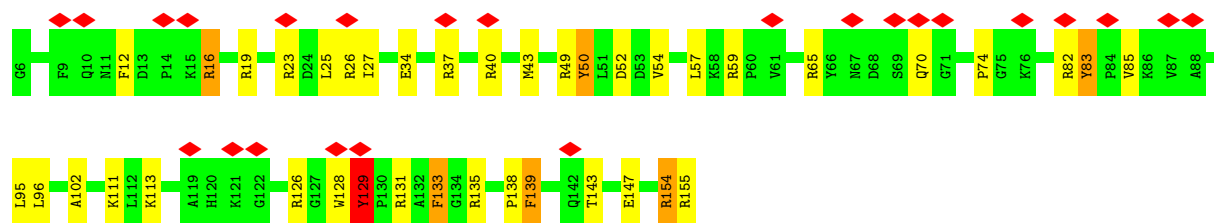
- Molecule 4: 50S ribosomal protein L19E



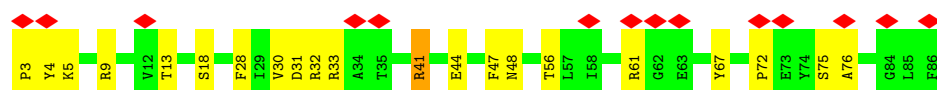
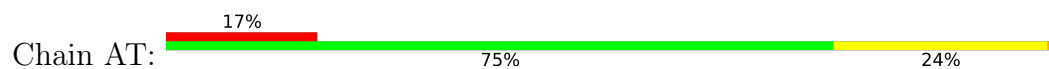
- Molecule 5: 50S ribosomal protein L22P



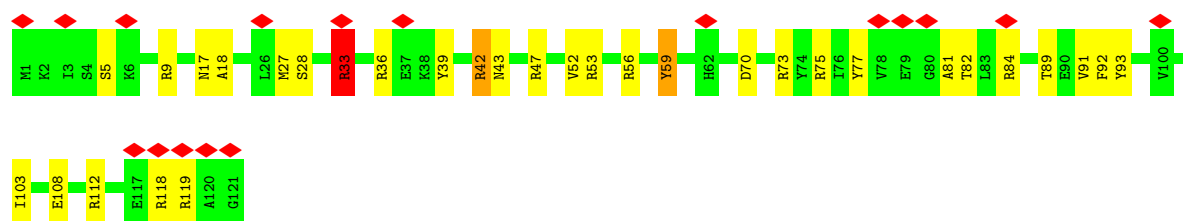
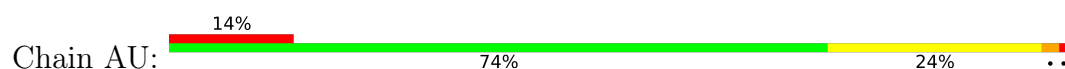




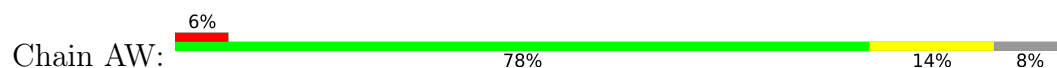
• Molecule 6: 50S ribosomal protein L23P



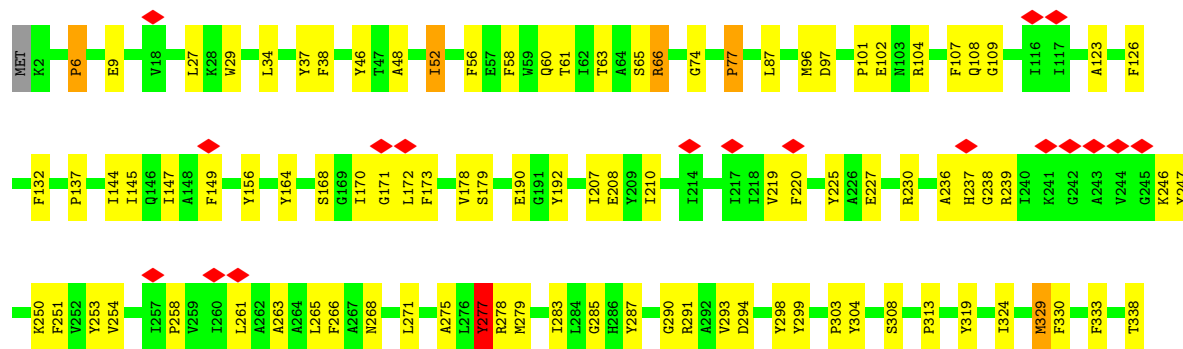
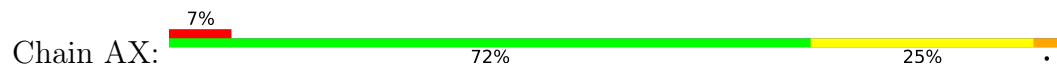
• Molecule 7: 50S ribosomal protein L24P

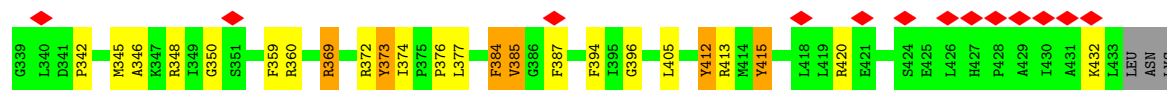


• Molecule 8: 50S ribosomal protein L29P

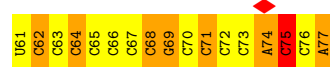
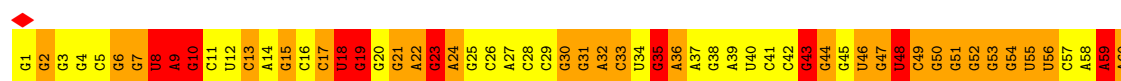


• Molecule 9: Protein translocase subunit SecY

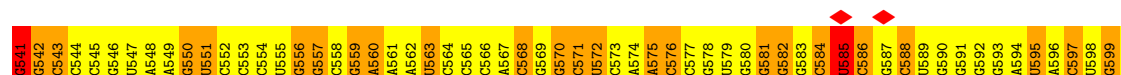
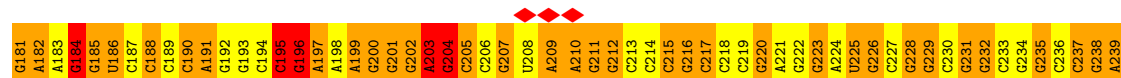
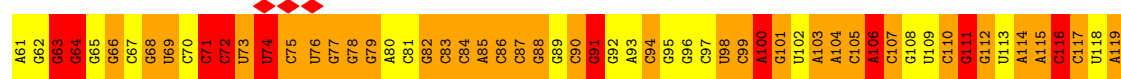




• Molecule 10: E-tRNA

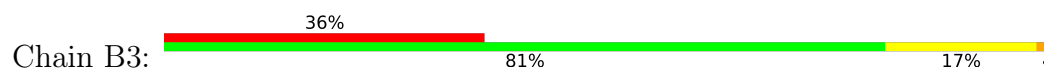


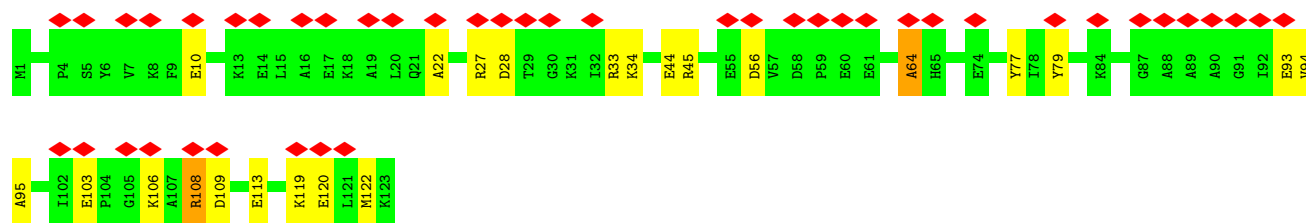
• Molecule 11: 16S ribosomal RNA



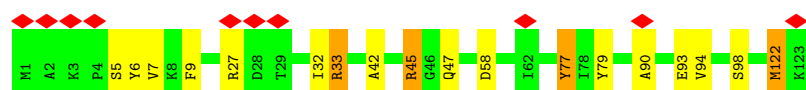
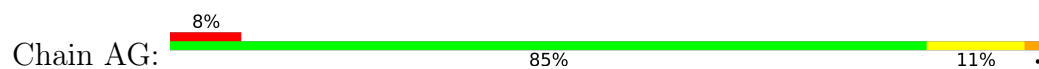
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• Molecule 12: 30S ribosomal protein L7AE

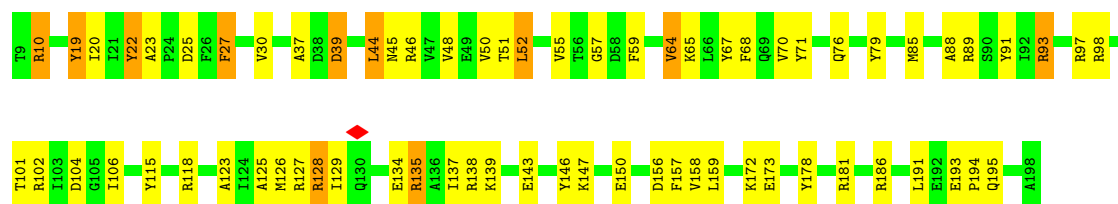




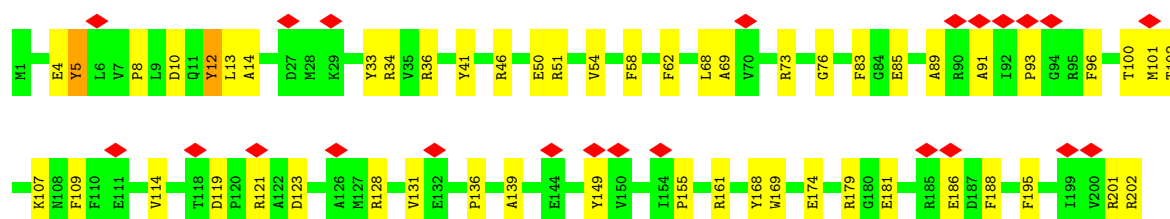
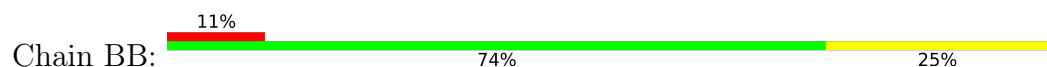
- Molecule 12: 30S ribosomal protein L7AE



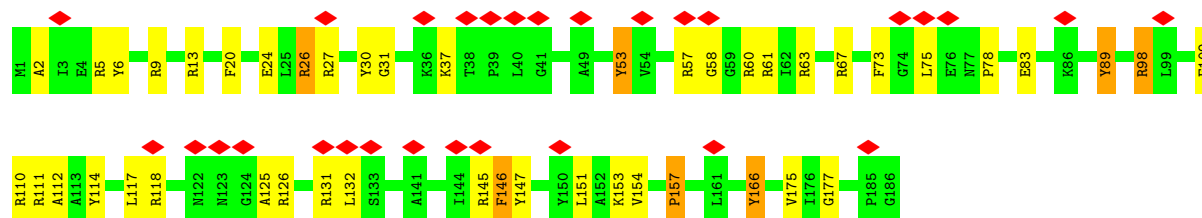
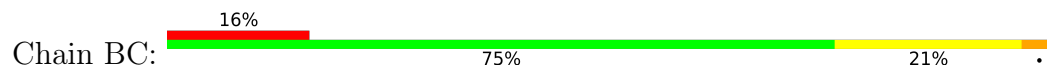
- Molecule 13: 30S ribosomal protein S3AE



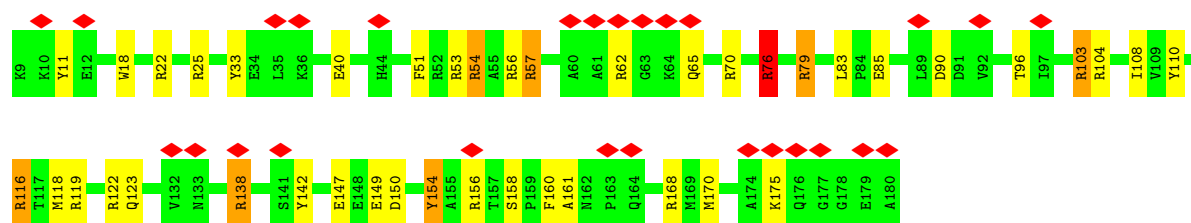
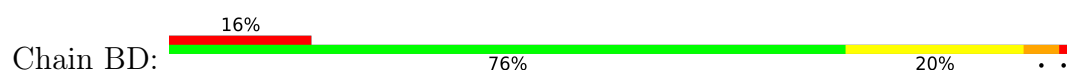
- Molecule 14: 30S ribosomal protein S2P



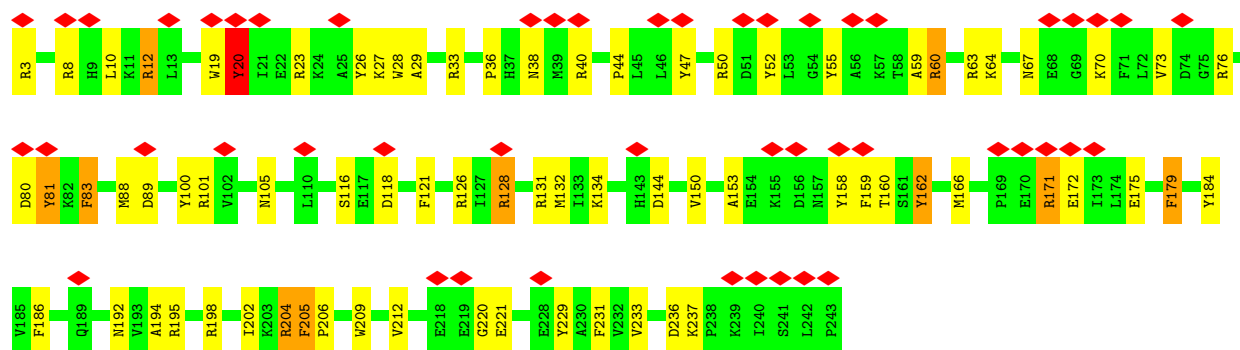
- Molecule 15: 30S ribosomal protein S3P



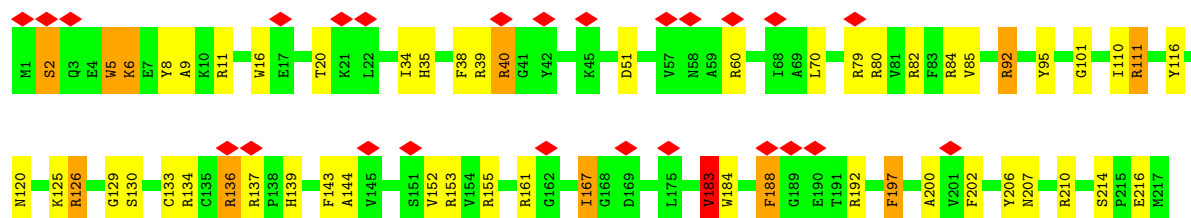
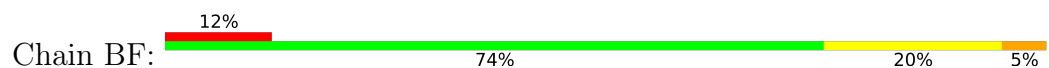
- Molecule 16: 30S ribosomal protein S4P



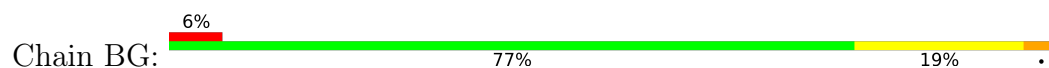
- Molecule 17: 30S ribosomal protein S4E



- Molecule 18: 30S ribosomal protein S5P

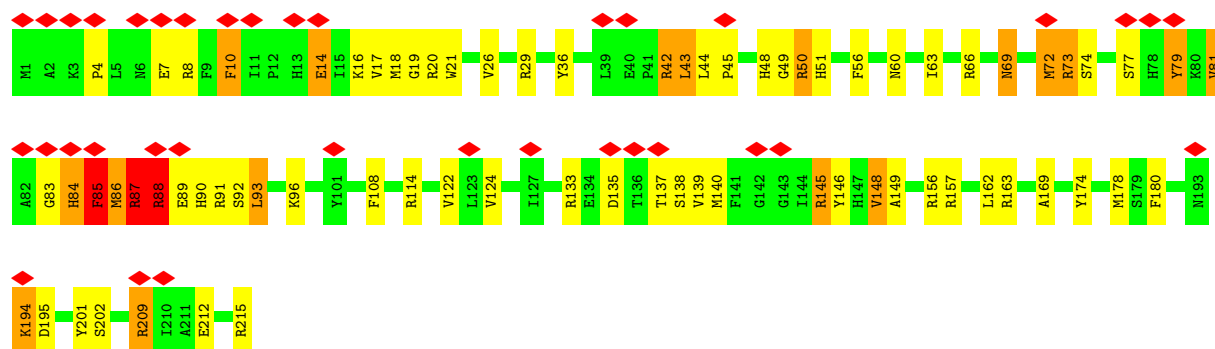


- Molecule 19: 30S ribosomal protein S6E

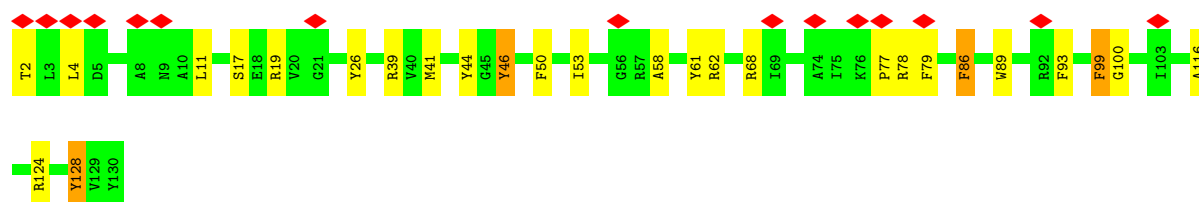
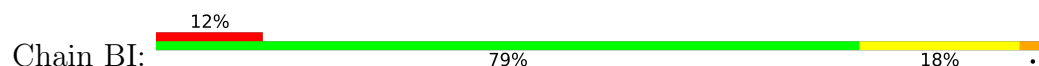


- Molecule 20: 30S ribosomal protein S7P

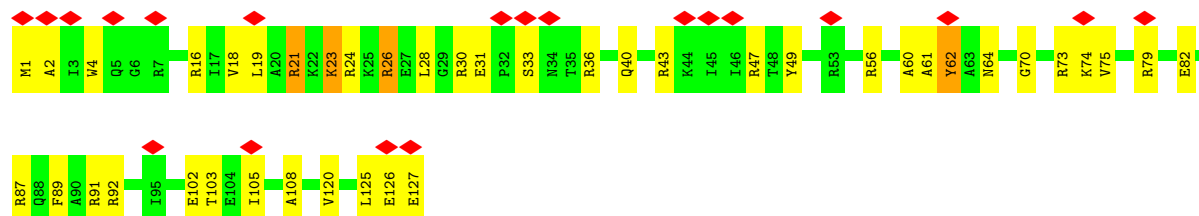




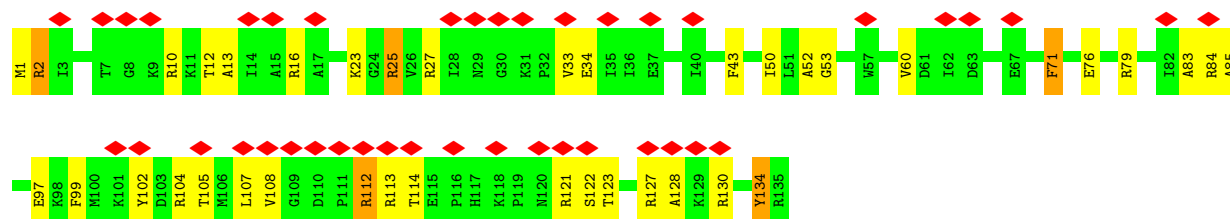
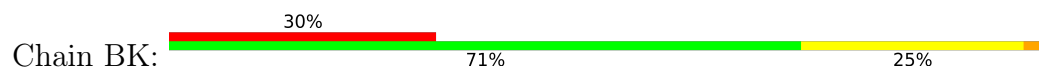
• Molecule 21: 30S ribosomal protein S8P



• Molecule 22: 30S ribosomal protein S8E

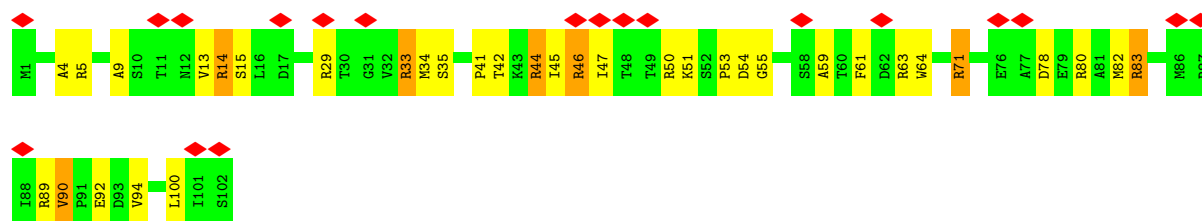


• Molecule 23: 30S ribosomal protein S9P

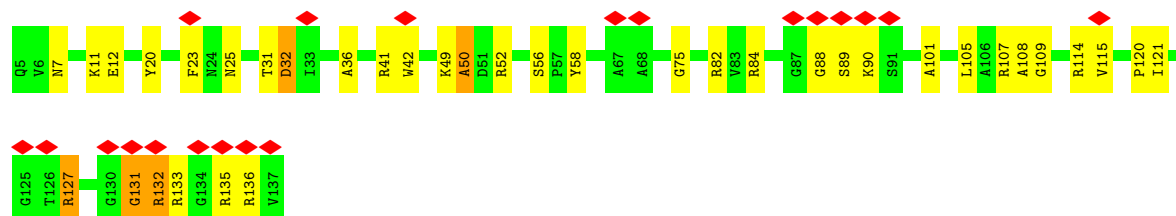
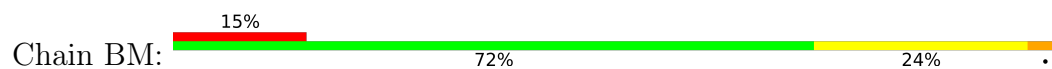


• Molecule 24: 30S ribosomal protein S10P

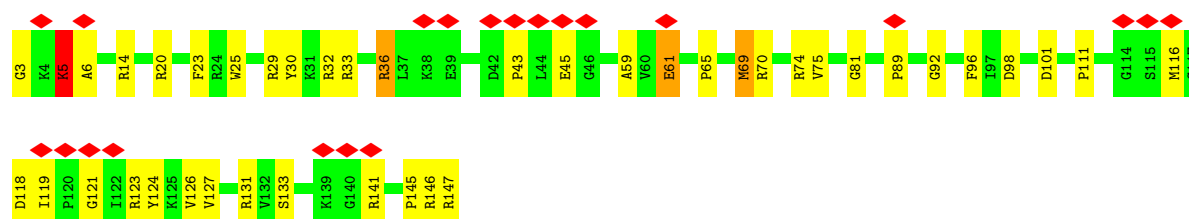
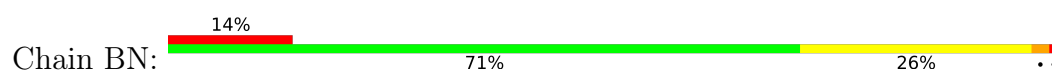




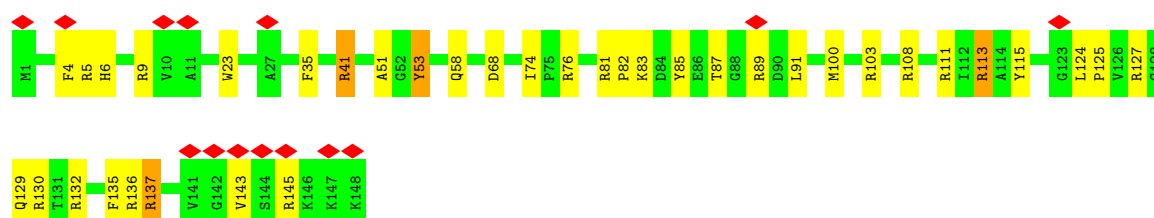
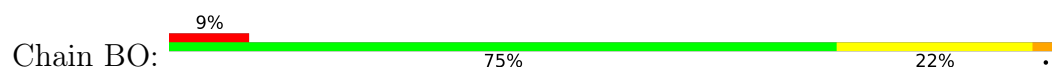
- Molecule 25: 30S ribosomal protein S11P



- Molecule 26: 30S ribosomal protein S12P




- Molecule 27: 30S ribosomal protein S13P

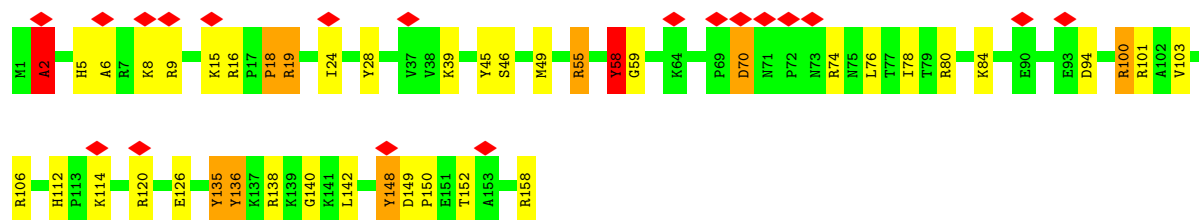


- Molecule 28: 30S ribosomal protein S14P




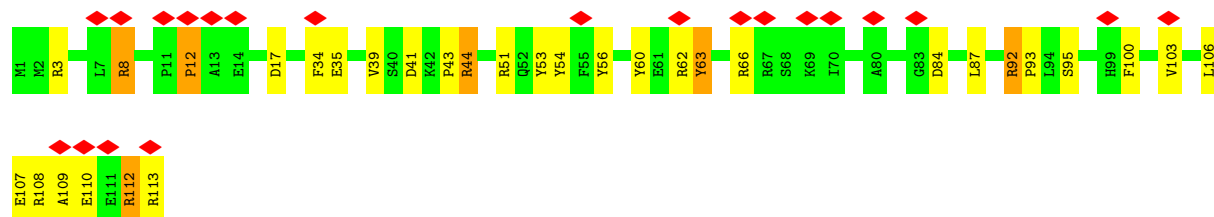
- Molecule 29: 30S ribosomal protein S15P/S13E

Chain BQ: 




- Molecule 30: 30S ribosomal protein S17P

Chain BR: 




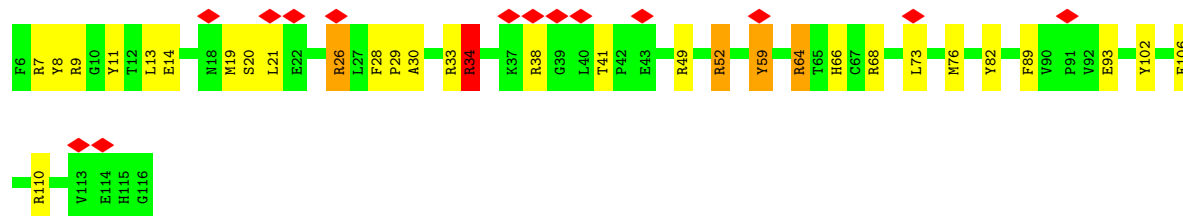
- Molecule 31: 30S ribosomal protein S17E

Chain BS: 




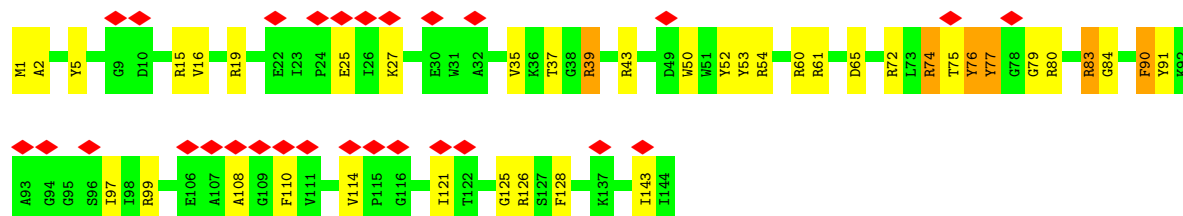
- Molecule 32: 30S ribosomal protein S19P

Chain BT: 



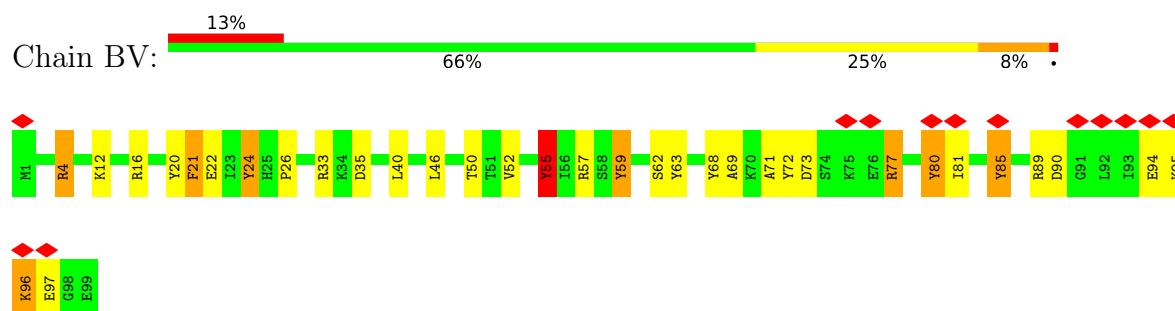
- Molecule 33: 30S ribosomal protein S19E

Chain BU: 

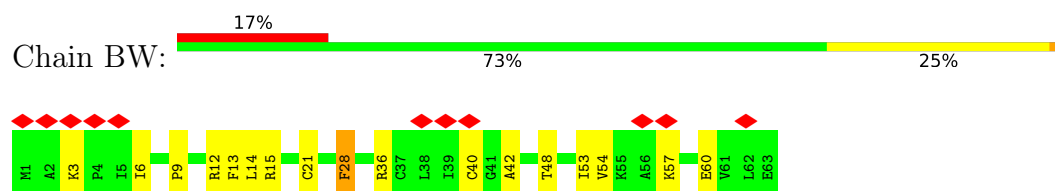




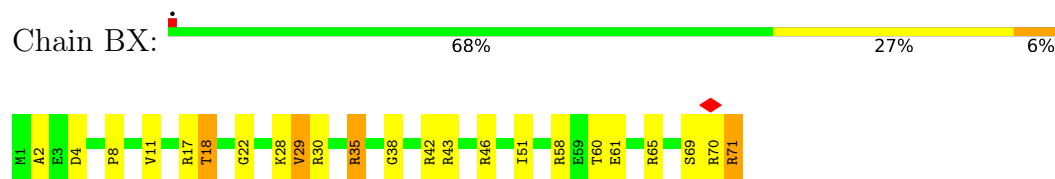
- Molecule 34: 30S ribosomal protein S24E



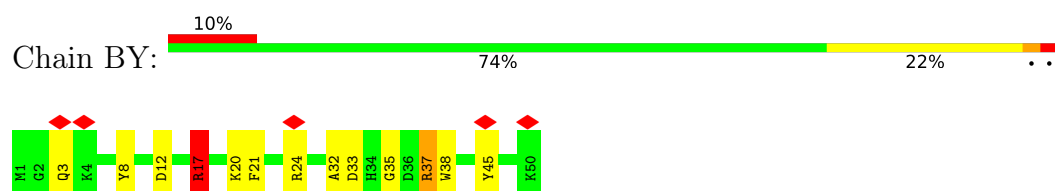
- Molecule 35: 30S ribosomal protein S27E



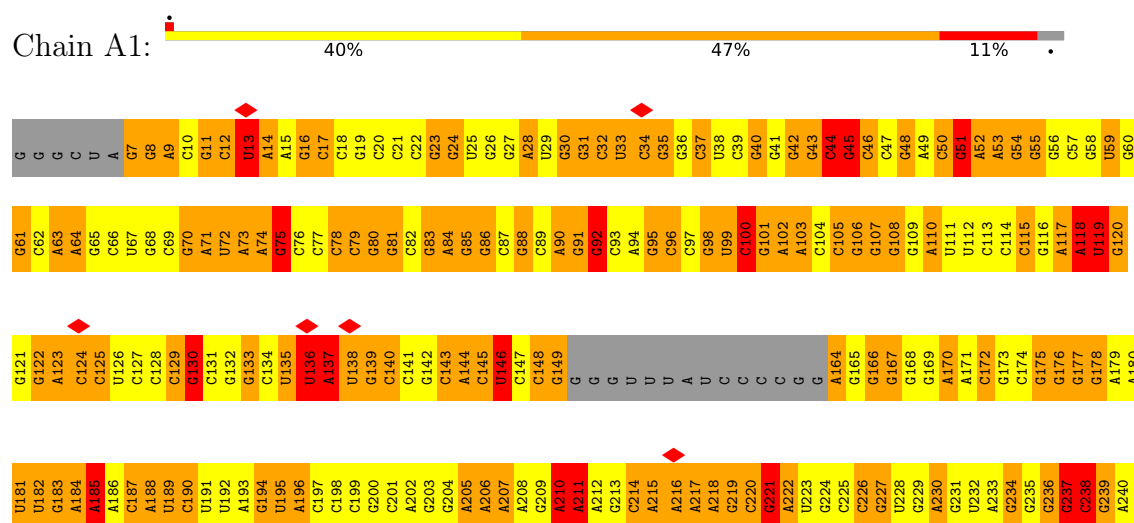
- Molecule 36: 30S ribosomal protein S28E



- Molecule 37: 30S ribosomal protein S27AE



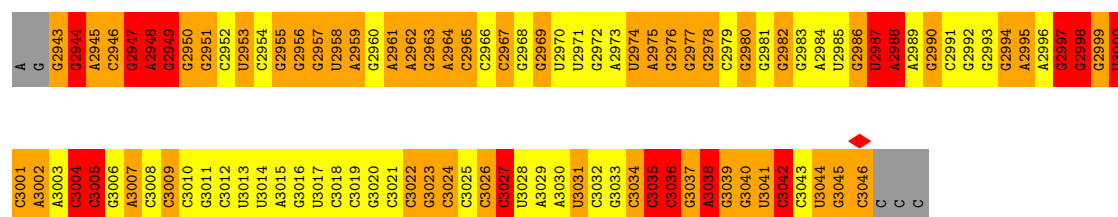
- Molecule 38: 23S ribosomal RNA



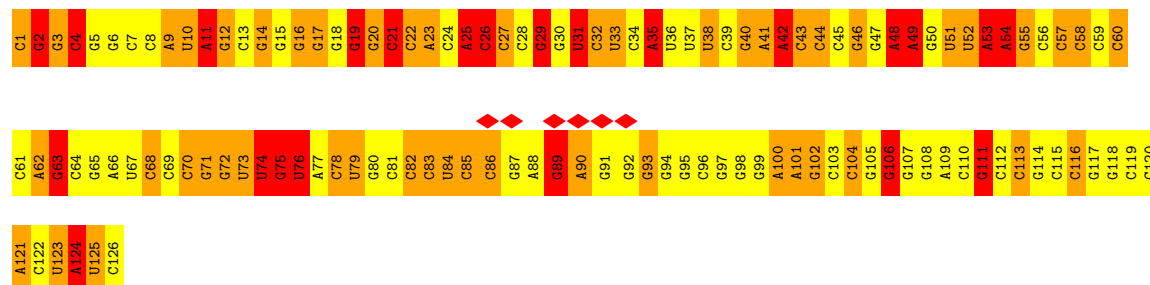
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A1143	G1083	C1023	G963	C903	C843	G783	A723	A663	G603	G543	◆	◆	G363	G423	G363	G303	C243
A1144	G1084	G1024	C964	G904	C844	G784	G724	A664	A604	A544	◆	◆	G364	U424	G364	G304	A244
G1145	G1085	A1025	A965	G905	U845	C785	G725	C665	A605	G545	◆	◆	G365	U425	G365	G305	A245
U1146	U1086	A1026	G966	G906	C846	G786	G726	A666	A606	G546	◆	◆	G366	G426	G366	G306	A246
G1147	G1087	A1027	G967	C907	A847	G787	A727	C667	C607	C547	◆	◆	G367	G427	G367	C307	A247
C1148	G1088	G1028	U968	U908	A848	A788	A728	C668	C608	U548	◆	◆	U368	A288	U368	C308	C248
C1149	G1089	C1029	U969	A909	C849	G789	A729	G669	G609	U549	◆	◆	G369	U429	G369	C309	C249
G1150	G1090	C1030	G970	G910	C850	U790	C729	C670	C610	G549	◆	◆	A370	A430	A370	C310	G250
G1151	G1091	C1031	G971	G911	G851	C791	G731	C671	G611	A550	◆	◆	G371	U431	G371	C311	C251
C1152	U1092	C1032	C972	G912	A852	A792	G732	C672	G612	A551	◆	◆	A372	A432	A372	G312	A252
U1153	G1093	C1033	C973	G913	G853	C793	A733	A673	C613	A552	◆	◆	U313	G433	G373	U313	G253
A1154	U1094	G1034	C974	U914	G854	G794	C734	G674	G614	C553	◆	◆	G374	G434	G374	A314	A254
A1155	A1095	G1035	C975	G915	C855	G795	A735	C675	A615	G554	◆	◆	C375	G435	C375	U315	G255
U1156	A1096	C1036	C976	A916	A856	C796	U736	C676	C616	G555	◆	◆	G376	G436	G376	G316	G256
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G1158	G1098	U1038	C978	A918	G858	G798	C738	G678	C618	G557	◆	◆	G378	G438	G378	G318	A258
U1159	C1099	C1039	G979	G919	G859	C799	C739	U679	G619	G558	◆	◆	U379	A439	U379	A319	A259
U1160	G1100	C1040	G980	G920	A860	G800	C740	U680	G620	G559	◆	◆	C500	A440	C500	A320	A260
A1161	U1101	U1041	G981	C921	G861	A801	G741	C681	G621	C561	◆	◆	G381	A441	G381	C321	A261
C1162	C1102	G1042	G982	C922	C862	G802	C742	C682	A622	C562	◆	◆	C382	G442	C382	G322	C262
U1163	C1103	U1043	G983	A923	C863	A803	A743	C683	G623	A563	◆	◆	C383	G443	C383	U323	U263
C1164	A1104	C1044	U984	A924	C864	C804	G744	G684	U624	U564	◆	◆	G384	U444	G384	C324	G264
C1165	C1105	A1045	A985	U925	C865	C805	C745	G685	A625	A564	◆	◆	U385	G445	U385	G325	A265
U1166	C1106	A1046	G986	C926	C866	C806	C746	C686	C626	A565	◆	◆	A386	G446	A386	C326	A266
A1167	G1107	U1047	G987	G927	C867	G807	G747	C687	G627	G566	◆	◆	A387	G447	A387	G327	C267
U1168	A1108	C1048	C988	A928	U868	A808	G748	G688	A628	G567	◆	◆	G388	U448	G388	C328	C268
G1169	G1109	U1049	G989	C929	A869	A809	C749	U689	G629	A568	◆	◆	C389	U449	C389	G329	C269
U1170	A1110	C1050	G990	G930	G870	A810	U749	C690	G630	G569	◆	◆	U390	A450	U390	C330	C270
G1171	G1111	U1051	U991	C931	G871	C811	C750	G691	G631	A510	◆	◆	C391	U451	C391	G331	G271
U1172	G1112	G1052	G992	C932	C872	C812	U751	C692	G632	G512	◆	◆	A332	A452	A332	G332	G272
G1173	G1113	C1053	G993	G933	C873	G813	A752	G693	A633	G513	◆	◆	C393	U453	C393	G333	G273
U1174	G1114	A1054	G994	G934	U874	G814	U753	U694	G634	G514	◆	◆	A394	G454	A394	G334	C274
C1175	A1115	C1055	G995	A935	C875	U815	U754	G695	G635	C574	◆	◆	G395	G455	G395	C335	C275
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C1177	C1117	U1057	A997	A937	U877	G817	G757	C697	G637	G576	◆	◆	G397	U457	G397	G337	A277
G1178	A1118	U1058	G998	U938	U878	A818	C758	U698	A638	C577	◆	◆	A338	U458	A338	C338	C278
U1179	C1119	C1059	A999	A939	U879	U819	G759	A699	C639	G578	◆	◆	A339	U459	A339	G339	C279
G1180	C1120	C1060	G1000	G940	U880	C820	G760	A700	C640	C579	◆	◆	G340	U460	G340	G340	A280
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G1186	C1126	C1066	A1006	U946	G886	C826	G766	G706	G646	G526	◆	◆	U406	C466	U406	G286	G286
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A1197	G1137	G1076	C1017	C957	U897	G837	A777	A717	U657	G536	◆	◆	U416	C477	U416	G297	G297
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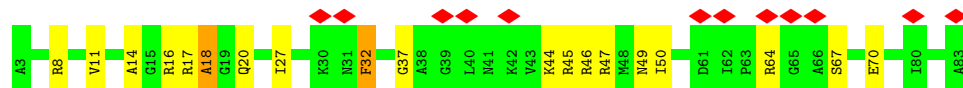
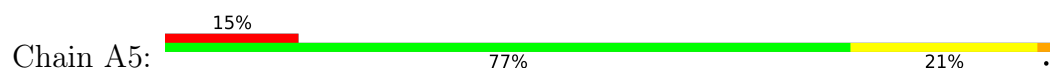




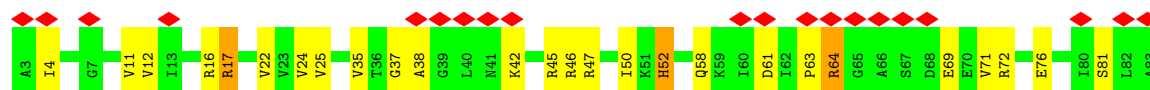
• Molecule 39: 5S ribosomal RNA



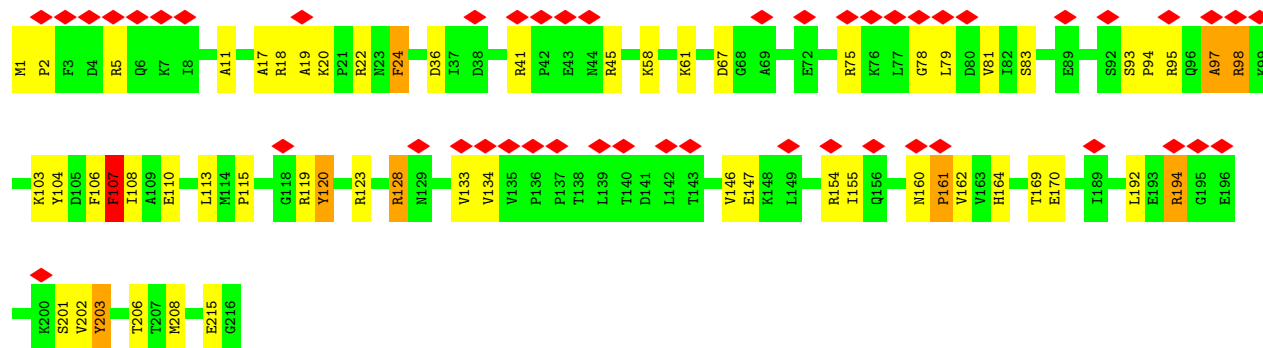
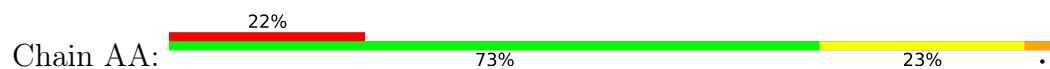
• Molecule 40: 50S ribosomal protein L14E



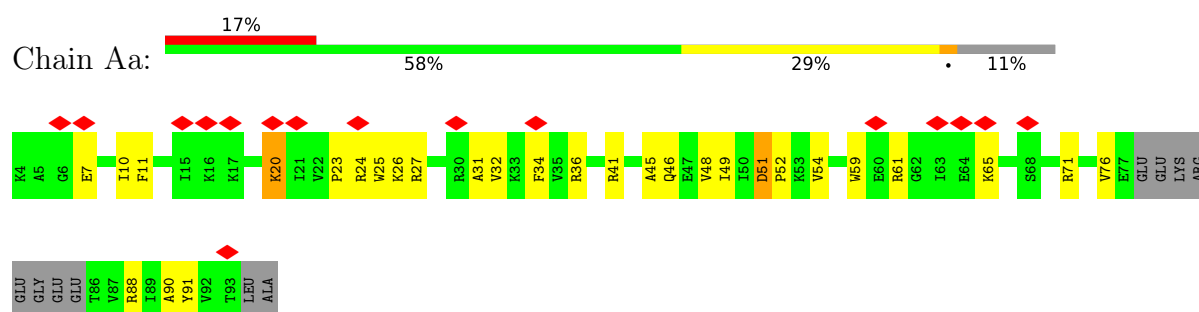
• Molecule 40: 50S ribosomal protein L14E



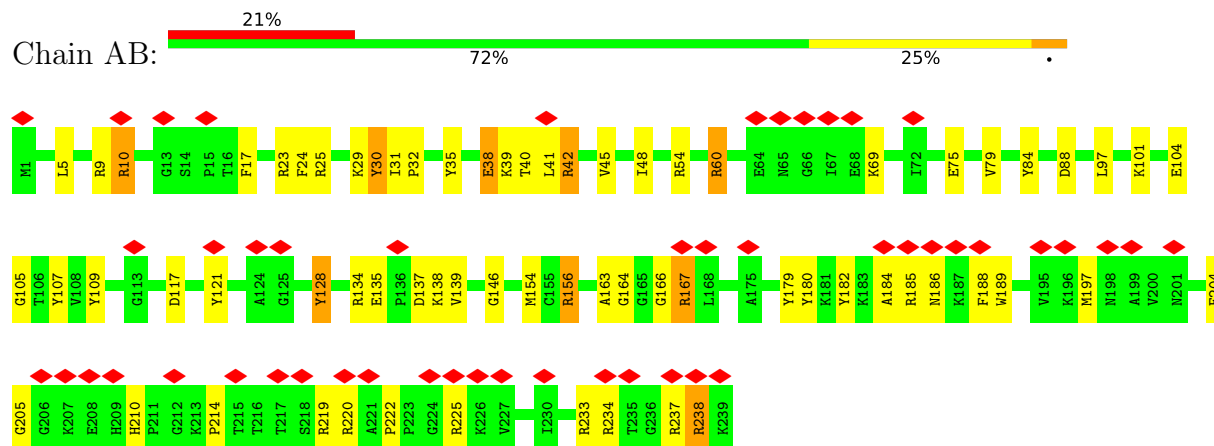
• Molecule 41: 50S ribosomal protein L1P



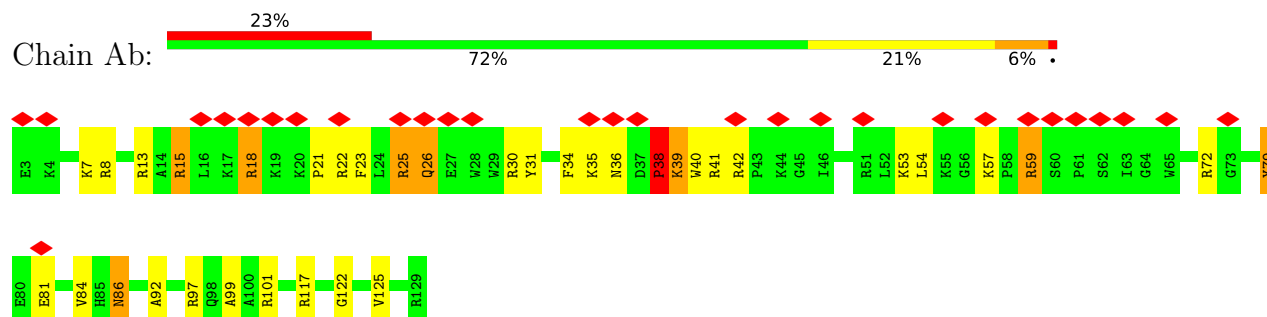
• Molecule 42: 50S ribosomal protein L31E



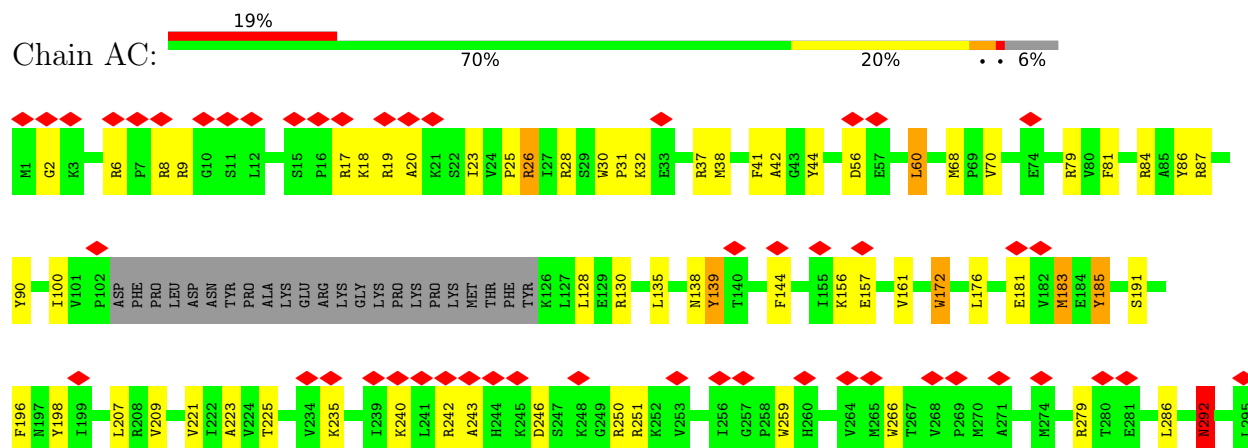
• Molecule 43: 50S ribosomal protein L2

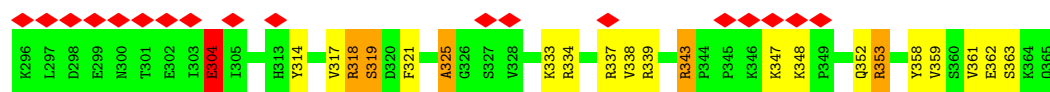


• Molecule 44: 50S ribosomal protein L32E

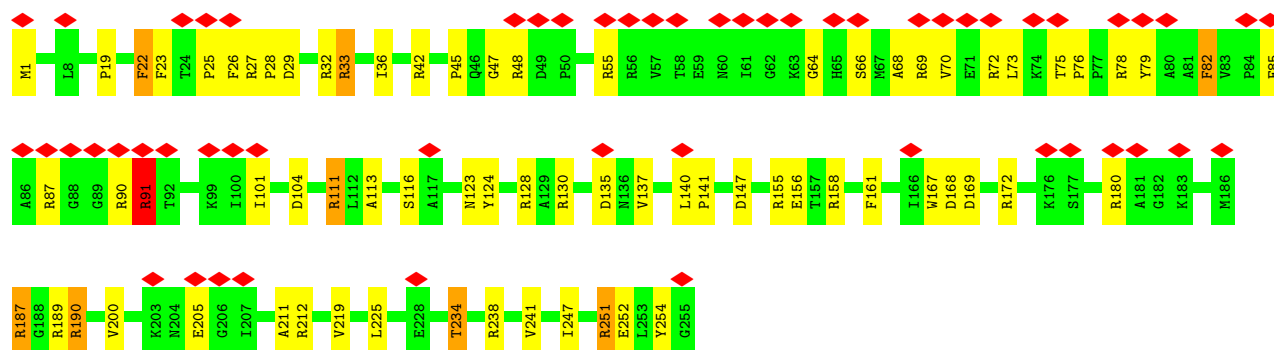
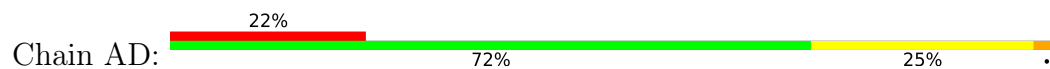


• Molecule 45: 50S ribosomal protein L3P

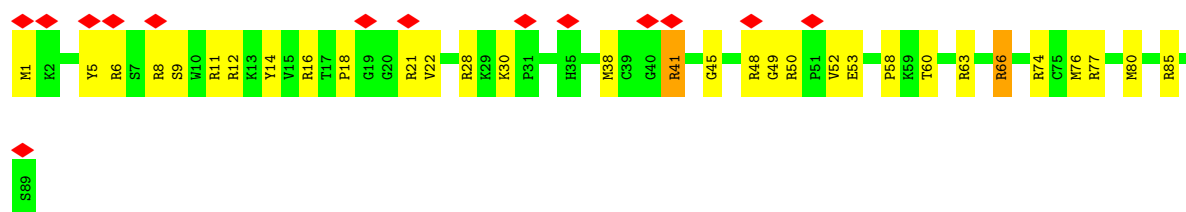




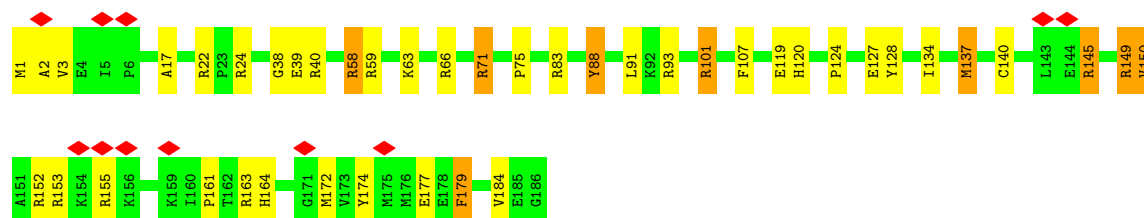
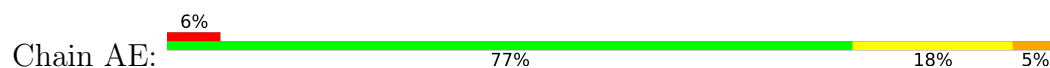
• Molecule 46: 50S ribosomal protein L4P



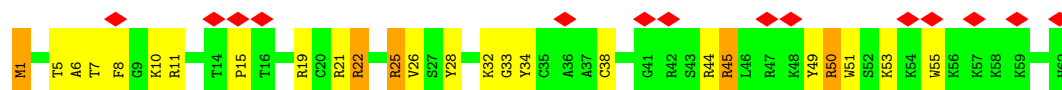
• Molecule 47: 50S ribosomal protein L34E



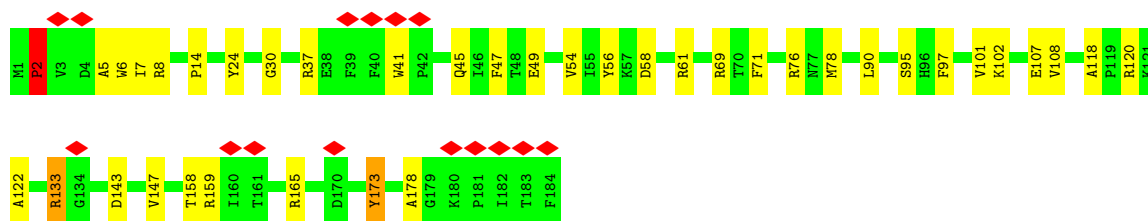
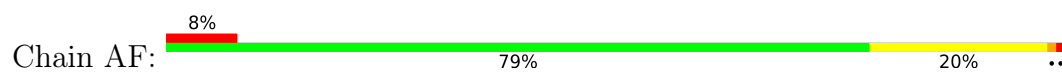
• Molecule 48: 50S ribosomal protein L5P



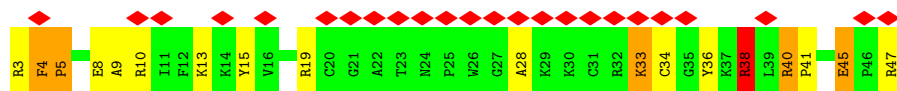
• Molecule 49: 50S ribosomal protein L37E



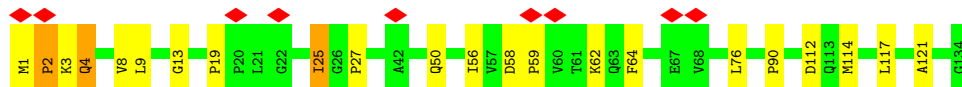
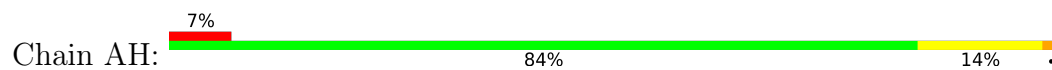
• Molecule 50: 50S ribosomal protein L6P



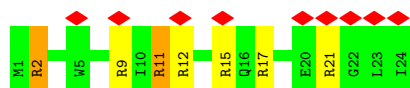
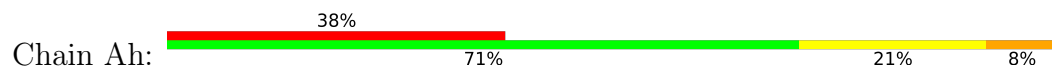
- Molecule 51: 50S ribosomal protein L40E



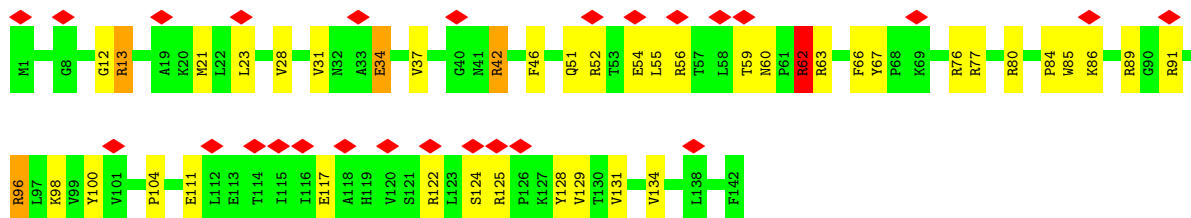
- Molecule 52: 50S ribosomal protein L11P



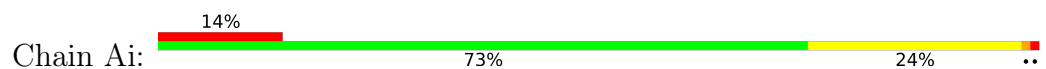
- Molecule 53: 50S ribosomal protein L41E



- Molecule 54: 50S ribosomal protein L13P

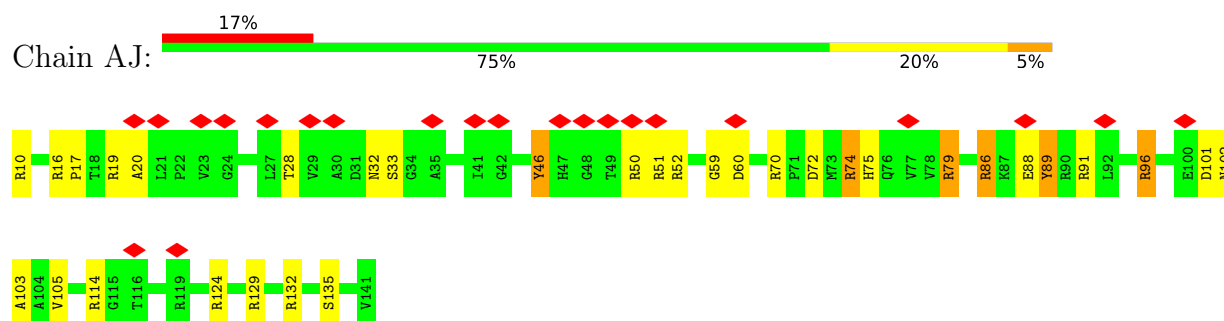


- Molecule 55: 50S ribosomal protein L37AE

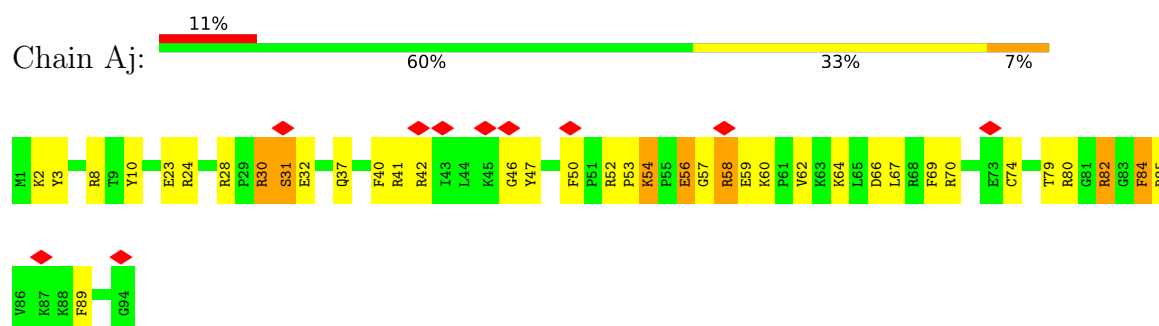




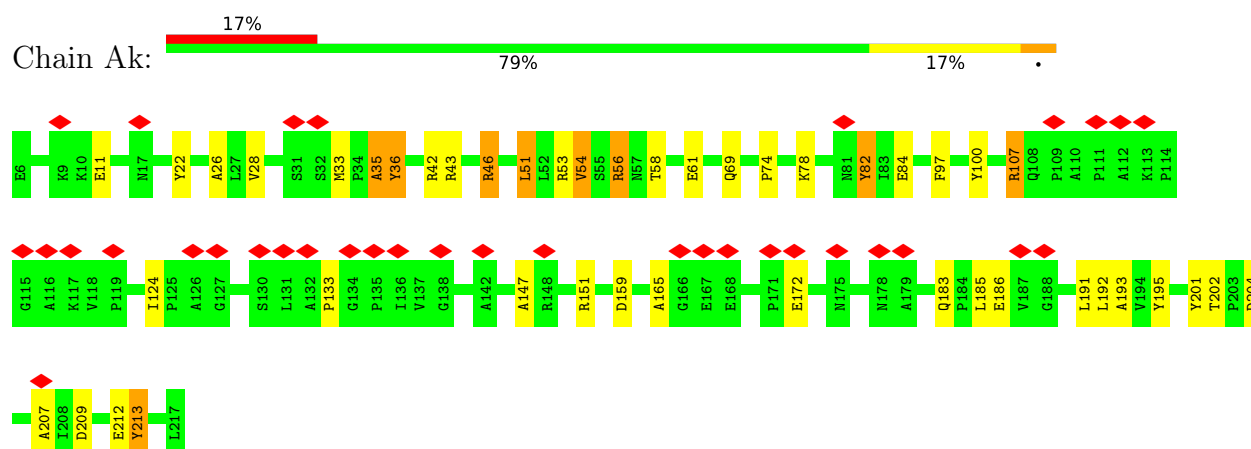
- Molecule 56: 50S ribosomal protein L14P



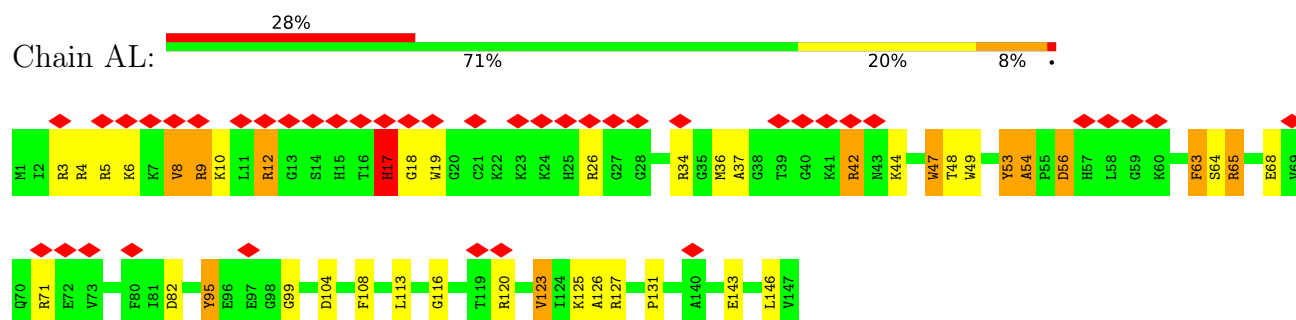
- Molecule 57: 50S ribosomal protein L44E



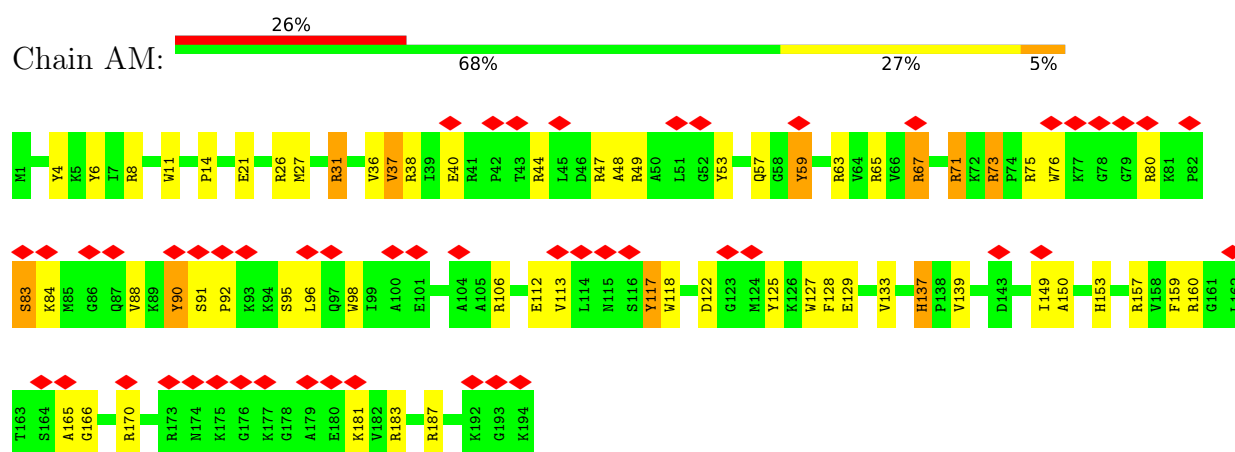
- Molecule 58: 50S ribosomal protein P0/L10E



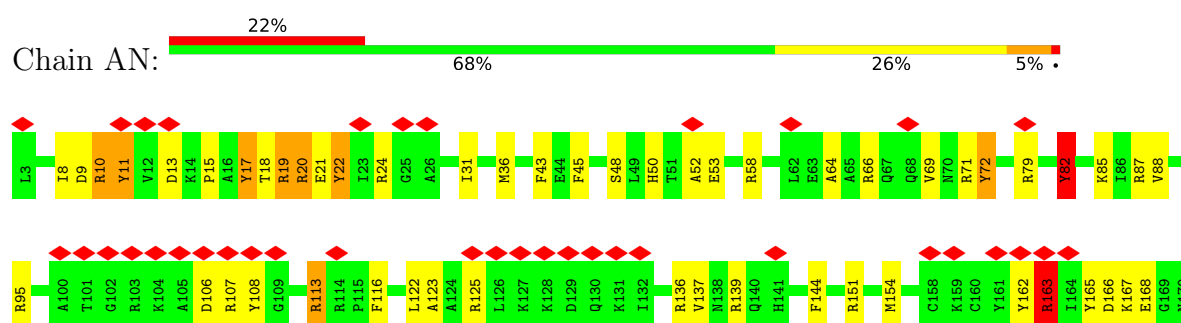
- Molecule 59: 50S ribosomal protein L15P



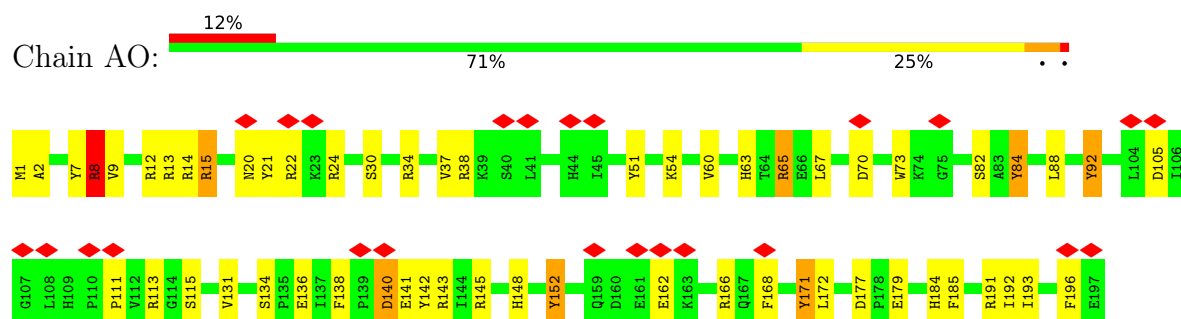
- Molecule 60: 50S ribosomal protein L15E



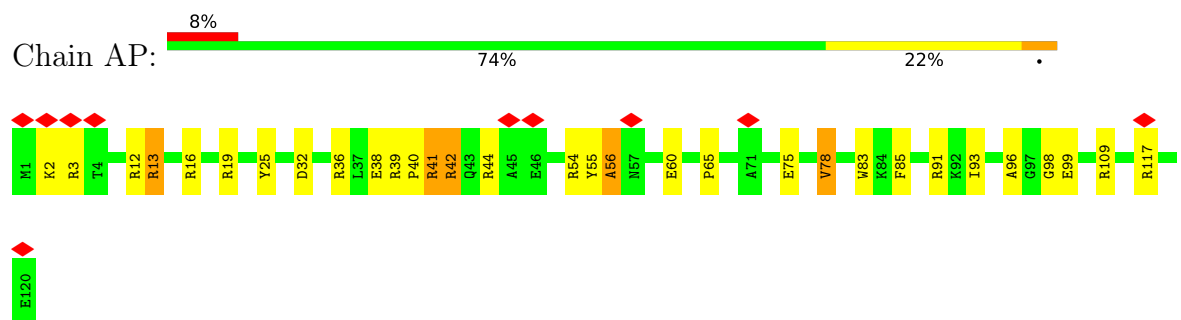
- Molecule 61: 50S ribosomal protein L10E/L16



- Molecule 62: 50S ribosomal protein L18P

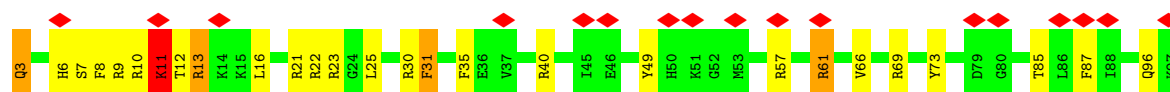


- Molecule 63: 50S ribosomal protein L18E

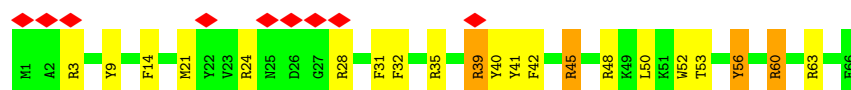
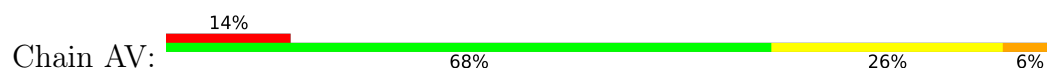


- Molecule 64: 50S ribosomal protein L21E

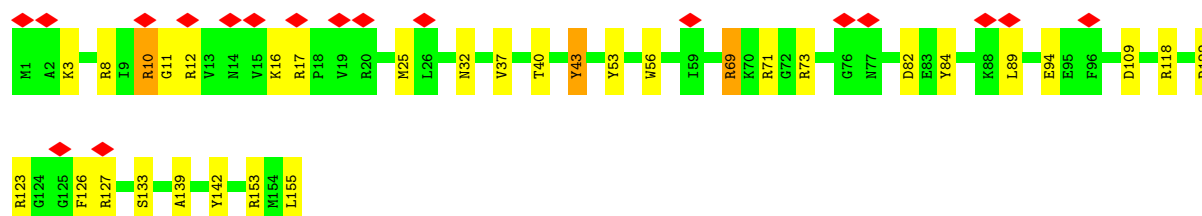
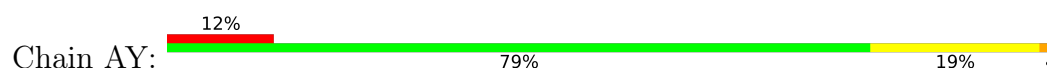




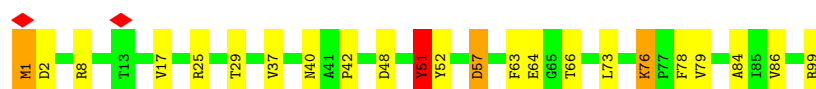
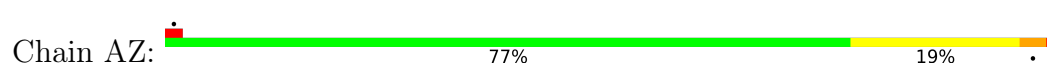
- Molecule 65: 50S ribosomal protein L24E



- Molecule 66: 50S ribosomal protein L30P



- Molecule 67: 50S ribosomal protein L30E



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	37000	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	per micrograph	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	20	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	51000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	3.556	Depositor
Minimum map value	-0.752	Depositor
Average map value	0.060	Depositor
Map value standard deviation	0.270	Depositor
Recommended contour level	0.93	Depositor
Map size ( $\text{\AA}$ )	444.99, 444.99, 442.26	wwPDB
Map dimensions	163, 163, 162	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	2.73, 2.73, 2.73	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	A7	1.64	2/534 (0.4%)	1.97	14/719 (1.9%)
2	A8	1.75	1/263 (0.4%)	1.81	4/354 (1.1%)
3	Af	1.83	4/453 (0.9%)	2.10	15/603 (2.5%)
4	AQ	1.80	16/1272 (1.3%)	2.05	35/1676 (2.1%)
5	AS	1.80	17/1226 (1.4%)	2.14	41/1649 (2.5%)
6	AT	1.69	6/689 (0.9%)	2.00	19/924 (2.1%)
7	AU	1.81	15/1024 (1.5%)	2.04	30/1365 (2.2%)
8	AW	1.76	5/547 (0.9%)	1.95	12/725 (1.7%)
9	AX	1.71	31/3383 (0.9%)	1.98	79/4593 (1.7%)
10	B1	3.41	257/1840 (14.0%)	3.87	460/2869 (16.0%)
11	B2	3.43	4996/35963 (13.9%)	3.79	8330/56134 (14.8%)
12	AG	1.71	4/951 (0.4%)	1.82	14/1281 (1.1%)
12	B3	1.62	3/951 (0.3%)	1.78	13/1281 (1.0%)
13	BA	1.74	21/1585 (1.3%)	2.02	45/2124 (2.1%)
14	BB	1.72	15/1654 (0.9%)	1.96	43/2233 (1.9%)
15	BC	1.82	18/1481 (1.2%)	2.03	41/1985 (2.1%)
16	BD	1.77	14/1457 (1.0%)	2.13	51/1953 (2.6%)
17	BE	1.76	25/2025 (1.2%)	2.01	58/2732 (2.1%)
18	BF	1.81	29/1746 (1.7%)	2.04	51/2350 (2.2%)
19	BG	1.72	9/999 (0.9%)	1.94	22/1337 (1.6%)
20	BH	1.79	22/1773 (1.2%)	2.00	62/2381 (2.6%)
21	BI	1.77	13/1049 (1.2%)	2.04	27/1408 (1.9%)
22	BJ	1.83	14/1013 (1.4%)	2.02	22/1349 (1.6%)
23	BK	1.76	10/1088 (0.9%)	1.96	31/1455 (2.1%)
24	BL	1.76	10/830 (1.2%)	2.00	26/1113 (2.3%)
25	BM	1.83	16/1022 (1.6%)	1.90	24/1375 (1.7%)
26	BN	1.74	8/1157 (0.7%)	2.06	37/1536 (2.4%)
27	BO	1.78	13/1208 (1.1%)	2.02	32/1619 (2.0%)
28	BP	1.94	12/471 (2.5%)	2.31	20/620 (3.2%)
29	BQ	1.75	14/1338 (1.0%)	1.95	34/1797 (1.9%)
30	BR	1.75	12/956 (1.3%)	2.06	24/1287 (1.9%)
31	BS	1.70	4/562 (0.7%)	1.95	10/744 (1.3%)
32	BT	1.78	11/943 (1.2%)	2.23	35/1257 (2.8%)
33	BU	1.80	13/1204 (1.1%)	2.01	30/1621 (1.9%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
34	BV	1.80	13/839 (1.5%)	2.13	29/1122 (2.6%)
35	BW	1.68	2/485 (0.4%)	1.93	11/651 (1.7%)
36	BX	1.84	7/570 (1.2%)	1.93	9/760 (1.2%)
37	BY	1.66	4/421 (1.0%)	2.22	16/558 (2.9%)
38	A1	3.42	9848/71524 (13.8%)	3.76	16432/111652 (14.7%)
39	A3	3.37	408/3007 (13.6%)	3.87	667/4689 (14.2%)
40	A5	1.85	11/618 (1.8%)	1.97	14/829 (1.7%)
40	AK	1.64	4/618 (0.6%)	1.97	16/829 (1.9%)
41	AA	1.71	17/1702 (1.0%)	2.12	52/2293 (2.3%)
42	Aa	1.72	11/690 (1.6%)	2.12	23/926 (2.5%)
43	AB	1.80	20/1883 (1.1%)	1.99	66/2540 (2.6%)
44	Ab	1.81	13/1100 (1.2%)	1.99	30/1466 (2.0%)
45	AC	1.73	29/2774 (1.0%)	1.98	77/3727 (2.1%)
46	AD	1.74	29/2068 (1.4%)	2.04	58/2787 (2.1%)
47	Ad	1.84	13/758 (1.7%)	2.12	28/1007 (2.8%)
48	AE	1.75	14/1513 (0.9%)	1.98	30/2026 (1.5%)
49	Ae	1.87	6/517 (1.2%)	2.04	15/681 (2.2%)
50	AF	1.71	18/1507 (1.2%)	1.89	24/2033 (1.2%)
51	Ag	1.89	5/381 (1.3%)	2.19	15/504 (3.0%)
52	AH	1.59	2/1002 (0.2%)	1.82	15/1351 (1.1%)
53	Ah	1.81	3/233 (1.3%)	2.32	10/301 (3.3%)
54	AI	1.81	11/1168 (0.9%)	1.94	31/1561 (2.0%)
55	Ai	1.86	10/599 (1.7%)	1.97	14/798 (1.8%)
56	AJ	1.86	13/1027 (1.3%)	1.92	17/1385 (1.2%)
57	Aj	1.85	12/806 (1.5%)	2.18	30/1065 (2.8%)
58	Ak	1.74	16/1660 (1.0%)	1.92	34/2253 (1.5%)
59	AL	1.82	14/1175 (1.2%)	2.03	34/1563 (2.2%)
60	AM	1.85	27/1634 (1.7%)	2.11	53/2179 (2.4%)
61	AN	1.85	24/1410 (1.7%)	2.05	43/1890 (2.3%)
62	AO	1.73	17/1636 (1.0%)	2.11	47/2196 (2.1%)
63	AP	1.82	12/980 (1.2%)	2.03	26/1313 (2.0%)
64	AR	1.74	10/808 (1.2%)	1.97	23/1080 (2.1%)
65	AV	1.91	9/570 (1.6%)	2.18	23/758 (3.0%)
66	AY	1.69	8/1262 (0.6%)	1.98	33/1687 (2.0%)
67	AZ	1.68	2/764 (0.3%)	1.94	21/1028 (2.0%)
All	All	2.89	16322/184366 (8.9%)	3.26	27857/271937 (10.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	A8	0	1
3	Af	0	6
4	AQ	0	5
5	AS	0	5
6	AT	0	2
7	AU	0	4
9	AX	0	9
10	B1	0	35
11	B2	0	725
12	AG	0	2
13	BA	0	11
14	BB	0	2
15	BC	0	8
16	BD	0	7
17	BE	0	9
18	BF	0	3
19	BG	1	4
20	BH	4	13
21	BI	0	3
22	BJ	0	6
23	BK	0	7
24	BL	0	8
25	BM	0	2
26	BN	0	4
27	BO	0	5
28	BP	0	1
29	BQ	0	7
30	BR	0	3
31	BS	0	2
32	BT	0	5
33	BU	0	4
34	BV	0	12
35	BW	0	1
36	BX	0	3
37	BY	0	3
38	A1	2	1412
39	A3	0	55
40	A5	0	2
40	AK	0	2
41	AA	0	4
42	Aa	0	2
43	AB	0	8
44	Ab	0	9

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Mol	Chain	#Chirality outliers	#Planarity outliers
45	AC	0	7
46	AD	0	9
47	Ad	0	1
48	AE	0	6
49	Ae	1	9
50	AF	0	3
51	Ag	1	5
52	AH	1	2
53	Ah	0	2
54	AI	0	7
55	Ai	0	2
56	AJ	0	4
57	Aj	0	7
58	Ak	0	4
59	AL	2	10
60	AM	0	4
61	AN	0	7
62	AO	0	10
63	AP	0	4
64	AR	0	1
65	AV	0	5
66	AY	0	2
67	AZ	0	1
All	All	12	2533

The worst 5 of 16322 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	B2	770	A	N7-C5	-18.72	1.28	1.39
11	B2	470	G	N9-C8	18.32	1.50	1.37
38	A1	2257	A	N7-C5	-18.29	1.28	1.39
38	A1	910	G	N7-C5	-17.89	1.28	1.39
38	A1	2164	G	N7-C5	-17.73	1.28	1.39

The worst 5 of 27857 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	B2	1445	A	N1-C6-N6	27.58	135.15	118.60
38	A1	277	A	N1-C6-N6	27.04	134.82	118.60
38	A1	2347	G	N1-C6-O6	26.94	136.06	119.90
38	A1	1281	A	N1-C6-N6	26.62	134.57	118.60
38	A1	2540	A	N1-C6-N6	26.19	134.31	118.60



5 of 12 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
19	BG	53	LYS	CA
20	BH	85	PHE	CA
20	BH	86	MET	CA
20	BH	87	ARG	CA
20	BH	96	LYS	CA

5 of 2533 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A8	49	TYR	Sidechain
3	Af	2	ALA	Peptide
3	Af	33	ARG	Peptide
3	Af	34	ARG	Sidechain
3	Af	37	THR	Peptide

## 5.2 Too-close contacts [i](#)

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

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A7	63/67 (94%)	43 (68%)	16 (25%)	4 (6%)	1	17
2	A8	30/52 (58%)	22 (73%)	7 (23%)	1 (3%)	4	26
3	Af	49/51 (96%)	40 (82%)	6 (12%)	3 (6%)	1	17
4	AQ	148/150 (99%)	139 (94%)	5 (3%)	4 (3%)	5	31
5	AS	148/150 (99%)	135 (91%)	10 (7%)	3 (2%)	7	38
6	AT	82/84 (98%)	75 (92%)	4 (5%)	3 (4%)	3	24
7	AU	119/121 (98%)	113 (95%)	5 (4%)	1 (1%)	19	60

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	AW	64/72 (89%)	64 (100%)	0	0	100	100
9	AX	430/436 (99%)	322 (75%)	77 (18%)	31 (7%)	1	14
12	AG	121/123 (98%)	114 (94%)	4 (3%)	3 (2%)	5	32
12	B3	121/123 (98%)	100 (83%)	14 (12%)	7 (6%)	1	18
13	BA	188/190 (99%)	164 (87%)	12 (6%)	12 (6%)	1	16
14	BB	200/202 (99%)	182 (91%)	12 (6%)	6 (3%)	4	28
15	BC	184/186 (99%)	171 (93%)	9 (5%)	4 (2%)	6	35
16	BD	170/172 (99%)	148 (87%)	20 (12%)	2 (1%)	13	50
17	BE	239/241 (99%)	207 (87%)	20 (8%)	12 (5%)	2	20
18	BF	215/217 (99%)	188 (87%)	16 (7%)	11 (5%)	2	19
19	BG	123/125 (98%)	103 (84%)	13 (11%)	7 (6%)	1	18
20	BH	213/215 (99%)	186 (87%)	14 (7%)	13 (6%)	1	17
21	BI	127/129 (98%)	118 (93%)	8 (6%)	1 (1%)	19	60
22	BJ	125/127 (98%)	107 (86%)	15 (12%)	3 (2%)	6	33
23	BK	133/135 (98%)	116 (87%)	10 (8%)	7 (5%)	2	19
24	BL	100/102 (98%)	90 (90%)	7 (7%)	3 (3%)	4	28
25	BM	131/133 (98%)	112 (86%)	9 (7%)	10 (8%)	1	13
26	BN	143/145 (99%)	128 (90%)	7 (5%)	8 (6%)	2	19
27	BO	146/148 (99%)	122 (84%)	16 (11%)	8 (6%)	2	19
28	BP	54/56 (96%)	44 (82%)	8 (15%)	2 (4%)	3	24
29	BQ	156/158 (99%)	137 (88%)	9 (6%)	10 (6%)	1	16
30	BR	111/113 (98%)	105 (95%)	5 (4%)	1 (1%)	17	57
31	BS	65/67 (97%)	60 (92%)	5 (8%)	0	100	100
32	BT	109/111 (98%)	102 (94%)	5 (5%)	2 (2%)	8	40
33	BU	142/144 (99%)	123 (87%)	11 (8%)	8 (6%)	2	19
34	BV	97/99 (98%)	88 (91%)	5 (5%)	4 (4%)	3	23
35	BW	61/63 (97%)	52 (85%)	6 (10%)	3 (5%)	2	20
36	BX	69/71 (97%)	62 (90%)	6 (9%)	1 (1%)	11	46
37	BY	48/50 (96%)	41 (85%)	5 (10%)	2 (4%)	3	22
40	A5	79/81 (98%)	67 (85%)	9 (11%)	3 (4%)	3	24
40	AK	79/81 (98%)	70 (89%)	4 (5%)	5 (6%)	1	17

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	AA	214/216 (99%)	186 (87%)	19 (9%)	9 (4%)	3	22
42	Aa	78/92 (85%)	69 (88%)	9 (12%)	0	100	100
43	AB	237/239 (99%)	209 (88%)	23 (10%)	5 (2%)	7	36
44	Ab	125/127 (98%)	108 (86%)	11 (9%)	6 (5%)	2	21
45	AC	338/365 (93%)	303 (90%)	21 (6%)	14 (4%)	3	23
46	AD	253/255 (99%)	220 (87%)	23 (9%)	10 (4%)	3	23
47	Ad	87/89 (98%)	78 (90%)	6 (7%)	3 (3%)	3	26
48	AE	184/186 (99%)	161 (88%)	15 (8%)	8 (4%)	2	22
49	Ae	60/62 (97%)	43 (72%)	13 (22%)	4 (7%)	1	15
50	AF	182/184 (99%)	165 (91%)	14 (8%)	3 (2%)	9	44
51	Ag	43/45 (96%)	30 (70%)	8 (19%)	5 (12%)	0	6
52	AH	132/134 (98%)	114 (86%)	11 (8%)	7 (5%)	2	19
53	Ah	22/24 (92%)	21 (96%)	1 (4%)	0	100	100
54	AI	140/142 (99%)	121 (86%)	13 (9%)	6 (4%)	2	22
55	Ai	76/78 (97%)	69 (91%)	4 (5%)	3 (4%)	3	23
56	AJ	130/132 (98%)	121 (93%)	6 (5%)	3 (2%)	6	34
57	Aj	92/94 (98%)	69 (75%)	18 (20%)	5 (5%)	2	19
58	Ak	210/212 (99%)	192 (91%)	11 (5%)	7 (3%)	4	26
59	AL	145/147 (99%)	129 (89%)	11 (8%)	5 (3%)	3	26
60	AM	192/194 (99%)	175 (91%)	11 (6%)	6 (3%)	4	27
61	AN	166/168 (99%)	141 (85%)	19 (11%)	6 (4%)	3	25
62	AO	195/197 (99%)	166 (85%)	20 (10%)	9 (5%)	2	21
63	AP	118/120 (98%)	107 (91%)	5 (4%)	6 (5%)	2	19
64	AR	93/95 (98%)	85 (91%)	3 (3%)	5 (5%)	2	19
65	AV	64/66 (97%)	61 (95%)	3 (5%)	0	100	100
66	AY	153/155 (99%)	137 (90%)	12 (8%)	4 (3%)	5	31
67	AZ	97/99 (98%)	84 (87%)	9 (9%)	4 (4%)	3	23
All	All	8708/8907 (98%)	7624 (88%)	733 (8%)	351 (4%)	5	23

5 of 351 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A7	30	LYS

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Mol	Chain	Res	Type
4	AQ	134	ASN
9	AX	239	ARG
9	AX	277	TYR
9	AX	346	ALA

### 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	A7	57/59 (97%)	55 (96%)	2 (4%)	36	59
2	A8	28/44 (64%)	28 (100%)	0	100	100
3	Af	47/47 (100%)	46 (98%)	1 (2%)	53	72
4	AQ	130/130 (100%)	125 (96%)	5 (4%)	33	57
5	AS	126/126 (100%)	119 (94%)	7 (6%)	21	46
6	AT	75/75 (100%)	73 (97%)	2 (3%)	44	65
7	AU	110/110 (100%)	105 (96%)	5 (4%)	27	52
8	AW	61/66 (92%)	60 (98%)	1 (2%)	62	79
9	AX	351/355 (99%)	341 (97%)	10 (3%)	43	65
12	AG	99/99 (100%)	95 (96%)	4 (4%)	31	55
12	B3	99/99 (100%)	94 (95%)	5 (5%)	24	48
13	BA	166/166 (100%)	152 (92%)	14 (8%)	11	33
14	BB	173/173 (100%)	168 (97%)	5 (3%)	42	64
15	BC	145/145 (100%)	141 (97%)	4 (3%)	43	65
16	BD	153/153 (100%)	148 (97%)	5 (3%)	38	61
17	BE	212/212 (100%)	201 (95%)	11 (5%)	23	48
18	BF	181/181 (100%)	173 (96%)	8 (4%)	28	53
19	BG	108/108 (100%)	108 (100%)	0	100	100
20	BH	184/184 (100%)	165 (90%)	19 (10%)	7	25
21	BI	107/107 (100%)	105 (98%)	2 (2%)	57	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	BJ	103/103 (100%)	95 (92%)	8 (8%)	12	36
23	BK	111/111 (100%)	108 (97%)	3 (3%)	44	65
24	BL	91/91 (100%)	87 (96%)	4 (4%)	28	53
25	BM	100/100 (100%)	96 (96%)	4 (4%)	31	55
26	BN	119/119 (100%)	114 (96%)	5 (4%)	30	54
27	BO	122/122 (100%)	120 (98%)	2 (2%)	62	79
28	BP	46/46 (100%)	43 (94%)	3 (6%)	17	42
29	BQ	143/143 (100%)	135 (94%)	8 (6%)	21	46
30	BR	102/102 (100%)	92 (90%)	10 (10%)	8	26
31	BS	61/61 (100%)	58 (95%)	3 (5%)	25	50
32	BT	99/99 (100%)	95 (96%)	4 (4%)	31	55
33	BU	121/121 (100%)	118 (98%)	3 (2%)	47	68
34	BV	89/89 (100%)	87 (98%)	2 (2%)	52	71
35	BW	54/54 (100%)	51 (94%)	3 (6%)	21	46
36	BX	60/60 (100%)	53 (88%)	7 (12%)	5	21
37	BY	41/41 (100%)	40 (98%)	1 (2%)	49	69
40	A5	64/64 (100%)	62 (97%)	2 (3%)	40	62
40	AK	64/64 (100%)	59 (92%)	5 (8%)	12	36
41	AA	182/182 (100%)	173 (95%)	9 (5%)	25	50
42	Aa	73/81 (90%)	68 (93%)	5 (7%)	16	41
43	AB	189/189 (100%)	183 (97%)	6 (3%)	39	61
44	Ab	114/114 (100%)	108 (95%)	6 (5%)	22	47
45	AC	291/312 (93%)	278 (96%)	13 (4%)	27	52
46	AD	213/213 (100%)	207 (97%)	6 (3%)	43	65
47	Ad	81/81 (100%)	81 (100%)	0	100	100
48	AE	158/158 (100%)	153 (97%)	5 (3%)	39	61
49	Ae	51/51 (100%)	49 (96%)	2 (4%)	32	56
50	AF	156/156 (100%)	150 (96%)	6 (4%)	33	57
51	Ag	37/37 (100%)	36 (97%)	1 (3%)	44	65
52	AH	110/110 (100%)	108 (98%)	2 (2%)	59	77
53	Ah	23/23 (100%)	23 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
54	AI	122/122 (100%)	118 (97%)	4 (3%)	38	61
55	Ai	57/57 (100%)	55 (96%)	2 (4%)	36	59
56	AJ	104/104 (100%)	98 (94%)	6 (6%)	20	45
57	Aj	83/83 (100%)	80 (96%)	3 (4%)	35	59
58	Ak	179/179 (100%)	173 (97%)	6 (3%)	37	60
59	AL	117/117 (100%)	112 (96%)	5 (4%)	29	53
60	AM	162/162 (100%)	155 (96%)	7 (4%)	29	53
61	AN	140/140 (100%)	134 (96%)	6 (4%)	29	53
62	AO	166/166 (100%)	159 (96%)	7 (4%)	30	54
63	AP	101/101 (100%)	99 (98%)	2 (2%)	55	74
64	AR	85/85 (100%)	79 (93%)	6 (7%)	14	39
65	AV	56/56 (100%)	56 (100%)	0	100	100
66	AY	133/133 (100%)	130 (98%)	3 (2%)	50	70
67	AZ	80/80 (100%)	73 (91%)	7 (9%)	10	31
All	All	7465/7521 (99%)	7153 (96%)	312 (4%)	33	54

5 of 312 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
50	AF	7	ILE
61	AN	137	VAL
12	AG	93	GLU
40	AK	24	VAL
64	AR	66	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 66 such sidechains are listed below:

Mol	Chain	Res	Type
62	AO	43	HIS
62	AO	76	HIS
66	AY	120	HIS
25	BM	29	HIS
24	BL	69	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	B1	76/77 (98%)	20 (26%)	4 (5%)
11	B2	1494/1495 (99%)	264 (17%)	103 (6%)
38	A1	2964/3049 (97%)	600 (20%)	158 (5%)
39	A3	125/126 (99%)	36 (28%)	11 (8%)
All	All	4659/4747 (98%)	920 (19%)	276 (5%)

5 of 920 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
10	B1	8	U
10	B1	9	A
10	B1	10	G
10	B1	18	U
10	B1	19	G

5 of 276 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
38	A1	2324	C
38	A1	2401	A
38	A1	2957	G
11	B2	1399	G
11	B2	1322	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 monosaccharides 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 ⓘ

There are no chain breaks in this entry.



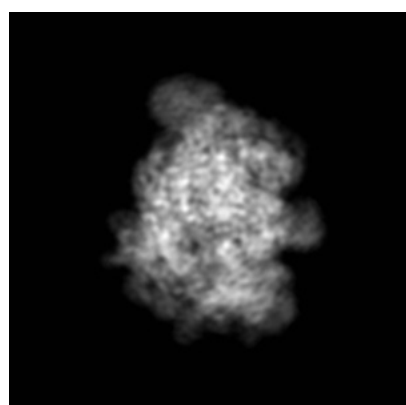
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5691. These allow visual inspection of the internal detail of the map and identification of artifacts.

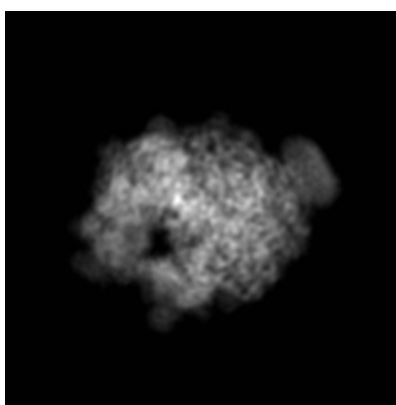
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

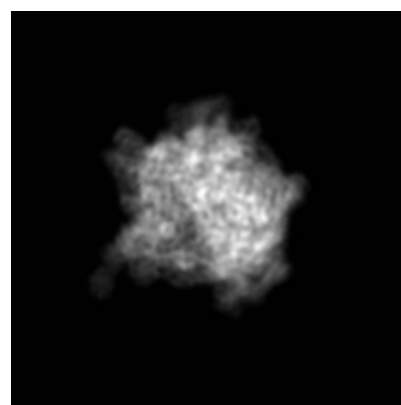
#### 6.1.1 Primary map



X



Y

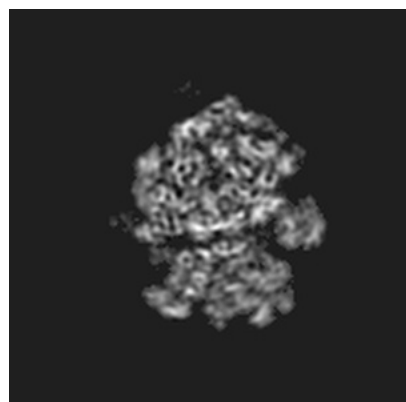


Z

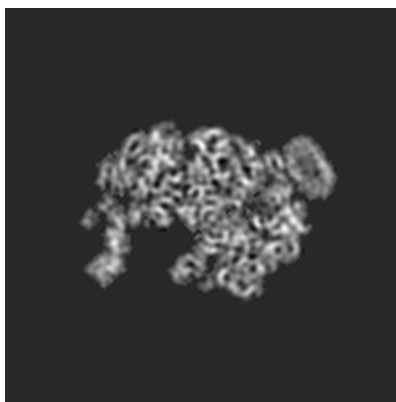
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

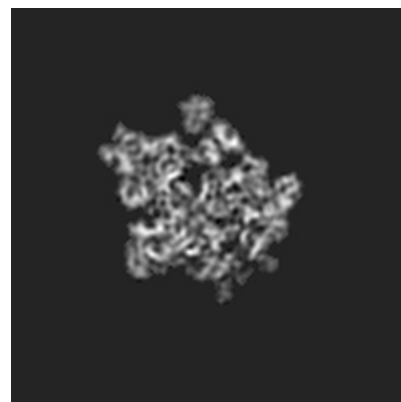
#### 6.2.1 Primary map



X Index: 81



Y Index: 81

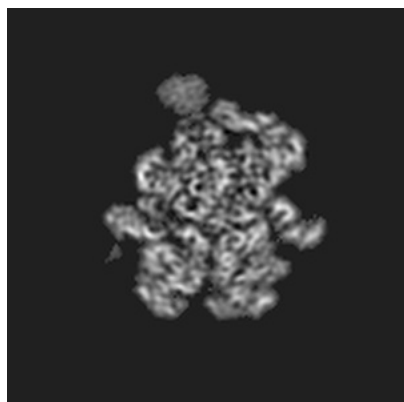


Z Index: 81

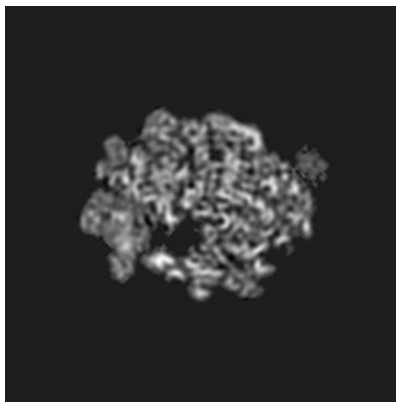
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

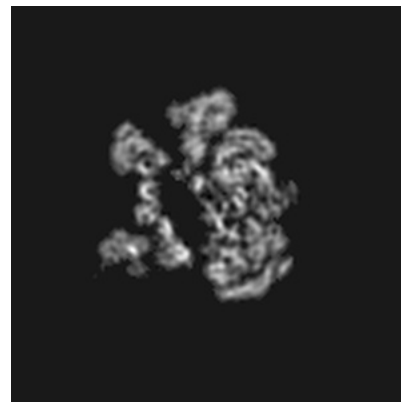
### 6.3.1 Primary map



X Index: 85



Y Index: 87



Z Index: 70

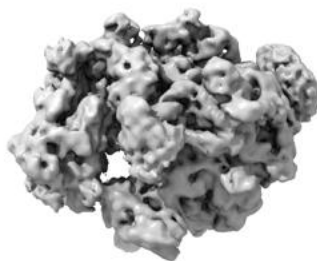
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal surface views [i](#)

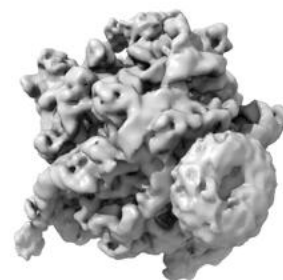
### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.93. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

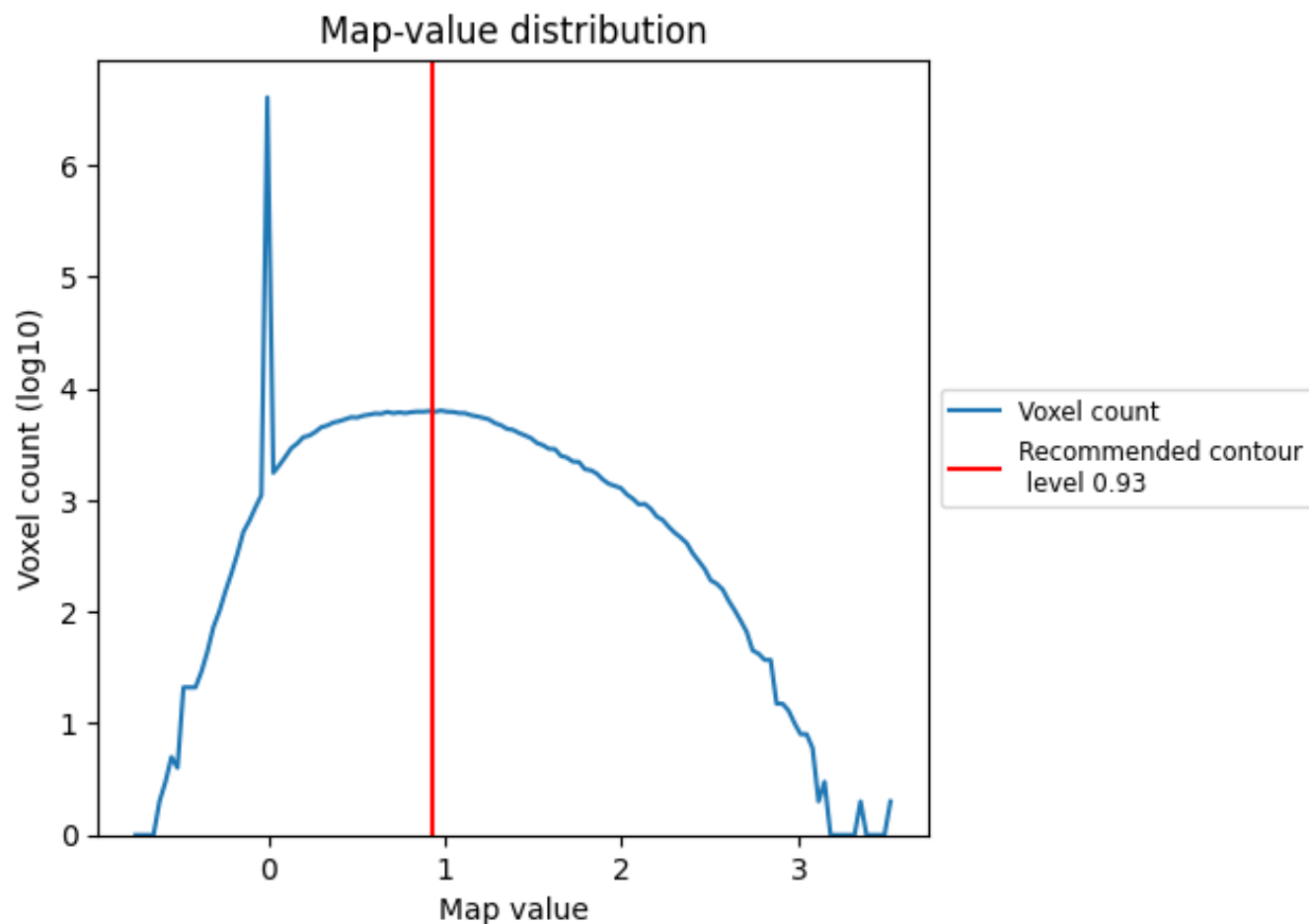
## 6.5 Mask visualisation

This section was not generated.

## 7 Map analysis [i](#)

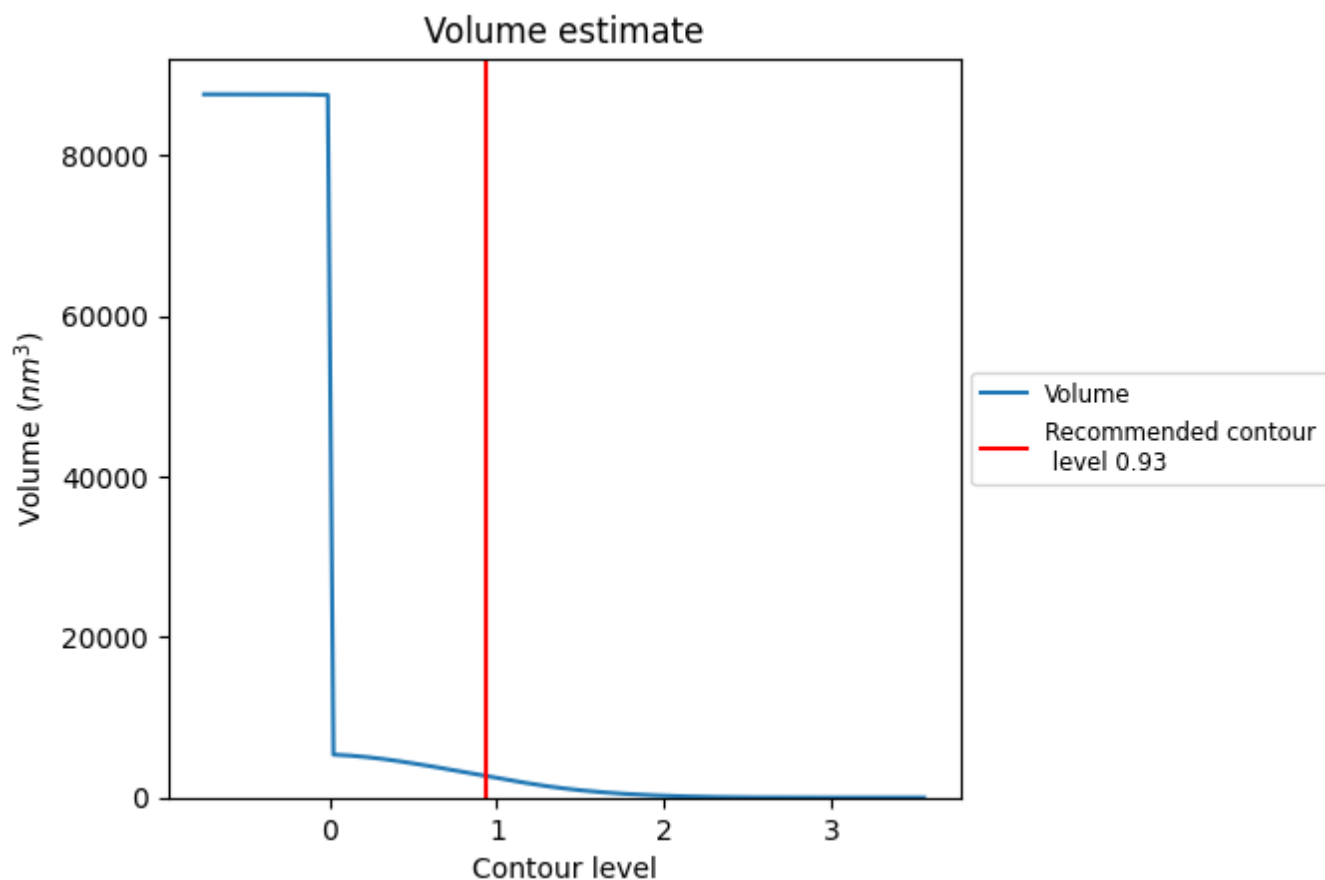
This section contains the results of statistical analysis of the map.

### 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 2715 nm<sup>3</sup>; this corresponds to an approximate mass of 2453 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 [i](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

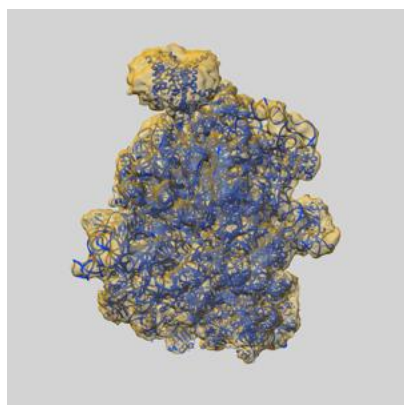
## 8 Fourier-Shell correlation

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

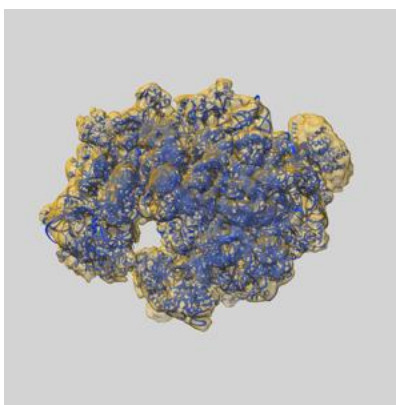
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-5691 and PDB model 4V4N. Per-residue inclusion information can be found in section [3](#) on page [16](#).

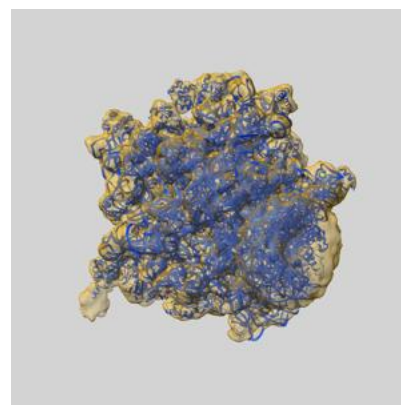
### 9.1 Map-model overlay [i](#)



X



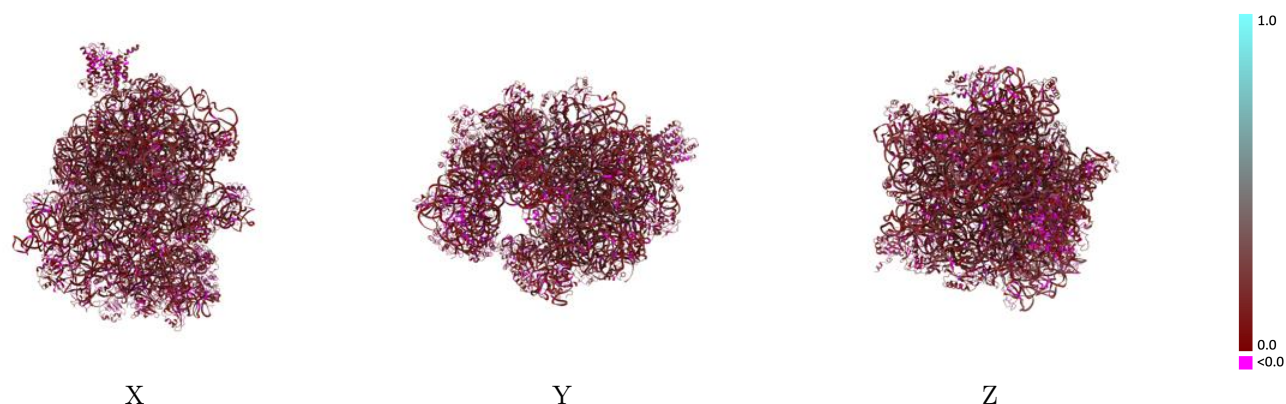
Y



Z

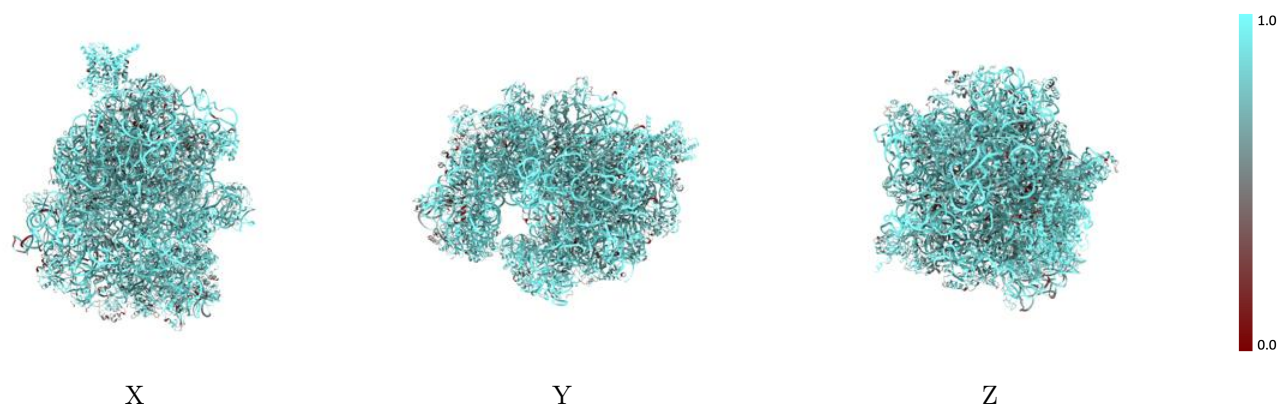
The images above show the 3D surface view of the map at the recommended contour level 0.93 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 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.

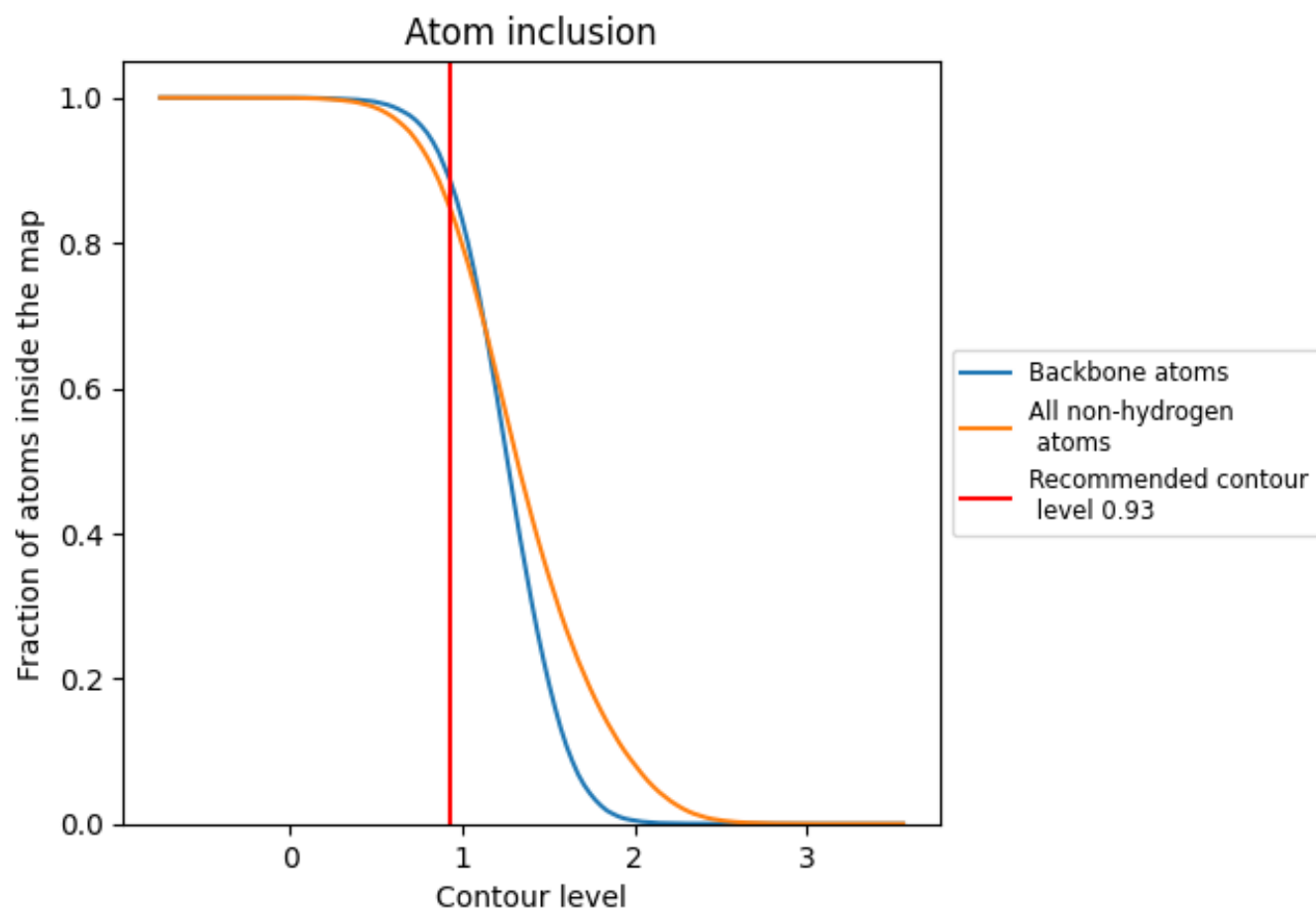
## 9.3 Atom inclusion mapped to coordinate model [i](#)



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 (0.93).









































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 85% 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 (0.93) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8468	 0.1240
A1	 0.9299	 0.1530
A3	 0.8967	 0.1350
A5	 0.7408	 0.1180
A7	 0.8859	 0.1390
A8	 0.9091	 0.0680
AA	 0.7119	 0.0850
AB	 0.6592	 0.0870
AC	 0.6824	 0.0840
AD	 0.6512	 0.0890
AE	 0.8355	 0.1010
AF	 0.7697	 0.1100
AG	 0.8006	 0.1310
AH	 0.8716	 0.0650
AI	 0.6352	 0.1030
AJ	 0.6965	 0.0860
AK	 0.6622	 0.1130
AL	 0.6146	 0.0750
AM	 0.6089	 0.0770
AN	 0.6760	 0.0960
AO	 0.7421	 0.1000
AP	 0.7634	 0.1130
AQ	 0.6741	 0.0980
AR	 0.6636	 0.0850
AS	 0.7079	 0.0980
AT	 0.6842	 0.1060
AU	 0.7181	 0.1020
AV	 0.7434	 0.0970
AW	 0.7586	 0.1270
AX	 0.8679	 0.1020
AY	 0.6907	 0.1130
AZ	 0.8212	 0.1280
Aa	 0.6626	 0.0790
Ab	 0.6234	 0.0900
Ad	 0.6936	 0.0790



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Chain	Atom inclusion	Q-score
Ae	 0.6112	 0.0430
Af	 0.2891	 0.0250
Ag	 0.4056	 0.0270
Ah	 0.5421	 0.0520
Ai	 0.6861	 0.1150
Aj	 0.7907	 0.0890
Ak	 0.7713	 0.1020
B1	 0.8524	 0.1170
B2	 0.9348	 0.1380
B3	 0.5797	 0.0800
BA	 0.8750	 0.1130
BB	 0.7500	 0.1120
BC	 0.7362	 0.1080
BD	 0.7167	 0.0920
BE	 0.6981	 0.0590
BF	 0.7389	 0.1020
BG	 0.7996	 0.0880
BH	 0.7543	 0.0780
BI	 0.7268	 0.0990
BJ	 0.7285	 0.0740
BK	 0.6322	 0.0360
BL	 0.7112	 0.0710
BM	 0.7706	 0.0910
BN	 0.6859	 0.0930
BO	 0.8357	 0.0850
BP	 0.7528	 0.0550
BQ	 0.7480	 0.0960
BR	 0.7179	 0.0820
BS	 0.5904	 0.0680
BT	 0.8168	 0.0770
BU	 0.7540	 0.0640
BV	 0.7531	 0.0910
BW	 0.7170	 0.0850
BX	 0.8835	 0.0910
BY	 0.7990	 0.0630