



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 05:55 PM UTC

PDB ID : 4V69 / pdb_00004v69
EMDB ID : EMD-5036
Title : Ternary complex-bound E.coli 70S ribosome.
Authors : Villa, E.; Sengupta, J.; Trabuco, L.G.; LeBarron, J.; Baxter, W.T.; Shaikh, T.R.; Grassucci, R.A.; Nissen, P.; Ehrenberg, M.; Schulten, K.; Frank, J.
Deposited on : 2008-12-11
Resolution : 6.70 Å(reported)
Based on initial models : 2J00, 2I2U, 2I2V, 1OB2

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

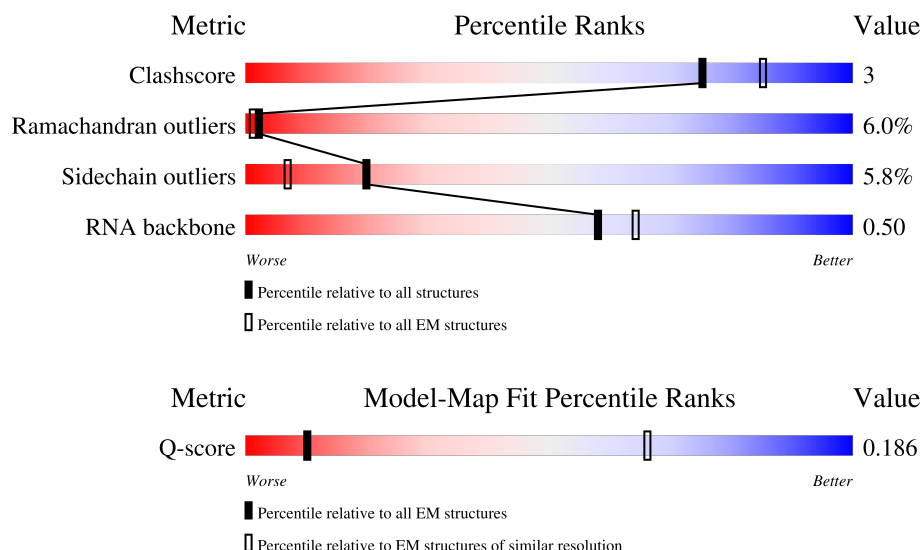
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 6.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	523 (6.20 - 7.20)

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

Mol	Chain	Length	Quality of chain
1	AJ	98	38% 39% 49% 9% .
2	AK	117	34% 42% 53% . .
3	AL	123	37% 39% 51% 9% .

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Mol	Chain	Length	Quality of chain
4	AM	113	
5	AN	96	
6	AO	88	
7	AP	80	
8	AQ	80	
9	AR	55	
10	AS	79	
11	AT	85	
12	AU	51	
13	AB	218	
14	AC	206	
15	AD	205	
16	AE	150	
17	AF	100	
18	AG	150	
19	AH	129	
20	AI	127	
21	AA	1530	
22	AY	76	
23	AW	76	
24	AX	11	
25	AZ	393	
26	AV	77	
27	B5	234	
28	BI	141	

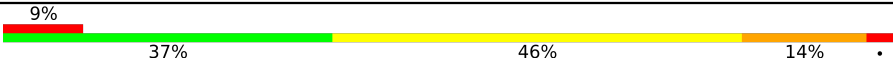
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Mol	Chain	Length	Quality of chain
29	BJ	142	
30	BK	121	
31	BL	143	
32	BM	136	
33	BN	120	
34	BO	116	
35	BP	114	
36	BQ	117	
37	BR	103	
38	BS	110	
39	BT	93	
40	BU	102	
41	BV	94	
42	BW	79	
43	BX	77	
44	BY	63	
45	BC	271	
46	BZ	58	
47	B0	56	
48	B1	50	
49	B2	46	
50	B3	64	
51	B4	38	
52	BD	209	
53	BE	201	

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Mol	Chain	Length	Quality of chain
54	BF	178	
55	BG	176	
56	BH	149	
57	BB	2903	
58	BA	117	

2 Entry composition [i](#)

There are 59 unique types of molecules in this entry. The entry contains 152250 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 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AJ	98	Total	C	N	O	S	0	0
			787	493	150	143	1		

- Molecule 2 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AK	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 3 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AL	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 4 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AM	113	Total	C	N	O	S	0	0
			877	541	177	156	3		

- Molecule 5 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AN	96	Total	C	N	O	S	0	0
			774	483	160	128	3		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AN	?	-	SER	deletion	UNP P0AG59
AN	?	-	ASP	deletion	UNP P0AG59
AN	?	-	GLU	deletion	UNP P0AG59

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Chain	Residue	Modelled	Actual	Comment	Reference
AN	?	-	ASP	deletion	UNP P0AG59

- Molecule 6 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AO	88	Total	C	N	O	S	0	0
			716	440	146	129	1		

- Molecule 7 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AP	80	Total	C	N	O	S	0	0
			639	400	126	112	1		

- Molecule 8 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AQ	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 9 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	AR	55	Total	C	N	O	0	0
			456	288	86	82		

- Molecule 10 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AS	79	Total	C	N	O	S	0	0
			638	408	120	108	2		

- Molecule 11 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AT	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 12 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AU	51	Total	C	N	O	S	0	0
			426	265	86	74	1		

- Molecule 13 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AB	218	Total	C	N	O	S	0	0
			1705	1081	305	312	7		

- Molecule 14 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AC	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 15 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AD	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 16 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AE	150	Total	C	N	O	S	0	0
			1106	687	211	202	6		

- Molecule 17 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AF	100	Total	C	N	O	S	0	0
			818	515	148	149	6		

- Molecule 18 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AG	150	Total	C	N	O	S	0	0
			1175	730	226	215	4		

- Molecule 19 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AH	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 20 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AI	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 21 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AA	1530	Total	C	N	O	P	0	0
			32832	14642	6024	10636	1530		

- Molecule 22 is a RNA chain called A/T-site tRNA Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AY	76	Total	C	N	O	P	0	0
			1622	725	293	529	75		

- Molecule 23 is a RNA chain called P-site tRNA fMet (Unmodified bases except for Thymine 54).

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AW	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		

- Molecule 24 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AX	11	Total	C	N	O	P	0	0
			232	106	44	72	10		

- Molecule 25 is a protein called Elongation factor Tu.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AZ	393	Total	C	N	O	S	0	0
			3035	1918	523	581	13		

- Molecule 26 is a RNA chain called E-site tRNA Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AV	77	Total	C	N	O	P	0	0
			1645	733	297	538	77		

- Molecule 27 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	B5	234	Total	C	N	O	S	0	0
			1733	1081	315	330	7		

- Molecule 28 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BI	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 29 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BJ	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 30 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BK	121	Total	C	N	O	S	0	0
			931	582	179	165	5		

- Molecule 31 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BL	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 32 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BM	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 33 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BN	120	Total	C	N	O	S	0	0
			961	593	196	167	5		

- Molecule 34 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BO	116	Total	C	N	O		0	0
			892	552	178	162			

- Molecule 35 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BP	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 36 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BQ	117	Total	C	N	O		0	0
			947	604	192	151			

- Molecule 37 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BR	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 38 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BS	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 39 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BT	93	Total	C	N	O	S	0	0
			739	466	139	132	2		

- Molecule 40 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	BU	102	Total	C	N	O		
			780	492	146	142	0	0

- Molecule 41 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	BV	94	Total	C	N	O	S	
			753	479	137	134	3	0

- Molecule 42 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	BW	79	Total	C	N	O	S	
			596	367	120	108	1	0

- Molecule 43 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	BX	77	Total	C	N	O	S	
			625	388	129	106	2	0

- Molecule 44 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	BY	63	Total	C	N	O	S	
			509	313	99	95	2	0

- Molecule 45 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	BC	271	Total	C	N	O	S	
			2083	1288	423	365	7	0

- Molecule 46 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	BZ	58	Total	C	N	O	S	
			449	281	87	79	2	0

- Molecule 47 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	B0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 48 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	B1	50	Total	C	N	O		0	0
			410	263	75	72			

- Molecule 49 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	B2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 50 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	B3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 51 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	B4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 52 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BD	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 53 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BE	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 54 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BF	178	Total	C	N	O	S	0	0
			1420	905	251	258	6		

- Molecule 55 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	BG	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 56 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BH	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

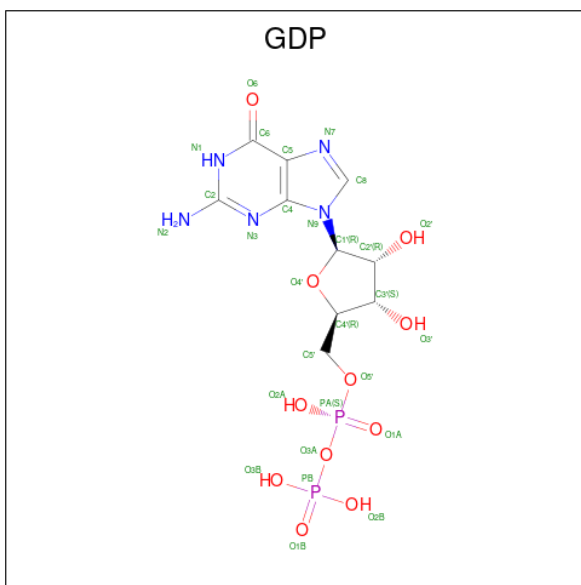
- Molecule 57 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	BB	2903	Total	C	N	O	P	0	0
			62321	27801	11467	20150	2903		

- Molecule 58 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	BA	117	Total	C	N	O	P	0	0
			2508	1116	459	816	117		

- Molecule 59 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).

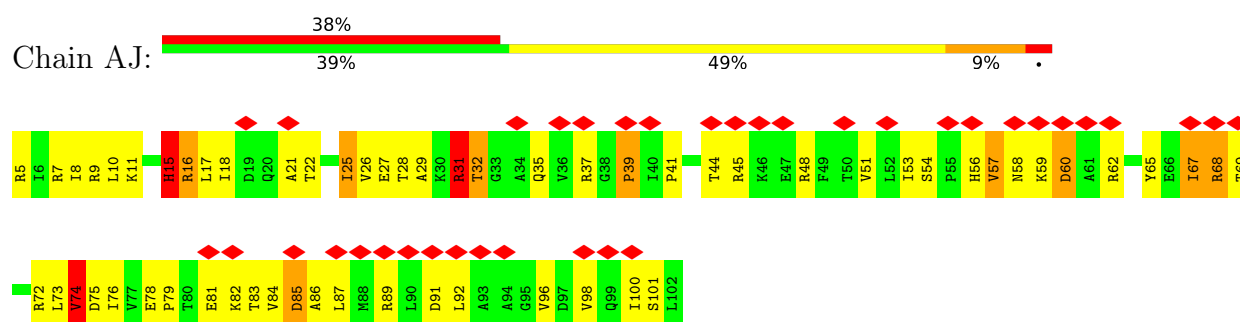


Mol	Chain	Residues	Atoms					AltConf
59	AZ	1	Total	C	N	O	P	0
			28	10	5	11	2	

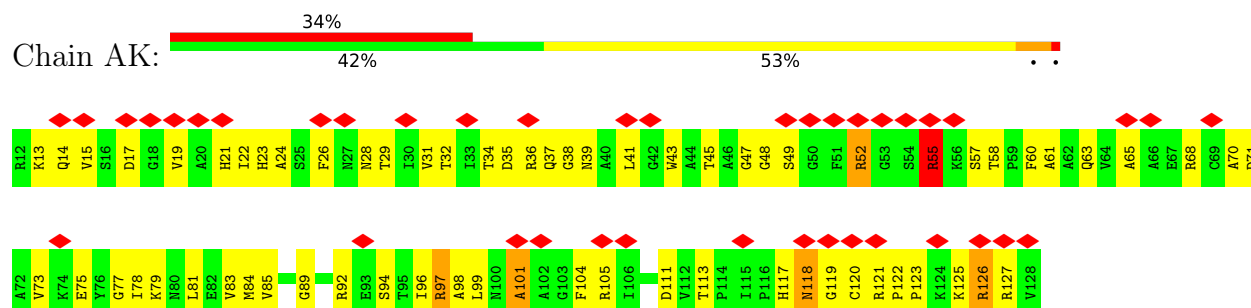
3 Residue-property plots [i](#)

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.

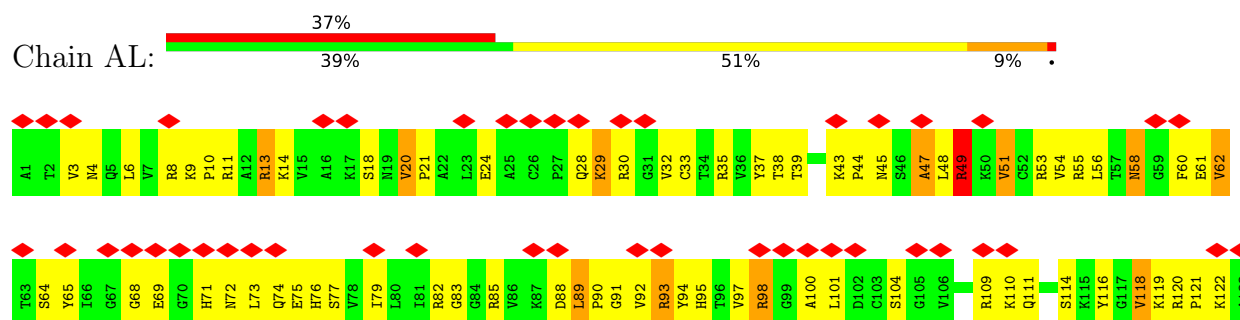
• Molecule 1: 30S ribosomal protein S10



• Molecule 2: 30S ribosomal protein S11

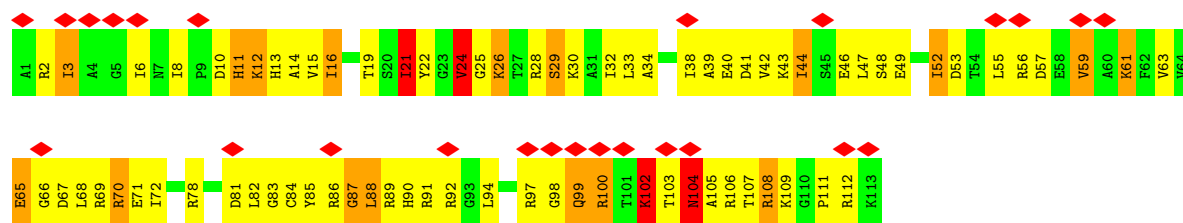


• Molecule 3: 30S ribosomal protein S12

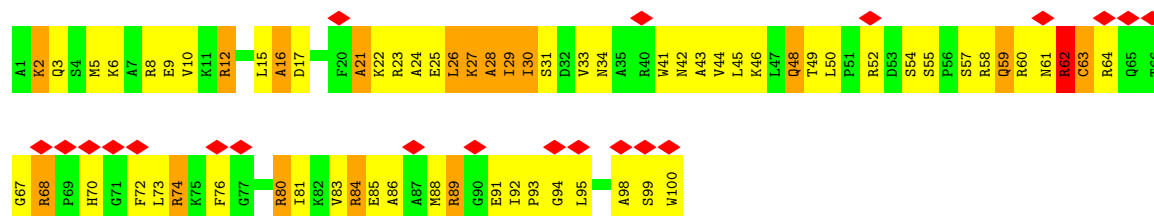


• Molecule 4: 30S ribosomal protein S13

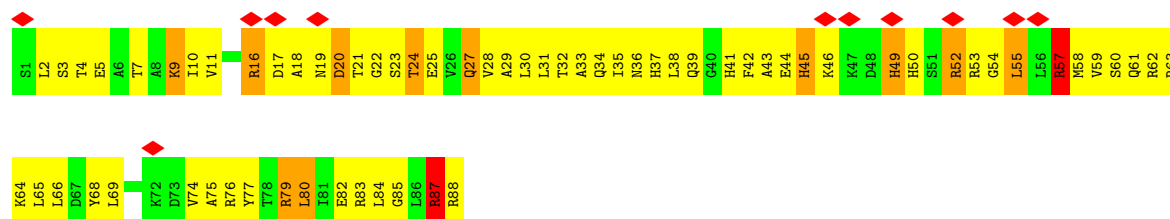




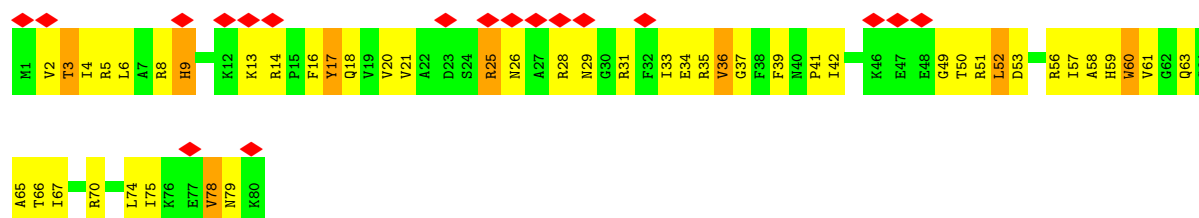
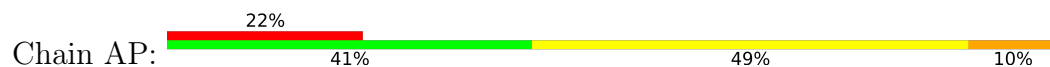
• Molecule 5: 30S ribosomal protein S14



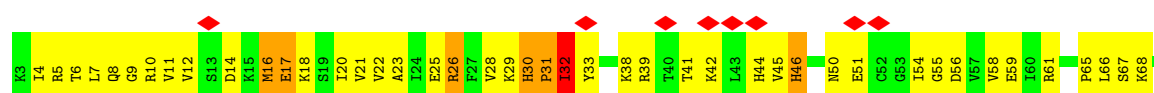
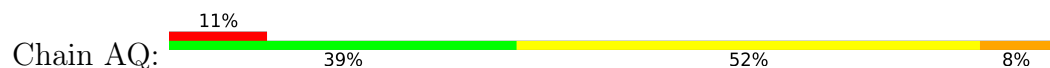
• Molecule 6: 30S ribosomal protein S15



• Molecule 7: 30S ribosomal protein S16

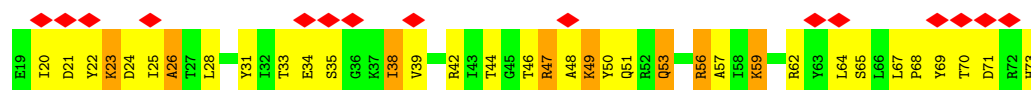


• Molecule 8: 30S ribosomal protein S17

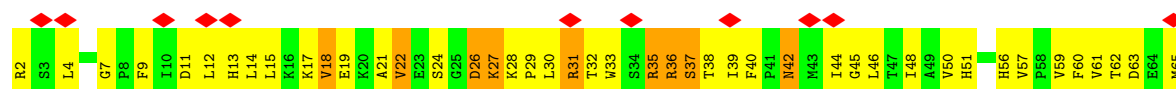




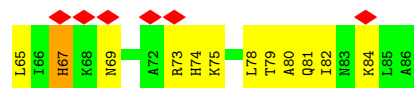
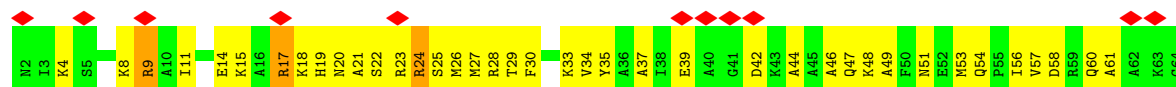
• Molecule 9: 30S ribosomal protein S18



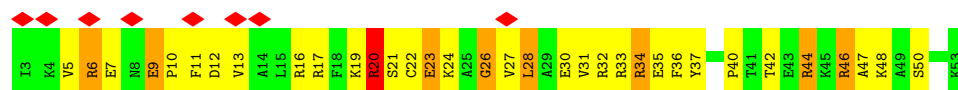
• Molecule 10: 30S ribosomal protein S19



• Molecule 11: 30S ribosomal protein S20

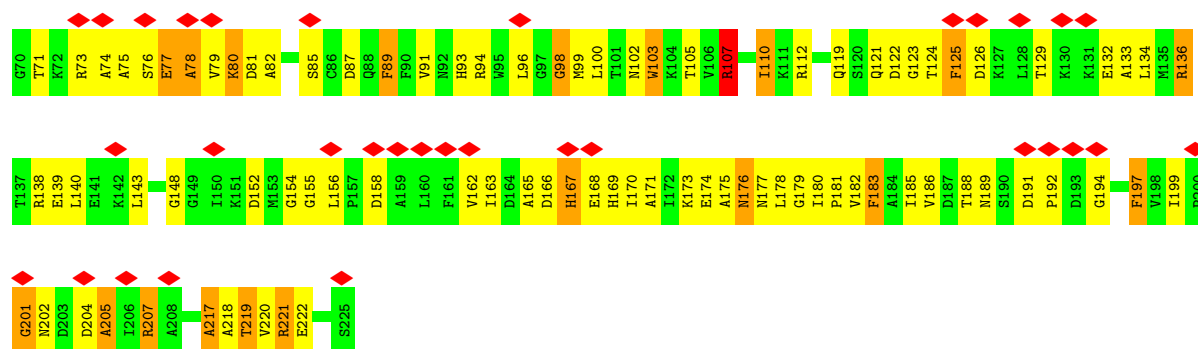


• Molecule 12: 30S ribosomal protein S21

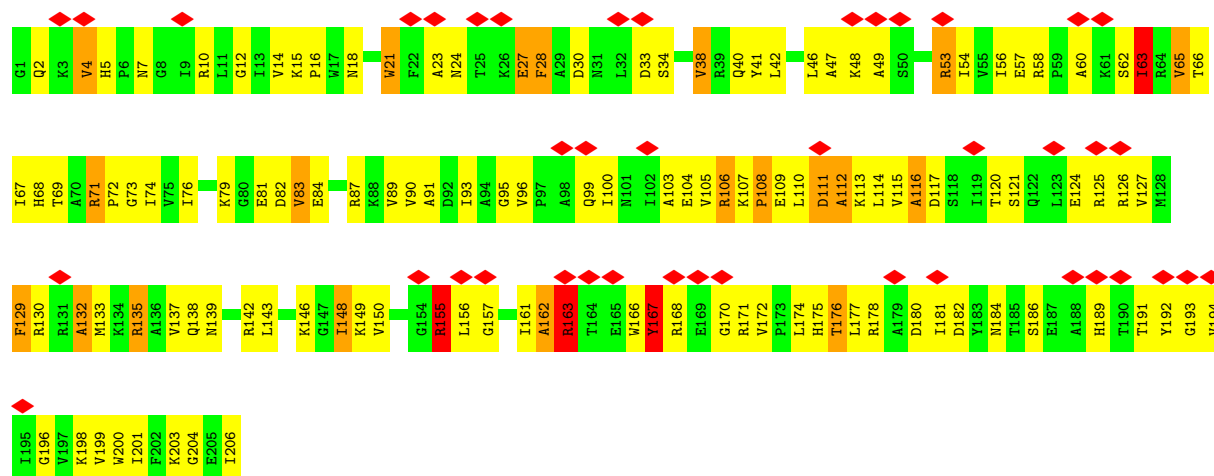


• Molecule 13: 30S ribosomal protein S2

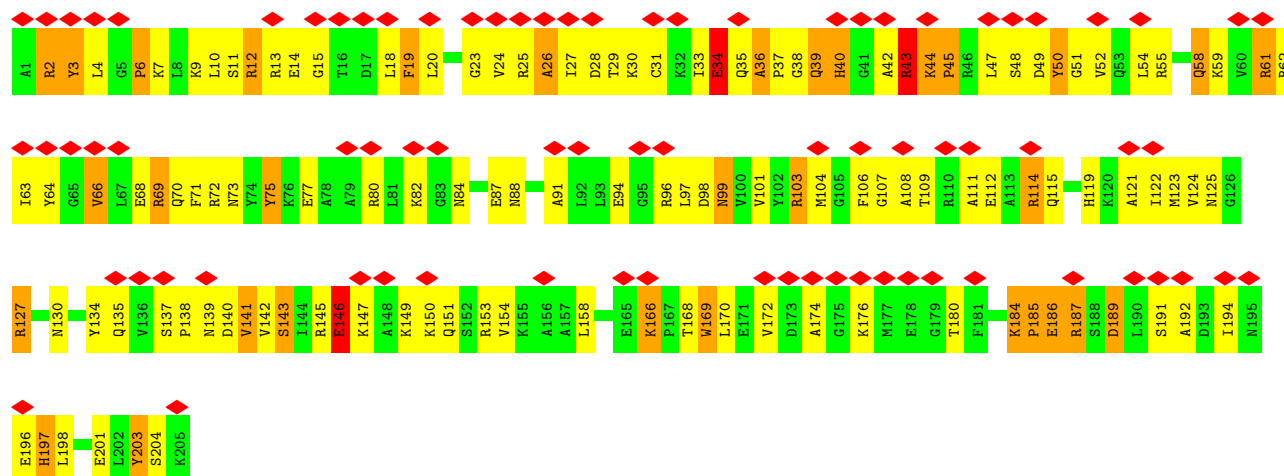




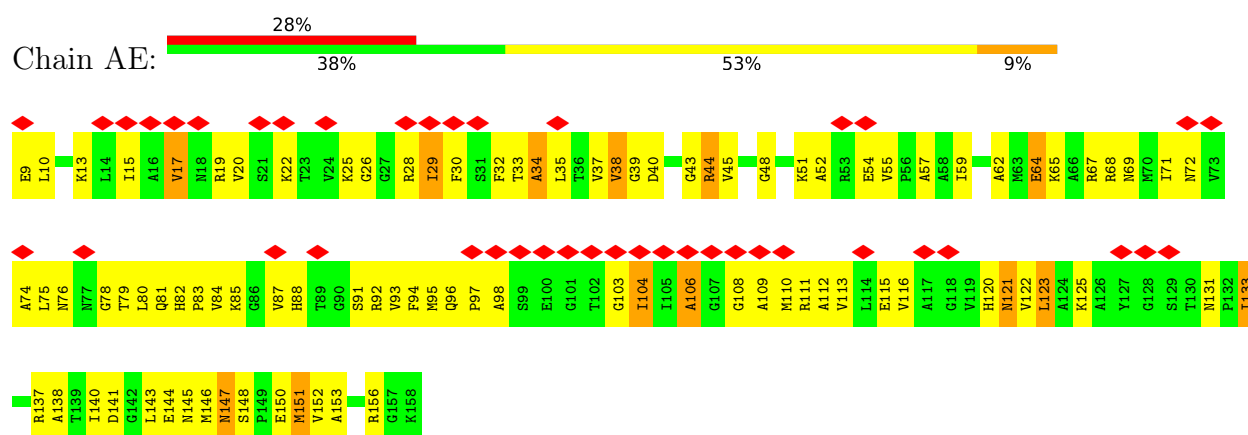
• Molecule 14: 30S ribosomal protein S3



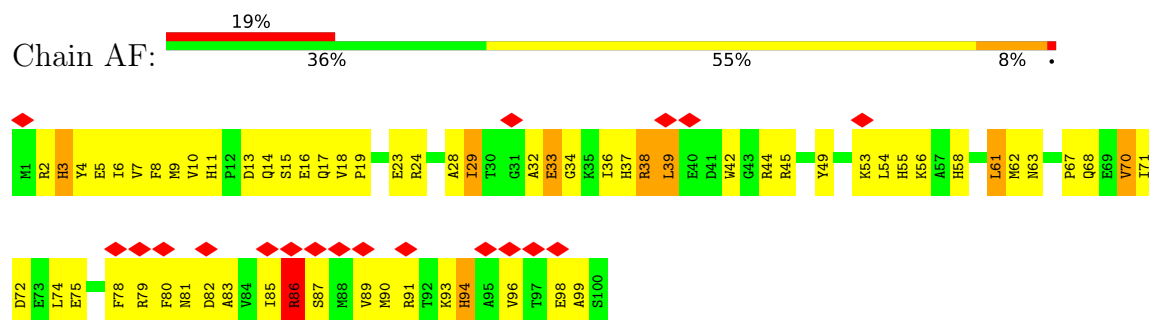
• Molecule 15: 30S ribosomal protein S4



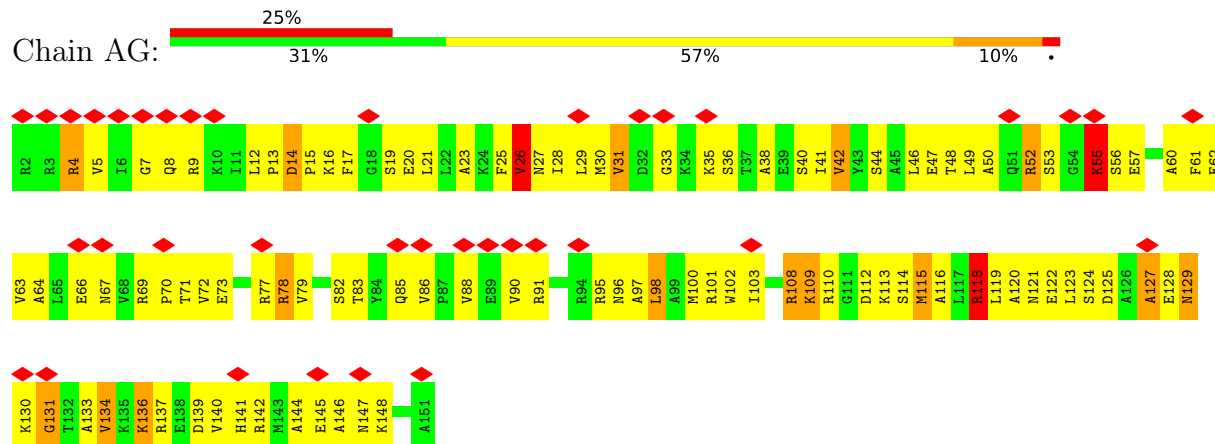
• Molecule 16: 30S ribosomal protein S5



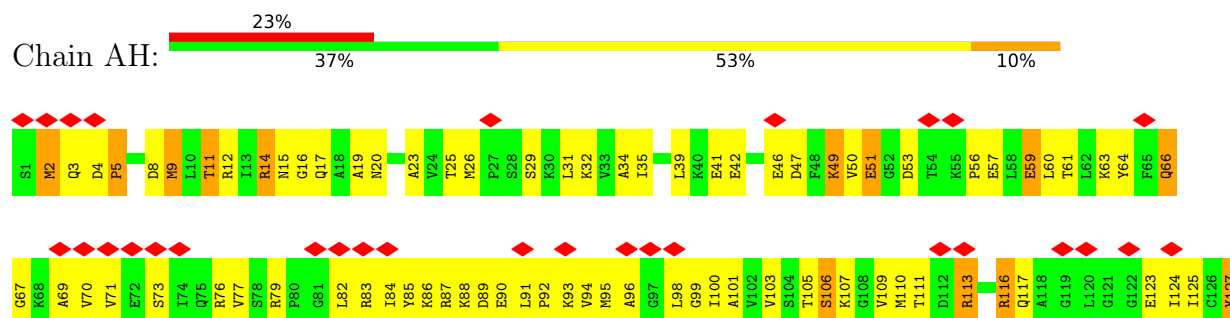
• Molecule 17: 30S ribosomal protein S6



• Molecule 18: 30S ribosomal protein S7



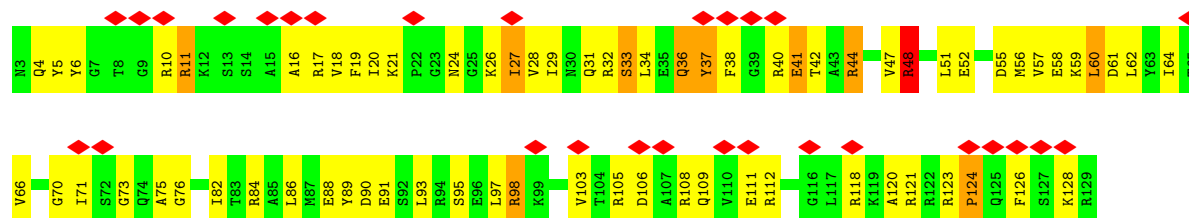
• Molecule 19: 30S ribosomal protein S8



V128
A129

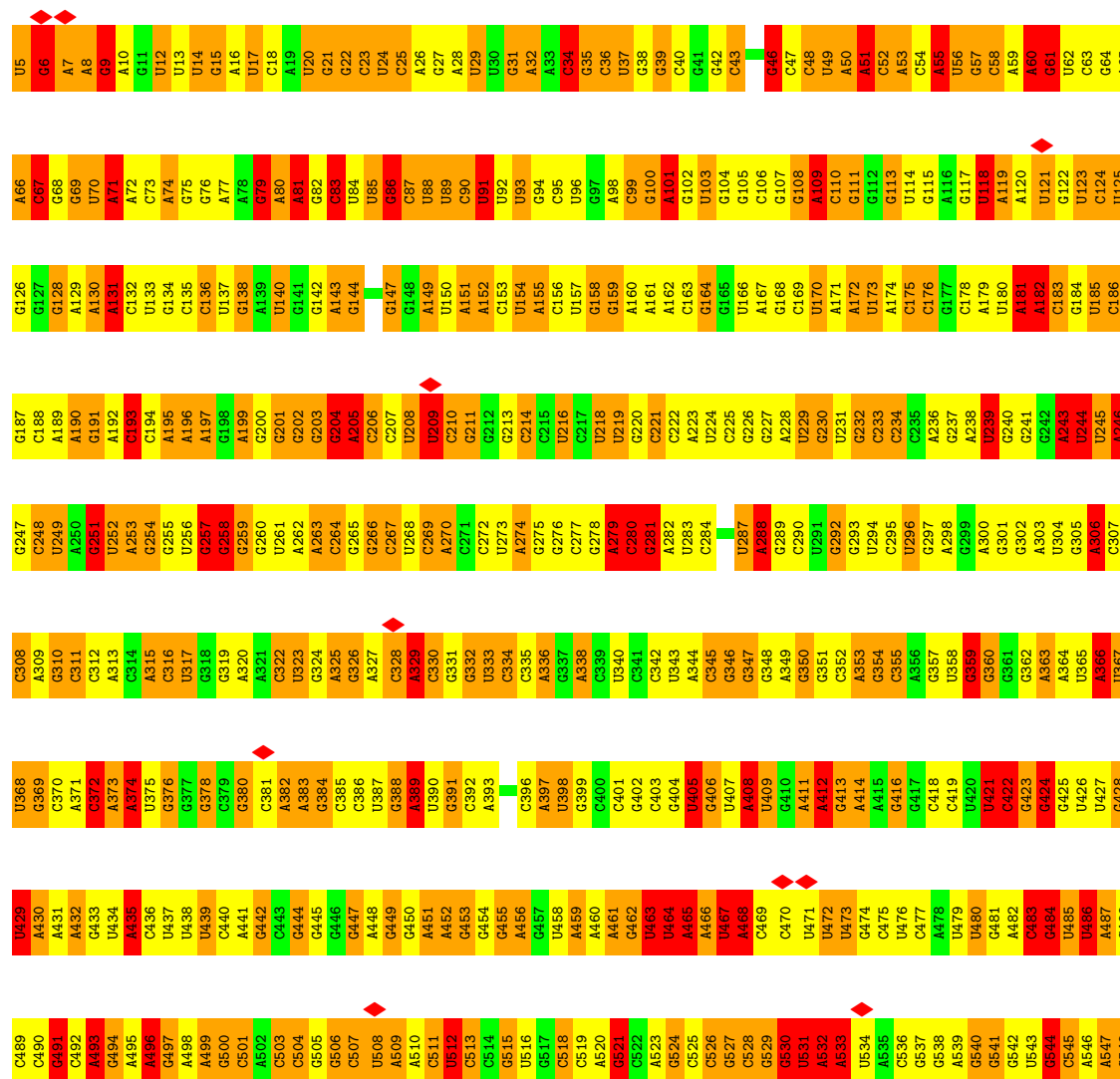
• Molecule 20: 30S ribosomal protein S9

Chain AI: 23% 44% 47% 8%

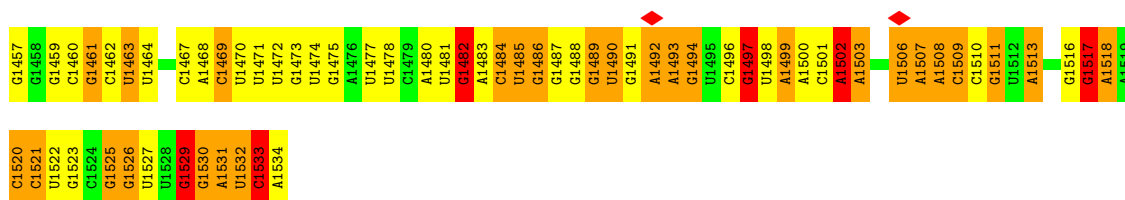


• Molecule 21: 16S rRNA

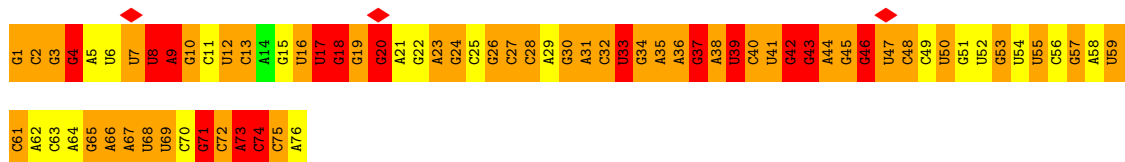
Chain AA: 11% 39% 37% 13%



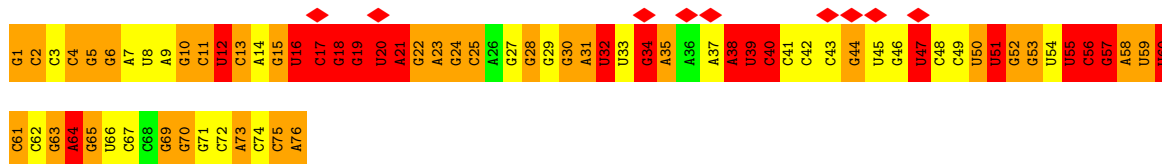




• Molecule 22: A/T-site tRNA Phe



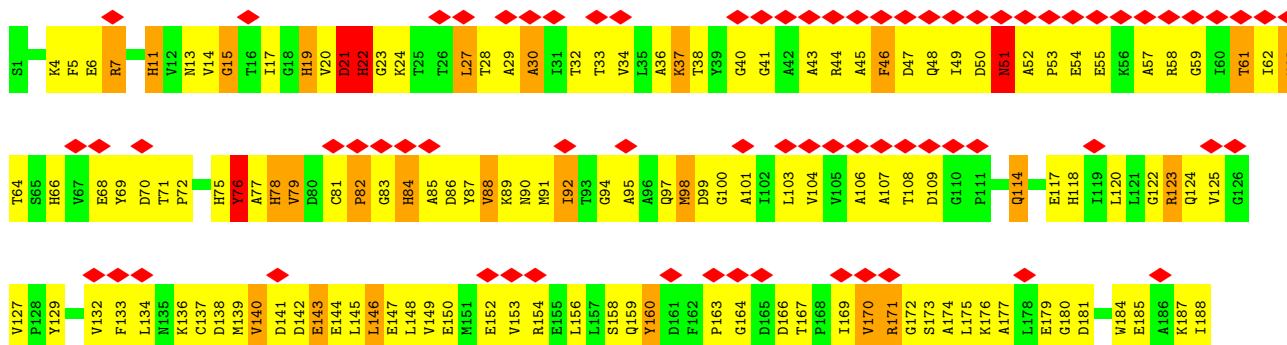
• Molecule 23: P-site tRNA fMet (Unmodified bases except for Thymine 54)

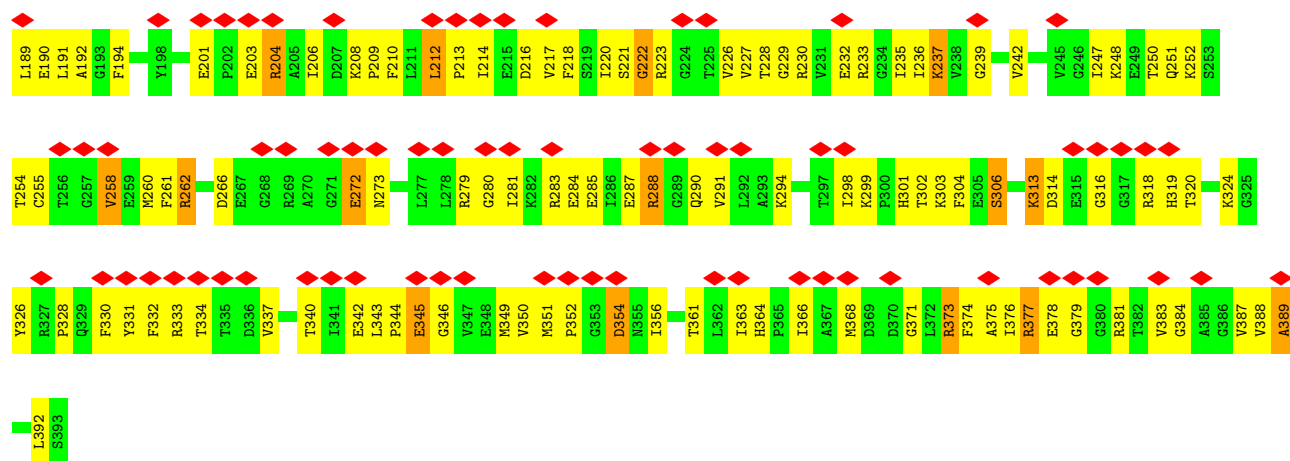


• Molecule 24: mRNA

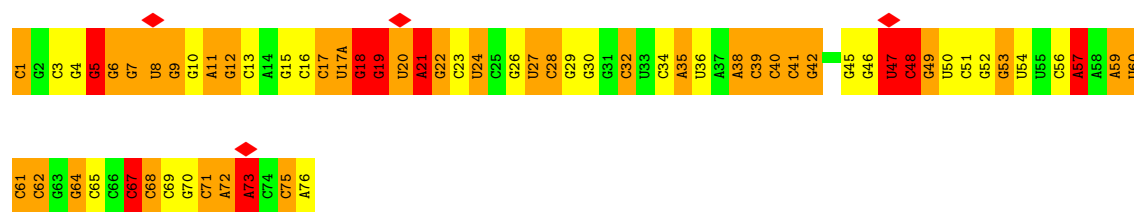


• Molecule 25: Elongation factor Tu

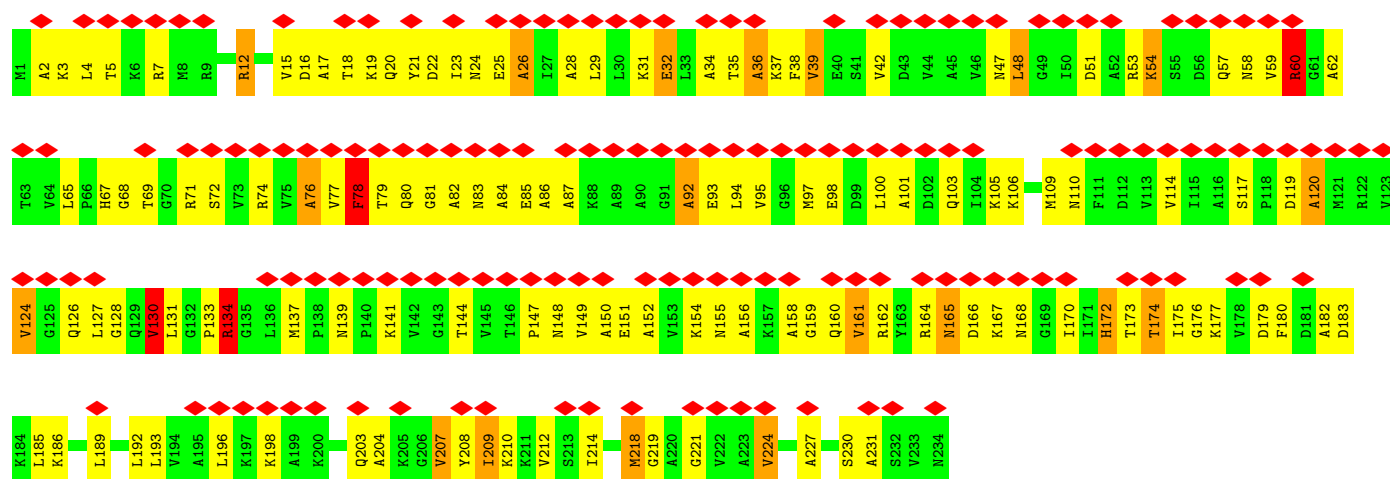




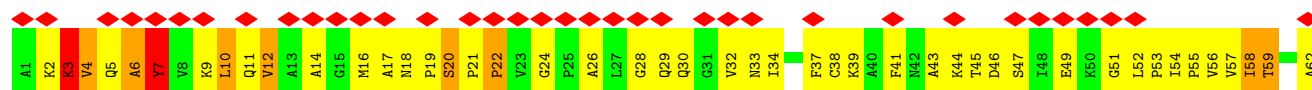
• Molecule 26: E-site tRNA Phe

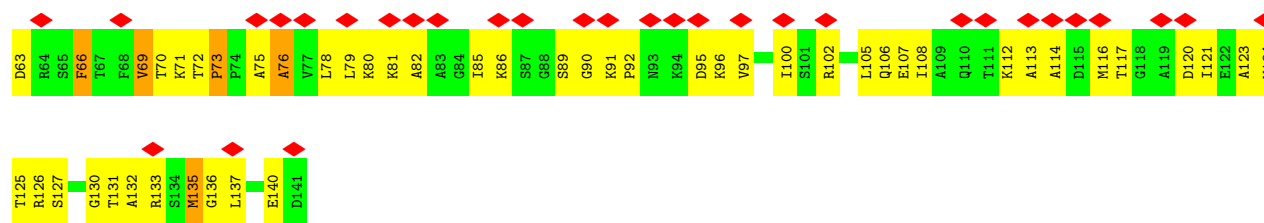


• Molecule 27: 50S ribosomal protein L1



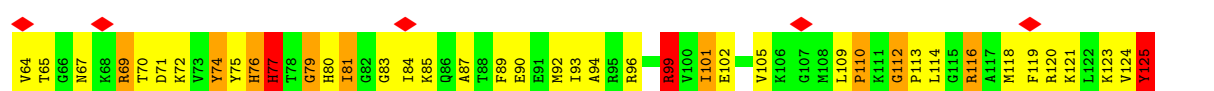
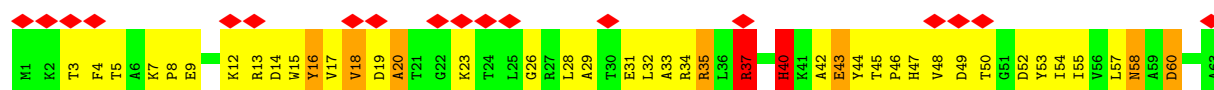
• Molecule 28: 50S ribosomal protein L11





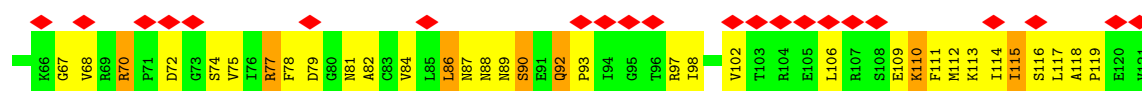
• Molecule 29: 50S ribosomal protein L13

Chain BJ: 18% 35% 51% 11% .



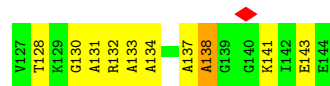
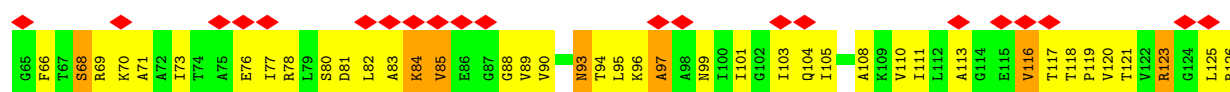
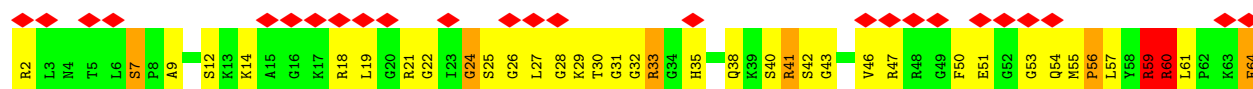
• Molecule 30: 50S ribosomal protein L14

Chain BK: 45% 45% 10%

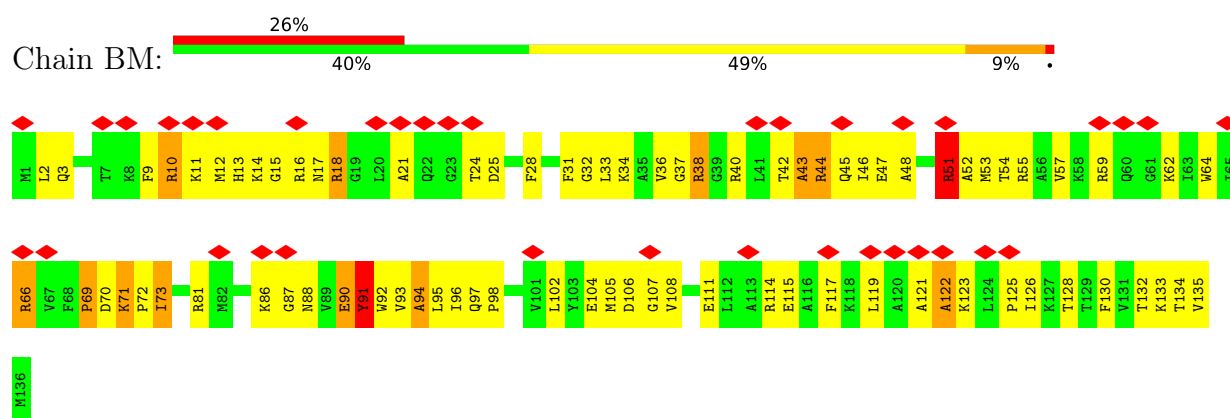


• Molecule 31: 50S ribosomal protein L15

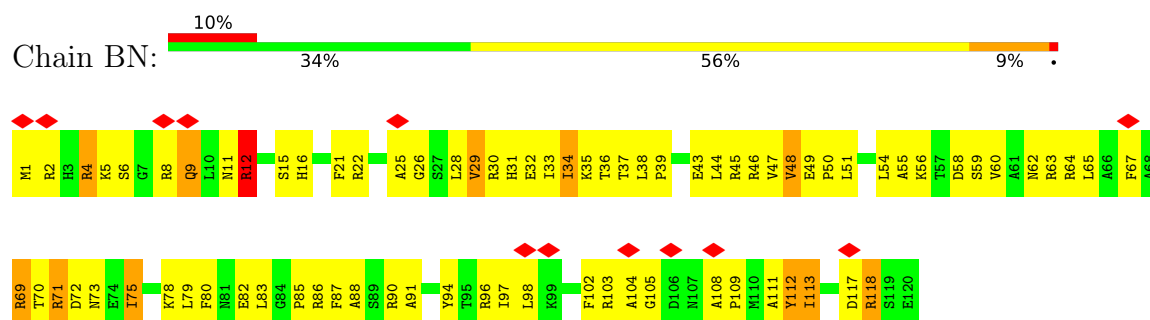
Chain BL: 33% 38% 51% 10% .



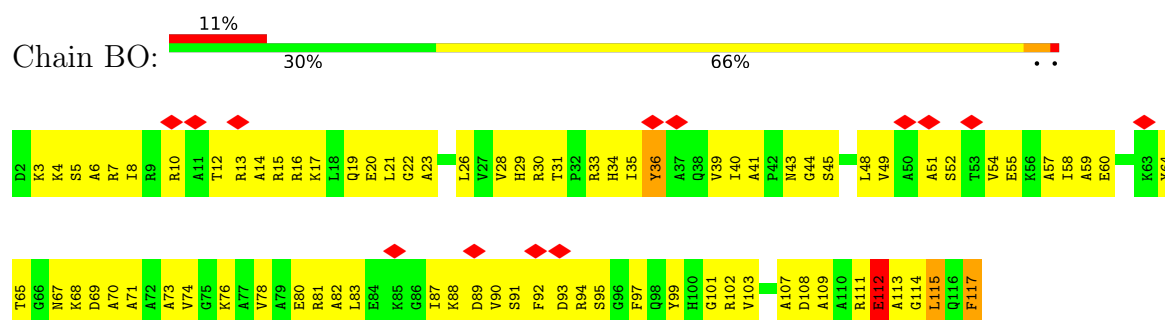
• Molecule 32: 50S ribosomal protein L16



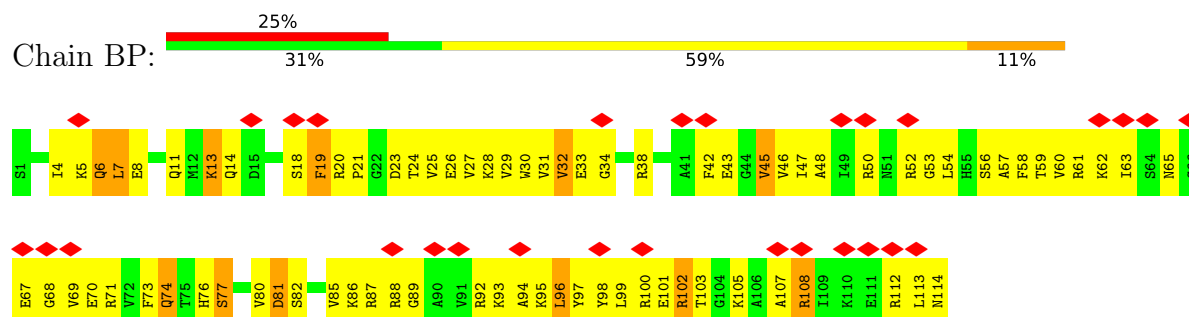
• Molecule 33: 50S ribosomal protein L17



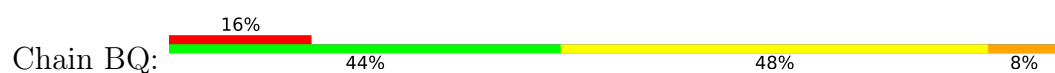
• Molecule 34: 50S ribosomal protein L18

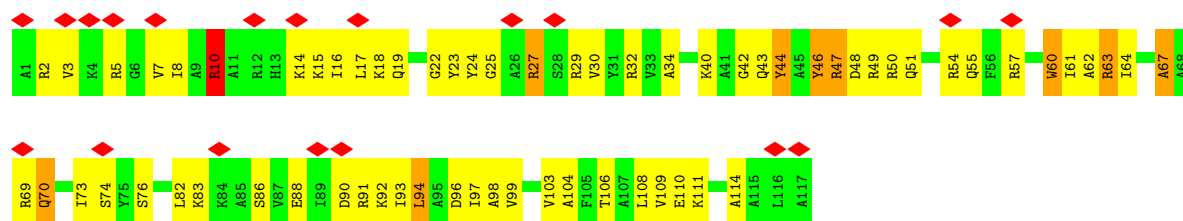


• Molecule 35: 50S ribosomal protein L19

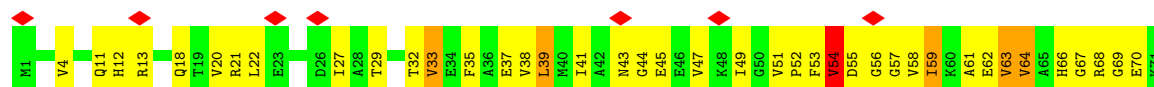


• Molecule 36: 50S ribosomal protein L20





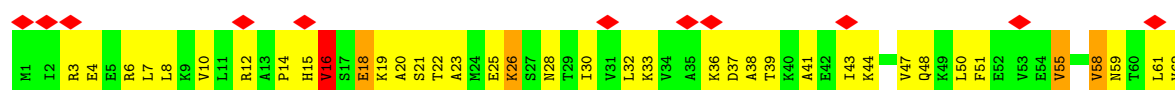
• Molecule 37: 50S ribosomal protein L21



• Molecule 38: 50S ribosomal protein L22



• Molecule 39: 50S ribosomal protein L23

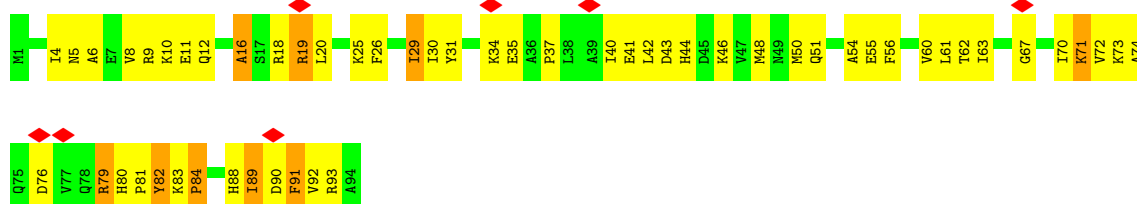
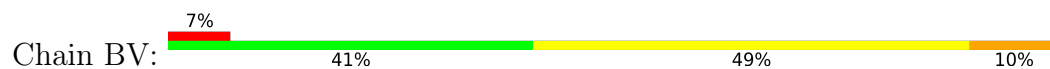


• Molecule 40: 50S ribosomal protein L24

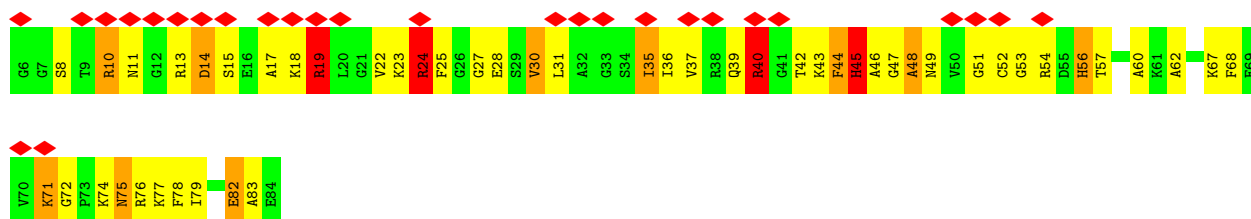




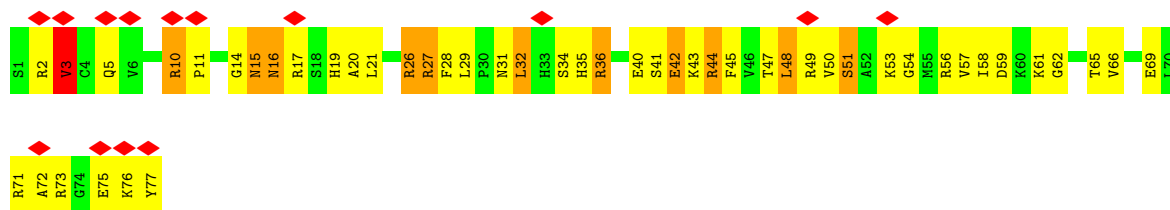
- Molecule 41: 50S ribosomal protein L25



- Molecule 42: 50S ribosomal protein L27



- Molecule 43: 50S ribosomal protein L28

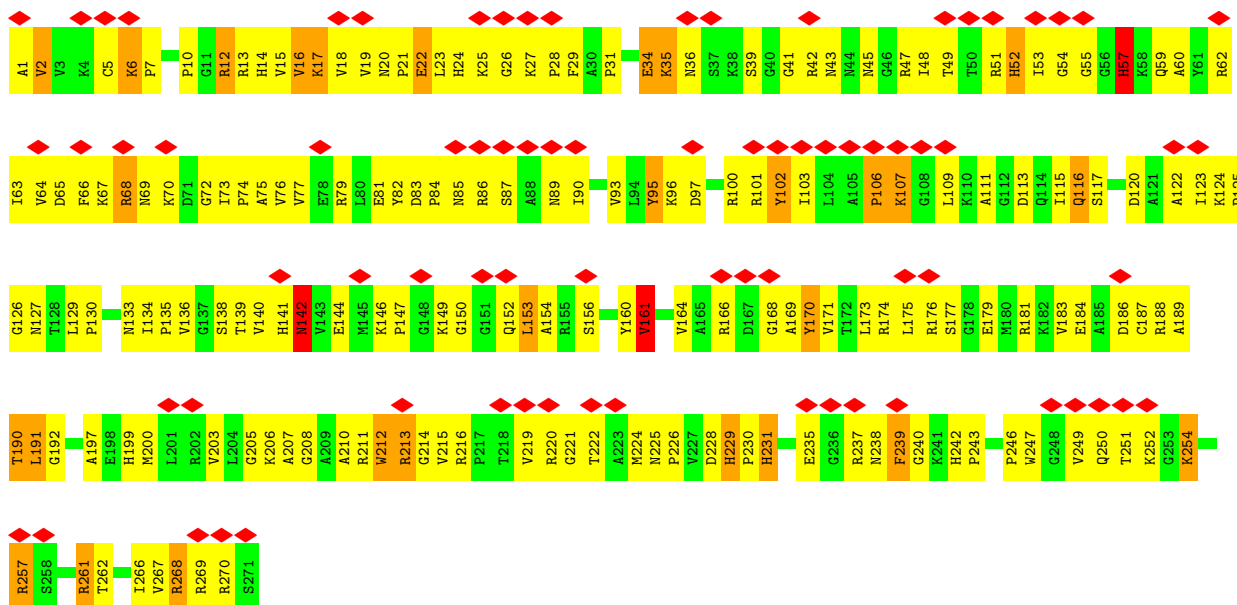


- Molecule 44: 50S ribosomal protein L29



- Molecule 45: 50S ribosomal protein L2

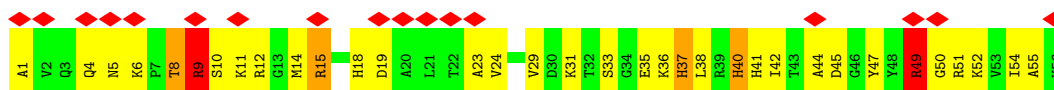
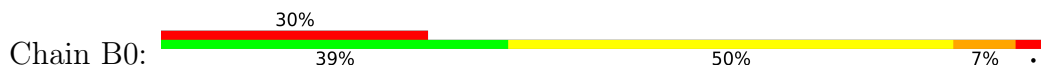




- Molecule 46: 50S ribosomal protein L30



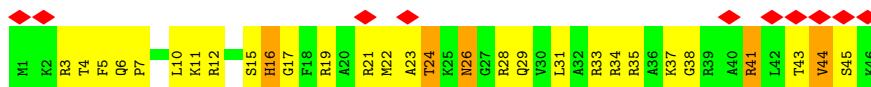
- Molecule 47: 50S ribosomal protein L32



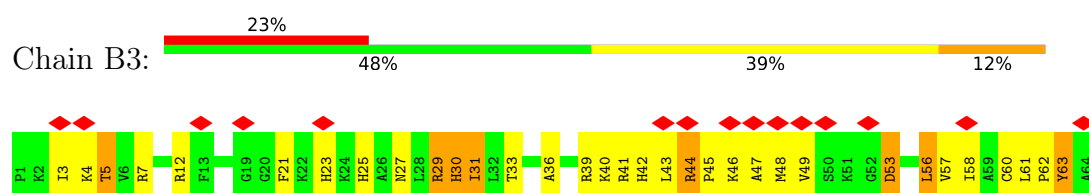
- Molecule 48: 50S ribosomal protein L33



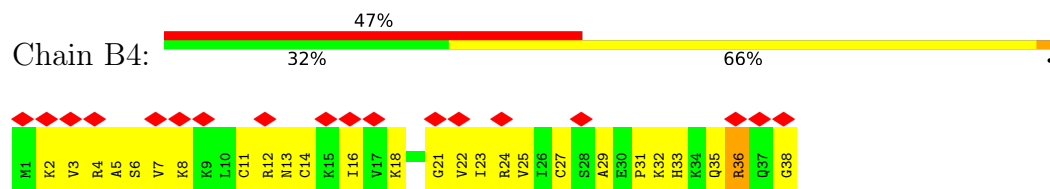
- Molecule 49: 50S ribosomal protein L34



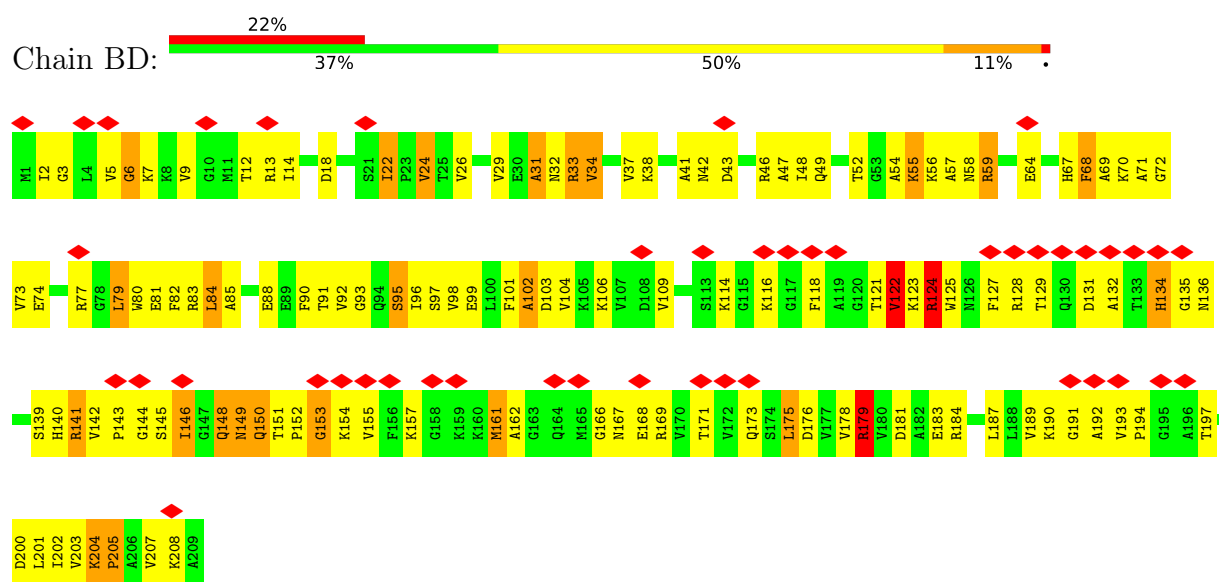
- Molecule 50: 50S ribosomal protein L35



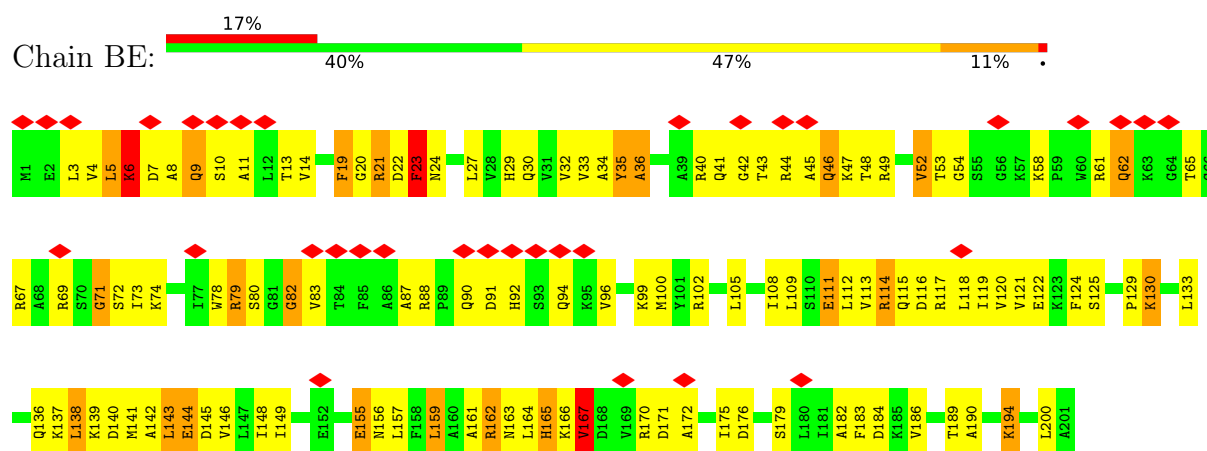
• Molecule 51: 50S ribosomal protein L36



• Molecule 52: 50S ribosomal protein L3

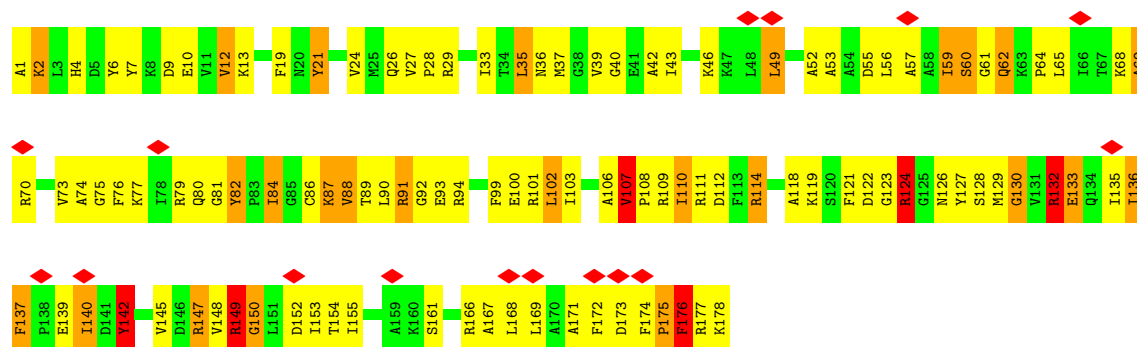


• Molecule 53: 50S ribosomal protein L4

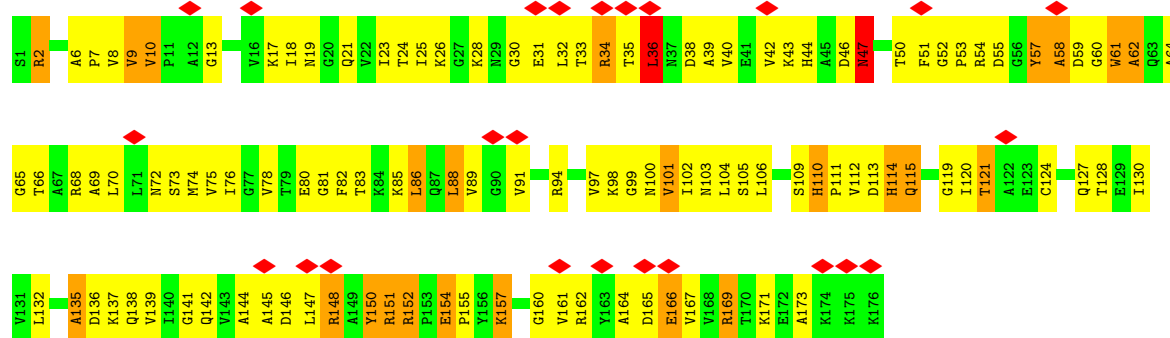


• Molecule 54: 50S ribosomal protein L5

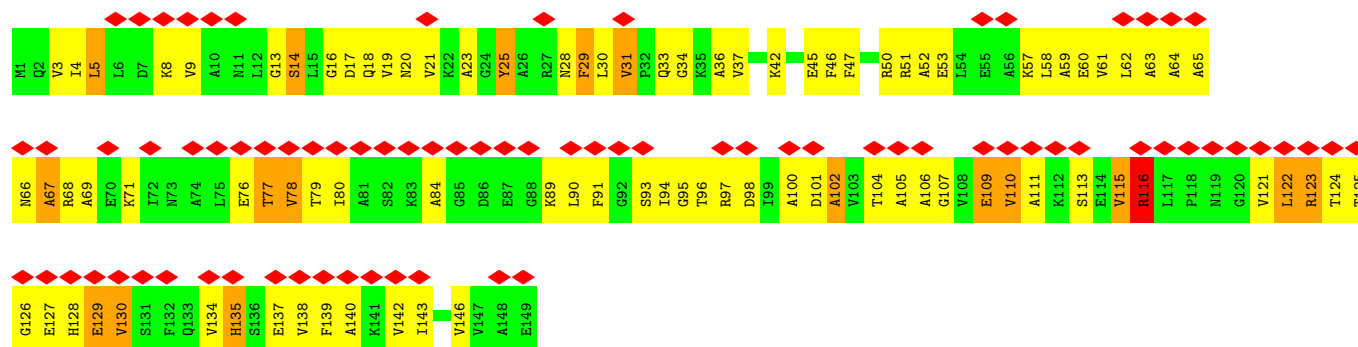




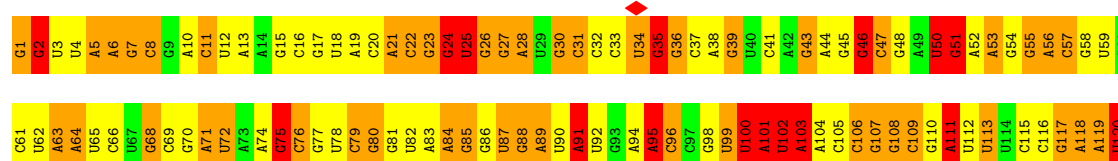
• Molecule 55: 50S ribosomal protein L6



• Molecule 56: 50S ribosomal protein L9



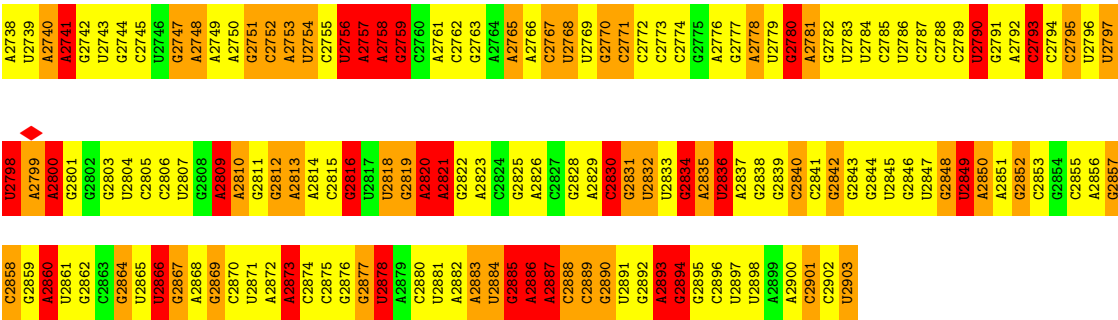
• Molecule 57: 23S ribosomal RNA



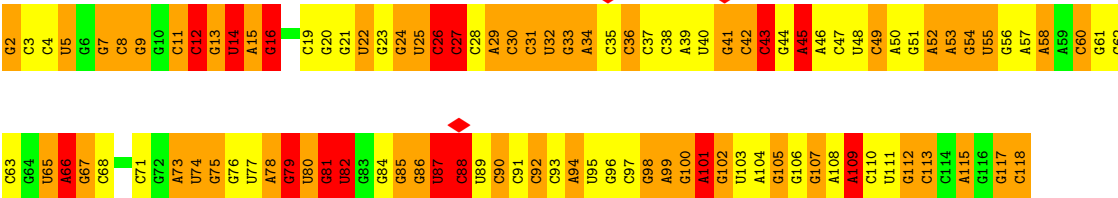
U1033	A973	A911	U850	U790	A730	A670	U607	U546	C485	G424	A382	C302	G242	A182	G121
G974	G974	C912	C851	C791	C731	C671	A608	A547	C486	G425	G363	G303	U243	C183	G122
U1035	A975	A913	U872	A792	A732	C672	A609	G548	C426	C426	G364	U304	A244	C184	G123
G1036	G976	C914	C853	C793	C733	C673	C610	G549	C427	U427	U365	C305	G245	G185	G124
G1037	G977	C915	C854	A794	A734	C674	C611	C550	C488	A428	C366	U306	C246	G186	A125
G1038	G978	G916	G855	C795	A735	A675	C612	G551	C490	A429	G367	G307	G247	G187	A126
A1039	A979	A917	G856	C796	C736	A676	A613	U552	C491	A430	A368	C308	G248	C188	A127
A1040	A980	A918	C857	C797	C737	A677	A614	G553	C492	U431	U369	A309	G249	G189	C128
G1041	A981	U919	G858	C798	A738	C678	U615	U554	C493	A432	G370	A310	C250	C189	C129
G1042	G982	U920	G859	C799	A739	A678	A616	G555	C494	A433	A371	A311	A251	A190	C130
A983	C921	C921	U860	A800	C740	C680	C617	U556	C495	U434	G372	G312	C252	C192	A131
A984			A861	G801	U741	C681	C618	C557	G496	C435	U373	G313	C253	C193	G132
G985	G824	G824	G862	A802	A742	C682	C619	U558	A497	C436	A374	C314	C254	C194	U135
A1046	A925	A925	A863	C803	A743	U683	G620	C559	C498	U437	G375	C315	A255	A195	U136
G1047	G926	G926	G864	A804	U744	C684	G620	C560	C499	G438	G376	C316	A256	A196	G136
A1048	A988	A927	C865	C805	U745	A685	C624	U561	G500	A439	G377	C317	C257	C197	U137
C1049	G989	A928	A866	C906	U746	U686	C625	U562	G501	C440	C378	C318	G258	C198	U138
A1050		U929	C867	U807	U747	C687	A627	C564	A502	U441	G379	C319	C259	A199	U139
G991	G930	G930	C870	G808	G748	U688	A628	C565	A503	G442	G380	A320	C260	U200	C140
U1051	C992	U931	U870	G809	A749	A689	C628	C566	A504	A443	G381	U321	G261	C201	G141
C1052	G993	U932	U871	U810	A750	C690	C629	U566	A505	C444	A382	A322	A262	U202	C142
C1053	A933	A933	U872	U811	A751	C691	C630	U567	G506	C445	C383	C323	A263	C203	C143
G1055	C995	U934	C873	C812	A752	C692	A631	U568	A507	C446	A384	A324	C264	A204	A144
G1056	A995	C935	G874	U813	A753	A693	A632	U569	A508	A447	C385	C325	A265	G205	C145
A1057	G997	A936	C876	C814	U754	U694	A633	G570	C509	U448	G386	G326	C266	U206	C146
C998	C937	C937	C877	C815	U755	C695	C634	U571	C510	A449	U387	G327	C267	A207	C147
U1058	U999	G938	A877	C816	A756	C696	C635	A572	U511	G450	C388	U328	C268	C208	U148
G1059	G937	G938	A878	C817	U757	C697	C636	U573	G512		C389	C329	C269	C209	A149
U1060	A1001	G939	G879	C818	C758	A698	A637	A574	A513		C390	A330	A270	C210	U150
U1061	G940	G940	A880	A819	A759	A699	C638	U575	A514	A454	C391	C331	C271	C211	G151
G1002	A941	A941	G881	C820	A760	G700	U639	U576	A515	A455	A272	A332	G272	G152	C152
G1003	G942	G942	G882	A821	A761	G701	C640	U577	C516	C456	C394	G333	C273	U153	C153
U1004	A943	A943	C883	G822	U762	U702	U641	G578	G518	A457	U395	C334	C274	C154	U154
C1006	C944	C944	U884	C823	C763	U703	C642	G579	G519	G458	G396	C335	C275	C155	A155
A1007	A945	A945	C885	U824	A764	G704	A643	U580	G520	U459	U397	C336	U276	A216	A156
C946	C946	C946	A886	A825	C765	A705	A644	C581	U521	A460	C461	C337	C277	C157	C157
A947	A947	A947	U887	U826	U766	U707	U646	A582	U522	C462	C400	G338	A278	U158	C158
A1009	C948	C948	C888	U827	U767	C707	C647	C583	A522	C463	A401	U339	C279	C159	G159
A1010	G949	G949	C889	U828	C768	U708	C648	C584	C523	G464	C402	U340	A279	C160	A160
G950	A950	A950	U889	C830	U769	U709	C649	C585	G524	U465	C281	C341	C281	A161	C161
C951	G951	G951	C890	A829	C770	U710	A649	C586	G525	C466	U403	C342	A282	C162	A162
U1013	A952	A952	C891	G830	A766	G704	C650	C587	G526	A466	A404	C343	A283	C163	C163
G953	G953	G953	A892	U832	C772	G712	C651	U588	G527	G467	U405	C344	U284	C164	G164
U1015	C954	C954	C893	U833	C773	G713	C652	U589	A528	G468	A406	A345	C285	C165	A165
G1016	G955	G955	C894	A833	C774	G714	U653	A590	A529	G469	G407	U346	C286	C166	U166
A1017	C956	C956	U895	G834	C774	U714	C653	C590	G530	A470	C408	A347	U287	C167	A167
U1078	A957	A957	C895	C835	C775	A715	A654	U591	G531	C471	C409	C348	U288	C168	C168
C1079	C957	C957	A896	G836	C776	A716	A655	A592	C532	A472	G410	U349	C289	C169	G169
U1019	G958	G958	C897	C837	C777	C717	C656	U593	A531	A473	C411	C350	C290	C170	U170
A1020	A959	A959	C898	G838	C778	G718	U657	U594	G533	G474	G411	C351	U290	C171	U171
U1081	C960	C960	A899	U839	U779	C719	U658	C595	U534	A475	A412	C352	C291	A172	C172
G1082	A1021	A1021	A899	C839	C779	G719	C659	U596	G535	C475	C413	C353	U292	C232	A173
U1083	C961	C961	A900	C840	C780	U720	C660	U597	G536	C476	C414	C354	U293	A233	C173
A1084	G962	G962	C899	G841	A781	A721	C660	U598	G537	A477	C415	C355	U294	C234	U174
A1085	U963	U963	C902	U842	C782	A722	C661	U599	G538	A478	C416	U355	C295	C175	G175
G1025	C964	C964	C903	G843	A783	C723	C662	A599	A538	A479	C417	C356	U296	C236	A176
A1026	G965	G965	G904	A844	C784	U724	C664	C600		A480	C418	C357	U297	C237	G177
G1027	A966	A966	A845	A845	C785	G725	U665	G600		A481	C419	U358	C297	C238	C178
A1028	U967	U967	U905	U846	C786	G726	U666	A603	C542	A482	C420	U359	C298	C239	G179
A1029	G967	G967	A906	U847	C787	G727	U667	G604	C543	A483	C421	U359	C299	C240	C180
C1030	U967	U967	C907	U847	C788	A727	U668	G605	C544	A484	C422	U360	C300	C241	G181
G1031	U970	U970	A908	U848	C789	G728	U669	A606	U545	C484	A423	G361	C301	A241	C182
A1032	G971	G971	A909	A849	A789	G729	C669	U606							C183

C1887	G1826	U1765	G1702	G1642	A1580	U1520	U1457	U1397	A1274	A1214	G1154	U1094
G1888	U1827	G1766	G1703	G1643	G1581	G1521	U1458	C1398	A1275	G1215	A1155	A1095
A1889	A1828	G1767	C1704	G1644	G1582	A1522	G1459	C1399	G1276	U1216	A1156	A1096
G1890	G1829	C1768	A1705	G1645	A1583	G1523	U1460	U1400	A1277	U1217	G1157	U1097
C1891	C1830	U1769	C1706	G1646	U1584	U1524	C1461	G1401	C1278	G1218	C1158	A1098
G1892	G1831	G1770	G1707	U1647	C1585	A1525	C1462	U1402	G1279	U1219	U1159	G1099
C1893	C1832	C1771	G1708	U1648	A1586	G1526	C1463	A1403	G1280	G1220	G1160	C1100
C1894	G1833	A1772	U1709	G1649	G1587	C1527	G1464	C1404	G1281	C1221	C1161	U1101
G1895	U1834	A1773	G1710	A1650	A1588	A1528	G1465	U1405	U1282	U1222	G1162	C1102
G1896	G1835	C1774	U1711	G1651	U1589	A1529	U1466	U1406	G1283	G1223	G1163	A1103
G1897	C1836	U1775	U1712	A1652	A1590	G1530	U1467	G1407	A1284	U1224	C1164	G1104
U1898	C1837	G1776	A1713	G1653	A1591	G1531	U1468	U1408	A1285	G1225	A1165	U1105
A1899	G1838	U1777	U1714	A1654	C1592	G1532	A1469	G1410	A1286	A1226	G1166	G1106
A1900	G1839	U1778	G1715	A1655	A1593	A1532	A1470	G1411	A1287	G1227	C1167	G1107
A1901	G1840	U1779	U1716	C1656	C1594	A1533	A1471	U1411	A1288	G1228	G1168	U1108
C1902	A1717	A1780	G1718	G1657	U1534	A1534	C1472	U1412	C1289	G1229	A1169	C1109
G1903	G1842	U1781	G1719	C1658	A1598	A1535	G1473	A1413	C1290	U1231	G1170	G1110
G1904	C1843	U1782	G1718	G1659	U1599	G1536	U1474	U1414	C1291	U1231	G1171	A1111
C1905	G1844	A1783	U1720	G1660	C1600	G1537	G1475	U1415	G1292	G1232	C1172	G1112
G1906	G1845	A1784	G1721	G1661	G1601	G1538	U1476	G1416	C1293	C1233	U1173	U1113
G1907	U1846	A1785	G1722	U1662	U1602	U1539	U1477	C1417	U1234	U1234	U1174	C1114
C1908	A1847	A1786	G1730	G1663	A1603	G1540	G1478	G1418	A1241	G1235	G1185	G1115
A1909	A1848	A1787	C1732	A1664	C1604	C1541	U1479	A1419	A1302	U1181	G1186	A1126
G1910	G1849	C1788	G1733	A1665	C1605	U1542	U1480	G1426	A1303	C1243	G1187	A1127
U1911	G1850	U1789	G1734	G1666	C1606	U1543	U1481	A1427	A1304	C1244	U1188	A1129
A1912	U1851	C1790	U1729	G1667	C1607	A1544	G1482	G1422	C1305	A1244	U1189	U1130
A1913	U1852	A1791	U1730	A1668	A1608	A1545	G1483	G1423	C1306	G1245	U1184	G1124
C1914	A1853	G1792	G1731	A1669	A1609	G1546	U1484	G1424	A1307	A1246	G1185	G1125
U1915	A1854	C1793	C1732	G1670	A1610	C1547	U1485	G1425	A1308	G1247	G1186	A1126
A1916	U1855	A1794	G1733	C1671	C1611	A1548	U1486	G1426	A1309	G1248	G1187	G1128
U1917	U1856	U1795	G1734	A1672	C1612	A1549	U1487	A1427	G1310	U1249	U1188	A1129
A1918	G1857	U1796	G1735	G1673	C1613	A1550	C1488	C1428	G1311	G1250	A1189	U1130
A1919	U1858	G1797	G1737	G1674	A1614	U1551	C1489	G1429	U1312	C1251	G1191	G1132
C1920	U1859	U1798	A1738	C1675	C1615	A1552	G1491	G1430	U1313	G1252	G1192	U1133
G1921	G1860	G1799	G1740	A1676	A1616	A1553	G1492	G1431	C1314	A1253	G1193	A1133
U1922	G1861	C1800	C1741	G1677	C1617	G1556	C1493	A1433	C1315	U1254	A1194	A1134
A1923	G1862	A1801	U1742	A1678	A1618	C1557	A1494	A1434	U1316	G1255	G1195	C1135
C1924	G1863	A1802	U1743	A1679	G1619	C1558	A1495	G1435	G1317	G1256	C1196	G1136
U1925	U1864	A1803	G1743	U1680	G1620	C1559	A1496	G1436	C1318	U1257	C1197	G1137
U1926	U1865	C1804	A1744	G1681	U1621	G1560	U1497	G1437	A1321	G1258	U1198	G1138
A1927	A1866	A1805	A1745	G1682	G1622	U1561	C1498	C1437	A1322	C1261	U1199	G1139
U1928	G1867	C1806	A1746	U1683	G1623	C1561	U1499	U1438	A1323	U1262	C1200	C1140
G1929	G1868	G1807	U1747	G1684	U1624	U1562	C1500	G1440	G1324	U1263	U1201	U1141
C1930	C1869	A1808	C1748	C1685	C1625	U1563	C1507	C1441	U1325	A1264	G1202	A1142
U1931	C1870	A1809	A1749	C1686	A1626	C1564	A1508	C1442	U1326	A1265	U1203	A1143
A1932	G1871	A1810	G1750	G1687	C1627	C1565	A1509	U1443	A1327	A1266	A1204	A1144
G1933	C1872	G1811	U1751	U1688	G1628	A1566	A1504	U1444	G1327	G1267	A1205	A1145
C1934	C1873	U1812	C1752	A1689	U1629	G1567	A1505	A1384	G1328	U1268	G1206	C1146
G1935	G1875	G1813	G1753	A1690	A1630	G1568	U1506	G1445	G1329	A1269	C1207	C1147
A1936	A1876	G1814	A1754	C1691	G1631	A1569	C1507	C1446	G1330	A1270	C1208	U1148
A1937	A1877	A1815	A1755	U1692	A1632	C1570	C1508	C1447	G1331	G1271	G1209	G1149
A1938	G1878	C1816	G1756	U1693	G1633	A1571	A1509	G1448	G1332	G1272	C1210	C1150
U1939	C1879	G1817	A1757	C1694	A1634	A1572	G1510	G1449	G1333	G1273	C1211	A1151
U1940	U1880	U1818	U1758	G1695	A1635	G1573	G1511	U1450	G1334	U1274	G1212	A1152
C1941	C1881	A1819	A1759	G1696	U1636	C1574	C1451	C1451	G1335	U1275	A1213	
A1942	U1882	U1820	C1760	G1697	A1637	C1575	U1513	A1452	G1336			
U1943	U1883	A1821	C1761	A1698	C1638	U1576	U1514	A1453	G1337			
U1944	G1884	A1822	A1762	G1699	C1639	U1577	G1515	C1454	G1338			
G1945	A1885	C1823	G1763	A1700	A1640	U1578	A1516	U1594	G1339			
U1946	U1886		C1764	A1701	A1641	A1579	G1517	G1456	G1340			

G2677	U2615	U2554	G2494	A2433	G2373	U2192	U2132	A2070	C2008	G1949
C2678	C2616	U2555	G2495	A2434	C2374	G2193	G2133	A2071	A2009	U1950
A2679	U2617	C2556	A2496	A2435	A2375	U2194	A2134	C2072	G2010	G1951
U2680	G2618	G2557	A2497	G2436	A2376	U2195	A2135	C2073	U2011	A1952
C2681	C2619	C2558	G2498	G2437	A2377	G2256	G2136	U2074	G2012	A1953
C2682	C2620	C2559	G2499	A2438	A2378	U2197	U2137	U2075	A2013	G1954
C2683	G2621	U2560	U2500	A2439	G2379	C2258	G2138	U2076	A2014	U1955
U2684	G2622	U2561	C2501	C2440	C2380	U2259	U2139	A2077	A2015	U1956
G2685	G2623	A2562	G2502	U2441	A2381	C2260	G2140	C2078	U2016	G1957
G2686	G2624	A2563	A2503	C2442	G2382	G2201	A2141	U2079	U2017	G1958
U2687	G2625	A2564	U2504	C2443	U2383	U2202	A2142	A2080	G2018	G1959
G2688	G2626	A2565	G2505	G2444	U2384	U2203	C2143	C2081	A2019	A1960
U2689	G2627	A2566	G2506	U2445	U2385	G2204	G2144	U2081	A2020	A1961
U2690	C2628	G2567	U2507	G2447	U2386	A2205	C2145	C2084	C2021	G1962
G2691	U2629	U2568	C2507	A2448	U2387	C2206	A2146	U2085	U2022	U1963
G2692	G2630	G2569	U2508	U2449	A2388	C2207	A2147	U2086	C2023	G1964
G2693	G2631	U2571	G2509	A2450	A2389	G2208	U2148	C2089	G2024	G1965
G2694	A2632	C2572	U2510	A2451	U2390	C2209	U2149	A2090	C2025	A1966
U2695	G2633	C2573	U2511	A2452	U2391	U2210	C2150	C2091	U2026	C1967
U2696	A2634	C2574	A2512	C2453	G2392	A2211	U2151	U2092	U2028	G1968
U2697	G2635	C2575	U2513	G2454	U2393	A2212	C2152	G2093	A2030	A1969
U2698	G2636	U2576	A2514	U2455	C2394	U2213	A2153	A2094	A2031	U1970
C2699	G2637	G2577	G2515	G2456	C2395	C2214	U2154	C2095	G2032	U1971
A2700	G2638	A2577	A2516	G2457	G2396	C2215	U2155	A2096	A2033	G1972
U2701	A2639	G2578	G2517	U2458	G2397	G2216	G2156	C2097	G2034	G1973
G2702	G2640	C2579	A2518	G2459	U2398	G2217	A2157	U2098	U2034	G1974
C2703	G2641	U2580	U2519	A2459	G2399	G2218	C2158	U2099	G2035	G1975
C2704	G2642	G2581	G2520	U2460	U2400	U2219	G2159	G2100	C2036	U1976
A2705	G2643	G2582	A2521	A2461	G2401	U2220	C2160	A2101	A2037	A1977
A2706	G2644	G2583	U2522	C2462	U2402	G2221	G2161	G2102	G2038	A1978
A2707	G2645	U2584	G2523	C2463	C2403	C2222	A2162	C2103	U2039	U1979
U2708	G2646	U2585	G2524	G2464	U2404	G2223	A2163	C2104	G2040	G1980
G2709	U2647	U2586	G2525	C2465	C2405	G2224	C2164	U2105	U2041	A1981
C2710	G2648	A2587	G2526	C2466	A2406	A2225	C2165	U2106	A2042	U1982
A2711	G2649	G2588	G2527	G2467	G2407	C2226	U2167	G2107	C2043	G1983
C2712	U2650	U2589	U2528	A2468	A2408	A2227	G2168	A2108	C2044	C1984
C2713	C2651	A2590	G2529	A2469	U2409	G2228	G2169	U2109	C2045	G1985
G2714	G2652	C2591	A2530	G2470	G2409	U2229	A2170	G2110	G2046	C1986
C2715	U2653	U2592	G2531	A2471	G2410	U2230	A2171	U2111	C2047	A1987
C2716	G2654	U2593	G2532	G2472	A2411	U2231	U2172	G2112	G2048	G1988
G2717	A2654	C2594	U2533	U2473	G2412	G2232	A2173	U2113	G2049	G1989
C2718	G2655	G2595	A2534	U2474	G2413	U2233	C2174	A2114	G2053	U1990
U2719	C2656	U2596	G2535	C2475	G2414	U2234	C2175	G2115	A2064	G1991
U2720	U2657	G2597	G2536	A2476	G2415	G2235	A2176	G2116	C2055	G1992
A2721	A2658	A2598	U2537	U2477	C2416	U2236	C2177	A2117	G2056	U1993
G2722	G2659	G2599	C2538	A2478	C2417	G2237	C2178	U2118	G2057	G1994
C2723	A2660	A2600	G2539	U2479	A2418	G2238	C2179	A2119	A2058	U1995
U2724	G2663	C2601	G2540	C2480	U2419	G2239	U2180	G2120	A2059	C1996
A2725	G2664	A2602	A2541	G2481	C2420	U2240	U2181	G2121	A2060	C1997
A2726	A2665	G2603	A2542	A2482	G2421	C2300	U2182	U2122	G2061	A1998
U2727	C2666	U2604	G2543	A2483	U2422	C2301	U2183	G2123	A2062	C1999
A2728	G2667	U2605	G2544	G2484	U2423	U2241	A2184	G2124	C2063	C2000
G2729	U2668	C2606	G2545	G2485	C2424	U2242	U2185	G2125	G2064	C2001
C2730	A2669	G2607	U2546	C2486	A2425	U2243	U2186	A2126	C2065	A2002
G2731	A2670	G2608	A2547	G2487	A2426	U2244	G2187	G2127	G2066	G2003
U2732	G2671	U2609	U2548	C2488	C2427	G2302	U2188	G2128	C2067	A2004
A2733	U2672	C2610	G2549	U2489	G2428	A2247	U2189	U2129	U2068	A2005
G2734	G2673	C2611	G2550	G2490	G2429	G2303	A2248	U2130	G2069	U2007
A2735	G2674	C2612	U2551	U2491	A2430	U2249	G2190			
A2736	A2675	U2613	U2552	U2492	U2431	G2250	A2191			
G2737	G2676	A2614	G2553	U2493	U2372	G2251				



● Molecule 58: 5S ribosomal RNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	131599	Depositor
Resolution determination method	Not provided	
CTF correction method	Correction of reconstruction of each defocus group	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	4520	Depositor
Maximum defocus (nm)	1200	Depositor
Magnification	58279	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	303.004	Depositor
Minimum map value	-114.578	Depositor
Average map value	6.031	Depositor
Map value standard deviation	29.145	Depositor
Recommended contour level	90	Depositor
Map size ($\text{\AA}$)	370.80002, 370.80002, 370.80002	wwPDB
Map dimensions	309, 309, 309	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.2, 1.2, 1.2	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 5MU, 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	AJ	2.35	37/797 (4.6%)	2.33	43/1077 (4.0%)
2	AK	2.42	47/893 (5.3%)	2.46	59/1205 (4.9%)
3	AL	2.28	41/969 (4.2%)	2.34	56/1300 (4.3%)
4	AM	2.49	46/885 (5.2%)	2.68	78/1181 (6.6%)
5	AN	2.40	31/786 (3.9%)	2.69	74/1046 (7.1%)
6	AO	2.40	37/724 (5.1%)	2.77	85/966 (8.8%)
7	AP	2.46	33/649 (5.1%)	2.37	39/870 (4.5%)
8	AQ	2.48	39/658 (5.9%)	2.41	32/881 (3.6%)
9	AR	2.35	21/463 (4.5%)	2.52	32/621 (5.2%)
10	AS	2.46	34/653 (5.2%)	2.37	41/877 (4.7%)
11	AT	2.31	27/671 (4.0%)	2.52	56/888 (6.3%)
12	AU	2.37	19/431 (4.4%)	2.48	29/570 (5.1%)
13	AB	2.24	60/1736 (3.5%)	2.49	120/2338 (5.1%)
14	AC	2.36	73/1652 (4.4%)	2.49	113/2225 (5.1%)
15	AD	2.34	70/1665 (4.2%)	2.50	118/2227 (5.3%)
16	AE	2.35	48/1119 (4.3%)	2.49	75/1504 (5.0%)
17	AF	2.41	38/836 (4.5%)	2.49	65/1128 (5.8%)
18	AG	2.40	59/1188 (5.0%)	2.63	104/1591 (6.5%)
19	AH	2.27	43/989 (4.3%)	2.57	75/1326 (5.7%)
20	AI	2.27	41/1034 (4.0%)	2.35	55/1375 (4.0%)
21	AA	2.00	688/36763 (1.9%)	1.85	1210/57350 (2.1%)
22	AY	2.39	69/1814 (3.8%)	2.27	147/2827 (5.2%)
23	AW	2.45	52/1809 (2.9%)	2.00	82/2819 (2.9%)
24	AX	2.06	3/260 (1.2%)	1.86	8/403 (2.0%)
25	AZ	2.42	154/3091 (5.0%)	2.53	247/4182 (5.9%)
26	AV	2.06	39/1814 (2.1%)	1.90	68/2825 (2.4%)
27	B5	2.30	75/1748 (4.3%)	2.62	139/2355 (5.9%)
28	BI	2.36	52/1046 (5.0%)	2.53	86/1410 (6.1%)
29	BJ	2.35	52/1152 (4.5%)	2.43	77/1551 (5.0%)
30	BK	2.34	37/940 (3.9%)	2.44	61/1258 (4.8%)
31	BL	2.45	49/1054 (4.6%)	2.52	86/1403 (6.1%)
32	BM	2.31	49/1093 (4.5%)	2.53	74/1460 (5.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	BN	2.39	46/974 (4.7%)	2.52	73/1301 (5.6%)
34	BO	2.42	39/902 (4.3%)	2.57	73/1209 (6.0%)
35	BP	2.39	44/929 (4.7%)	2.38	54/1242 (4.3%)
36	BQ	2.25	36/960 (3.8%)	2.48	63/1278 (4.9%)
37	BR	2.37	41/829 (4.9%)	2.46	52/1107 (4.7%)
38	BS	2.31	35/864 (4.1%)	2.54	62/1156 (5.4%)
39	BT	2.13	19/745 (2.6%)	2.57	57/994 (5.7%)
40	BU	2.30	29/788 (3.7%)	2.53	48/1051 (4.6%)
41	BV	2.30	32/766 (4.2%)	2.52	58/1025 (5.7%)
42	BW	2.42	27/603 (4.5%)	2.47	40/797 (5.0%)
43	BX	2.42	34/635 (5.4%)	2.44	40/848 (4.7%)
44	BY	2.26	21/510 (4.1%)	2.46	37/677 (5.5%)
45	BC	2.37	91/2122 (4.3%)	2.54	154/2852 (5.4%)
46	BZ	2.25	24/453 (5.3%)	2.65	32/605 (5.3%)
47	B0	2.35	18/450 (4.0%)	2.48	27/599 (4.5%)
48	B1	2.33	16/417 (3.8%)	2.38	29/554 (5.2%)
49	B2	2.41	16/380 (4.2%)	2.68	34/498 (6.8%)
50	B3	2.26	25/513 (4.9%)	2.45	32/676 (4.7%)
51	B4	2.49	15/303 (5.0%)	2.56	25/397 (6.3%)
52	BD	2.31	73/1586 (4.6%)	2.41	101/2134 (4.7%)
53	BE	2.30	65/1571 (4.1%)	2.51	108/2113 (5.1%)
54	BF	2.31	55/1444 (3.8%)	2.57	117/1937 (6.0%)
55	BG	2.42	68/1343 (5.1%)	2.52	100/1816 (5.5%)
56	BH	2.24	46/1122 (4.1%)	2.60	97/1515 (6.4%)
57	BB	1.99	1355/69800 (1.9%)	1.84	2283/108892 (2.1%)
58	BA	2.00	55/2804 (2.0%)	1.86	100/4371 (2.3%)
All	All	2.12	4488/165195 (2.7%)	2.05	7530/246683 (3.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AJ	0	3
2	AK	0	4
3	AL	0	7
4	AM	0	5
5	AN	0	5
6	AO	0	5
7	AP	0	3
8	AQ	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
9	AR	0	4
10	AS	0	1
11	AT	0	3
12	AU	0	5
13	AB	0	4
14	AC	0	5
15	AD	0	9
16	AE	0	1
17	AF	0	2
18	AG	0	4
19	AH	0	4
20	AI	0	6
21	AA	0	713
22	AY	0	40
23	AW	3	39
24	AX	0	3
25	AZ	0	8
26	AV	0	37
27	B5	1	7
28	BI	0	3
29	BJ	0	9
30	BK	0	1
31	BL	0	8
32	BM	0	4
33	BN	0	3
34	BO	0	4
35	BP	0	2
36	BQ	0	4
37	BR	0	6
38	BS	0	1
39	BT	0	2
40	BU	0	2
41	BV	0	4
42	BW	0	3
43	BX	0	3
44	BY	0	2
45	BC	0	9
46	BZ	0	3
47	B0	0	4
48	B1	0	2
49	B2	0	1
50	B3	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
51	B4	0	1
52	BD	0	5
53	BE	0	7
54	BF	0	9
55	BG	0	5
56	BH	0	3
57	BB	0	1349
58	BA	0	56
All	All	4	2445

The worst 5 of 4488 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	AW	63	G	N9-C8	29.59	1.97	1.37
23	AW	63	G	N9-C4	26.14	1.90	1.38
23	AW	63	G	C5-C4	24.33	1.87	1.38
23	AW	63	G	N7-C5	23.42	1.86	1.39
23	AW	63	G	C8-N7	18.36	1.67	1.30

The worst 5 of 7530 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	B5	36	ALA	CA-C-N	18.25	154.55	121.70
27	B5	36	ALA	C-N-CA	18.25	154.55	121.70
27	B5	36	ALA	O-C-N	-17.55	99.25	122.59
57	BB	880	G	P-O3'-C3'	15.65	143.67	120.20
21	AA	1256	A	P-O3'-C3'	15.62	143.63	120.20

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
23	AW	17	C	C1'
23	AW	47	U	C1'
23	AW	70	G	C3'
27	B5	37	LYS	CA

5 of 2445 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AJ	16	ARG	Sidechain
1	AJ	68	ARG	Sidechain
1	AJ	9	ARG	Sidechain

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Mol	Chain	Res	Type	Group
2	AK	26	PHE	Sidechain
2	AK	55	ARG	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	AJ	787	0	828	4	0
2	AK	877	0	887	1	0
3	AL	955	0	1019	9	0
4	AM	877	0	937	8	0
5	AN	774	0	828	9	0
6	AO	716	0	742	8	0
7	AP	639	0	656	2	0
8	AQ	649	0	691	3	0
9	AR	456	0	478	4	0
10	AS	638	0	665	7	0
11	AT	665	0	714	1	0
12	AU	426	0	449	0	0
13	AB	1705	0	1732	10	0
14	AC	1625	0	1699	7	0
15	AD	1643	0	1710	18	0
16	AE	1106	0	1148	7	0
17	AF	818	0	808	6	0
18	AG	1175	0	1230	11	0
19	AH	979	0	1034	4	0
20	AI	1022	0	1070	5	0
21	AA	32832	0	16503	180	0
22	AY	1622	0	812	11	0
23	AW	1619	0	822	22	0
24	AX	232	0	120	2	0
25	AZ	3035	0	3049	17	0
26	AV	1645	0	834	6	0
27	B5	1733	0	1824	10	0
28	BI	1032	0	1088	5	0
29	BJ	1129	0	1162	8	0
30	BK	931	0	1003	5	0
31	BL	1045	0	1117	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	BM	1074	0	1157	1	0
33	BN	961	0	1000	7	0
34	BO	892	0	923	2	0
35	BP	917	0	965	5	0
36	BQ	947	0	1022	4	0
37	BR	816	0	839	3	0
38	BS	857	0	922	3	0
39	BT	739	0	807	4	0
40	BU	780	0	834	5	0
41	BV	753	0	780	3	0
42	BW	596	0	610	5	0
43	BX	625	0	655	3	0
44	BY	509	0	543	2	0
45	BC	2083	0	2157	16	0
46	BZ	449	0	491	0	0
47	B0	444	0	461	6	0
48	B1	410	0	440	4	0
49	B2	377	0	418	3	0
50	B3	504	0	574	3	0
51	B4	302	0	343	0	0
52	BD	1565	0	1616	16	0
53	BE	1552	0	1619	8	0
54	BF	1420	0	1460	10	0
55	BG	1323	0	1374	7	0
56	BH	1111	0	1148	4	0
57	BB	62321	0	31298	326	0
58	BA	2508	0	1268	8	0
59	AZ	28	0	12	0	0
All	All	152250	0	103395	782	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 3.

The worst 5 of 782 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)
23:AW:63:G:C5	23:AW:63:G:C4	1.87	1.59
23:AW:63:G:C8	23:AW:63:G:N7	1.67	1.56
23:AW:63:G:C5	23:AW:63:G:N7	1.86	1.43
23:AW:63:G:C4	23:AW:63:G:N9	1.90	1.40
23:AW:63:G:C8	23:AW:63:G:N9	1.97	1.31

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AJ	96/98 (98%)	77 (80%)	11 (12%)	8 (8%)	0	9
2	AK	115/117 (98%)	90 (78%)	18 (16%)	7 (6%)	1	13
3	AL	121/123 (98%)	107 (88%)	11 (9%)	3 (2%)	4	26
4	AM	111/113 (98%)	81 (73%)	20 (18%)	10 (9%)	0	8
5	AN	94/96 (98%)	67 (71%)	18 (19%)	9 (10%)	0	7
6	AO	86/88 (98%)	73 (85%)	8 (9%)	5 (6%)	1	13
7	AP	78/80 (98%)	61 (78%)	14 (18%)	3 (4%)	2	19
8	AQ	78/80 (98%)	62 (80%)	13 (17%)	3 (4%)	2	19
9	AR	53/55 (96%)	43 (81%)	10 (19%)	0	100	100
10	AS	77/79 (98%)	55 (71%)	17 (22%)	5 (6%)	1	12
11	AT	83/85 (98%)	73 (88%)	8 (10%)	2 (2%)	4	27
12	AU	49/51 (96%)	35 (71%)	10 (20%)	4 (8%)	0	9
13	AB	216/218 (99%)	166 (77%)	37 (17%)	13 (6%)	1	13
14	AC	204/206 (99%)	168 (82%)	26 (13%)	10 (5%)	1	16
15	AD	203/205 (99%)	161 (79%)	28 (14%)	14 (7%)	1	11
16	AE	148/150 (99%)	118 (80%)	21 (14%)	9 (6%)	1	13
17	AF	98/100 (98%)	79 (81%)	15 (15%)	4 (4%)	2	18
18	AG	148/150 (99%)	122 (82%)	18 (12%)	8 (5%)	1	14
19	AH	127/129 (98%)	96 (76%)	26 (20%)	5 (4%)	2	18
20	AI	125/127 (98%)	102 (82%)	21 (17%)	2 (2%)	7	38
25	AZ	391/393 (100%)	319 (82%)	52 (13%)	20 (5%)	1	15
27	B5	232/234 (99%)	195 (84%)	31 (13%)	6 (3%)	4	25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	BI	139/141 (99%)	121 (87%)	11 (8%)	7 (5%)	1	16
29	BJ	140/142 (99%)	116 (83%)	11 (8%)	13 (9%)	0	8
30	BK	119/121 (98%)	96 (81%)	18 (15%)	5 (4%)	2	17
31	BL	141/143 (99%)	118 (84%)	16 (11%)	7 (5%)	1	16
32	BM	134/136 (98%)	101 (75%)	26 (19%)	7 (5%)	1	15
33	BN	118/120 (98%)	97 (82%)	17 (14%)	4 (3%)	3	21
34	BO	114/116 (98%)	100 (88%)	8 (7%)	6 (5%)	1	14
35	BP	112/114 (98%)	87 (78%)	15 (13%)	10 (9%)	0	8
36	BQ	115/117 (98%)	99 (86%)	14 (12%)	2 (2%)	7	36
37	BR	101/103 (98%)	83 (82%)	13 (13%)	5 (5%)	1	16
38	BS	108/110 (98%)	85 (79%)	15 (14%)	8 (7%)	1	10
39	BT	91/93 (98%)	64 (70%)	19 (21%)	8 (9%)	0	8
40	BU	100/102 (98%)	79 (79%)	13 (13%)	8 (8%)	1	9
41	BV	92/94 (98%)	76 (83%)	14 (15%)	2 (2%)	5	29
42	BW	77/79 (98%)	56 (73%)	10 (13%)	11 (14%)	0	3
43	BX	75/77 (97%)	60 (80%)	10 (13%)	5 (7%)	1	12
44	BY	61/63 (97%)	47 (77%)	11 (18%)	3 (5%)	1	16
45	BC	269/271 (99%)	201 (75%)	43 (16%)	25 (9%)	0	8
46	BZ	56/58 (97%)	49 (88%)	7 (12%)	0	100	100
47	B0	54/56 (96%)	43 (80%)	9 (17%)	2 (4%)	2	19
48	B1	48/50 (96%)	44 (92%)	2 (4%)	2 (4%)	2	17
49	B2	44/46 (96%)	32 (73%)	11 (25%)	1 (2%)	5	28
50	B3	62/64 (97%)	54 (87%)	5 (8%)	3 (5%)	2	16
51	B4	36/38 (95%)	31 (86%)	4 (11%)	1 (3%)	4	24
52	BD	207/209 (99%)	152 (73%)	39 (19%)	16 (8%)	1	10
53	BE	199/201 (99%)	157 (79%)	29 (15%)	13 (6%)	1	12
54	BF	176/178 (99%)	129 (73%)	28 (16%)	19 (11%)	0	6
55	BG	174/176 (99%)	137 (79%)	23 (13%)	14 (8%)	1	9
56	BH	147/149 (99%)	107 (73%)	23 (16%)	17 (12%)	0	4
All	All	6242/6344 (98%)	4971 (80%)	897 (14%)	374 (6%)	2	13

5 of 374 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AJ	67	ILE
3	AL	24	GLU
4	AM	3	ILE
4	AM	29	SER
4	AM	99	GLN

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AJ	86/86 (100%)	78 (91%)	8 (9%)	8	26
2	AK	90/90 (100%)	87 (97%)	3 (3%)	33	55
3	AL	103/103 (100%)	99 (96%)	4 (4%)	28	49
4	AM	91/91 (100%)	82 (90%)	9 (10%)	7	24
5	AN	79/79 (100%)	79 (100%)	0	100	100
6	AO	76/76 (100%)	74 (97%)	2 (3%)	40	62
7	AP	65/65 (100%)	62 (95%)	3 (5%)	24	45
8	AQ	74/74 (100%)	69 (93%)	5 (7%)	14	36
9	AR	48/48 (100%)	45 (94%)	3 (6%)	16	37
10	AS	70/70 (100%)	67 (96%)	3 (4%)	26	47
11	AT	65/65 (100%)	65 (100%)	0	100	100
12	AU	44/44 (100%)	40 (91%)	4 (9%)	9	27
13	AB	180/180 (100%)	170 (94%)	10 (6%)	19	40
14	AC	170/170 (100%)	156 (92%)	14 (8%)	10	31
15	AD	172/172 (100%)	161 (94%)	11 (6%)	16	37
16	AE	113/113 (100%)	106 (94%)	7 (6%)	16	38
17	AF	87/87 (100%)	84 (97%)	3 (3%)	32	54
18	AG	123/123 (100%)	117 (95%)	6 (5%)	22	43
19	AH	104/104 (100%)	94 (90%)	10 (10%)	8	25
20	AI	105/105 (100%)	99 (94%)	6 (6%)	18	40

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	AZ	325/326 (100%)	307 (94%)	18 (6%)	19	41
27	B5	181/181 (100%)	167 (92%)	14 (8%)	12	32
28	BI	109/109 (100%)	101 (93%)	8 (7%)	13	34
29	BJ	116/116 (100%)	110 (95%)	6 (5%)	21	42
30	BK	102/102 (100%)	95 (93%)	7 (7%)	14	36
31	BL	102/102 (100%)	99 (97%)	3 (3%)	37	58
32	BM	109/109 (100%)	99 (91%)	10 (9%)	8	27
33	BN	100/100 (100%)	95 (95%)	5 (5%)	22	43
34	BO	86/86 (100%)	83 (96%)	3 (4%)	32	53
35	BP	99/99 (100%)	93 (94%)	6 (6%)	17	38
36	BQ	89/89 (100%)	87 (98%)	2 (2%)	45	64
37	BR	84/84 (100%)	79 (94%)	5 (6%)	17	39
38	BS	93/93 (100%)	89 (96%)	4 (4%)	26	47
39	BT	80/80 (100%)	74 (92%)	6 (8%)	12	33
40	BU	83/83 (100%)	73 (88%)	10 (12%)	5	17
41	BV	78/78 (100%)	77 (99%)	1 (1%)	61	74
42	BW	59/59 (100%)	54 (92%)	5 (8%)	10	29
43	BX	67/67 (100%)	60 (90%)	7 (10%)	7	22
44	BY	55/55 (100%)	54 (98%)	1 (2%)	51	68
45	BC	216/216 (100%)	204 (94%)	12 (6%)	19	40
46	BZ	48/48 (100%)	45 (94%)	3 (6%)	16	37
47	B0	47/47 (100%)	44 (94%)	3 (6%)	16	37
48	B1	45/45 (100%)	42 (93%)	3 (7%)	15	36
49	B2	38/38 (100%)	38 (100%)	0	100	100
50	B3	51/51 (100%)	48 (94%)	3 (6%)	18	39
51	B4	34/34 (100%)	34 (100%)	0	100	100
52	BD	164/164 (100%)	153 (93%)	11 (7%)	15	36
53	BE	165/165 (100%)	156 (94%)	9 (6%)	19	41
54	BF	149/149 (100%)	138 (93%)	11 (7%)	13	33
55	BG	137/137 (100%)	126 (92%)	11 (8%)	11	31
56	BH	114/114 (100%)	110 (96%)	4 (4%)	32	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	5170/5171 (100%)	4868 (94%)	302 (6%)	20	40

5 of 302 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
44	BY	53	VAL
54	BF	175	PRO
45	BC	183	VAL
52	BD	34	VAL
56	BH	129	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 165 such sidechains are listed below:

Mol	Chain	Res	Type
39	BT	70	HIS
49	B2	13	ASN
41	BV	75	GLN
45	BC	43	ASN
52	BD	130	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
21	AA	1529/1530 (99%)	281 (18%)	42 (2%)
22	AY	75/76 (98%)	20 (26%)	5 (6%)
23	AW	75/76 (98%)	24 (32%)	6 (8%)
24	AX	10/11 (90%)	3 (30%)	0
26	AV	76/77 (98%)	14 (18%)	0
57	BB	2902/2903 (99%)	496 (17%)	63 (2%)
58	BA	116/117 (99%)	20 (17%)	4 (3%)
All	All	4783/4790 (99%)	858 (17%)	120 (2%)

5 of 858 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
21	AA	6	G
21	AA	7	A
21	AA	8	A
21	AA	9	G
21	AA	14	U

5 of 120 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
57	BB	548	G
57	BB	2402	U
57	BB	1068	G
57	BB	2336	A
58	BA	66	A

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

1 non-standard protein/DNA/RNA residue is 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
26	5MU	AV	54	26	19,22,23	1.33	4 (21%)	27,32,35	1.22	3 (11%)

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
26	5MU	AV	54	26	-	0/7/25/26	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	AV	54	5MU	C6-N1	2.46	1.42	1.38
26	AV	54	5MU	O4'-C1'	2.35	1.47	1.42
26	AV	54	5MU	O2'-C2'	-2.33	1.37	1.43
26	AV	54	5MU	C2-N1	2.26	1.42	1.38

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	AV	54	5MU	C6-N1-C2	-3.02	118.30	121.30
26	AV	54	5MU	O4'-C1'-N1	2.80	114.70	108.36
26	AV	54	5MU	C1'-N1-C6	2.41	125.13	121.15

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	$\# Z > 2$
59	GDP	AZ	401	-	29,30,30	1.86	4 (13%)	45,47,47	1.33	6 (13%)

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
59	GDP	AZ	401	-	-	2/16/32/32	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	AZ	401	GDP	PA-O3A	7.75	1.67	1.59
59	AZ	401	GDP	O4'-C1'	3.01	1.48	1.42
59	AZ	401	GDP	C4-N3	2.23	1.39	1.34
59	AZ	401	GDP	O3'-C3'	-2.03	1.37	1.43

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	AZ	401	GDP	C5-C4-N3	-3.11	123.43	128.39
59	AZ	401	GDP	C6-C5-N7	-2.44	125.85	130.29
59	AZ	401	GDP	O3'-C3'-C2'	2.28	119.11	111.82
59	AZ	401	GDP	C2-N3-C4	2.20	116.08	112.30
59	AZ	401	GDP	C6-C5-C4	2.13	122.03	118.83

There are no chirality outliers.

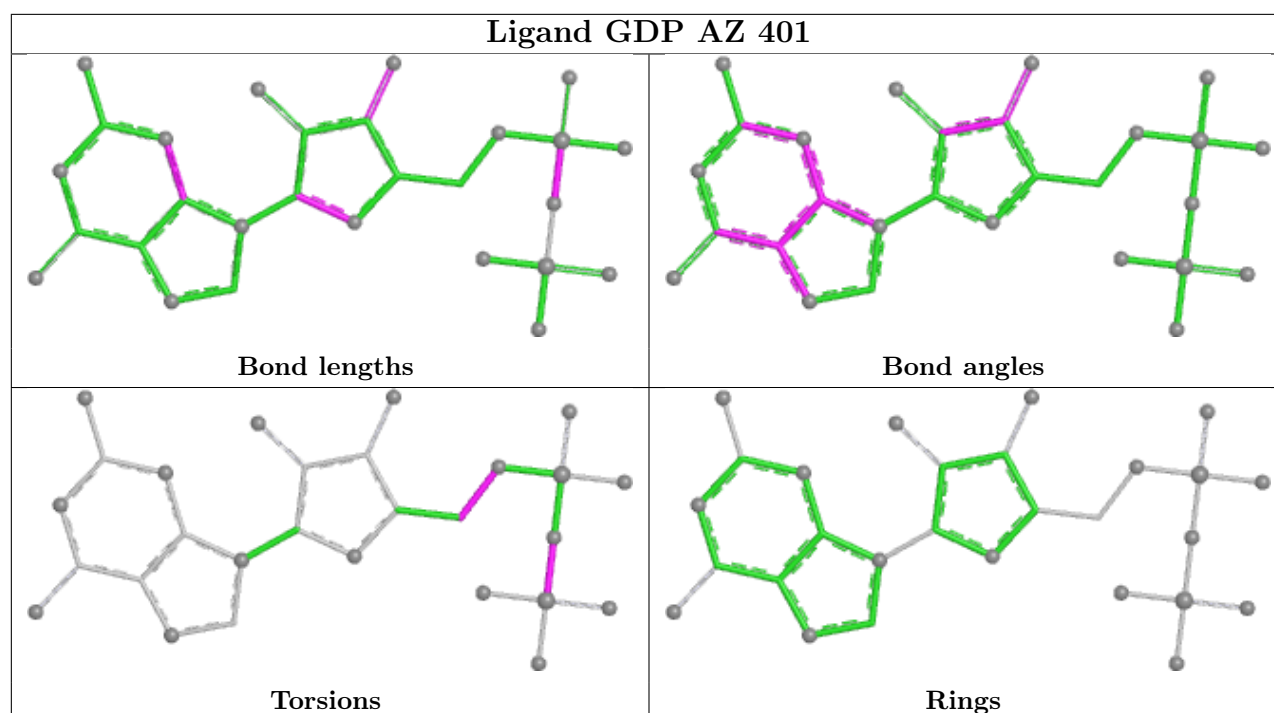
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	AZ	401	GDP	PA-O3A-PB-O3B
59	AZ	401	GDP	C4'-C5'-O5'-PA

There are no ring outliers.

No monomer is involved in short contacts.

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.

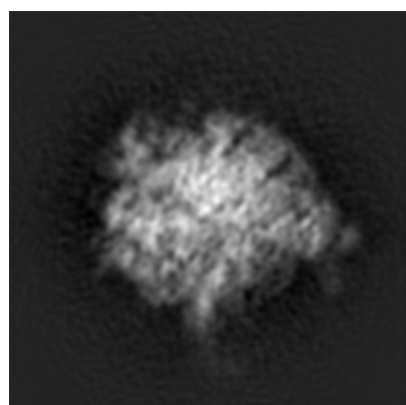
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5036. These allow visual inspection of the internal detail of the map and identification of artifacts.

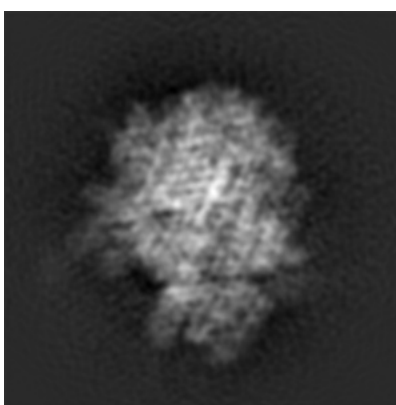
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

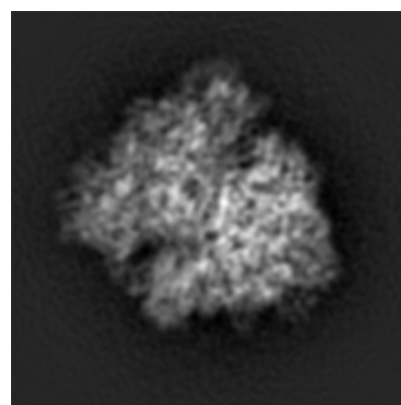
6.1.1 Primary map



X



Y

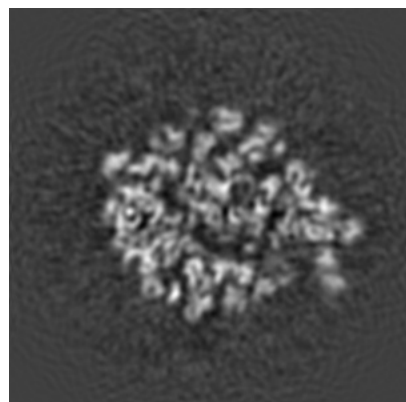


Z

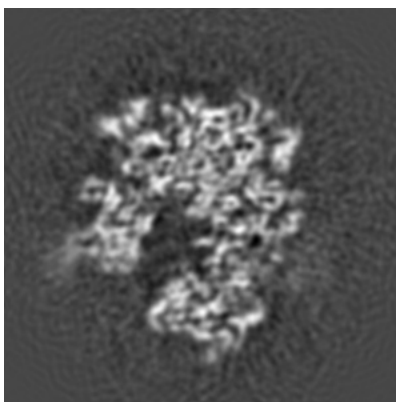
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

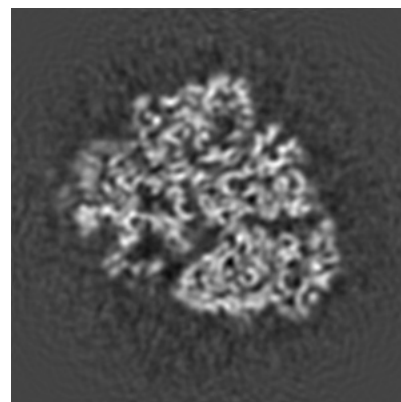
6.2.1 Primary map



X Index: 154



Y Index: 154

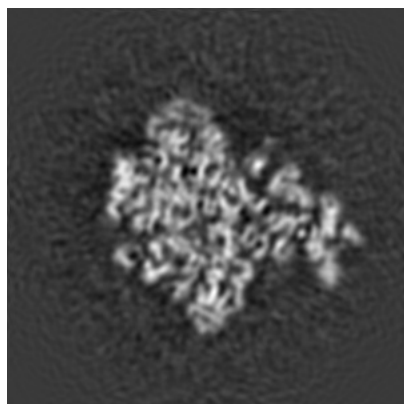


Z Index: 154

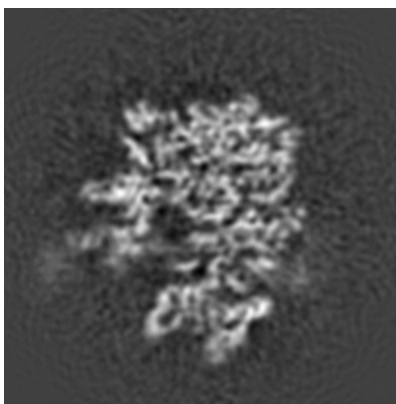
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

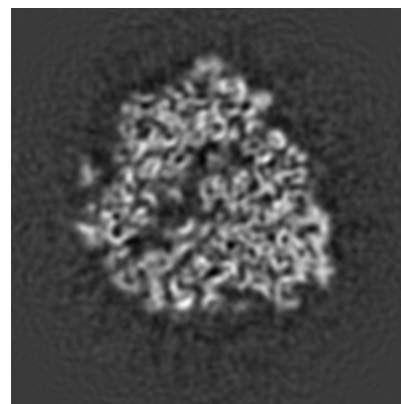
6.3.1 Primary map



X Index: 164



Y Index: 160

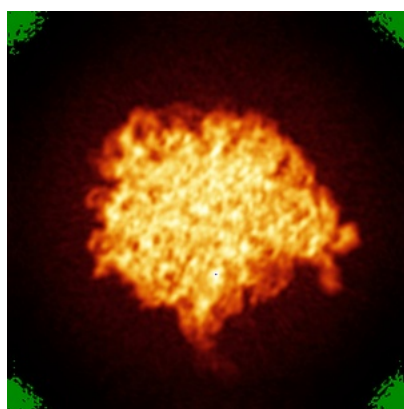


Z Index: 142

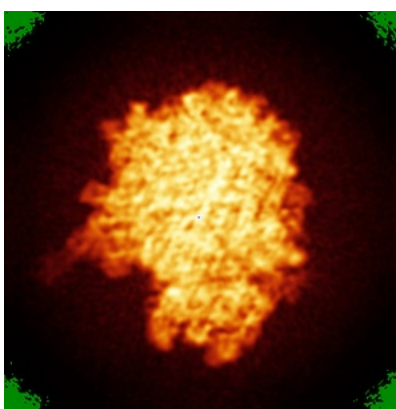
The images above show the largest variance slices of the map in three orthogonal directions.

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

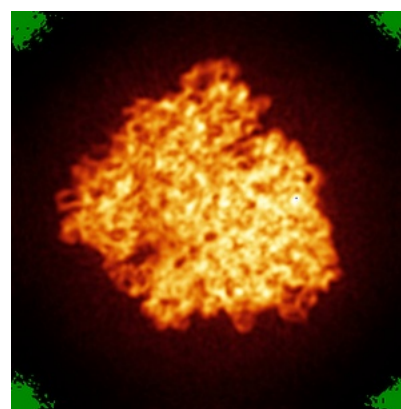
6.4.1 Primary map



X



Y

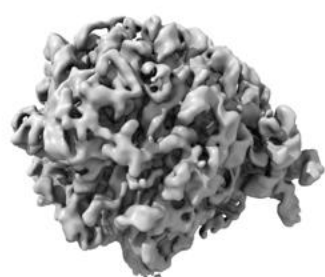


Z

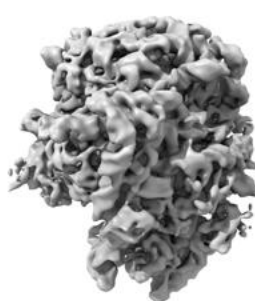
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

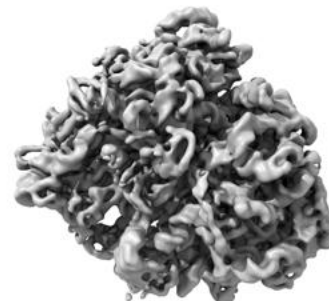
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 90.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

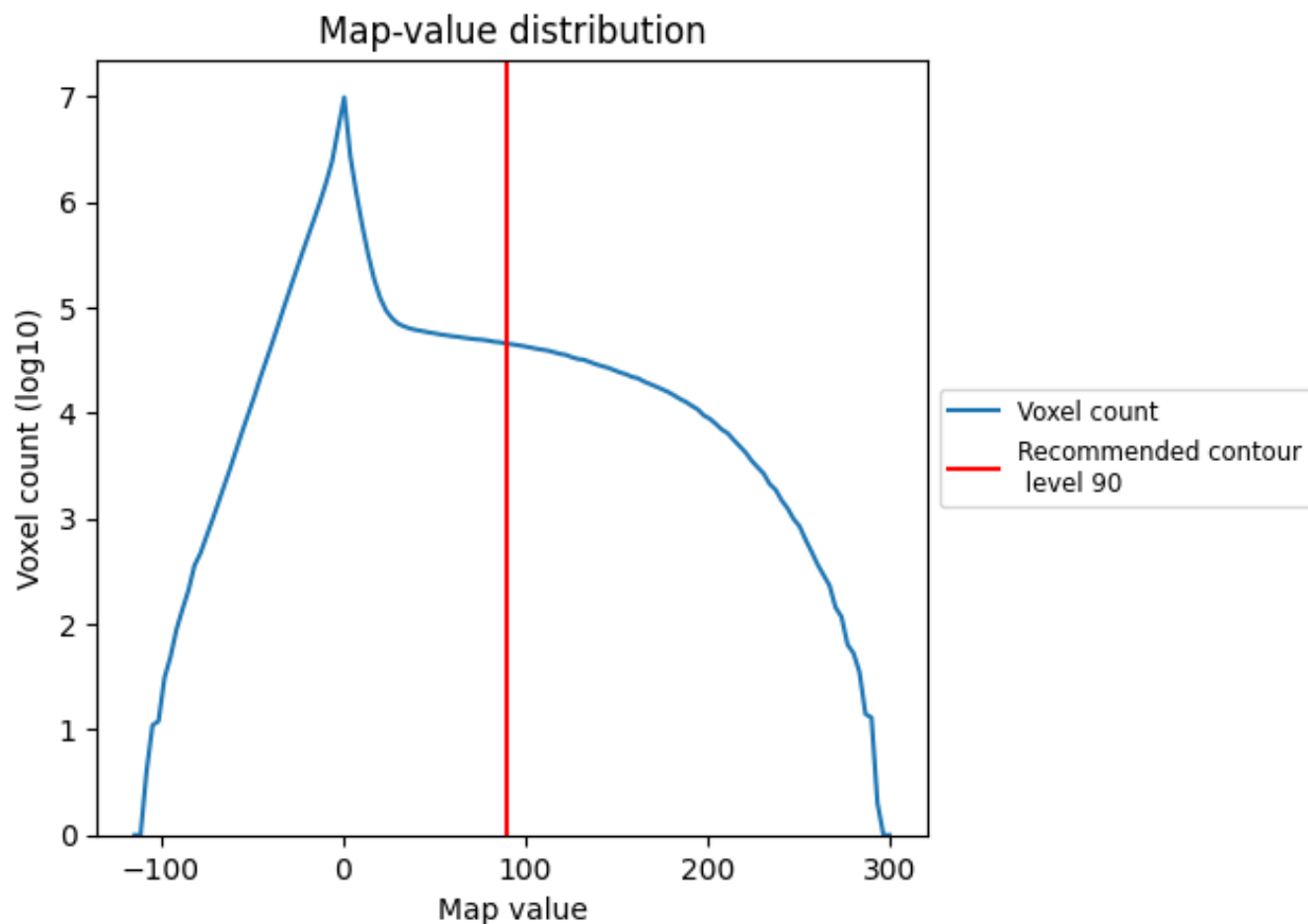
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

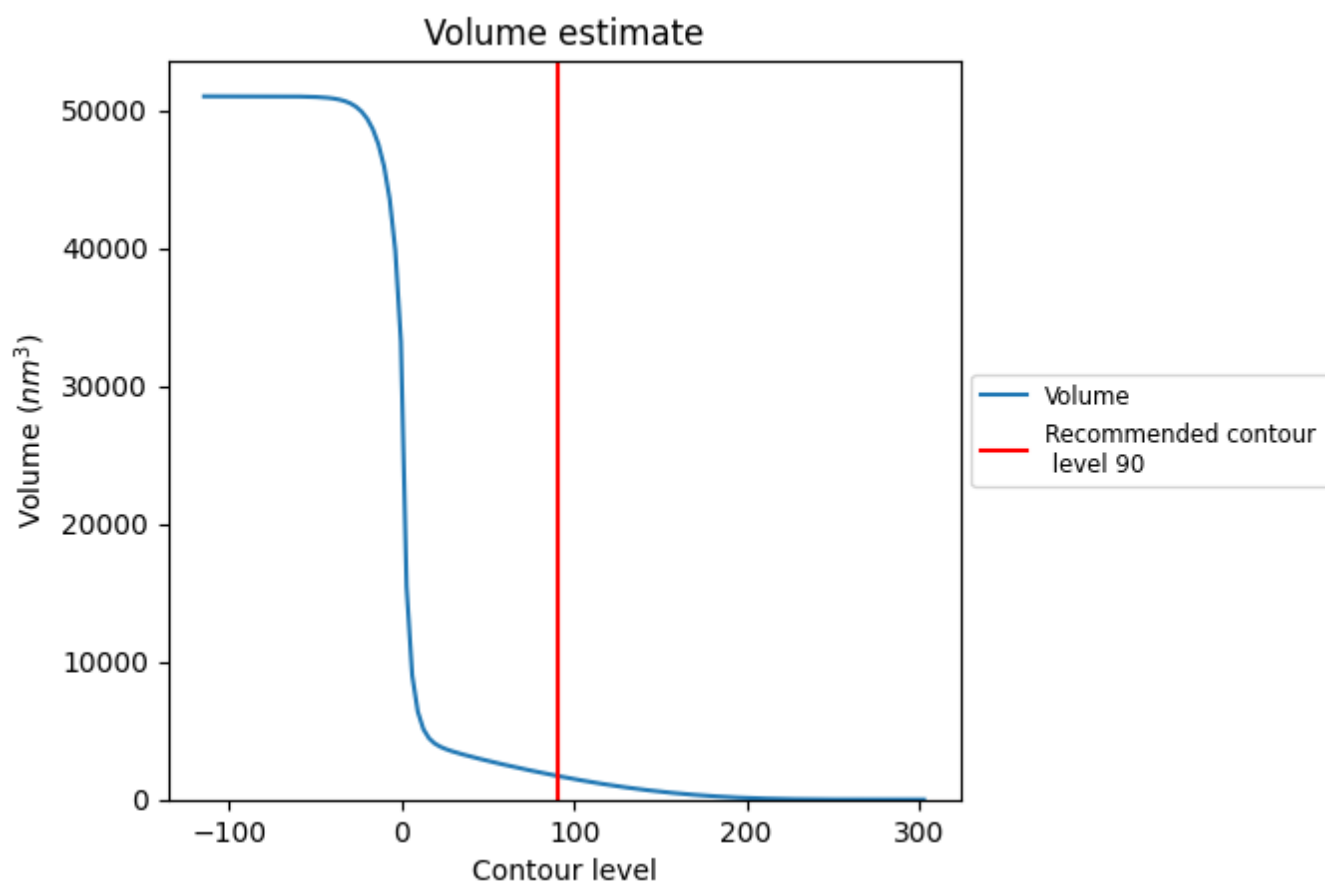
This section contains the results of statistical analysis of the map.

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.

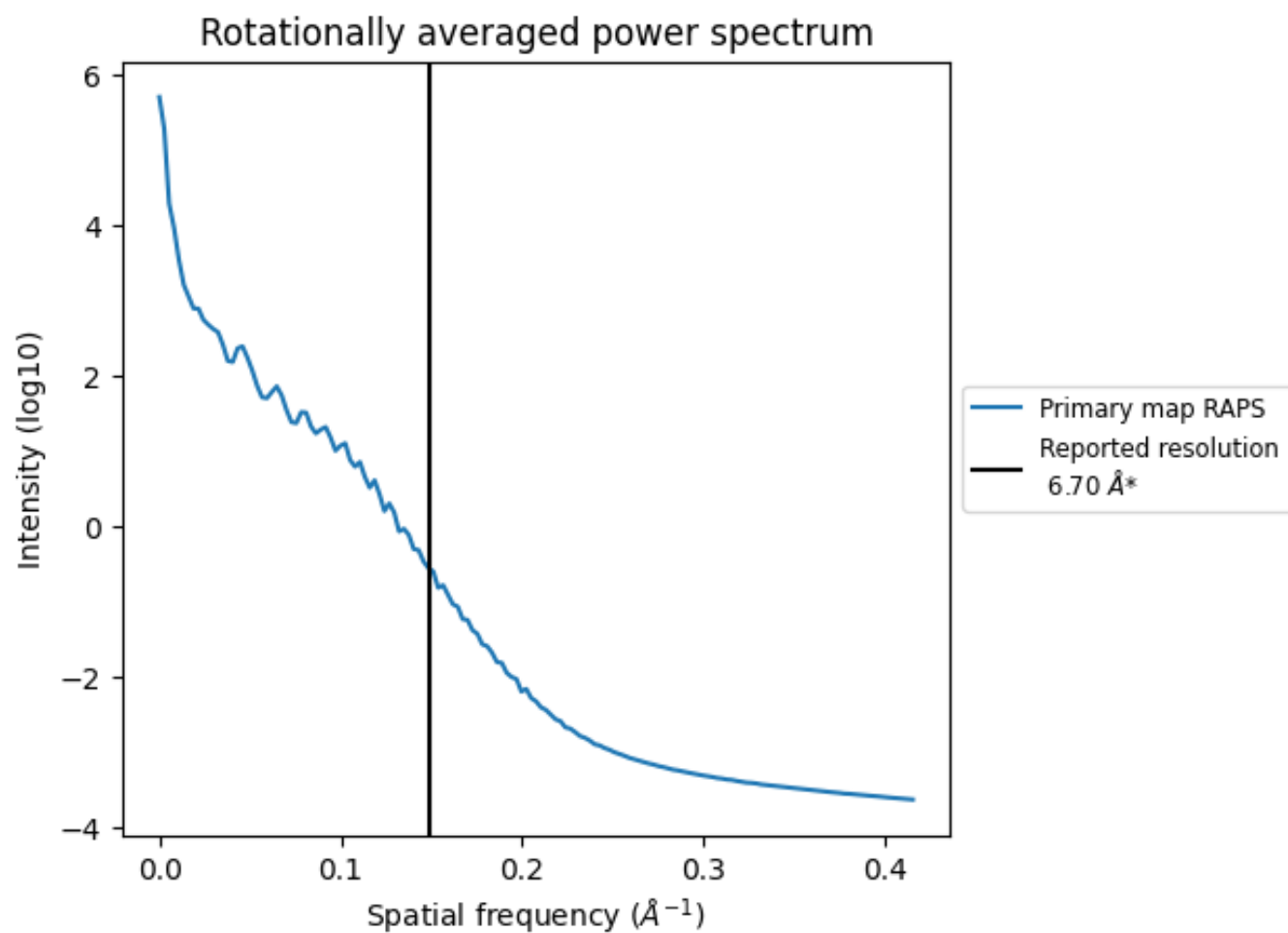
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1724 nm³; this corresponds to an approximate mass of 1557 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 0.149 Å⁻¹

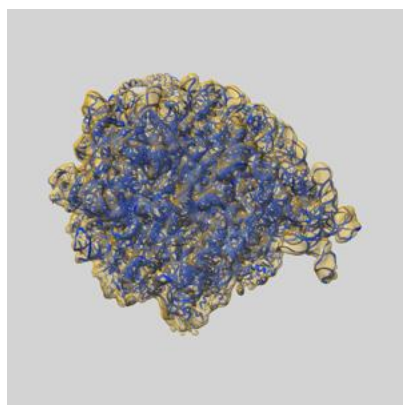
8 Fourier-Shell correlation

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

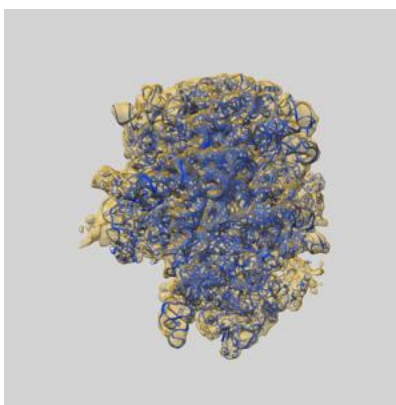
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-5036 and PDB model 4V69. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

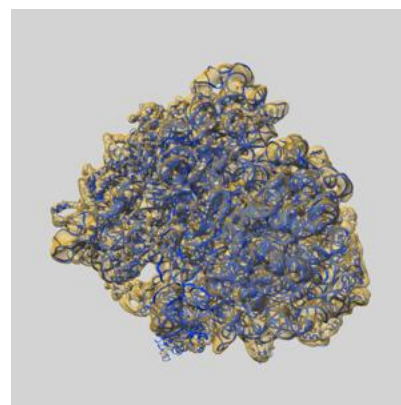
9.1 Map-model overlay [i](#)



X



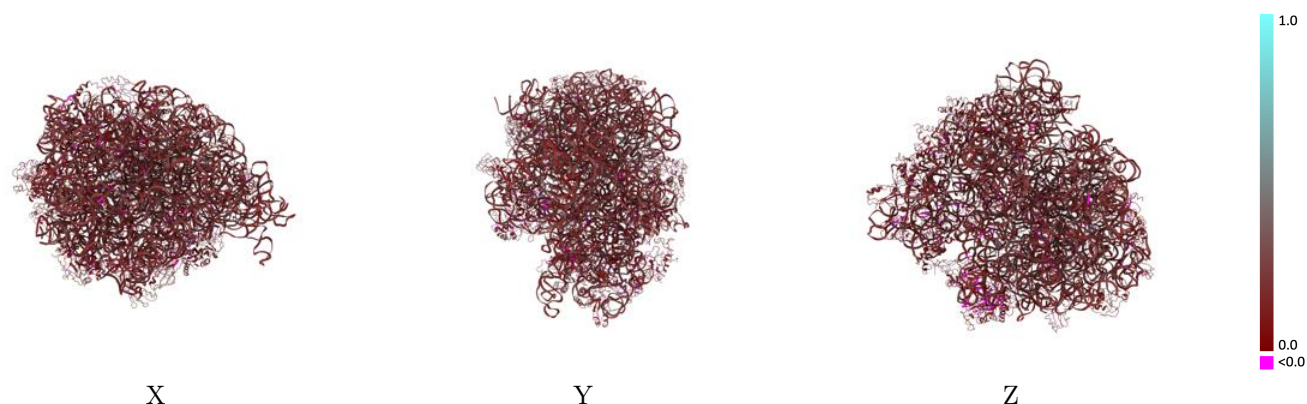
Y



Z

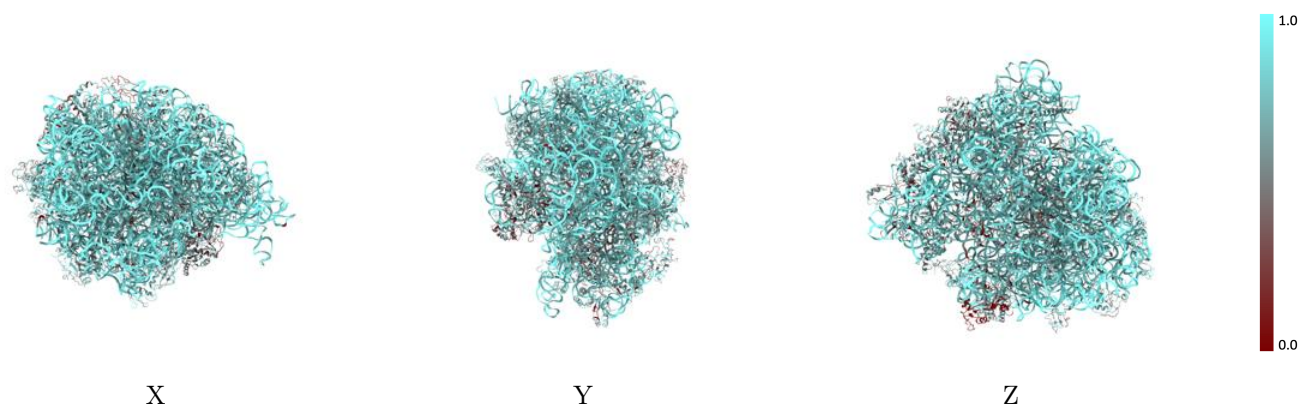
The images above show the 3D surface view of the map at the recommended contour level 90.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



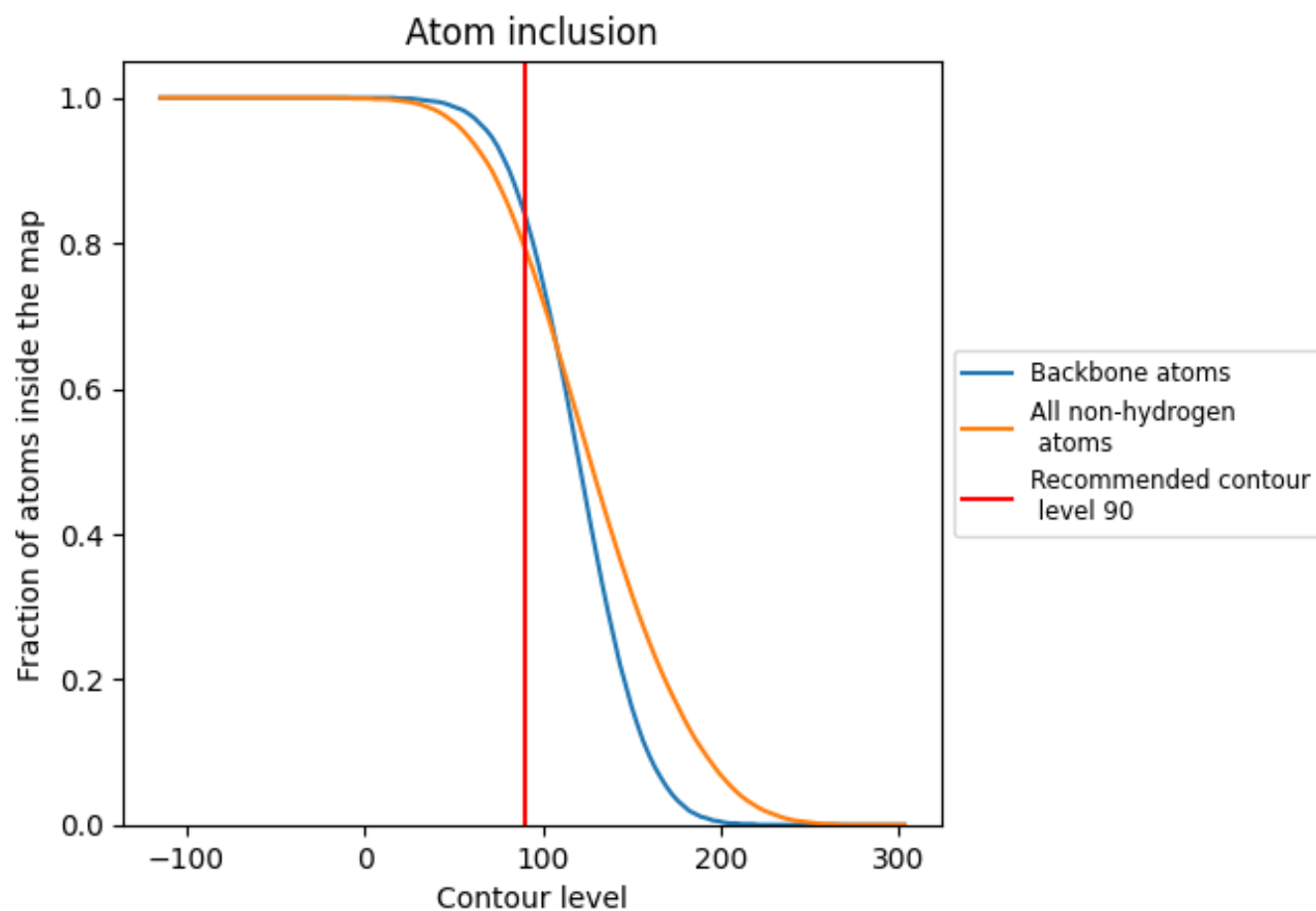
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (90).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 79% 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 (90) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7930	 0.1860
AA	 0.8950	 0.2030
AB	 0.5980	 0.1550
AC	 0.6000	 0.1680
AD	 0.4980	 0.1540
AE	 0.5930	 0.1600
AF	 0.6510	 0.1650
AG	 0.6070	 0.1460
AH	 0.5600	 0.1590
AI	 0.6100	 0.1320
AJ	 0.4580	 0.1330
AK	 0.5100	 0.1580
AL	 0.4790	 0.1550
AM	 0.6190	 0.1590
AN	 0.6060	 0.1390
AO	 0.6230	 0.1520
AP	 0.6140	 0.1330
AQ	 0.6820	 0.1460
AR	 0.5490	 0.1480
AS	 0.6740	 0.1430
AT	 0.6030	 0.1520
AU	 0.7470	 0.2000
AV	 0.7940	 0.1990
AW	 0.7090	 0.1720
AX	 0.7540	 0.2270
AY	 0.7890	 0.1930
AZ	 0.4790	 0.1640
B0	 0.6400	 0.1350
B1	 0.6170	 0.1530
B2	 0.5970	 0.1010
B3	 0.5890	 0.1460
B4	 0.4970	 0.1260
B5	 0.3000	 0.0990
BA	 0.9240	 0.2090
BB	 0.9050	 0.2040



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Chain	Atom inclusion	Q-score
BC	 0.5800	 0.1420
BD	 0.5850	 0.1460
BE	 0.6170	 0.1630
BF	 0.7330	 0.1620
BG	 0.6840	 0.1710
BH	 0.4090	 0.1420
BI	 0.4640	 0.1380
BJ	 0.6030	 0.1590
BK	 0.4080	 0.1560
BL	 0.5300	 0.1450
BM	 0.5420	 0.1470
BN	 0.6650	 0.1340
BO	 0.7220	 0.1530
BP	 0.5630	 0.1700
BQ	 0.6130	 0.1150
BR	 0.6270	 0.1580
BS	 0.5920	 0.1460
BT	 0.6280	 0.1380
BU	 0.6730	 0.1560
BV	 0.7250	 0.1700
BW	 0.5380	 0.0990
BX	 0.5810	 0.1520
BY	 0.7060	 0.1360
BZ	 0.6590	 0.1660