



wwPDB EM Validation Summary Report ⓘ

Nov 9, 2024 – 02:59 pm GMT

PDB ID : 4V5M
EMDB ID : EMD-1798
Title : tRNA tranlocation on the 70S ribosome: the pre-translocational translocation intermediate TI(PRE)
Authors : Ratje, A.H.; Loerke, J.; Mikolajka, A.; Bruenner, M.; Hildebrand, P.W.; Starosta, A.L.; Doenhoefer, A.; Connell, S.R.; Fucini, P.; Mielke, T.; Whitford, P.C.; Onuchic, J.N.; Yu, Y.; Sanbonmatsu, K.Y.; Hartmann, R.K.; Penczek, P.A.; Wilson, D.N.; Spahn, C.M.T.
Deposited on : 2010-10-01
Resolution : 7.80 Å(reported)
Based on initial models : 2WRJ, 2WRI

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

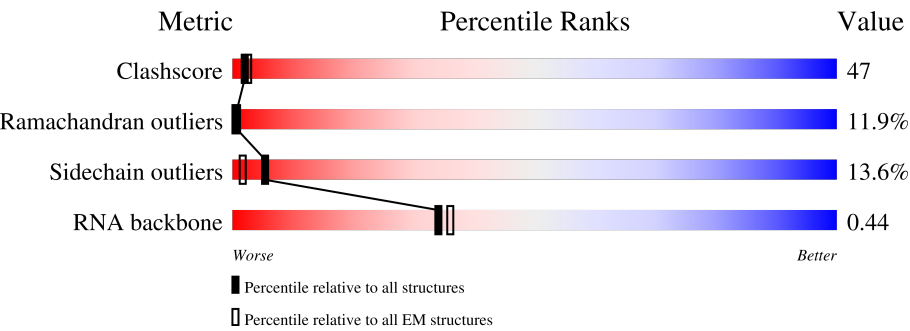
EMDB validation analysis : 0.0.1.dev113
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

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 7.80 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

Mol	Chain	Length	Quality of chain
1	AA	1522	<div><div></div><div>24%57%17%</div></div>
2	AB	256	<div><div>37%</div><div>23%48%16%9%</div></div>
3	AC	239	<div><div>26%</div><div>22%46%14%14%</div></div>
4	AD	209	<div><div>26%</div><div>29%49%17%</div></div>
5	AE	162	<div><div>21%</div><div>27%52%13%7%</div></div>

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Mol	Chain	Length	Quality of chain
6	AF	101	
7	AG	156	
8	AH	138	
9	AI	128	
10	AJ	105	
11	AK	129	
12	AL	132	
13	AM	126	
14	AN	61	
15	AO	89	
16	AP	88	
17	AQ	105	
18	AR	88	
19	AS	93	
20	AT	106	
21	AU	27	
22	AV	77	
23	AX	11	
24	AY	691	
25	B0	85	
26	B1	98	
27	B2	72	
28	B3	60	
29	B4	71	
30	B5	60	

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Mol	Chain	Length	Quality of chain
31	B6	54	
32	B7	49	
33	B8	65	
34	B9	37	
35	BA	2915	
36	BB	122	
37	BC	229	
38	BD	276	
39	BE	206	
40	BF	210	
41	BG	182	
42	BH	180	
43	BK	147	
44	BL	121	
45	BN	140	
46	BO	122	
47	BP	150	
48	BQ	141	
49	BR	118	
50	BS	112	
51	BT	146	
52	BU	118	
53	BV	101	
54	BW	113	
55	BX	96	

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Mol	Chain	Length	Quality of chain
56	BY	110	<div><div></div><div>32%</div><div>9%</div><div>57%</div><div>24%</div><div>6%</div><div></div></div>
57	BZ	206	<div><div></div><div>42%</div><div>17%</div><div>45%</div><div>22%</div><div>5%</div><div>11%</div></div>

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 152777 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 16S RRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	1504	Total	C	N	O	P	0	0
			32329	14390	5992	10444	1503		

- Molecule 2 is a protein called 30S RIBOSOMAL PROTEIN S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	234	Total	C	N	O	S	0	0
			1900	1213	341	341	5		

- Molecule 3 is a protein called 30S RIBOSOMAL PROTEIN S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AC	206	Total	C	N	O	S	0	0
			1612	1016	314	281	1		

- Molecule 4 is a protein called 30S RIBOSOMAL PROTEIN S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AD	208	Total	C	N	O	S	0	0
			1703	1066	339	291	7		

- Molecule 5 is a protein called 30S RIBOSOMAL PROTEIN S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AE	150	Total	C	N	O	S	0	0
			1146	724	217	201	4		

- Molecule 6 is a protein called 30S RIBOSOMAL PROTEIN S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AF	101	Total	C	N	O	S	0	0
			843	531	155	154	3		

- Molecule 7 is a protein called 30S RIBOSOMAL PROTEIN S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AG	155	Total	C	N	O	S	0	0
			1257	781	252	218	6		

- Molecule 8 is a protein called 30S RIBOSOMAL PROTEIN S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AH	138	Total	C	N	O	S	0	0
			1116	705	215	193	3		

- Molecule 9 is a protein called 30S RIBOSOMAL PROTEIN S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AI	127	Total	C	N	O	S	0	0
			1010	639	197	174			

- Molecule 10 is a protein called 30S RIBOSOMAL PROTEIN S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AJ	98	Total	C	N	O	S	0	0
			794	499	156	138	1		

- Molecule 11 is a protein called 30S RIBOSOMAL PROTEIN S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AK	119	Total	C	N	O	S	0	0
			885	549	168	165	3		

- Molecule 12 is a protein called 30S RIBOSOMAL PROTEIN S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AL	124	Total	C	N	O	S	0	0
			970	611	195	163	1		

- Molecule 13 is a protein called 30S RIBOSOMAL PROTEIN S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AM	124	Total	C	N	O	S	0	0
			987	611	205	169	2		

- Molecule 14 is a protein called 30S RIBOSOMAL PROTEIN S14 TYPE Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AN	60	Total	C	N	O	S	0	0
			492	312	104	72	4		

- Molecule 15 is a protein called 30S RIBOSOMAL PROTEIN S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AO	88	Total	C	N	O	S	0	0
			734	459	147	126	2		

- Molecule 16 is a protein called 30S RIBOSOMAL PROTEIN S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AP	83	Total	C	N	O	S	0	0
			700	443	139	117	1		

- Molecule 17 is a protein called 30S RIBOSOMAL PROTEIN S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AQ	99	Total	C	N	O	S	0	0
			823	528	151	142	2		

- Molecule 18 is a protein called 30S RIBOSOMAL PROTEIN S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	AR	70	Total	C	N	O	0	0
			574	367	112	95		

- Molecule 19 is a protein called 30S RIBOSOMAL PROTEIN S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AS	78	Total	C	N	O	S	0	0
			629	403	114	110	2		

- Molecule 20 is a protein called 30S RIBOSOMAL PROTEIN S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AT	99	Total	C	N	O	S	0	0
			763	470	162	129	2		

- Molecule 21 is a protein called 30S RIBOSOMAL PROTEIN THX.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	AU	24	Total	C	N	O	0	0
			208	128	50	30		

- Molecule 22 is a RNA chain called TRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AV	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 23 is a RNA chain called MRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AX	11	Total	C	N	O	P	0	0
			230	105	41	74	10		

- Molecule 24 is a protein called ELONGATION FACTOR G.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AY	666	Total	C	N	O	S	0	0
			5214	3316	892	988	18		

- Molecule 25 is a protein called 50S RIBOSOMAL PROTEIN L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	B0	84	Total	C	N	O	S	0	0
			662	410	140	111	1		

- Molecule 26 is a protein called 50S RIBOSOMAL PROTEIN L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	B1	93	Total	C	N	O	S	0	0
			731	460	145	125	1		

- Molecule 27 is a protein called 50S RIBOSOMAL PROTEIN L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	B2	71	Total	C	N	O	S	0	0
			598	370	121	106	1		

- Molecule 28 is a protein called 50S RIBOSOMAL PROTEIN L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	B3	59	Total	C	N	O	S	0	0
			467	298	90	78	1		

- Molecule 29 is a protein called 50S RIBOSOMAL PROTEIN L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	B4	57	Total	C	N	O	S	0	0
			450	285	77	83	5		

- Molecule 30 is a protein called 50S RIBOSOMAL PROTEIN L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	B5	59	Total	C	N	O	S	0	0
			459	288	90	76	5		

- Molecule 31 is a protein called 50S RIBOSOMAL PROTEIN L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	B6	50	Total	C	N	O	S	0	0
			433	270	88	71	4		

- Molecule 32 is a protein called 50S RIBOSOMAL PROTEIN L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	B7	48	Total	C	N	O	S	0	0
			418	257	104	55	2		

- Molecule 33 is a protein called 50S RIBOSOMAL PROTEIN L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	B8	63	Total	C	N	O	S	0	0
			507	326	101	78	2		

- Molecule 34 is a protein called 50S RIBOSOMAL PROTEIN L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	B9	37	Total	C	N	O	S	0	0
			307	188	68	47	4		

- Molecule 35 is a RNA chain called 23S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BA	2901	Total	C	N	O	P	0	0
			62474	27806	11681	20087	2900		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BB	119	Total	C	N	O	P	0	0
			2551	1136	471	826	118		

- Molecule 37 is a protein called 50S RIBOSOMAL PROTEIN L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BC	228	Total	C	N	O	S	0	0
			1742	1101	319	319	3		

- Molecule 38 is a protein called 50S RIBOSOMAL PROTEIN L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BD	275	Total	C	N	O	S	0	0
			2145	1353	428	361	3		

- Molecule 39 is a protein called 50S RIBOSOMAL PROTEIN L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BE	204	Total	C	N	O	S	0	0
			1563	988	299	270	6		

- Molecule 40 is a protein called 50S RIBOSOMAL PROTEIN L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BF	207	Total	C	N	O	S	0	0
			1623	1035	303	282	3		

- Molecule 41 is a protein called 50S RIBOSOMAL PROTEIN L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BG	181	Total	C	N	O	S	0	0
			1474	942	268	260	4		

- Molecule 42 is a protein called 50S RIBOSOMAL PROTEIN L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BH	166	Total	C	N	O	S	0	0
			1268	803	237	227	1		

- Molecule 43 is a protein called 50S RIBOSOMAL PROTEIN L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BK	139	Total	C	N	O	S	0	0
			1025	653	181	186	5		

- Molecule 44 is a protein called 50S RIBOSOMAL PROTEIN L7/L12.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	BL	67	Total	C	N	O	0	0
			477	301	81	95		

- Molecule 45 is a protein called 50S RIBOSOMAL PROTEIN L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BN	138	Total	C	N	O	S	0	0
			1104	712	206	182	4		

- Molecule 46 is a protein called 50S RIBOSOMAL PROTEIN L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BO	122	Total	C	N	O	S	0	0
			933	588	171	170	4		

- Molecule 47 is a protein called 50S RIBOSOMAL PROTEIN L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BP	146	Total	C	N	O	S	0	0
			1114	692	227	193	2		

- Molecule 48 is a protein called 50S RIBOSOMAL PROTEIN L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BQ	141	Total	C	N	O	S	0	0
			1122	715	212	188	7		

- Molecule 49 is a protein called 50S RIBOSOMAL PROTEIN L17.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	BR	117	Total	C	N	O	0	0
			960	599	202	159		

- Molecule 50 is a protein called 50S RIBOSOMAL PROTEIN L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	BS	98	Total	C	N	O	0	0
			770	486	154	130		

- Molecule 51 is a protein called 50S RIBOSOMAL PROTEIN L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BT	137	Total	C	N	O	S	0	0
			1141	710	234	196	1		

- Molecule 52 is a protein called 50S RIBOSOMAL PROTEIN L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BU	117	Total	C	N	O	S	0	0
			958	604	202	151	1		

- Molecule 53 is a protein called 50S RIBOSOMAL PROTEIN L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BV	101	Total	C	N	O	S	0	0
			779	501	142	135	1		

- Molecule 54 is a protein called 50S RIBOSOMAL PROTEIN L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BW	113	Total	C	N	O	S	0	0
			896	563	176	155	2		

- Molecule 55 is a protein called 50S RIBOSOMAL PROTEIN L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	BX	92	Total	C	N	O	0	0
			725	471	131	123		

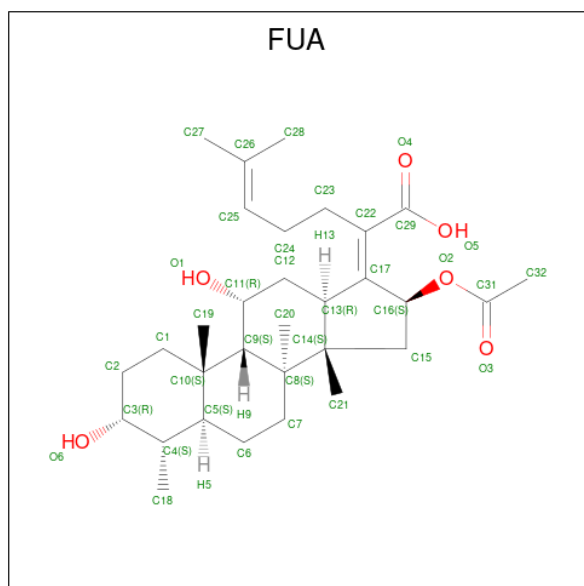
- Molecule 56 is a protein called 50S RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BY	106	Total	C	N	O	S	0	0
			810	520	154	131	5		

- Molecule 57 is a protein called 50S RIBOSOMAL PROTEIN L25.

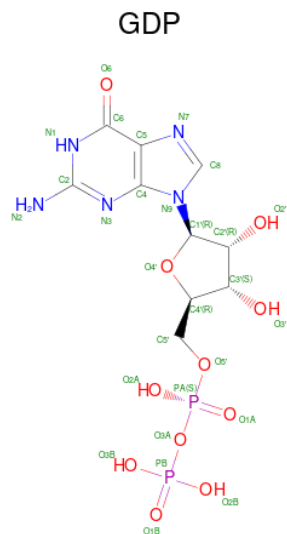
Mol	Chain	Residues	Atoms					AltConf	Trace
57	BZ	184	Total	C	N	O	S	0	0
			1467	936	261	268	2		

- Molecule 58 is FUSIDIC ACID (three-letter code: FUA) (formula: $C_{31}H_{48}O_6$).



Mol	Chain	Residues	Atoms			AltConf
58	AY	1	Total	C	O	0
			37	31	6	

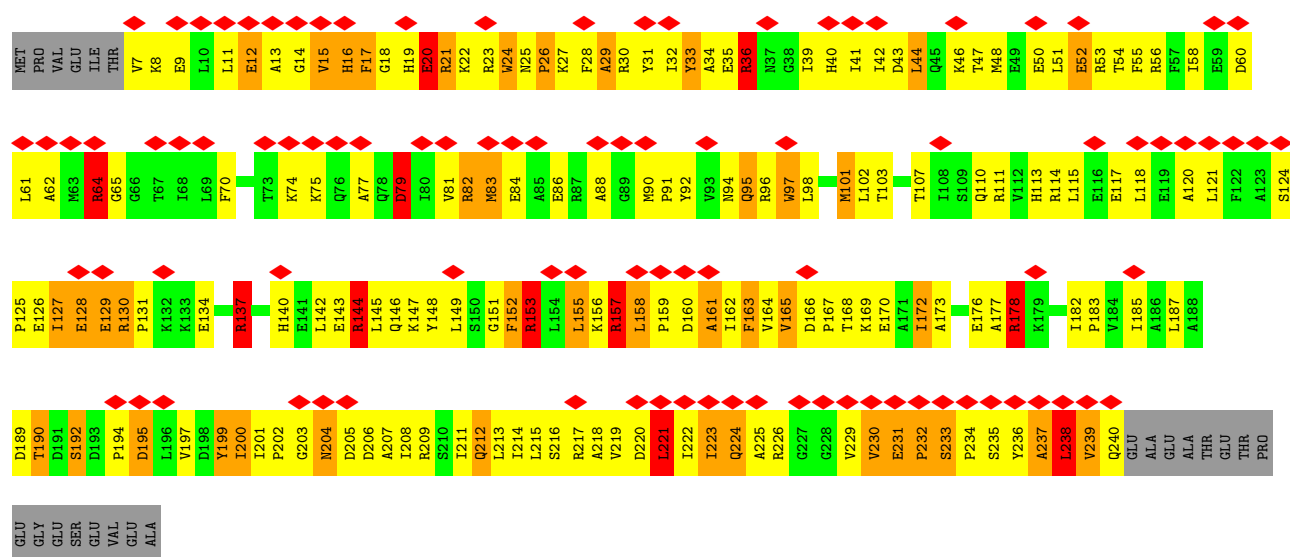
- Molecule 59 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



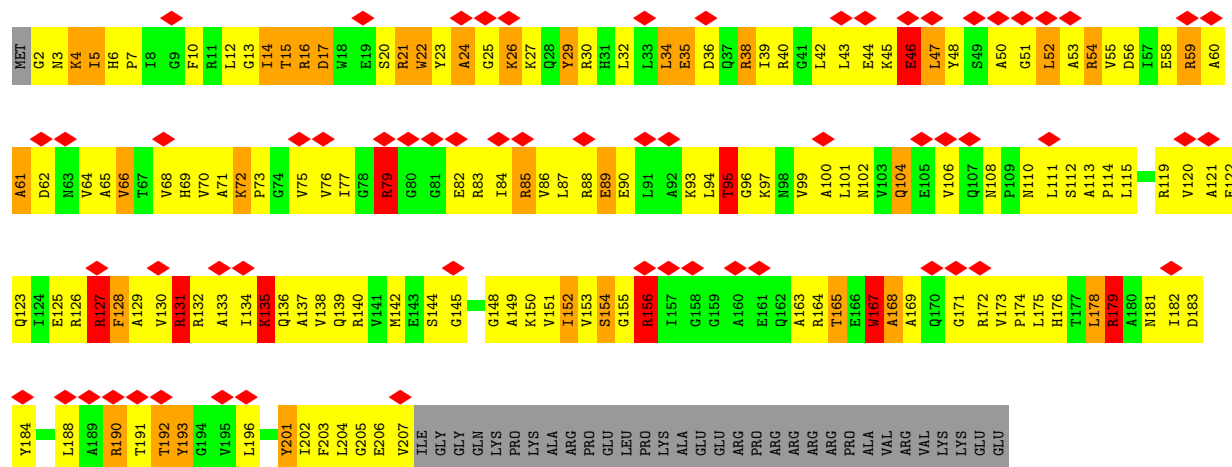
Mol	Chain	Residues	Atoms					AltConf
59	AY	1	Total	C	N	O	P	0
			28	10	5	11	2	



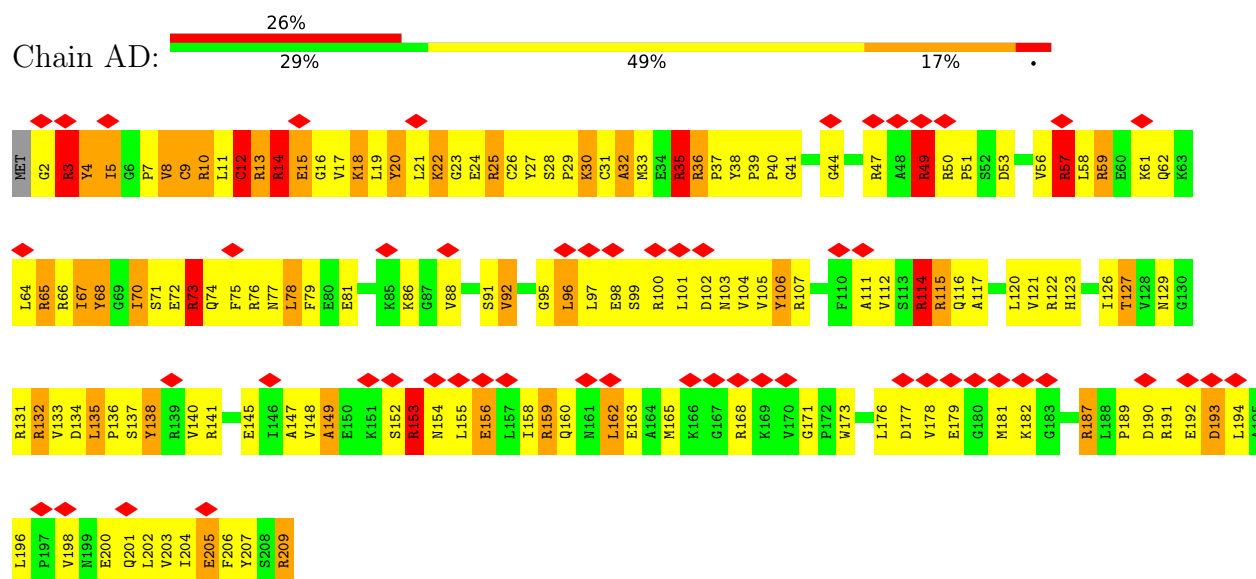
- Molecule 2: 30S RIBOSOMAL PROTEIN S2



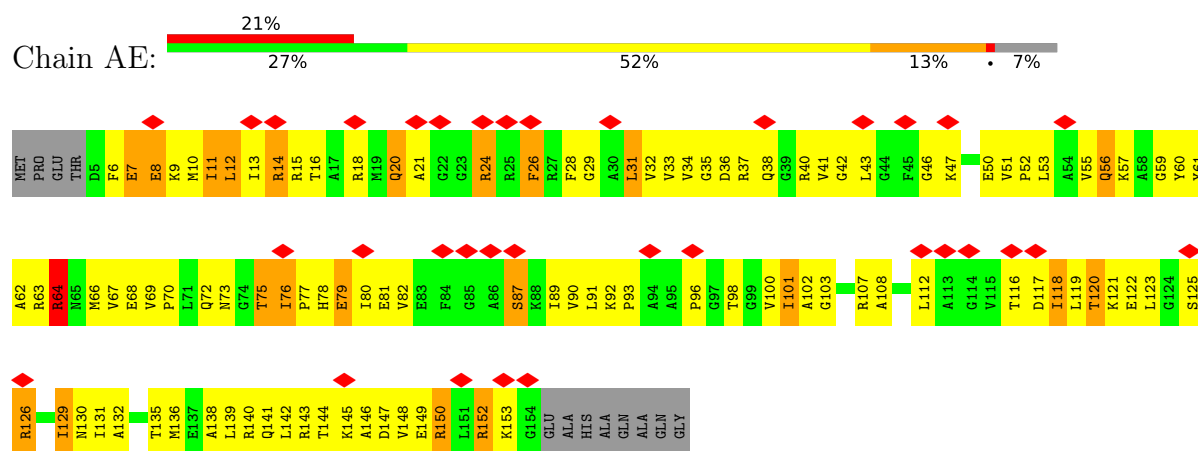
- Molecule 3: 30S RIBOSOMAL PROTEIN S3

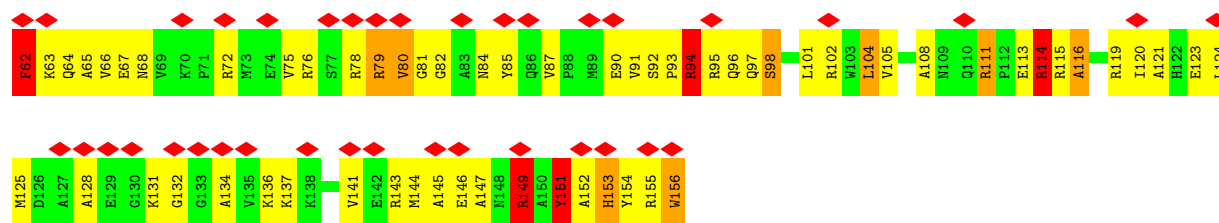


- Molecule 4: 30S RIBOSOMAL PROTEIN S4

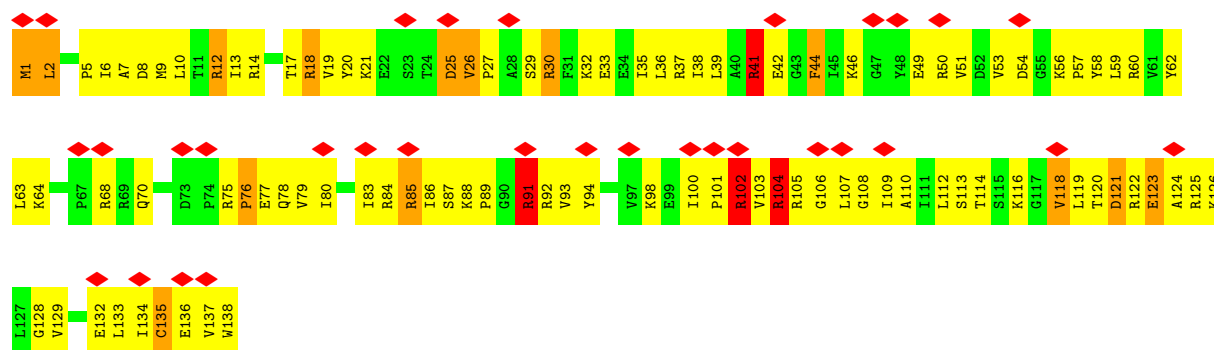


• Molecule 5: 30S RIBOSOMAL PROTEIN S5

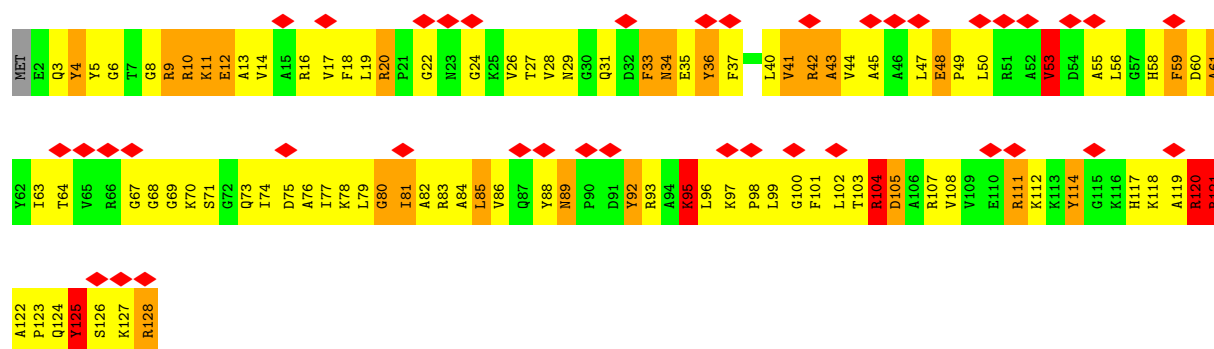




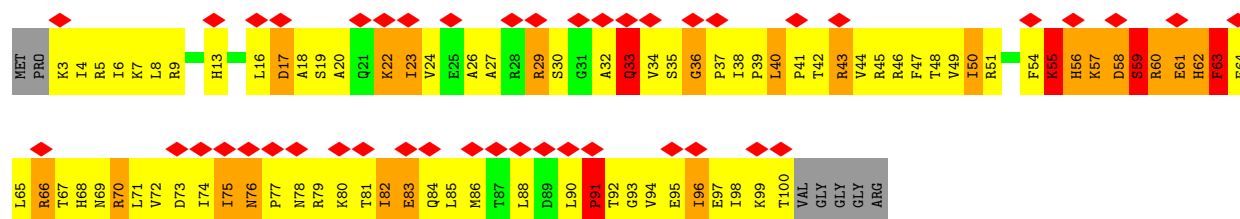
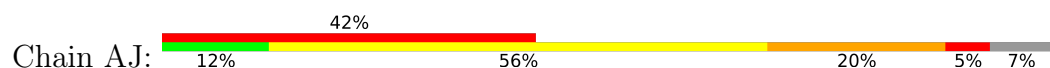
• Molecule 8: 30S RIBOSOMAL PROTEIN S8



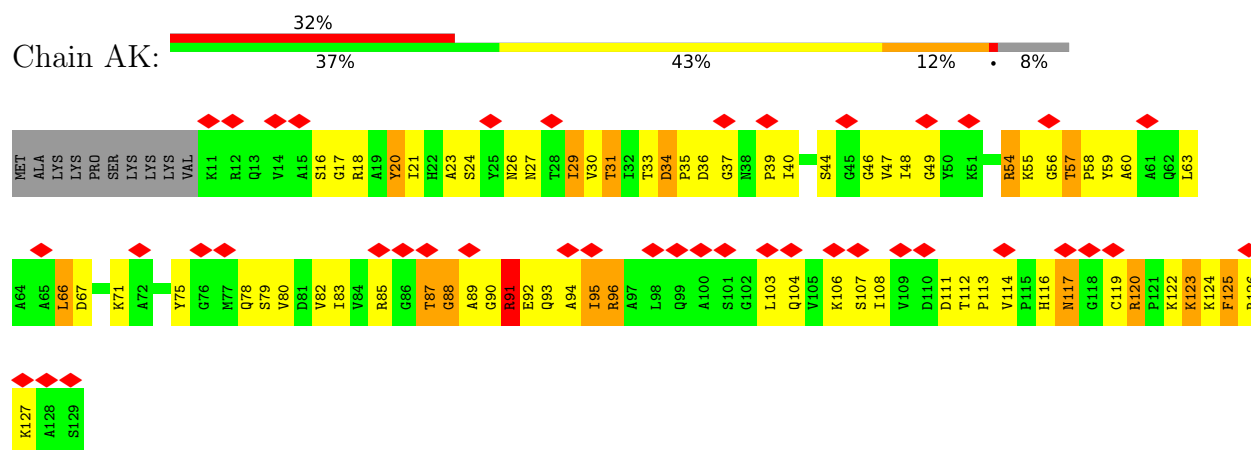
• Molecule 9: 30S RIBOSOMAL PROTEIN S9



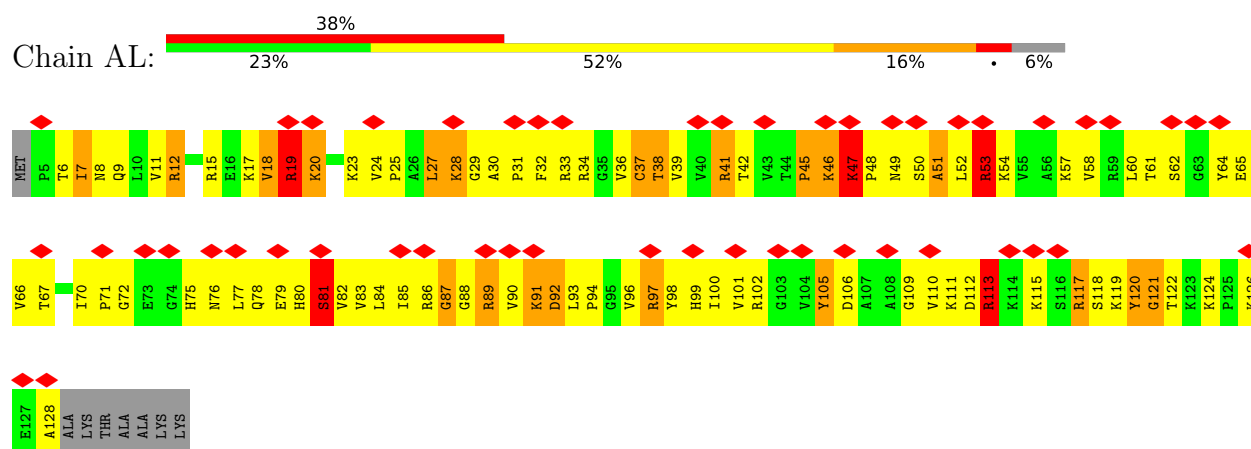
• Molecule 10: 30S RIBOSOMAL PROTEIN S10



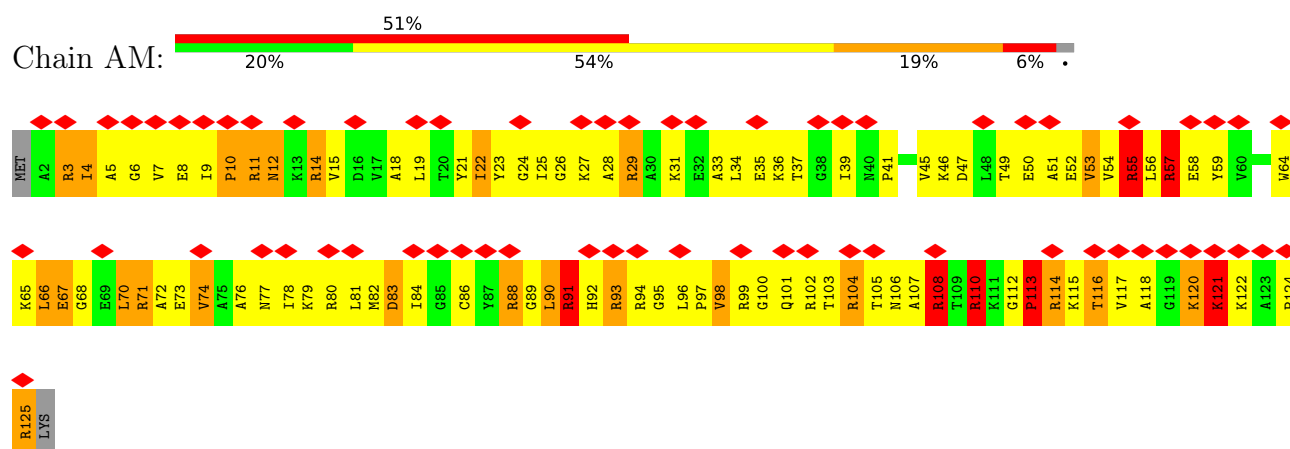
• Molecule 11: 30S RIBOSOMAL PROTEIN S11



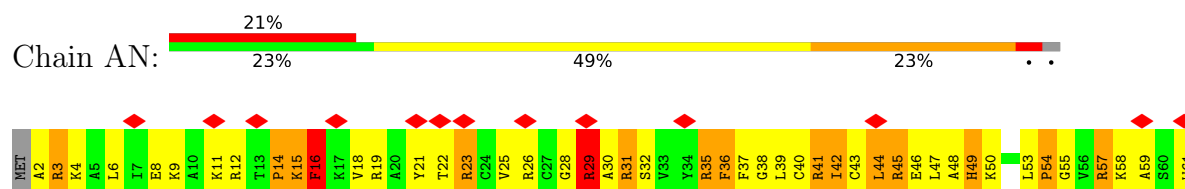
• Molecule 12: 30S RIBOSOMAL PROTEIN S12



• Molecule 13: 30S RIBOSOMAL PROTEIN S13

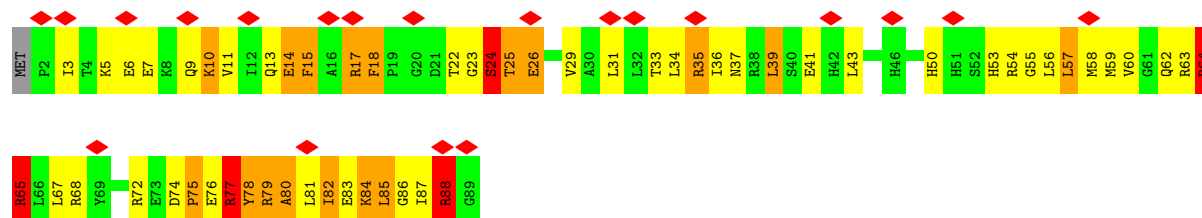


• Molecule 14: 30S RIBOSOMAL PROTEIN S14 TYPE Z



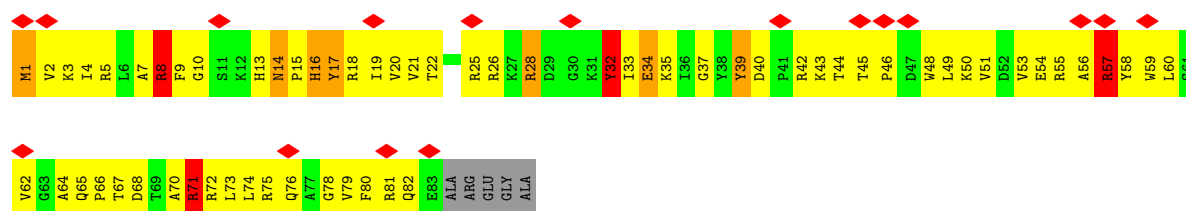
- Molecule 15: 30S RIBOSOMAL PROTEIN S15

Chain AO: 



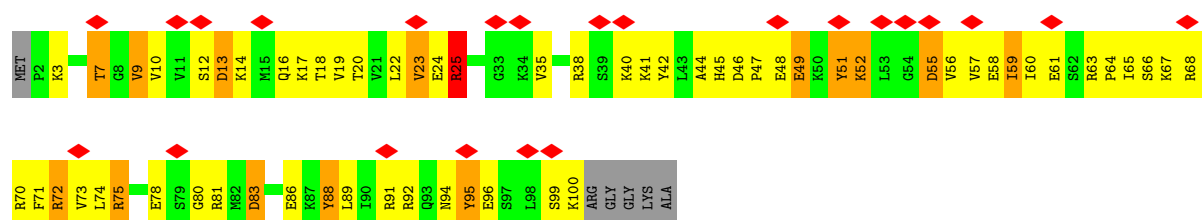
- Molecule 16: 30S RIBOSOMAL PROTEIN S16

Chain AP: 




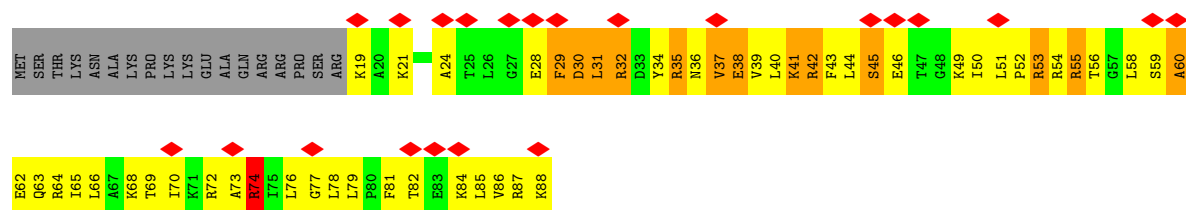
- Molecule 17: 30S RIBOSOMAL PROTEIN S17

Chain AQ: 



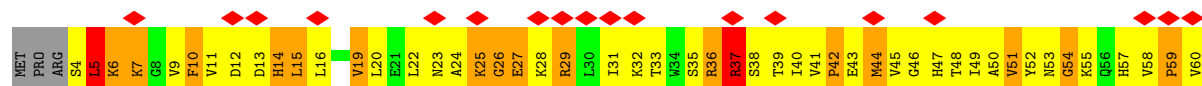
- Molecule 18: 30S RIBOSOMAL PROTEIN S18

Chain AR: 



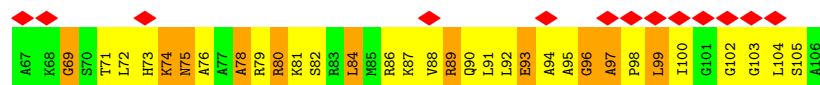
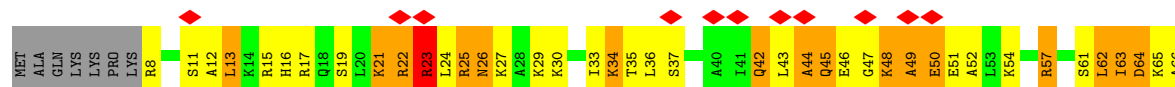
- Molecule 19: 30S RIBOSOMAL PROTEIN S19

Chain AS: 

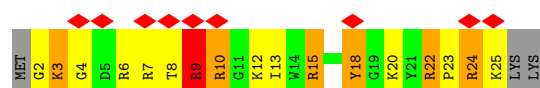
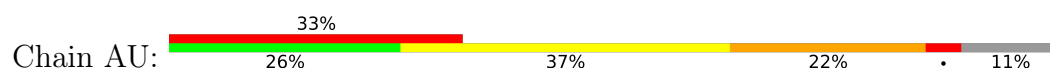




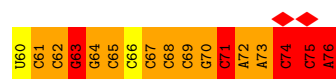
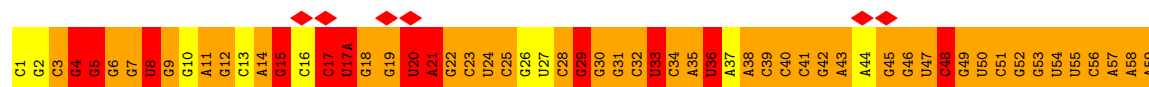
• Molecule 20: 30S RIBOSOMAL PROTEIN S20



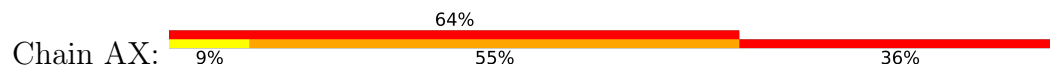
• Molecule 21: 30S RIBOSOMAL PROTEIN THX



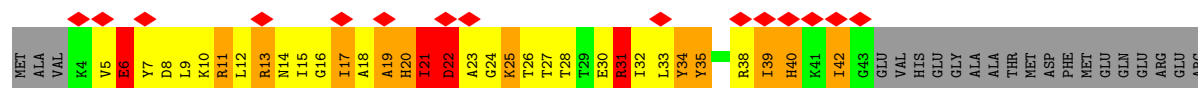
• Molecule 22: TRNA

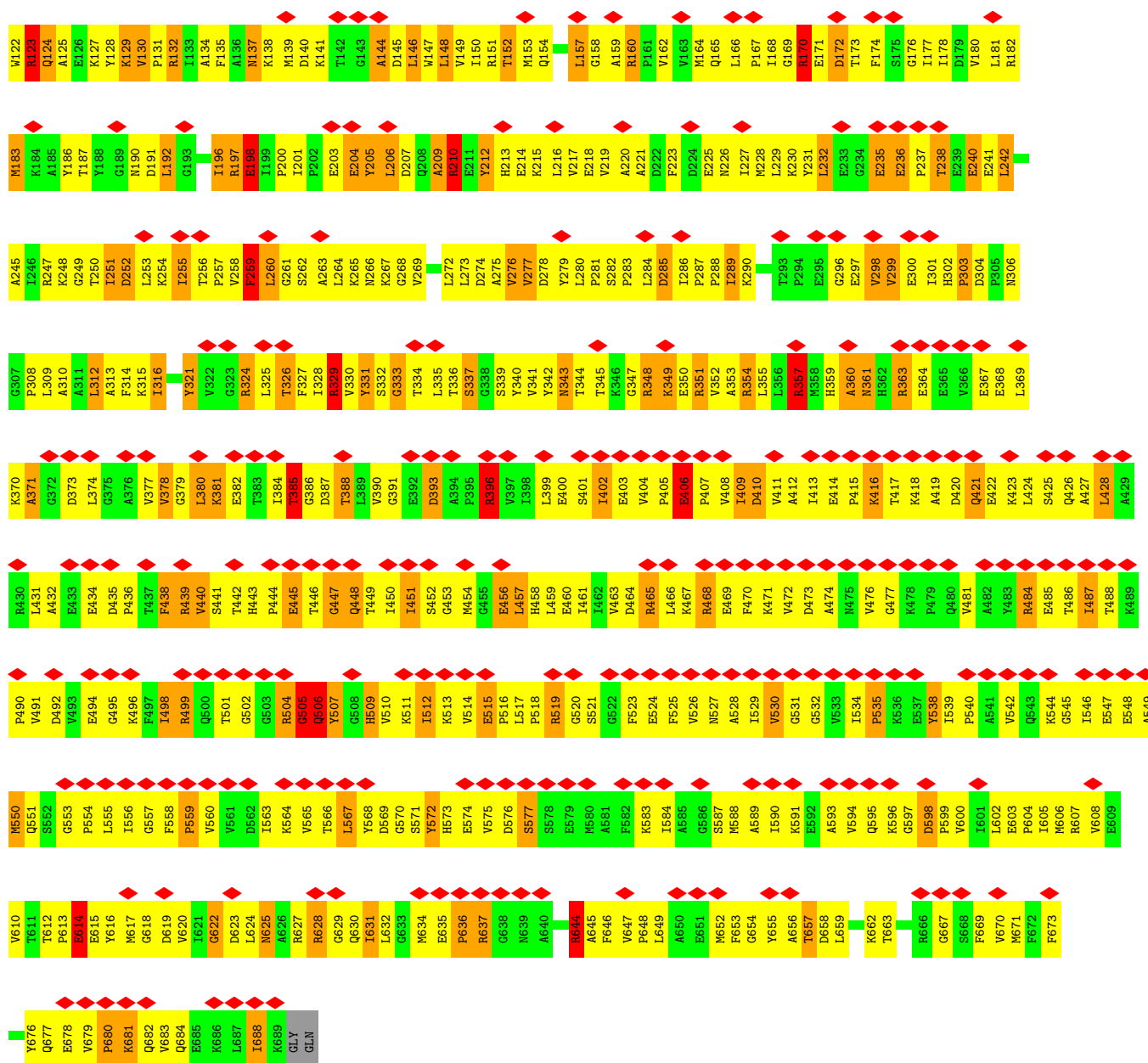


• Molecule 23: MRNA

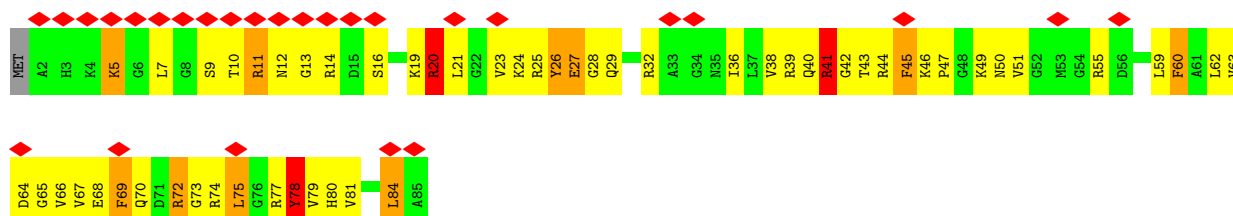


• Molecule 24: ELONGATION FACTOR G



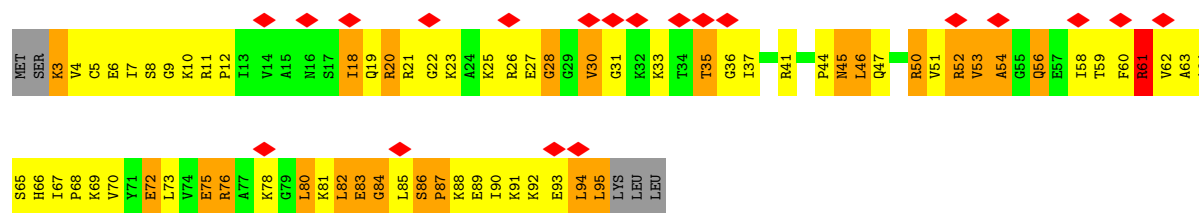


• Molecule 25: 50S RIBOSOMAL PROTEIN L27

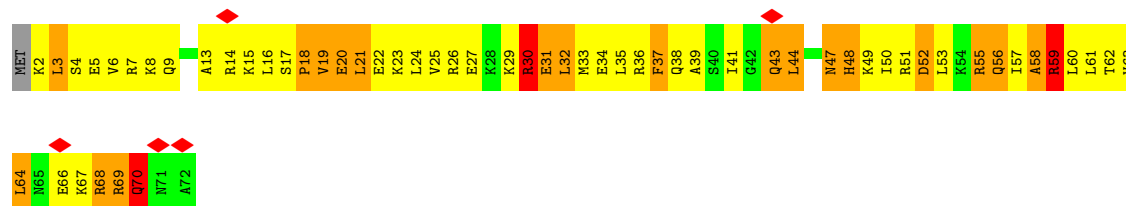
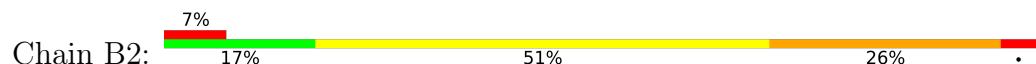


• Molecule 26: 50S RIBOSOMAL PROTEIN L28

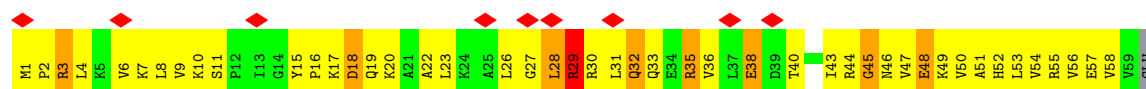




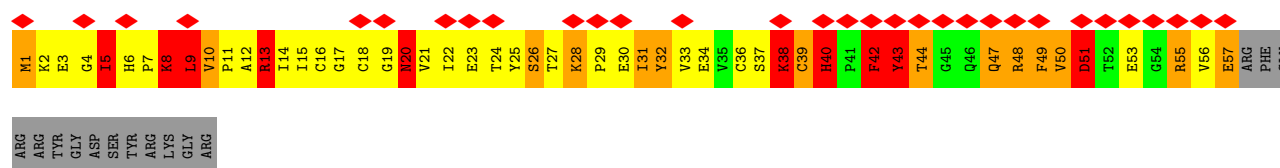
• Molecule 27: 50S RIBOSOMAL PROTEIN L29



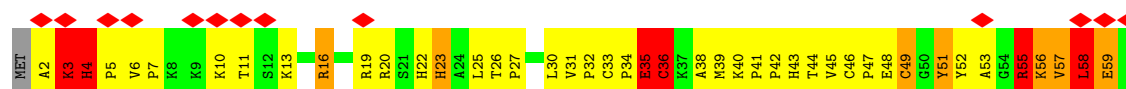
• Molecule 28: 50S RIBOSOMAL PROTEIN L30



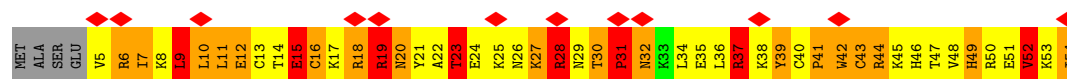
• Molecule 29: 50S RIBOSOMAL PROTEIN L31



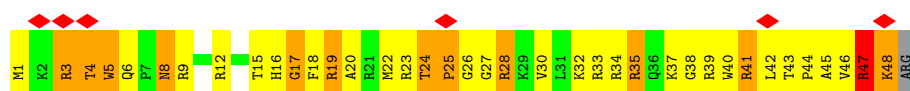
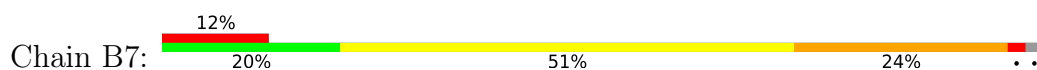
• Molecule 30: 50S RIBOSOMAL PROTEIN L32



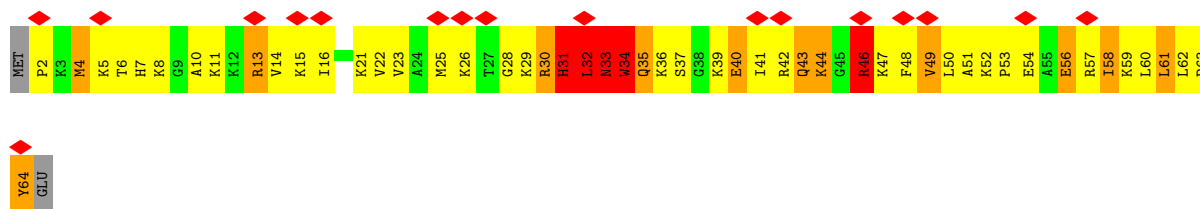
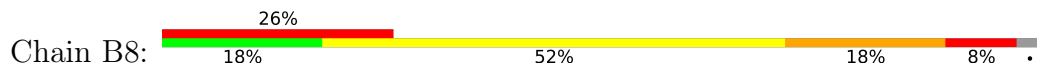
• Molecule 31: 50S RIBOSOMAL PROTEIN L33



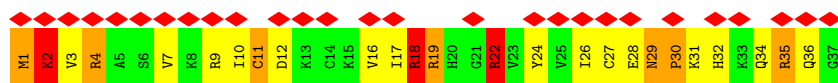
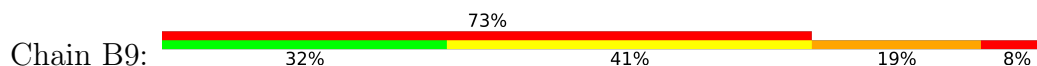
• Molecule 32: 50S RIBOSOMAL PROTEIN L34



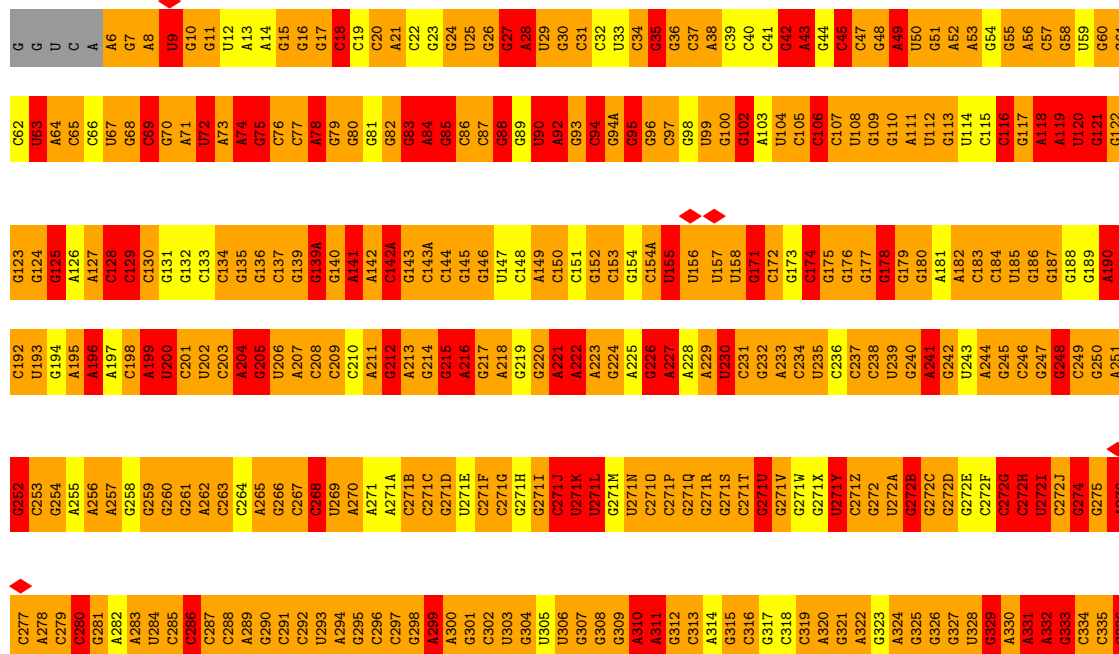
• Molecule 33: 50S RIBOSOMAL PROTEIN L35



• Molecule 34: 50S RIBOSOMAL PROTEIN L36



• Molecule 35: 23S RIBOSOMAL RNA

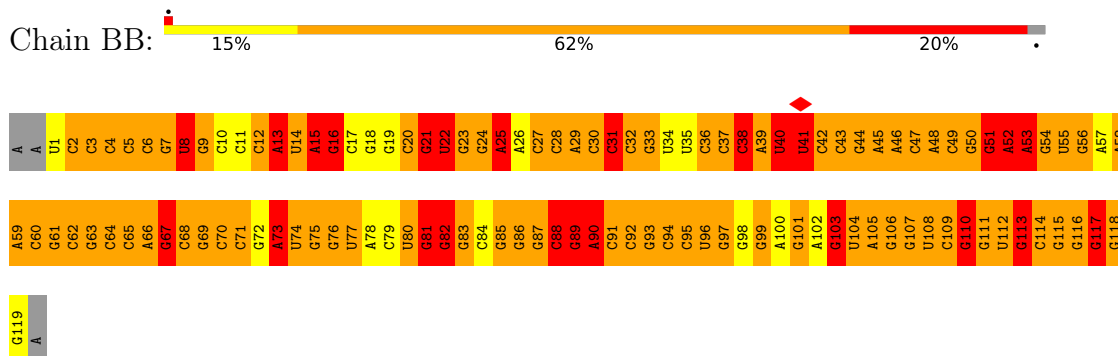


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C1158	A1098	C1038	G978	A918	C857	C797	G737	A677	U639	C581	U519	A458	C397	U340
U1159	U1099	G1039	G979	A919	U858	G798	G738	C678	C640	G582	G520	U459	C398	G341
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G1162	C1102	G1042	C982	U922	A861	G801	G741	G681	A643	G585	C523	C462	A401	C344
G1163	A1103	C1043	A983	C923	G862	A802	G742	G682	A644	A586	U524	C463	A402	A345
G1164	U1104	A1044	A984	C924	A863	U803	G743	G683	C645	C587	U525	U464	U403	A346
U1165	C1105	A1045	C985	C925	G864	A804	G744	G684	A646	U588	A526	C465	C404	A347
C1166	G1106	A1046	C986	A926	C865	G805	G745	A685	G647	C589	C527	A466	U405	U348
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G1171	A1111	G1051	C991	U932	A870	U810	A750	G690	C652	U594	A532	A471	G410	G353
G1172	G1112	C1052	C992	A933	U871	U811	A751	C691	A653	C595	G533	A472	G411	G354
U1173	U1113	C1053	G993	C934	A872	C812	A752	C692	A654	G596	U534	C473	G412	G355
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C1181	C1121	U1061	A1001	G942	A878	A820	G760	G700	C654H	G604	C542	C481	C420	G363
A1182	G1122	G1062	G1002	U943	G879	A821	A761	G701	C654I	C605	C543	A482	U421	A363A
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G1190	U1130	A1070	C951	G952	C886	A829	G769	U709	C654Q	G613	G553	C491	A429	C366
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G1192	A1132	C1072	U1012	A953	A887	G831	G771	G711	C654S	U614A	U555	C493	U431	A371
G1193	U1133	A1073	C1013	G954	C888	G832	C772	G712	C654T	G614B	U557	C494	A432	G372
A1194	C1135	G1074	U1014	C955	C889	U833	U773	G713	A654U	G615	G558	C495	C433	U373
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U1200	U1200	A1080	U1019	U1019	C894	U839	U779	C719	C659	G622	C564	A502	G440	G379
C1201	U1201	U1081	A1021	G962	U895	C840	G780	C720	G660	G623	C565	A503	U441	U380
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C1208	A1148	A1088	A1028	U969	A901	U847	U787	A727	U667	G630	A572	C510	A449	U387
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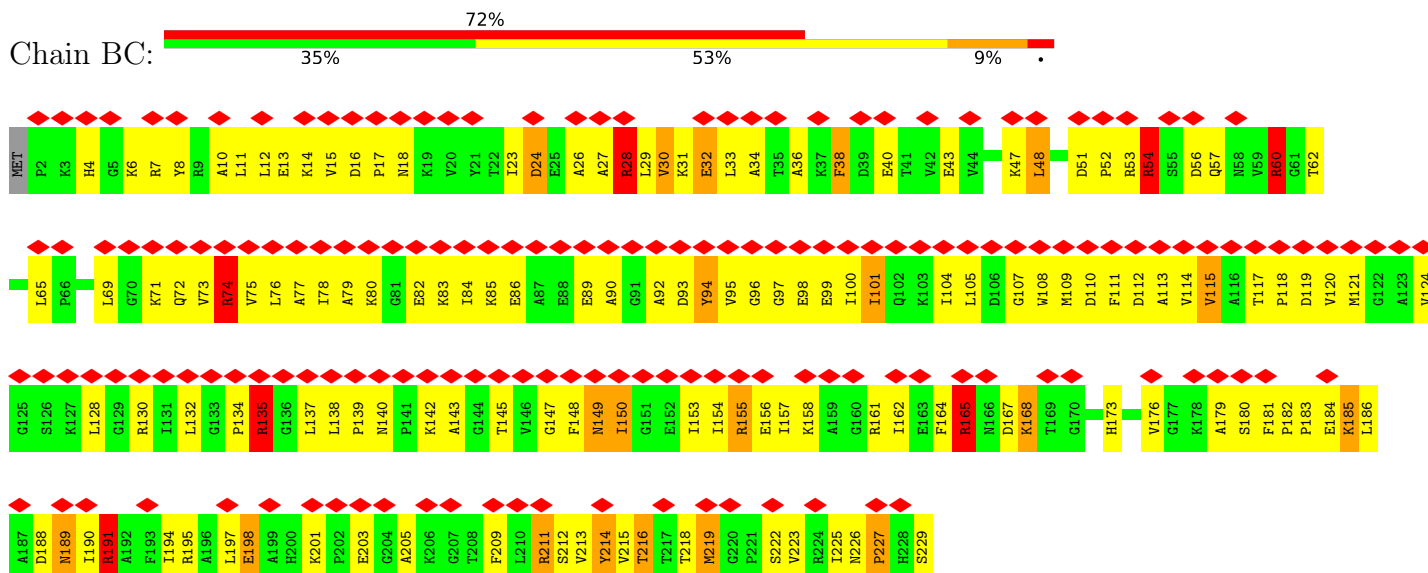
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G2024	G1964	G1903	U1834	C1774	A1698	C1638	A1578	G1517	C1458	C1399	U1339	G1279	A1220
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C2063	G2003	U1942	G1883	G1814	C1754	G1678	G1619	C1558	C1498	U1439	G1379	G1319	G1259
C2064	A2004	C1942	A1884	A1815	A1755	U1679	G1620	G1559	G1499	G1380	C1320	C1320	G1260
C2065	U1943	U1944	C1885	G1816	G1756	U1680	U1621	G1560	G1500	G1381	G1321	C1321	C1261
C2066	A2005	G1945	C1886	G1817	U1757	G1681	G1622	G1561	C1501	G1440	A1322	A1322	A1262
G2067	G2006	C1946	C1887	U1818	G1758	G1682	G1623	A1562	C1502	G1441	C1382	U1323	G1263
U2068	C2007	G1947	C1888	G1819	A1759	C1683	G1624	G1563	U1503	G1442	C1383	U1324	G1264
G2069	C2008	C1947	G1889	G1820	C1759	C1684	C1625	C1564	C1504	G1443	A1384	G1324	A1265
G2070	G2009	A1948	A1890	U1821	A1760	C1685	G1626	C1565	C1505	A1445	G1385	U1326	G1266
A2071	U2011	G1949	G1891	G1822	C1761	C1686	G1627	C1566	C1446	C1445A	C1387	U1327	G1267
G2072	C2012	G1950	C1892	G1823	A1762	G1687	G1628	A1567	A1507	G1447	G1388	C1327	A1268
U2073	A2013	C1951	C1893	G1824	G1763	U1688	U1567	G1568	U1508	G1448	U1389	U1329	A1269
U2074	A2014	A1952	C1894	G1825	C1765	A1689	G1630	A1569	C1509	G1449	U1390	U1330	G1270
U2075	A2015	G1953	C1895	G1826	U1766	A1690	C1631	A1570	A1509B	G1450	U1391	A1331	G1271
U2076	U2016	G1954	G1896	C1827	C1767	C1691	A1631A	A1571	A1509B	C1450A	A1392	G1332	A1272
A2077	C2017	U1955	G1897	G1828	U1768	U1692	A1632	A1572	G1511	C1451	A1393	U1273	U1273
C2078	G2018	C1958	U1898	A1829	G1769	U1693	G1633	G1573	U1512	A1452	U1394	G1334	A1274

C2871	C2811	A2748	U2889	A2829	G2569	G2509	U2449	G2389	G2329	A2269	A2199	C2139	U2079
C2872	G2812	A2749	C2690	G2630	G2570	C2510	A2450	U2389	G2330	G2270	C2200	C2140	G2080
A2873	A2813	A2750	C2691	G2631	C2571	U2511	A2451	U2390	G2331	G2271	C2201	C2141	C2081
C2874	C2814	G2751	C2692	G2632	A2572	C2512	C2452	A2392	U2332	G2272	C2202	C2142	A2082
C2875	C2815	G2752	A2693	G2633	C2573	G2513	A2453	A2393	A2333	A2273	U2203	C2143	C2083
C2876	C2816	A2753	G2694	G2634	G2574	U2514	G2454	C2394	G2334	C2274	C2205	U2144	C2084
G2877	G2817	U2754	C2695	G2635	C2575	C2515	G2455	C2395	A2335	C2275	G2206	C2145	C2085
U2878	G2818	G2755	U2696	U2636	G2576	G2516	C2456	G2396	A2336	G2276	G2207	C2146	U2086
C2879	A2820	U2756	G2697	U2637	A2577	C2517	U2457	U2397	G2337	G2277	A2208	G2147	G2087
C2880	A2821	A2757	U2698	G2638	G2578	U2518	G2458	U2398	G2338	A2278	U2218	G2148	U2088
A2881	G2822	A2758	C2699	A2639	C2579	U2519	A2459	U2399	G2339	G2279	G2219	G2149	U2089
A2882	A2823	G2759	C2700	G2640	U2580	C2520	U2460	G2400	G2340	G2280	G2220	U2150	G2090
A2883	A2824	G2760	C2701	G2641	U2581	C2521	U2461	U2401	G2341	C2281	G2221	G2151	U2091
U2884	G2824	G2761	U2702	G2642	G2582	U2522	U2462	C2402	C2342	G2282	G2222	G2152	U2092
C2885	C2825	G2762	C2703	G2643	G2583	G2523	C2463	C2403	U2343	C2283	G2223	G2153	G2093
G2886	A2826	G2763	C2704	G2644	U2584	G2524	G2464	C2404	C2344	C2284	G2224	G2154	G2094
U2887	C2827	A2764	A2705	G2645	U2585	G2525	C2465	G2405	G2345	G2285	A2225	G2155	C2095
C2888	C2828	A2765	G2706	G2646	C2586	G2526	C2466	U2406	A2346	A2286	G2226	U2156	U2096
C2889	C2829	G2766	G2707	U2647	A2587	C2527	C2467	G2407	G2347	A2287	A2227	G2157	C2097
G2890	G2830	C2767	G2708	C2648	U2588	U2528	G2468	U2408	U2348	G2288	G2228	A2158	U2098
A2892	G2831	C2768	G2709	G2649	A2589	G2529	A2469	G2409	G2349	A2289	C2229	G2159	U2099
C2893	U2832	G2769	C2710	G2650	A2590	A2530	G2470	G2410	C2350	G2290	G2230	G2160	G2100
G2894	G2833	G2770	A2711	C2651	C2591	A2531	C2471	A2411	C2351	U2291	C2231	C2161	G2101
U2895	G2834	C2771	U2712	C2652	G2592	G2532	G2472	A2412	A2352	C2292	U2232	G2162	U2102
A2896	A2835	C2772	A2712A	U2653	G2593	A2533	U2473	G2413	G2353	C2293	U2233	G2163	C2103
U2897	U2836	C2773	A2713	A2654	C2594	A2534	C2474	G2414	G2354	C2294	U2234	G2164	G2104
U	G2837	C2774	G2714	G2655	U2595	G2535	A2475	G2415	C2355	C2295	U2235	G2165	C2105
G	G2838	A2775	C2715	U2656	U2596	G2536	C2476	C2416	G2356	C2296	G2236	G2166	G2106
A	C2839	A2776	U2716	C2657	G2597	U2537	C2477	C2417	U2357	A2297	G2237	U2167	C2107
C	C2840	G2777	C2717	C2658	A2598	C2538	G2478	A2418	C2358	G2298	G2238	A2168	U2108
C	A2841	A2778	G2718	G2659	C2599	C2539	G2479	U2419	C2359	G2299	G2239	A2169	U2109
C	G2842	U2779	G2719	U2660	A2600	C2540	C2480	C2420	A2360	G2300	C2240	A2170	G2110
C	G2843	G2780	U2720	G2661	C2601	A2541	G2481	G2421	A2361	C2301	A2241	A2171	C2111
U	A2844	A2781	A2721	A2662	A2602	A2542	G2482	U2422	G2362	G2302	G2242	A2172	G2112
C	G2845	G2782	G2722	G2663	G2603	G2543	C2483	U2423	G2363	G2303	U2243	A2173	U2113
C	G2846	G2783	C2723	G2664	U2604	G2544	G2484	C2424	C2364	G2304	U2244	C2174	A2114
C	U2847	G2784	C2724	A2665	U2605	G2545	G2485	A2425	G2365	A2305	U2245	G2175	G2115
C	G2848	C2785	A2725	C2666	G2606	U2546	G2486	A2426	A2366	C2306	G2246	A2176	G2116
U2849	U2786	C2786	U2726	C2667	G2607	U2547	G2487	C2427	G2367	G2307	A2247	A2177	A2117
A2850	C2787	G2787	G2727	G2668	G2608	G2548	A2488	G2428	C2368	G2308	G2248	C2178	U2118
A2851	G2788	C2788	U2728	G2669	G2609	G2549	G2489	G2429	A2369	A2309	U2249	C2179	A2119
G2852	C2789	A2789	G2729	A2670	U2609	G2550	G2490	A2430	G2370	A2310	G2250	U2180	G2120
C2853	G2790	C2790	C2730	G2671	C2610	C2551	U2491	U2431	G2371	A2311	G2251	G2181	G2121
G2854	C2791	G2791	G2731	A2672	U2611	U2552	U2492	A2432	G2372	U2312	G2252	G2182	U2122
C2855	G2792	G2792	G2732	G2673	C2612	G2553	U2493	A2433	G2373	C2313	G2253	C2183	G2123
C2856	G2793	C2793	A2733	G2674	U2613	U2554	G2494	A2434	C2374	C2314	G2254	G2184	G2124
C2857	C2794	A2794	G2734	A2675	A2614	U2555	G2495	A2435	G2375	G2315	C2255	C2185	G2125
G2858	G2795	G2795	G2735	C2676	U2615	C2556	G2496	G2436	G2376	G2316	G2256	G2186	A2126
G2859	U2796	G2796	G2736	C2677	C2616	G2557	U2497	U2437	A2377	C2317	U2257	G2187	G2127
A2860	C2797	G2797	A2737	C2678	C2617	C2558	U2498	U2438	G2378	G2318	G2258	G2188	C2128
G2861	A2801	C2799	U2739	C2679	C2618	C2559	G2499	A2439	G2379	G2319	G2259	U2189	C2129
C2862	G2802	A2802	U2740	C2680	C2619	U2560	U2500	C2440	C2380	A2320	G2260	U2190	U2130
C2863	G2803	G2803	A2741	U2681	A2620	A2561	G2501	C2441	C2381	G2321	C2261	G2191	G2131
U2865	C2804	C2804	C2742	U2682	C2622	U2562	G2502	C2442	G2382	A2322	U2262	G2192	U2132
U2866	G2805	C2805	C2743	U2683	G2623	U2563	A2503	G2443	G2383	G2323	C2263	G2193	G2133
G2867	G2806	C2806	G2744	G2684	G2624	A2564	U2504	G2444	G2384	C2324	U2264	G2194	A2134
A2868	U2807	C2807	G2745	G2685	G2625	G2565	G2505	G2445	G2385	G2325	U2265	C2195	A2135
G2869	U2808	U2808	U2746	G2686	G2626	A2566	U2506	G2446	G2386	C2326	A2266	C2196	C2136
C2870	A2809	C2809	G2747	U2687	G2627	A2567	G2507	G2447	U2387	A2327	A2267	U2197	C2137
	A2810		G2747	U2688	C2628	C2568	G2508	A2448	A2388	A2328	A2268	A2198	C2138

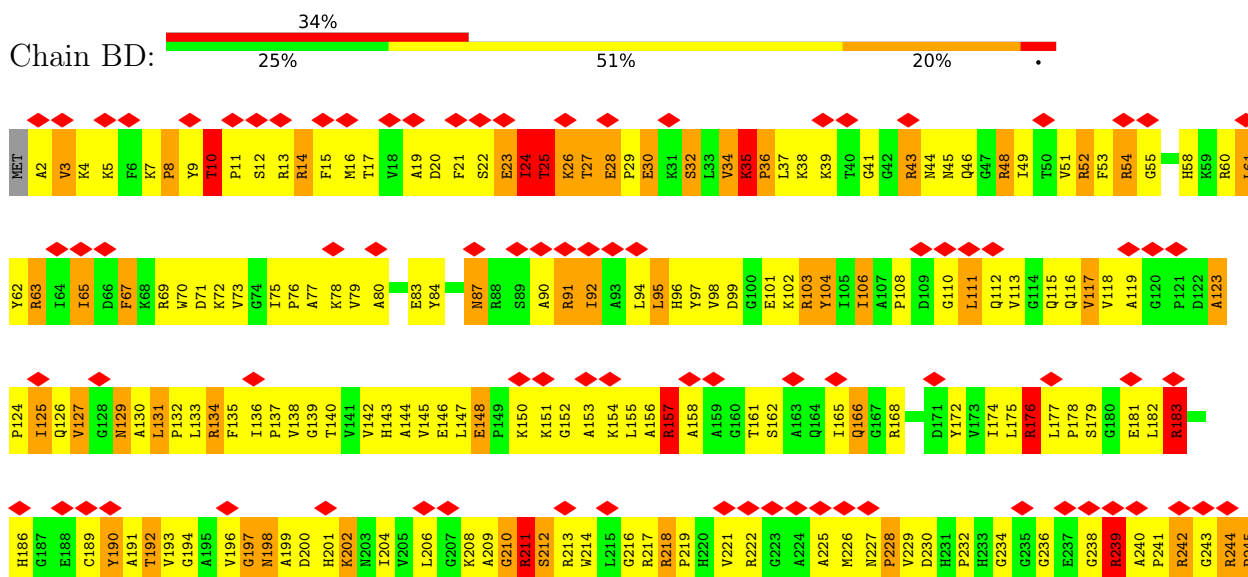
• Molecule 36: 5S RIBOSOMAL RNA

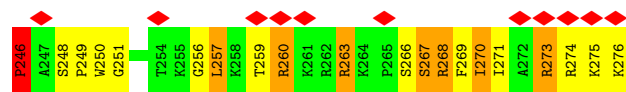


• Molecule 37: 50S RIBOSOMAL PROTEIN L1

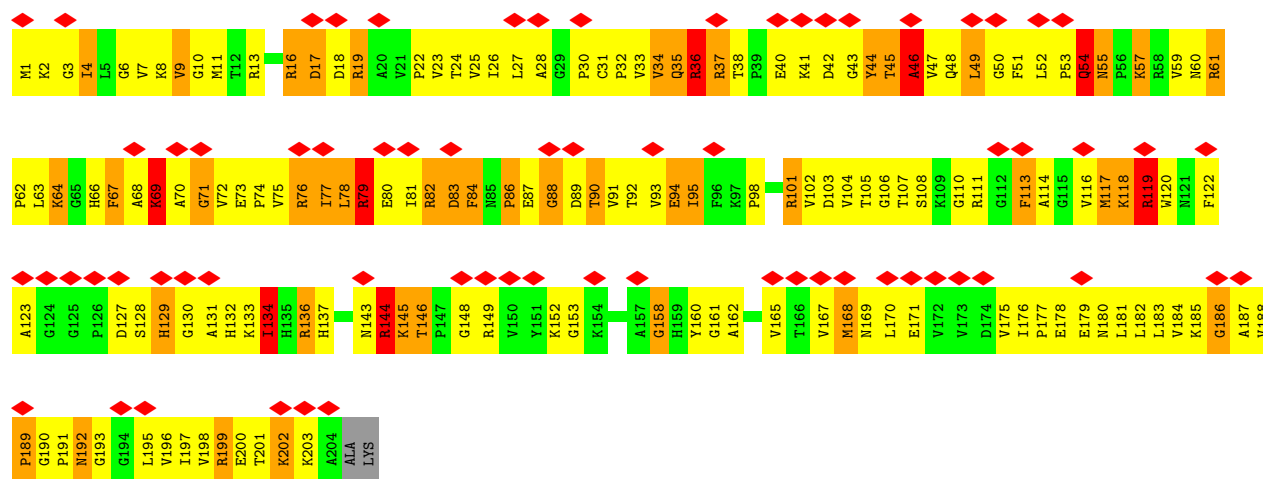


• Molecule 38: 50S RIBOSOMAL PROTEIN L2

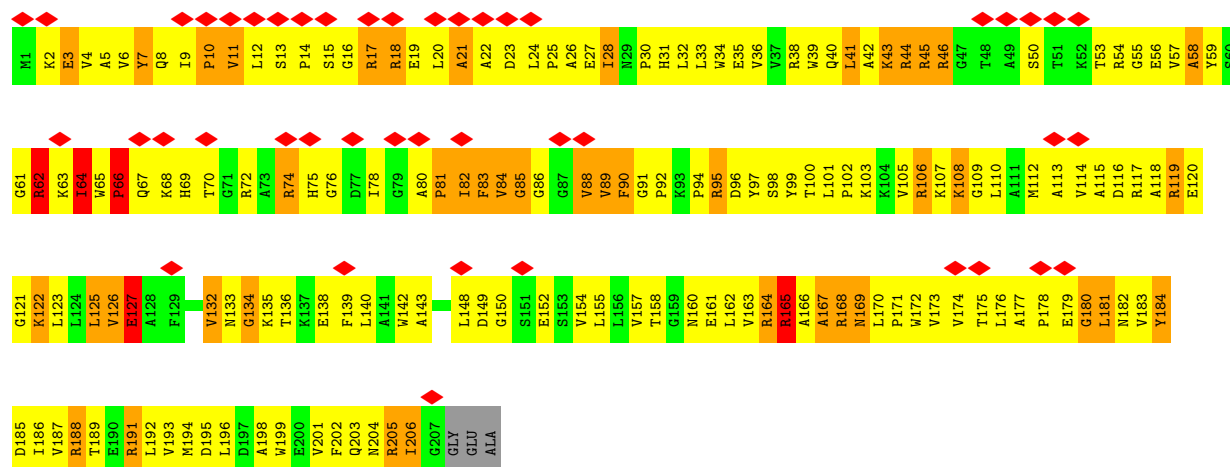




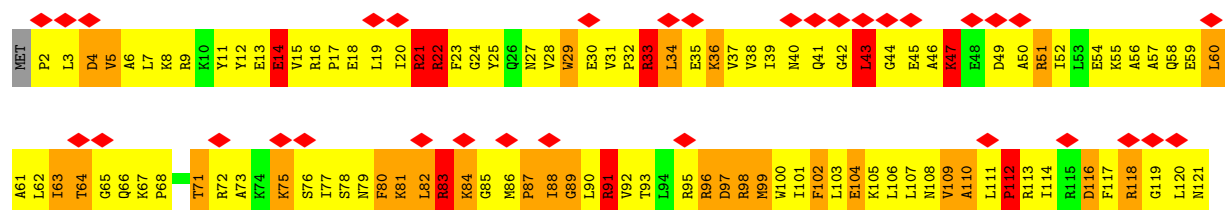
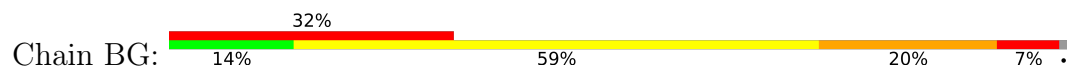
• Molecule 39: 50S RIBOSOMAL PROTEIN L3

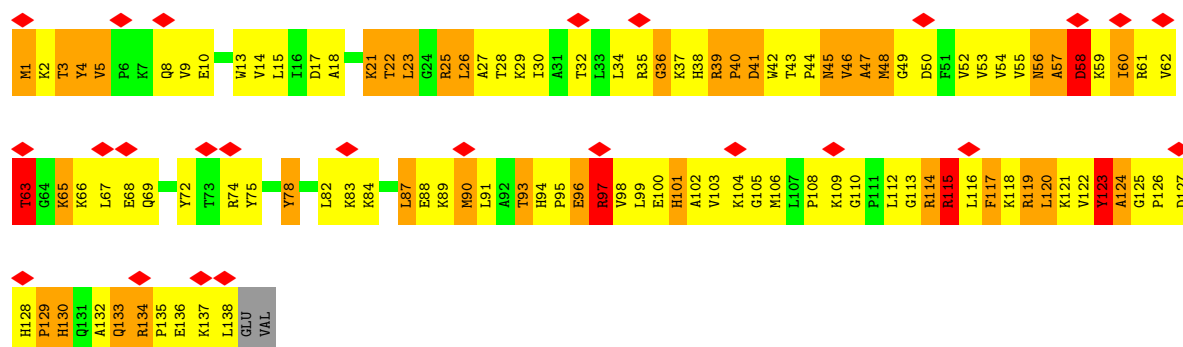


• Molecule 40: 50S RIBOSOMAL PROTEIN L4

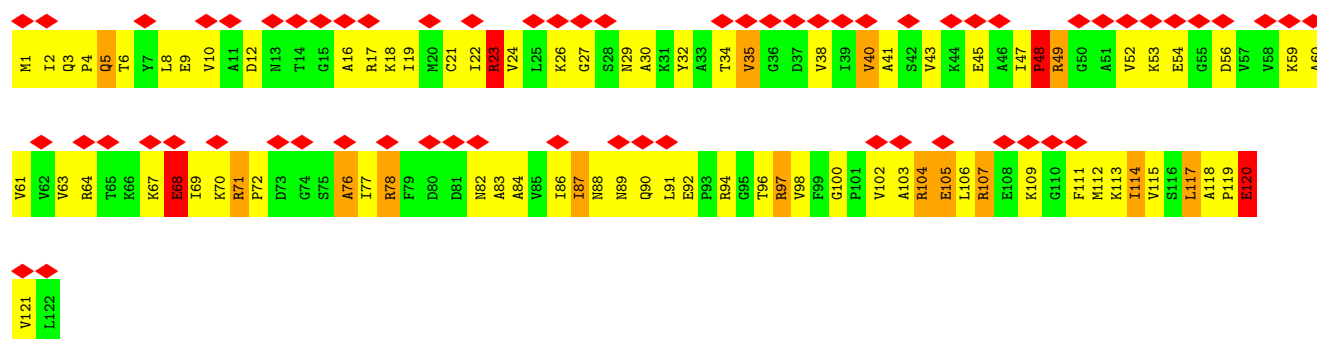


• Molecule 41: 50S RIBOSOMAL PROTEIN L5

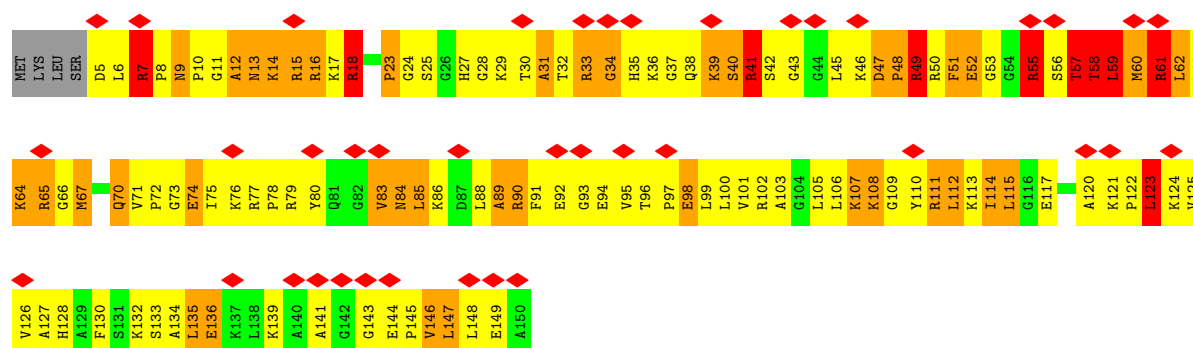
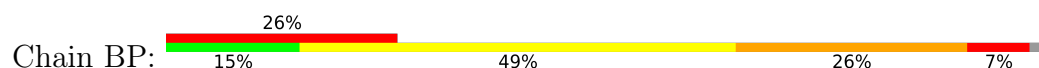




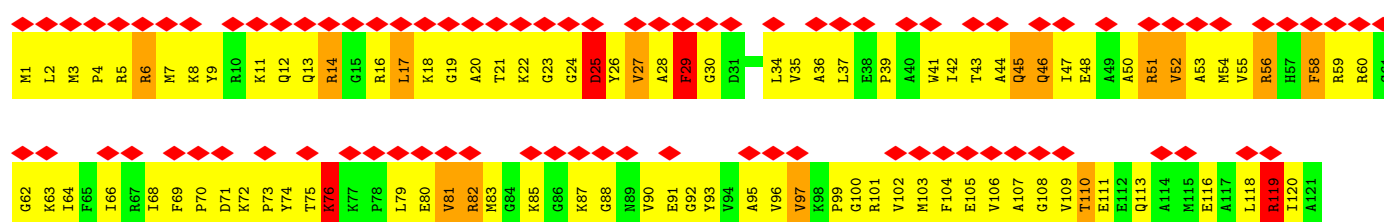
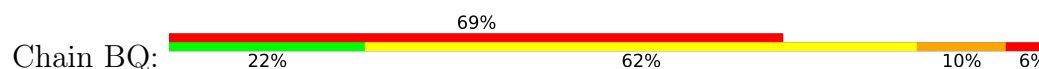
• Molecule 46: 50S RIBOSOMAL PROTEIN L14

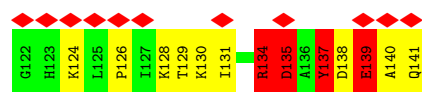


• Molecule 47: 50S RIBOSOMAL PROTEIN L15

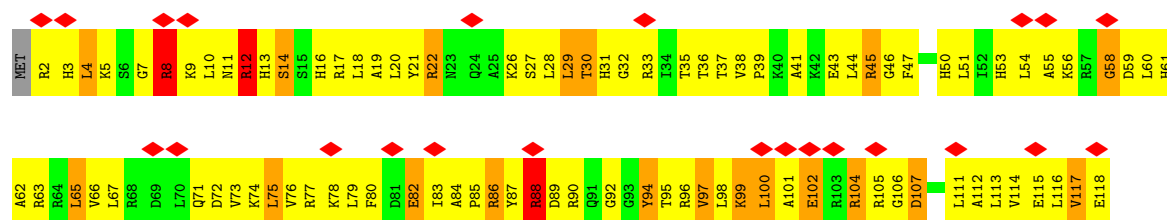


• Molecule 48: 50S RIBOSOMAL PROTEIN L16

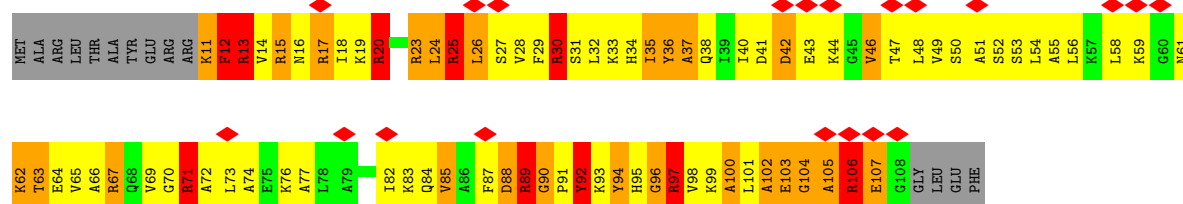




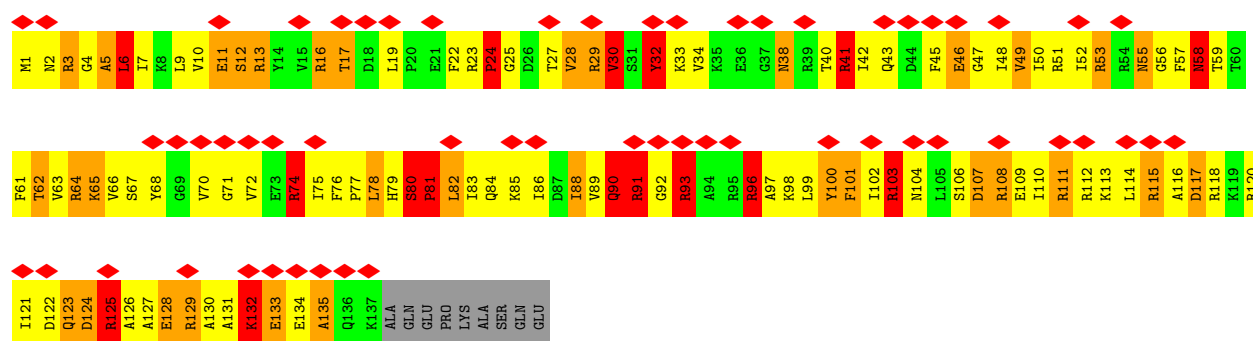
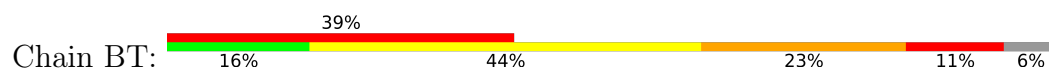
• Molecule 49: 50S RIBOSOMAL PROTEIN L17



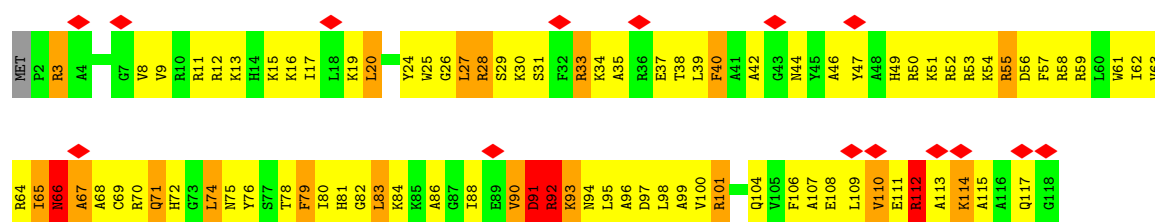
• Molecule 50: 50S RIBOSOMAL PROTEIN L18



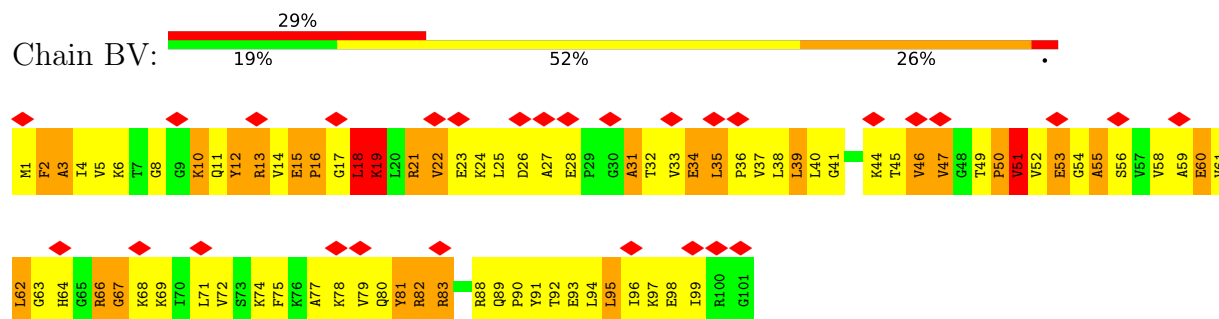
• Molecule 51: 50S RIBOSOMAL PROTEIN L19



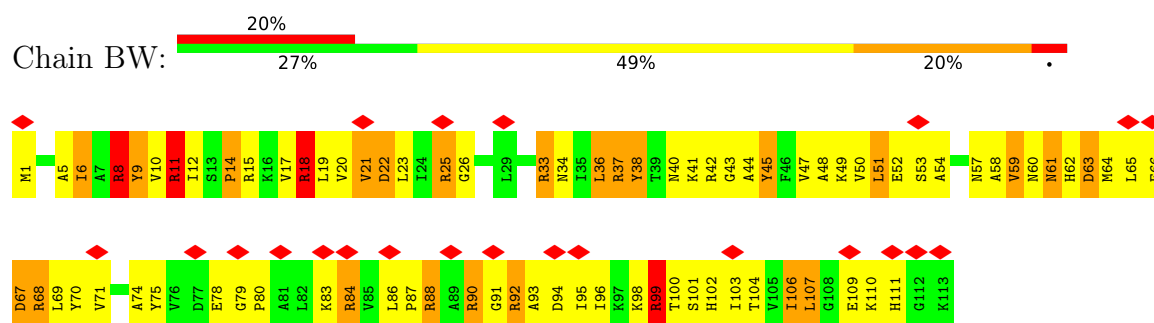
• Molecule 52: 50S RIBOSOMAL PROTEIN L20



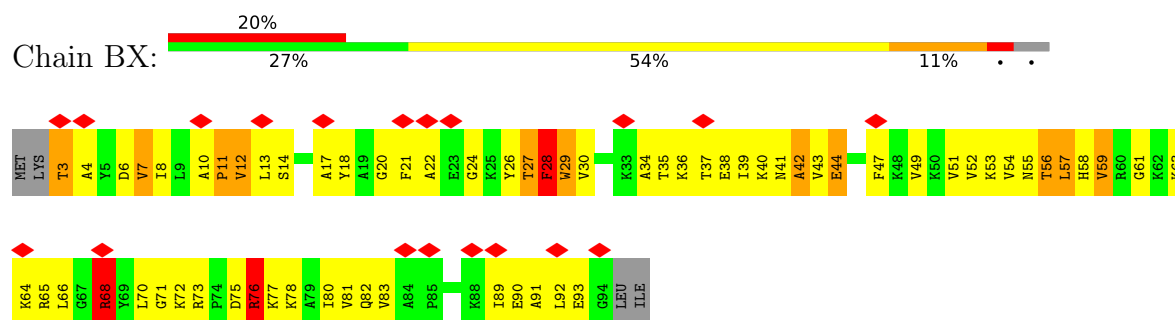
- Molecule 53: 50S RIBOSOMAL PROTEIN L21



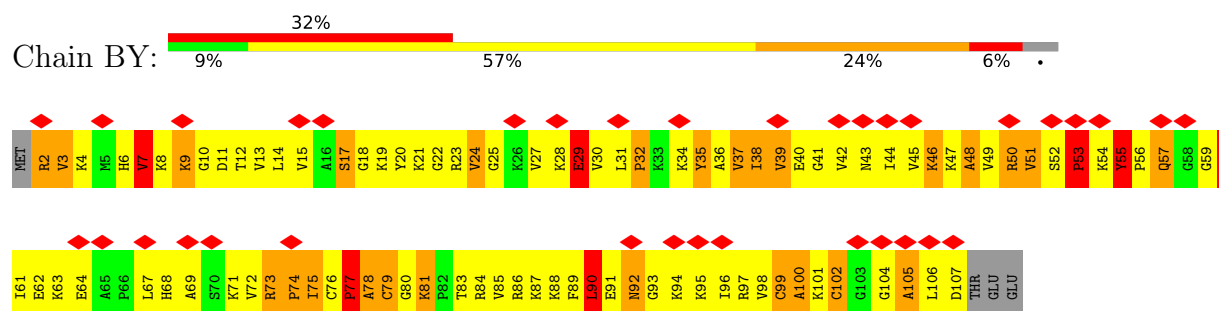
- Molecule 54: 50S RIBOSOMAL PROTEIN L22



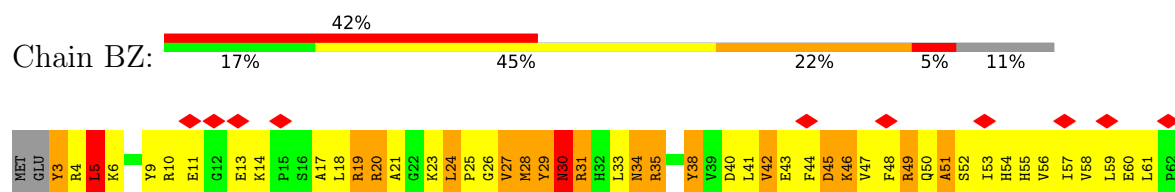
- Molecule 55: 50S RIBOSOMAL PROTEIN L23

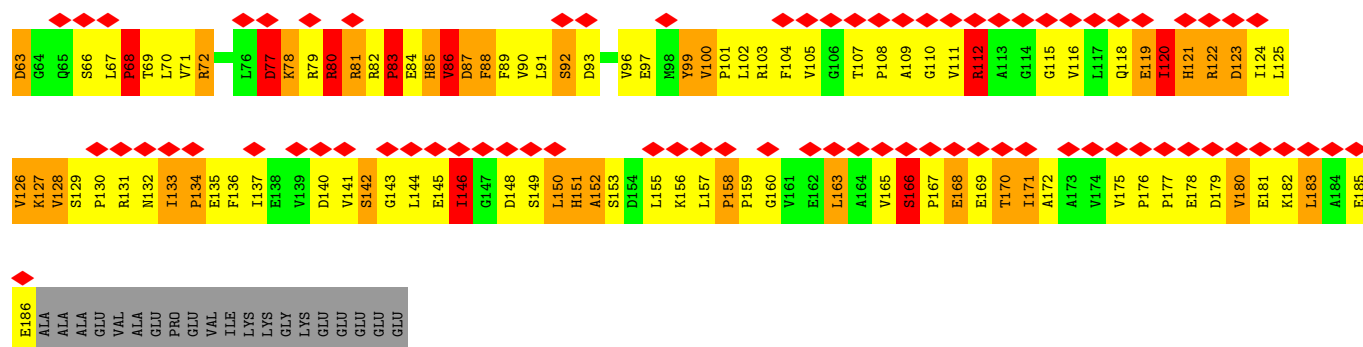


- Molecule 56: 50S RIBOSOMAL PROTEIN L24



- Molecule 57: 50S RIBOSOMAL PROTEIN L25





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	Not provided	
Resolution determination method	Not provided	
CTF correction method	DEFOCUS GROUPS	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	65520	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	13410.900	Depositor
Minimum map value	-6356.590	Depositor
Average map value	213.063	Depositor
Map value standard deviation	916.721	Depositor
Recommended contour level	3000	Depositor
Map size (\AA)	378, 378, 378	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90, 90, 90	wwPDB
Pixel spacing (\AA)	1.26, 1.26, 1.26	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: FUA, GDP

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	AA	2.74	2653/36190 (7.3%)	2.42	3123/56486 (5.5%)
2	AB	1.43	2/1935 (0.1%)	1.55	20/2609 (0.8%)
3	AC	1.49	3/1636 (0.2%)	1.59	25/2205 (1.1%)
4	AD	1.40	1/1733 (0.1%)	1.59	25/2318 (1.1%)
5	AE	1.48	1/1162 (0.1%)	1.54	9/1564 (0.6%)
6	AF	1.39	3/856 (0.4%)	1.69	15/1154 (1.3%)
7	AG	1.39	1/1276 (0.1%)	1.51	15/1709 (0.9%)
8	AH	1.48	2/1136 (0.2%)	1.67	20/1527 (1.3%)
9	AI	1.47	2/1029 (0.2%)	2.08	19/1379 (1.4%)
10	AJ	1.35	0/807	1.50	6/1085 (0.6%)
11	AK	1.40	1/900 (0.1%)	1.48	9/1213 (0.7%)
12	AL	1.45	0/986	1.56	9/1320 (0.7%)
13	AM	1.39	1/998 (0.1%)	1.64	17/1336 (1.3%)
14	AN	1.49	2/501 (0.4%)	1.71	9/664 (1.4%)
15	AO	1.35	0/745	1.59	13/992 (1.3%)
16	AP	1.34	1/716 (0.1%)	1.62	11/963 (1.1%)
17	AQ	1.45	2/836 (0.2%)	1.57	11/1117 (1.0%)
18	AR	1.40	0/579	1.59	7/768 (0.9%)
19	AS	1.28	0/642	1.48	5/865 (0.6%)
20	AT	1.31	0/765	1.52	12/1007 (1.2%)
21	AU	1.33	0/212	1.76	6/277 (2.2%)
22	AV	2.74	134/1832 (7.3%)	2.54	182/2855 (6.4%)
23	AX	2.60	15/257 (5.8%)	2.50	24/398 (6.0%)
24	AY	1.31	7/5312 (0.1%)	1.51	49/7193 (0.7%)
25	B0	1.27	0/671	1.52	11/892 (1.2%)
26	B1	1.37	2/738 (0.3%)	1.59	6/981 (0.6%)
27	B2	1.25	0/600	1.51	4/793 (0.5%)
28	B3	1.35	0/472	1.46	4/634 (0.6%)
29	B4	1.32	0/460	1.78	10/621 (1.6%)
30	B5	1.35	1/473 (0.2%)	1.48	3/639 (0.5%)
31	B6	1.49	3/440 (0.7%)	1.68	7/586 (1.2%)
32	B7	1.38	0/426	1.66	9/561 (1.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	B8	1.33	1/515 (0.2%)	1.56	6/679 (0.9%)
34	B9	1.37	0/310	1.59	6/407 (1.5%)
35	BA	2.69	4866/69972 (7.0%)	2.42	6058/109237 (5.5%)
36	BB	2.71	196/2853 (6.9%)	2.45	289/4451 (6.5%)
37	BC	1.35	0/1774	1.44	16/2391 (0.7%)
38	BD	1.38	3/2195 (0.1%)	1.59	25/2955 (0.8%)
39	BE	1.37	1/1596 (0.1%)	1.58	19/2153 (0.9%)
40	BF	1.40	2/1658 (0.1%)	1.63	27/2244 (1.2%)
41	BG	1.35	1/1499 (0.1%)	1.93	24/2016 (1.2%)
42	BH	1.35	4/1292 (0.3%)	1.51	12/1744 (0.7%)
43	BK	1.29	2/1044 (0.2%)	1.38	4/1416 (0.3%)
44	BL	1.10	0/478	1.50	2/640 (0.3%)
45	BN	1.33	2/1131 (0.2%)	1.57	13/1525 (0.9%)
46	BO	1.43	1/943 (0.1%)	1.50	11/1269 (0.9%)
47	BP	1.34	0/1131	1.64	13/1504 (0.9%)
48	BQ	1.38	2/1143 (0.2%)	1.52	11/1527 (0.7%)
49	BR	1.28	0/974	1.52	12/1302 (0.9%)
50	BS	1.31	1/778 (0.1%)	1.74	23/1036 (2.2%)
51	BT	1.37	1/1155 (0.1%)	1.78	25/1542 (1.6%)
52	BU	1.38	0/975	1.51	8/1297 (0.6%)
53	BV	1.34	2/790 (0.3%)	1.49	7/1057 (0.7%)
54	BW	1.31	1/907 (0.1%)	1.59	14/1216 (1.2%)
55	BX	1.39	0/739	1.46	5/993 (0.5%)
56	BY	1.24	1/823 (0.1%)	1.55	9/1098 (0.8%)
57	BZ	1.34	0/1499	1.53	18/2035 (0.9%)
All	All	2.36	7924/165495 (4.8%)	2.21	10352/246445 (4.2%)

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
1	AA	0	107
2	AB	0	5
3	AC	0	3
4	AD	0	3
5	AE	0	4
6	AF	0	6
7	AG	0	6
8	AH	0	4
9	AI	0	5

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Mol	Chain	#Chirality outliers	#Planarity outliers
10	AJ	0	2
11	AK	0	2
12	AL	0	3
13	AM	0	3
14	AN	0	2
15	AO	0	3
16	AP	0	6
17	AQ	0	3
18	AR	0	3
19	AS	0	3
20	AT	0	2
21	AU	0	3
22	AV	0	5
23	AX	0	1
24	AY	0	13
25	B0	0	1
26	B1	0	3
27	B2	0	6
28	B3	0	2
29	B4	0	3
30	B5	0	2
31	B6	0	3
32	B7	0	1
33	B8	0	2
34	B9	0	2
35	BA	1	152
36	BB	0	6
37	BC	0	6
38	BD	0	2
39	BE	0	3
40	BF	0	3
41	BG	0	5
42	BH	0	8
43	BK	0	3
45	BN	0	3
46	BO	0	3
47	BP	0	5
48	BQ	0	3
49	BR	0	2
50	BS	0	6
51	BT	0	6
52	BU	0	4

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Mol	Chain	#Chirality outliers	#Planarity outliers
53	BV	0	2
54	BW	0	4
55	BX	0	2
56	BY	0	3
57	BZ	0	4
All	All	1	457

The worst 5 of 7924 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AA	473	G	N7-C5	-17.52	1.28	1.39
1	AA	710	G	C8-N7	-15.43	1.21	1.30
1	AA	809	G	C8-N7	-15.17	1.21	1.30
1	AA	188	C	N1-C6	-15.00	1.28	1.37
1	AA	1311	G	C8-N7	-14.67	1.22	1.30

The worst 5 of 10352 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	BG	112	PRO	O-C-N	-40.65	57.66	122.70
9	AI	53	VAL	O-C-N	-36.52	64.27	122.70
9	AI	104	ARG	O-C-N	-30.37	74.11	122.70
41	BG	112	PRO	CA-C-N	21.56	164.63	117.20
26	B1	20	ARG	NE-CZ-NH2	-18.37	111.11	120.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
35	BA	1992	G	C3'

5 of 457 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	106	C	Sidechain
1	AA	108	G	Sidechain
1	AA	30	U	Sidechain
1	AA	5	U	Sidechain
1	AA	69	G	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	AA	32329	0	16041	1543	0
2	AB	1900	0	1951	244	0
3	AC	1612	0	1677	208	0
4	AD	1703	0	1767	205	0
5	AE	1146	0	1207	140	0
6	AF	843	0	857	95	0
7	AG	1257	0	1296	119	0
8	AH	1116	0	1177	110	0
9	AI	1010	0	1037	142	0
10	AJ	794	0	840	185	0
11	AK	885	0	904	92	0
12	AL	970	0	1057	144	0
13	AM	987	0	1059	139	0
14	AN	492	0	533	78	0
15	AO	734	0	771	74	0
16	AP	700	0	720	83	0
17	AQ	823	0	891	68	0
18	AR	574	0	644	77	0
19	AS	629	0	652	116	0
20	AT	763	0	861	112	0
21	AU	208	0	221	28	0
22	AV	1640	0	831	100	0
23	AX	230	0	114	17	0
24	AY	5214	0	5288	791	0
25	B0	662	0	688	91	0
26	B1	731	0	808	116	0
27	B2	598	0	653	94	0
28	B3	467	0	523	53	0
29	B4	450	0	449	93	0
30	B5	459	0	480	98	0
31	B6	433	0	461	148	0
32	B7	418	0	467	58	0
33	B8	507	0	576	103	0
34	B9	307	0	338	35	0
35	BA	62474	0	31032	3276	0
36	BB	2551	0	1281	164	0
37	BC	1742	0	1798	171	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	BD	2145	0	2234	305	0
39	BE	1563	0	1629	246	0
40	BF	1623	0	1677	283	0
41	BG	1474	0	1535	287	0
42	BH	1268	0	1337	232	0
43	BK	1025	0	1066	177	0
44	BL	477	0	509	14	0
45	BN	1104	0	1180	202	0
46	BO	933	0	996	124	0
47	BP	1114	0	1187	295	0
48	BQ	1122	0	1179	166	0
49	BR	960	0	1021	158	0
50	BS	770	0	832	168	0
51	BT	1141	0	1202	228	0
52	BU	958	0	1015	170	0
53	BV	779	0	852	148	0
54	BW	896	0	953	103	0
55	BX	725	0	778	93	0
56	BY	810	0	901	186	0
57	BZ	1467	0	1492	230	0
58	AY	37	0	47	12	0
59	AY	28	0	12	7	0
All	All	152777	0	105584	12183	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 47.

The worst 5 of 12183 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)
1:AA:509:A:H5'	1:AA:510:A:OP2	1.26	1.30
24:AY:496:LYS:HE2	24:AY:498:ILE:CD1	1.66	1.25
53:BV:15:GLU:HB3	53:BV:16:PRO:HD2	1.23	1.20
41:BG:63:ILE:HA	41:BG:143:GLU:HG3	1.22	1.19
35:BA:925:C:H2'	35:BA:926:A:H5''	1.24	1.18

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	
2	AB	232/256 (91%)	146 (63%)	55 (24%)	31 (13%)	0	4
3	AC	204/239 (85%)	129 (63%)	58 (28%)	17 (8%)	0	9
4	AD	206/209 (99%)	133 (65%)	52 (25%)	21 (10%)	0	7
5	AE	148/162 (91%)	116 (78%)	27 (18%)	5 (3%)	3	21
6	AF	99/101 (98%)	78 (79%)	15 (15%)	6 (6%)	1	13
7	AG	153/156 (98%)	107 (70%)	34 (22%)	12 (8%)	1	10
8	AH	136/138 (99%)	106 (78%)	23 (17%)	7 (5%)	1	15
9	AI	125/128 (98%)	84 (67%)	26 (21%)	15 (12%)	0	4
10	AJ	96/105 (91%)	64 (67%)	19 (20%)	13 (14%)	0	4
11	AK	117/129 (91%)	93 (80%)	18 (15%)	6 (5%)	1	15
12	AL	122/132 (92%)	81 (66%)	26 (21%)	15 (12%)	0	4
13	AM	122/126 (97%)	77 (63%)	25 (20%)	20 (16%)	0	2
14	AN	58/61 (95%)	48 (83%)	6 (10%)	4 (7%)	1	11
15	AO	86/89 (97%)	53 (62%)	25 (29%)	8 (9%)	0	8
16	AP	81/88 (92%)	58 (72%)	19 (24%)	4 (5%)	2	16
17	AQ	97/105 (92%)	76 (78%)	16 (16%)	5 (5%)	1	15
18	AR	68/88 (77%)	51 (75%)	11 (16%)	6 (9%)	0	9
19	AS	76/93 (82%)	39 (51%)	20 (26%)	17 (22%)	0	1
20	AT	97/106 (92%)	52 (54%)	30 (31%)	15 (16%)	0	3
21	AU	22/27 (82%)	14 (64%)	6 (27%)	2 (9%)	0	8
24	AY	662/691 (96%)	442 (67%)	135 (20%)	85 (13%)	0	4
25	B0	82/85 (96%)	64 (78%)	16 (20%)	2 (2%)	5	27
26	B1	91/98 (93%)	60 (66%)	20 (22%)	11 (12%)	0	4
27	B2	69/72 (96%)	34 (49%)	22 (32%)	13 (19%)	0	2
28	B3	57/60 (95%)	41 (72%)	12 (21%)	4 (7%)	1	11

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	B4	55/71 (78%)	25 (46%)	16 (29%)	14 (26%)	0	1
30	B5	57/60 (95%)	40 (70%)	6 (10%)	11 (19%)	0	2
31	B6	48/54 (89%)	22 (46%)	10 (21%)	16 (33%)	0	0
32	B7	46/49 (94%)	35 (76%)	9 (20%)	2 (4%)	2	17
33	B8	61/65 (94%)	35 (57%)	17 (28%)	9 (15%)	0	3
34	B9	35/37 (95%)	23 (66%)	8 (23%)	4 (11%)	0	5
37	BC	226/229 (99%)	173 (76%)	42 (19%)	11 (5%)	2	16
38	BD	273/276 (99%)	185 (68%)	55 (20%)	33 (12%)	0	4
39	BE	202/206 (98%)	121 (60%)	49 (24%)	32 (16%)	0	2
40	BF	205/210 (98%)	134 (65%)	44 (22%)	27 (13%)	0	4
41	BG	179/182 (98%)	113 (63%)	44 (25%)	22 (12%)	0	4
42	BH	164/180 (91%)	89 (54%)	37 (23%)	38 (23%)	0	1
43	BK	137/147 (93%)	89 (65%)	36 (26%)	12 (9%)	0	9
44	BL	65/121 (54%)	56 (86%)	9 (14%)	0	100	100
45	BN	136/140 (97%)	89 (65%)	31 (23%)	16 (12%)	0	4
46	BO	120/122 (98%)	94 (78%)	17 (14%)	9 (8%)	1	10
47	BP	144/150 (96%)	75 (52%)	44 (31%)	25 (17%)	0	2
48	BQ	139/141 (99%)	104 (75%)	28 (20%)	7 (5%)	1	16
49	BR	115/118 (98%)	79 (69%)	24 (21%)	12 (10%)	0	6
50	BS	96/112 (86%)	43 (45%)	34 (35%)	19 (20%)	0	2
51	BT	135/146 (92%)	76 (56%)	34 (25%)	25 (18%)	0	2
52	BU	115/118 (98%)	70 (61%)	33 (29%)	12 (10%)	0	6
53	BV	99/101 (98%)	67 (68%)	15 (15%)	17 (17%)	0	2
54	BW	111/113 (98%)	80 (72%)	18 (16%)	13 (12%)	0	4
55	BX	90/96 (94%)	62 (69%)	23 (26%)	5 (6%)	1	14
56	BY	104/110 (94%)	45 (43%)	35 (34%)	24 (23%)	0	1
57	BZ	182/206 (88%)	108 (59%)	41 (22%)	33 (18%)	0	2
All	All	6645/7104 (94%)	4378 (66%)	1475 (22%)	792 (12%)	1	4

5 of 792 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	13	ALA

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Mol	Chain	Res	Type
2	AB	20	GLU
2	AB	95	GLN
2	AB	190	THR
2	AB	195	ASP

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	
2	AB	202/220 (92%)	178 (88%)	24 (12%)	4	16
3	AC	160/188 (85%)	133 (83%)	27 (17%)	1	9
4	AD	180/181 (99%)	158 (88%)	22 (12%)	4	15
5	AE	115/123 (94%)	101 (88%)	14 (12%)	4	15
6	AF	90/90 (100%)	80 (89%)	10 (11%)	5	17
7	AG	126/127 (99%)	113 (90%)	13 (10%)	6	20
8	AH	119/119 (100%)	106 (89%)	13 (11%)	5	18
9	AI	98/99 (99%)	88 (90%)	10 (10%)	6	20
10	AJ	88/92 (96%)	75 (85%)	13 (15%)	2	12
11	AK	90/99 (91%)	82 (91%)	8 (9%)	8	25
12	AL	104/109 (95%)	93 (89%)	11 (11%)	5	19
13	AM	99/101 (98%)	86 (87%)	13 (13%)	3	14
14	AN	49/50 (98%)	42 (86%)	7 (14%)	2	12
15	AO	79/80 (99%)	70 (89%)	9 (11%)	4	16
16	AP	72/74 (97%)	69 (96%)	3 (4%)	25	46
17	AQ	94/97 (97%)	86 (92%)	8 (8%)	8	27
18	AR	61/77 (79%)	58 (95%)	3 (5%)	21	42
19	AS	69/80 (86%)	59 (86%)	10 (14%)	2	12
20	AT	76/82 (93%)	66 (87%)	10 (13%)	3	14
21	AU	19/22 (86%)	19 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	AY	563/582 (97%)	481 (85%)	82 (15%)	2	12
25	B0	66/67 (98%)	56 (85%)	10 (15%)	2	11
26	B1	78/83 (94%)	64 (82%)	14 (18%)	1	8
27	B2	66/67 (98%)	58 (88%)	8 (12%)	4	15
28	B3	51/52 (98%)	47 (92%)	4 (8%)	10	29
29	B4	51/63 (81%)	36 (71%)	15 (29%)	0	2
30	B5	51/52 (98%)	45 (88%)	6 (12%)	4	16
31	B6	49/52 (94%)	37 (76%)	12 (24%)	0	3
32	B7	41/42 (98%)	34 (83%)	7 (17%)	1	9
33	B8	53/55 (96%)	46 (87%)	7 (13%)	3	14
34	B9	34/34 (100%)	28 (82%)	6 (18%)	1	8
37	BC	180/181 (99%)	162 (90%)	18 (10%)	6	20
38	BD	217/218 (100%)	178 (82%)	39 (18%)	1	8
39	BE	165/166 (99%)	141 (86%)	24 (14%)	2	12
40	BF	165/166 (99%)	154 (93%)	11 (7%)	13	34
41	BG	155/156 (99%)	129 (83%)	26 (17%)	1	9
42	BH	136/148 (92%)	118 (87%)	18 (13%)	3	14
43	BK	104/111 (94%)	88 (85%)	16 (15%)	2	11
44	BL	46/85 (54%)	41 (89%)	5 (11%)	5	18
45	BN	117/119 (98%)	95 (81%)	22 (19%)	1	7
46	BO	100/100 (100%)	92 (92%)	8 (8%)	10	29
47	BP	112/116 (97%)	86 (77%)	26 (23%)	0	4
48	BQ	111/111 (100%)	94 (85%)	17 (15%)	2	11
49	BR	100/101 (99%)	89 (89%)	11 (11%)	5	18
50	BS	77/88 (88%)	66 (86%)	11 (14%)	2	12
51	BT	120/127 (94%)	95 (79%)	25 (21%)	1	6
52	BU	92/94 (98%)	82 (89%)	10 (11%)	5	18
53	BV	82/82 (100%)	70 (85%)	12 (15%)	2	12
54	BW	91/92 (99%)	78 (86%)	13 (14%)	2	12
55	BX	74/78 (95%)	63 (85%)	11 (15%)	2	11
56	BY	87/91 (96%)	75 (86%)	12 (14%)	3	13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
57	BZ	162/179 (90%)	134 (83%)	28 (17%)	1 9
All	All	5586/5868 (95%)	4824 (86%)	762 (14%)	5 13

5 of 762 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	BE	61	ARG
45	BN	96	GLU
39	BE	192	ASN
39	BE	54	GLN
42	BH	53	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 177 such sidechains are listed below:

Mol	Chain	Res	Type
39	BE	129	HIS
48	BQ	12	GLN
39	BE	192	ASN
43	BK	30	HIS
50	BS	38	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1503/1522 (98%)	277 (18%)	47 (3%)
22	AV	76/77 (98%)	17 (22%)	0
23	AX	10/11 (90%)	5 (50%)	0
35	BA	2900/2915 (99%)	633 (21%)	77 (2%)
36	BB	118/122 (96%)	27 (22%)	2 (1%)
All	All	4607/4647 (99%)	959 (20%)	126 (2%)

5 of 959 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	9	G
1	AA	31	G
1	AA	32	A
1	AA	33	A
1	AA	39	G

5 of 126 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
35	BA	332	A
35	BA	2425	A
35	BA	1020	A
35	BA	2422	A
35	BA	2779	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
58	FUA	AY	701	-	39,40,40	2.10	12 (30%)	49,64,64	1.79	11 (22%)
59	GDP	AY	702	-	24,30,30	1.57	6 (25%)	30,47,47	1.71	7 (23%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
58	FUA	AY	701	-	-	5/15/92/92	0/4/4/4
59	GDP	AY	702	-	-	2/12/32/32	0/3/3/3

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	AY	701	FUA	C23-C22	-5.40	1.37	1.51
58	AY	701	FUA	C23-C24	-4.19	1.39	1.53
59	AY	702	GDP	C5-C6	-4.16	1.39	1.47
58	AY	701	FUA	C15-C14	-3.97	1.46	1.54
58	AY	701	FUA	C29-C22	3.88	1.53	1.47

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	AY	701	FUA	C8-C9-C10	-6.55	109.63	116.34
58	AY	701	FUA	C6-C5-C10	-4.41	106.16	111.65
59	AY	702	GDP	PA-O3A-PB	-4.24	118.26	132.83
59	AY	702	GDP	C2-N1-C6	-3.60	118.46	125.10
58	AY	701	FUA	O6-C3-C2	-3.46	101.66	109.96

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
58	AY	701	FUA	C13-C17-C22-C29
58	AY	701	FUA	C17-C22-C23-C24
58	AY	701	FUA	C29-C22-C23-C24
59	AY	702	GDP	C5'-O5'-PA-O3A
59	AY	702	GDP	C5'-O5'-PA-O1A

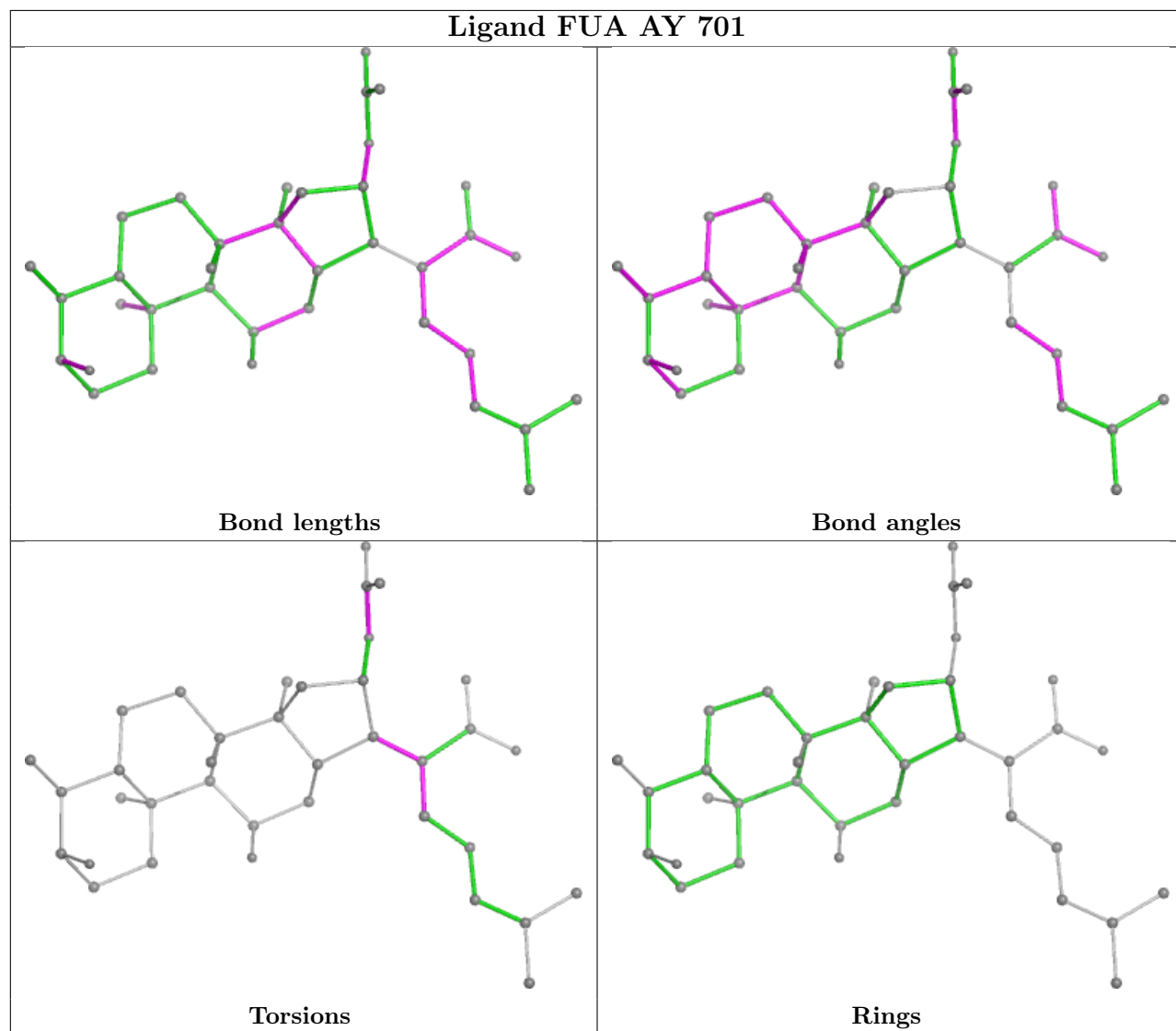
There are no ring outliers.

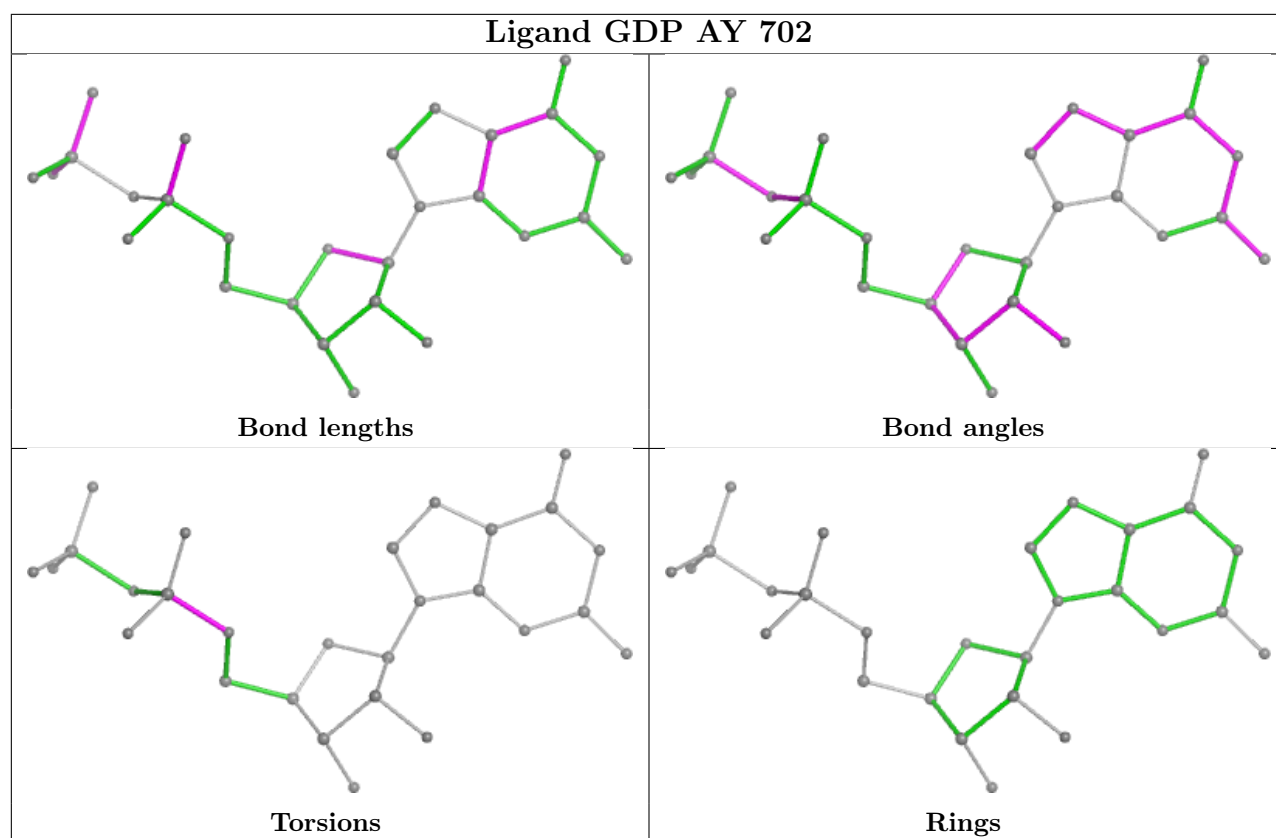
2 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
58	AY	701	FUA	12	0
59	AY	702	GDP	7	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and

any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

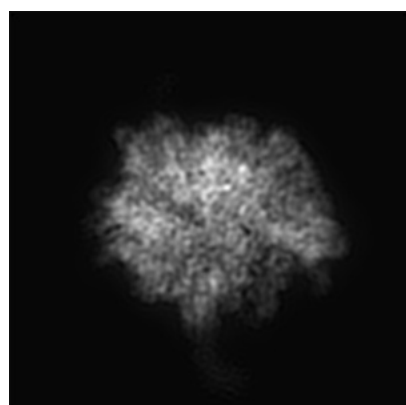
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1798. These allow visual inspection of the internal detail of the map and identification of artifacts.

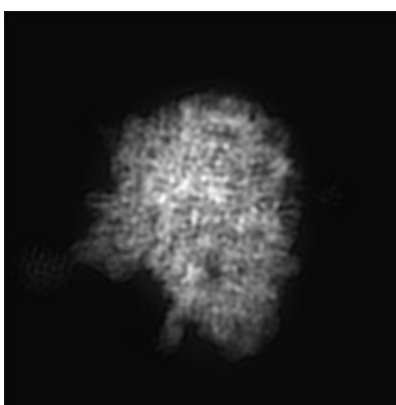
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

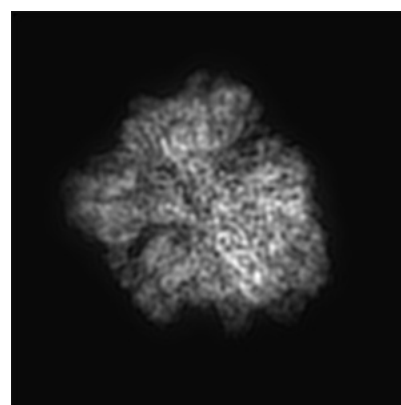
6.1.1 Primary map



X



Y

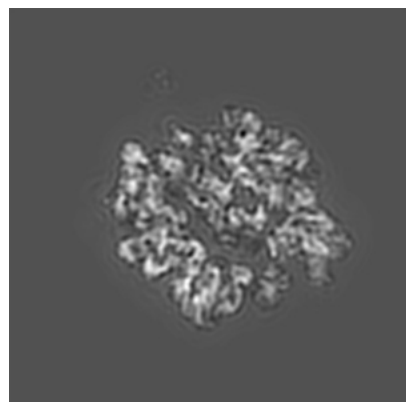


Z

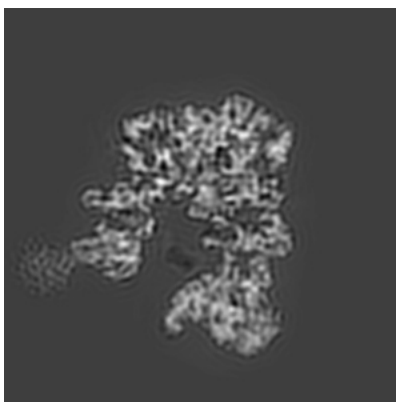
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

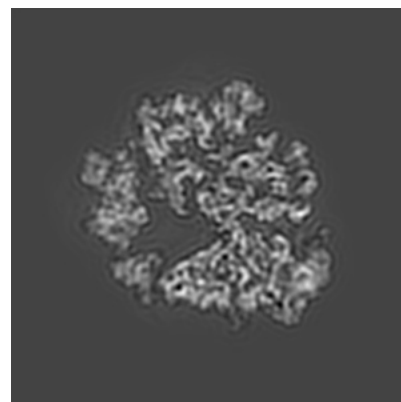
6.2.1 Primary map



X Index: 150



Y Index: 150

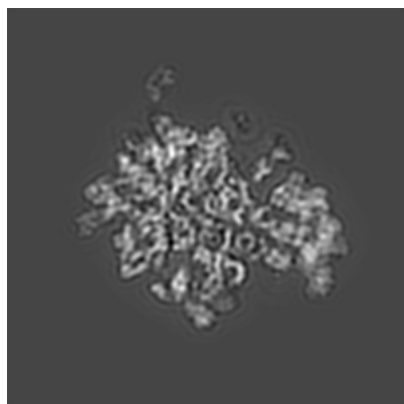


Z Index: 150

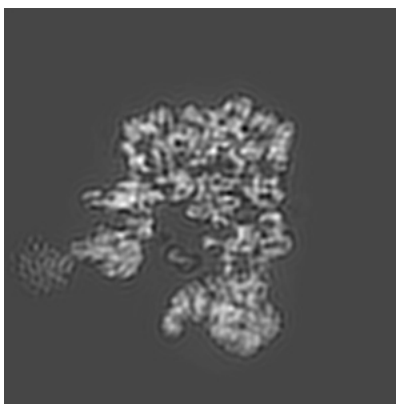
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

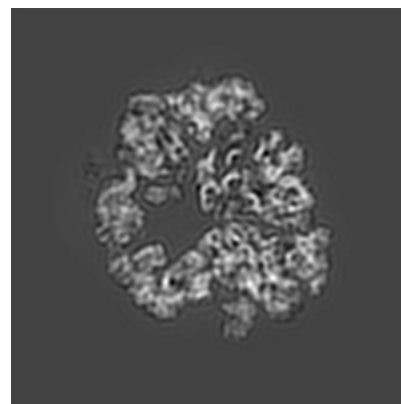
6.3.1 Primary map



X Index: 162



Y Index: 152

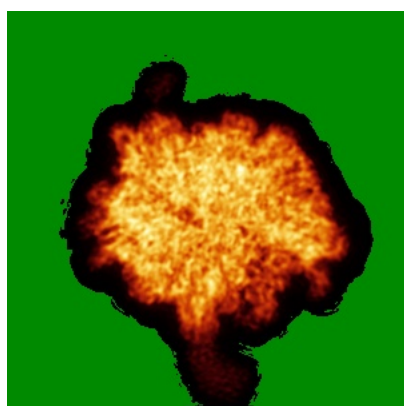


Z Index: 142

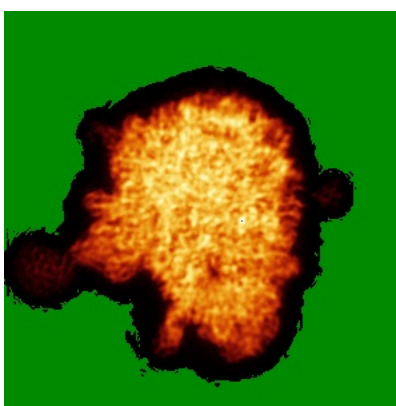
The images above show the largest variance slices of the map in three orthogonal directions.

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

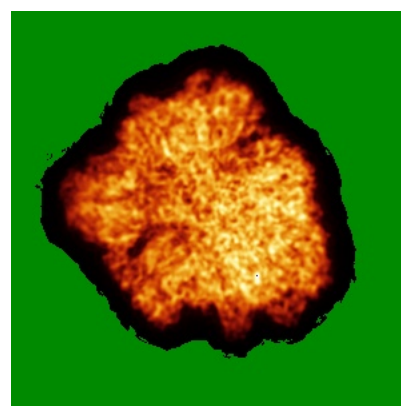
6.4.1 Primary map



X



Y



Z

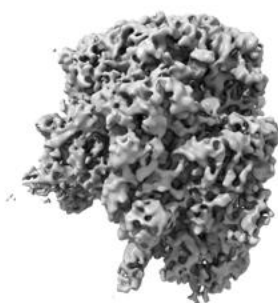
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 3000.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

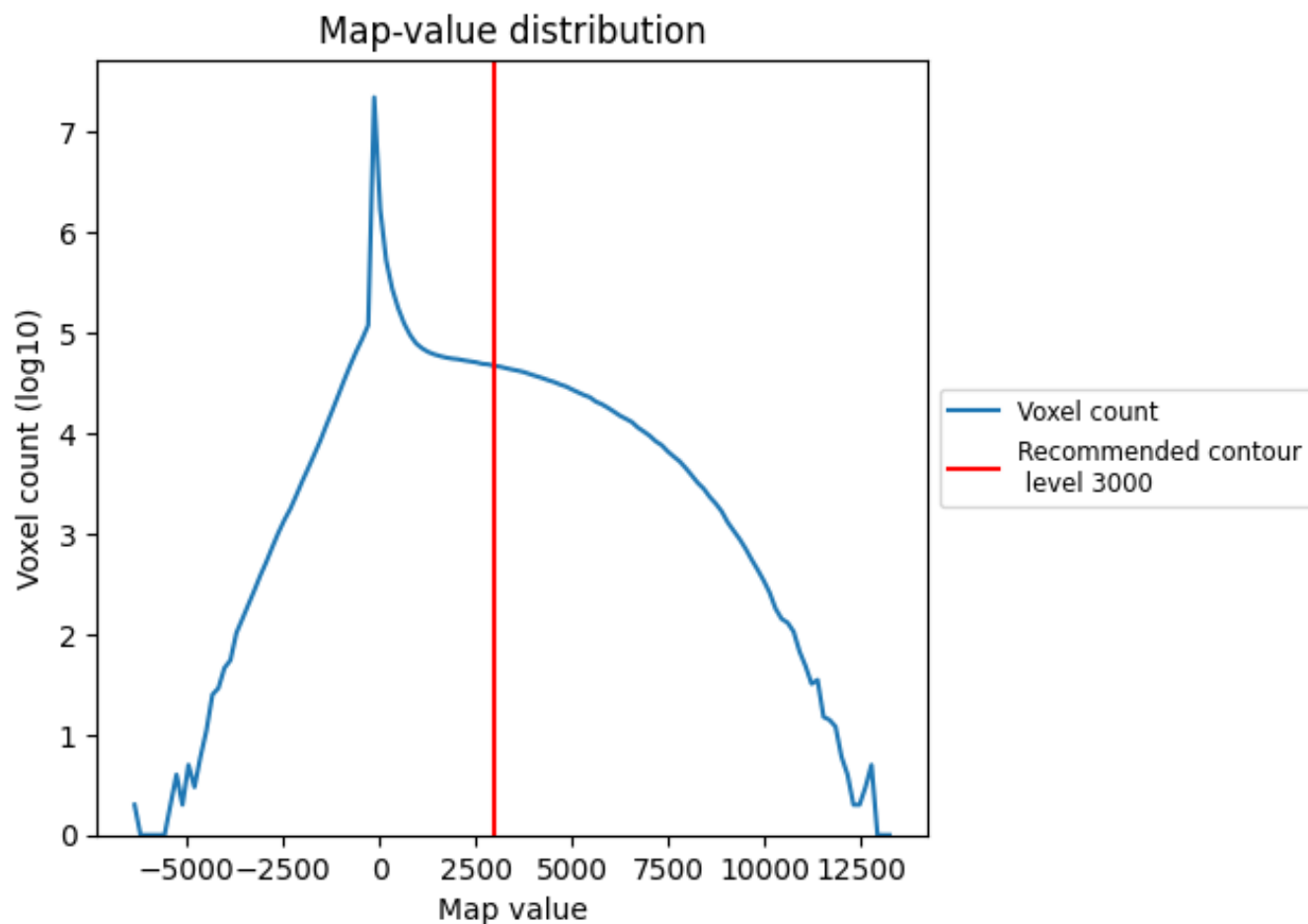
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

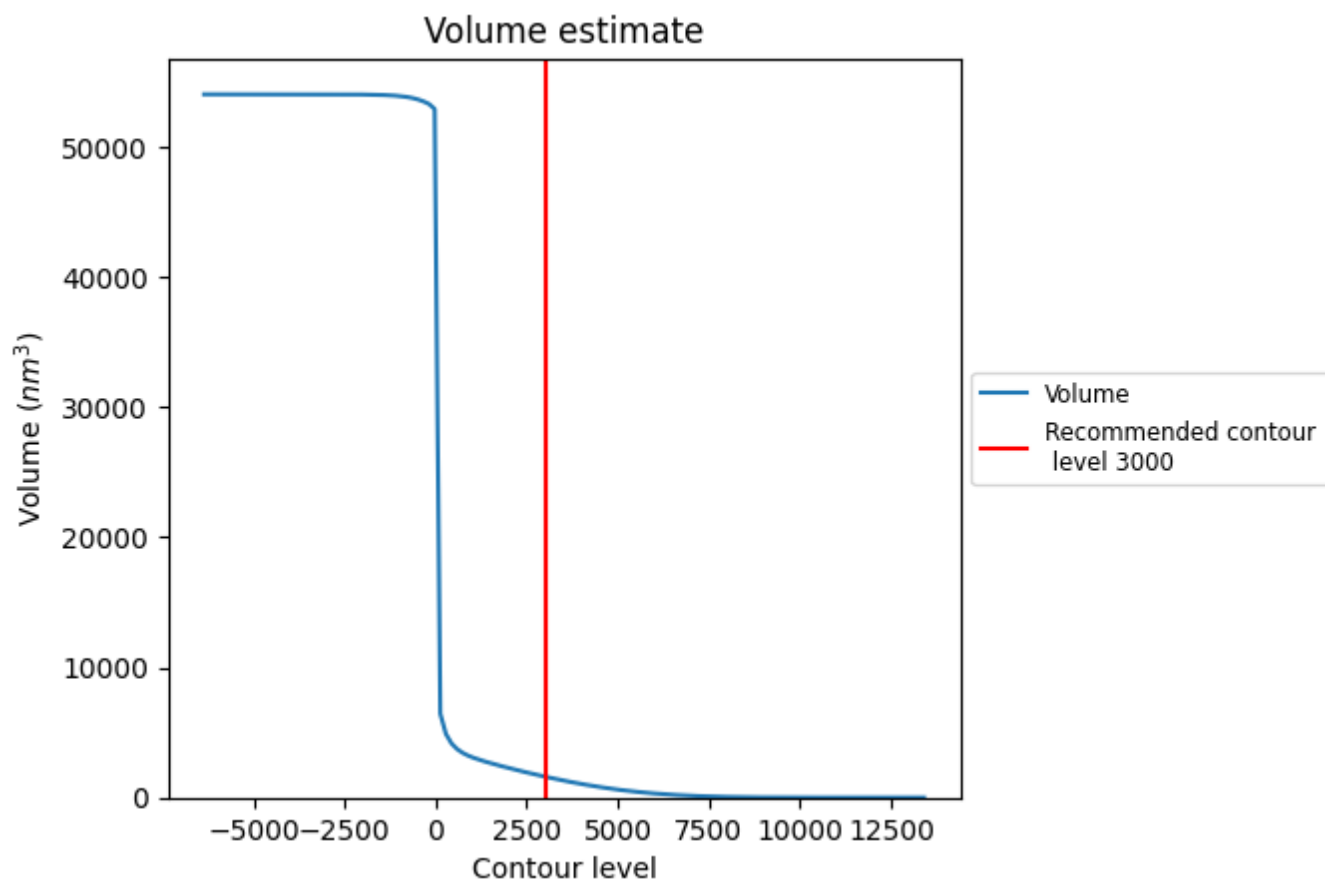
This section contains the results of statistical analysis of the map.

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.

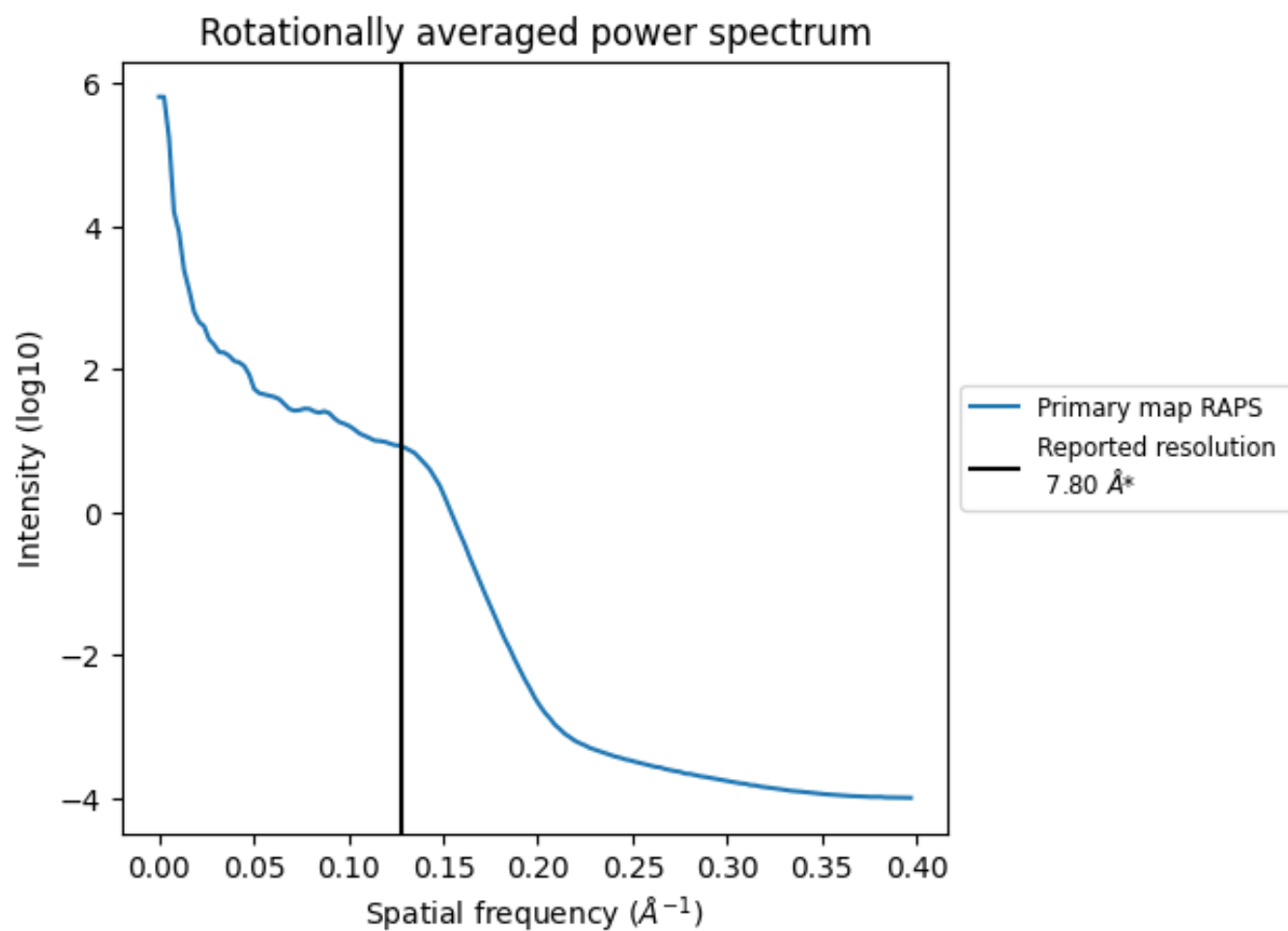
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1609 nm³; this corresponds to an approximate mass of 1453 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 0.128 Å⁻¹

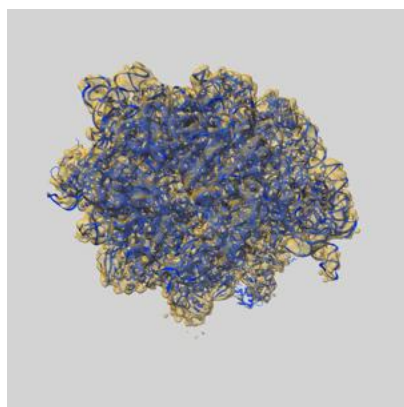
8 Fourier-Shell correlation

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

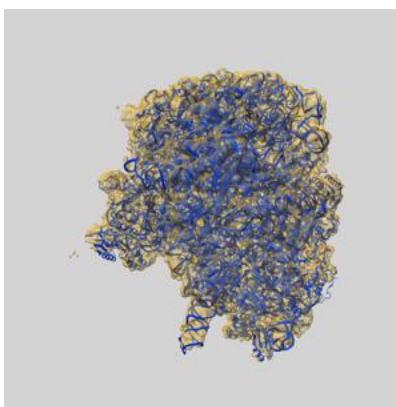
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-1798 and PDB model 4V5M. Per-residue inclusion information can be found in section 3 on page 16.

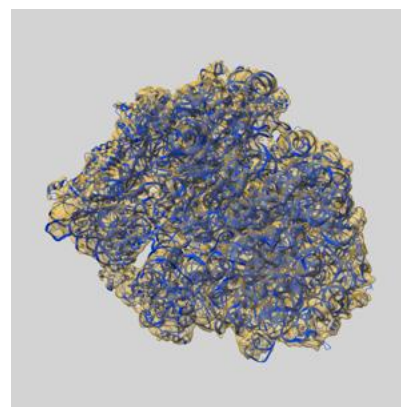
9.1 Map-model overlay [i](#)



X



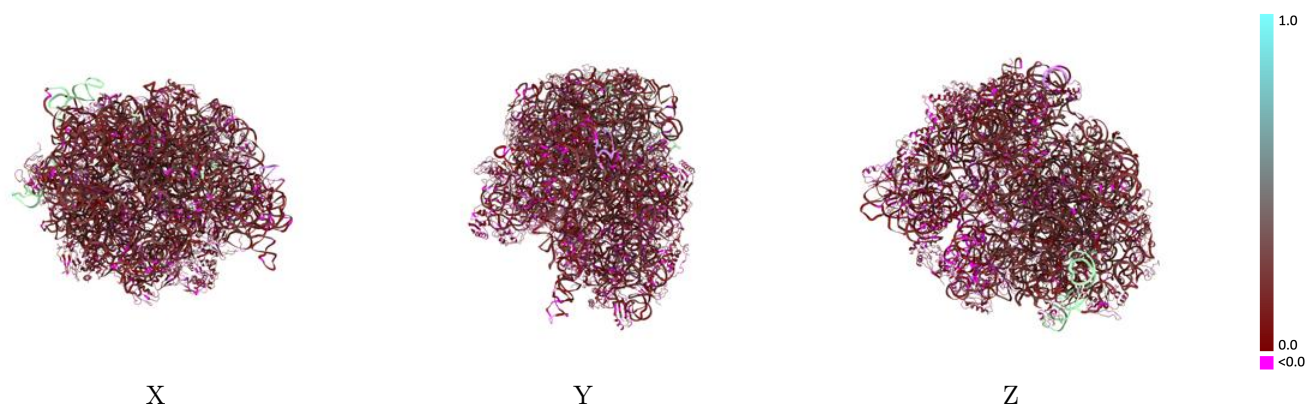
Y



Z

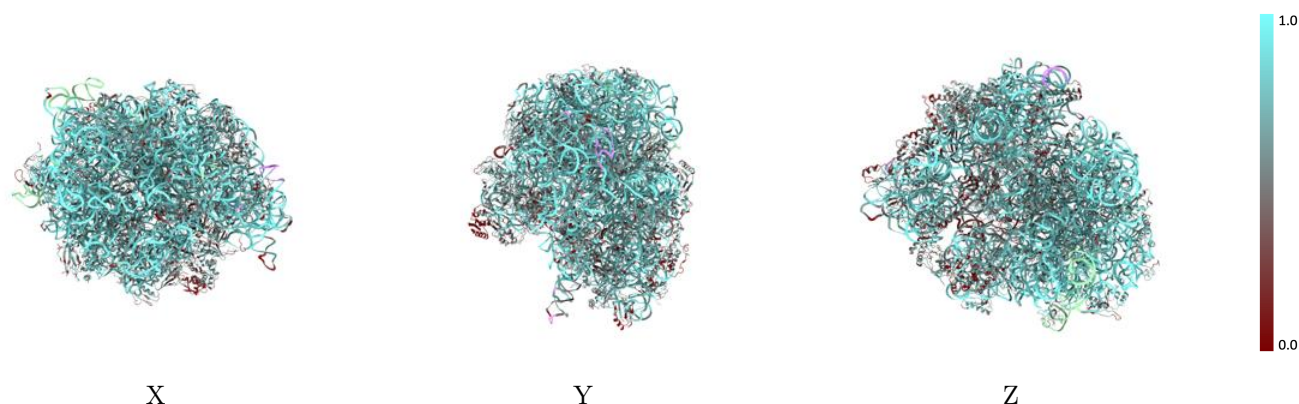
The images above show the 3D surface view of the map at the recommended contour level 3000.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



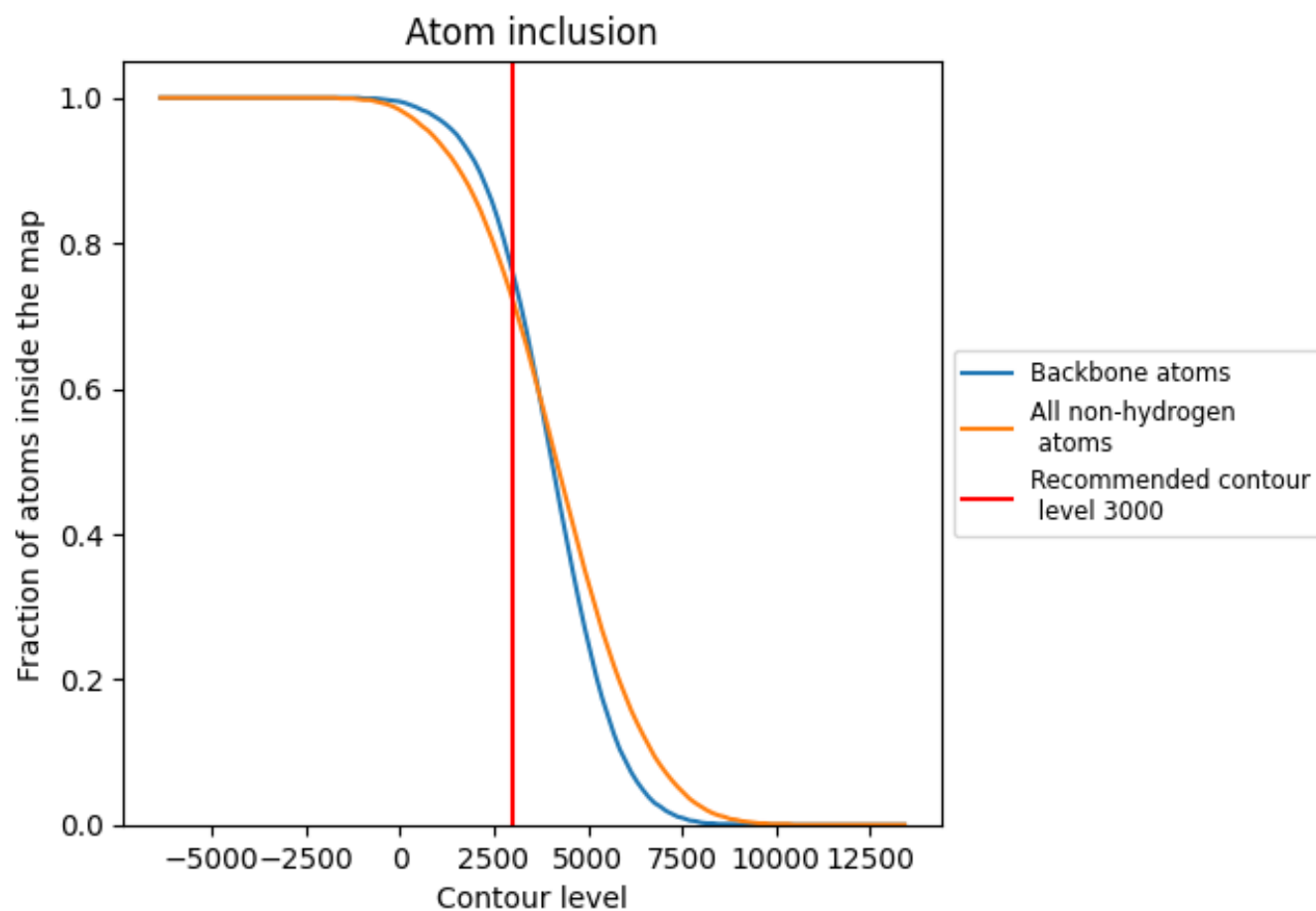
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3000).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 72% 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 (3000) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7220	 0.1590
AA	 0.8290	 0.1700
AB	 0.4670	 0.1320
AC	 0.5500	 0.1360
AD	 0.5930	 0.1270
AE	 0.5820	 0.1350
AF	 0.5400	 0.1510
AG	 0.4980	 0.1130
AH	 0.5840	 0.1400
AI	 0.5860	 0.0960
AJ	 0.4570	 0.0840
AK	 0.5290	 0.1310
AL	 0.4580	 0.1200
AM	 0.4250	 0.0790
AN	 0.5970	 0.1230
AO	 0.5990	 0.1410
AP	 0.6300	 0.1120
AQ	 0.5510	 0.1200
AR	 0.5230	 0.1210
AS	 0.5220	 0.0840
AT	 0.5600	 0.1220
AU	 0.4760	 0.0650
AV	 0.6490	 0.1350
AX	 0.2700	 0.0910
AY	 0.4490	 0.1190
B0	 0.5200	 0.0990
B1	 0.5770	 0.1340
B2	 0.6330	 0.1500
B3	 0.6040	 0.1520
B4	 0.3880	 0.1080
B5	 0.6000	 0.1540
B6	 0.5940	 0.0930
B7	 0.6160	 0.1230
B8	 0.5530	 0.1240
B9	 0.2820	 0.0620



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Chain	Atom inclusion	Q-score
BA	 0.8410	 0.1880
BB	 0.8680	 0.1790
BC	 0.2520	 0.0480
BD	 0.5130	 0.1240
BE	 0.5330	 0.1270
BF	 0.6150	 0.1380
BG	 0.5160	 0.0980
BH	 0.5730	 0.1330
BK	 0.3590	 0.0890
BL	 0.0590	 0.0440
BN	 0.5870	 0.1450
BO	 0.3680	 0.1210
BP	 0.5850	 0.1430
BQ	 0.2790	 0.0930
BR	 0.6000	 0.1370
BS	 0.6620	 0.1480
BT	 0.4780	 0.1260
BU	 0.6310	 0.1220
BV	 0.5540	 0.1420
BW	 0.6050	 0.1280
BX	 0.6140	 0.1420
BY	 0.4970	 0.1340
BZ	 0.4570	 0.0750