



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 08:40 AM UTC

PDB ID : 4V6T / pdb_00004v6t
EMDB ID : EMD-5386
Title : Structure of the bacterial ribosome complexed by tmRNA-SmpB and EF-G during translocation and MLD-loading
Authors : Ramrath, D.J.F.; Yamamoto, H.; Rother, K.; Wittek, D.; Pech, M.; Mielke, T.; Loerke, J.; Scheerer, P.; Ivanov, P.; Teraoka, Y.; Shpanchenko, O.; Nierhaus, K.H.; Spahn, C.M.T.
Deposited on : 2012-01-27
Resolution : 8.30 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

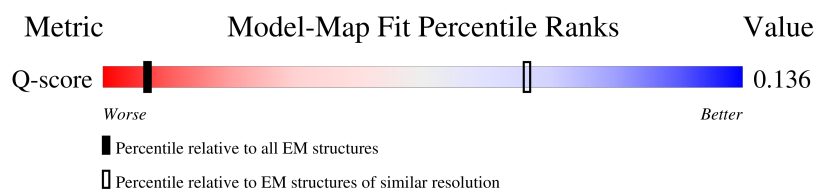
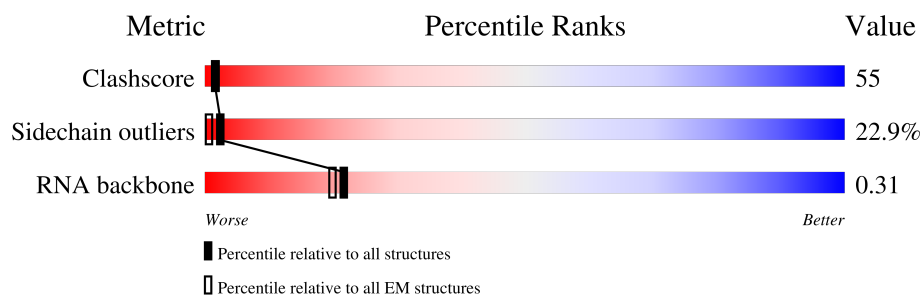
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 8.30 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	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	280 (7.82 - 8.80)

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	1539	
2	AB	218	
3	AC	206	
4	AD	205	

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Mol	Chain	Length	Quality of chain
5	AE	150	
6	AF	100	
7	AG	151	
8	AH	129	
9	AI	127	
10	AJ	98	
11	AK	117	
12	AL	123	
13	AM	114	
14	AN	100	
15	AO	88	
16	AP	82	
17	AQ	80	
18	AR	55	
19	AS	79	
20	AT	85	
21	AU	51	
22	AV	363	
23	AW	123	
24	AX	77	
25	AY	691	
26	BA	2903	
27	BC	271	
28	BD	209	
29	BE	201	

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Mol	Chain	Length	Quality of chain
30	BF	177	
31	BG	176	
32	BH	149	
33	BI	141	
34	BJ	142	
35	BK	122	
36	BL	143	
37	BM	136	
38	BN	120	
39	BO	116	
40	BP	114	
41	BQ	117	
42	BR	103	
43	BS	110	
44	BT	93	
45	BU	102	
46	BV	94	
47	BW	76	
48	BX	77	
49	BY	63	
50	BZ	58	
51	B0	56	
52	B1	50	
53	B2	46	
54	B3	64	

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Mol	Chain	Length	Quality of chain
55	B4	38	
56	BB	119	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
22	PSU	AV	347	-	-	X	-

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 157519 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 ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	1538	Total	C	N	O	P	0	0
			32995	14716	6050	10691	1538		

- Molecule 2 is a protein called 30S ribosomal protein S2.

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

- 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
			1625	1028	305	289	3		

- Molecule 4 is a protein called 30S ribosomal protein S4.

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

- 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
			1106	687	211	202	6		

- Molecule 6 is a protein called 30S ribosomal protein S6.

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

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AG	151	Total	C	N	O	S	0	0
			1182	735	227	216	4		

- Molecule 8 is a protein called 30S ribosomal protein S8.

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

- 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
			1022	634	206	179	3		

- 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
			787	493	150	143	1		

- Molecule 11 is a protein called 30S ribosomal protein S11.

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

- Molecule 12 is a protein called 30S ribosomal protein S12.

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

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AM	114	Total	C	N	O	S	0	0
			884	546	178	157	3		

- Molecule 14 is a protein called 30S ribosomal protein S14.

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

- 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
			714	439	144	130	1		

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AP	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 17 is a protein called 30S ribosomal protein S17.

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

- Molecule 18 is a protein called 30S ribosomal protein S18.

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

- Molecule 19 is a protein called 30S ribosomal protein S19.

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

- Molecule 20 is a protein called 30S ribosomal protein S20.

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

- Molecule 21 is a protein called 30S ribosomal protein S21.

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

- Molecule 22 is a RNA chain called full length transfer messenger RNA (tmRNA).

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AV	334	Total	C	N	O	P	0	0
			7135	3185	1286	2330	334		

- Molecule 23 is a protein called SsrA-binding protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	AW	122	Total	C	N	O	0	0
			993	637	181	175		

- Molecule 24 is a RNA chain called formyl-methionine specific initiator transfer RNA.

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

- Molecule 25 is a protein called elongation factor G.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AY	667	Total	C	N	O	S	0	1
			5215	3316	893	988	18		

- Molecule 26 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BA	2903	Total	C	N	O	P	0	0
			62319	27801	11467	20149	2902		

- Molecule 27 is a protein called 50S ribosomal protein L2.

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

- Molecule 28 is a protein called 50S ribosomal protein L3.

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

- Molecule 29 is a protein called 50S ribosomal protein L4.

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

- Molecule 30 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BF	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

- Molecule 31 is a protein called 50S ribosomal protein L6.

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

- Molecule 32 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BH	149	Total	C	N	O	S	0	0
			1110	699	197	213	1		

- Molecule 33 is a protein called 50S ribosomal protein L11.

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

- Molecule 34 is a protein called 50S ribosomal protein L13.

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

- Molecule 35 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BK	122	Total	C	N	O	S	0	0
			939	587	180	166	6		

- Molecule 36 is a protein called 50S ribosomal protein L15.

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

- Molecule 37 is a protein called 50S ribosomal protein L16.

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

- Molecule 38 is a protein called 50S ribosomal protein L17.

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

- Molecule 39 is a protein called 50S ribosomal protein L18.

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

- Molecule 40 is a protein called 50S ribosomal protein L19.

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

- Molecule 41 is a protein called 50S ribosomal protein L20.

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

- Molecule 42 is a protein called 50S ribosomal protein L21.

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

- Molecule 43 is a protein called 50S ribosomal protein L22.

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

- Molecule 44 is a protein called 50S ribosomal protein L23.

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

- Molecule 45 is a protein called 50S ribosomal protein L24.

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

- Molecule 46 is a protein called 50S ribosomal protein L25.

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

- Molecule 47 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BW	76	Total	C	N	O	S	0	0
			575	356	117	101	1		

- Molecule 48 is a protein called 50S ribosomal protein L28.

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

- Molecule 49 is a protein called 50S ribosomal protein L29.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L32.

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

- Molecule 52 is a protein called 50S ribosomal protein L33.

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

- Molecule 53 is a protein called 50S ribosomal protein L34.

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

- Molecule 54 is a protein called 50S ribosomal protein L35.

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

- Molecule 55 is a protein called 50S ribosomal protein L36.

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

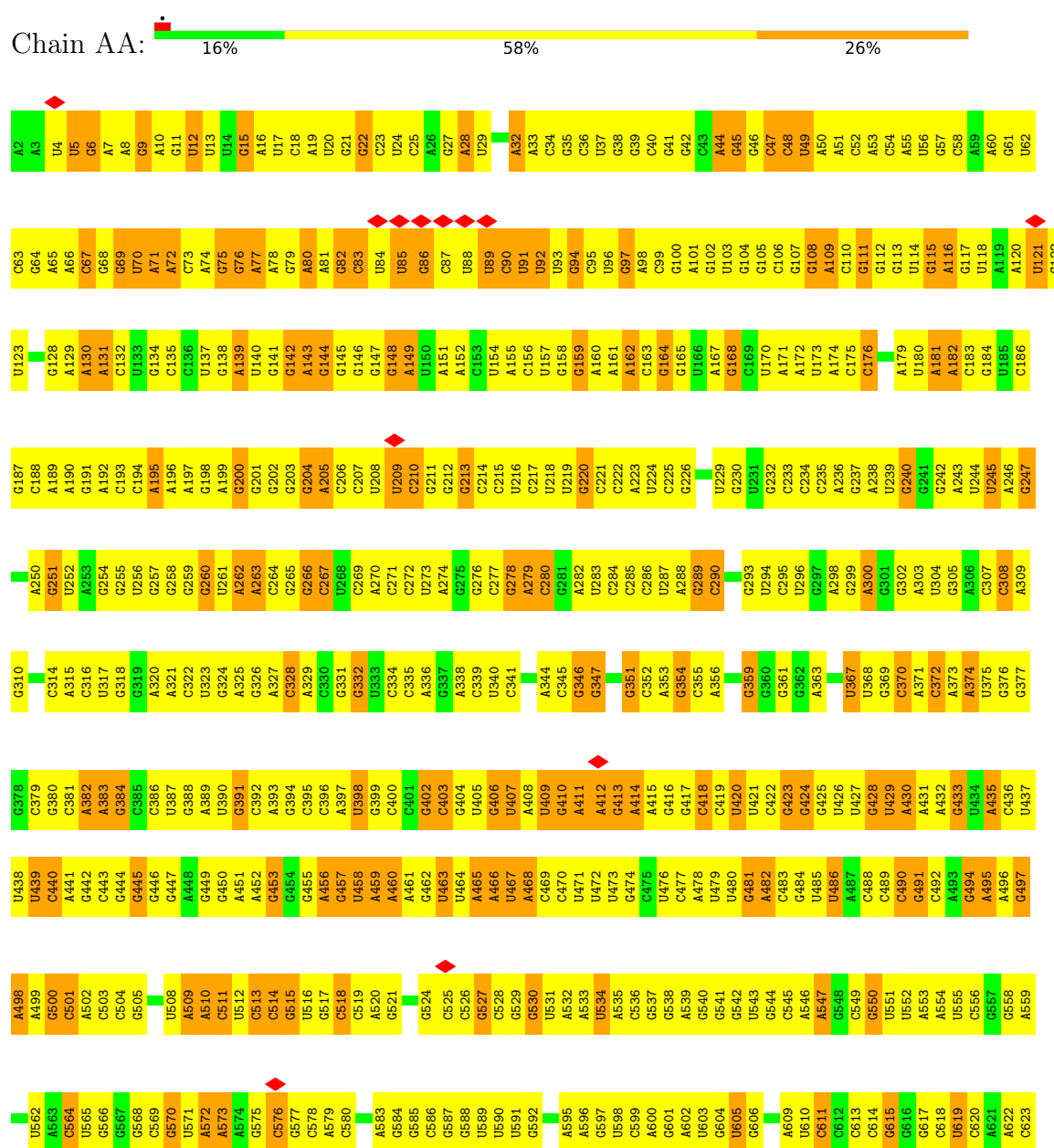
- Molecule 56 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BB	119	Total	C	N	O	P	0	0
			2548	1135	466	829	118		

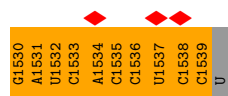
3 Residue-property plots

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

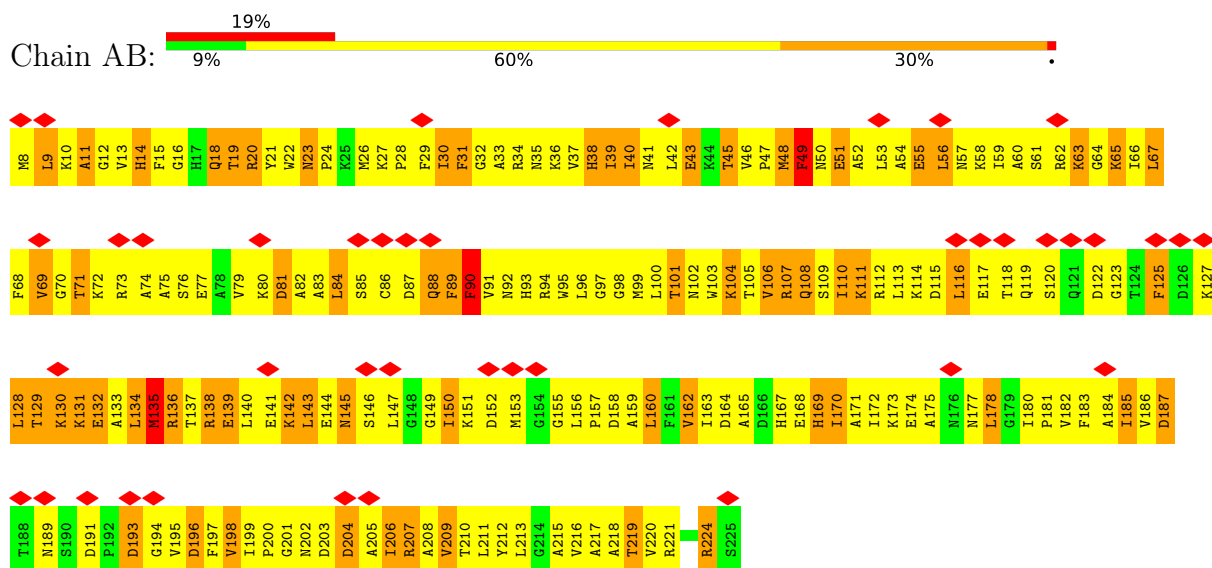
• Molecule 1: 16S ribosomal RNA



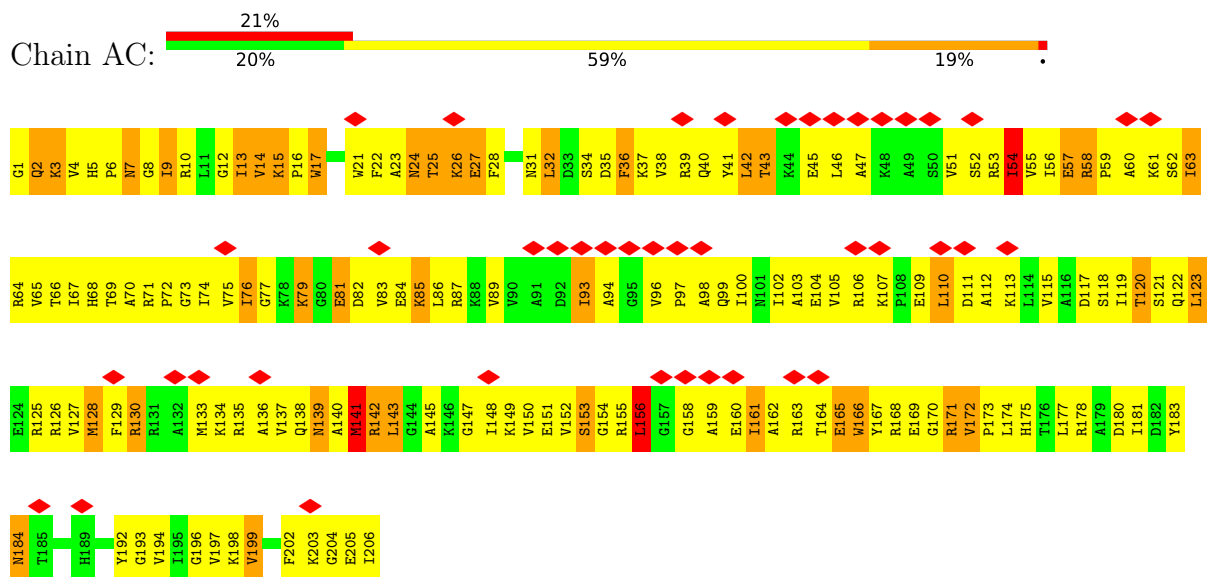




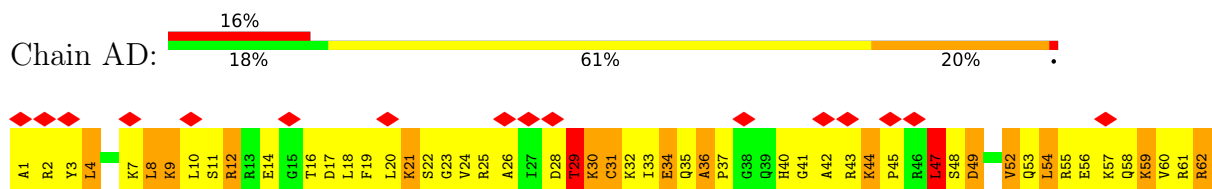
• Molecule 2: 30S ribosomal protein S2

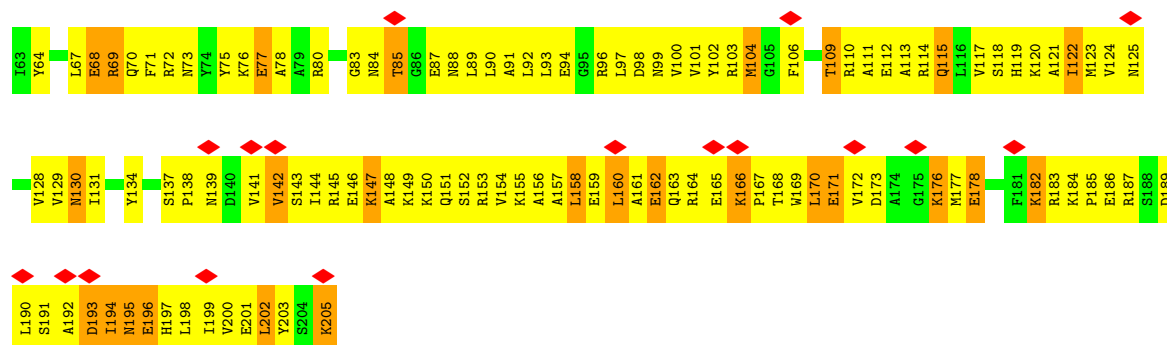


• Molecule 3: 30S ribosomal protein S3



• Molecule 4: 30S ribosomal protein S4

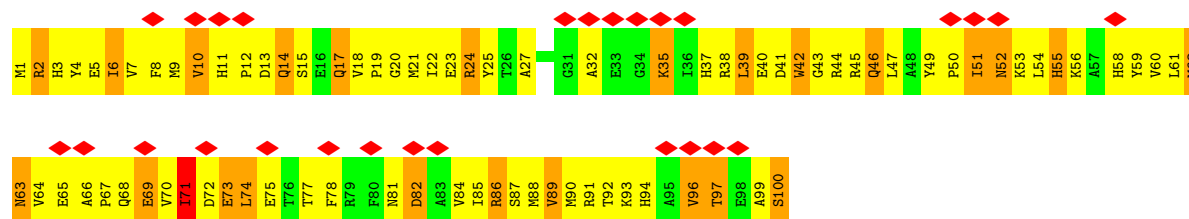




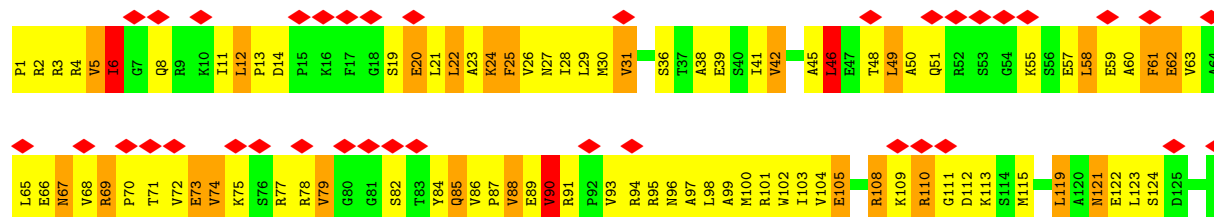
• Molecule 5: 30S ribosomal protein S5



• Molecule 6: 30S ribosomal protein S6

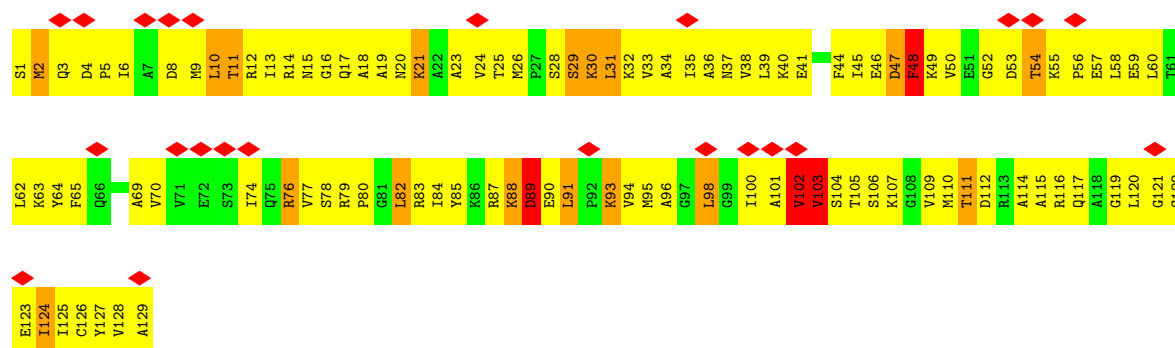


• Molecule 7: 30S ribosomal protein S7

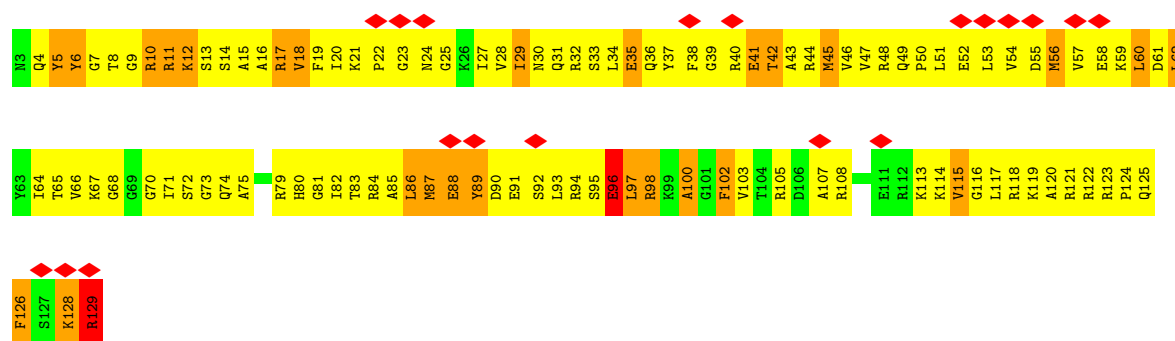
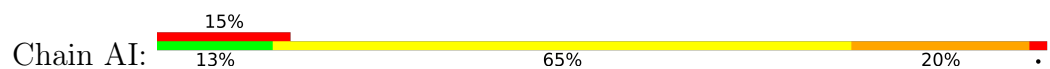




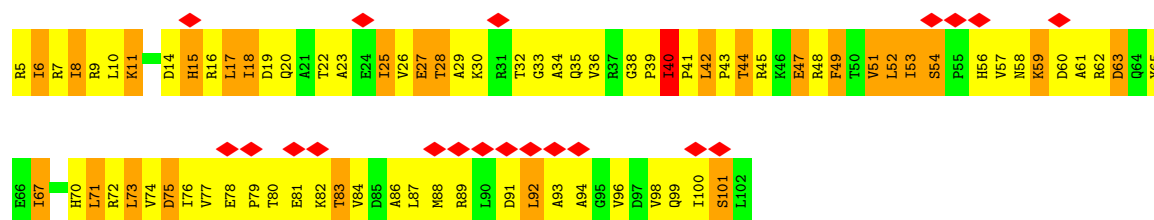
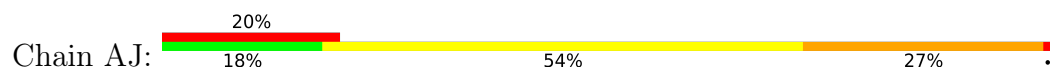
• Molecule 8: 30S ribosomal protein S8



• Molecule 9: 30S ribosomal protein S9

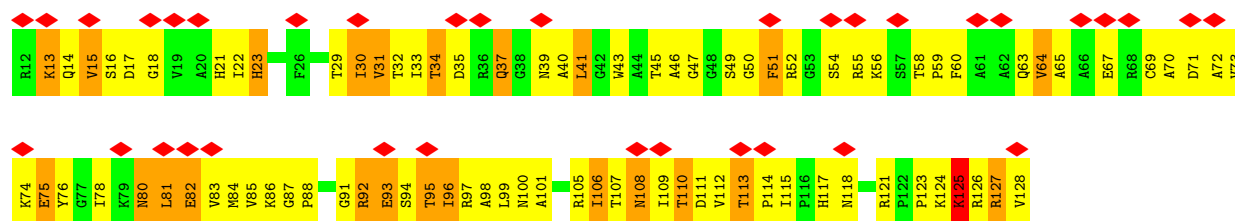


• Molecule 10: 30S ribosomal protein S10

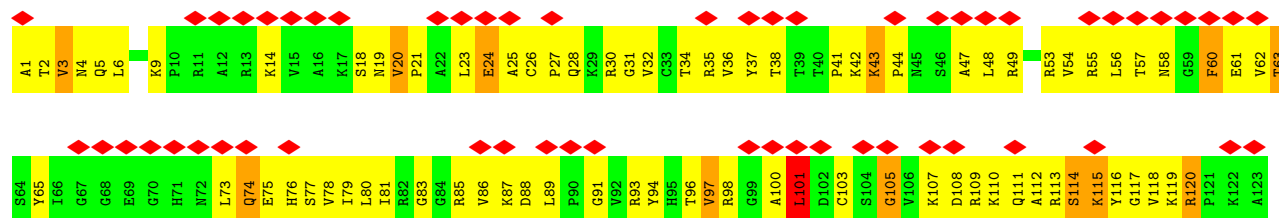


• Molecule 11: 30S ribosomal protein S11

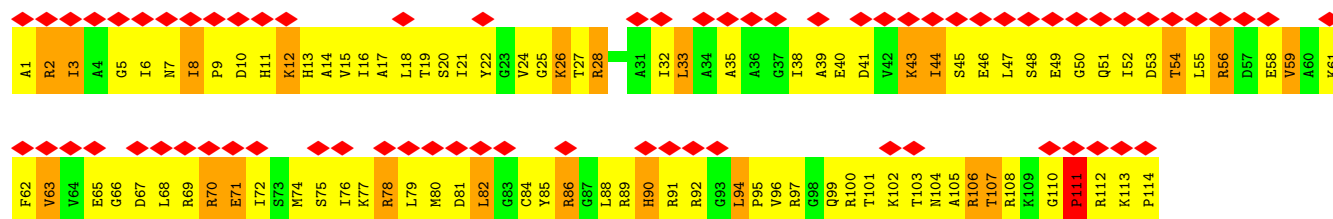




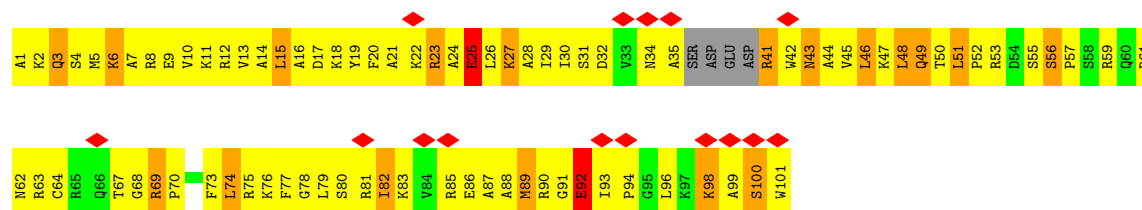
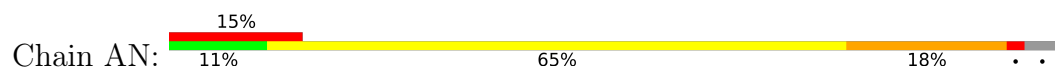
• Molecule 12: 30S ribosomal protein S12



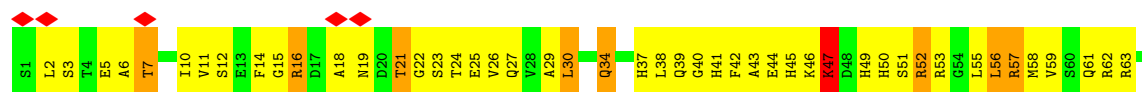
• Molecule 13: 30S ribosomal protein S13



• Molecule 14: 30S ribosomal protein S14

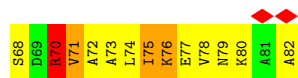
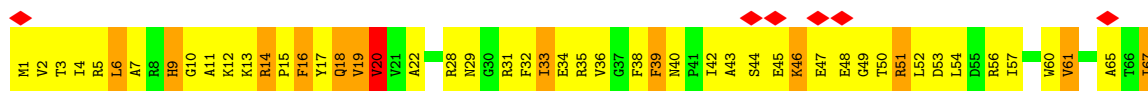


• Molecule 15: 30S ribosomal protein S15

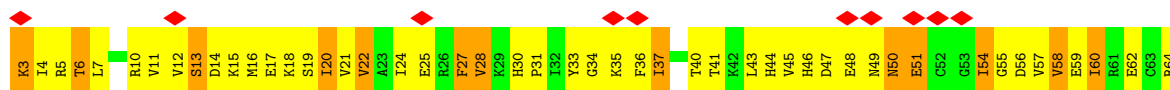




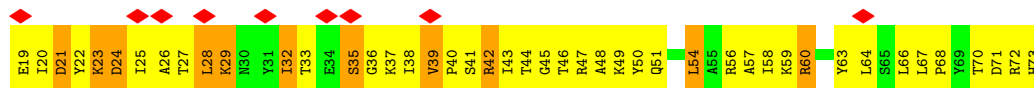
- Molecule 16: 30S ribosomal protein S16



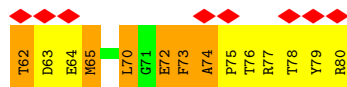
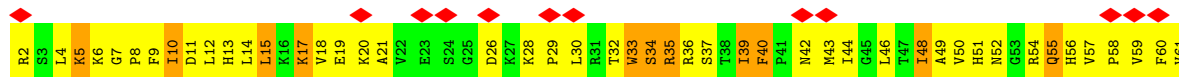
- Molecule 17: 30S ribosomal protein S17



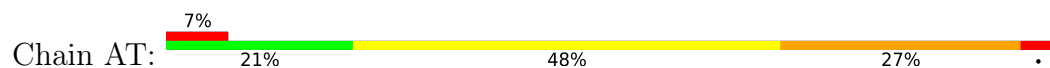
- Molecule 18: 30S ribosomal protein S18

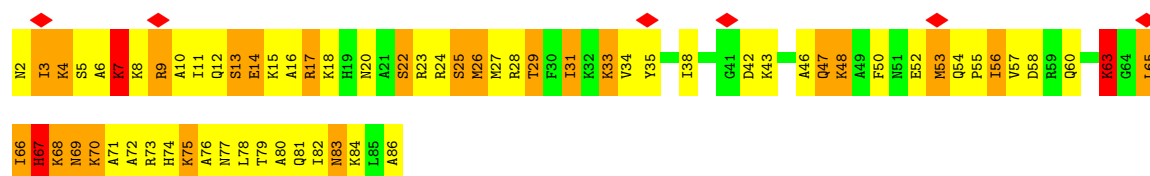


- Molecule 19: 30S ribosomal protein S19

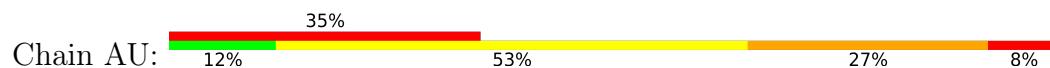


- Molecule 20: 30S ribosomal protein S20

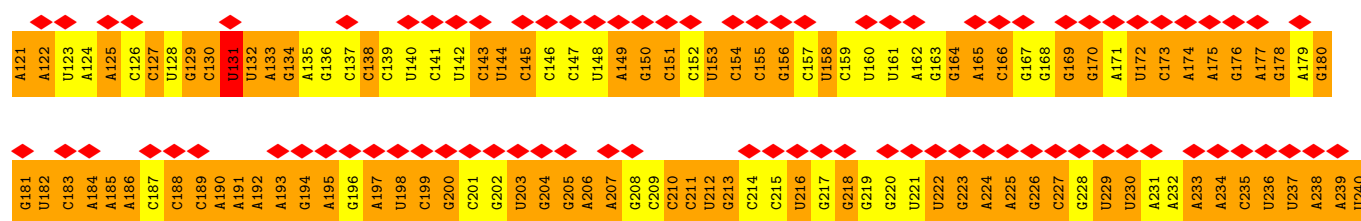




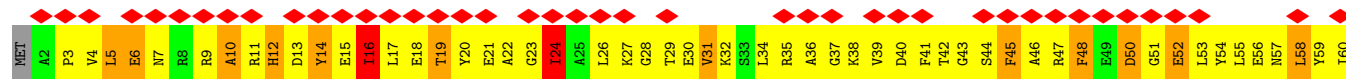
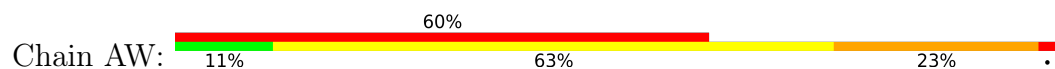
• Molecule 21: 30S ribosomal protein S21

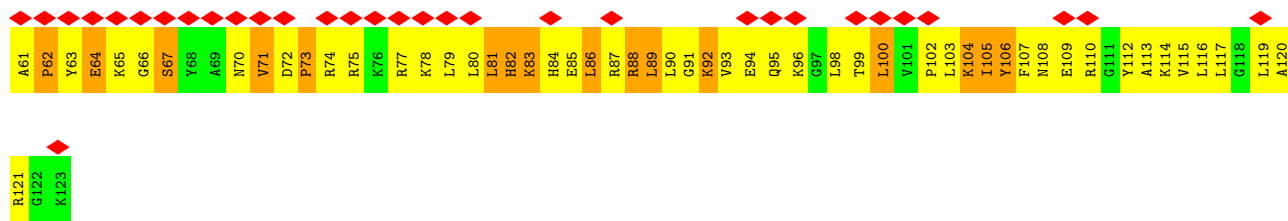


• Molecule 22: full length transfer messenger RNA (tmRNA)

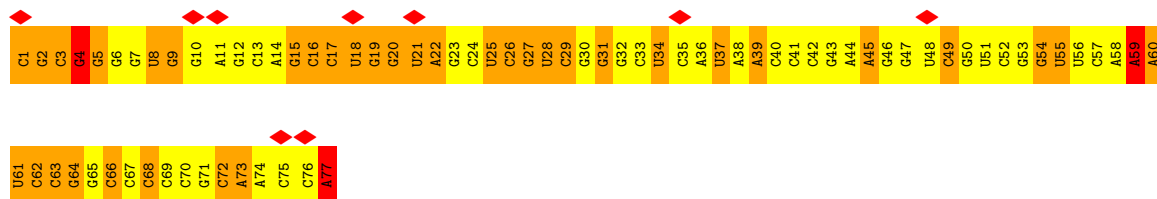


• Molecule 23: SsrA-binding protein

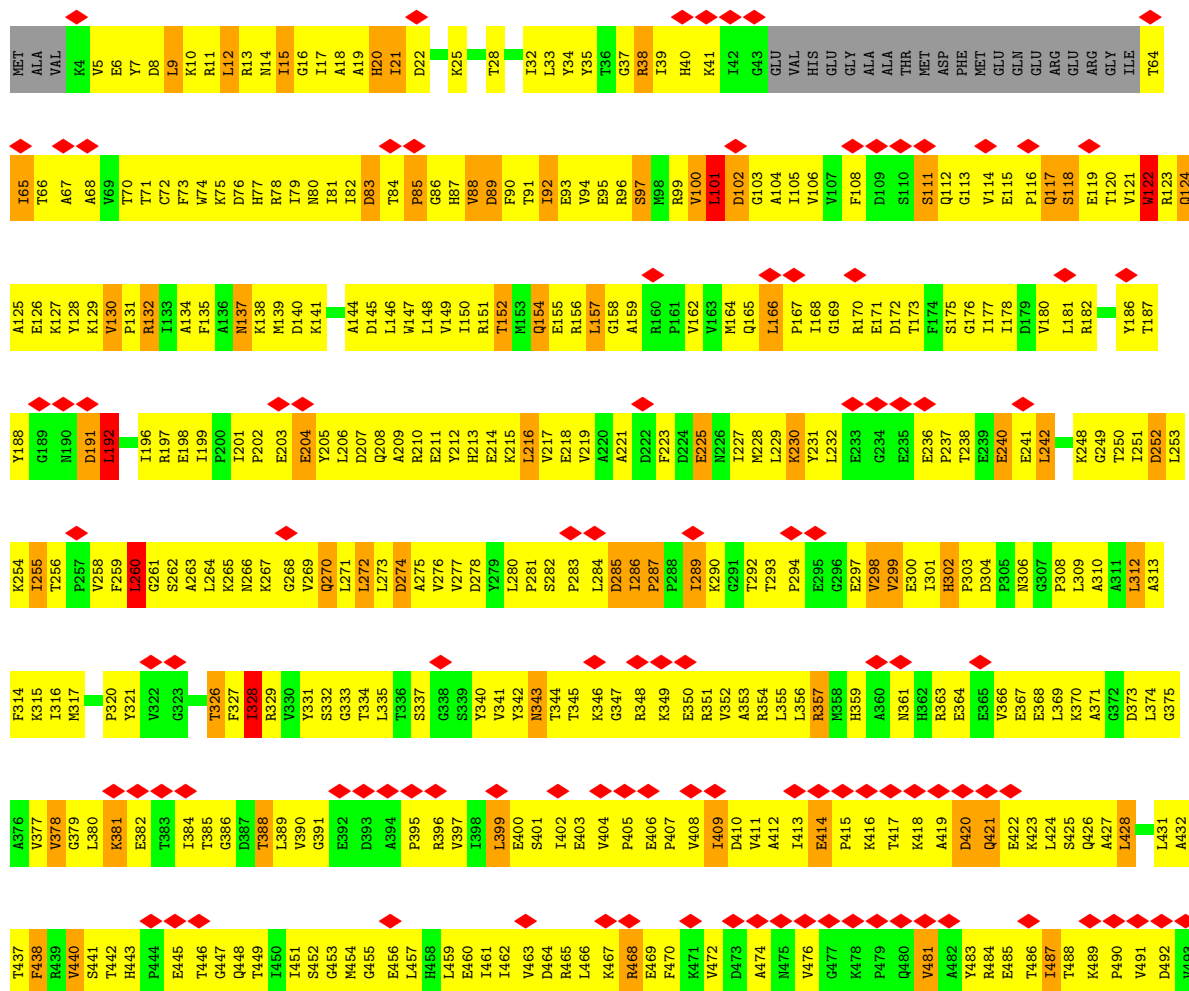


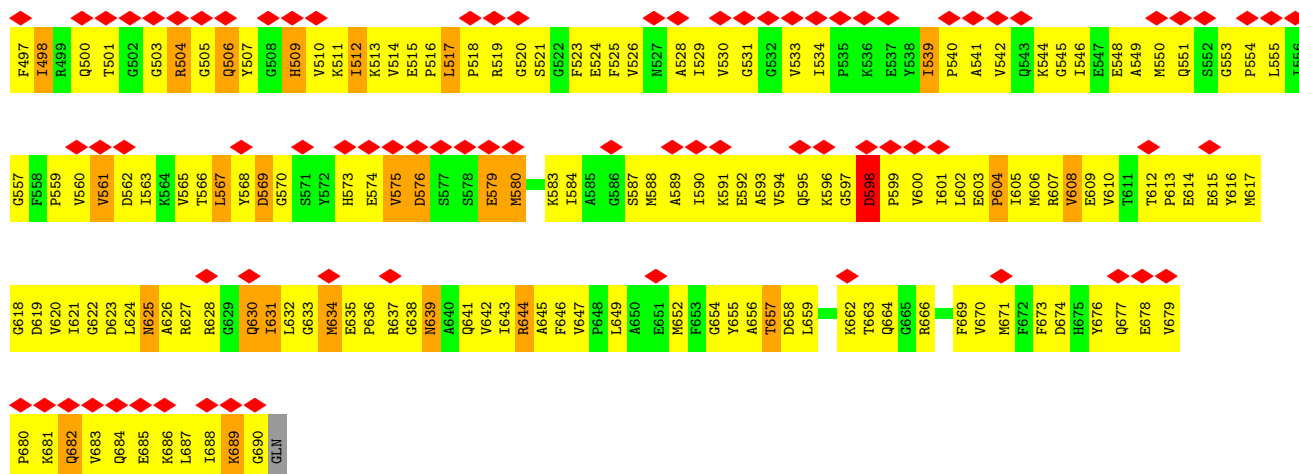


- Molecule 24: formyl-methionine specific initiator transfer RNA

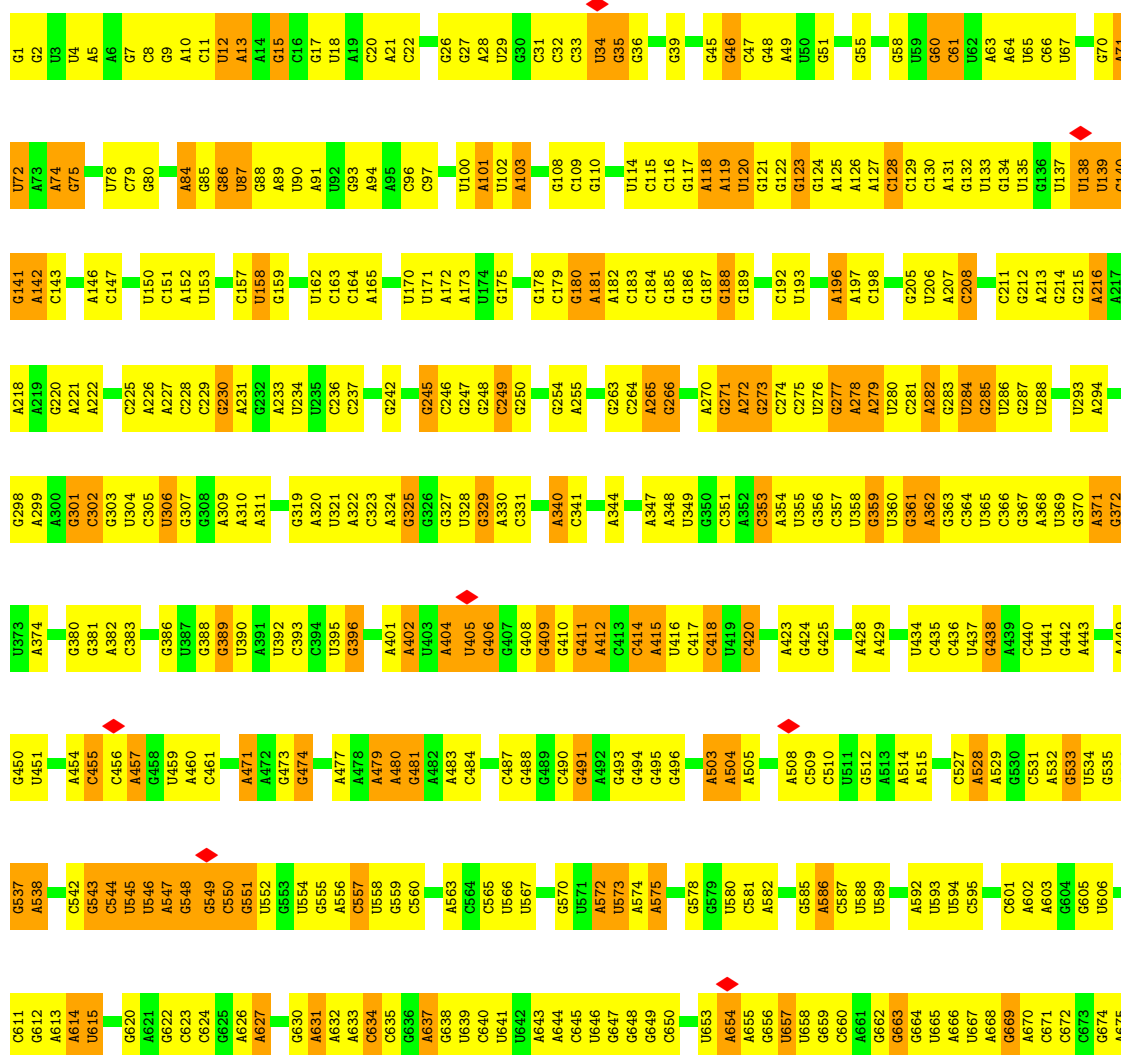


- Molecule 25: elongation factor G



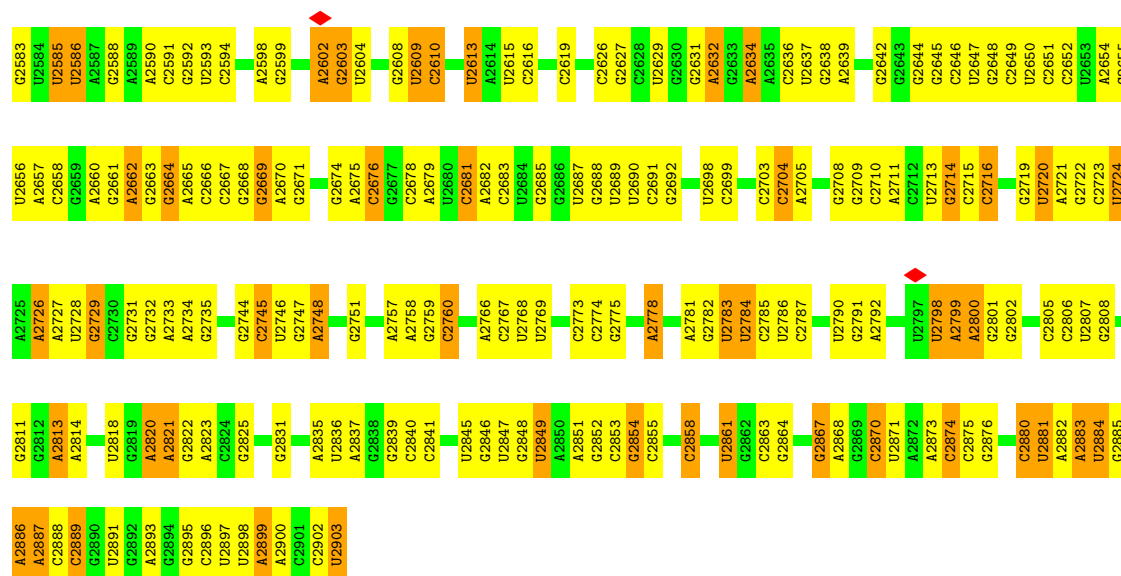


• Molecule 26: 23S ribosomal RNA

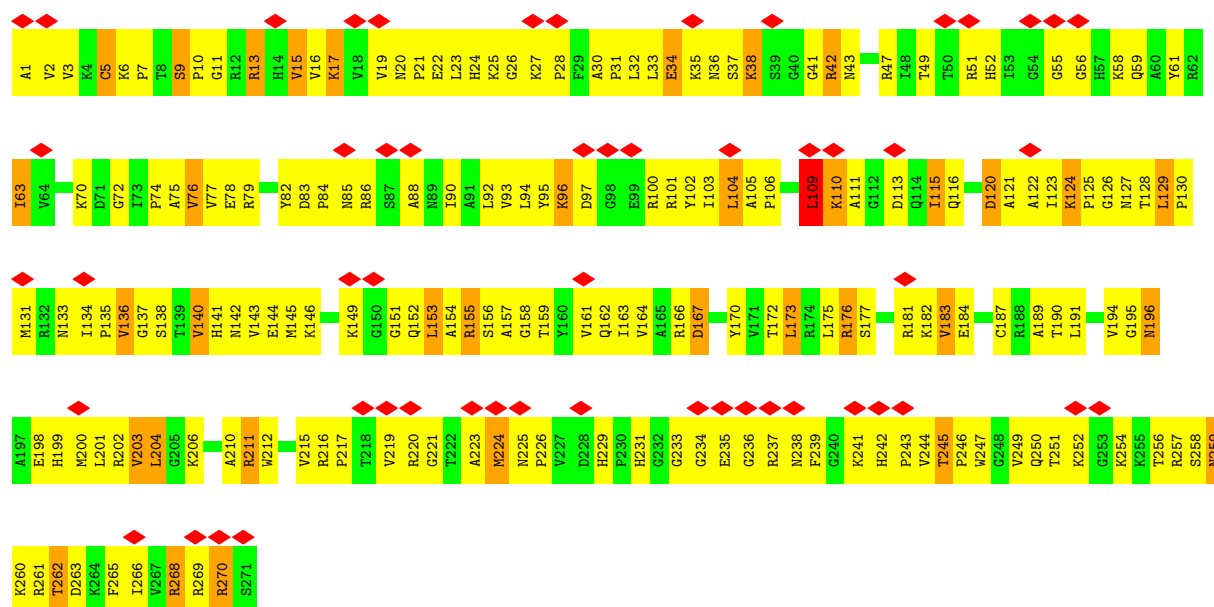




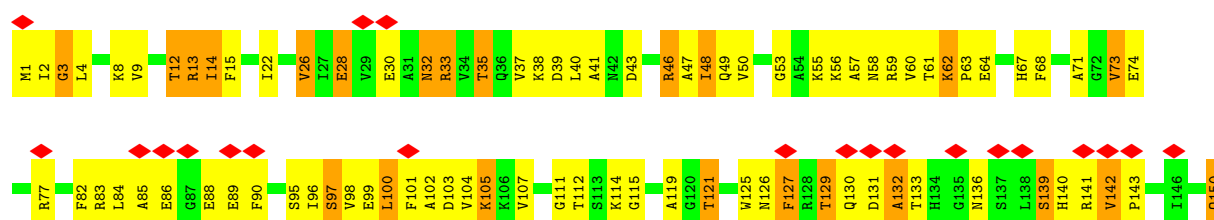
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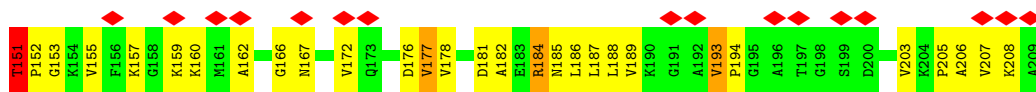


• Molecule 27: 50S ribosomal protein L2

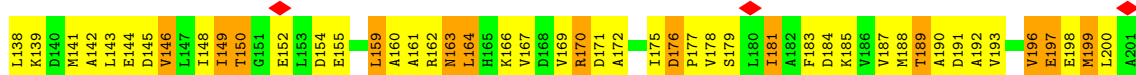
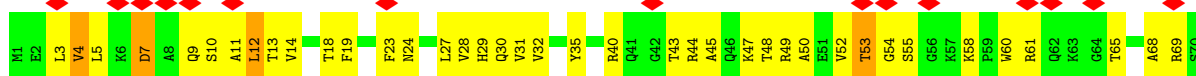


• Molecule 28: 50S ribosomal protein L3

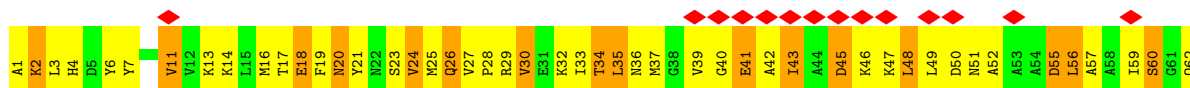




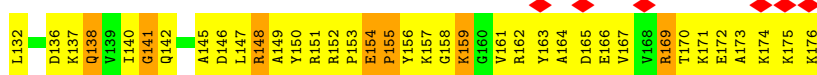
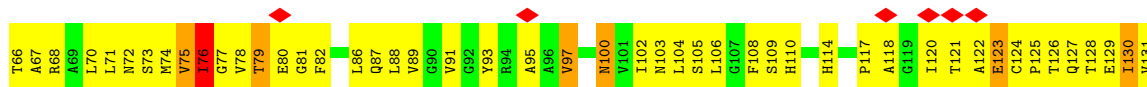
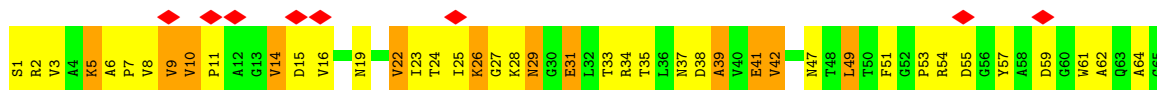
• Molecule 29: 50S ribosomal protein L4



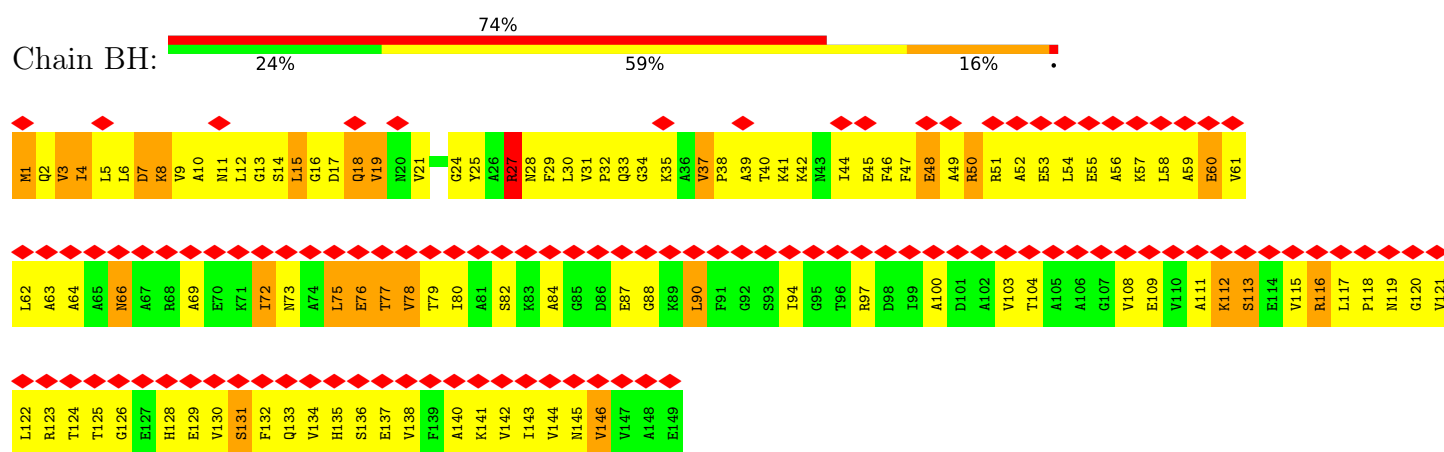
• Molecule 30: 50S ribosomal protein L5



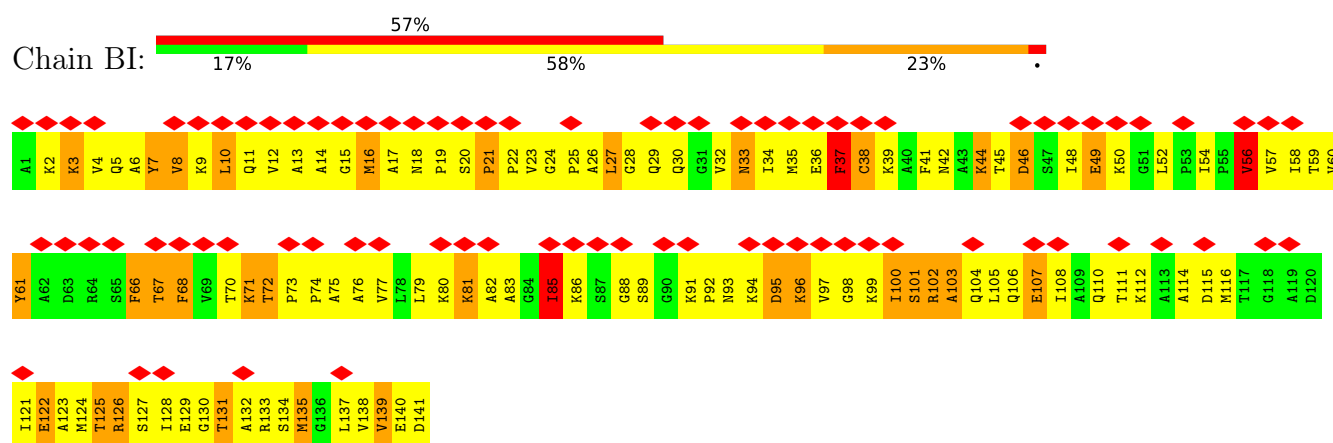
• Molecule 31: 50S ribosomal protein L6



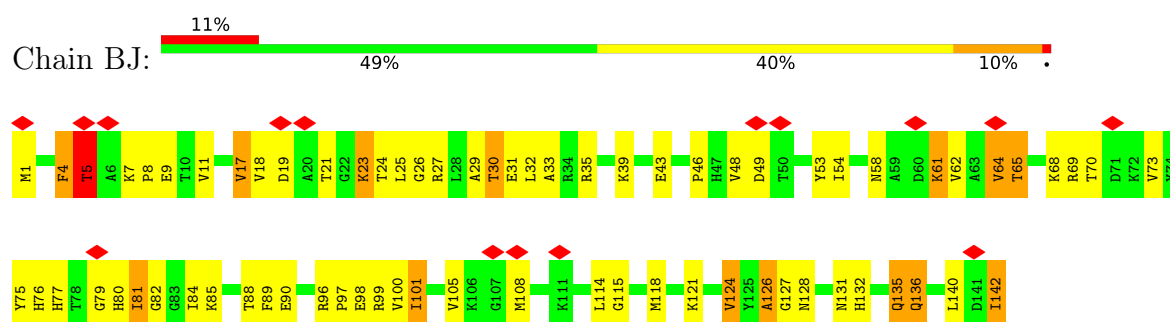
• Molecule 32: 50S ribosomal protein L9



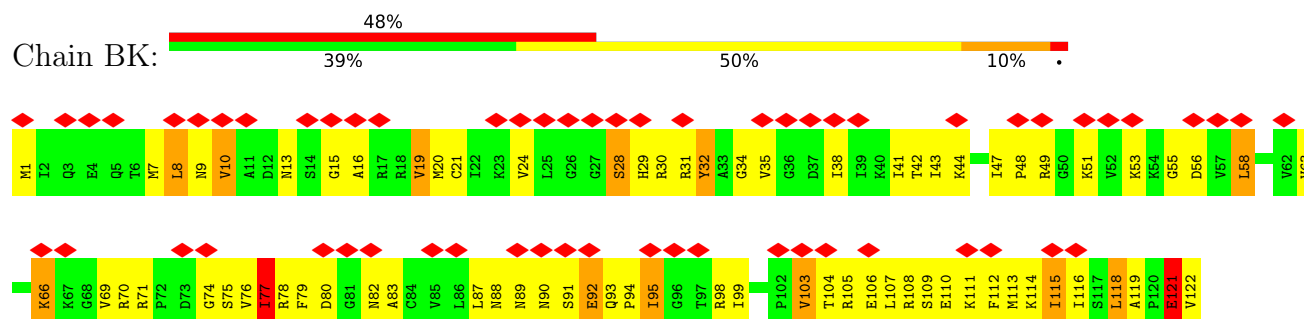
• Molecule 33: 50S ribosomal protein L11



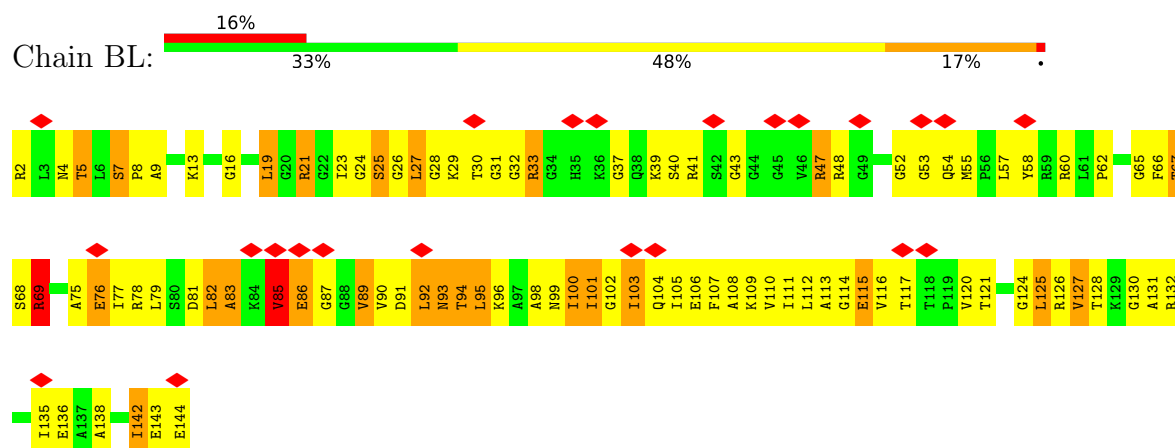
• Molecule 34: 50S ribosomal protein L13



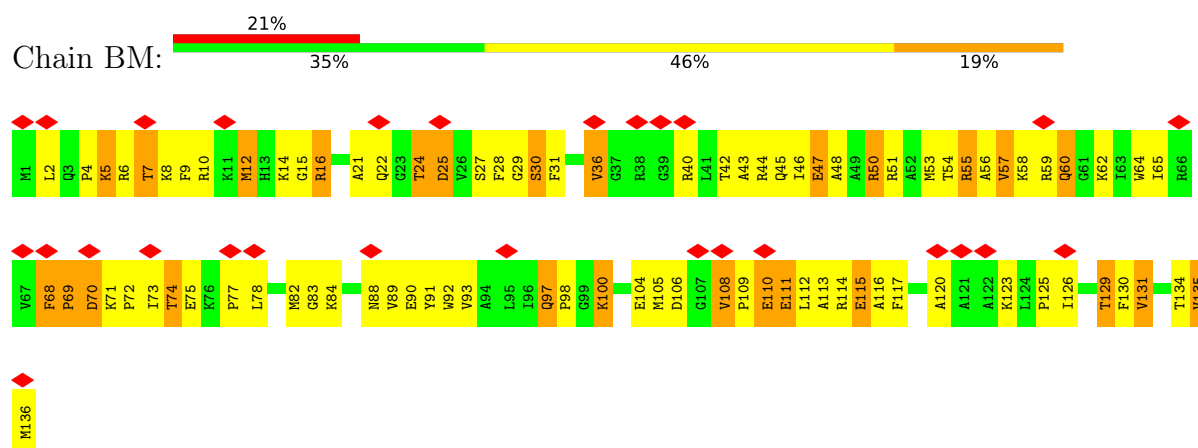
• Molecule 35: 50S ribosomal protein L14



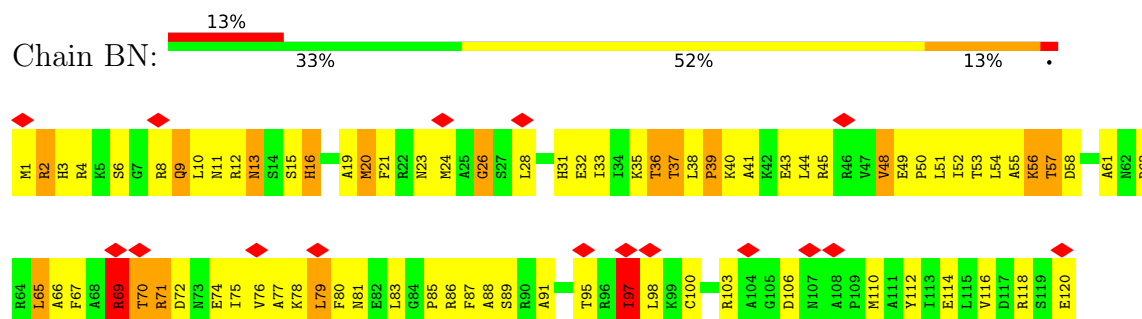
- Molecule 36: 50S ribosomal protein L15



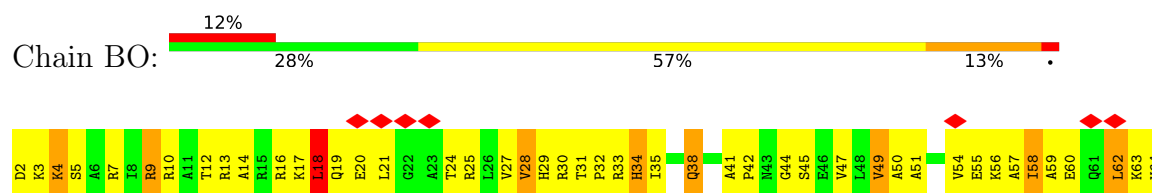
- Molecule 37: 50S ribosomal protein L16

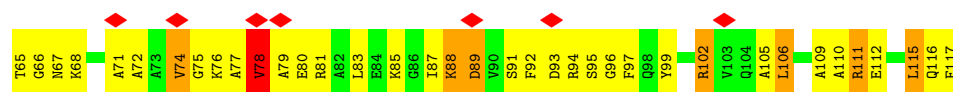


- Molecule 38: 50S ribosomal protein L17

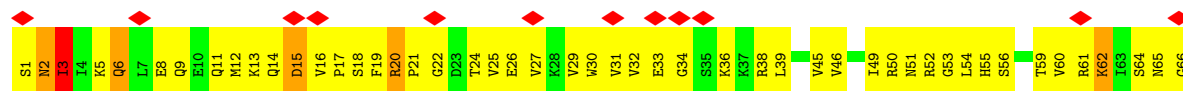


- Molecule 39: 50S ribosomal protein L18

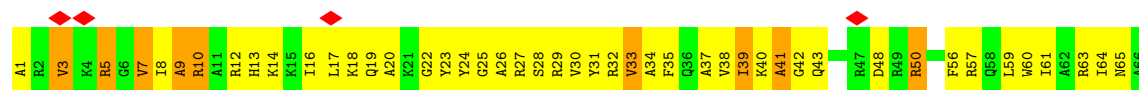




- Molecule 40: 50S ribosomal protein L19



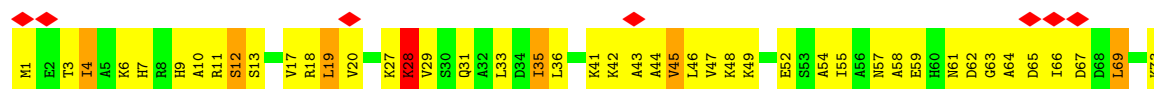
- Molecule 41: 50S ribosomal protein L20



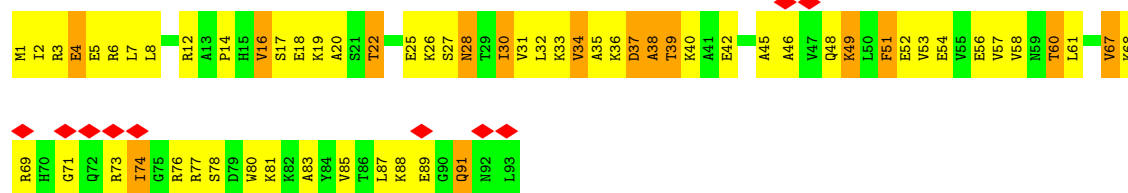
- Molecule 42: 50S ribosomal protein L21



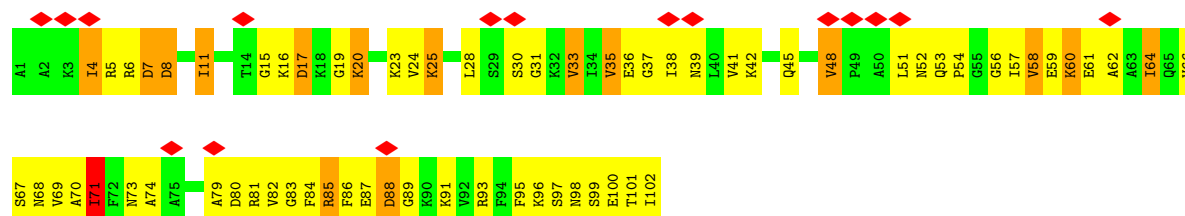
- Molecule 43: 50S ribosomal protein L22



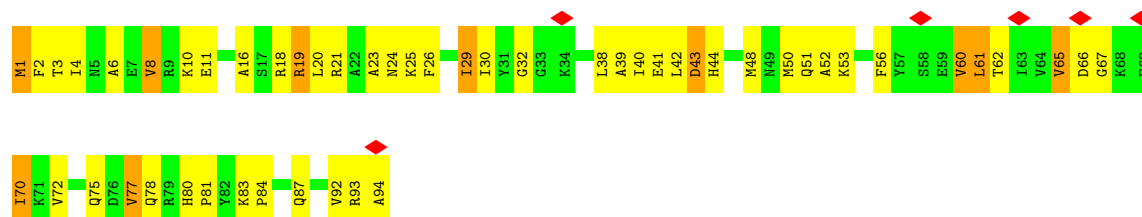
- Molecule 44: 50S ribosomal protein L23



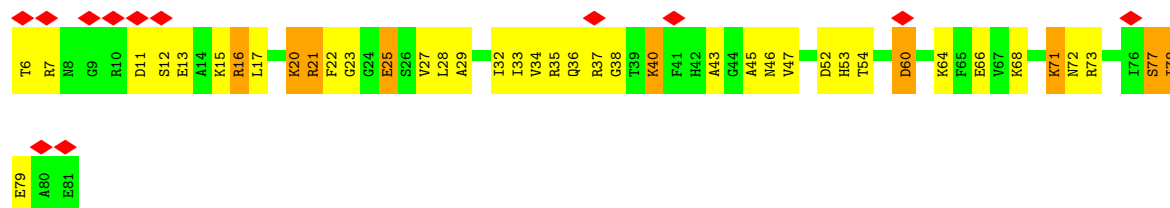
• Molecule 45: 50S ribosomal protein L24



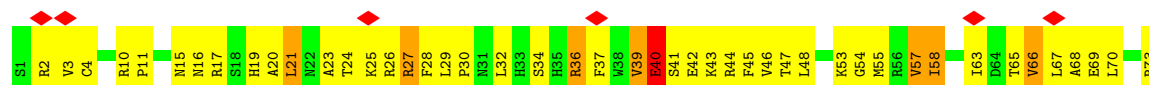
• Molecule 46: 50S ribosomal protein L25



• Molecule 47: 50S ribosomal protein L27



• Molecule 48: 50S ribosomal protein L28





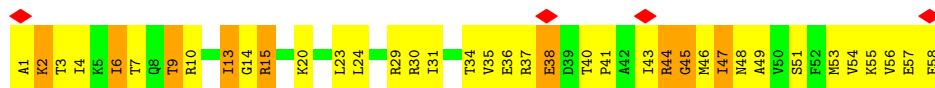
- Molecule 49: 50S ribosomal protein L29

Chain BY: 8% 25% 52% 17% 5%



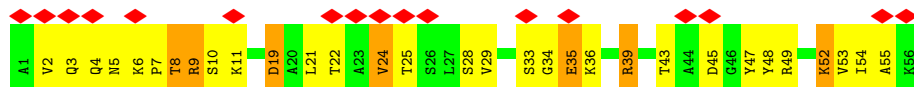
- Molecule 50: 50S ribosomal protein L30

Chain BZ: 7% 34% 50% 16%



- Molecule 51: 50S ribosomal protein L32

Chain B0: 30% 45% 43% 12%



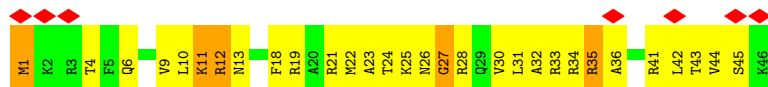
- Molecule 52: 50S ribosomal protein L33

Chain B1: 24% 28% 58% 14%



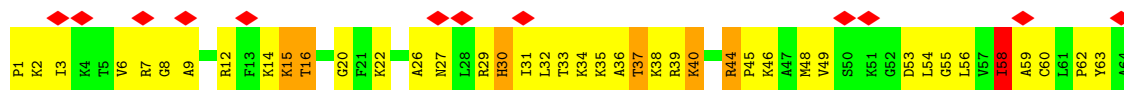
- Molecule 53: 50S ribosomal protein L34

Chain B2: 15% 35% 54% 11%

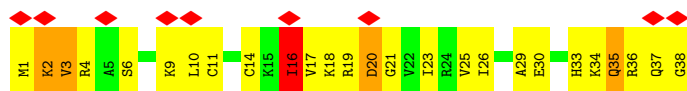


- Molecule 54: 50S ribosomal protein L35

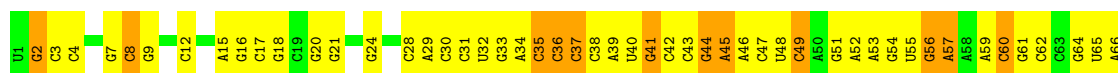
Chain B3: 19% 36% 53% 9%



- Molecule 55: 50S ribosomal protein L36



- Molecule 56: 5S ribosomal RNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	68843	Depositor
Resolution determination method	Not provided	
CTF correction method	The volumes were CTF-corrected in defocus groups, with an average of approximately 215 individual images per group	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	2500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	39000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	9.001	Depositor
Minimum map value	-3.389	Depositor
Average map value	0.205	Depositor
Map value standard deviation	0.751	Depositor
Recommended contour level	2	Depositor
Map size (Å)	378.0, 378.0, 378.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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: 5MU, PSU

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	0.49	0/36944	0.51	0/57632
2	AB	0.77	0/1736	1.13	10/2338 (0.4%)
3	AC	0.70	0/1652	1.01	4/2225 (0.2%)
4	AD	0.70	0/1665	1.07	11/2227 (0.5%)
5	AE	0.81	1/1119 (0.1%)	1.20	8/1504 (0.5%)
6	AF	0.81	0/836	1.15	5/1128 (0.4%)
7	AG	0.64	0/1196	1.04	7/1602 (0.4%)
8	AH	0.74	0/989	1.14	9/1326 (0.7%)
9	AI	0.63	1/1034 (0.1%)	1.01	5/1375 (0.4%)
10	AJ	0.76	0/797	1.05	4/1077 (0.4%)
11	AK	0.91	0/893	1.14	1/1205 (0.1%)
12	AL	0.77	0/969	1.09	5/1300 (0.4%)
13	AM	0.68	0/893	1.07	3/1193 (0.3%)
14	AN	0.67	0/785	1.11	6/1043 (0.6%)
15	AO	0.73	0/722	1.04	3/964 (0.3%)
16	AP	0.70	0/659	1.16	5/884 (0.6%)
17	AQ	0.65	0/658	1.04	3/881 (0.3%)
18	AR	0.75	0/463	1.03	3/621 (0.5%)
19	AS	0.60	0/653	1.16	10/877 (1.1%)
20	AT	0.69	0/671	0.97	3/888 (0.3%)
21	AU	1.04	0/431	1.27	6/570 (1.1%)
22	AV	0.48	15/7912 (0.2%)	0.79	19/12332 (0.2%)
23	AW	0.92	1/1011 (0.1%)	1.23	6/1354 (0.4%)
24	AX	0.55	1/1832 (0.1%)	0.81	2/2855 (0.1%)
25	AY	0.53	1/5313 (0.0%)	1.10	41/7195 (0.6%)
26	BA	0.88	6/69795 (0.0%)	0.61	4/108884 (0.0%)
27	BC	1.04	0/2122	1.20	6/2852 (0.2%)
28	BD	1.28	2/1586 (0.1%)	1.35	12/2134 (0.6%)
29	BE	1.18	0/1571	1.19	5/2113 (0.2%)
30	BF	0.81	0/1435	1.10	7/1926 (0.4%)
31	BG	0.94	0/1343	1.28	11/1816 (0.6%)
32	BH	0.87	0/1121	1.04	3/1515 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	BI	1.05	1/1046 (0.1%)	1.15	10/1410 (0.7%)
34	BJ	1.36	4/1152 (0.3%)	1.15	4/1551 (0.3%)
35	BK	1.17	1/948 (0.1%)	1.24	8/1268 (0.6%)
36	BL	1.27	2/1054 (0.2%)	1.38	11/1403 (0.8%)
37	BM	1.27	4/1093 (0.4%)	1.31	7/1460 (0.5%)
38	BN	1.25	0/974	1.24	9/1301 (0.7%)
39	BO	0.99	1/902 (0.1%)	1.19	6/1209 (0.5%)
40	BP	1.10	0/929	1.20	5/1242 (0.4%)
41	BQ	1.46	3/960 (0.3%)	1.29	5/1278 (0.4%)
42	BR	1.26	1/829 (0.1%)	1.39	7/1107 (0.6%)
43	BS	1.46	3/864 (0.3%)	1.29	6/1156 (0.5%)
44	BT	1.02	2/745 (0.3%)	1.20	7/994 (0.7%)
45	BU	1.19	3/788 (0.4%)	1.23	3/1051 (0.3%)
46	BV	1.02	0/766	1.17	4/1025 (0.4%)
47	BW	1.37	2/582 (0.3%)	1.21	0/769
48	BX	1.03	1/635 (0.2%)	1.13	4/848 (0.5%)
49	BY	0.98	0/510	1.39	8/677 (1.2%)
50	BZ	1.38	2/453 (0.4%)	1.35	5/605 (0.8%)
51	B0	1.23	1/450 (0.2%)	1.32	4/599 (0.7%)
52	B1	0.90	0/417	1.02	0/554
53	B2	1.39	0/380	1.38	5/498 (1.0%)
54	B3	1.21	1/513 (0.2%)	1.11	1/676 (0.1%)
55	B4	1.13	0/303	1.24	1/397 (0.3%)
56	BB	0.74	0/2847	0.60	0/4440
All	All	0.82	60/170946 (0.0%)	0.79	347/255354 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
4	AD	0	1
5	AE	0	1
9	AI	0	1
11	AK	0	1
13	AM	0	1
14	AN	0	1
21	AU	0	2
23	AW	0	1
24	AX	0	4
27	BC	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
28	BD	0	2
33	BI	0	1
42	BR	0	1
45	BU	0	1
50	BZ	0	1
All	All	0	20

The worst 5 of 60 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	AW	24	ILE	CA-CB	8.32	1.66	1.54
22	AV	110	U	C1'-N1	7.20	1.59	1.48
41	BQ	103	VAL	CA-CB	-7.17	1.45	1.54
22	AV	26	U	C1'-N1	7.13	1.59	1.48
26	BA	870	U	C1'-N1	7.12	1.59	1.48

The worst 5 of 347 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	BD	151	THR	CA-C-N	15.77	139.55	119.84
28	BD	151	THR	C-N-CA	15.77	139.55	119.84
42	BR	51	VAL	CA-C-N	-12.33	104.43	119.84
42	BR	51	VAL	C-N-CA	-12.33	104.43	119.84
49	BY	16	THR	N-CA-C	-12.14	98.05	111.28

There are no chirality outliers.

5 of 20 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	AD	47	LEU	Peptide
5	AE	100	GLU	Peptide
9	AI	5	TYR	Peptide
11	AK	125	LYS	Peptide
13	AM	111	PRO	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	32995	0	16600	2517	0
2	AB	1705	0	1731	437	0
3	AC	1625	0	1695	277	0
4	AD	1643	0	1710	310	0
5	AE	1106	0	1147	243	0
6	AF	818	0	808	118	0
7	AG	1182	0	1238	140	0
8	AH	979	0	1034	168	0
9	AI	1022	0	1070	226	0
10	AJ	787	0	828	187	0
11	AK	877	0	887	167	0
12	AL	955	0	1019	113	0
13	AM	884	0	944	168	0
14	AN	774	0	827	145	0
15	AO	714	0	736	70	0
16	AP	649	0	666	112	0
17	AQ	649	0	691	123	0
18	AR	456	0	478	49	0
19	AS	638	0	665	82	0
20	AT	665	0	714	94	0
21	AU	426	0	449	145	0
22	AV	7135	0	3594	2247	0
23	AW	993	0	1030	336	0
24	AX	1640	0	835	262	0
25	AY	5215	0	5279	983	0
26	BA	62319	0	31328	3015	0
27	BC	2083	0	2157	233	0
28	BD	1565	0	1616	123	0
29	BE	1552	0	1619	144	0
30	BF	1411	0	1443	248	0
31	BG	1323	0	1374	161	0
32	BH	1110	0	1148	160	0
33	BI	1032	0	1086	296	0
34	BJ	1129	0	1162	68	0
35	BK	939	0	1012	81	0
36	BL	1045	0	1117	134	0
37	BM	1074	0	1157	136	0
38	BN	961	0	1000	94	0
39	BO	892	0	923	94	0
40	BP	917	0	965	98	0
41	BQ	947	0	1022	69	0
42	BR	816	0	839	86	0
43	BS	857	0	922	48	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	BT	739	0	807	76	0
45	BU	780	0	834	66	0
46	BV	753	0	780	62	0
47	BW	575	0	589	31	0
48	BX	625	0	655	42	0
49	BY	509	0	543	89	0
50	BZ	449	0	491	31	0
51	B0	444	0	461	35	0
52	B1	410	0	440	37	0
53	B2	377	0	418	32	0
54	B3	504	0	574	44	0
55	B4	302	0	343	23	0
56	BB	2548	0	1292	104	0
All	All	157519	0	106792	14467	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 55.

The worst 5 of 14467 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:38:LYS:HE2	26:BA:1910:G:P	1.23	1.71
22:AV:172:U:H2'	22:AV:173:C:C6	1.25	1.65
25:AY:633:GLY:HA2	26:BA:1068:G:C8	1.19	1.62
22:AV:323:A:H2'	22:AV:324:G:C8	1.34	1.62
22:AV:48:C:C2'	22:AV:49:C:H5''	1.25	1.62

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

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	180/180 (100%)	110 (61%)	70 (39%)	0	1
3	AC	170/170 (100%)	122 (72%)	48 (28%)	0	3
4	AD	172/172 (100%)	130 (76%)	42 (24%)	1	4
5	AE	113/113 (100%)	75 (66%)	38 (34%)	0	2
6	AF	87/87 (100%)	57 (66%)	30 (34%)	0	1
7	AG	124/124 (100%)	85 (68%)	39 (32%)	0	2
8	AH	104/104 (100%)	79 (76%)	25 (24%)	1	4
9	AI	105/105 (100%)	80 (76%)	25 (24%)	1	4
10	AJ	86/86 (100%)	60 (70%)	26 (30%)	0	2
11	AK	90/90 (100%)	63 (70%)	27 (30%)	0	2
12	AL	103/103 (100%)	86 (84%)	17 (16%)	2	10
13	AM	92/92 (100%)	69 (75%)	23 (25%)	0	4
14	AN	79/83 (95%)	59 (75%)	20 (25%)	0	3
15	AO	76/76 (100%)	62 (82%)	14 (18%)	1	8
16	AP	65/65 (100%)	47 (72%)	18 (28%)	0	3
17	AQ	74/74 (100%)	54 (73%)	20 (27%)	0	3
18	AR	48/48 (100%)	37 (77%)	11 (23%)	1	6
19	AS	70/70 (100%)	54 (77%)	16 (23%)	1	6
20	AT	65/65 (100%)	35 (54%)	30 (46%)	0	0
21	AU	44/44 (100%)	26 (59%)	18 (41%)	0	0
23	AW	101/102 (99%)	75 (74%)	26 (26%)	0	3
25	AY	563/582 (97%)	480 (85%)	83 (15%)	3	13
27	BC	216/216 (100%)	173 (80%)	43 (20%)	1	7
28	BD	164/164 (100%)	135 (82%)	29 (18%)	2	9
29	BE	165/165 (100%)	138 (84%)	27 (16%)	2	10
30	BF	148/148 (100%)	111 (75%)	37 (25%)	0	4
31	BG	137/137 (100%)	110 (80%)	27 (20%)	1	7
32	BH	114/114 (100%)	87 (76%)	27 (24%)	1	4
33	BI	109/109 (100%)	74 (68%)	35 (32%)	0	2
34	BJ	116/116 (100%)	95 (82%)	21 (18%)	2	9

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	BK	103/103 (100%)	85 (82%)	18 (18%)	2	9
36	BL	102/102 (100%)	77 (76%)	25 (24%)	1	4
37	BM	109/109 (100%)	81 (74%)	28 (26%)	0	3
38	BN	100/100 (100%)	80 (80%)	20 (20%)	1	7
39	BO	86/86 (100%)	65 (76%)	21 (24%)	1	4
40	BP	99/99 (100%)	77 (78%)	22 (22%)	1	6
41	BQ	89/89 (100%)	76 (85%)	13 (15%)	3	13
42	BR	84/84 (100%)	68 (81%)	16 (19%)	1	8
43	BS	93/93 (100%)	79 (85%)	14 (15%)	3	12
44	BT	80/80 (100%)	67 (84%)	13 (16%)	2	10
45	BU	83/83 (100%)	64 (77%)	19 (23%)	1	6
46	BV	78/78 (100%)	63 (81%)	15 (19%)	1	8
47	BW	56/58 (97%)	45 (80%)	11 (20%)	1	7
48	BX	67/67 (100%)	55 (82%)	12 (18%)	2	9
49	BY	55/55 (100%)	44 (80%)	11 (20%)	1	7
50	BZ	48/48 (100%)	36 (75%)	12 (25%)	0	4
51	B0	47/47 (100%)	42 (89%)	5 (11%)	6	21
52	B1	45/45 (100%)	35 (78%)	10 (22%)	1	6
53	B2	38/38 (100%)	32 (84%)	6 (16%)	2	11
54	B3	51/51 (100%)	42 (82%)	9 (18%)	2	9
55	B4	34/34 (100%)	27 (79%)	7 (21%)	1	6
All	All	5327/5353 (100%)	4108 (77%)	1219 (23%)	2	6

5 of 1219 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	BK	88	ASN
47	BW	78	ILE
36	BL	142	ILE
35	BK	82	ASN
40	BP	108	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 134 such sidechains are listed below:

Mol	Chain	Res	Type
42	BR	43	ASN
43	BS	57	ASN
52	B1	45	HIS
20	AT	47	GLN
20	AT	20	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1537/1539 (99%)	458 (29%)	27 (1%)
22	AV	332/363 (91%)	187 (56%)	32 (9%)
24	AX	76/77 (98%)	37 (48%)	3 (3%)
26	BA	2901/2903 (99%)	777 (26%)	58 (1%)
56	BB	118/119 (99%)	24 (20%)	1 (0%)
All	All	4964/5001 (99%)	1483 (29%)	121 (2%)

5 of 1483 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	5	U
1	AA	6	G
1	AA	7	A
1	AA	9	G
1	AA	12	U

5 of 121 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
22	AV	332	G
26	BA	2211	A
26	BA	479	A
26	BA	2157	G
26	BA	2848	G

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

3 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
22	5MU	AV	341	22	19,22,23	1.02	1 (5%)	27,32,35	2.40	8 (29%)
22	PSU	AV	347	22	18,21,22	1.59	2 (11%)	21,30,33	1.54	3 (14%)
22	PSU	AV	342	22	18,21,22	0.81	0	21,30,33	1.61	4 (19%)

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
22	5MU	AV	341	22	-	0/7/25/26	0/2/2/2
22	PSU	AV	347	22	-	1/7/25/26	0/2/2/2
22	PSU	AV	342	22	-	1/7/25/26	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	AV	347	PSU	C2-N1	5.09	1.43	1.36
22	AV	347	PSU	C6-C5	2.97	1.38	1.35
22	AV	341	5MU	C6-N1	2.68	1.42	1.38

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	AV	341	5MU	C5-C4-N3	5.96	120.50	115.32
22	AV	341	5MU	C4-N3-C2	-5.70	119.86	127.34
22	AV	341	5MU	O4-C4-C5	-4.97	119.23	124.92
22	AV	342	PSU	C6-C5-C4	4.32	121.09	118.17
22	AV	341	5MU	N3-C2-N1	4.05	120.17	114.89

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
22	AV	347	PSU	C4'-C5'-O5'-P
22	AV	342	PSU	O4'-C1'-C5-C4

There are no ring outliers.

3 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
22	AV	341	5MU	5	0
22	AV	347	PSU	7	0
22	AV	342	PSU	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

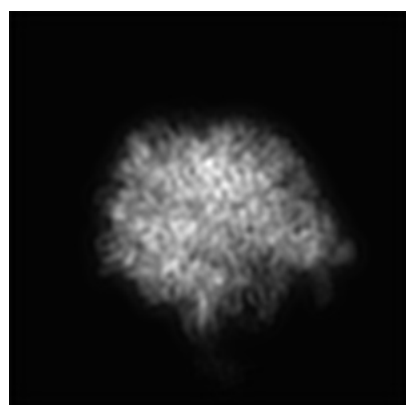
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5386. These allow visual inspection of the internal detail of the map and identification of artifacts.

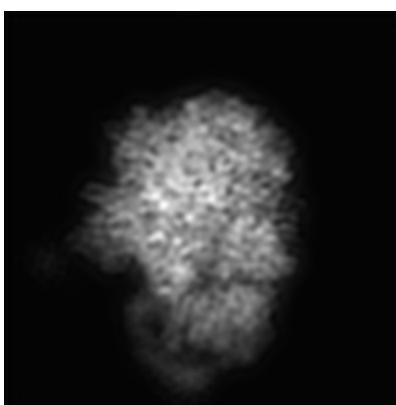
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

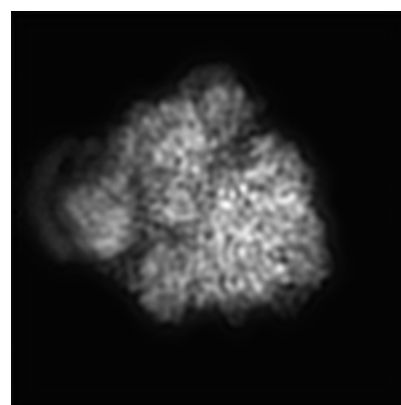
6.1.1 Primary map



X



Y

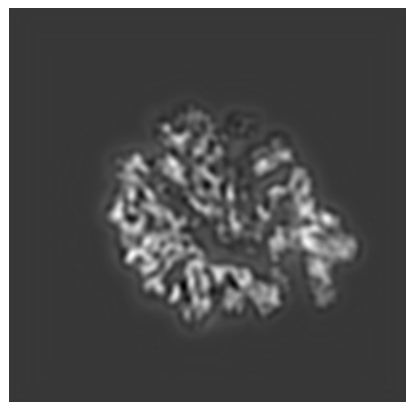


Z

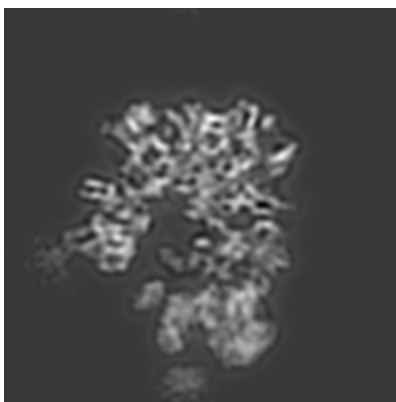
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

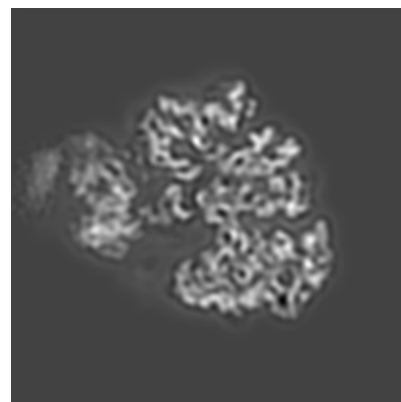
6.2.1 Primary map



X Index: 150



Y Index: 150

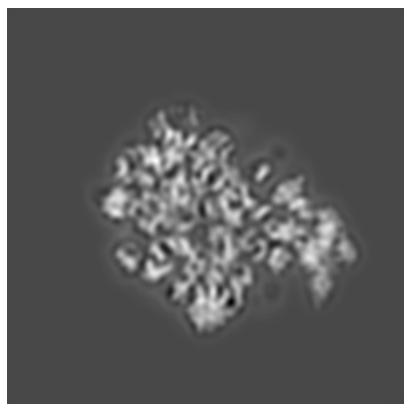


Z Index: 150

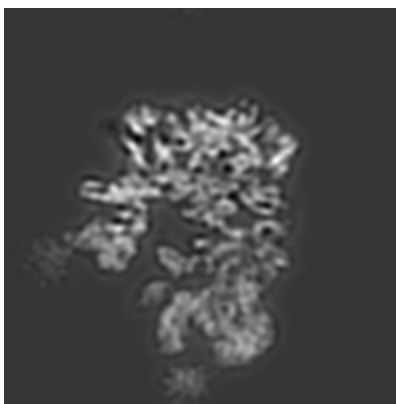
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

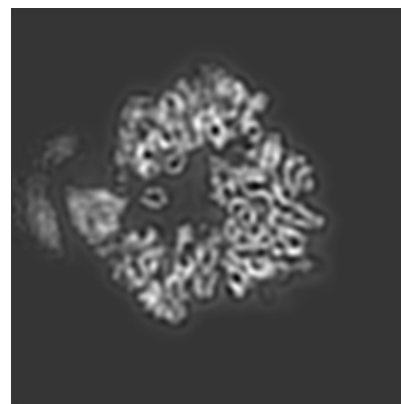
6.3.1 Primary map



X Index: 158



Y Index: 153



Z Index: 130

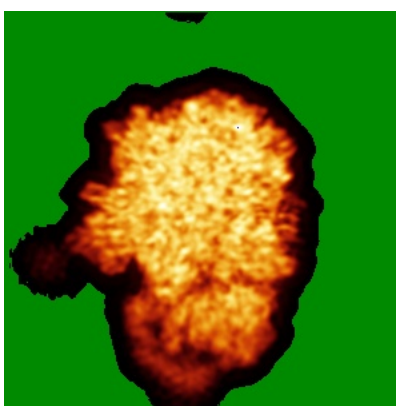
The images above show the largest variance slices of the map in three orthogonal directions.

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

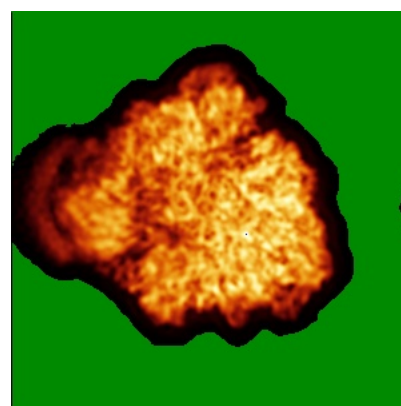
6.4.1 Primary map



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

This section was not generated.

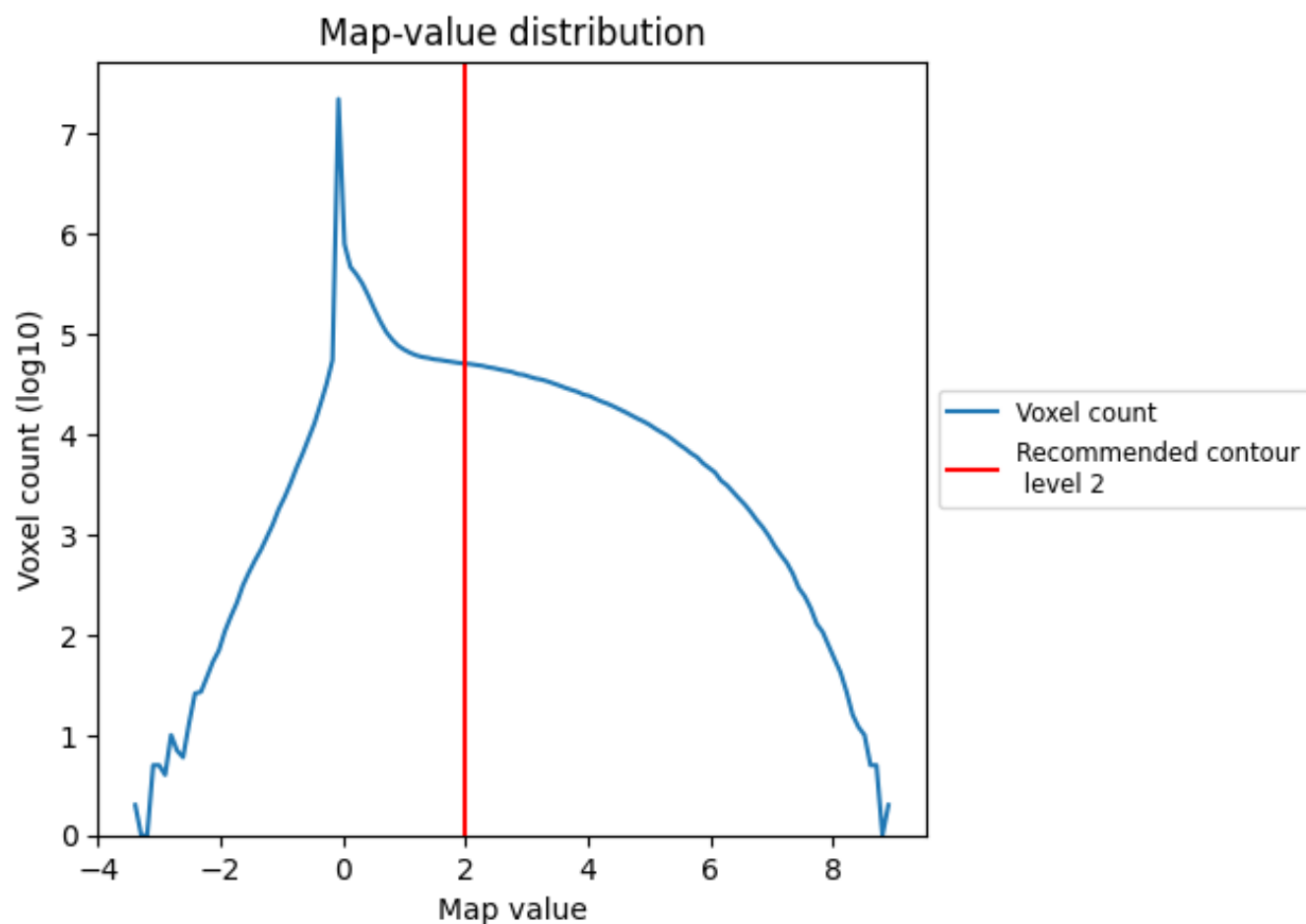
6.6 Mask visualisation

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

7 Map analysis [i](#)

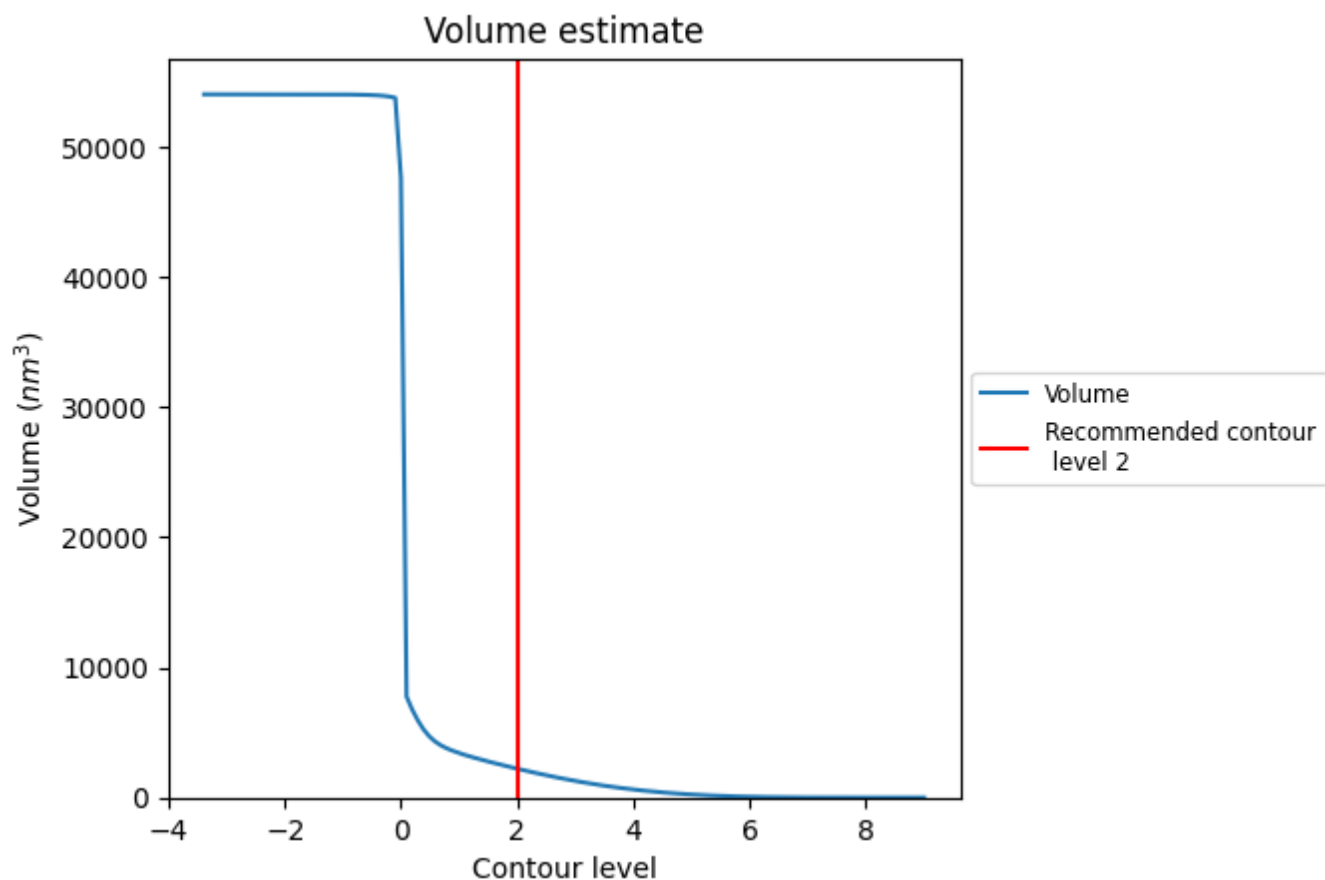
This section contains the results of statistical analysis of the map.

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.

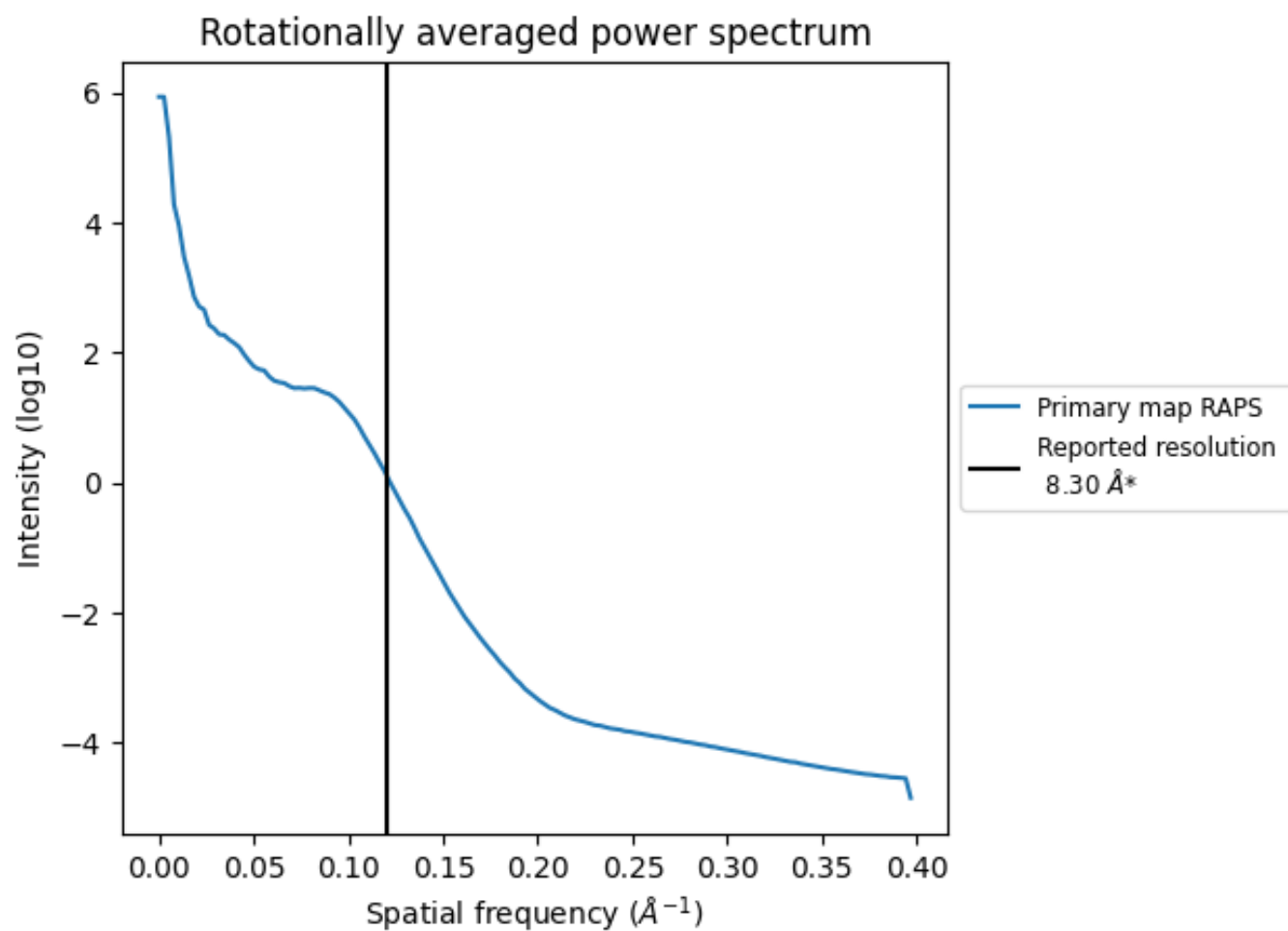
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2217 nm³; this corresponds to an approximate mass of 2002 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 0.120 Å⁻¹

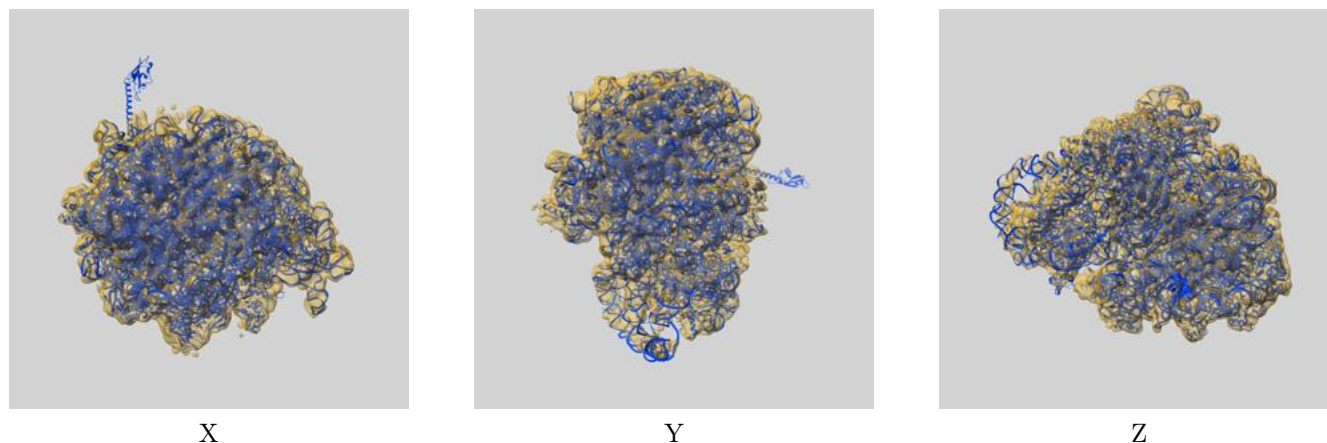
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

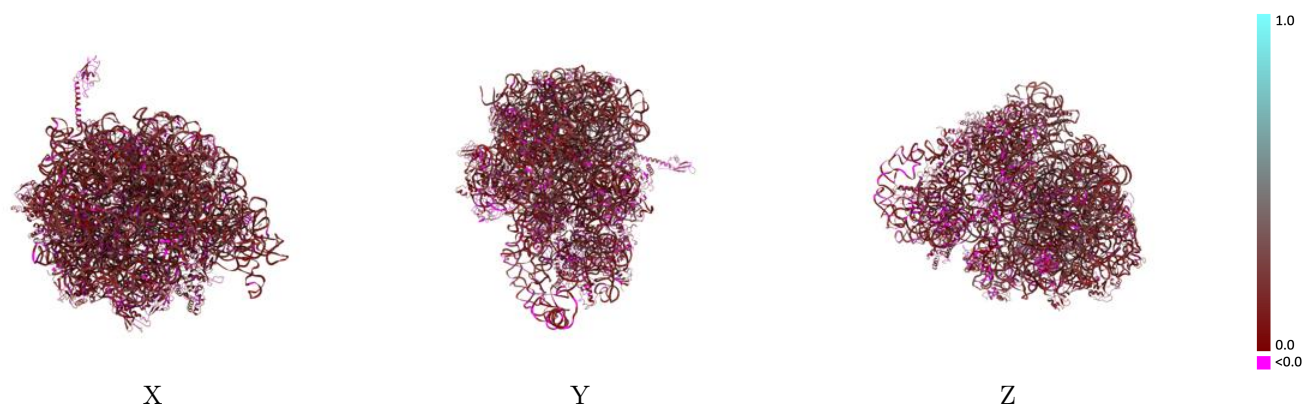
This section contains information regarding the fit between EMDB map EMD-5386 and PDB model 4V6T. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 2.0 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](#)

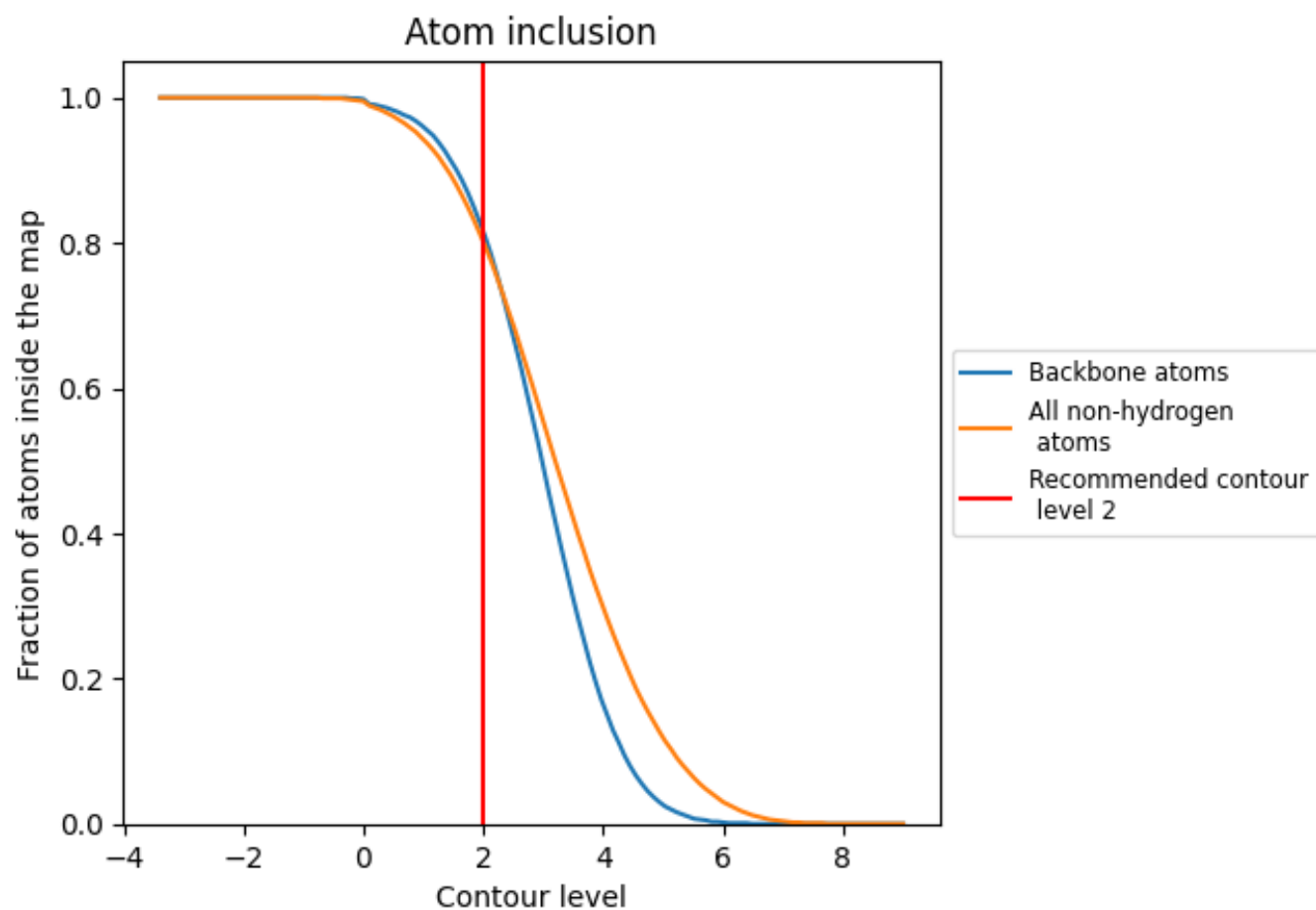


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 80% 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 (2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8010	 0.1360
AA	 0.8940	 0.1490
AB	 0.6720	 0.1300
AC	 0.6810	 0.1110
AD	 0.7120	 0.1150
AE	 0.6780	 0.1240
AF	 0.6190	 0.1010
AG	 0.5340	 0.0810
AH	 0.6880	 0.1120
AI	 0.7390	 0.0930
AJ	 0.7220	 0.0580
AK	 0.5870	 0.0750
AL	 0.4210	 0.0930
AM	 0.3630	 0.0840
AN	 0.7600	 0.0880
AO	 0.7100	 0.1200
AP	 0.7430	 0.1090
AQ	 0.7130	 0.1020
AR	 0.7070	 0.0780
AS	 0.6640	 0.0700
AT	 0.7630	 0.1540
AU	 0.5680	 0.1290
AV	 0.5070	 0.0940
AW	 0.3210	 0.0650
AX	 0.6980	 0.1370
AY	 0.5990	 0.1110
B0	 0.6520	 0.0730
B1	 0.6870	 0.0940
B2	 0.6820	 0.0990
B3	 0.6560	 0.1000
B4	 0.6810	 0.0760
BA	 0.9100	 0.1620
BB	 0.9320	 0.1580
BC	 0.6440	 0.1040
BD	 0.6680	 0.1030



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Chain	Atom inclusion	Q-score
BE	 0.7100	 0.1270
BF	 0.6380	 0.0640
BG	 0.7290	 0.1210
BH	 0.2270	 0.0470
BI	 0.3760	 0.0160
BJ	 0.7320	 0.1140
BK	 0.4610	 0.1000
BL	 0.6900	 0.1020
BM	 0.6150	 0.1210
BN	 0.7130	 0.0930
BO	 0.7800	 0.1080
BP	 0.6310	 0.1080
BQ	 0.7650	 0.1160
BR	 0.7330	 0.1150
BS	 0.7020	 0.1150
BT	 0.7170	 0.1190
BU	 0.7810	 0.1130
BV	 0.7890	 0.1230
BW	 0.7170	 0.0720
BX	 0.7060	 0.1180
BY	 0.7730	 0.1420
BZ	 0.7550	 0.1300